

**STUDIES ON INDOOR FUNGI**

by

James Alexander Scott

A thesis submitted in conformity with the requirements  
for the degree of Doctor of Philosophy in Mycology,  
Graduate Department of Botany in the University of Toronto

Copyright by James Alexander Scott, 2001

When I heard the learn'd astronomer,  
When the proofs, the figures, were ranged in columns before  
me,  
When I was shown the charts and diagrams, to add, divide, and  
measure them,  
When I sitting heard the astronomer where he lectured with  
much applause in the lecture-room,  
How soon unaccountable I became tired and sick,  
Till rising and gliding out I wander'd off by myself,  
In the mystical moist night-air, and from time to time,  
Look'd up in perfect silence at the stars.

Walt Whitman, "Leaves of Grass", 1855

# STUDIES ON INDOOR FUNGI

James Alexander Scott

Department of Botany, University of Toronto

2001

## ABSTRACT

Fungi are among the most common microbiota in the interiors of buildings, including homes. Indoor fungal contaminants, such as dry-rot, have been known since antiquity and are important agents of structural decay, particularly in Europe. The principal agents of indoor fungal contamination in North America today, however, are anamorphic (asexual) fungi mostly belonging to the phyla Ascomycota and Zygomycota, commonly known as “moulds”.

Broadloom dust taken from 369 houses in Wallaceburg, Ontario during winter, 1994, was serial dilution plated, yielding approximately 250 fungal taxa, over 90% of which were moulds. The ten most common taxa were: *Alternaria alternata*, *Aureobasidium pullulans*, *Eurotium herbariorum*, *Aspergillus versicolor*, *Penicillium chrysogenum*, *Cladosporium cladosporioides*, *P. spinulosum*, *Cl. sphaerospermum*, *As. niger* and *Trichoderma viride*. Chi-square association analysis of this mycoflora revealed several ecological groups including phylloplane-, soil-, and xerophilic food-spoilage fungi.

Genotypic variation was investigated in two common dust-borne species, *Penicillium brevicompactum* and *P. chrysogenum*. Nine multilocus haplotypes comprising 75 isolates of *P. brevicompactum* from 50 houses were detected by heteroduplex mobility assay (HMA) of

polymorphic regions in beta-tubulin (*benA*), nuclear ribosomal RNA spanning the internal transcribed spacer regions (ITS1-2) and histone 4 (*his4*) genes. Sequence analysis of the *benA* and rDNA loci showed two genetically divergent groups. Authentic strains of *P. brevicompactum* and *P. stoloniferum* clustered together in the predominant clade, accounting for 86% of isolates. The second lineage contained 14% of isolates, and included collections from the rotting fruit bodies of macrofungi.

Similarly, 5 multilocus haplotypes based on acetyl coenzyme-A synthase (*acuA*), *benA*, ITS1-2 and thioredoxin reductase (*trxB*) genes comprised 198 isolates of *P. chrysogenum* obtained from 109 houses. A strictly clonal pattern of inheritance was observed, indicating the absence of recombination. Phylogenetic analyses of allele sequences segregated the population into three divergent lineages, encompassing 90%, 7% and 3% of the house dust isolates, respectively. Type isolates of *P. chrysogenum* and its synonym *P. notatum* clustered within the secondary lineage, confirming this synonymy. No isolates of nomenclatural status clustered within the predominant lineage; however, this clade contained Alexander Fleming's historically noteworthy penicillin-producing strain from 1929. Similarly, there was no available name for the minor lineage.

## ACKNOWLEDGEMENTS

I am profoundly grateful to my advisors, Dave Malloch and Neil Straus, for their thoughtful mentorship, both intentional and unintentional, on all matters of science and life. They have given me gifts of their patience and wisdom that I cannot repay. I thank the members of my supervisory committee, Jim Anderson, David Miller and Richard Summerbell, for their gentle encouragement and sincere enthusiasm which helped me to stay on-track. Linda Kohn and Keith Seifert are thanked for their excellent and thoughtful feedback on the thesis in conjunction with the senate oral examination.

I could not have completed this thesis nor the research it presents without the friendship, dedication and benevolence of Brenda Koster, Bess Wong and Wendy Untereiner.

I have laughed, cried and grown immeasurably from my friendships and discussions, often over beer, pizza or #49, with my fellow graduate students Jacquie Bede, Cameron Currie, Laurie Ketch and Simona Margaritescu, along with many others. I am grateful for the assistance of Len Hutchison, Brett Couch, Wendy Malloch, Colleen McGee, Emily Taylor and Megan Weibe during the early stages of this work. More recently, Michael Warnock helped with proofreading and correcting this thesis. Barry Neville and Shanelle Lum kindly kept me informed of many news items on indoor fungi that otherwise I would certainly have missed. Carolyn Babcock and Steve Peterson graciously provided cultures. I thank John Pogacar for insightful conversations on building science and for help in final thesis preparation. Financial support was provided by NSERC as operating grants and a strategic grant to DM and NS, and a doctoral scholarship to JS. Jim Gloer generously funded my early mycological training.

Wieland Meyer has been a superlative collaborator on the aspects of this project involving DNA fingerprinting of *Penicillium chrysogenum*. Steve Peterson, John Pitt and Rob Samson are thanked for many insightful discussions on *Penicillium* taxonomy.

I owe the greatest debt of gratitude to my parents, Kay and Alex Scott, for nurturing my eclectic interests from a very young age, for their compassion and understanding of the many turns my life has taken, and for the unconditional freedom, support and love that they have given me as I have pursued my dreams. For all this and much more, I dedicate this thesis to them.

On a muggy, summer day when I was a very young boy, my cousin, Jim Guillet inspired me to study biology. As we stood together in my grandmother's garden, Jim explained that the stems of the rhubarb plant could be eaten but that the leaves could not, because they were poisonous. How could it be so? And why? I stared in utter disbelief and hotly challenged this absurd idea, while my parents, grimacing, looked on. I stopped just short of biting into a leaf myself to see its effect. In the very many intervening years since, I have reflected on our exchange countless times. Jim, perhaps unintentionally, taught me four very valuable lessons that day: 1) Nature is fascinating and intricate, her properties and processes are rarely apparent or intuitive; 2) Never be afraid to question any notion proffered as fact, no matter how high the authority; 3) Science embodies a set of methods that can provide insight into the delicate inner workings of Nature when applied thoughtfully and skillfully; and above all, 4) Don't eat rhubarb leaves.

# TABLE OF CONTENTS

	PAGE
ABSTRACT .....	II
ACKNOWLEDGEMENTS .....	IV
TABLE OF CONTENTS.....	VI
LIST OF TABLES .....	X
LIST OF FIGURES .....	XI
LIST OF APPENDICES.....	XIII
LIST OF ABBREVIATED TERMS.....	XIV
LIST OF NOMENCLATURAL ABBREVIATIONS .....	XVI
<b>CHAPTER 1. INTRODUCTION .....</b>	<b>1</b>
The biology of house dust.....	1
Interactions between mites and fungi.....	3
Fungi in household dust.....	3
Indoor sources of dust mycoflora .....	5
<i>Penicillium</i> in indoor environments.....	6
Health effects of exposure to indoor fungi .....	9
Allergic rhinitis and sinusitis.....	10
Type I allergic syndromes.....	10
Dust mites and allergy.....	11
Hypersensitivity syndromes.....	12
Asthma.....	12
Mycotoxins.....	15
Volatile fungal metabolites .....	17
Objectives of the current study .....	17
<b>CHAPTER 2. ANALYSIS OF HOUSE DUST MYCOFLORA .....</b>	<b>19</b>
Abstract.....	19
Introduction .....	19
Materials and methods .....	20
Collection of dust samples.....	20
Analysis of dust samples .....	23
Identification and isolation of cultures .....	25
Reliability of identifications .....	26

Storage of cultures .....	26
Organization and analysis of data .....	27
Results .....	29
Species diversity and distribution .....	29
Efficiency of sampling.....	29
Species abundance .....	35
Association analysis .....	35
Discussion.....	45
Conclusions .....	50
<b>CHAPTER 3.    A REVIEW OF TECHNIQUES FOR THE ASSESSMENT</b>	
<b>OF GENOTYPIC DIVERSITY.....</b>	<b>52</b>
Introduction .....	52
The detection of genetic variation.....	53
The use of proteins to distinguish variation.....	53
Hybridization-based markers .....	54
Low-stringency PCR.....	55
Randomly amplified polymorphic DNA (RAPD).....	55
Amplified fragment length polymorphism (AFLP).....	57
High-stringency PCR -- site-specific polymorphisms.....	59
Detection of low-level sequence variability.....	60
Restriction endonuclease digestion of PCR products.....	61
Denaturing-gradient gel electrophoresis (DGGE) .....	62
Single-strand conformation polymorphism (SSCP) .....	62
Heteroduplex mobility assay (HMA) .....	64
Summary .....	69
<b>CHAPTER 4.    DEVELOPMENT OF METHODS FOR THE ASSESSMENT</b>	
<b>OF GENOTYPIC DIVERSITY OF PENICILLIA .....</b>	<b>70</b>
Abstract.....	70
Isolate selection .....	70
Isolation of DNA from <i>Penicillium</i> conidia.....	71
Materials and methods, DNA isolation.....	71
Results and discussion, DNA isolation .....	73
Heteroduplex mobility assay .....	74
Materials and methods, HMA .....	74
DNA amplification .....	74
Cloning and sequencing of PCR products .....	75
Preparation and analysis of DNA heteroduplexes .....	76
Electrophoresis and imaging .....	77
Resolution of heteroduplexed DNAs on Phast system.....	77
Results and discussion, HGE.....	81
Vertical gel electrophoresis (VGE) in HMA .....	84
HMA Screening approaches .....	85
Overlapped pairs .....	85
Universal heteroduplex generator.....	86
Results and discussion, VGE.....	86



Identification of polymorphic genetic loci .....	90
Phylogenetic analysis of <i>Penicillium sensu stricto</i> .....	91
<i>Penicillium chrysogenum</i> .....	99
<i>Penicillium brevicompactum</i> .....	99
<b>CHAPTER 5. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES</b>	
<b>OF <i>PENICILLIUM BREVICOMPACTUM</i> .....</b>	<b>101</b>
Abstract .....	101
Introduction .....	102
Materials and methods .....	103
Collection and characterization of isolates .....	103
Sequence analysis .....	105
Results .....	109
Heteroduplex mobility assay .....	110
DNA sequence analysis .....	110
Discussion .....	118
<i>Penicillium stoloniferum</i> .....	122
<i>Penicillium paxilli</i> .....	122
Affiliations of <i>P. brevicompactum</i> .....	123
Conclusions .....	124
<b>CHAPTER 6. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES</b>	
<b>OF <i>PENICILLIUM CHRYSOGENUM</i> .....</b>	<b>125</b>
Abstract .....	125
Introduction .....	126
Materials and methods .....	128
Isolation and identification of strains .....	128
DNA preparation and heteroduplex analysis .....	132
PCR fingerprinting .....	132
Random primer-pair fingerprinting .....	135
Cluster analysis .....	136
DNA sequencing .....	137
Sequence analysis .....	137
Spatial analysis .....	138
Dendrogram construction .....	138
Results .....	138
Heteroduplex analysis .....	138
Individual data sets .....	143
Combined sequence data .....	148
Spatial analysis .....	155
PCR fingerprinting .....	155
Random primer fingerprinting .....	163
Discussion .....	169
Morphological and physiological variation .....	171
History of <i>P. chrysogenum</i> .....	173
Nomenclatural stability of <i>P. chrysogenum</i> .....	174
Synonyms of <i>P. chrysogenum</i> .....	177

<i>Penicillium chrysogenum</i> and the indoor environment.....	178
Conclusions .....	179
<b>CHAPTER 7. CONCLUSIONS AND GENERAL SUMMARY.....</b>	<b>180</b>
Fungal decay in early structures .....	181
Ventilation.....	182
Early housing and urbanization .....	183
Modern era.....	184
The changing urban landscape.....	186
Suburban life.....	187
North American dependence on petroleum .....	187
The energy crisis and the sick building .....	188
Heating and ventilation .....	189
Gypsum-based wallboard products.....	194
The dawn of “Sick Building Syndrome” .....	195
Ecology of dust-borne fungi .....	195
Association analysis of dust-borne fungi.....	196
<i>Penicillium brevicompactum</i> .....	198
<i>Penicillium chrysogenum</i> .....	200
Summary .....	202
 <b>LITERATURE CITED .....</b>	 <b>205</b>
 <b>APPENDIX A</b>	 Summary of dust mycoflora by house.....229
<b>APPENDIX B</b>	Chi square statistics for association analysis of dustborne taxa.....290
<b>APPENDIX C</b>	Calculations of sampling efficiency.....340
<b>APPENDIX D</b>	Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S-ITS2 and partial 28S region from 85 <i>Penicillium</i> species .....344
<b>APPENDIX E</b>	Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S-ITS2 region from 46 taxa from Subgenus <i>Penicillium</i> .....393
<b>APPENDIX F</b>	Alignments of <i>P. brevicompactum</i> sequences
<b>F-1</b>	Beta-tubulin (benA), partial sequence.....406
<b>F-2</b>	Nuclear ribosomal RNA, ITS1-5.8S-ITS2.....409
<b>APPENDIX G</b>	Alignments of <i>P. chrysogenum</i> sequences
<b>G-1</b>	Acetyl coenzyme A synthase (acuA), partial sequence.....413
<b>G-2</b>	Beta-tubulin (benA), partial sequence.....418
<b>G-3</b>	Nuclear ribosomal RNA, ITS1-5.8S-ITS2.....426
<b>G-4</b>	Thioredoxin reductase (trxB), partial sequence.....436

## LIST OF TABLES

<b>TABLE 1-1.</b>	Selected hypersensitivity pneumonitides of microbial etiology.....	14
<b>TABLE 1-2.</b>	Mycotoxins of significance produced by indoor fungi.....	16
<b>TABLE 2-1.</b>	Summary of significantly-associated couplets of taxa.....	44
<b>TABLE 2-2.</b>	Distribution of samples in houses manifesting visible mould growth.....	46
<b>TABLE 4-1.</b>	Loci screened for polymorphisms in <i>P. brevicompactum</i> .....	92
<b>TABLE 4-2.</b>	Loci screened for polymorphisms in <i>P. chrysogenum</i> .....	93
<b>TABLE 4-3.</b>	Sources of nuclear ribosomal ITS1-5.8S-ITS2 and partial 28S sequences.....	94
<b>TABLE 5-1.</b>	List of isolates of <i>P. brevicompactum</i> and related species from other sources.....	106
<b>TABLE 5-2.</b>	Primer sequences used to amplify polymorphic regions in <i>P. brevicompactum</i> .....	108
<b>TABLE 5-3.</b>	Summary of isolate haplotypes of <i>P. brevicompactum</i> isolates.....	111
<b>TABLE 5-4.</b>	Haplotype frequencies of <i>P. brevicompactum</i> isolates.....	112
<b>TABLE 6-1.</b>	Sources of house dust isolates.....	130
<b>TABLE 6-2.</b>	List of culture collection strains of <i>P. chrysogenum</i> and related species.....	131
<b>TABLE 6-3.</b>	Primer sequences used to amplify polymorphic regions in <i>P. chrysogenum</i> .....	134
<b>TABLE 6-4.</b>	Summary of haplotypes of <i>P. chrysogenum</i> isolates.....	139
<b>TABLE 6-5.</b>	Haplotype frequencies of <i>P. chrysogenum</i> isolates.....	142
<b>TABLE 6-6.</b>	Summary of MPITs produced for each of the 4 gene sequences examined.....	152
<b>TABLE 6-7.</b>	Comparison of Clade A (from FIG. 6-10) and combined fingerprint data.....	173

## LIST OF FIGURES

<b>FIGURE 2-1.</b>	Map of Ontario, Canada, indicating the location of Wallaceburg .....	21
<b>FIGURE 2-2.</b>	Locations of houses sampled .....	22
<b>FIGURE 2-3.</b>	Plating regimen for dust samples.....	24
<b>FIGURE 2-4.</b>	Frequency of dustborne fungi.....	30
<b>FIGURE 2-5.</b>	Sampling efficiency for house dust mycoflora as estimated using Good's Hypothesis.....	36
<b>FIGURE 2-6.</b>	Trellis diagram summarizing significant associations of dustborne taxa .....	37
<b>FIGURE 2-7.</b>	Cluster analysis based on significance of association between dustborne fungi .....	39
<b>FIGURE 2-8.</b>	Inter-relationships between taxa in significant clusters (> 2 taxa) .....	40
<b>FIGURE 4-1.</b>	Demonstration of DNA heteroduplexes using the Phast gel system .....	78
<b>FIGURE 4-2</b>	Cross-section of band front on horizontal PAG cast and run without top-plate .....	80
<b>FIGURE 4-3.</b>	Comparison of media in horizontal gel electrophoresis for the resolution of DNA heteroduplexes.....	82
<b>FIGURE 4-4.</b>	Vertical PAG using Overlapping Pairs screening method for HMA.....	87
<b>FIGURE 4-5.</b>	Vertical PAG using Universal Heteroduplex Generator screening method for HMA.....	88
<b>FIGURE 4-6.</b>	Distance tree of <i>Penicillium</i> spp. inferred from ITS1-5.8S-ITS2 and partial 28S rDNA data.....	96
<b>FIGURE 4-7.</b>	Unrooted distance tree of <i>Penicillium</i> spp. inferred from ITS1-5.8S-ITS2 and partial 28S rDNA data .....	97
<b>FIGURE 4-8.</b>	Distance tree of <i>Penicillium</i> subgen. <i>Penicillium</i> inferred from ITS1-5.8S-ITS2 rDNA data .....	100
<b>FIGURE 5-1.</b>	Street map of Wallaceburg, Ontario, indicating collection sites for <i>P. brevicompactum</i> isolates used in this study.....	104
<b>FIGURE 5-2.</b>	Locations of primers used to amplify polymorphic regions in <i>P. brevicompactum</i> .....	107
<b>FIGURE 5-3.</b>	Results of Partition Homogeneity Test for combined benA/ ITS sequence data for <i>P. brevicompactum</i> .....	113
<b>FIGURE 5-4A.</b>	Distance tree of <i>P. brevicompactum</i> isolates based on combined benA data .....	114
<b>FIGURE 5-4B.</b>	Distance tree of <i>P. brevicompactum</i> isolates based on combined ITS data .....	114
<b>FIGURE 5-4C.</b>	Distance tree of <i>P. brevicompactum</i> isolates based on combined benA-ITS data .....	115
<b>FIGURE 5-5.</b>	Strict consensus tree of 20 MPTs for <i>P. brevicompactum</i> isolates based on combined benA-ITS data.....	117
<b>FIGURE 5-6.</b>	Cluster analysis based on Euclidean distance between collection sites, indicating <i>P. brevicompactum</i> haplotype .....	119
<b>FIGURE 6-1.</b>	Street map of Wallaceburg, Ontario, indicating collection sites for <i>P. chrysogenum</i> isolates used in this study .....	129
<b>FIGURE 6-2.</b>	Locations of primers used to amplify polymorphic regions in <i>P. chrysogenum</i> .....	133

## LIST OF FIGURES (cont'd)

<b>FIGURE 6-3.</b>	Neighbor-Joining tree of <i>P. chrysogenum</i> isolates based on partial <i>acuA</i> gene .....	144
<b>FIGURE 6-4.</b>	Neighbor-Joining tree of <i>P. chrysogenum</i> isolates based on partial <i>benA</i> gene .....	145
<b>FIGURE 6-5.</b>	Neighbor-Joining tree of <i>P. chrysogenum</i> isolates based on sequence data from the ITS1-5.8S-ITS2 region of nuclear rDNA.....	146
<b>FIGURE 6-6.</b>	Neighbor-Joining tree of <i>P. chrysogenum</i> isolates based on partial <i>trxB</i> gene .....	147
<b>FIGURE 6-7.</b>	Strict consensus of two MPITs produced from partial <i>trxB</i> sequence .....	149
<b>FIGURE 6-8.</b>	Results of PHT for <i>acuA</i> , <i>benA</i> , ITS and <i>trxB</i> sequence data.....	150
<b>FIGURE 6-9.</b>	Results of PHT for <i>acuA</i> , <i>benA</i> and <i>trxB</i> sequence data for dust isolates only.....	153
<b>FIGURE 6-10.</b>	MPIT produced from combined <i>acuA</i> , <i>benA</i> and <i>trxB</i> sequences, including representative dust isolates and authentic strains .....	154
<b>FIGURE 6-11.</b>	Cluster analysis based on Euclidean distance between collection sites, indicating <i>P. chrysogenum</i> haplotype .....	156
<b>FIGURE 6-12.</b>	DNA fingerprinting gel based on single-primer PCR using the M13 core sequence.....	157
<b>FIGURE 6-13.</b>	Cluster analysis of band similarity based on single-primer PCR using M13 core sequence.....	159
<b>FIGURE 6-14.</b>	DNA fingerprinting gel based on single-primer PCR using (GACA) <sub>4</sub> .....	160
<b>FIGURE 6-15.</b>	Cluster analysis of band similarity based on single-primer PCR using (GACA) <sub>4</sub> .....	162
<b>FIGURE 6-16.</b>	DNA fingerprinting gel based on RAPD primed by 5SOR/MYC1 .....	164
<b>FIGURE 6-17.</b>	Cluster analysis of similarity based on RAPD primed by 5SOR/MYC1 .....	166
<b>FIGURE 6-18.</b>	Cluster analysis of combined fingerprint data .....	167
<b>FIGURE 6-19.</b>	Comparison of combined fingerprint data and combined gene tree .....	168
<b>FIGURE 6-20.</b>	Comparison of combined fingerprint data and distance tree based on collection site location.....	170
<b>FIGURE 7-1.</b>	Crude oil cost from 1883 to present .....	190
<b>FIGURE 7-2.</b>	Crude oil consumption from 1955 to present .....	191
<b>FIGURE 7-3.</b>	Minimum ventilation rates from 1836 to present .....	192

## LIST OF APPENDICES

<b>APPENDIX A</b>	Summary of dust mycoflora by house.....	229
<b>APPENDIX B</b>	Chi square statistics for association analysis of dustborne taxa.....	290
<b>APPENDIX C</b>	Calculations of sampling efficiency.....	340
<b>APPENDIX D</b>	Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S-ITS2 and partial 28S region from 85 <i>Penicillium</i> species .....	344
<b>APPENDIX E</b>	Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S- ITS2 region from 46 taxa from <i>Penicillium</i> subgen. <i>Penicillium</i> .....	393
<b>APPENDIX F</b>	Alignments of <i>P. brevicompactum</i> sequences	
<b>F-1</b>	Beta-tubulin (benA), partial sequence.....	406
<b>F-2</b>	Nuclear ribosomal RNA, ITS1-5.8S-ITS2.....	409
<b>APPENDIX G</b>	Alignments of <i>P. chrysogenum</i> sequences	
<b>G-1</b>	Acetyl coenzyme A synthase (acuA), partial sequence.....	413
<b>G-2</b>	Beta-tubulin (benA), partial sequence.....	418
<b>G-3</b>	Nuclear ribosomal RNA, ITS1-5.8S-ITS2.....	426
<b>G-4</b>	Thioredoxin reductase (trxB), partial sequence.....	436

## LIST OF ABBREVIATED TERMS

<b>acuA</b>	Acetyl Co-Enzyme A Synthase gene
<b>AFLP</b>	Amplified Fragment Length Polymorphism
<b>AIHA</b>	American Industrial Hygiene Association
<b>ASHRAE</b>	American Society for Heating, Refrigeration and Air-Conditioning Engineers
<b>ASHVE</b>	American Society for Heating and Ventilation Engineers
<b>benA</b>	Beta-tubulin gene
<b>bp</b>	Base pairs
<b>CFM</b>	Cubic feet (of air) per minute (per person)
<b>CFU</b>	Colony Forming Unit
<b>CI</b>	Consistency Index
<b>CMHC</b>	Canada Mortgage and Housing Corporation
<b>CSA</b>	Creatine sucrose agar ( <i>see</i> Frisvad, 1985)
<b>CYA</b>	Czapek's yeast autolysate agar ( <i>see</i> Malloch, 1981)
<b>DG18</b>	Dichloran 18 % Glycerol agar ( <i>see</i> Hocking and Pitt, 1980)
<b>DGGE</b>	Denaturing Gradient Gel Electrophoresis
<b>DNA</b>	Deoxyribonucleic acid
<b>ds</b>	Double stranded
<b>GM</b>	General Motors Corporation
<b>his4</b>	Histone 4 gene
<b>HDX</b>	Heteroduplexed DNA structure
<b>HGE</b>	Horizontal gel electrophoresis
<b>HMA</b>	Heteroduplex mobility assay
<b>HP</b>	Hypersensitivity pneumonitis
<b>HVAC</b>	Heating, Ventilating and Air-Conditioning
<b>IAQ</b>	Indoor Air Quality
<b>ICPAT</b>	International Commission on <i>Penicillium</i> and <i>Aspergillus</i> Taxonomy
<b>ILD</b>	Incongruence Length Difference test
<b>ISIAQ</b>	International Society for Indoor Air Quality and Climate
<b>ITS</b>	Internal transcribed spacer region, nuclear rDNA
<b>kbp</b>	Kilo-base pairs
<b>MLA</b>	Modified Leonian's agar ( <i>see</i> Malloch, 1981)
<b>NAT</b>	N-acrylyltrishydroxymethylaminomethane
<b>NCU-2</b>	Names in Current Use in the Trichocomaceae ( <i>see</i> Pitt and Samson, 1993)
<b>OPEC</b>	Organization of Petroleum Exporting Countries
<b>OTU</b>	Operational Taxonomic Unit
<b>PAW-I</b>	First International <i>Penicillium</i> and <i>Aspergillus</i> Workshop
<b>PAW-II</b>	Second International <i>Penicillium</i> and <i>Aspergillus</i> Workshop
<b>PAW-III</b>	Third International <i>Penicillium</i> and <i>Aspergillus</i> Workshop
<b>PAG</b>	Polyacrylamide gel
<b>PCR</b>	Polymerase Chain Reaction
<b>PHT</b>	Partition Homogeneity Test
<b>RAPD</b>	Random-Amplified Polymorphic DNA
<b>rDNA</b>	DNA subrepeat encoding nuclear ribosomal RNA
<b>RFLP</b>	Restriction Fragment Length Polymorphism
<b>RI</b>	Retention Index

## LIST OF ABBREVIATED TERMS (cont'd)

<b>rRNA</b>	Ribosomal ribonucleic acid
<b>ss</b>	Single stranded
<b>SSCP</b>	Single Strand Conformation Polymorphism
<b>TAE</b>	Tris-acetate-EDTA ( <i>see</i> Sambrook et al., 1989)
<b>TBE</b>	Tris-borate-EDTA ( <i>see</i> Sambrook et al., 1989)
<b>TEMED</b>	N,N,N',N'-tetramethyl-ethylenediamine
<b>trxB</b>	Thioredoxin reductase gene
<b>UFFI</b>	Urea-formaldehyde foam insulation
<b>UPGMA</b>	Unweighted pair group method using arithmetic averages
<b>USD</b>	US dollars
<b>USDA</b>	United States Department of Agriculture
<b>V8A</b>	V8 Juice agar (Malloch, 1981)
<b>VGE</b>	Vertical gel electrophoresis
<b>VNTR</b>	Variable-number tandem repeat
<b>VOCs</b>	Volatile organic compounds
<b>WWII</b>	World War II

---

Acronyms of herbaria and culture collections follow Holmgren et al. (1990) and Takishima et al. (1989).



## LIST OF NOMENCLATURAL ABBREVIATIONS

ABSI CORY	<i>Absidia corymbifera</i>	CONI SP__	<i>Coniothyrium</i> sp.
ABSI SP__	<i>Absidia</i> sp.	CONI SPOR	<i>Coniothyrium sporulosum</i>
ACRE BUTY	<i>Acremonium butyri</i>	CUNN SP__	<i>Cunninghamella</i> sp.
ACRE FURC	<i>Acremonium furcatum</i>	CURV PRAS	<i>Curvularia prasadii</i>
ACRE KILI	<i>Acremonium kiliense</i>	CURV PROT	<i>Curvularia protuberata</i>
ACRE RUTI	<i>Acremonium rutilum</i>	CURV SENE	<i>Curvularia senegalensis</i>
ACRE SCLE	<i>Acremonium sclerotigenum</i>	CYLI SP__	<i>Cylindrocarpon</i> sp.
ACRE SP__	<i>Acremonium</i> sp.	DIPL SPIC	<i>Diplococcium spicatum</i>
ACRE STRI	<i>Acremonium strictum</i>	DORA MICR	<i>Doratomyces microsporus</i>
ALTE ALTE	<i>Alternaria alternata</i>	DOTH CZSP	<i>Dothichiza</i> sp.
ALTE CITR	<i>Alternaria citri</i>	DOTH LASP	<i>Dothiorella</i> sp.
ALTE SP__	<i>Alternaria</i> sp.	DREC BISE	<i>Drechslera biseptata</i>
ALTE TENU	<i>Alternaria tenuissima</i>	DREC SP__	<i>Drechslera</i> sp.
APIO MONT	<i>Apiospora montagnei</i>	EMER NIDU	<i>Emericella nidulans</i>
APIO SP__	<i>Apiospora</i> sp.	EMER SP__	<i>Emericella</i> sp.
ASPE CAND	<i>Aspergillus candidus</i>	EMER VARI	<i>Emericella varicolor</i>
ASPE CERV	<i>Aspergillus cervinus</i>	EPIC NIGR	<i>Epicoccum nigrum</i>
ASPE CLAV	<i>Aspergillus clavatus</i>	EPIC SP__	<i>Epicoccum</i> sp.
ASPE FLAP	<i>Aspergillus flavipes</i>	EUPE OCHR	<i>Eupenicillium ochrosalmonium</i>
ASPE FLAV	<i>Aspergillus flavus</i>	EURO AMST	<i>Eurotium amstelodami</i>
ASPE FUMI	<i>Aspergillus fumigatus</i>	EURO CHEV	<i>Eurotium chevalieri</i>
ASPE GLAU	<i>Aspergillus glaucus</i>	EURO HERB	<i>Eurotium herbariorum</i>
ASPE NIGE	<i>Aspergillus niger</i>	EURO RUBR	<i>Eurotium rubrum</i>
ASPE NIVE	<i>Aspergillus niveus</i>	EURO SP__	<i>Eurotium</i> sp.
ASPE OCHR	<i>Aspergillus ochraceus</i>	EXOP JEAN	<i>Exophiala jeanselmei</i>
ASPE ORNA	<i>Aspergillus ornatus</i>	EXOP SP__	<i>Exophiala</i> sp.
ASPE ORYZ	<i>Aspergillus oryzae</i>	FUSA EQUI	<i>Fusarium equiseti</i>
ASPE PARS	<i>Aspergillus parasiticus</i>	FUSA FLOC	<i>Fusarium flocciferum</i>
ASPE PARX	<i>Aspergillus paradoxus</i>	FUSA OXYS	<i>Fusarium oxysporum</i>
ASPE PENI	<i>Aspergillus penicilloides</i>	FUSA SP__	<i>Fusarium</i> sp.
ASPE REST	<i>Aspergillus restrictus</i>	GEOM PANN	<i>Geomyces pannorum</i>
ASPE SCLE	<i>Aspergillus sclerotiorum</i>	GEOM SP__	<i>Geomyces</i> sp.
ASPE SP__	<i>Aspergillus</i> sp.	GEOT CAND	<i>Geotrichum candidum</i>
ASPE SYDO	<i>Aspergillus sydowii</i>	GILM HUMI	<i>Gilmaniella humicola</i>
ASPE TAMA	<i>Aspergillus tamarii</i>	GLIO MUFE	<i>Gliomastix murorum</i> v. <i>felina</i>
ASPE TERR	<i>Aspergillus terreus</i>	GLIO MUMU	<i>Gliomastix murorum</i> v. <i>murorum</i>
ASPE USTU	<i>Aspergillus ustus</i>	GLIO MURO	<i>Gliomastix murorum</i>
ASPE VERS	<i>Aspergillus versicolor</i>	GLIO ROSE	<i>Gliocladium roseum</i>
ASPE WENT	<i>Aspergillus wentii</i>	GLIO SP__	<i>Gliocladium</i> sp.
AURE PULL	<i>Aureobasidium pullulans</i>	GLIO VIRE	<i>Gliocladium virens</i>
BASI DIOM	<i>basidiomycete</i>	GRAP SP__	<i>Graphium</i> sp.
BLAS SP__	<i>Blastobotrys</i> sp.	HAIN LYTH	<i>Hainesia lythri</i>
BOTR ALLI	<i>Botrytis allii</i>	HORM DEMA	<i>Hormonema dematioides</i>
BOTR CINE	<i>Botrytis cinerea</i>	HORT WERN	<i>Hortaea werneckii</i>
BOTR PILU	<i>Botryotrichum piluliferum</i>	HUMI FUSC	<i>Humicola fuscoatra</i>
BOTR SP__	<i>Botrytis</i> sp.	HYAL SP__	<i>Hyalodendron</i> sp.
CAND SP__	<i>Candida</i> sp.	LECY HOFF	<i>Lecythophora hoffmannii</i>
CHAE AURE	<i>Chaetomium aureum</i>	LECY SP__	<i>Lecythophora</i> sp.
CHAE CIRC	<i>Chaetomium circinatum</i>	LEPT AUST	<i>Leptosphaerulina australis</i>
CHAE COCH	<i>Chaetomium cochliodes</i>	MICR OLIV	<i>Microsphaeropsis olivaceus</i>
CHAE FUNI	<i>Chaetomium funicola</i>	MICR SP__	<i>Microsphaeropsis</i> sp.
CHAE GLOB	<i>Chaetomium globosum</i>	MONA RUBE	<i>Monascus ruber</i>
CHAE NOZD	<i>Chaetomium nozdrenkoae</i>	MONI SP__	<i>Moniliella</i> sp.
CHAE SP__	<i>Chaetomium</i> sp.	MRTR AMAT	<i>Mortierella ramanniana</i> v. <i>autotrophica</i>
CHAE SUBS	<i>Chaetomium subspirale</i>	MUCO CIRC	<i>Mucor circinelloides</i>
CHRN SITO	<i>Chrysonilia sitophila</i>	MUCO HIEM	<i>Mucor hiemalis</i>
CHRN SP__	<i>Chrysonilia</i> sp.	MUCO MUCE	<i>Mucor mucedo</i>
CHRS SP__	<i>Chrysosporium</i> sp.	MUCO PLUM	<i>Mucor plumbeus</i>
CLAD CHLO	<i>Cladosporium chlorocephalum</i>	MUCO RACE	<i>Mucor racemosus</i>
CLAD CLAD	<i>Cladosporium cladosporioides</i>	MUCO SP__	<i>Mucor</i> sp.
CLAD HERB	<i>Cladosporium herbarum</i>	MYRO CINC	<i>Myrothecium cinctum</i>
CLAD MACR	<i>Cladosporium macrocarpum</i>	MYRO OLIV	<i>Myrothecium olivaceum</i>
CLAD SP__	<i>Cladosporium</i> sp.	MYRO RORI	<i>Myrothecium roridum</i>
CLAD SPHA	<i>Cladosporium sphaerospermum</i>	MYRO SP__	<i>Myrothecium</i> sp.
COCH GENI	<i>Cochliobolus geniculatus</i>	NEOS SP__	<i>Neosartorya</i> sp.
COCH SATI	<i>Cochliobolus sativus</i>	NIGR SPHA	<i>Nigrospora sphaerica</i>
CONI FUCK	<i>Coniothyrium fuckelii</i>		

## LIST OF NOMENCLATURAL ABBREVIATIONS (cont'd)

OIDI RHOD	<i>Oidiodendron rhodogenum</i>	PHIA SP__	<i>Phialophora</i> sp.
OIDI SP__	<i>Oidiodendron</i> sp.	PHOM CHRY	<i>Phoma chrysanthemicola</i>
OPHI SP__	<i>Ophiostoma</i> sp.	PHOM EUPY	<i>Phoma eupyrena</i>
OPHI TENE	<i>Ophiostoma tenellum</i>	PHOM EXIG	<i>Phoma exigua</i>
PAEC FULV	<i>Paecilomyces fulva</i>	PHOM FIME	<i>Phoma fimeti</i>
PAEC FUMO	<i>Paecilomyces fumosoroseus</i>	PHOM GLOM	<i>Phoma glomerata</i>
PAEC INFL	<i>Paecilomyces inflatus</i>	PHOM HERB	<i>Phoma herbarum</i>
PAEC SP__	<i>Paecilomyces</i> sp.	PHOM LEVE	<i>Phoma leveillei</i>
PAEC VARI	<i>Paecilomyces variotii</i>	PHOM MEDI	<i>Phoma medicaginis</i>
PENI ATRA	<i>Penicillium atramentosum</i>	PHOM SP__	<i>Phoma</i> sp.
PENI AURA	<i>Penicillium aurantiogriseum</i>	PITH CHAR	<i>Pithomyces chartarum</i>
PENI BREV	<i>Penicillium brevicompactum</i>	PITH SP__	<i>Pithomyces</i> sp.
PENI CANE	<i>Penicillium canescens</i>	PYRE SP__	<i>Pyrenochaeta</i> sp.
PENI CHRY	<i>Penicillium chrysogenum</i>	PYTH SP__	<i>Pythium</i> sp.
PENI COMM	<i>Penicillium commune</i>	RHIZ ORYZ	<i>Rhizopus oryzae</i>
PENI COPR	<i>Penicillium coprophilum</i>	RHIZ STOL	<i>Rhizopus stolonifer</i>
PENI CORY	<i>Penicillium corylophilum</i>	SCOL CONS	<i>Scolecobasidium constrictum</i>
PENI CRUS	<i>Penicillium crustosum</i>	SCOP BREV	<i>Scopulariopsis brevicaulis</i>
PENI CTNG	<i>Penicillium citreonigrum</i>	SCOP BRUM	<i>Scopulariopsis brumptii</i>
PENI CTRM	<i>Penicillium citrinum</i>	SCOP CAND	<i>Scopulariopsis candida</i>
PENI DECU	<i>Penicillium decumbens</i>	SCOP CHAR	<i>Scopulariopsis chartarum</i>
PENI DIGI	<i>Penicillium digitatum</i>	SCOP FUSC	<i>Scopulariopsis fusca</i>
PENI ECHI	<i>Penicillium echinulatum</i>	SCOP SP__	<i>Scopulariopsis</i> sp.
PENI EXPA	<i>Penicillium expansum</i>	SCYT SP__	<i>Scytalidium</i> sp.
PENI FUNI	<i>Penicillium funiculosum</i>	SORD SP__	<i>Sordaria</i> sp.
PENI GLAN	<i>Penicillium glandicola</i>	SPHA SP__	<i>Sphaeropsis</i> sp.
PENI GRIS	<i>Penicillium griseofulvum</i>	SPOR PRUI	<i>Sporotrichum pruinatum</i>
PENI HIRS	<i>Penicillium hirsutum</i>	SPOR THSP	<i>Sporothrix</i> sp.
PENI IMPL	<i>Penicillium implicatum</i>	SPRB SP__	<i>Sporobolomyces</i> sp.
PENI ISLA	<i>Penicillium islandicum</i>	STAC CHAR	<i>Stachybotrys chartarum</i>
PENI ITAL	<i>Penicillium italicum</i>	STAC PARV	<i>Stachybotrys parvispora</i>
PENI JANT	<i>Penicillium janthinellum</i>	STEM BOTR	<i>Stemphylium botryosum</i>
PENI MELI	<i>Penicillium melinii</i>	STEM SOLA	<i>Stemphylium solani</i>
PENI MICZ	<i>Penicillium miczynskii</i>	STEM SP__	<i>Stemphylium</i> sp.
PENI OXAL	<i>Penicillium oxalicum</i>	SYNC RACE	<i>Syncephalastrum racemosum</i>
PENI PURP	<i>Penicillium purpurogenum</i>	SYNC SP__	<i>Syncephalastrum</i> sp.
PENI RAIS	<i>Penicillium raistrickii</i>	SYNC VERR	<i>Syncephalastrum verruculosum</i>
PENI REST	<i>Penicillium restrictum</i>	TALA FLAV	<i>Talaromyces flavus</i>
PENI ROQU	<i>Penicillium roquefortii</i>	TALA TRAC	<i>Talaromyces trachyspermus</i> var. macrocarpus
PENI SIMP	<i>Penicillium simplicissimum</i>	THAM ELEG	<i>Thamnidium elegans</i>
PENI SP__	<i>Penicillium</i> sp.	TOLY SP__	<i>Tolypocladium</i> sp.
PENI SP01	<i>Penicillium</i> sp. #1	TORU HERB	<i>Torula herbarum</i>
PENI SP13	<i>Penicillium</i> sp. #13	TRIC ASPE	<i>Trichocladium asperum</i>
PENI SP26	<i>Penicillium</i> sp. #26	TRIC HARZ	<i>Trichoderma harzianum</i>
PENI SP35	<i>Penicillium</i> sp. #35	TRIC KONI	<i>Trichoderma koningii</i>
PENI SP38	<i>Penicillium</i> sp. #38	TRIC POLY	<i>Trichoderma polysporum</i>
PENI SP44	<i>Penicillium</i> sp. #44	TRIC ROSE	<i>Trichothecium roseum</i>
PENI SP52	<i>Penicillium</i> sp. #52	TRIC SP__	<i>Trichoderma</i> sp.
PENI SP64	<i>Penicillium</i> sp. #64	TRIC VIRI	<i>Trichoderma viride</i>
PENI SP84	<i>Penicillium</i> sp. #84	TRPH TONS	<i>Trichophyton tonsurans</i>
PENI SP87	<i>Penicillium</i> sp. #87	TRUN ANGU	<i>Truncatella angustata</i>
PENI SPIN	<i>Penicillium spinulosum</i>	ULOC ATRU	<i>Ulocladium atrum</i>
PENI VARI	<i>Penicillium variabile</i>	ULOC CHAR	<i>Ulocladium chartarum</i>
PENI VERR	<i>Penicillium verrucosum</i>	ULOC SP__	<i>Ulocladium</i> sp.
PENI VIRI	<i>Penicillium viridicatum</i>	VERT SP__	<i>Verticillium</i> sp.
PENI VULP	<i>Penicillium vulpinum</i>	WALL SEBI	<i>Walleimia sebi</i>
PENI WAKS	<i>Penicillium waksmanii</i>	WARD HUMI	<i>Wardomyces humicola</i>
PEST PALU	<i>Pestalotiopsis palustris</i>	YEAS T__	yeast
PEST SP__	<i>Pestalotiopsis</i> sp.	ZETI HETE	<i>Zetiasplozna heteromorpha</i>
PHIA FAST	<i>Phialophora fastigiata</i>		

## **CHAPTER 1. INTRODUCTION**

Fungi inhabit nearly all terrestrial environments. In this regard, the interiors of human dwellings and workspaces are no exception. The mould flora of human-inhabited indoor environments consists of a distinctive group of organisms that collectively are not normally encountered elsewhere. The biology and taxonomy of selected members of the fungal flora of household dust are the focus of the research and discussion presented in this thesis.

Household dust itself is not a substance that evokes a rich sense of practical or historical importance aside from its relentless contribution to the stereotypical plight of suburban housewives obsessed with its elimination. Shakespeare used *dust* as a metaphor to evoke the cyclical nature of life, and the fact that neither class nor creed exempts us from this binding cycle. The spirit of Shakespeare's metaphor provides a fitting framework within which to study the substance itself, as a thriving and complex community comprising a vast diversity of organisms whose lives secretly parallel our own.

### **THE BIOLOGY OF HOUSE DUST**

Dust formation occurs as a result of the ongoing elutriation of airborne organic and inorganic particulate matter that originates from a multiplicity of indoor and outdoor sources. House dust is a fibrous material composed primarily of a matrix of textile fibres, hairs and shed epithelial debris (Bronswijk, 1981). The majority of particles comprising household dust fall within the size range from  $10^{-3}$  to 1 mm (ibid.). Airborne particles smaller than this (e.g. smoke, fumes, etc.) tend to behave as a colloidal system and do not sediment efficiently even in still air due to

their relative buoyancy; thus, their presence within dust is often a function of filtration, diffusion or electrostatic effects (Cox and Wathes, 1995).

The large daily influx of organic debris to the dust of inhabited houses provides a rich primary nutrient source that supports an intricate microcommunity encompassing three kingdoms of organisms: animals (arthropods, and to some extent larger animals such as rodents, etc.), bacteria and fungi (Bronswijk, 1981; Harvey and May, 1990; Harving et al., 1993; Hay et al., 1992a, 1992b; Miyamoto et al., 1969; Samson and Lustgraaf, 1978; Sinha et al., 1970). The fibrous nature of a stable dust matt composed predominantly of hygroscopic fibres acts to harvest atmospheric moisture and simultaneously provides shelter from desiccation for the organisms contained within. While the variety of fibres themselves (particularly cellulosic fibres) may serve as sources of carbon nutrition for the heterotrophic dust inhabitants, a more readily available source of organic carbon and nitrogen comes from food crumbs and excoriated epithelia. Although the latter makes up a considerable mass-fraction of house dust, its microbial availability is largely limited to non-keratin proteins and lipids due to the refractory nature of keratin itself (Currah, 1985). Plant pollen arising from the phylloplane likely provide additional nutritional input to the house dust ecosystem (Bronswijk, 1981). Bronswijk (1981) compiled a list of taxa of different groups of dust-borne organisms based on reports by numerous workers. The fauna in her inventory included isopods (5 taxa), roaches (47 taxa), lepidoptera (8 taxa), psocoptera (20 taxa) and mites (147 taxa), while the microbiota was dominated by fungi (163 taxa) with only few bacterial taxa (8).

## INTERACTIONS BETWEEN MITES AND FUNGI

Bronswijk (1981) speculated considerably on trophic interactions between microarthropods and fungi within dust-bound habitats. She suggested that xerophilic fungi, notably *Wallemia sebi* and members of the *Aspergillus glaucus* series were responsible for the hydrolysis of fats in dustborne dander, facilitating the consumption of these materials by various mite species. Bronswijk (1981) further proposed that *Acremonium*, *Penicillium* and *Scopulariopsis* along with mesophilic species of *Aspergillus* provided food for oribatid mites by the colonization of crumbs and other food debris. Samson and Lustgraaf (1978) demonstrated an association between *Dermatophagoides pteronyssinus* and the microfungi *Aspergillus penicillioides* and *Eurotium halophilicum* whereby these fungi frequently co-occurred with certain dust-borne mite species, and the mites preferred consuming materials upon which the fungi had grown. Hay and co-workers (1992a) showed antigenic cross-reactivity between *Aspergillus penicillioides* and the mite *D. pteronyssinus*, however these workers later suggested that this association may have been an artifact of laboratory culture conditions under which the mites were reared (Hay et al., 1992b)<sup>1</sup>.

## FUNGI IN HOUSEHOLD DUST

The fungal component of dust biodiversity probably remains underestimated since only a few studies to date have provided thorough mycological characterizations of house dust (Davies, 1960; Gravesen, 1978a; Lustgraaf and Bronswijk, 1977; Ostrowski, 1999; Schober, 1991). An analysis of dust from 60 households in the Netherlands by Hoekstra and co-workers (1994)

---

<sup>1</sup> I have observed dramatic overgrowths on the cadavers of predatory mites (Macrochaelidae) from composting marine seaweeds incubated in moist chamber culture by a mould species that compared to *P. olsonii*. Similarly, fungus-feeding mites occurring as inquilines in laboratory cultures of leaf-cutting ants of the tribe Attini often become overgrown by *Penicillium* spp., when incubated under damp chamber conditions. In the latter case, it is reasonably clear that *Penicillia* are uncommon allochthonous members of the fungal flora of the fungal gardens of leaf-cutting ants. The colonisation of these mites by *Penicillium* is most likely an artifact of high arthropod population density under unnatural conditions of laboratory culture, and neither supports an hypothetical role for *Penicillium* in the mite lifecycles nor suggests that *Penicillium* is important in the nutrient cycling of this system.

revealed 108 fungal species in 54 genera using V8 juice agar and Dichloran 18 % glycerol agar (DG18) as isolation media. Species recovery showed temporal variation in samples taken 6 wks apart. Also, considerable variation was observed according to the isolation media used. A similar study by Ostrowski (1999) from 219 households in the Netherlands reported 143 fungal taxa of which 113 were also observed in air samples taken from kitchen areas, where the highest level of fungal species diversity was observed.

Innumerable reservoirs of fungal material exist outdoors that may contribute to the fungal burden of indoor air and dust according to the continuous input of outdoor air into indoor environments. Levels of phylloplane fungal spores in indoor air are typically correlated with prevailing weather conditions, including wind speed and precipitation that are responsible for mediating spore release in the outdoor environment (Ingold, 1965; Li and Kendrick, 1994, 1995). As such, surveys of fungi from indoor air and dust usually demonstrate the presence of phylloplane taxa that are qualitatively similar to outdoor air albeit at lower levels (Abdel-Hafez et al., 1993; Bunnag et al., 1982; Calvo et al., 1980; Dillon et al., 1996; Ebner et al., 1992).

Fungal propagules in household dust can be divided into two ecological categories according to their origin. Dustborne fungi may be **1**) active inhabitants of dust (autochthonic *sensu* Bronswijk, 1981); or, **2**) they may be imported, as passive entrants from other sources (allochthonic *ibid.*; *see also* Cohen et al., 1935; Davies, 1960; Gravesen, 1978; Morey, 1990). Davies (1960) reported dust-bound concentrations of viable fungal propagules in excess of 300 CFU/mg. The magnitude of this concentration prompted Bronswijk (1981) to infer that this dust-bound spora could not have been imported and must have been produced within the dust. Even when fungi

are not produced within dust proper, an indoor fungal amplification site produces a characteristic pattern of species distribution in indoor air and consequently house dust.

#### **INDOOR SOURCES OF DUST MYCOFLORA**

Indoor fungal growth contributes to disproportionately high spore levels in indoor air relative to those observed in outdoor air (Agrawak et al., 1988; Berk et al., 1957; Grant et al., 1989).

Furthermore, when a fungal amplifier is local, the composition of the indoor fungal flora usually differs qualitatively, in being dominated by a single or few abundant species which may not be components of the background flora (Giddings, 1986; Miller, 1992; Miller et al., 1988; Moriyama et al., 1992). For instance, *Cladosporium sphaerospermum* is a frequent colonist of indoor finishes as a consequence of excessive indoor relative humidity (Burge and Otten, 1999). This species has a proclivity for many characteristically refractile substrates such as oil-based paints, and polymeric decorative finishes (e.g. vinyl wall coverings) (Domsch et al., 1980). Interestingly, *Cl. sphaerospermum* is a comparatively rare component of outdoor air flora where species such as *Cl. herbarum* and *Cl. cladosporioides* typically dominate (Burge and Otten, 1999). Despite the abundance of *Mycosphaerella* and its *Cladosporium* anamorphs in outdoor epiphyllous habitats and consequently as spora in outdoor air (Farr et al., 1989; Ho et al., 1999), *Cl. sphaerospermum* is comparably rare in these habitats and even low levels of this fungus in indoor air are unusual and strongly indicate active indoor fungal growth.

Indoor plantings can also serve as reservoirs of fungal material (Burge et al., 1982; Summerbell, 1992). Summerbell and co-workers (1989) examined soils from potted plants in hospital wards and found a large number of potential human pathogenic fungi including *Aspergillus fumigatus* and *Scedosporium apiospermum*, an anamorph of *Pseudallescheria boydii*. Although these workers did not

investigate airborne concentrations of these fungi related to their presence in soil, based upon the results of Kaitzis (1977) and Smith and co-workers (1988) Summerbell and colleagues theorized that activities such as watering were likely to cause spore release. The recognition and elimination of indoor amplifiers of opportunistic human pathogenic fungi within the hospital environment are important in the reduction of nosocomial infection. *Aspergillus fumigatus* and *A. flavus* are of particular concern because these fungi are frequent agents of pulmonary aspergillosis especially in immunocompromised patients such as organ recipients and HIV patients (Summerbell, 1998).

#### ***PENICILLIUM* IN INDOOR ENVIRONMENTS**

Perhaps the most famous of all indoor fungi was made so in a 10 page paper written in 1929 by Alexander Fleming, which described the inhibition of several groups of cocciform bacteria by a fungus in the genus *Penicillium*. This fungus, identified for Fleming by St. Mary's Hospital mycologist Charles La Touche as *P. rubrum* Grassberger-Stoll ex. Biourge, was sent by Fleming to Harold Raistrick at the University of London, who in turn sent it to Charles Thom of the US Department of Agriculture in Peoria, Illinois (Fleming, 1929; Gray, 1959; Howard, 1994). Thom (1930) considered Fleming's isolate to be *P. notatum*, a species described by Westling (1911) from the branches of *Hyssopus* L. (Lamiaceae) in Norway. Over a decade after Fleming's discovery, Ernst Chain and Howard Florey isolated the active principal, penicillin, and demonstrated its success in clinical trials, a collective achievement for which the three shared the Nobel Prize for Physiology and Medicine in 1945 (Howard, 1994).

The discovery of penicillin ranks as one of the most significant events in the history of medicine and possibly of human civilization and has been the subject of much discussion (Hare, 1970;



MacFarlane, 1979, 1984; Williams, 1984). Fleming's pivotal role in the penicillin story has been described as a most remarkable case of serendipity, since the vast majority of *Penicillia* produce metabolites with profound mammalian toxicity (Gray, 1959; Samson et al., 1996). Others have alleged that this discovery was inevitable. From knowledge of the substrate of Westling's (1911) species *P. notatum*, Selwyn (1980) and later Lowe and Elander (1983) inferred the naïve use of penicillin from the following passage of the Old Testament Book of Psalms:

“Purge me with hyssop, and I shall be clean, wash me, and I shall be whiter than snow.

(Psalms 51:7)

Similarly, a passage from the Third Book of Moses describes a treatment for leprosy<sup>2</sup>:

“This is the law of the leper in the day of his cleansing... He shall take... the cedarwood, and the scarlet and the hyssop, and shall dip them... in the blood of the bird... And he shall sprinkle upon him that is to be cleansed from the leprosy...

(Lev. 14:2-7)

Certainly the habitat of *P. chrysogenum* is not restricted to *Hyssopus*, as this fungus is known from a vast range of outdoor substrates (Domsch et al., 1980; Pitt and Hocking, 1999). Despite the ubiquitous nature of *P. chrysogenum* outdoors, however, it remains poorly represented in samples of outdoor air where typical phylloplane fungi such as *Alternaria*, *Aureobasidium*, *Cladosporium*, *Epicoccum* and *Ulocladium* dominate (Dillon et al., 1996; Scott et al., 1999b; Tobin et al., 1987). Indoors, *P. chrysogenum* is typically the most commonly occurring airborne and dustborne species of this genus (Abdel-Hafez et al., 1986; Mallea et al., 1982; Summerbell et al., 1992). Certainly an important factor in the establishment of high indoor levels of *P. chrysogenum* is its role as an agent of food spoilage. Pitt and Hocking (1999) indicated that *P. chrysogenum* was the most common species of this genus associated with food contamination, known from numerous fruits, vegetables, cereals, meats and dairy products (Domsch et al., 1980; Pitt and Hocking, 1999;

---

<sup>2</sup> In biblical translations and allusions, leprosy refers to any disfiguring skin disease, whose cause is not necessarily limited to Hansen's bacillus, *Mycobacterium leprae* (Brown, 1993).

Samson et al., 1996). Indeed, most high penicillin-producing strains of this species were derived from a single isolate obtained from cantaloupe (Gray, 1956; Lowe and Elander, 1983; Raper and Thom, 1949). The growth of *P. chrysogenum* on wooden food-shipping crates has also been responsible for the tainting of foodstuffs by the release of chloroanisole produced during the breakdown of phenolic wood preservatives (Pitt and Hocking, 1999; Hill et al., 1995). Frisvad and Gravesen (1994) speculated that the indoor abundance of this species could not be explained by its occurrence on foodstuffs alone, and suggested that the somewhat xerophilic nature of both *P. chrysogenum* and *P. brevicompactum* may facilitate their colonization of other indoor substrates such as wood and paint. Adan and Samson (1994) listed *P. chrysogenum* as a common colonist of acrylic-based paint finishes, noting that this species exhibited growth at relative humidities as low as 79 %. This species is also known from wallpaper, textiles, broadloom, visual art and optical lenses (Samson et al., 1994). Similarly, *P. brevicompactum* is known from a wide range of indoor substrates including foods, building materials and decorative finishes (Adan and Samson, 1994; Domsch et al., 1981; Scott et al., 1999a).

Many of the microfungi that are routinely observed as colonists on indoor finishes and construction materials, such as *Aspergillus*, *Paecilomyces*, *Penicillium* and *Scopulariopsis* species tend to grow at relatively low water activity often on refractile substrates (Samson et al., 1996). These genera form the core of the group commonly referred to as “domicile fungi” owing to their inordinate abundance in the air and dust of residential interiors. While these fungi are common agents of structural deterioration in North America, the dry rot fungus *Serpula lacrimans* remains the principal agent of structural decay in Britain and Northern Europe (Singh, 1994). Similarly, the importance of indoor exposure to fungal spores indoors in the development of allergic asthma is greater in North America than in Europe, where dust mite and dander exposures are

the primary exposure risk factors for this disease (Beaumont et al., 1985; Flannigan and Miller, 1994).

## **HEALTH EFFECTS OF EXPOSURE TO INDOOR FUNGI**

Although environmental fungal reservoirs have rarely been implicated in human infection (Miller, 1992; Summerbell et al., 1992), their presence has long been accepted as an important risk factor to respiratory morbidity (Dillon et al., 1996). Human exposure to indoor fungi has been implicated in the etiology of a multiplicity of health problems that ranges from allergies and respiratory diseases to toxicoses and neoplastic diseases. To the extent that fungi are involved in these processes, the inhalation or ingestion of fungal cellular debris is thought to be the principal route of exposure. Ancillary products of mould growth such as volatile organic metabolites (e.g. alcohols) or volatile breakdown products from extracellular processes (e.g. formaldehyde) may contribute to symptoms of illness or discomfort independent of exposure to fungal biomass (Miller, 1992). The diversity in clinical scope of building-related illnesses makes their diagnosis difficult. Similarly, the identification and localization of agents that may contribute to decreased indoor air quality (IAQ) is often problematic. Over the past 30 years, "Sick Building Syndrome", in which the air quality in a building is compromised as a result of biological or chemical pollutants, has been recognized as a serious threat to modern public health (Mishra et al., 1992; Su et al., 1992; Tobin et al., 1987).

Despite the ubiquity of fungi in indoor air and dust, indoor fungal exposures are rarely implicated in the etiology of human infection (Burge, 1989; Summerbell et al., 1992). However, their involvement in irritative disorders (i.e. primarily non-infective diseases such as allergy and asthma) has long been recognised (Al-Doory, 1984; Cohen et al., 1935; Flannigan et al., 1991;

Gravesen, 1979; Reymann and Schwartz, 1946). Bioaerosols of fungal origin, consisting of spores and hyphal fragments are readily respirable, and are potent elicitors of bronchial irritation and allergy (Brunekreef et al., 1989; Burge, 1990a; Dales et al., 1991a, 1991b; Platt et al., 1989; Sakamoto et al., 1989; Samet et al., 1988; Sherman and Merksamer, 1964; Strachan et al., 1990).

## **ALLERGIC RHINITIS AND SINUSITIS**

### **Type I allergic syndromes**

Concern regarding human exposure to mould aerosols in indoor environments is mainly related to direct mucosal irritation and elicitation of an IgE-mediated hypersensitivity response that precipitates rhinitis and upper airways irritation, eye irritation and frequently sinusitis that characterize allergic syndromes (Pope et al., 1993). The symptoms of allergy are not manifested until sensitisation in which an individual incurs repeated exposures to the antagonistic agent. During this process, antigen-specific IgE is produced that attaches to receptors on mast cells that are concentrated on gastric and respiratory mucosa. In a sensitised individual, the IgE on mast cells binds to antigen following exposure, mediating mast cell rupture, histamine release and the ensuing hypersensitivity response (Guyton, 1982). The principal fungal allergens are either high molecular weight carbohydrates (e.g. beta 1-3 glucans) or water soluble glycoproteins (such as enzymes) (ibid.). Typically, these compounds are sequestered within fungal spores or secreted into fungus-contaminated debris. These allergens become airborne which when these materials are aerosolized. A link between respiratory exposure to fungal material and seasonal allergy was first proposed in 1873 by Blackley who demonstrated the provocation of allergic respiratory symptoms by exposure to *Penicillium* spores (*vide* Nilsby, 1949). Latgé and Paris (1991) listed 106 fungal genera with members documented to elicit allergy, although it is likely that the true number is actually much larger (Li, 1994). Although the principal allergenic vehicles

of fungal allergies are spores and other cellular debris, the culprit allergens are not always constitutively present in these materials. Savolainen and co-workers (1990) suggested that certain allergenic enzymes may only be produced upon germination. Exposure to these compounds requires inhalation of germinable propagules, followed by germination on upper respiratory tract mucosa.

### **Dust mites and allergy**

Other notable biological elicitors of similar allergic cascades include plant pollen (particularly *Ambrosia* spp. in northern temperate North America *vide* Jelks, 1994), and so-called “dust mites”, typically of the genus *Dermatophagoides* (especially *D. pteronyssinus* and *D. farinae*, Bronswijk, 1981). Considerable research has examined the relationship of dust mite allergen exposure to clinical allergy. Bronswijk (1981) provides an excellent review of this work. Dust mite sensitisation in domestic settings appears to be influenced by additional biotic agents. Miyamoto and colleagues (1969) showed allergenic cross-reactivity between domestic dust mites and other biological sensitizers including dust and fungi. It is likely that this cross-reactivity is a consequence of correlated exposures because mites often occur together with fungi on water-damaged indoor materials (Bronswijk, 1981)<sup>3</sup>. The feces of dust mites are considerably allergenic because of the large content of partially digested food materials and intact digestive enzymes (Tovey et al., 1981). In addition, mite fecal pellets often contain large numbers of intact and partially degraded fungal spores because these materials are a preferred food of many dustborne mite taxa (Samson and Lustgraaf, 1978).

---

<sup>3</sup> It is common to observe dense mite colonization on superficial fungal growth on wall surfaces, especially where *Cl. sphaerospermum* has disfigured the finished sides of exterior walls pursuant to excessive indoor relative humidity during the winter months. In such cases, elevated mite populations are a predictable consequence. Indeed, by gauging the level of mite activity on a fungus-contaminated surface it is often possible to determine the time-course of contamination, since mite populations do not generally develop until 3-6 months after the emergence of fungal growth (data not presented).

## HYPERSENSITIVITY SYNDROMES

Extrinsic allergic alveolitis, or hypersensitivity pneumonitis (HP) is an acute inflammatory reaction of the lower airways upon exposure to an agent to which a sensitivity has developed from prior exposure. Hypersensitivity pneumonitis involves cell-mediated immunity (Type IV allergic response), in contrast to Type I allergic syndromes that are IgE-mediated, and thus may exist independently of the latter. Numerous environmental antigens have been implicated as elicitors of HP, including fungal aerosols. The majority of case literature on fungus-mediated HP involves occupational exposures where exposures to mould aerosol exceed background by several orders of magnitude. Furthermore, these exposures often involve a stable, low species diversity related to a particular substrate or process. Although the clinical presentation of these disorders is relatively uniform, a florid nomenclature has developed based primarily on the particular occupation or the sensitising agent implicated (*see* Table 1-1). In non-industrial, non-agricultural settings, some case reports suggest that sufficiently high airborne levels of otherwise innocuous fungal particulates have caused HP where patients exhibited pneumonia-like symptoms following even low exposures to irritant agents (Jacob et al., 1989; Pepys, 1969; Samet et al., 1988; Weissman and Schuyler, 1991). Four of the hypersensitivity pneumonitides in Table 1-1 have been reported from indoor environments: Humidifier Lung (fungal etiologic agents include *Penicillium* spp. and *Cephalosporium* [= *Acremonium*] spp.), Cephalosporium HP (*Cephalosporium* spp.) and Japanese Summer-Type HP (probable etiologic agent *Trichosporon cutaneum*) (Pope et al., 1993).

## ASTHMA

Asthma is a disease characterized by reversible airway obstruction triggered by any of a number of provocation agents, including allergens, cold and exercise stress, and relieved by the inhalation

of aerosolised beta-adrenergic antagonists (Hunninghake and Richardson, 1998; Pope et al., 1993). Asthmatic conditions are loosely categorized as **1)** allergic asthma, with typical onset at an early age in patients with positive skin tests to common allergens or a family history of allergy; and, **2)** idiosyncratic asthma, where onset is usually later in life, in the absence of immunological allergic predisposition, family history indicators or comorbid stimuli such as smoking. Asthma symptoms include wheezing, usually accompanied by dyspnea (shortness of breath) and cough, often in an episodic pattern with intermittent or extended periods of remission. For over a decade, it has been quite clear that the presence of moulds (as indicated by dampness) in housing exerts an adverse effect on the respiratory health of children (Martin et al., 1987; Platt et al., 1989). Strachan and co-workers (1988; 1990) showed an increase in symptoms of wheezing in children living in mouldy homes in Edinburgh, Scotland; however, these workers found little quantitative difference in the airborne mycoflora of households in which asthmatic children lived, as measured by viable sampling. These workers postulated that the disagreement between objective measurement of airborne mould levels and subjective assessment of housing conditions by occupants indicated a reporting bias in which asthmatics were more likely to report mould conditions than non-asthmatics. A Canadian cross-sectional study of over 13,000 children by Dales and colleagues (1991a) also showed a significant increase in respiratory symptoms according to reported mould or damp conditions in housing. These workers suggested that short-term indoor air samples (“grab samples”) such as those employed by Strachan and co-workers (1988; 1990) were not necessarily reflective of longer-term conditions, due to the periodic nature of spore release. An earlier US-based cross-sectional study (“The Harvard Six-Cities Study”, Brunekreef et al., 1989) showed a significantly lower prevalence of wheeze than the Edinburgh study, yet demonstrated a comparable odds ratio between this symptom and mouldy housing conditions, suggesting that wheeze may have been over-reported

**TABLE 1-1:** Selected hypersensitivity pneumonitides with probable microbial etiologies

<b>DISEASE</b>	<b>SOURCE</b>	<b>PROBABLE ALLERGEN</b>
Bagassosis	Mouldy bagasse (sugar cane)	Thermophilic actinomycetes
<i>Cephalosporium</i> HP	Basement sewage contamination	<i>Cephalosporium</i> spp. (= <i>Acremonium</i> )
Cheese washer's lung	Mouldy cheese	<i>Penicillium casei</i> (= <i>P. roquefortii</i> )
Compost lung	Compost	<i>Aspergillus</i> spp.
Familial HP	Contaminated wood dust in walls	<i>Bacillus subtilis</i>
Farmer's lung	Mouldy hay, grain or silage	<i>Aspergillus fumigatus</i> and thermophilic actinomycetes
Hot tub lung	Mould on ceiling	<i>Cladosporium</i> spp.
Housewife's lung	Moldy wooden flooring	<i>Penicillium expansum</i> and other moulds
Humidifier/ Air-conditioner lung	Contaminated water or coils in humidifiers and air-conditioners	<i>Aureobasidium pullulans</i> , <i>Cephalosporium</i> spp., <i>Penicillium</i> spp. and thermophilic actinomycetes
Japanese summer house HP	Bird droppings, house dust	<i>Trichosporon cutaneum</i>
Lycoperdonosis	Puffballs	<i>Lycoperdon</i> spp.
Malt worker's lung	Mouldy barley	<i>Aspergillus fumigatus</i> or <i>As. clavatus</i>
Maple bark disease	Maple bark	<i>Cryptostroma corticale</i>
Mushroom worker's lung	Mushroom compost	Thermophilic actinomycetes and other microorganisms
Potato riddler's lung	Mouldy hay around potatoes	<i>Aspergillus</i> spp. and thermophilic actinomycetes
Sauna taker's lung	Contaminated sauna water	<i>Cladosporium</i> spp. and others
Suberosis	Mouldy cork dust	unknown
Tap water lung	Contaminated tap water	unknown
Thatched roof disease	Dried grasses and other leaves	<i>Saccharomonospora viridis</i>
Tobacco worker's disease	Mouldy tobacco	<i>Aspergillus</i> spp.
Winegrower's lung	Mouldy grapes	<i>Botrytis cinerea</i>
Wood trimmer's disease	Contaminated wood trimmings	<i>Rhizopus</i> spp. and <i>Mucor</i> spp.
Woodman's disease	Oak and maple trees	<i>Penicillium</i> spp.
Woodworker's lung	Oak, cedar and mahogany dusts, pine and spruce pulp	<i>Alternaria</i> spp. and wood dust

**SOURCES:** Hunninghake and Richardson (1998); Park et al. (1994); Pope et al. (1993)



in the study by Strachan and co-workers (1988). In their review of asthma trends, Pope and co-workers (1993) noted that the magnitude of allergen exposure increased the potential for allergic sensitisation, and was both a risk factor for lowered age of asthma onset as well as increased disease severity. Furthermore, these workers proposed a recent increase in asthma morbidity and mortality as reflected by hospital admission statistics.

### **MYCOTOXINS**

In addition to their roles as irritants and allergens, many fungi produce toxic chemical constituents (Kendrick, 1992; Miller, 1992; Wyllie and Morehouse, 1977). Samson and co-workers (1996) defined mycotoxins as “fungal secondary metabolites that in small concentrations are toxic to vertebrates and other animals when introduced via a natural route”. These compounds are non-volatile and may be sequestered in spores and vegetative mycelium or secreted into the growth substrate. The mechanism of toxicity of many mycotoxins involves interference with various aspects of cell metabolism, producing neurotoxic, carcinogenic or teratogenic effects (Rylander, 1999). Other toxic fungal metabolites such as the cyclosporins exert potent and specific toxicity on the cellular immune system (Hawksworth et al., 1995); however, most mycotoxins are known to possess immunosuppressant properties that vary according to the compound (Flannigan and Miller, 1994). Indeed, the toxicity of certain fungal metabolites such as aflatoxin, ranks them among the most potently toxic, immunosuppressive and carcinogenic substances known (ibid.). There are unambiguous links between ingestion as well as inhalation exposures to outbreaks of human and animal mycotoxicoses (Abdel-Hafez and Shoreit, 1985; Burg et al., 1982; Croft et al., 1986; Hintikka, 1978; Jarvis, 1986; Norbäck et al., 1990; Sorenson et al., 1987; Schiefer, 1986). Several common mycotoxigenic indoor fungi and their respective toxins are listed in Table 1-2.

**TABLE 1-2:** Mycotoxins of significance produced by indoor fungi

<b>MYCOTOXIN</b>	<b>PRIMARY HEALTH EFFECT</b>	<b>FUNGAL PRODUCERS</b>
Aflatoxins	Carcinogens, hepatotoxins	<i>Aspergillus flavus</i> <i>As. parasiticus</i>
Citrinin	Nephrotoxin	<i>Penicillium citrinum</i> <i>Pe. verrucosum</i>
Cyclosporin	Immunosuppressant	<i>Tohyocladium inflatum</i>
Fumonisin	Carcinogens, neurotoxins	<i>Fusarium moniliforme</i> (=F. <i>verticillioides</i> ) <i>F. proliferatum</i>
Ochratoxin A	Carcinogen	<i>As. ochraceus</i> <i>Pe. verrucosum</i>
Patulin	Protein synthesis inhibitor, nephrotoxin	<i>As. terreus</i> <i>Paecilomyces variotii</i> <i>Pe. expansum</i> <i>Pe. griseofulvum</i> <i>Pe. roquefortii</i>
Sterigmatocystin	Carcinogen, hepatotoxin	<i>As. nidulans</i> <i>As. versicolor</i> <i>Chaetomium</i> spp.
Trichothecenes, macrocyclic		
Satratoxins	Protein synthesis inhibitors	<i>Stachybotrys chartarum</i> <i>Myrothecium</i> spp.
Trichothecenes, non-macrocyclic		
Deoxynivalenol (vomitoxin)	Emetic	<i>F. cerealis</i> <i>F. culmorum</i> <i>F. graminearum</i>
T-2 toxin	Hemorrhagic, emetic, carcinogen	<i>F. sporotrichioides</i>
Verrucosidin	Neurotoxin	<i>Pe. aurantiogriseum</i> group
Xanthomegnin	Hepatotoxin, nephrotoxin	<i>As. ochraceus</i> <i>Pe. aurantiogriseum</i> group
Zeralenone	Estrogenic	<i>Fusarium</i> spp.

**SOURCES:** Burge and Ammann (1999); Rodricks et al. (1977); Samson et al. (1996)

## **VOLATILE FUNGAL METABOLITES**

During exponential growth, many fungi release low molecular weight, volatile organic compounds (VOCs) as products of secondary metabolism. These compounds comprise a great diversity of chemical structure, including ketones, aldehydes and alcohols as well as moderately to highly modified aromatics and aliphatics. Cultural studies of some common household moulds suggest that the composition of VOCs remains qualitatively stable over a range of growth media and conditions (Sunesson et al., 1995). Furthermore, the presence of certain marker compounds common to multiple species, such as 3-methylfuran, may be monitored as a proxy for the presence of a fungal amplifier (Sunesson et al., 1995). This method has been suggested as a means of monitoring fungal contamination in grain storage facilities (Börjesson et al., 1989; 1990; 1992; 1993). Limited evidence suggests that exposure to low concentrations of VOCs may induce respiratory irritation independent of exposure to allergenic particulate (Koren et al., 1992). Volatile organic compounds may also arise through indirect metabolic effects. A well-known example of this is the fungal degradation of urea formaldehyde foam insulation. Fungal colonization of this material results in the cleavage of urea from the polymer, presumably to serve as a carbon or nitrogen source for primary metabolism. During this process formaldehyde is evolved as a derivative, contributing to a decline in IAQ (Bissett, 1987).

## **OBJECTIVES OF THE CURRENT STUDY**

The present study was conceived with two primary objectives. First, this investigation shall characterize the fungal biodiversity of house dust. This work shall investigate correlations between dustborne fungal species, and examine the ecological similarity of positively associated taxa based on the hypothesis that positively associated dustborne fungi are likely to share habitat

characteristics. From this, a second hypothesis follows that mechanisms that permit the entry or concentration a given species will tend to facilitate the entry of other positively correlated taxa.

A second objective of this research is to assess the extent of genotypic variability in two dustborne *Penicillia*, *P. brevicompactum* and *P. chrysogenum*. The goal of this work shall be to examine the extent of clonality within these two species, and to determine if the observed patterns of genotypic variation support the current species concepts.

## **CHAPTER 2. ANALYSIS OF HOUSE DUST MYCOFLORA**

### **ABSTRACT**

Broadloom dust samples were enumerated for culturable fungi from 369 homes in Wallaceburg, Ontario, Canada in winter, 1994. In total, 253 fungal taxa were identified. The taxa observed were consistent with other published reports on the fungal flora of household dust and indoor air. Taxa observed in the present study followed a Raunkiaer-type distribution, where several species accounted for the majority of observations (abundance), and the greater proportion of species documented were observed only rarely. A calculation of sampling efficiency according to Good's Hypothesis suggested high overall sampling efficiency, averaging over 92 % of the total expected biodiversity. Association analysis based on two-way chi-square contingency resolved a number of species assemblages. These assemblages were primarily correlated to ecological specialization. The three main ecological categories that characterized the main assemblages comprised **1)** phylloplane fungi; **2)** soil fungi and **3)** food spoilage/ xerophilic fungi. A number of smaller assemblages contained species known to be active contaminants of water damaged building materials.

### **INTRODUCTION**

It has long been hypothesized that indoor dusts possess allergenic properties (Lucretius, 50 BC). However, the importance of fungal materials as dust-borne allergens, was not demonstrated with fair certainty until early in the 20<sup>th</sup> century (Flood, 1931; Hopkins et al., 1930). Recently, however, there have been efforts to study household dust as an ecosystem, in an attempt to determine the characteristics of dust-borne fungi that facilitated their diversification into this relatively new habitat (Davies, 1960; Bronswijk, 1981; Bronswijk et al., 1986; Swaebly and

Christensen, 1952; Verhoeff et al., 1994). It is difficult to interpret much of the existing literature in this area for two main reasons: 1) many authors provide only genus-level identifications of fungi, or employ species names that are antiquated or confused; and, 2) the lack of voucher isolates precludes the confirmation of results.

The present study is an examination of the fungal flora of household broodloom dust obtained during the course of a larger research project funded by the Canada Mortgage and Housing Corporation (CMHC) (Ottawa). This project sought to measure various parameters of environmental exposure incurred by housing occupants, and attempted to correlate these findings to objective measures of illness. Within this context, the present study shall (1) determine the numbers and kinds of moulds present in household broodloom dust in a study site in Wallaceburg, and (2) investigate statistical associations between different mould taxa in an attempt to form hypotheses on sources and contamination pathways.

## **MATERIALS AND METHODS**

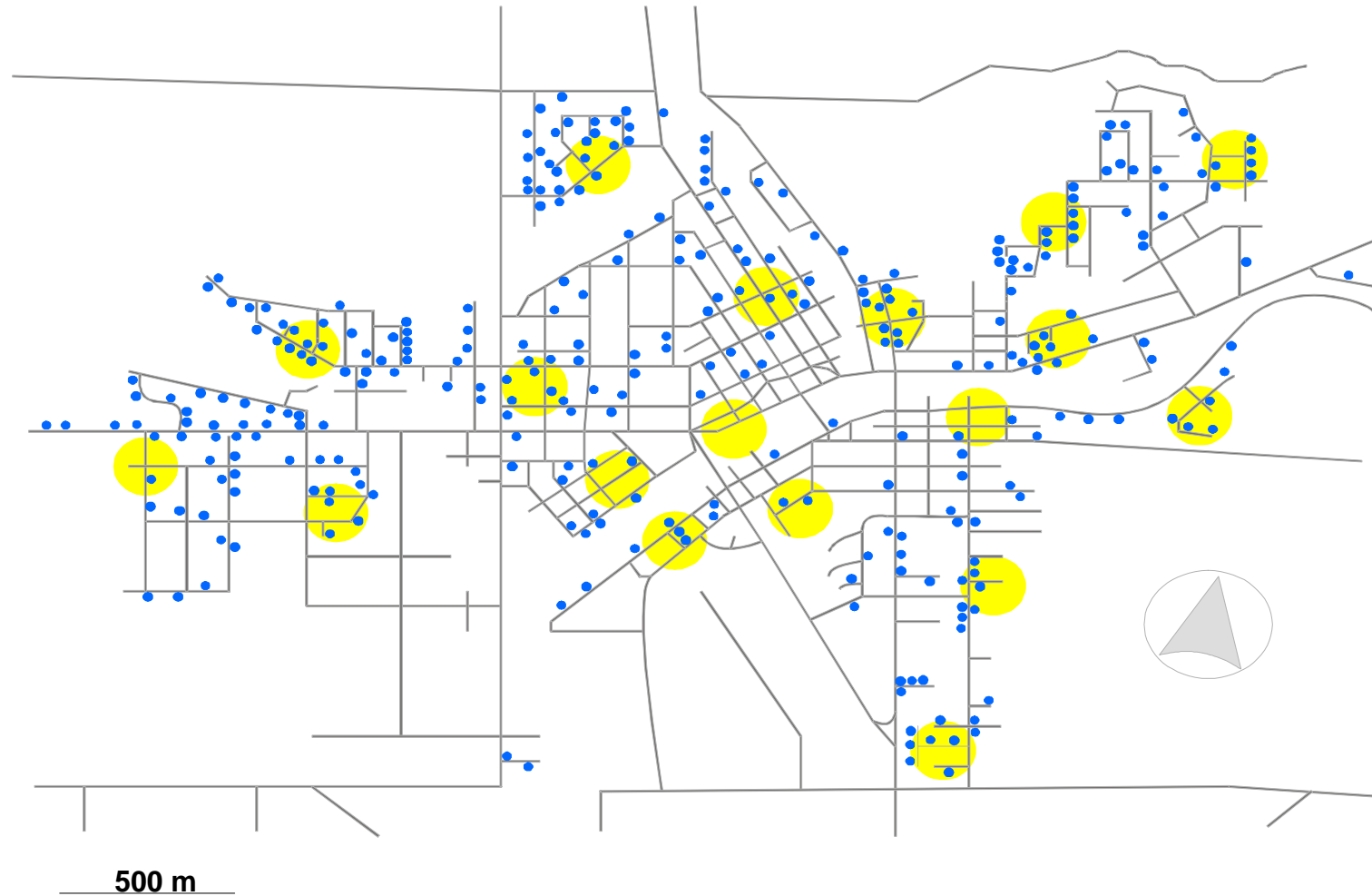
Field work for this study was conducted by a private company under contract to CMHC over a period of five months starting in January, 1994. Initially, 400 households in Wallaceburg, Ontario agreed to participate in Phase I the study (*see* Figure 2-1).

### **COLLECTION OF DUST SAMPLES**

Vacuum cleaner bag samples of carpet dust were collected from 369 houses. Sample coverage is illustrated on the residential street map shown in Figure 2-2. These samples were supplied in sealed, 10 mL polypropylene vials which were stored at room temperature until analysis.



**FIGURE 2-1.** Map of Ontario, Canada, indicating the location of Wallaceburg



**Figure 2-2:** Locations of urban houses sampled (small blue dots). Locations of air samples taken during late summer, 1995 using the RCS sampler (each sample tested 80,000 cc of air) are indicated by large yellow circles.



### **ANALYSIS OF DUST SAMPLES**

Two subsamples of approximately 50 mg (the actual mass was recorded) were added individually to 10 mL of sterile 2% peptone broth and suspended by vortexing at medium speed. Two serial dilutions of these stock suspensions were made subsequently using an adaptation of the standard technique reviewed by Malloch (1981); the first was made by diluting 1 mL of stock suspension in 9 mL of 2% peptone broth and the second was made by diluting 1 mL of the first serial dilution in 9 mL of 2% peptone broth. Four aliquots of 1 mL each were taken from each of the two sets of dilutions and dispensed individually into polystyrene 100 mm Petri dishes (Fisher). Two Petri plates were set up in this manner for each of the two stock suspensions. Molten sterile Rose Bengal agar (RBA) (Malloch, 1981) and RBA containing 25 % glycerol (RBGA) as an osmoticant. Both media were amended with 60 ppm of chlortetracycline hydrochloride (Sigma), streptomycin sulphate (Sigma) and benzylpenicillin (penicillin-G, Sigma), were cooled to 45 °C and aseptically dispensed each into half of the Petri plate replicates at a volume of 25 mL per plate using a Pour-o-matic Petri plate filling machine (New Brunswick Scientific, New Jersey). The medium was mixed with the dilution aliquot by gently swirling the Petri plates prior to solidification. A schematic of the plating regime is provided in Figure 2-3.

After 12 to 18 hr the plates were removed from the machine, wrapped with Parafilm (Alcan) and inverted in stacks of 20 plates each. The plates were incubated under 12 hr artificial daylight at room temperature (ca. 24 °C) for 7 days. One of the three sets of dilutions averaging between 15 and 60 colonies per plate was selected for identification and enumeration. Except where one of the media used could not be enumerated at the dilution selected (due to excessively high- or low numbers of colonies or contamination) the same dilution set was enumerated for both media. This method was refined by multiple preliminary experiments.

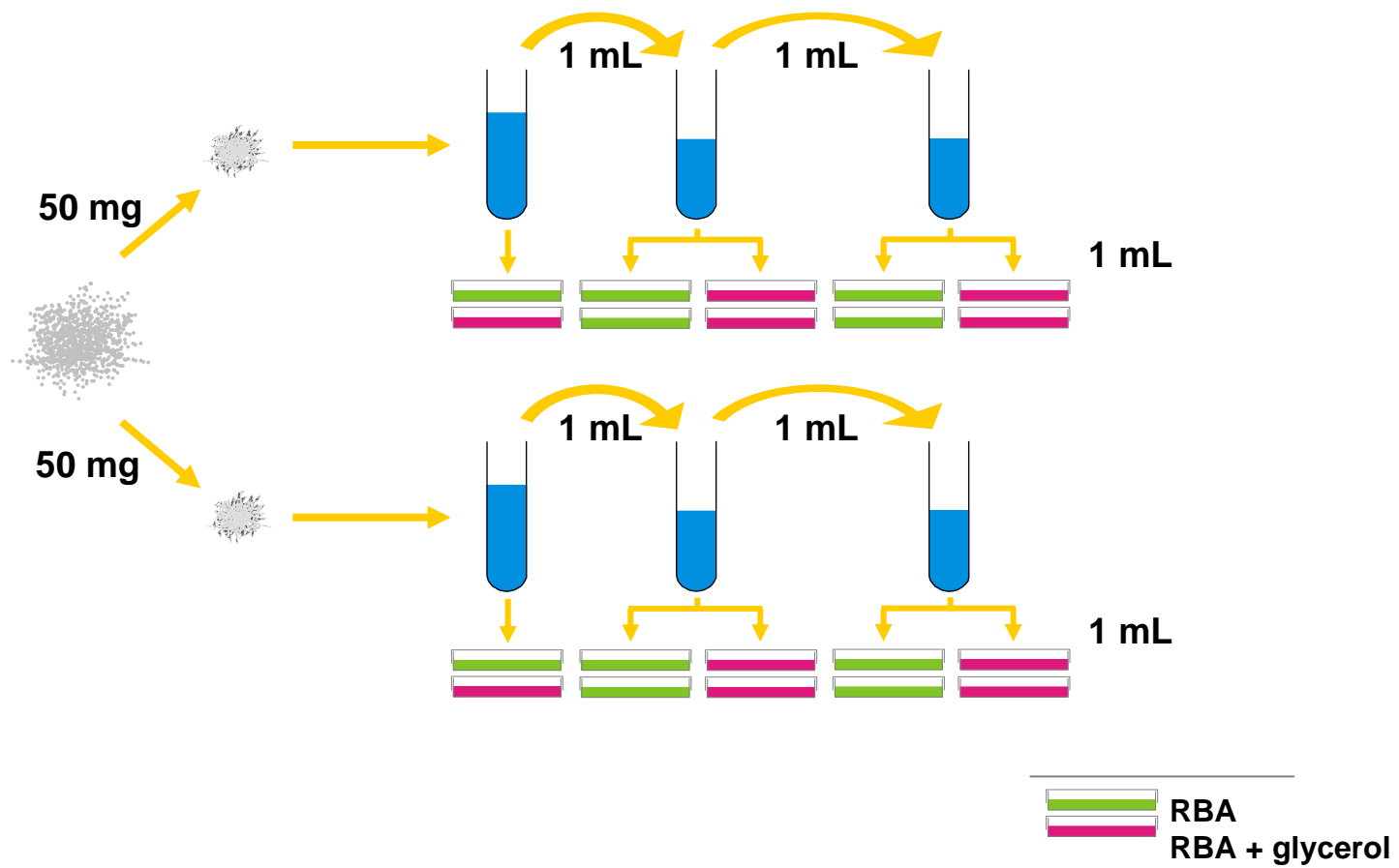


Figure 2-3. Plating regimen for dust samples.

Microscopic mounts were made in either distilled water with Photoflo (Kodak) or lacto-fuchsin (Carmichael, 1955). All culture media and stock solutions were autoclaved for 20 min at 15 psi prior to use. Sterile glass- and plasticware were used for all aseptic procedures.

#### **IDENTIFICATION AND ISOLATION OF CULTURES**

Where possible, fungi were identified to the genus level directly from colonies on the Rose Bengal isolation media using well-established techniques of macroscopic and microscopic examination and standard reference works for the identification of moulds (e.g. Arx, 1970; Barnett and Hunter, 1986; Barron, 1968; Carmichael et al., 1980; Domsch et al. 1980; Ellis, 1971, 1976; Hanlin, 1990; Malloch, 1981). Many isolates were further identified to species level using appropriate monographs.

Species of *Penicillium* were grouped according to macroscopic and microscopic similarity, averaging five groups per house. Representatives of each of the groups with similar penicillia were subcultured on four diagnostic media for further identification using a central-point inoculation technique modified from Pitt (1979). The Petri plates were wrapped with Parafilm, and incubated inverted under 12 hr artificial daylight at room temperature for 7 to 14 days prior to examination. The following media were employed in the identification of cultures of *Penicillium* to species level: Czapek's yeast-autolysate agar (CYA) (Pitt, 1979), Creatine sucrose agar (CREA) (as modified by Frisvad, 1985), 25% Glycerol-nitrate agar (G25N) (Pitt, 1979) and Modified Leonian's agar (MLA) (Malloch, 1981). Multiple unique isolates of *Penicillium* spp. were retained for subsequent use. Cultures were identified according to colonial and microscopic morphologies produced on these media and compared to the species descriptions given by Pitt (1980, 1988). Other fungi that could not be identified directly on RBA and RBGA plates were

subcultured on a range of other growth media (including CYA, MLA, 2% water agar, Weitzman-Silva Hutner's agar and Sabouraud's glucose agar (Malloch, 1981)) and incubated in a manner similar to that used for the species identification of *Penicillium* cultures.

### **RELIABILITY OF IDENTIFICATIONS**

This study involved the examination and identification of over 200,000 individual fungal colonies. Over half of these identifications were performed by the author; the balance were carried out by B.M. Koster, D. Malloch and L.J. Hutchison in addition to several contracted student assistants (*see* Acknowledgements, p. iv). Discussions between the author and other project workers during the plating/ isolation phase suggested that the rate of misidentifications was relatively low, and typically restricted to rare or difficult taxa (e.g. *Penicillium aurantiogriseum* group). This speculation has been supported by retrospective examination of many retained cultures. For the purposes of the analyses presented in this chapter, all identifications were accepted as accurate and comparable; however, the reader is cautioned that the reliability of identifications may vary to some extent according to the skill of the investigator and the condition of the particular isolate examined.

### **STORAGE OF CULTURES**

Each representative isolate of *Penicillium* was subcultured in duplicate into 2 mL screw cap (with rubber "O"-ring) flat-bottom microcentrifuge (microculture) tubes (Sarstedt) containing 1 mL per tube of 2 % MLA. Additional representatives of *Penicillium* and other genera were subcultured in a similar manner pending future need. The tubes were capped and incubated under 12 hr artificial daylight at room temperature for 7 to 10 days prior to transfer to 5 °C for short-term storage. Cultures requiring long-term preservation (e.g. for use in fingerprinting)

were subcultured subsequently and checked for purity. Axenic cultures were subcultured in triplicate in microculture tubes and incubated as outlined above. After colonies had grown out, cultures were aseptically overlaid with 1 mL sterile 20 % glycerol combined with 17 % skim milk as a cryoprotectant and stored at -70 °C (McGinnis and Pasarell, 1992).

#### **ORGANIZATION AND ANALYSIS OF DATA**

Data were compiled using the Borland Paradox database (ver. 3.0, Borland Corp.). The database consisted of one record for each occurrence of a species on each plate examined (for both RBA and RBGA). Each record comprised 6 fields: House number; Plate identifier; Species name; Number of colonies counted; Mass of dust used in subsample (mg); and, Total number of plates of each medium (RBA or RBGA) that were examined for that house. Subsequent manipulations of the data including statistical analyses were carried out by means of specific software routines programmed and compiled by the author using QuickBasic (ver. 4.5, Microsoft Corp.).

An index of sampling efficiency ( $I$ ) was calculated using Good's Hypothesis as modified by Moore and Holdeman (Good, 1953; Moore and Holdeman, 1974), such that;

$$I = (1 - N_1/N_T) \times 100 \quad (1)$$

where,

$$\begin{aligned} N_1 &= \text{number of species observed once} \\ N_T &= \text{total number of observations of all species} \end{aligned}$$

Presence-absence (occurrence) data for taxa present in 2 % or more of samples were analysed using chi-square association analysis with Yate's correction factor for small datasets (Greig-Smith, 1964; Kent and Coker, 1992), such that:

$$\chi^2 = \frac{n(ad-bc-n/2)^2}{(a+b) \cdot (c+d) \cdot (a+c) \cdot (b+d)} \quad (2)$$

where,

- a* = observed number of relevés containing “a & b”
- b* = observed number of relevés containing “a” only
- c* = observed number of relevés containing “b” only
- d* = observed number of relevés lacking “a & b”
- n* = total number of relevés examined

The relative degree of association was summarized graphically for all combinations of taxa involved in one or more significant associations based on negative inverse logarithms of chi-square values. These values were compiled into an artificial “distance matrix” in which closely-associated pairs of taxa had smaller interposing distances relative to those with lesser associations, which were separated by greater distance. A cluster analysis of this matrix was conducted using the UPGMA method in the PAUP\* software package (PAUP\* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts). It is acknowledged that as test statistics, chi-square values calculated from pair-wise contingency of nominal data such as those in the present study represent multiple non-independent comparisons, and thus should not properly be analysed in un-corrected combination. It is important to note, however, that the use of chi-square values in the present application is solely a measure of the degree of association and not an assessment of the statistical significance of correlation (*see* Causton, 1988). Following UPGMA cluster analysis, terminal clusters of three or more closely-associated taxa were pruned from the dendrogram and re-examined graphically as 2-way matrices upon which the level of significance and polarity of association of individual chi-square statistics were encoded.

## RESULTS

### SPECIES DIVERSITY AND DISTRIBUTION

Two hundred and fifty-three fungal taxa were isolated from the 369 dust samples analysed. The proportion of house dust samples containing each taxon are summarized in Figure 2-4. A complete list of abbreviations used is given in the front matter. The distribution of fungal taxa in the study site was of a Raunkiaer-type, whereby species were distributed unevenly in abundance. In this model, most species were observed only rarely, and the majority of individuals in the population comprised relatively few species (Daubenmire, 1968; Raunkiaer, 1934).

Thirty-three taxa were observed in 10 % or more of samples; six of these taxa, *Alternaria alternata*, *Aureobasidium pullulans*, *Eurotium herbariorum*, *Epicoccum nigrum*, *Aspergillus versicolor* and *Penicillium chrysogenum* were present in 50 % or more of the samples analysed. Forty-three taxa were observed in 2 to 10 % of samples, while an additional 177 taxa were present in fewer than 2 % of samples. Interestingly, unidentified yeasts were observed in 85 % of samples analysed while the most commonly encountered filamentous fungus, *Alternaria alternata*, was observed in 89 % of samples. The most commonly occurring species of *Penicillium* were: *P. chrysogenum* (52 % of samples), *P. spinulosum* (39 %), *P. corylophilum* (29 %), *P. commune* (26 %) and *P. brevicompactum* (23 %). Most taxa observed were anamorphic species; however, a few sexual species were encountered (e.g. *Eurotium herbariorum*, *Sordaria* spp., and *Eupenicillium ochrosalmonium*).

### EFFICIENCY OF SAMPLING

According to Moore and Holdeman's modification of Good's hypothesis (Good, 1953; Moore and Holdeman, 1974), the species that were observed comprised, on average, 92.1 % (8.8 %,

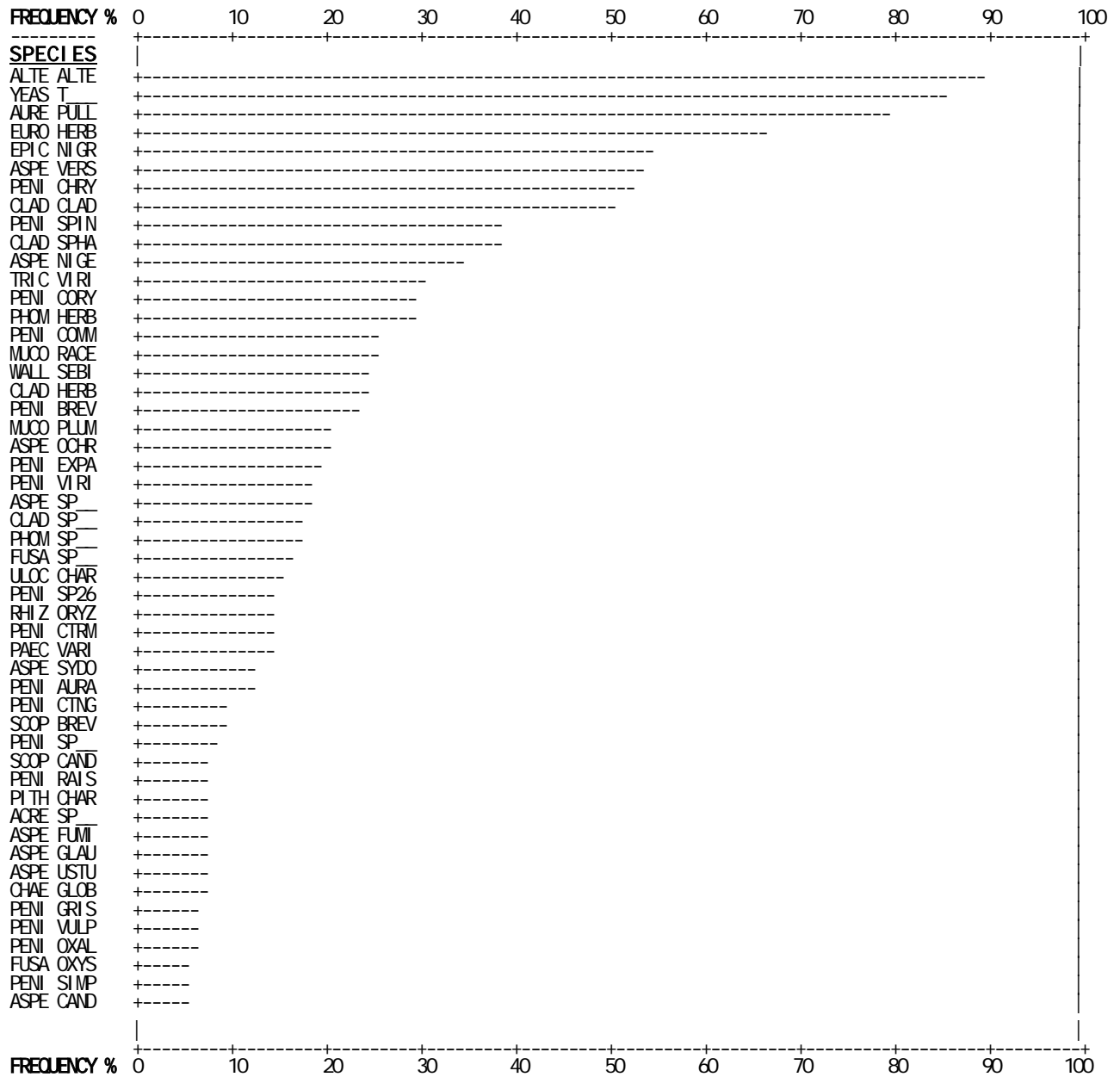


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.



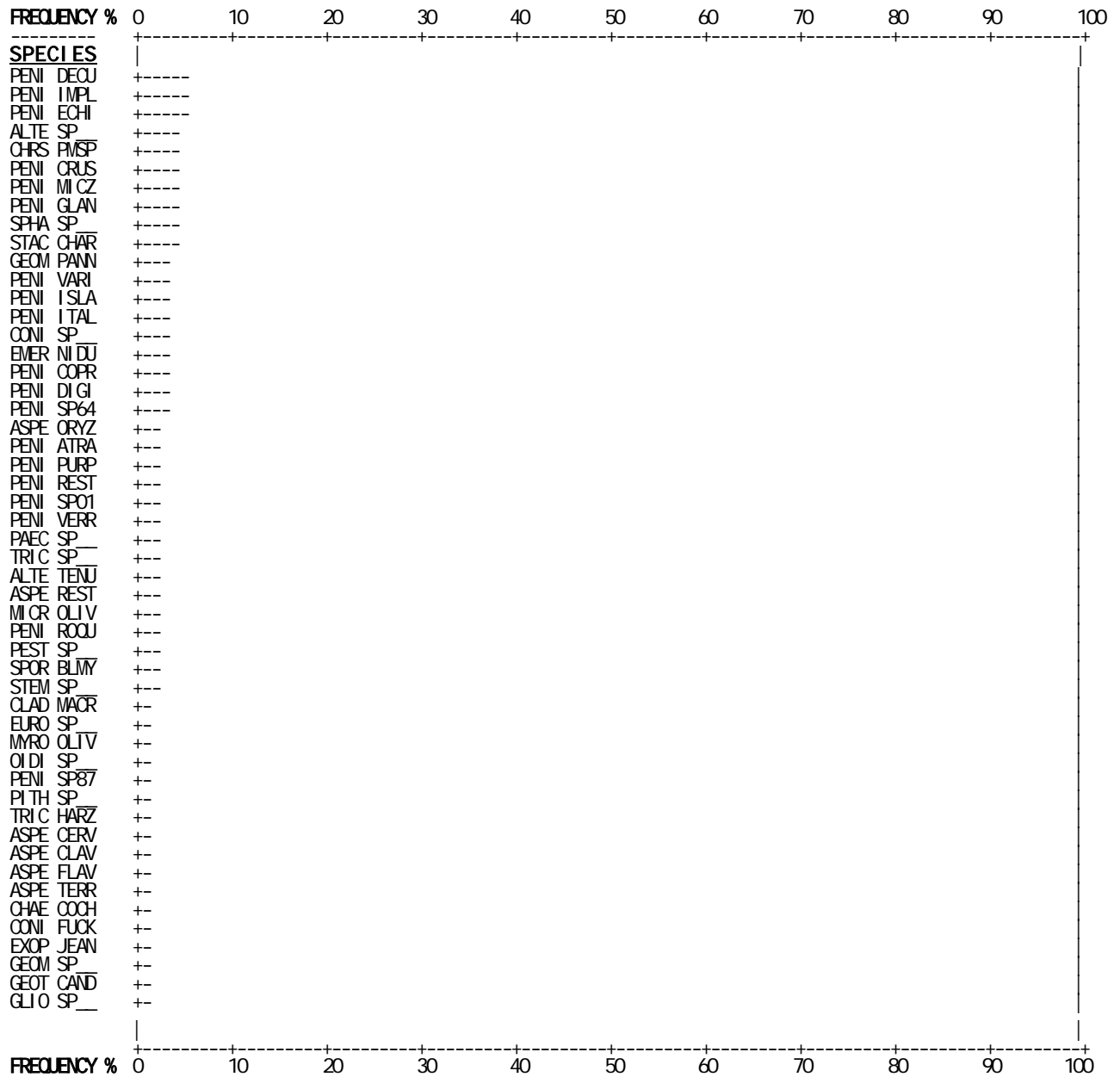


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

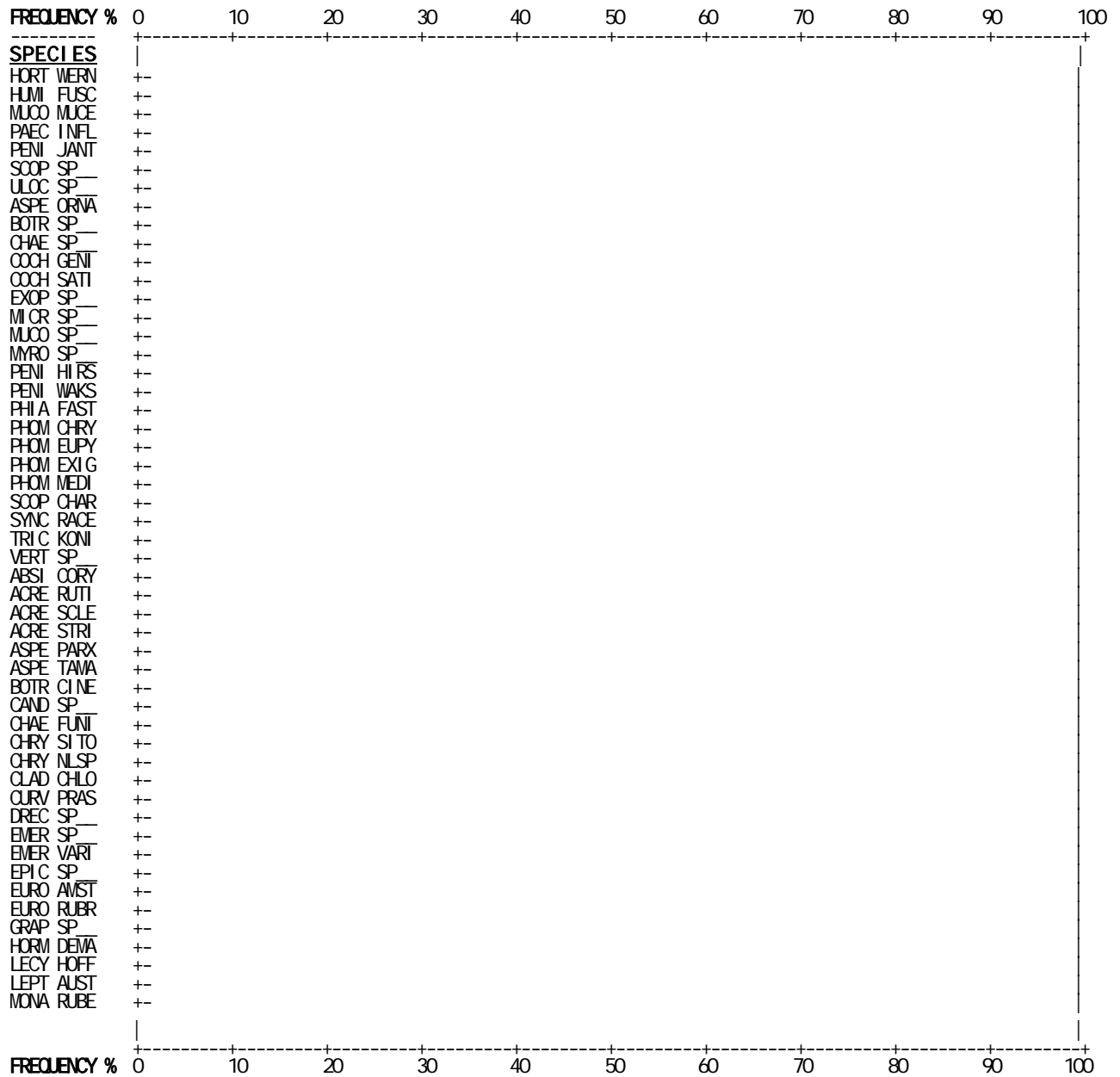


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

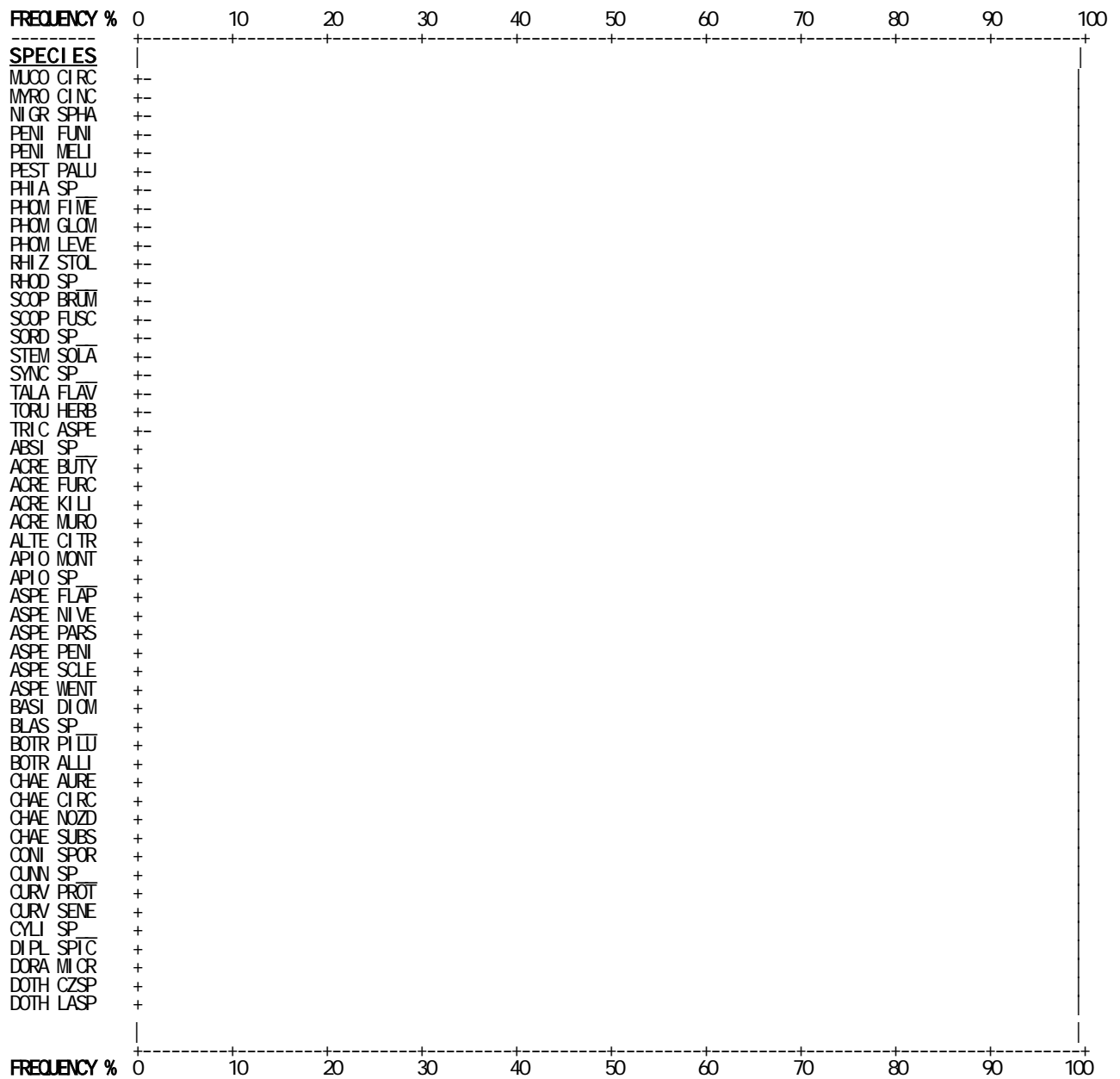


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

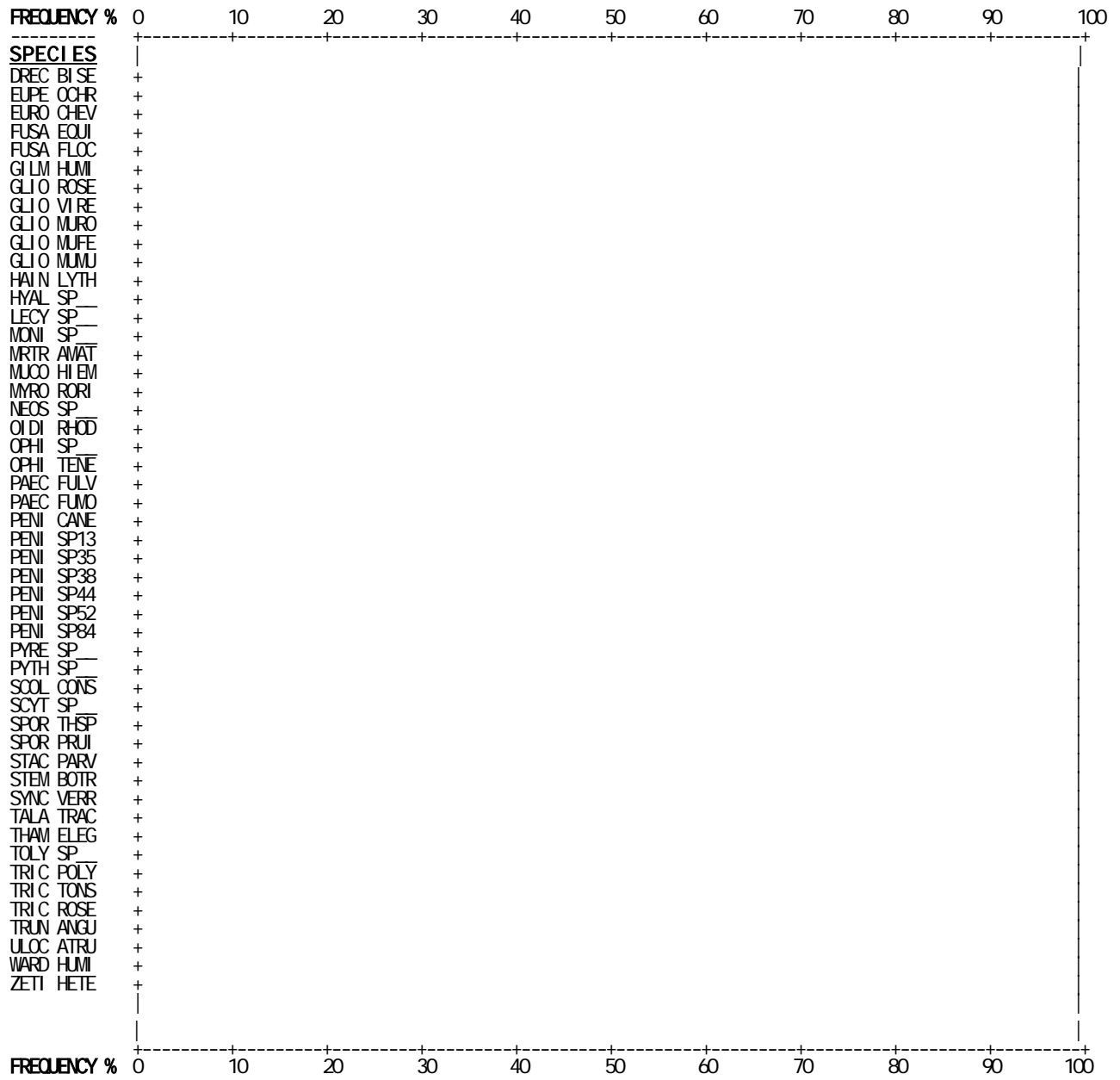


FIGURE 2-4. Frequency of dustborne fungi observed in broadloom dust samples from Wallaceburg, Ontario.

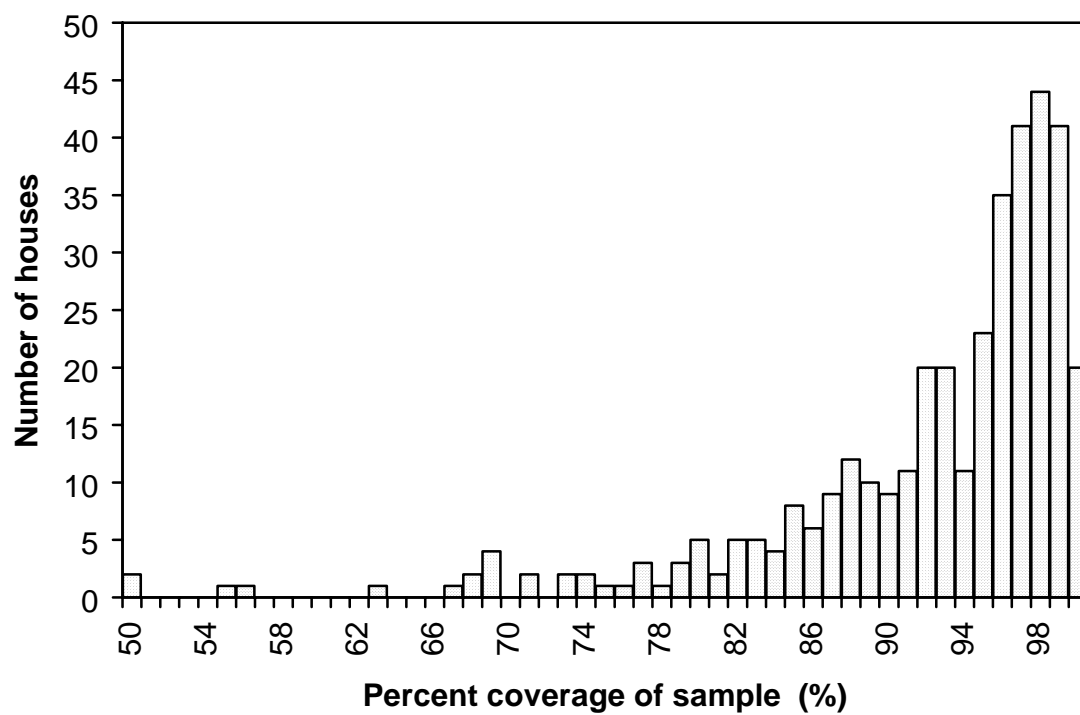
SD) of the total expected biodiversity in the study site. This result, in combination with the Raunkiaer-type distribution of taxa within the sample set, suggests that an increase in the number of sample sites would have only contributed to an increase in the number of rare species observed (*see* Figure 2-5).

### **SPECIES ABUNDANCE**

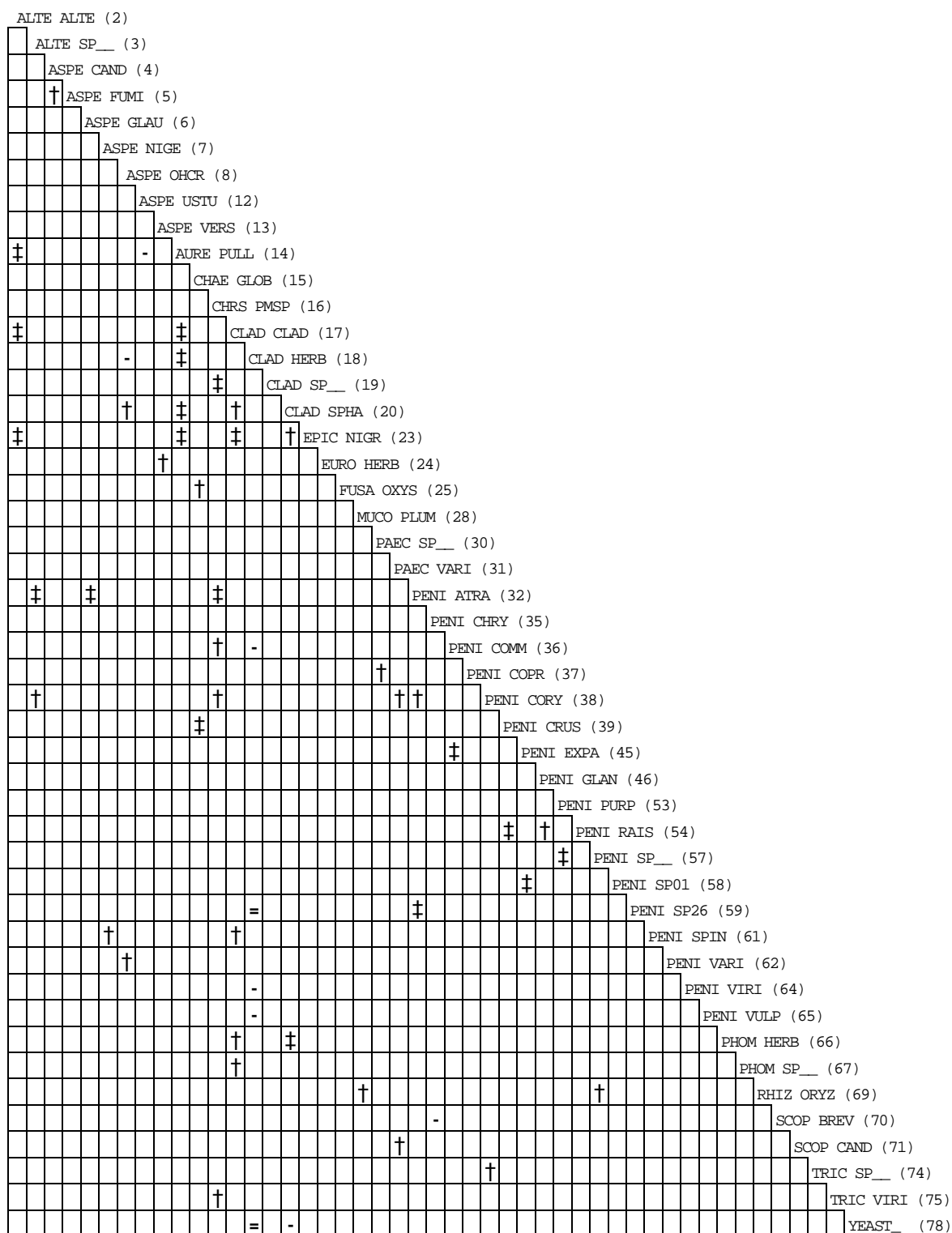
The calculated abundance data (not presented here) showed numbers of colony-forming units (CFUs) per gram of dust that ranged, on average, from 2 to 10 CFUs/mg; but, species abundance occasionally was observed as high as 500 CFUs/mg. Generally, yeasts and yeast-like fungi (e.g. *Aureobasidium pullulans*) tended to occur at greater abundances than strictly filamentous species. Due to the relatively low number of replications per sample (i.e. the number of plates examined) which varied from 4 to 8, the standard deviations of average species abundances tended to be excessive, often in excess of calculated means. For this reason, excessive outlying data would not permit trends of species associations to be resolved using canonical correspondence analysis (Braak, 1992). Species that occurred at a low frequency (i.e. in fewer than 2 % of samples) tended to skew the chi-statistic artifactually towards significance. For this reason, rare species were eliminated from this analysis. The results of significant chi-square associations are shown in trellis-diagram format in Figure 2-6. The 52 pairings of species represent the significant associations ( $\alpha = .05$ ,  $df = 1$ ) that resulted from the inspection of 3,003 pairings (*see* Appendix B). The first 21 couplets were highly significant ( $\alpha=.001$ , *see* Appendix B).

### **ASSOCIATION ANALYSIS**

The 52 associations of significance involved forty-seven taxa (including a category of unidentified yeasts); forty-three of these associations were positive correlations while the



**FIGURE 2-5.** Sampling efficiency for house dust mycoflora as estimated based on Good's Hypothesis.



**LEGEND:** Positive association significant at  $\alpha = .05$  (†) and  $\alpha = .001$  (‡)  
 Negative association significant at  $\alpha = .05$  (-) and  $\alpha = .001$  (=)

**FIGURE 2-6.** Treillis diagram summarizing significant associations of dustborne taxa. Positive associations are indicated by † ( $\alpha=0.05$ ) ‡ ( $\alpha=0.001$ ). Negative associations are indicated by - ( $\alpha=0.05$ ) and = ( $\alpha=0.001$ ).

remainder (9) were negatively associated. Interestingly, *Cladosporium herbarum* was a partner in two thirds of the negative associations.

The results of this association analysis are presented as a dendrogram based on average distance by an inverse logarithmic transformation of the  $\chi^2$  value. Overall, 14 clusters of more than two taxa were observed (see Figure 2-7). These terminal clusters of 3 or more taxa are shown in Figure 2-8, and their polarity is indicated. Each terminal branch is shown as a matrix, in which the positive or negative nature of the correlation is shown by a shaded circle at each node. Following is a summary of these terminal clusters:

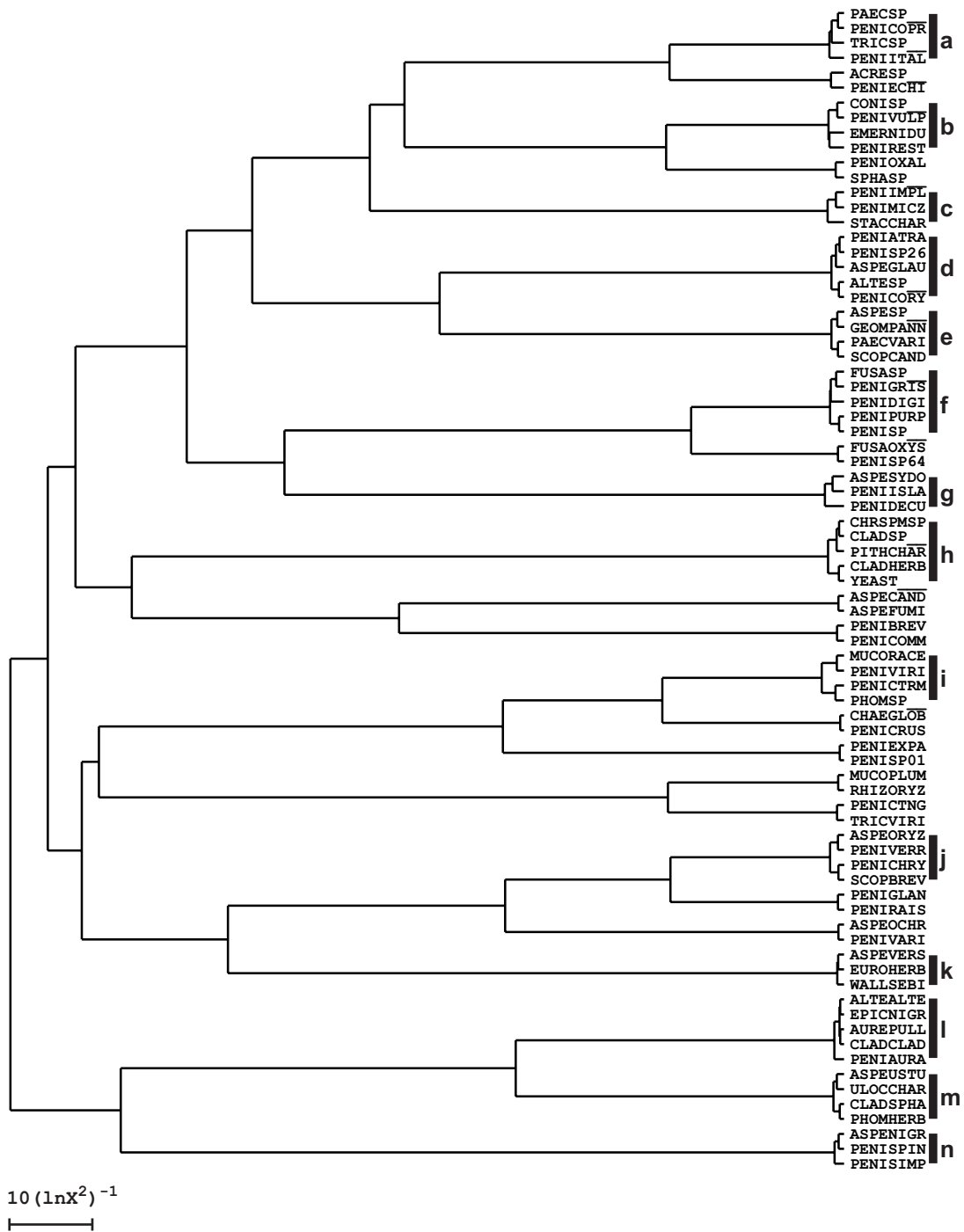
**Cluster a)** An unidentified species of *Paecilomyces* was positively correlated to *Penicillium coprophilum* (see Figure 2-8a). This pair was negatively correlated to *Trichoderma* sp. and *Penicillium italicum* (the latter pair also showed a negative correlation).

**Cluster b)** A similar arrangement was observed in Figure 2-8 cluster b, in which *Coniothyrium* sp. was positively correlated to *Penicillium vulpinum* yet this pair showed negative correlation to *Emericella nidulans* and *Penicillium restrictum* (the latter two also showed negative correlation).

**Cluster c)** *Stachybotrys chartarum* was negatively correlated to the positively-associated pair *Penicillium implicatum* and *Penicillium miczynskii* (see Figure 2-8c).

**Cluster d)** Cluster d (Figure 2-8d) showed positive associations between *Penicillium atramentosum*, *Penicillium* sp. #26, *Aspergillus glaucus*, *Alternaria* sp. and *Penicillium corylophilum*. Within this





**FIGURE 2-7.** Cluster analysis based on associations between dustborne fungi determine by pair-wise Chi-square contingency.

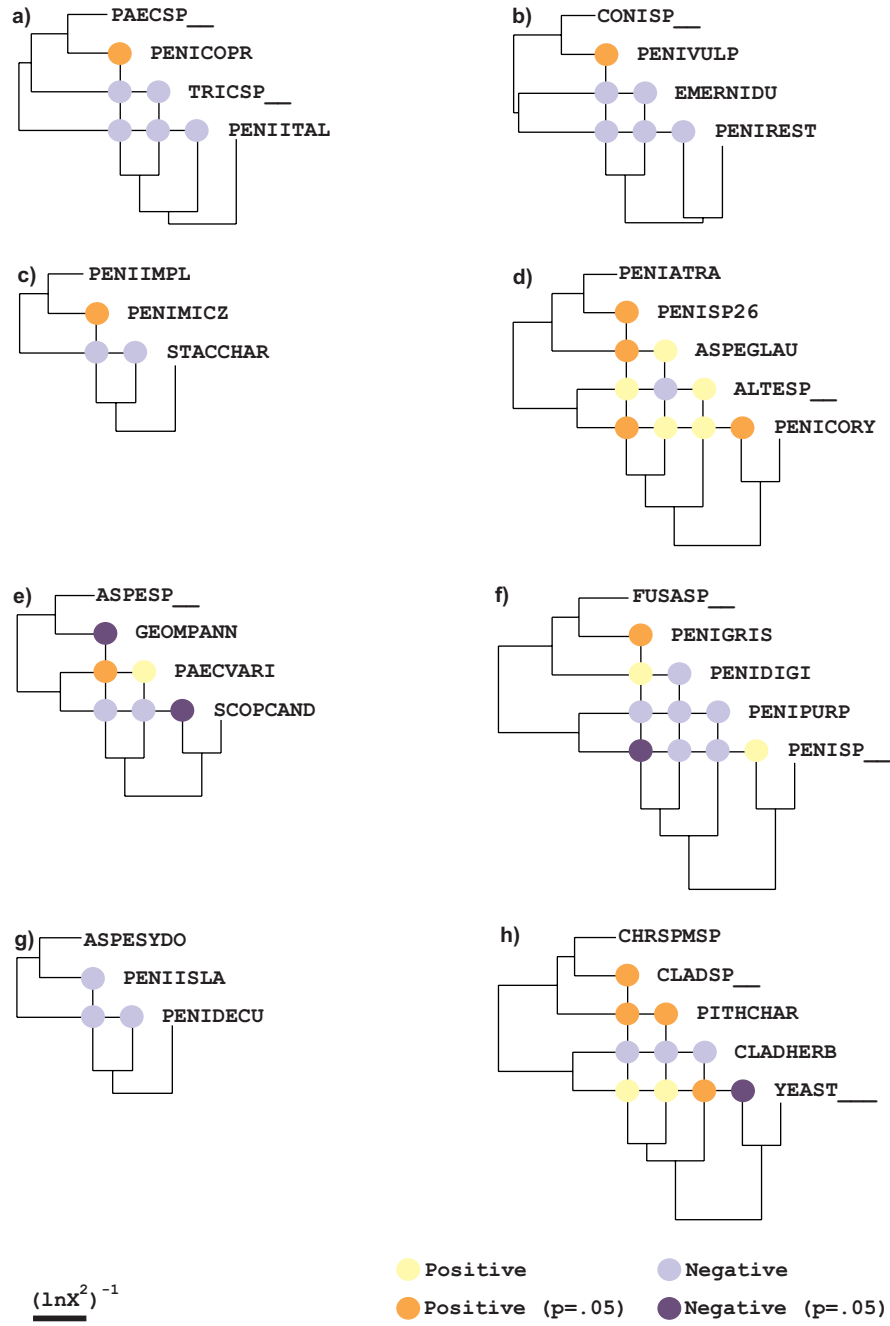


FIGURE 2-8. Significant associations between taxa in significant clusters (> 2 taxa).

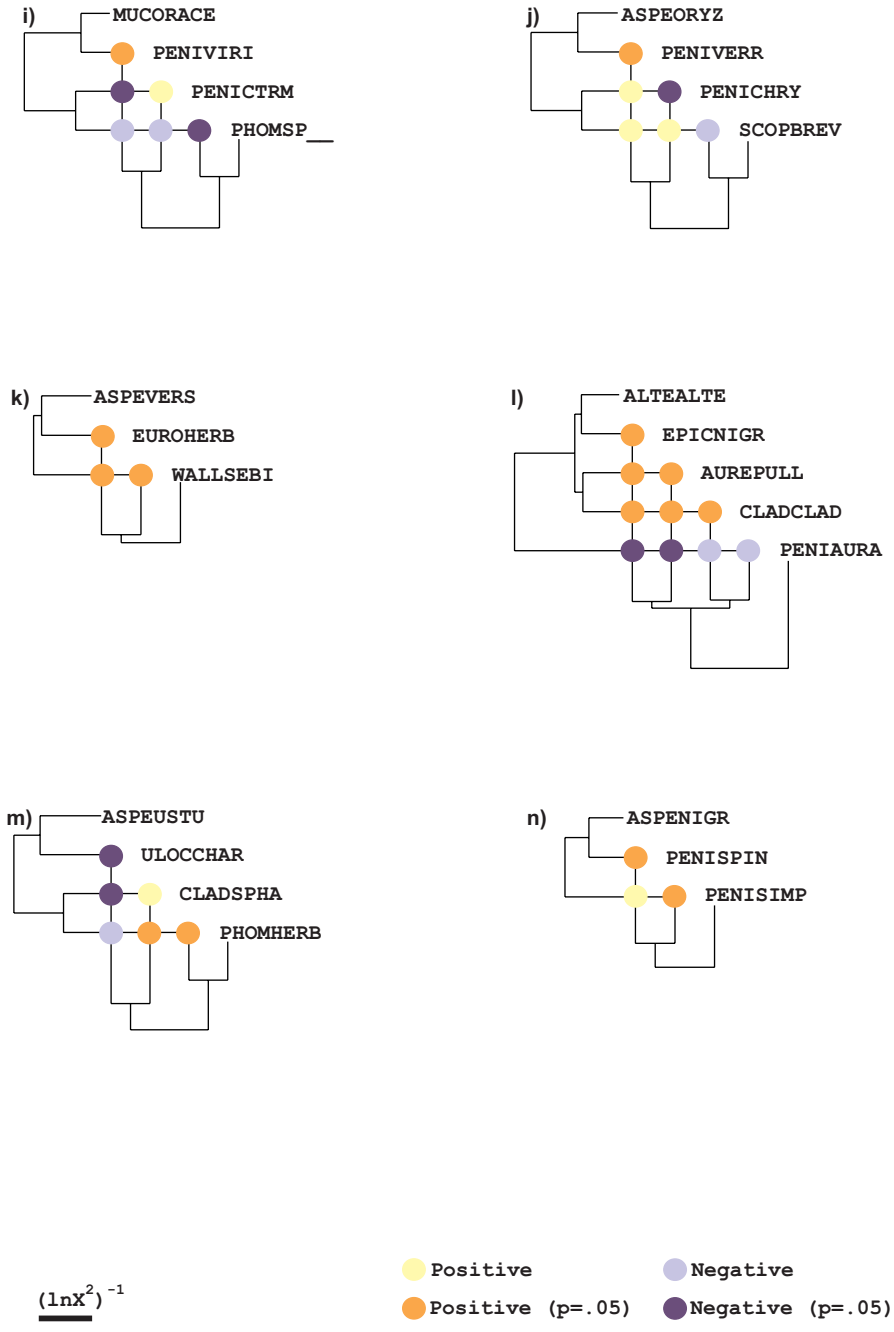


FIGURE 2-8 (cont'd). Significant associations between taxa in significant clusters (> 2 taxa).

assemblage, however, a negative association was observed between *Alternaria* sp. and *Penicillium* sp. #26.

**Cluster e)** *Geomyces pannorus* was positively associated with *Paecilomyces variotii* (see Figure 2-8e). An unidentified species of *Aspergillus* showed a negative correlation to the former, and a positive correlation to the latter. Collectively, this group was negatively associated with *Scopulariopsis candida*.

**Cluster f)** *Fusarium* sp. in cluster f (Figure 2-8f) was positively allied with *Penicillium griseofulvum* and *Penicillium digitatum* (the latter two were negatively associated). This group was negatively associated with the positively correlated pair of *Penicillium purpurogenum* and an un-named *Penicillium* species.

**Cluster g)** The species negatively-associated assemblage in cluster g (Figure 2-8g) comprised *Aspergillus sydowii*, *Penicillium islandicum* and *Penicillium decumbens*.

**Cluster h)** The three taxa *Chrysosporium* sp., *Cladosporium* sp., *Pithomyces chartarum* and uncategorized yeast were positively associated in cluster h (Figure 2-8h). This group was negatively correlated to *Cladosporium herbarum*.

**Cluster i)** *Mucor racemosus* was positively correlated with *Penicillium viridicatum*, which was further positively correlated to *Penicillium citrinum* (see Figure 2-8i). However, *Penicillium citrinum* showed a strongly negative correlation to *Mucor racemosus*. As well, an unidentified species of *Phoma* showed negative correlations to all taxa in this cluster (Figure 2-8i).

**Cluster j)** *Penicillium chrysogenum* was negatively correlated with *Penicillium brevicompactum*, yet these two taxa were positively correlated with *Aspergillus oryzae* (see Figure 2-8j). Within this assemblage, *Penicillium verrucosum* showed a positive association with *Aspergillus oryzae* and *Penicillium brevicompactum* and a strongly negative association with *Penicillium chrysogenum*.

**Cluster k)** The xerophilic fungi *Aspergillus versicolor*, *Eurotium herbariorum* and *Wallemia sebi* formed a positively correlated assemblage (see Figure 2-8k).

**Cluster l)** There were positive associations between the typical phylloplane fungi, *A. alternata*, *Aureobasidium pullulans*, *C. cladosporioides*, and *Epicoccum nigrum* (see Figure 2-8l). This assemblage tended to be negatively associated with *Penicillium aurantiogriseum*.

**Cluster m)** The phylloplane taxon *Ulocladium chartarum* was positively associated with *Cladosporium sphaerospermum* and *Phoma herbarum*. This assemblage was collectively negatively associated with the xerophilic fungus *Aspergillus ustus* (see Figure 2-8m).

**Cluster n)** Similar to Cluster k (*As. versicolor*, *Eu. herbariorum* and *W. sebi*), *Aspergillus niger* was positively associated with *Penicillium spinulosum* and *Penicillium simplicissimum* (see Figure 2-8n).

The remaining couplet assemblages are summarized in Table 2-1. Ten of these associations were positive and one was negative (*Acremonium* sp. with *Penicillium echinulatum*). Of the positive associations, several are of interest. In particular, the soil fungi *Aspergillus candidus* and *Aspergillus fumigatus* were associated. *Aspergillus ochraceus* was positively associated with *Penicillium variabile*.

Both of these taxa are common indoor contaminants on damp building materials (Adan and

**Table 2-1:** Couplets of associated dustborne taxa

<b>Polarity</b>	<b>Taxon #1</b>	<b>Taxon #2</b>	<b>p-value</b>
Positive	<i>Aspergillus candidus</i>	<i>Aspergillus fumigatus</i>	0.003
	<i>Aspergillus ochraceus</i>	<i>Penicillium variable</i>	0.002
	<i>Chaetomium globosum</i>	<i>Penicillium crustosum</i>	< 0.001
	<i>Fusarium oxysporum</i>	<i>Penicillium</i> sp. #64	0.006
	<i>Mucor plumbeus</i>	<i>Rhizopus oryzae</i>	0.003
	<i>Penicillium brevicompactum</i>	<i>Penicillium commune</i>	0.015
	<i>Penicillium citreonigrum</i>	<i>Trichoderma viride</i>	0.014
	<i>Penicillium expansum</i>	<i>Penicillium</i> sp. #1	< 0.001
	<i>Penicillium glandicola</i>	<i>Penicillium raistrickii</i>	0.004
	<i>Sphaeropsis</i> sp.	0.032	
Negative	<i>Acremonium</i> sp.	<i>Penicillium echinulatum</i>	0.103

Samson, 1994). Similarly, *Chaetomium globosum* showed an association with *Penicillium crustosum*. These taxa are common colonists of very wet gypsum wall board. *Mucor plumbeus* was correlated with *Rhizopus oryzae*. Both of these taxa are rapid colonists of substrates under high disturbance, particularly in the presence of simple carbohydrates (e.g. such as decaying fruits) (Samson and Reenen-Hoekstra, 1988). *Penicillium brevicompactum* showed a positive association with *Penicillium commune*. These *Penicillia* occur frequently on indoor finishes, particularly wall paper or drywall which incurs intermittent wetting. The soil fungi *Penicillium citreonigrum* and *Trichoderma viride* were positively associated. For comparative purposes, the houses which were observed to have active mould growth on indoor surfaces are summarized in Table 2-2.

## DISCUSSION

The most commonly occurring species found in the present study are consistent with reports on the species composition of household dust by other authors (Bronswijk, 1981; Calvo et al., 1982; Davies, 1960; Gravesen, 1978; Hamada and Yamada, 1991; Ishii et al., 1979; Lustgraaf and Bronswijk, 1977; Mallea et al., 1982; Saad and El-Gindy, 1990; Schober, 1991; Swaebly and Christensen, 1952; Wickman et al., 1992). The species assemblages of dust microfungi observed in this study comprised a mixture of ecologically homogeneous groups:

- 1) Phylloplane (leaf surface) moulds (e.g. *Alternaria alternata*, *Aureobasidium pullulans*, *Cladosporium cladosporioides* and *Epicoccum nigrum*), all of which were negatively correlated to *Penicillium aurantiogriseum*, a typical xerophilic food spoilage fungus.
- 2) Xerophilic moulds typically associated with food spoilage such as *Aspergillus versicolor* group, *Eurotium herbariorum* and *Wallemia sebi* (see Pitt and Hocking, 1985; Samson and Reenen-Hoekstra, 1988)

**Table 2-2:** Houses with visible mould growth observed

House Number	Number of isolates recovered	
	<i>P. brevicompactum</i>	<i>P. chrysogenum</i>
10		
24		
28		
30		
31		
<b>34</b>		2
43		
<b>45</b>	2	5
<b>48</b>		5
55		
86		
96		
<b>100</b>	1	
<b>102</b>		1
<b>111</b>		1
115		
117		
122		
<b>132</b>	2	1
134		
<b>136</b>	1	
150		
<b>154</b>		2
157		
167		
<b>177</b>		3
190		
197		
<b>201</b>	1	
<b>206</b>		1
<b>216</b>		1
235		
<b>247</b>		1
250		
<b>276</b>		1
332		
377		
395		
396		



- 3) Soilborne fungi such as *Trichoderma viride* and *Penicillium citreonigrum* (see Barron, 1968; Domsch et al., 1980). The existence of these distinct species assemblages was corroborated by chi-square association analysis.

Besides the groups with obvious ecological similarity, several species assemblages were noted that contained taxa notable as contaminants of water-damaged building materials or finishes (e.g. *Aspergillus versicolor*, *As. ustus*, *Chaetomium globosum*, *Penicillium aurantiogriseum*, *Pe. brevicompactum*, *Pe. chrysogenum* and *Stachybotrys chartarum*). Often these taxa (e.g. *As. ustus*, *Pe. aurantiogriseum*, etc.) were negatively correlated to clusters of taxa from defined ecological groups discussed above. It is likely that these taxa are true household residents, as agents of structural contamination or growing in dust following episodic wetting.

The results of this study showed disproportionately high viable levels of small-spored fungi, such as *Aspergillus* or *Penicillium* (data presented in Appendix A). This observation is consistent with those of other workers (e.g. Flannigan and Miller, 1994), who have suggested that additional factors besides proliferation *in situ* may lead to accumulation of these spores in dust in homes absent of indicators of mould problems (e.g. in good repair, clean and free from water damage) and objective measurements demonstrate a high standard of IAQ (Flannigan and Miller, 1994; Scott et al., 1999a). Scott and co-workers (1999a) postulated that dilute levels of spores of these taxa from outdoors might enter houses passively and accumulate in dust, either because of differentially long viability period of spores of these species or through mechanical means. The large component of phylloplane fungi in house dust suggests that, although these fungi may in some cases become resident in homes, their collective occurrence in dust is a function of their abundance in outdoor air; thus, in house dust, the accumulation of propagules of these fungi

likely results from the settling of spores from ambient air. The fact that many small spored taxa are often well-represented in carpet dust may relate to the tendency of these spore types to be produced by phialidic species, many of which produce spores prolifically on compound conidiophores with the number of spores per conidiophore greatly in excess of many common, non-phialidic phylloplane moulds (e.g. *Alternaria*, *Cladosporium*). Differences in viability over time between these two spore types may also be important. For instance, the relatively thick-walled nature of these typically phylloplane spores intuitively suggests an adaptation to increased spore viability; however, Sussman (1968) documented the disproportionate longevity of small, thin-walled globose spores such as *Aspergillus* and *Penicillium*, relative to larger, thicker walled spores of phylloplane moulds. Despite the lack of input of xerophilic species into the indoor environment from outdoors during winter months while windows remain closed to conserve heat, a stable reservoir of propagules of phylloplane moulds remains in the biological "memory" of the carpet. Flannigan and Miller (1994) recognized the longevity of *Aspergillus* and *Penicillium* spores in household dust, and suggested that this property may permit the use of dust as a long-term spore trap which, by analysis, could reveal transient bursts of airborne spores of these taxa over time. However, Verhoeff and co-workers (1994) found only a weak correlation between houses that had objectively demonstrable mould problems and a substantial change in the dust mycoflora, suggesting that dust analysis may not be a reliable predictor of indoor contamination.

The viability of the mycoflora was followed over three years for dust samples from selected Wallaceburg stored under dry conditions. Fifteen dust samples (indicated in bold in Table 2-2) in follow-up testing showed the complete dying off of all taxa except *Aureobasidium pullulans* and *Penicillium* spp. These results confirmed the observation of Sussman (1968) that spores of species of *Aspergillus* and *Penicillium* remain viable for a much longer period of time compared to

most phylloplane fungi under our storage conditions (e.g. *Alternaria*, *Cladosporium*, *Epicoccum* and *Ulocladium* and support the hypothesis that the culture-presence of high numbers of *Aspergillus* and *Penicillium* relative to phylloplane taxa from household dust may be an artifact of the longer period of spore viability of the former group. Davies (1960) proposed that mould colonization of house dust required at least one of several conditions to be met: **1)** the direct observation of conidiophores in the dust; **2)** the ability to culture particular fungi from dust-borne mycelial fragments; and, **3)** an abundance of a particular fungus in dilution plates that significantly exceeds the representation of that same species in control samples. These principles are supported by the present study.

I hypothesize that various routine mechanical processes within houses permit the accumulation of fungal spores. Since spores of *Aspergillus* and *Penicillium* are typically in the size range of 2-5  $\mu\text{m}$  in diameter it is possible that these particles may penetrate inefficient filters, such as dust bags in portable vacuum cleaners or filters in forced-air heating systems, and thus, not be efficiently removed from the indoor environment by these processes (Stetzenbach et al., 1999). This being the case, a properly installed, externally-vented central vacuum cleaner may help to reduce the accumulation of indoor mould spores.

The negative correlation of *C. herbarum* with a number of other, presumably resident carpet dust fungi may result from its particular abundance in outdoor air during early spring (Abdel-Hafez et al., 1986, 1993; Ripe, 1962). Additional examinations of outdoor air samples by the author have shown that *C. herbarum* is typically the most abundant species of *Cladosporium* isolated from outdoor air from early spring through summer in Toronto. This species remained relatively uncommon in dust samples until late spring, at which point, the colony counts of *C. herbarum*

became sufficiently high that higher orders of dilution were used in order to maintain overall counting efficiency (data not shown). As such, the occurrences of other species that remained present at roughly constant background levels were displaced by the high input of *C. herbarum* and proportionally were observed to decrease.

Soilborne fungi occur only at very low levels in indoor air, and their presence in indoor environments is mostly limited to the soil of indoor, potted ornamental plants (Summerbell et al., 1992). The results of the present study indicate that many common soilborne taxa occur frequently in carpet dust as well. This may result from the commonplace North American practice of wearing footwear in the house, a custom uncommon in most parts of Europe and Asia.

The indices of coverage that were calculated using Good's hypothesis showed that in all but a few cases (e.g. house numbers 137, 288 and 291) the sampling technique employed was adequate to detect close to the total number of species expected in each dust sample (see Appendix C). Nevertheless, the number of replications that would be required to establish statistical confidence in abundance data is prohibitively large in a study of this magnitude. Even so, the interpretation of abundance data is complicated by the tendency of heavily sporulating fungi such as *Aspergillus*, *Penicillium* and fungi exhibiting yeast-like growth forms to be over-represented in surveys employing serial dilution techniques.

## CONCLUSIONS

The fungal flora of broadloom-bound house dust consists of a mixture of active and passive residents. The passive occupants of carpet substrates are mainly allochthonous, and arise from

ecologically diverse habitats, mostly outside of the indoor environment. The main sources of allochthonous indoor moulds are 1) the phylloplane; 2) soil and 3) xerophilic fungal food-spoilage. The accumulation of spores of these fungi within broadloom dust is a result of multiple mechanical processes operating within the indoor environment. These processes may include the propagation of phylloplane spores indoors on air currents and clothing and the movement of soil-borne fungi indoor on footwear and by pets.

The small-spored nature of many xerophilic food spoilage fungi may favor their passage through inefficient filters, such as on vacuum cleaners and forced air furnaces. This likelihood, coupled with the differentially greater longevity relative to phylloplane taxa may facilitate their artifactual accumulation within broadloom over time. Many of the taxa common to any of these groupings may undergo active growth in the indoor environment under suitable conditions, however, the primary sources of inoculum for these fungi are allochthonous. The active residents of broadloom dust are mostly restricted to a small subset of the total fungal biodiversity contained within this substrate. These species proliferate within broadloom dust (autochthonous), and are similarly often responsible for fungal disfigurement of other indoor finishes and building elements under conditions of water accumulation (e.g. *As versicolor*, *W. sebi*).

## CHAPTER 3. A REVIEW OF TECHNIQUES FOR THE ASSESSMENT OF GENOTYPIC DIVERSITY<sup>4</sup>

### INTRODUCTION

The development of the polymerase chain reaction (PCR) in the mid 1980s precipitated a series of rapid technological advancements in DNA-based diagnostics as well as DNA sequencing technology. Many such improvements have led to the widespread acceptance and, indeed, routine use of DNA sequencing as a tool for addressing a myriad of previously untenable biological hypotheses. In particular, DNA sequencing has permitted the inferential elucidation of phylogeny in many difficult taxonomic groups, such as the Trichocomaceae.

As problems of relatedness and species concept among the anamorphs of the Trichocomaceae are resolved, questions of population biology or genetic variation below the species level become germane. To date, many molecular genetic techniques have been devised to discriminate 'individuals'. These methods include the classical hybridisation approach of Restriction Fragment Length Polymorphism (RFLP) as well as several PCR-based approaches such as Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), RFLP of PCR products (PCR-RFLP), Single-Strand Conformation Polymorphism (SSCP), Microsatellite Single-Locus Fingerprinting and Heteroduplex Mobility Assay (HMA).

---

<sup>4</sup> This chapter is reprinted with the kind consent of the copyright owners, Overseas Publishers Association (OPA) N.V., with permission from Gordon and Breach Publishers, from Scott, J.A. and Straus, N.A. 2000. A review of current methods in DNA fingerprinting. pp. 209-224. In Integration of Modern Taxonomic Methods for *Penicillium* and *Aspergillus* Classification. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers. This work was a contribution to the Third International Workshop on *Penicillium* and *Aspergillus*, held in Baarn, The Netherlands, from 26-29 May 1997, and is presented here as justification for the use of heteroduplex mobility assay as a method of genotypic comparison in this dissertation. For up-to-date discussion of DNA fingerprinting techniques, the reader is referred to Blears et al. (1998), Ryskov (1999), Savelkoul et al. (1999), Smouse and Chevillon (1998) and Soll (2000).

This chapter presents a critical assessment of these techniques and comments upon their appropriate uses.

## **THE DETECTION OF GENETIC VARIATION**

The ability to analyse and characterize genetic variation between individuals of the same species with both accuracy and precision has been a technological grail of biological science since Gregor Mendel's pioneering work on heredity in the mid-nineteenth century. Traditionally, morphological and later physiological characteristics of phenotype served as proxy measurements of genotypic variation. However, most phenotypic traits do not behave as strict Mendelian determinants and instead are regulated by multifactorial genetic expression (i.e. polygenetic inheritance) coupled with complex environmental influences. Thus, while useful as taxonomic and ecological indicators, these markers pose problems in population genetic studies. In more recent time, molecular approaches have attempted to solve these shortcomings, first with studies on protein variation and later, following the emergence of recombinant DNA technology, by analyses of the genetic material itself. The recent introduction of the polymerase chain reaction (PCR) (Mullis, 1990; Saiki et al., 1985, 1988) represents a quantum technological advance in applied molecular genetics, and has driven the development of a great diversity of ancillary methodologies (White et al., 1989).

## **THE USE OF PROTEINS TO DISTINGUISH VARIATION**

Early approaches to the assessment of genetic diversity exploited polymorphisms in a variety of well characterized enzymes. Extracted proteins were separated by gel electrophoresis and allozymes (allelic variants of the same enzyme) were detected by reacting the gel with an appropriate substrate and dye. Allozymes with differing amino acid sequences appeared as

bands with unique electrophoretic mobilities in native gels. With the development of allozyme analysis in the mid 1960s, it at once became possible to address questions about spatial and temporal distribution of genetic variability within and between populations and to investigate fundamental aspects of mating systems, recombination, gene flow and genetic drift. This early form of molecular genetic analysis remained prominent until the mid 1980s.

### **HYBRIDIZATION-BASED MARKERS**

In the early 1970s, DNA-based technologies began to replace protein analyses. Initially, DNA-DNA reassociation kinetics coupled with DNA hybrid stability was used to analyse phylogenetic relationships of single-copy DNA in eukaryotic organisms (e.g. Shields and Straus, 1975; Sohn et al., 1975). These pioneering techniques of the 1970s rapidly gave way to the more powerful methodologies of genetic engineering. Unlike allozyme assays, the still-widespread analysis of restriction fragment length polymorphisms (RFLP) had the advantage of examining DNA variability directly. In RFLP, genomic DNA is digested with a restriction endonuclease. The resulting DNA fragments are separated by gel electrophoresis, chemically denatured and transferred by Southern blotting to a DNA-binding membrane. The membrane is incubated in a solution containing a labelled nucleic acid probe and the hybridising fragment bands are visualized by autoradiographic or chemiluminescent techniques. The resulting patterns may represent polymorphic forms of a structural gene with implication for breeding strategies or may be the result of more complex patterns arising from repeated elements of cryptic function.

Variable number tandem repeats (VNTRs) range from short, interspersed repeats of short nucleotide sequences to long stretches of recurrent, tandem sequence motifs. Families of VNTR sequences are known variously as "satellite" DNAs, appropriately prefixed to indicate the



relative size category of the repeated element and its extent of dispersion within the genome (e.g. microsatellite, minisatellite). Variable minisatellite DNA was first investigated for DNA fingerprinting by Jefferies and co-workers (1985a, 1985b), and is discussed in detail by Jefferies (1987). RFLP technology has been widely exploited for mycological analysis. This method has been reviewed in depth by Weising and colleagues (1995).

Although RFLP methodologies have been powerful analytical tools, they require large amounts of genomic DNA, are difficult to automate and require substantial time to complete. The discovery of the polymerase chain reaction (PCR) (Saiki et al., 1985, 1988) provided an opportunity to alleviate all of these constraints and in addition, offered new strategies of exploiting sequence variation.

## **LOW-STRINGENCY PCR**

### **Randomly amplified polymorphic DNA (RAPD)**

Perhaps the most widespread PCR-based fingerprinting techniques currently in use are based on random-primed PCR. The use of single oligonucleotide primers of arbitrary sequence was introduced simultaneously by the independent groups of Williams and co-workers (1990) and Welsh and McClelland (1990). Williams et al. (1990) systematically studied single primer PCR using a set of randomly designed decamers as well as sequentially truncated versions of a selected primer. In their methodology, known as random amplified polymorphic DNA (RAPD), amplified fragments were separated using agarose gel electrophoresis and visualized by ethidium bromide staining. In contrast, Welsh and McClelland (1990) described a similar method, where single primers of arbitrary sequence of various lengths (optimally 20 bp) were used in PCR of candidate template DNAs, into which  $\alpha$ -<sup>32</sup>P dCTP was incorporated as a radiolabel. The

fingerprint generated consists of a unique profile of fragment sizes separated by denaturing polyacrylamide gel electrophoresis and visualized by autoradiography. A third variation was proposed by Caetano-Anollés and colleagues (1992) where even shorter oligonucleotide primers (5 bp) were used in a single-primer PCR. Fragment profiles were separated using denaturing polyacrylamide gel electrophoresis and visualized by silver staining. Of these three related methods, RAPD (*sensu* Williams et al., 1990) has enjoyed the greatest acceptance to date (Hedrick, 1992; Weising et al., 1995). These techniques offer a cheaper and less time-consuming alternative to RFLPs. In addition, markers may be developed rapidly by screening a panel of candidate arbitrary-sequence oligonucleotide primers without *a priori* knowledge of target sequence (Williams et al., 1990). Also, polymorphisms that are inaccessible by RFLP analysis may be accessed by these methods (Williams et al., 1990). However, marker dominance is not a complication for the analysis of true fungi since with few exceptions, their vegetative mycelia are haploid (Weising et al., 1995; Williams et al., 1990).

With time, numerous authors have advanced general modifications and application-specific refinements to the basic concept behind RAPD technology, such as varying the concentrations of reactants (Tommerup et al., 1995), thermal cycling set-up protocols and profiles (Bielawski et al., 1995; Kelly et al., 1994; Yu and Pauls, 1992) and using paired primers (Micheli et al., 1993; Welsh and McClelland, 1991). However, many investigators have found random primer fingerprinting methods to be hampered by problems relating to reproducibility and consequently have questioned RAPD reliability for certain types of analyses. These problems largely stem from a critical dependence of the fragment profile and relative yield on all of the basic parameters of PCR (Bielawski et al., 1995), such as annealing temperature and extension time (Ellsworth et al., 1993; Penner et al., 1993), primer concentration (Ellsworth et al., 1993;

MacPherson et al., 1993; Muralidharan and Wakeland, 1993), template quality (Micheli et al., 1993) and concentration (Davin-Regli et al., 1995; Micheli et al., 1993; Muralidharan and Wakeland, 1993), reactant concentration (Ellsworth et al., 1993), the particular commercial brand of DNA polymerase (Meunier and Grimont, 1993; Schierwater and Ender, 1993; Tommerup et al., 1995) and the make and model of thermocycler (He et al., 1994; MacPherson et al., 1993; Meunier and Grimont, 1993). Penner and co-workers (1993) noted problems with RAPD reproducibility between seven laboratories utilizing the same primers and templates with some varied reaction conditions. Also, several workers have described the presence of non-parental bands resulting from PCR artifacts such as heteroduplexes (Ayliffe et al., 1994) or other interference (Hallden et al., 1996; Micheli et al., 1993; Riedy et al., 1992). The observation of heteroduplexed DNAs as RAPD bands, however, has been suggested as a means of identifying codominant RAPD markers (Davis et al., 1995). While useful as initial screens for polymorphic loci which subsequently may be cloned and sequenced to construct site-specific primers (e.g. Groppe et al., 1995), PCR-based fingerprinting techniques relying on random primers are not robust and generally unsuitable for use as population markers, particularly in critical or demanding situations such as human diagnostics or courtroom evidence (Riedy et al., 1992).

### **Amplified fragment length polymorphism (AFLP)**

A fingerprinting method that combines elements of both RFLP and random primer PCR was described by Zabeau and Vos (1993) and Vos and co-workers (1995). The authors called this technique amplification fragment length polymorphism (AFLP<sup>5</sup>, Vos et al., 1995), a clearly intentional allusion to the acronym "RFLP". Although RFLPs originally examined

---

<sup>5</sup> "AFLP" as "amplification fragment length polymorphism" had been applied previously by Caetano-Anollés and co-workers (1992) as a general term referring to PCR fingerprinting methods directed by single primers of arbitrary sequence.

polymorphisms at identified loci by hybridisation, AFLP compares polymorphic patterns in fragments generated from the selected amplification of a subset of restriction fragments. In the first stage of this method, a template DNA is digested with restriction endonucleases. Concomitantly, one or two "adapter" molecules, consisting of 18-20 bp duplexed oligomers synthesized with 5'- and 3' sequence homology to the respective "sticky" ends produced by restriction digestion of the template DNA are ligated such that the original restriction sites are not restored. A panel of single primers (Mueller et al., 1996) or primer pairs (Vos et al., 1995; Zabeau and Vos, 1993) designed with homology to core sequences in the adaptor molecules, but with the addition of two arbitrary bases at the 3' termini were used in high stringency, "touchdown" PCR (Don et al., 1991). In the seminal paper by Vos and colleagues (1995), primers were end-labelled using T4 polynucleotide kinase with either  $\gamma$ -<sup>32</sup>P- or  $\gamma$ -<sup>33</sup>P-dATP to facilitate detection of the amplified fragments by autoradiography following separation by denaturing polyacrylamide gel electrophoresis. Curiously, this paper specifically stated that "adapters were not phosphorylated", in which case it is apparent that the template strand of the adapters could not ligate to the 3'-OH terminus of the cleaved genomic DNA. As such, it is not clear how the primers initiate the first round of PCR.

To date, several studies have demonstrated the use of a practical variation of this methodology in resolving relatedness within bacterial (Lin et al., 1996) and fungal populations (Majer et al., 1996; Mueller et al., 1996). Mueller and co-workers (1996) used a single adapter, and the double-stranded PCR products were resolved by agarose gel electrophoresis and visualized with ethidium bromide staining. However, the study by Majer and colleagues (1996) followed more closely the original AFLP technique (Vos et al., 1995). They suggest that AFLP appears to be more robust than RAPD and related methods because the longer primers and known target

sequence permit a higher stringency of hybridisation during the amplification procedure (Majer et al., 1996). High stringency hybridisations in PCR inherently produce fewer artifactual bands due to spurious priming events (Cha and Thilly, 1993; Dieffenbach et al., 1993).

### **HIGH-STRINGENCY PCR -- SITE-SPECIFIC POLYMORPHISMS**

The identification of specific, polymorphic loci circumvents the problem of irreproducibility common to random-primer fingerprinting methods. However, unlike random primer techniques, locus-specific methods often require a substantial initial effort to identify and characterize suitable loci.

One category of site-specific polymorphisms exploits microsatellite DNA. Microsatellite regions are PCR-amplified using primers either based on adjacent, conserved sequences (Groppe et al., 1995) or consisting of a short, repeated sequence known to be present in the test organism from probe hybridisation data (Buscot, 1996; Meyer et al., 1992; Morgante and Olivieri, 1993; Schönian et al., 1993). Polymorphisms in microsatellite DNA consist of variation in the number of repeated elements and are detected as relative length polymorphisms following electrophoretic separation. Due to the high degree of variation in these sequences, however, individual loci may be quite taxon-specific, restricting their use as general markers. Several current reviews discuss applications of microsatellite single-locus fingerprinting (Bruford and Wayne, 1993; Weising et al., 1995).

Another source of site-specific genetic variability can be found in the sequences of introns (short stretches of non-coding sequences which punctuate many genes) of single copy metabolic and structural genes. Although these loci, like microsatellite markers, are difficult to develop, they

are particularly useful when fingerprint data from multiple loci are needed to study patterns of genetic variability (e.g. clonality vs. mating and recombination) (Anderson and Kohn, 1995). Primers designed using highly conserved sequences flanking introns have been described in a number of genes for filamentous fungi and yeasts (Glass and Donaldson, 1995). The variability of intron sequences, however, may not necessarily involve length polymorphism and may result solely from alterations in base sequence between fragments of identical size, necessitating a more sophisticated method of detection than that used for microsatellite typing. Several of the more commonly used methods are discussed below. These techniques and others have been reviewed by Prosser (1993) and Cotton (1993).

Unquestionably the most widely used locus for genetic discrimination to date is the subrepeat of the nuclear and mitochondrial ribosomal RNA (rRNA) genes (Gargas and DePriest, 1996; White et al., 1990). These genes provide a wide range of useful polymorphism, with highly variable regions suitable for fingerprinting (e.g. internal transcribed- and intergenic, non-transcribed spacer regions) as well as more conserved domains appropriate for several levels of phylogenetic study (e.g. small and large ribosomal subunit genes). Numerous primer sequences have been described for PCR mediated amplification of specific regions of rDNA from filamentous fungi and yeasts (Gargas and DePriest, 1996; White et al., 1990). Like intron loci, polymorphisms in rRNA may be cryptic and not necessarily reflected by length polymorphism of PCR-amplified fragments, requiring a sensitive detection method.

#### **DETECTION OF LOW-LEVEL SEQUENCE VARIABILITY**

The determination of base sequence is the ultimate, definitive method for the discrimination of occult genetic differences and the defining of mutations. However, despite recent extraordinary

technological advancements in DNA sequencing technologies since the introduction of these methods (Maxam and Gilbert, 1980; Sanger et al., 1977), the resources required for large-scale sequencing projects remain untenable for most laboratories (Chowdhury et al., 1993; Cotton, 1993). Therefore, a number of techniques have been described which permit the inferential comparison of base sequence, each aspiring to offer a high degree of sensitivity and reliability with low cost and ease of use.

### **Restriction endonuclease digestion of PCR products**

The simplest method for screening sequence variability in PCR products is digestion by restriction endonucleases (PCR-RFLP) in which subject PCR products are digested individually with a set of restriction enzymes. Typically, restriction endonucleases that cleave at quadrameric recognition sequences are chosen because the occurrence of the shorter recognition motif statistically occurs with greater frequency. Polymorphisms are recognized by different fragment profiles following electrophoretic separation. Variation detected by this method is limited to either fragment length differences or changes in base sequence that result in the loss or gain of a restriction enzyme recognition site. Several studies of fungal populations have used this method with some success (Buscot et al., 1996; Donaldson et al., 1995; Gardes et al., 1991; Glass and Donaldson, 1995). As well, PCR-RFLP has been used as a means of taxonomic positioning (Vilgalys and Hester, 1990). However, relatively little sequence information can be inferred from PCR-RFLP analysis since the probability of encountering a change in a specific site of four nucleotides is quite low. Although the inclusion of additional restriction enzymes improves the analysis, very little base sequence can be compared using this method.

### **Denaturing-gradient gel electrophoresis (DGGE)**

Denaturing-gradient gel electrophoresis (DGGE) is a method that has long been used to identify single base mutations in DNA fragments (Fisher and Lerman, 1983). This technique relies upon the alteration of melting domains between DNA fragments differing in base composition when separated electrophoretically on gels containing an ascending gradient of chemical denaturant. Partially annealed DNA duplexes migrate differentially, modulated by the degree and relative location of melted domains. Thus, the resolution of the technique is dependent upon at least partial association of the DNA strands, and ceases to provide further useful separation upon complete denaturation. Myers and co-workers (1985) attached a segment of G/C-rich sequence (a "GC-clamp") to one end of the DNA fragment prior to DGGE, to maintain partial duplex association at higher concentrations of denaturant in order to achieve better resolution. Sheffield and colleagues (1989, 1992) described the inclusion of similar G/C-rich sequences using PCR. Several reviews discuss applications of DGGE (Cotton, 1993; Prosser, 1993).

### **Single-strand conformation polymorphism (SSCP)**

A popular method for studying low-level sequence variability in PCR products known as single-strand conformation polymorphism (SSCP) was described by Orita and co-workers (1989a, 1989b). In this technique, radiolabelled PCR products are chemically denatured, separated by electrophoresis in native polyacrylamide gels and visualized by autoradiography. The electrophoretic migration of single strands is a function of secondary structure formed due to spontaneous self-annealing upon entry into the non-denaturing gel matrix. Single base substitutions may alter this secondary structure, hence changing the relative electrophoretic mobility of the molecule.



SSCP analysis has been used widely to identify deleterious mutations relating to human genetic diseases such as color vision defects (Zhang and Minoda, 1996), cystic fibrosis (Ravnikglavac et al., 1994), Tay-Sachs disease (Ainsworth et al., 1991), phenylketonuria (Dockhorn-Dworniczak et al., 1991), and a number of p53-associated carcinomas including lung cancer (Suzuki et al., 1990), lymphoblastic leukemia and non-Hodgkin lymphoma (Gaidano et al., 1991), breast- and colon cancer (Soto and Sukumar, 1992) and resistance to thyroid hormone (Grace et al., 1995). As well, SSCP has been employed in numerous investigations of organismal variability such as human papilloma virus (HPV) (Spinardi et al., 1991), major histocompatibility complex in Swedish moose (Ellegren et al., 1996), and differentiation of species of *Aspergillus* section *Flavi* (Kumeda and Asao, 1996).

Sheffield and co-workers (1993) studied the sensitivity of SSCP analysis for the detection of single base substitutions using an assortment of 64 characterized mutations (e.g. murine globulin promoter, p53 and rhodopsin). Using SSCP, they were able to detect roughly 80 % of these single base mutations. This detection rate is consistent with results from other studies (Hayashi, 1992; Spinardi et al., 1991). Hayashi (1991, 1992) and Sheffield and colleagues (1993) found that fragment size<sup>6</sup> as well as location of the substituted base are the major factors governing the sensitivity and thus the success of this technique. Dideoxy-fingerprinting (ddf) is a hybrid variant of SSCP (Orita et al., 1989a, 1989b) and dideoxy sequencing (Sanger et al., 1977) in which a typical Sanger reaction with one dideoxynucleotide is followed by chemical denaturation and electrophoresis on a non-denaturing polyacrylamide gel (Blaszyk et al., 1995). This technique has been used to detect single base mutations with an astonishingly high level of

---

<sup>6</sup> The ability to discriminate mutations diminishes with increased fragment size, e.g. > 200 bp.

sensitivity (Blaszyk et al., 1995; Ellison et al., 1994; Felmlee et al., 1995; Fox et al., 1995; Stratakis et al., 1996).

A number of procedural modifications have been proposed to enhance the sensitivity and reproducibility of SSCP, including concentrating a single strand using asymmetric PCR (Ainsworth et al., 1991); decreasing dNTP concentration in initial PCR to increase incorporation of radiolabel (Dean and Gerrard, 1991); using non-isotopic detection systems including silver staining (Ainsworth et al., 1991; Dockhorn-Dworniczak et al., 1991; Mohabeer et al., 1991); fluorescence-based methods (Makino et al., 1992), and ethidium bromide staining (Grace et al., 1995); modifying the gel substrate (Dean and Gerrard, 1991; Spinardi et al., 1991); altering electrophoresis conditions such as temperature (Dean and Gerrard, 1991; Spinardi et al., 1991), ionic strength of the electrophoresis buffer and gel matrix (Spinardi et al., 1991) and various changes to facilitate large-scale screening (Mashiyama et al., 1990). Liu and Sommer (1995) performed multiple restriction enzyme digests on large PCR-amplified fragments and combined the products prior to SSCP, permitting this technique to be used effectively on larger amplicons. Several authors however have noted that results of SSCP analyses vary considerably between experiments under identical conditions (Dean and Gerrard, 1991; Soto and Sukumar, 1992).

### **Heteroduplex mobility assay (HMA)**

Heteroduplex mobility assay (HMA) (Delwart et al., 1993; Keen et al, 1991) is a relatively new technique which is comparable in sensitivity to SSCP, but not so widely used (Cotton, 1993). In HMA, the PCR amplification products of a pair of isolates are combined in equimolar proportion, heat denatured and reannealed at lower temperature. The resulting mixture comprises duplexed molecules of all possible combinations of compatible DNAs including two

populations of homoduplexes identical to the fragments of each original amplification product, as well as two hybrid DNAs (heteroduplexes) created by the cross-annealing of compatible strands originating from different "parent" duplexes. Differences in base sequence such as substitutions, insertions or deletions between the two strands of heteroduplexed DNAs produce local "bubbles" or "kinks" in these hybrid molecules. Indeed, Wang and co-workers (1992) confirmed the bent physical conformation of heteroduplexed DNA fragments by visualizing fragments containing deletional kinks using electron microscopy. These structural instabilities result in the slower migration of the heteroduplex molecules to duplexes with total base complementarity when separated by electrophoresis in native polyacrylamide gels. The rate of detection of single base mutations by this technique is comparable to that observed in SSCP (Ganguly et al., 1993; Ravnikglavac et al., 1994; White et al., 1992). Other authors have suggested significantly better discrimination of small mutations using HMA relative to SSCP (Offermans et al., 1996). However, a number of studies using heteroduplexed DNA employ excessively long annealing times, or inappropriate annealing temperatures which unintentionally favour the reannealing of homoduplexes (e.g. Bachmann et al., 1994; Cheng et al., 1994; D'Amato and Sorrentino, 1994; Delwart et al., 1993, 1994; El-Borai et al., 1994; Gross and Nilsson, 1995; Soto and Sukumar, 1992; Wilson et al., 1995; Winter et al., 1985).

While DNA heteroduplexes were first noted as artifacts of PCR (Jensen and Straus, 1993; Nagamine et al., 1989), the differential mobility of deliberate DNA heteroduplexes has since been used in the recognition of various human genetic mutations including human p53-related tumours (Soto and Sukumar, 1992), *ras* oncogenes (Winter et al., 1985; ), type 1 antithrombin (Chowdhury et al., 1993), cystic fibrosis (Dodson and Kant, 1991; Ravnikglavac et al., 1994), endometrial adenocarcinoma (Doherty et al., 1995), sickle cell anaemia (Wood et al., 1993) and

$\beta$ -thalassaemia (Cai et al., 1991; Hatcher et al., 1993; Law et al., 1994; Savage et al., 1995). As well, heteroduplex technology has been proposed as a means of human leukocyte antigen typing (HLA typing) (D'Amato and Sorrentino, 1994; El-Borai et al., 1994; Martinelli et al., 1996).

HMA has also been used to study genetic variation in viruses such as human immunodeficiency virus (HIV) (Bachmann et al., 1994; Delwart et al., 1993, 1994; Louwagie et al., 1994) and hepatitis C virus (Gretch et al., 1996; Wilson et al., 1995), as well as eukaryotes such as European populations of the basidiomycete plant pathogen *Heterobasidion annosum* (Cheng et al., 1994), Swedish populations of brown trout (Gross and Nilsson, 1995) and eastern Australian rabbit populations (Fuller et al., 1996).

Since the introduction of HMA as a diagnostic tool, a number of modifications have been proposed including the use of ethidium bromide staining (Bachmann et al., 1994; Chowdhury et al., 1993; D'Amato and Sorrentino, 1994; Delwart et al., 1994; Dodson and Kant, 1991; El-Borai et al., 1994; Hatcher et al., 1993; Pulyaeva et al., 1994; Soto and Sukumar, 1992; Wood et al., 1993) or silver staining (Gross and Nilsson, 1995) for visualization, lower ionic strength of electrophoresis buffer (Chowdhury et al., 1993; Soto and Sukumar, 1992), the use of buffering system other than TBE (D'Amato and Sorrentino, 1994; Ganguly et al., 1993), detection of heteroduplexed fragments by capillary electrophoresis (Cheng et al., 1994), electrophoresis on temperature gradient gels (Campbell et al., 1995) and the use of heteroduplex generators or universal comparative DNAs (D'Amato and Sorrentino, 1995; Doherty et al., 1995; El-Borai et al., 1994; Gross and Nilsson, 1995; Law et al., 1994; Louwagie et al., 1994; Martinelli et al., 1996; Savage et al., 1995; Wack et al., 1996; Wood et al., 1993).

Much of the earlier work using DNA heteroduplex analysis used Hydrolink MDE, which forms a vinyl polymer as an electrophoresis medium (Soto and Sukumar, 1992). Zakharov and Chrambach (1994) demonstrated increased resolution of DNA heteroduplexes by electrophoresis in low-crosslinked polyacrylamide gels, noting however that the gel matrix is more prone to swelling when synthesized with lower concentrations of N,N'-methylenebisacrylamide (Bis) due to less reproducible fibre properties (Zakharov and Chrambach, 1994). Pulyaeva and co-workers (1994) used uncrosslinked polyacrylamide gels with similar success. However, they noted that uncrosslinked polyacrylamide media lacked the mechanical strength of low, or standard crosslinked gels and thus were not suitable for many applications (Pulyaeva et al., 1994). Xing and colleagues (1996) amended 12 % polyacrylamide gels with 10 % glycerol and 2 % agarose for resolving DNA heteroduplexes. Several investigators have incorporated chemical denaturants such as ethylene glycol, formamide (Ganguly et al., 1993) and urea (White et al., 1992) into polyacrylamide gels as a means of destabilizing small heteroduplexes to facilitate their detection.

A number of related techniques have developed from HMA including the enzymatic cleavage of mismatched bases in RNA/RNA or RNA/DNA heteroduplexes using RNase A as a way of facilitating the detection of heteroduplexed molecules by gel electrophoresis (Winter et al., 1985), and the use of bacteriophage resolvases to cleave mismatched bases in DNA/DNA heteroduplexes (Marshall et al., 1995). Gross and Nilsson (1995) performed a restriction digest of PCR-amplified growth hormone 2 (GH2) gene from brown trout prior to heteroduplex generation as a means reducing fragment size and thus enhancing electrophoretic resolution of heteroduplexes.

Oka and co-workers (1994) demonstrated that a carefully controlled thermal annealing gradient can be used to cause the preferential formation of DNA homoduplexes relative to heteroduplexes. Using double-labelled DNA fragments (one strand labelled with biotin, the other strand labelled with dinitrophenyl (DNP)) they performed a temperature-gradient annealing with a test DNA, following which the duplexes bearing a biotin-labelled strand were captured onto a streptavidin-coated microtitre plate. The treatment of these fragments with an anti-DNP conjugated alkaline phosphatase followed by the introduction of a chromogenic substrate permitted the quantification of original double-labelled homoduplexes by spectrophotometry. The population of regenerated double-labelled homoduplexes was inversely proportional to the degree of homology of the double-labelled DNA to the tester DNA. Using this method, which they named PCR-dependent preferential homoduplex formation assay (PCR-PHFA), Oka and colleagues (1994) were able to detect differences of as little as a single nucleotide substitution between the double-labelled fragment and the tester. Although proposed as an alternative to HLA typing, PCR-PHFA may hold promise for other automated diagnostic applications.

Like SSCP, HMA is a rapid technique that takes into account the entirety of the sequence variability of a PCR-amplified DNA fragment, rather than the limited amount of sequence information available from PCR-RFLP. Both SSCP and HMA require less sample manipulation than PCR-RFLP and fewer gel runs. However, SSCP requires the ability to compare lanes both within and between gel runs to assess similarity or difference between different products. This necessitates a high degree of quality control and thus is demanding of hardware technology capable of precisely duplicating run conditions on an ongoing basis. On the other hand, because

HMA compares two individual products in the same gel lane, there is little need for comparison of migration distances between different gels.

## **SUMMARY**

A review of various commonly-used approaches to assessing fungal genotypic diversity shows that methods based on site specific polymorphisms offer a more robust approach than RAPD or other non-specific methods. For the identification of different strains heteroduplex mobility analysis (HMA) may be superior to single-strand conformation polymorphism (SSCP) because two strains/isolates are compared in the same gel lane, eliminating difficulties in gel-to-gel comparison due to mobility variations from differences in running conditions inherent to SSCP analysis.

## CHAPTER 4. DEVELOPMENT OF METHODS FOR THE ASSESSMENT OF GENOTYPIC DIVERSITY OF PENICILLIA<sup>7</sup>

### ABSTRACT

Techniques for 1) small-scale isolation of high molecular weight total DNA; 2) heteroduplex mobility assay for screening genotypic diversity; and, 3) identification of polymorphic genetic loci in *P. brevicompactum* and *P. chrysogenum* are described.

### ISOLATE SELECTION

Isolates of *Penicillium* for genetic studies were collected and stored according to the methods presented in Chapter 2. Two species of *Penicillium* were selected for intensive study based on the strong representation in the culture collection and their good representation across the set of houses studied. *Penicillium chrysogenum* was selected because this was the most commonly occurring species of the genus in broadloom dust (see Figure 2-4) and was represented by 700 isolates in the accumulated collection. *Penicillium brevicompactum* was also chosen for further investigation. Although this species was outnumbered in the dataset and culture collection by isolates of *P. spinulosum*, *P. corylophilum*, and *P. commune*, its species circumscription seemed to be more stable and its identification less prone to confusion.

---

<sup>7</sup> Parts of this chapter are reprinted with the kind permission of: 1) Eastern New York Occupational and Environmental Health Centre (ENYOEHC), Albany, New York, USA, from Scott, J.A., Straus, N.A. and Wong, B. 1999. Heteroduplex DNA fingerprinting of *Penicillium brevicompactum* from house dust. pp. 335-342, In Bioaerosols, fungi and mycotoxins: health effects, assessment, prevention and control. E. Johannig (ed). Albany, New York: ENYOEHC. 638 pp.; and 2) Overseas Publishers Association (OPA) N.V., with permission from Gordon and Breach Publishers, from Scott, J.A., D. Malloch, B. Wong, T. Sawa and Straus, N.A. 2000. DNA heteroduplex fingerprinting in *Penicillium*. pp. 225-236, In Integration of Modern Taxonomic Methods for *Penicillium* and *Aspergillus* Classification. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers, as a contribution to the Third International Workshop on *Penicillium* and *Aspergillus*, held in Baarn, The Netherlands, from 26-29 May 1997.



All isolates of *P. brevicompactum* and *P. chrysogenum* that had been catalogued during the collection phase of this project were subcultured on several diagnostic media including modified Leonian's agar (MLA), Czapek's yeast autolysate agar (CYA) and modified Creatine-sucrose agar (CSA). Cultures were incubated at room temperature and rated for colony characteristics at 1, 2 and 3-week intervals. Microscopic preparations were made after 1 wk from cultures on MLA. Subcultures on MLA were also rated for growth after 1 wk at 5 °C and 37 °C. Based on the results of these tests, a subset of isolates that demonstrated high phenotypic homogeneity were selected for each species for further study (data not shown).

#### **ISOLATION OF DNA FROM *PENICILLIUM* CONIDIA**

Many of the existing techniques for isolating fungal DNA were designed for methods requiring milligram amounts of total DNA (Weising et al., 1995). These methods typically involve the preparation of broth cultures, followed by mycelial harvest and grinding. On a small-scale, these procedures are practical; however, the labour-intensive nature of these techniques makes them ill-suited to projects requiring DNA isolations from large numbers of samples. Furthermore, the potential for aerosol generation posed by such large-scale grinding risks potential biological hazards as well as sample cross-contamination. For the purposes of the current project, a modified technique was developed which permits rapid small-scale preparation of total DNA which facilitates the processing of large numbers of samples.

#### **Materials and methods, DNA isolation**

Fungal isolates were inoculated centrally on a Petri plate of Weitzman and Silva-Hutner's agar (WSHA) (Weitzman and Silva Hutner, 1967), and grown for 7 days at room temperature under 12 hr artificial daylight. The plates were flooded with 2 mL of 95 % ethanol and the conidia and

mycelium were suspended by gently scraping the surface of the colonies with a sterile bent glass rod. The conidial suspensions were collected in microcentrifuge tubes, centrifuged at 12 K rpm and the supernatant ethanol was discarded. The pellets were dried for 30 min in a vacuum concentrator centrifuge. This protocol yielded approximately 15 mg of pelleted conidia per vial. Each vial was sufficient for a single DNA isolation.

Approximately 15 mg of sterile, acid-cleaned Dicalite 1400 (diatomaceous earth-based swimming pool filter, Grefco Inc., Torrance, California), was added to a tube containing a roughly equal volume of dry, pelleted, ethanol-killed conidia. Following the addition of 10  $\mu$ L of 70 % EtOH, the mixture was ground with a sterile glass rod for 1 min and suspended in 600  $\mu$ L of lysis buffer containing 1.4 M NaCl, 2 % w/v CTAB, 200 mM Tris-HCl pH 8.0 and 20 mM EDTA (adapted from Weising et al., 1995). Tubes were incubated at 65 °C for 1 hr, during which they were mixed by inversion at 30 min intervals.

After extraction, the tubes were cooled to room temperature and centrifuged at 10 K rpm for 1 min to pellet the Dicalite and cellular debris. The supernatant liquid was extracted twice with chloroform:isoamyl alcohol (24:1) and the DNA was precipitated with 100 % isopropanol for 10 min at -80 °C. The pellets were rinsed with 70 % ethanol and dried. The DNA was resuspended in 200  $\mu$ L Tris-EDTA (10 mM and 1 mM, respectively) (TE) pH 8.0 (Sambrook et al., 1989). Ribonuclease A was added to the DNA at a final concentration of 0.2  $\mu$ g/ $\mu$ L, and incubated for 30 min at 37 °C. The DNA was subsequently extracted with chloroform:isoamyl alcohol as above, and following the addition of sodium acetate to a concentration of 0.3 M, the DNA was precipitated with 250  $\mu$ L of 100 % ethanol at -80 °C. The DNA solution was pelleted

and pellets were rinsed with 70 % ethanol, dried and resuspended in 100  $\mu$ L TE pH 8.0. The concentration of DNA in solution was determined spectrophotometrically.

### **Results and discussion, DNA isolation**

Dicalite was selected as a grinding agent because it is commercially available and inexpensive. It acts both as an abrasive to disrupt conidial walls, and as a bulking agent to ensure surface contact between the abrasive and the biological material. Although tight binding between DNA and glass powder in the presence of high concentrations of chaotropic salts (e.g. sodium iodide) forms the basis of several proprietary technologies for DNA purification (e.g. GeneClean® II, Bio 100 Inc.; Qiagen purification spin-columns), controlled experiments using herring sperm DNA indicated that negligible DNA bound to the Dicalite under the conditions used in this procedure (data not shown). Typically, a single Petri plate of *P. brevicompactum* grown for 14 days yielded 10 to 100 mg, dry weight, of harvestable conidia. From this, 10 to 100  $\mu$ g of high molecular weight DNA was isolated.

Many of the currently used methods for the isolation of DNA from harvested cellular material involve grinding procedures that risk generating aerosols. In cases where the fungi submitted to these procedures are either pathogenic, opportunistic or heavily sporulating, a potential biological hazard exists from the generation of viable fungal aerosols. Other risks independent of the viability of conidial or cellular aerosols, such as mycotoxins and allergenic beta-glucans, are greater with large mycelial isolations. In the procedure presented, ethanol serves as the initial harvesting medium. Ethanol is an efficient wetting agent for hydrophobic conidia, which prevents conidial aerosolization during the early stages of preparation. In addition, ethanol treatment kills *Penicillium* conidia, thereby eliminating the potential of cross culture

contamination during the DNA isolation procedures. The small scale of the preparations, and the limited use of grinding due to the inclusion of diatomaceous earth further reduce the potential for the generation of cellular aerosols which could cross-contaminate sample preparations.

### **HETERODUPLEX MOBILITY ASSAY**

This section describes a PCR-based heteroduplex analysis to screen for variability between homologous amplification products from different isolates of *P. brevicompactum* (Jensen and Straus, 1993). In this method, the PCR-amplified products of a pair of isolates are combined in equal proportion, denatured at 94 °C for 3 min and reannealed at 65 °C for 5 min. The resulting mixture comprises all possible combinations of compatible DNA strands including two homoduplexes identical to each original amplification product, along with two hybrid DNAs (heteroduplexes) created from the cross-annealing of compatible strands originating from different "parents". Any sequence differences, including base substitutions, insertions or deletions produce local "bubbles" or "kinks" in the hybrid molecules. These anomalies result in differential electrophoretic migration of these structures relative to duplexed strands 100 % base complementarity. Thus, small dissimilarities in sequence between two isolates at a given locus can be detected readily.

### **Materials and methods, HMA**

#### **DNA amplification**

An identified polymorphic region near the 5'-end of the beta-tubulin gene *benA* was amplified using primer sequences Bt2a and Bt2b described by Glass and Donaldson (1995). PCRs consisted of 1 unit of Taq DNA polymerase (Boehringer Mannheim), 50 mM KCl, 2.0 mM

MgCl<sub>2</sub>, 250 μM each of dATP, dTTP, dCTP and dGTP, 0.2 mM of each primer and approximately 60 ng high molecular weight template DNA in a total reaction volume of 50 μL overlaid with a drop of sterile mineral oil to prevent evaporation. A template-free reaction was included in each set of reactions. Reactions were carried out in a PTC-100 thermocycler (MJ Research). The typical PCR profile used consisted of 94 °C for 30 s to denature, 58 °C for 30 s to anneal primers and 72 °C for 30 s to extend. This profile was repeated for 30 cycles, followed by a final extension at 72 °C for 2 min. PCR yield was roughly quantified based on ethidium bromide staining and UV visualization following electrophoresis on 1.2% agarose gels.

### **Cloning and sequencing of PCR products**

Initial work on the heteroduplex screening method used cloned homologous fragments from a polymorphic region at the 5' end of the beta tubulin gene, benA. During the initial investigations into the use of the heteroduplex technique, cloned products were used to eliminate the influence of potential PCR artifacts.

Products for cloning were amplified directly from genomic template DNA using 5'-phosphorylated primers. Primers were phosphorylated in 0.2 μL 10 mM ATP, 1 μL 10x polynucleotide kinase buffer (Promega) and 0.5 μL T4 polynucleotide kinase (Promega), 7.3 μL sterile distilled deionized water and 1 μL of 500 μM oligonucleotide primer, incubated at 37 °C for 30 min and the enzyme was inactivated by incubation at 65 °C for 20 min.

Following amplification and soft gel purification of products (Sambrook et al., 1989), 42 μL aliquots of products were blunt-ended with 5 μL 10x T4 DNA polymerase buffer, 0.25 μL

acetylated bovine serum albumin, 100  $\mu$ M deoxynucleotide triphosphates (dNTPs) and 0.25  $\mu$ L T4 DNA polymerase (New England Biologicals). The resulting products were extracted once with phenol:chloroform (1:1) and once with chloroform and precipitated at -80  $^{\circ}$ C by the addition of 0.1 M NaCl and two volumes of cold 100 % ethanol. Prior to ligation, plasmid vector was digested to completion with *Hinc*II and treated with shrimp alkaline phosphatase according to suppliers instructions (US Biochemical). Ligation was performed using 45 ng of linearized pUC19 vector, 45 ng insert DNA, 2.4% polyethylene glycol 8000, 2  $\mu$ L 5x DNA ligase buffer and 0.6  $\mu$ L DNA ligase (BRL) in a reaction volume made to 10  $\mu$ L with sterile distilled deionized water and incubated at room temperature for 3-4 hr. Following ligation, reactions were diluted to 40  $\mu$ L total volume with 1x DNA ligase buffer and transformed into *E. coli* strains DH5 $\alpha$  and JM109 using the method described by Hanahan (1985). Cells were plated in 3 replicates of 100  $\mu$ L aliquots of transformation reaction onto LB agar containing 60  $\mu$ g/mL ampicillin. Isopropylthio- $\beta$ -D-galactoside (IPTG) (80  $\mu$ g/mL) and 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactoside (XGAL) (20 ng/mL) were incorporated to permit blue/white selection. Recombinant plasmids were isolated by alkaline lysis (Sambrook et al., 1989). Cloned DNA fragments were sequenced by the method of Sanger and co-workers (1977), using universal and reverse primers for pUC19.

### **Preparation and analysis of DNA heteroduplexes**

Preliminary experiments used cloned, sequenced DNA fragments which were PCR-amplified as described above using the Bt2 primer set. Products were amplified directly from total DNA. For each locus examined, PCRs were diluted to 50 % of the original concentration, with 4 mM EDTA and 50 mM KCl and combined in equimolar proportion in a total volume of 10  $\mu$ L, and

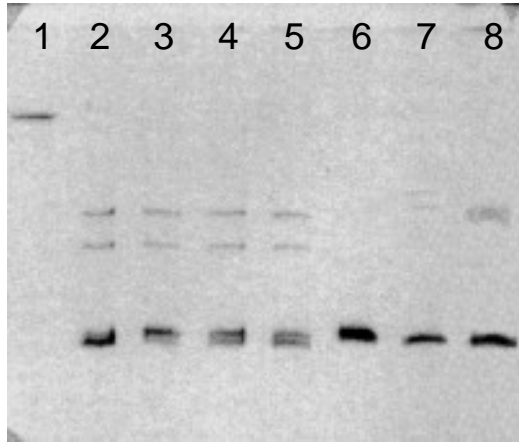
overlaid with a drop of sterile mineral oil. PCRs of sequentially numbered isolates were combined in a pair-wise manner such that each numerically adjacent pair were combined with each-other, and the first and last isolate of each series were combined. Reactions were heated to boiling for 4 min and immediately annealed at 65°C for 6 min. Based upon the results of this first pass, all adjacent “like” isolates were reduced to a single representative strain by transitive property. Subsequent rounds of HMA compared non- numerically juxtaposed “proxy” isolates ultimately reducing the entire population to a set of genotypically distinct alleles represented by a minimum number of proxy isolates for each locus tested.

#### **ELECTROPHORESIS AND IMAGING**

Prior to use in heteroduplexing reactions, the quality and yield of PCRs was assessed by electrophoresis on 1.5 % agarose gels in 1 x TAE. Agarose and proprietary gels were stained in 250 ng/mL ethidium bromide for 5-30 min and destained in distilled water for 10-30 min. Polyacrylamide gels were stained in 250 ng/mL ethidium bromide for 2-4 hr and destained in distilled water for 2 hr to overnight. All gels were visualized on an ultraviolet light transilluminator at 300 nm (Fotodyne).

#### **Resolution of heteroduplexed DNAs on Phast system**

Initial experiments to resolve heteroduplexed DNAs were conducted using the Phast gel electrophoresis system (Pharmacia, New Jersey). The Phast gel depicted in Figure 4-1 shows slow-migrating heteroduplexed DNA bands in lanes 2-5 and 7-8. The homoduplex band front is shown by the migration of native PCR product in lane 6. Despite that the Phast system provided good resolution of heteroduplexed DNAs, this system was not amenable to scale-up use given the 12 lane capacity of Phast gels.



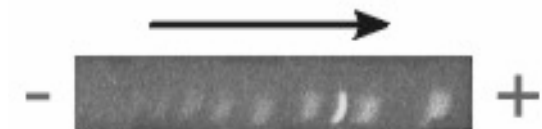
**FIGURE 4-1.** Demonstration of DNA heteroduplexes using the Phast gel system. Lanes contain (*from left to right*) **1**) 1 ug HindIII-digested  $\lambda$ -DNA; lanes 2-8 contain heteroduplexed PCR products for the following pairs of *P. brevicompactum* isolates: **2**) B91 + B119; **3**) B119 + B132; **4**) B 132 + B166; **5**) B166 + ALG1; **6**) ALG1 + DAOM 214776; **7**) DAOM 214776 + DAOM 214783 (deposited as *P. chrysogenum*, but appears to be misidentified); and **8**) DAOM 214783 + B36.



### **Horizontal gel electrophoresis (HGE) in HMA**

A technique of horizontal gel electrophoresis (HGE) was investigated for use in resolving heteroduplexed DNAs. In this method, agarose gel casting trays (BioRad minisubmarine) were modified by gluing a spacer strip of 6 mm square extruded poly(methyl-methacrylate) (PMMA) rod (General Electric), equal in length to the casting tray, into each corner of the tray using a glue that consisted of 1 % (w/v) PMMA and 1 % (v/v) acetic acid in dichloromethane. The volume of the gel tray was recalculated based on the decreased width. A removable cover plate designed to rest on top of the square rods was cut from 1/8" thick PMMA (Plexiglass, General Electric). The cover plate was cut to approximately 1 cm shorter than the total length of the gel tray to accommodate insertion of the comb. The use of a cover plate ensured a uniform thickness for the gel. In addition, the cover plate prevented contact with air during polymerization. The ends of the tray were sealed with masking tape (3M). The cover plate and comb were put in place prior to pouring. A solution of 7.7 % acrylamide, 0.3 % bisacrylamide and 0.04 % ammonium persulfate was prepared in 1 x TAE (Sambrook et al., 1989), to which 0.2 % N,N,N',N'-tetramethylethylenediamine (TEMED) was added immediately prior to casting after degassing of the solution.

Preliminary experiments using this method were conducted in which running buffer was in contact with the upper surface of the gel. In this configuration, it was found that a vertical ionic gradient was established during electrophoresis. This ionic gradient caused the differential migration of the lower portion of bands relative to the upper portion, producing an appearance of bending in cross-section (Figure 4-2). Visualization of these gels in face view showed smeared bands (not shown).



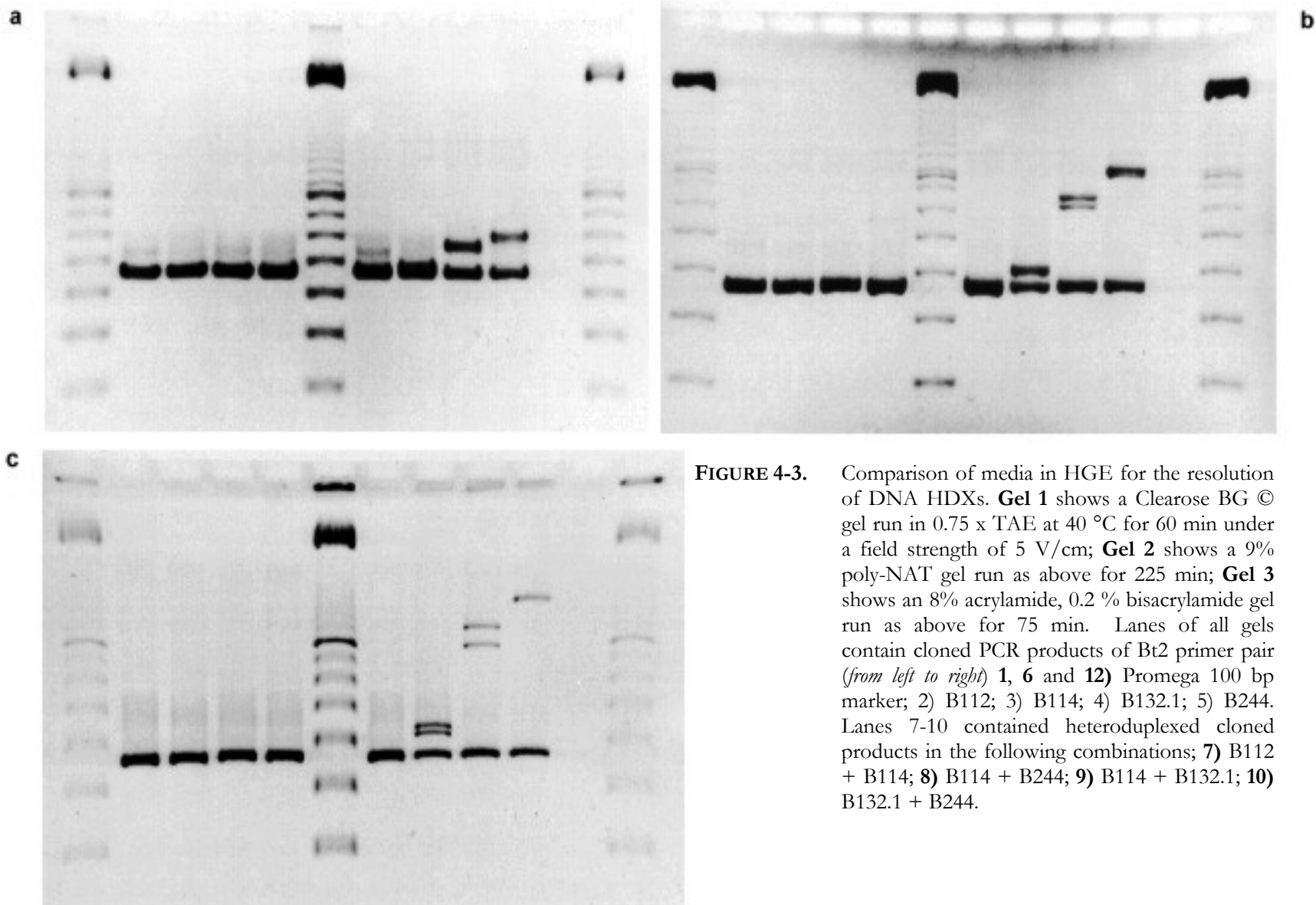
**FIGURE 4-2** Cross-section of band fronts of Promega 100 bp marker run on horizontal PAG cast and run without top-plate. Arrow indicates direction of electrophoretic migration. Note the convex configuration of band fronts in direction of anode (+). This bent morphology produced considerable blurring of bands in face view (not shown).

To address this problem, a cover plate was kept in position on the upper surface of the gel during electrophoresis to prevent contact with the running buffer. Exclusion of the running buffer from contacting the upper surface of the gel prevented ionic migration across the gel-buffer interface, thus preventing the formation of a vertical, ionic gradient in the gel matrix. This modification tended to sharpen the appearance of bands greatly.

Comparative sets of samples were electrophoresed in 1.5 % agarose (BioRad) as well as the proprietary media, Clearose®, a modified agarose (Elchrom), and 9 % Poly-NAT® (poly N-acryloyltris-(hydroxymethylaminomethane)) (Elchrom). Proprietary gel media electrophoresed in 0.75 x TAE (30 mM tris-acetate, 0.75 mM EDTA adjusted to pH 8.0) (Sambrook, 1989) using a temperature controlled, buffer-recirculating electrophoresis system (SEA 2000, Elchrom) running at 40 °C with a field strength of 5 Vcm<sup>-1</sup>. Polyacrylamide and poly-NAT gels were stained for 1 hr in 250 ng/mL ethidium bromide and destained in distilled water for 3-4 hr. Concentrations of amplification products were standardized based on band intensity as compared to a quantitative standard.

## **Results and discussion, HGE**

Preliminary investigations for appropriate electrophoresis methods used a set of morphologically and physiologically indistinguishable isolates of *P. brevicompactum*, notably three isolates, 114, 132 and 244 which were shown to differ in the Bt2 locus by sequencing on cloned PCR-amplified products (Figure 4-3). Different allelic forms of Bt2 were observed for each of these isolates using heteroduplex techniques. An additional isolate, 112, which did not form a heteroduplex with 114, was selected as a control. Aligned sequences of the cloned fragments for the Bt2 locus of isolates 114, 132 and 244 are shown in Appendix F-1. Isolates 114 and 244 have the greatest



**FIGURE 4-3.** Comparison of media in HGE for the resolution of DNA HDXs. **Gel 1** shows a Clearose BG © gel run in 0.75 x TAE at 40 °C for 60 min under a field strength of 5 V/cm; **Gel 2** shows a 9% poly-NAT gel run as above for 225 min; **Gel 3** shows an 8% acrylamide, 0.2 % bisacrylamide gel run as above for 75 min. Lanes of all gels contain cloned PCR products of Bt2 primer pair (from left to right) **1, 6** and **12**) Promega 100 bp marker; **2)** B112; **3)** B114; **4)** B132.1; **5)** B244. Lanes 7-10 contained heteroduplexed cloned products in the following combinations; **7)** B112 + B114; **8)** B114 + B244; **9)** B114 + B132.1; **10)** B132.1 + B244.

sequence similarity (15 base substitutions and two non-contiguous insertions/ deletions).

Isolates 114 and 132 differ by 42 base substitutions, 9 non-contiguous insertions/deletions and a four-base contiguous insertion/deletion. Isolates 132 and 244 differ by 44 base substitutions, 8 non-contiguous insertions/deletions, and the same four-base contiguous insertion/deletion. Sequence obtained for the Bt2 amplicon from isolate 112 was identical to that of isolate 114 (data not shown).

Each of these clones was amplified by PCR and heteroduplexed as described in Materials and Methods. The resulting reassociated structures were compared under three different conditions of electrophoresis (Figure 4-3). These conditions included Clearose BG (Elchrom) (Figure 4-3a), 9 % poly-NAT (Elchrom) (Figure 4-3b) and 8 % polyacrylamide (crosslinked with 0.2 % bisacrylamide) (Fig. 4-3c). These gels show that the low-crosslinked polyacrylamide provided the greatest level discriminate of heteroduplexed structures. Of the pre-cast gels, 9 % poly-NAT provide an acceptable degree of resolution for situations where the volume of analyses precludes in-house gel preparation. All of these analyses were completed on a temperature-regulated horizontal gel apparatus that is amenable to polyacrylamide or other polymeric gel substrates (SEA 2000, Elchrom). Horizontal gel electrophoresis system gels have the advantages of rapid loading, and easy gel casting and manipulation inherent to this configuration (Bellomy and Record, 1989).

The heteroduplex patterns that appeared in the poly-NAT and polyacrylamide electrophoretic gels (Figs. 4-3b &-c, respectively) corresponded to the mobilities expected based on the differences in sequence of the fragments such that the order of retardation of heteroduplex mobility corresponds to the degree of sequence dissimilarity. However, as pointed out by White

et al. (1992) and Ganguly et al. (1993), the actual gel mobility retardation in heteroduplex structures is related in a complex manner both to the type and distribution of sequence differences. Clustered base sequence changes that are centrally located produce local destabilization domains and have a much larger effect on mobility than non-contiguous differences dispersed throughout the molecule. However, the most pronounced heteroduplex mobility shifts result from molecular kinks caused by insertions or deletions between paired strands (Ganguly et al., 1993; Wang et al., 1992). This is seen in the substantial difference between the heteroduplex mobilities of the 114/132 and 132/244 heteroduplexes. Although the structures produced from 114/132 and 132/244 pairings show substantial difference in electrophoretic mobilities, the cumulative dissimilarities are only 55 and 56, respectively. The differences between these mobilities relative to both the homoduplexed DNAs and the 114/244 heteroduplexes seem unduly large because this total cumulative sequence difference between the 114/132 and 132/244 heteroduplexes is only one additional single base insertion/deletion in the latter.

### **Vertical gel electrophoresis (VGE) in HMA**

The low level of sequence variation between PCR fragments necessitated a greater running distance to achieve adequate resolution of DNA heteroduplexes. To address this need, the method of vertical gel electrophoresis (VGE) described by Xing and colleagues (1996) was used, in which a hybrid low crosslinked polyacrylamide / agarose gel was cast between large glass plates using a vertically-oriented protein-type electrophoresis apparatus (e.g. Protean II, BioRad, La Jolla, CA). The gel matrix was made to be weakly denaturing by the addition of glycerol prior to casting. This weakly denaturing gel matrix destabilized small heteroduplexes and facilitated their detection. This system was used for scaled-up evaluation of PCR-amplified polymorphic

loci from numerous fungal isolates since the system permitted the simultaneous electrophoresis of 100 products per run.

Similar to the horizontal method, a solution of 12.0 % acrylamide, 0.2 % bisacrylamide and 0.04 % ammonium persulfate was prepared in 1 x TBE to which 1.2 % agarose and 0.2 % N,N,N',N'-tetramethyl-ethylenediamine (TEMED) were added after degassing of the solution and immediately prior to casting. Gels were cast in a BioRad Protean electrophoresis apparatus at 1 mm thick, and allowed to polymerise for 4-5 hours prior to use. For electrophoresis, gels were cooled to 12 °C using a constant temperature refrigerated water bath and electrophoresed at 10 V/cm for up to 20 hr. Following electrophoresis, gels were stained in 250 ng/mL ethidium bromide for 2 hr, destained in distilled water for 3-4 hr prior to imaging. The large size of the gels and their relative fragility made their handling difficult. Custom plexiglass staining trays were constructed to accommodate these large gels. The trays were assembled using walls of PMMA plexiglass (General Electric) glued with 1 % (w/v) PMMA and 1 % (v/v) acetic acid in dichloromethane to a bottom plate of Acrylite OP-4 (General Electric), an ultraviolet transparent plastic sheet. The use of these trays allowed the gels to be stained, destained and visualized in a manner that limited their direct handling.

### **HMA Screening approaches**

For scale-up comparison of PCR products, two general screening approaches were used.

#### **Overlapped pairs**

In the first method, all isolates were screened in overlapping pairs. In this technique, PCR products of all isolates were arranged in fixed, arbitrary sequence. For the initial round of HMA, all adjacent pairs were compared. For example, the hypothetical set A, B, C & D, would be

compared in the pairs A+B, B+C, C+D and D+A. Following this initial round of HMA, all like-isolates were collapsed to a single representative by transitive property. A smaller second round of HMA compared alternating combinations of the remaining representative isolates. Often, with four rounds of reductive HMA, it was possible to determine haplotype for the entire set of 198 isolates of *P. chrysogenum* and 75 isolates of *P. brevicompactum*. An example of this approach is shown in Figure 4-4.

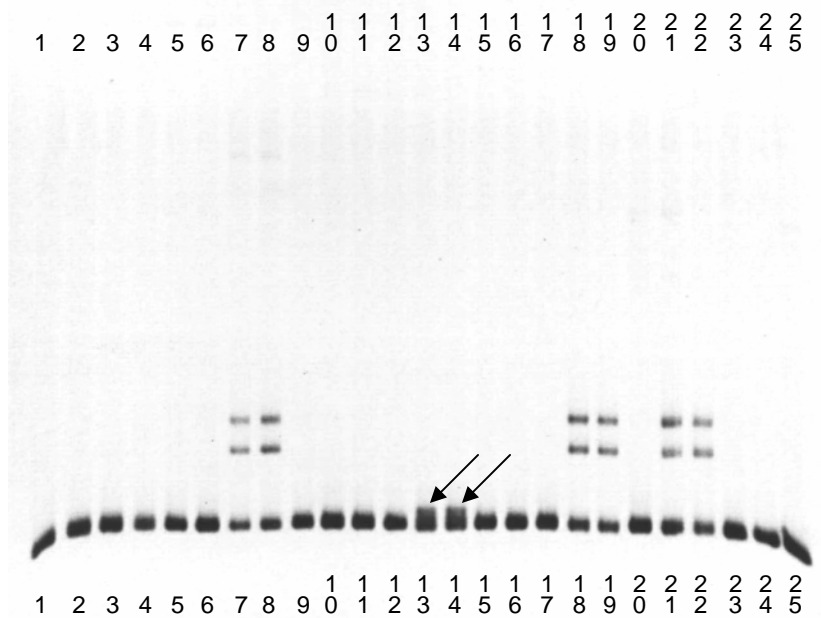
### **Universal heteroduplex generator**

A second screening approach used for HMA involved the selection of a single isolate as a “universal heteroduplex generator”. This isolate was selected on the basis of it being relatively distant from the panel of test isolates, typically from a closely related species. For example, *P. polonicum* was used as a universal heteroduplex generator for *P. chrysogenum* test panel. In this approach, each isolate was paired with the universal heteroduplex generator and submitted to electrophoresis (as above) under identical conditions. An example gel run using this approach is shown in Figure 4-5.

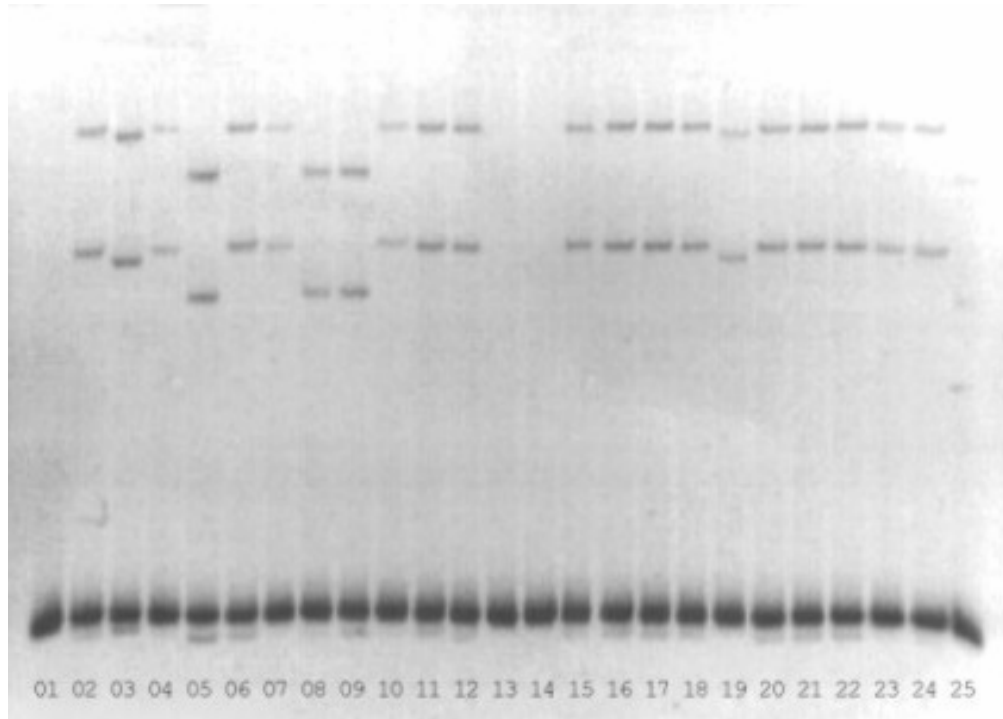
### **Results and discussion, VGE**

Overall, the use of the vertical electrophoresis method increased the resolution of small differences by HMA due to the greater length of the gels. As well, the larger format of the BioRad system allowed the electrophoresis of 25 lanes per gel. Gels were run back-to-back in the configuration recommended by the manufacturer. Thus, the operation of two electrophoresis apparatuses in this configuration permitted the simultaneous screening of 100 isolates.





**FIGURE 4-4.** Vertical 12% PAG run in 1 x TBE at 5 °C under a field strength of 10 V/cm using the “Overlapping Pairs” screening method for HMA. Lanes contain heteroduplexed pairs of *P. chrysogenum* isolates as follows (from left to right): **1)** C52.2 + C53; **2)** C53 + C56.3; **3)** C56.3 + C56.4; **4)** C56.4 + C56.5; **5)** C56.5 + C58.3; **6)** C58.3 + C58.4; **7)** C58.4 + C58.7; **8)** C58.7 + C58.8; **9)** C58.8 + C58.11; **10)** C58.11 + C58.12; **11)** C58.12 + C58.13; **12)** C58.13 + C58.14; **13)** C58.14 + C58.15; **14)** C58.15 + C58.16; **15)** C58.16 + C59.2; **16)** C59.2 + 64.1; **17)** C64.1 + 64.2; **18)** C64.2 + C67.3; **19)** C67.3 + C70; **20)** C70 + C70.1; **21)** C70.1 + C70.3; **22)** C70.3 + C70.5; **23)** C70.5 + C70.6; **24)** C70.6 + C70.7; **25)** C70.7 + C71.2. Note the large heteroduplex band shifts in lanes 7-8, 18-19 and 21-22. Small heteroduplex band shifts are indicated by the arrows in lanes 13-14.



**FIGURE 4-5.** Vertical 12% PAG run in 1 x TBE at 5 °C under a field strength of 10 V/cm using the “Universal Heteroduplex Generator” screening method for HMA. Lanes contain PCR products amplified using the Bt2 primer set of *P. brevicompactum* isolates heteroduplexed against isolate B91, as follows (*from left to right*): **1)** B91 (negative control); **2)** B98; **3)** B99; **4)** B100.2; **5)** B109.1; **6)** B109.2; **7)** B65.4 (positive control) **8)** B112; **9)** B114; **10)** B117; **11)** B119.1; **12)** B119.2; **13)** 132.1; **14)** B132.2; **15)** B136; **16)** B165; **17)** B166; **18)** B170.1; **19)** 183; **20)** 185; **21)** 189; **22)** 192.1; **23)** 192.2; **24)** 201; and **25)** B204. Lanes 1, 13 and 14 did not show heteroduplex bands. Note the large distinctive heteroduplex band shifts in lanes 5, 8, 9 and 25, and the minor shifts in lanes 3 and 19, relative to the heteroduplex migrations in remaining lanes.

The overlapping pairs screening method was used to assess haplotype for all loci in both *P. brevicompactum* and *P. chrysogenum*. This technique performed well for both test panels which in both cases were dominated by a single genotype. Using this method it was possible to reduce the test panel by an average of approximately 80 % in all cases following the first round of HMA. This screening approach was also convenient since it did not require the inclusion of external lane standards to account for slight variation in electrophoretic conditions or the separation of gel runs in time. Rather, each lane compared two contiguously accessioned isolates directly, eliminating the need for relative assessment of band migration in different lanes. Figure 4-4 shows a gel in which *P. chrysogenum* isolates were compared at the Bt2 locus employing the overlapping pairs screening approach. Note that heteroduplex bands are absent in lanes 1-6, 9-12, 15-17, 20 and 23-25, indicating that these lanes contain isolate pairs with indistinguishable sequences at this locus. In contrast, the isolate common to lanes 7-8, 18-19 and 21-22 differs from its paired isolates in these two lanes by a total of 4 non-contiguous base substitutions at positions 127 (A/G), 267 (A/G) and 351 (T/C) (total product length of 433 bp) and a deletion of 2 contiguous bases at position 242-243 (*see Appendix G*). The small heteroduplex shift indicated by arrows in lanes 13-14 differed from its paired isolates in these two lanes by a total of 7 non-contiguous base substitutions at positions 134 (C/T), 195 (G/A), 198 (T/C), 233 (A/G), 246 (G/A), 267 (A/G) and 351 (T/C). The smallest difference revealed using this technique was a single base substitution between isolates C8.12 and C8.24 at position 363 (T/G) in the 548 bp ITS fragment amplified from *P. chrysogenum* isolates (gel not shown) (*see Appendix G*).

For loci that demonstrated greater frequency of allelic differences, a screening method employing a universal heteroduplex generator method was used in addition to the overlapping pairs method. The use of a divergent universal heteroduplex generator increased the separation

between heteroduplex and homoduplex band fronts, reducing interference of the latter in evaluating band shifts. Figure 4-5 shows an HDX gel of *P. brevicompactum* using the Bt2 locus using a universal heteroduplex generator (in this case the same locus amplified from a distant isolate of *P. brevicompactum*, B91 (=B132.1, see Chapter 5, Table 5-3)). A small shift in mobility can be seen in the heteroduplex bands in lanes 3 and 19, relative to lanes 2, 4, 6, 7, 10-12, 15-18 and 20-24. This shift between these two groups was correlated to a difference of 4 non-contiguous base substitutions at positions 55 (G/A), 75 (A/T), 258 (T/G) and 420 (G/A), along with a single, contiguous 2-base substitution at position 71-71 (AT/GC) in a total product length of 438 bp (see Appendix F). Similarly, a larger shift between the latter group and lanes 5, 8 and 9 was correlated to 5 non-contiguous base substitutions at positions 60 (T/A), 148 (C/T), 158 (T/G), 259 (G/T) and 420 (A/G), with a contiguous 2-base substitution at position 74-75 (CT/TA) in a product of 438 bp in length. Lanes 13 and 14 contained control of isolate B91.

#### **IDENTIFICATION OF POLYMORPHIC GENETIC LOCI**

Preliminary investigation to determine polymorphic loci for use in the characterization of isolates of *P. brevicompactum* and *P. chrysogenum* used a randomly selected test panel of 10 isolates for each of these species. Primer pairs that amplified intron regions in conserved metabolic and structural proteins as well as the internal transcribed spacer regions (ITS1-2) of nuclear ribosomal DNA were assessed for their ability to discriminate strains using HMA. Tables 4-1 and 4-2 summarize the loci investigated for the screening of *P. brevicompactum* and *P. chrysogenum* isolates, respectively. For *P. brevicompactum* 7 loci were investigated, three of which, *benA*, *his4* and ITS, showed readily observable polymorphisms with HMA (see Table 4-1). Similarly, four informative loci (*acuA*, *benA*, ITS and *trxB*) were identified from preliminary studies of a *P. chrysogenum* test panel that investigated 13 candidate loci (see Table 4-2).

### PHYLOGENETIC ANALYSIS OF *PENICILLIUM* SENSU STRICTO

An analysis of phylogeny within the genus *Penicillium* was conducted in an effort to determine 1) the placement of *P. brevicompactum* and *P. chrysogenum* within the genus, and 2) to assist in the selection of appropriate outgroup taxa for later use in this study. Subgenus *Biverticillium* was not included in the present analysis because this group consists of anamorphs of the genus *Talaromyces*, which is only distantly related to *Eupenicillium* (Lobuglio et al., 1993).

Sequence data for the internal transcribed spacer and partial 28S regions of nuclear ribosomal DNA collected by Dr. Steve Peterson (United States Department of Agriculture, Northern Regional Research Laboratories in Peoria, Illinois) were obtained from GenBank for a set of 85 species of *Penicillium* including representatives of all accepted subgenera comprising the genus in the strict sense (e.g. subgen. *Aspergilloides*, *Exilicaulis*, *Divaricatum*, *Furcatum* and *Penicillium*) (see Table 4-3). A similar analysis of this dataset by parsimony methods is presented by Peterson (2000). Most of these sequences originated from authentic isolates from the NRRL culture collection. Sequences were aligned using Clustal X (version 1.8) (see Jeannmougin et al., 1998; Thompson et al., 1997) and a distance tree was generated using Neighbor-Joining. Alignment of the dataset is provided in Appendix D. Tree branch support was determined by 1000 bootstrap replications. Trees were generated using version 1.5.2 of TreeView for Microsoft Windows 32 bit (Roderick Page, Oxford University), and formatted using Corel Draw version 8.232 (Corel Corporation, Ottawa). *Penicillioopsis clavariiformis* was used as an outgroup taxon. The absence of partial 28S sequence prohibited the inclusion of *P. brevicompactum* in this analysis.

A Neighbor-Joining tree rooted using *Penicillioopsis clavariiformis* is shown in Figure 4-6. An unrooted version of this tree is presented for comparison in Figure 4-7. Branches for which

**Table 4-1:** Candidate loci examined for polymorphisms in *P. brevicompactum*

<b>Gene</b>	<b>Source of primers</b>	<b>No. primer pairs tested</b>	<b>No. with polymorphisms</b>
anonymous locus (A1)	Glass & Donaldson, 1995	1	
Beta-tubulin (benA)	Glass & Donaldson, 1995	2	1
Histone 3 (his3)	Glass & Donaldson, 1995	1	
Histone 4 (his4)	Glass & Donaldson, 1995	1	1
Phosphoglycerate kinase (pgk)	Glass & Donaldson, 1995	1	
rDNA Intergenic spacer region (IGS)	this study*	2	
rDNA Internal transcribed spacer region (ITS1-5.8S-ITS2)	White et al., 1989	1	1

\* Primer pairs developed in this study were based on gene sequences available in GenBank

**Table 4-2** Candidate loci examined for polymorphisms in *P. chrysogenum*

Gene	Source of primers	No. primer pairs tested	No. with polymorphisms
Acid phosphatase (phoG)	this study*	1	
Antifungal protein PAF (paf)	this study	1	
Acetyl co-enzyme A synthase (acuA)	this study	2	2
Beta-tubulin (benA)	Glass & Donaldson, 1995	2	1
Histone 3 (his3)	Glass & Donaldson, 1995	1	
Histone 4 (his4)	Glass & Donaldson, 1995	1	
Nitrogen regulation protein (areA)	this study	1	
Orotidine-5'-phosphate decarboxylase (pyrG)	this study	1	
Phosphoglycerate kinase (pgk)	Glass & Donaldson, 1995 & this study	2	
rDNA Intergenic spacer region (IGS)	this study	2	
rDNA Internal transcribed spacer region (ITS1-5.8S-ITS2)	White et al., 1989	1	1
Thioredoxin reductase (trxB)	this study	1	1
Xylanase (xyl)	this study	3	

\* Primer pairs developed in this study were based on gene sequences from *P. chrysogenum* deposited in GenBank

**Table 4-3:** Sources of nuclear ribosomal ITS and partial 28S sequences used in this study

Identification	Strains number	Status	GenBank accession
<i>Eupenicillium cinnamopurpureum</i> DB Scott & Stolk	NRRL 3326	ex-type	AF033414
<i>Eu. crustaceum</i> F Ludw.	NRRL 3332	ex-type	AF033466
<i>Eu. egyptiacum</i> Beyma	NRRL 2090	ex-type	AF033467
<i>Eu. lapidosum</i> DB Scott & Stolk	NRRL 718	ex-type	AF033409
<i>Eu. shearii</i> Stolk & DB Scott	NRRL 715	ex-type	AF033420
<i>Hemicarpenales paradoxus</i> AK Sarbhoy & Elphick	NRRL 2162	ex-type	AF033484
<i>Penicillioopsis clavariiformis</i> Solms	NRRL 2482	ex-type	AF033391
<i>Penicillium adametzii</i> Zalesky	NRRL 736		AF034459
<i>P. adametzii</i>	NRRL 737	ex-type	AF033401
<i>P. adametziioides</i> * Abe ex G Smith	NRRL 3405	ex-type	AF033403
<i>P. aspersorum</i> G Smith	NRRL 3411	ex-type	AF033412
<i>P. atramentosum</i> Thom	NRRL 795	ex-type	AF033483
<i>P. atrovenetum</i> G Smith	NRRL 2571	ex-type	AF033492
<i>P. aurantiogriseum</i> Dierckx	NRRL 971	ex-type	AF033476
<i>P. bilaii</i> Chalab.	NRRL 3391	ex-type	AF033402
<i>P. camemberti</i> Thom	NRRL 874	ex-type	AF034453
<i>P. camemberti</i>	NRRL 875		AF033474
<i>P. canescens</i> Sopp	NRRL 2147		AF034463
<i>P. canescens</i>	NRRL 910	ex-type	AF033493
<i>P. charlesii</i> * G Smith	NRRL 778	ex-type	AF033400
<i>P. chermesinum</i> Biourge	NRRL 735	ex-type	AF033413
<i>P. chrysogenum</i> Thom	NRRL 807	ex-type	AF033465
<i>P. chrysogenum</i>	NRRL 824	Fleming	AF034450
<i>P. cinerascens</i> Biourge	NRRL 748		AF033455
<i>P. citreonigrum</i> Dierckx	NRRL 761	ex-type	AF033456
<i>P. citrinum</i> Thom	NRRL 1841	ex-type	AF033422
<i>P. coprophilum</i> * (Berk. & Curtis) Siefert & Samson	NRRL 13627	ex-type	AF033469
<i>P. corylophilum</i> (Berk. & Curtis) Siefert & Samson	NRRL 793		AF034456
<i>P. corylophilum</i>	NRRL 802	ex-type	AF033450
<i>P. corylophilum</i>	NRRL 803		AF034457
<i>P. crustosum</i> Thom	NRRL 968		AF033472
<i>P. daleae</i> Zalesky	NRRL 922	ex-type	AF033442
<i>P. decumbens</i> Thom	NRRL 741	ex-type	AF033453
<i>P. decumbens</i>	NRRL 742		AF034458
<i>P. digitatum</i> (Pers.:Fr.) Sacc.	NRRL 786	ex-type	AF033471
<i>P. donkii</i> Stolk	NRRL 5562	ex-type	AF033445
<i>P. echinulatum</i> Raper & Thom	NRRL 1151	ex-type	AF033473
<i>P. expansum</i> Link	NRRL 974		AF033479
<i>P. fellutanum</i> Biourge	NRRL 746	ex-type	AF033399
<i>P. fuscum</i> * (Sopp) Biourge	NRRL 721	ex-type	AF033443
<i>P. glabrum</i> (Wehmer) Westling	NRRL 766	ex-type	AF033407
<i>P. griseofulvum</i> Dierckx	NRRL 2300	ex-type	AF033468
<i>P. griseofulvum</i>	NRRL 734		AF034452
<i>P. griseoroseum</i> Dierckx	NRRL 820		AF034857
<i>P. griseoroseum</i>	NRRL 832		AF034449
<i>P. herquei</i> Bainier & Sartory	NRRL 1040	ex-type	AF033405
<i>P. janthinellum</i> Biourge	NRRL 2016	ex-type	AF033434
<i>P. kojigenum</i> * G Smith	NRRL 3442	ex-type	AF033489
<i>P. lividum</i> Westling	NRRL 754	ex-type	AF033406
<i>P. melinii</i> Thom	NRRL 2041	ex-type	AF033449

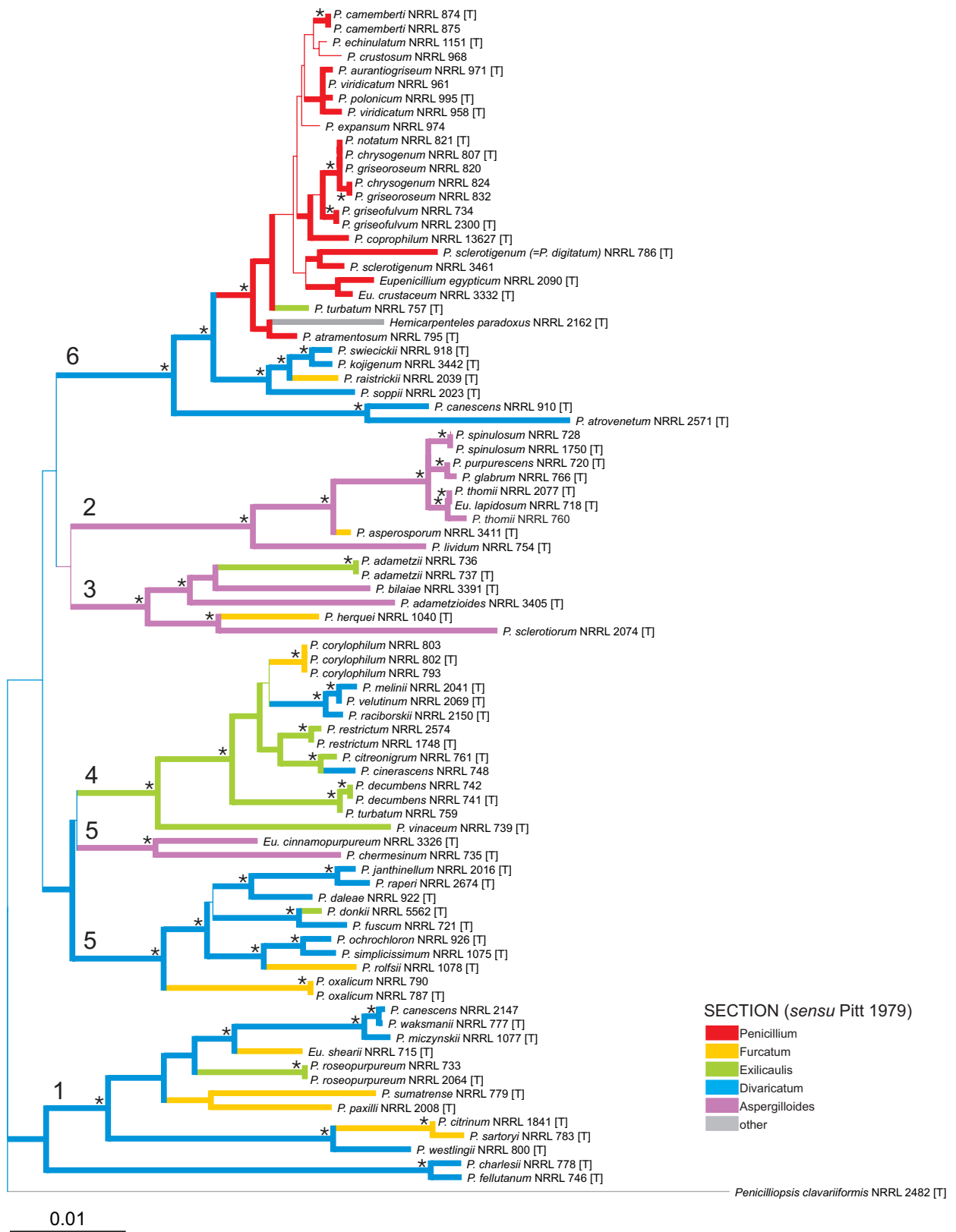
\*names not accepted by Pitt and Samson (1993), NCU-2



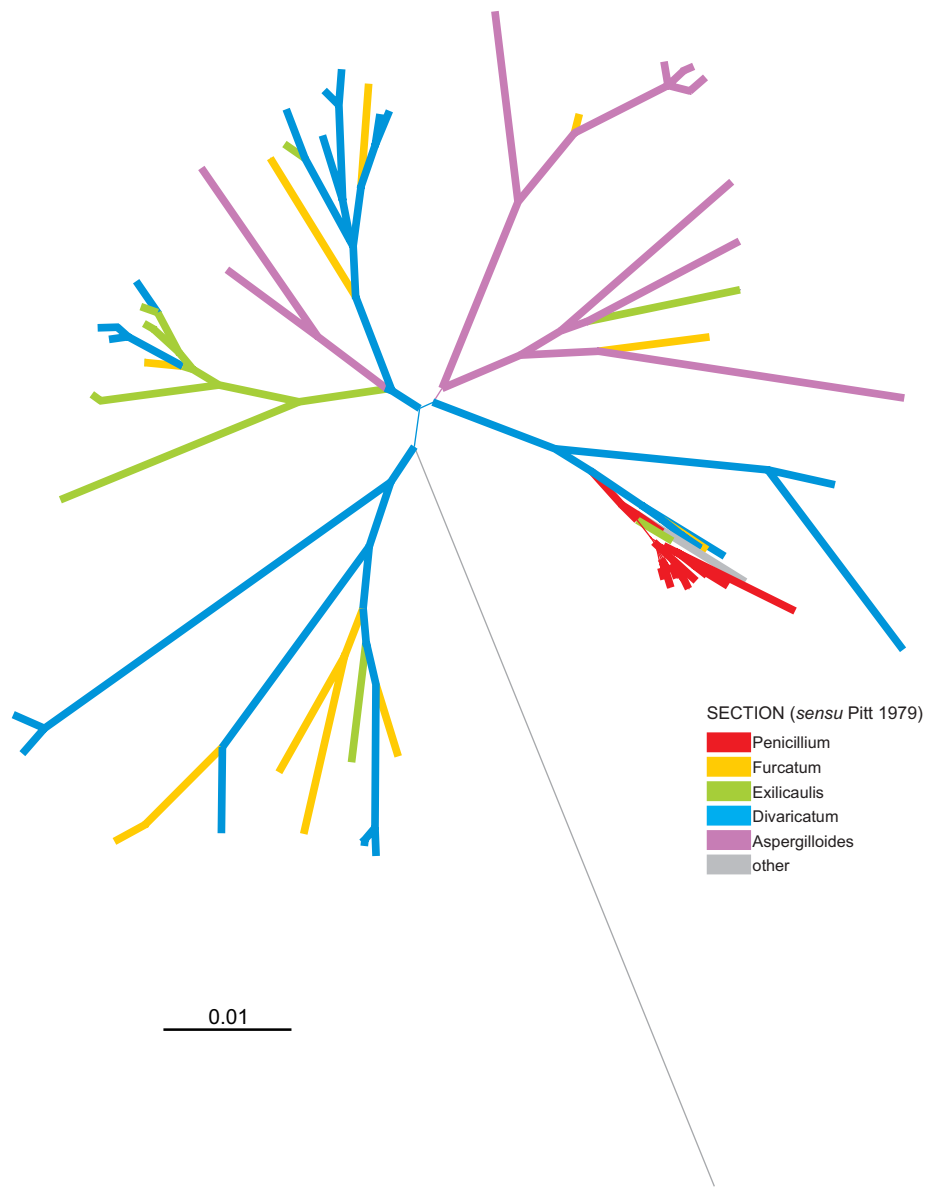
**Table 4-3:** Sources of nuclear ribosomal ITS and partial 28S sequences used in this study

Identification	Strains number	Status	GenBank accession
<i>P. miczynskii</i> Zalesky	NRRL 1077	ex-type	AF033416
<i>P. notatum</i> * Westling	NRRL 821	ex-type	AF034451
<i>P. ochrochloron</i> Biourge	NRRL 926	ex-type	AF178516
<i>P. oxalicum</i> Currie & Thom	NRRL 787	ex-type	AF033438
<i>P. oxalicum</i>	NRRL 790		AF034455
<i>P. paxilli</i> Bainier	NRRL 2008	ex-type	AF033426
<i>P. polonicum</i> * Zalesky	NRRL 995	ex-type	AF033475
<i>P. purpurens</i> (Sopp) Biourge	NRRL 720	ex-type	AF033408
<i>P. raciborskii</i> * Zalesky	NRRL 2150	ex-type	AF033447
<i>P. raistrickii</i> G Smith	NRRL 2039	ex-type	AF033491
<i>P. raperi</i> G Smith	NRRL 2674	ex-type	AF033433
<i>P. restrictum</i> Gilman & Abbott	NRRL 1748	ex-type	AF033457
<i>P. restrictum</i>	NRRL 25744		AF033459
<i>P. rolfsii</i> Thom	NRRL 1078	ex-type	AF033439
<i>P. roseopurpureum</i> * Dierckx	NRRL 2064	ex-type	AF033415
<i>P. roseopurpureum</i> *	NRRL 733		AF034462
<i>P. sartoryi</i> Thom	NRRL 783	ex-type	AF033421
<i>P. sclerotigenum</i> W Yamam.	NRRL 3461		AF033470
<i>P. sclerotiorum</i> Beyma	NRRL 2074	ex-type	AF033404
<i>P. simplicissimum</i> HZ Kong & ZT Qi	NRRL 1075	ex-type	AF033440
<i>P. soppii</i> Zalesky	NRRL 2023	ex-type	AF033488
<i>P. spinulosum</i> Thom	NRRL 1750	ex-type	AF033410
<i>P. spinulosum</i>	NRRL 728		AF034461
<i>P. sumatrense</i> * v. Szilvinyi	NRRL 779	ex-type	AF033424
<i>P. swiecickii</i> * Zalesky	NRRL 918	ex-type	AF033490
<i>P. thomii</i> Maire	NRRL 2077	ex-type	AF034448
<i>P. thomii</i>	NRRL 760		AF034460
<i>P. turbatum</i> Westling	NRRL 757	ex-type	AF034454
<i>P. turbatum</i>	NRRL 759		AF033452
<i>P. velutinum</i> Beyma	NRRL 2069	ex-type	AF033448
<i>P. vinaceum</i> Gilman & Abbott	NRRL 739	ex-type	AF033461
<i>P. viridicatum</i> Westling	NRRL 958	ex-type	AF033477
<i>P. viridicatum</i>	NRRL 961		AF033478
<i>P. waksmanii</i> Zalesky	NRRL 777	ex-type	AF033417
<i>P. westlingii</i> Zalesky	NRRL 800	ex-type	AF033423

\*names not accepted by Pitt and Samson (1993), NCU-2



**FIGURE 4-6.** Neighbor-Joining tree depicting phylogenetic relationships within *Penicillium sensu stricto* inferred from nuclear ribosomal ITS1-5.8S-ITS2 and partial 28S sequences rooted using *Penicillium clavariiformis*. Thick branches demonstrated over 50% bootstrap support, and branches marked with an asterisk showed over 80% bootstrap support in 1000 replications. Branch colour indicates taxonomic affiliation (*sensu* Pitt 1979). Numbered branches correspond to the clades identified by Peterson (2000).



**FIGURE 4-7.** Unrooted Neighbor-Joining tree depicting phylogenetic relationships within *Penicillium sensu stricto* inferred from nuclear ribosomal ITS1-5.8S-ITS2 and partial 28S sequences rooted using *Penicillioopsis clavariiformis*. Thick branches demonstrated over 50% bootstrap support, and branches marked with an asterisk showed over 80% bootstrap support in 1000 replications. Branch colour indicates taxonomic affiliation (*sensu* Pitt 1979).

bootstrap values were greater than 50 % are indicated as thick lines. Bootstrap support at greater than 80 % is indicated by an asterisk. Ex-type strains are indicated by “[I]”, and subgeneric classification following Pitt (1979) is indicated by color-coded branches.

The terverticillate taxa classified in *Penicillium* subgen. *Penicillium* formed a well-supported monophyletic clade at the top of the tree (indicated in red). *Penicillium chrysogenum* isolates grouped centrally within this clade, and were sister to *P. griseofulvum*. Isolates of *Penicillium* subgen. *Aspergilloides* formed a clade (bootstrap support less than 50 %) that was sister to the subgenus *Penicillium* clade. Several extraneous taxa, including *P. adametzii*, *P. herquei* and *P. asperosporum* (subgen. *Furcatum sensu* Pitt, 1980) were also found within this group.

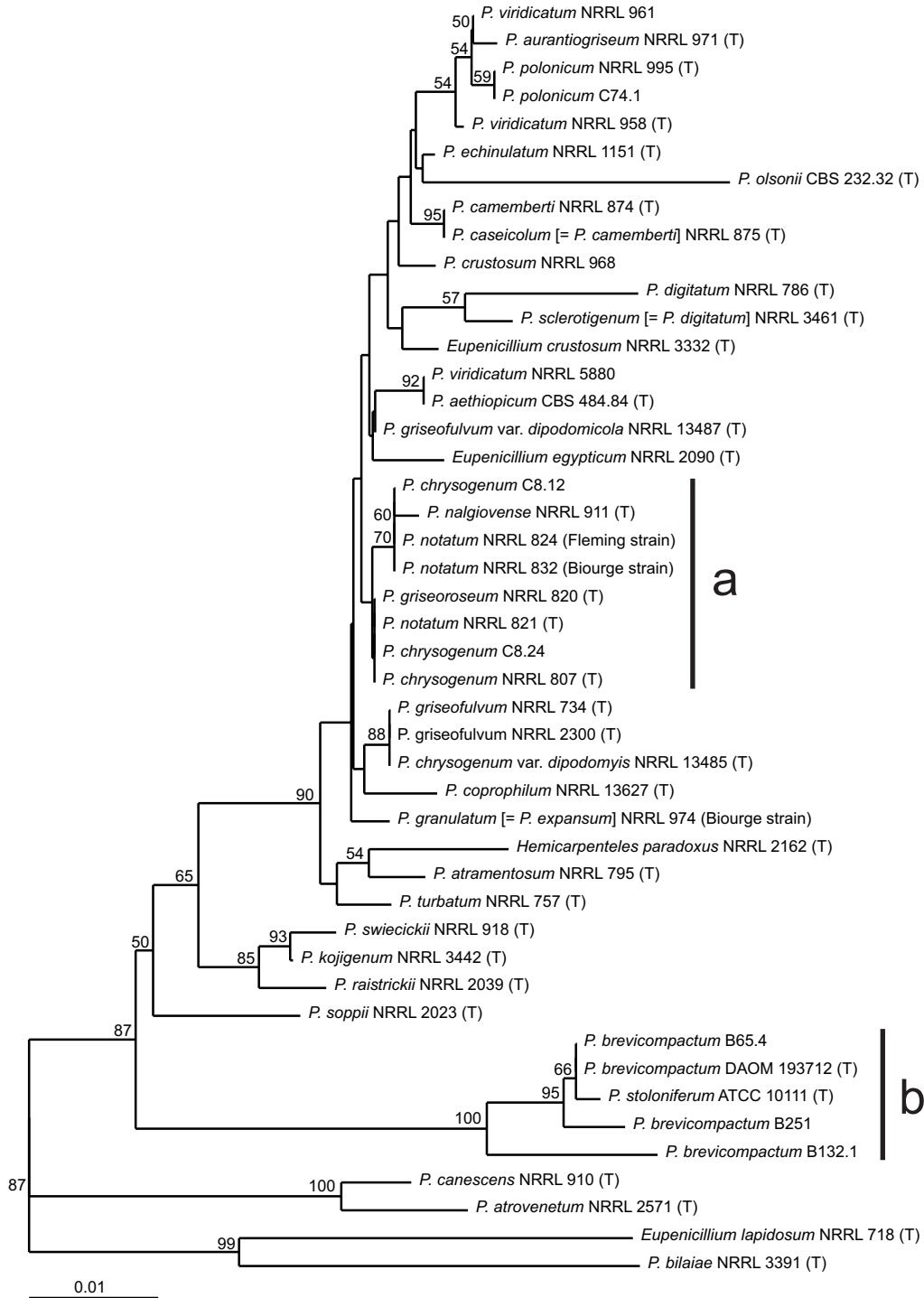
Representatives of subgenus *Furcatum* (indicated in yellow) were interspersed throughout the tree, indicating the multiple origin of the furcate conidiophore form characteristic of this group. Similarly, isolates of subgenus *Divaricatum* (indicated in blue) appeared throughout the tree. Divaricate conidiophore morphology appears to be the ancestral branching state, as it forms the backbone of the phylogeny. A multiple origin for the furcate form and an ancestral divaricate morphology for the genus provide the best interpretation of the internal branching topology of this tree. The principal clades identified in this analysis corresponded well to those observed by Peterson (2000) in a parsimony-based analysis of this dataset. The numbered groups observed by Peterson (2000) are indicated on the dendrogram in Figure 4-6 on the corresponding branches. Peterson’s results concur that penicillius complexity is not a reliable phylogenetic predictor, and that this feature is likely influenced by aspects of life history and dispersal of the species (or lineage) in question. The exception is the terverticillate *Penicillia*, which in both analyses formed a well-supported monophyletic group. Within this group, however, species were poorly separated. The employment of faster-evolving genes may better resolve these taxa.

### ***PENICILLIUM CHRYSOGENUM***

A subset of the above dataset limited to ITS1-5.8S-ITS2 region of GenBank sequences of 36 taxa in *Penicillium sensu stricto* collected by Dr. Steve Peterson (USDA, Peoria) were reanalyzed as above. Other sequences included in this dataset were representatives of Wallaceburg isolates of *P. brevicompactum*, *P. chrysogenum* and *P. polonicum*, as well as ex-type strains of species considered to be closely related to these taxa (e.g. *P. aethiopicum* CBS 484.84; *P. olsonii* CBS 232.32, *P. stoloniferum* ATCC 10111 and *P. brevicompactum* DAOM 193712). Sequences were analyzed and a distance tree was generated, as described above. The Neighbor-Joining tree shown in Figure 4-8 was rooted using *Eupenicillium lapidosum* and *Penicillium biliariae* (subgenus *Aspergilloides*). Isolates representing the *P. chrysogenum* complex group together in a weakly supported clade centrally within subgenus *Penicillium* (indicated as clade **a**, Figure 4-8). Within this group, two voucher strains deposited as *P. notatum* (NRRL 824 from Fleming and NRRL 832 from Biourge), the Wallaceburg strains represented by C8.12 (179 isolates in total) and *P. nalgiovense* (ex-type strain NRRL 911) formed a well-supported clade.

### ***PENICILLIUM BREVICOMPACTUM***

Isolates of *P. brevicompactum* formed a well-supported clade sister to the terverticillates (indicated as clade **b**, Figure 4-8). Within the *P. brevicompactum* clade, two well-defined groups were observed. The first of these contained the ex-type strains of *P. brevicompactum* (DAOM 193712) and *P. stoloniferum* (ATCC 10111) along with 60 isolates from the Wallaceburg collection represented by B65.4 (46 isolates) and B251 (15 isolate). The second group consisted of 10 Wallaceburg isolates represented by B132.1.



**FIGURE 4-8.** Distance tree of *Penicillium* subgen. *Penicillium* inferred from ITS1-5.8S-ITS2 rDNA data outgroup-rooted using *Eupenicillium lapidosum* and *P. bilaiae*.

## CHAPTER 5. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES OF *PENICILLIUM BREVICOMPACTUM*<sup>s</sup>

### ABSTRACT

*Penicillium brevicompactum* is a commonly occurring putatively asexual soilborne fungus and inhabitant of the decaying fruit bodies of fleshy fungi. This species is also known as a frequent contaminant of water-damaged building materials such as gypsum wallboard (Scott, 1999a). The present study examined the distribution of genotypic diversity based on sequences of two genes between indoor and outdoor populations of this fungus. The primary objective of this study was to test the current species concept applied to *P. brevicompactum*.

Seventy-five morphologically and physiologically uniform isolates of *P. brevicompactum* were obtained from 54 houses in Wallaceburg, Ontario, Canada. Three polymorphic genetic loci, beta-tubulin (*benA*), internal transcribed spacer regions of ribosomal DNA (ITS1-2) and histone 4 (*his4*) were amplified using PCR and compared by heteroduplex mobility assay (HMA). Nine unique multilocus haplotypes were observed in which alleles showed strong association indicating predominantly clonal reproduction. Two major genotypes were observed, which dominated the houses sampled, accounting for 88.6 % and 5.4 % of the sample, respectively. Other haplotypes were observed at low frequency in several of the houses from which multiple isolates were obtained.

---

<sup>s</sup> Parts of this chapter are reprinted with the kind permission of Eastern New York Occupational and Environmental Health Centre (ENYOEH), Albany, New York, USA, from Scott, J.A., Straus, N.A. and Wong, B. 1999. Heteroduplex DNA fingerprinting of *Penicillium brevicompactum* from house dust. pp. 335-342, *In* Bioaerosols, fungi and mycotoxins: health effects, assessment, prevention and control. E. Johanning (ed). Albany, New York: ENYOEH. 638 pp.

DNA sequence analysis of the beta-tubulin and rDNA loci for all alleles confirmed two genetically divergent groups within *P. brevicompactum* as currently circumscribed. Authentic strains of *P. brevicompactum* and *P. stoloniferum* clustered together in the predominant indoor clade which accounted for 86 % of the Wallaceburg isolates. The second lineage contained 14 % of the Wallaceburg isolates, and clustered with voucher collections obtained from the rotting fruit bodies of macrofungi.

## INTRODUCTION

There is widespread agreement that the outdoor environment contributes substantially to the burden of biological particulate present in building interiors (Miller, 1992). Although airborne fungal spores of outdoor origin are accepted to be amongst the principal allergenic mediators of seasonal allergic rhinitis, the presence of amplifiers of fungi within the building envelope presents a more serious concern. This is so for two main reasons: 1) In contrast to most outdoor surfaces, building materials of organic origin remain devoid of active growth until they become water damaged, at which point the absence of microbial competition facilitates the unbridled growth of primary fungal colonists; and 2) the indoor environment contains a finite dilution volume of air, permitting the establishment of airborne concentrations of these contaminants which may profoundly exceed outdoor levels. In the case of persistently wet drywall, the species most often observed are *Aspergillus nidulans* group, *As. versicolor*, *Chaetomium* spp., *Penicillium brevicompactum* and *Stachybotrys chartarum*. Curiously however, certain species, notably *As. versicolor*, *P. brevicompactum* and *P. chrysogenum* may be observed in abundance even in building environments lacking conspicuous amplifiers (Scott et al., 1999a, b). Investigations of both outdoor air and organic substrata fail to demonstrate sufficient presence of propagules of these fungi to account for their predominance in the indoor spora relative to other typical



background taxa, such as phylloplane moulds (Scott et al., 1999a). Thus, the culture-presence of these taxa from dust isolations, many of which range from xerotolerant to xerophilic, has been interpreted as evidence for the proliferation of these species in the dust substrate under "normal" conditions (e.g. low water activity) (e.g. Davies, 1960; Bronswijk, 1981). Despite considerable observation and documentation of these species from household dust and indoor air, there is scant empirical evidence to support this widespread hypothesis of generalized cryptic indoor proliferation under normal circumstances. Furthermore, the phylogenetic placement of *P. brevicompactum* within *Penicillium* has not been tested using molecular methods.

The present study was undertaken in cooperation with the Canada Mortgage and Housing Corporation (CMHC) in which multiple isolates of *P. brevicompactum* were obtained from houses in Wallaceburg, Ontario (see Figure 2-1). The amount of genotypic variability in PCR-amplified polymorphic genetic loci was assessed using a heteroduplex mobility assay. This method has been used previously in the screening of human genes for mutations of clinical diagnostic significance (e.g. White et al., 1992), and in the epidemiological investigation of human viral populations (Delwart et al., 1993; 1994). Chapters 3 and 4 present a more detailed discussion of this method.

## **MATERIALS AND METHODS**

### **COLLECTION AND CHARACTERIZATION OF ISOLATES**

Vacuum cleaner bag samples of carpet dust were collected from 369 houses in Wallaceburg, Ontario, Canada by a private company under contract to the Canada Mortgage and Housing Corporation over a period of five months starting in January, 1994. The distribution of house locations sampled is shown on the street map in Figure 5-1. Fungal isolates were obtained using



**FIGURE 5-1.** Street map of Wallaceburg, Ontario, indicating collection sites for *P. brevicompactum* isolates used in this study.

a standard dilution plating technique (Malloch, 1981). Isolates of *Penicillium* were identified using conventional methods (e.g. Pitt, 1980). Isolates selected for genetic screening were indistinguishable based upon microscopic morphology and physiological profiles on standard growth media (Pitt, 1979). Chapter 4 contains detailed information on these procedures. A set of isolates of *P. brevicompactum* from other locations was included for comparison (*see* Table 5-1).

DNA isolation and PCRs were performed according to the methods described in Chapter 4. Three polymorphic loci consisting of introns in the genes encoding beta-tubulin (BenA), histone 4 (H4) and the region spanning the internal transcribed spacers (ITS1 to ITS2) of nuclear ribosomal DNA (rDNA) were PCR-amplified using the primer sequences given in Table 5-2. The position of these primers is shown in Figure 5-2. Methods used for heteroduplex analysis of PCR products are given in Chapter 4.

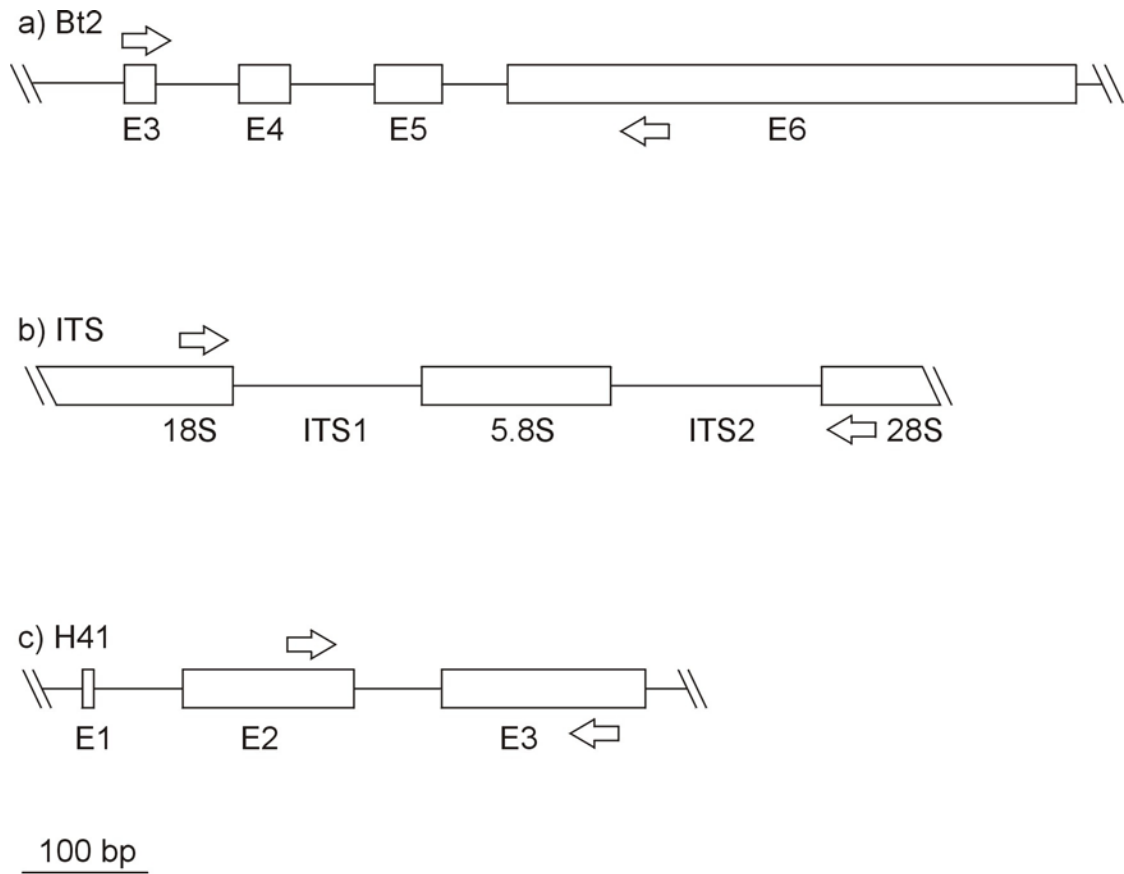
### **SEQUENCE ANALYSIS**

PCR templates were purified using QIAquick PCR purification kit (Qiagen, Inc., Valencia, Calif.). PCR templates were sequenced using the Taq DyeDeoxy cycle sequencing kit (Applied Biosystems, Inc., Foster City, Calif.) and extension products were analysed on an ABI-50 fluorescent automated sequencer (Applied Biosystems, Inc.). Sequences were determined on both sense and anti-sense strands using the same primers that were used for amplification (*see* Table 5-2).

Alignments of sequences were performed using Clustal X software package (version 1.8) (*see* Jeanmougin et al., 1998; Thompson et al., 1997) and adjusted by visual inspection using a text editor. Sequences were combined for analysis based on congruence as determined by the

**Table 5-1:** List of comparative strains used in this study

Strain number	Identification	Status	Substratum
ALG1	<i>P. brevicompactum</i>		decaying agaric, Algonquin Prov. Pk., Ontario, Canada
ALG2	<i>P. brevicompactum</i>		decaying agaric, Algonquin Prov. Pk., Ontario, Canada
ATCC 10111	<i>P. stoloniferum</i> Thom	ex-type	decaying bolete, Connecticut, USA
CBS 232.60	<i>P. olsonii</i>	ex-type	root of <i>Picea</i> ,
DAOM 147648	<i>P. brevicompactum</i> Dierckx		mushroom, Ottawa, Ontario
DAOM 191327	<i>P. brevicompactum</i> Dierckx		<i>Cytospora</i> sp. on <i>Prunus persica</i> , Harrow, Ontario
DAOM 192262	<i>P. brevicompactum</i> Dierckx		urea formaldehyde foam insulation, Ottawa Ontario
DAOM 193710	<i>P. chrysogenum</i>	ex-type	cheese, Connecticut, USA
DAOM 193712	<i>P. brevicompactum</i> Dierckx	ex-type	<i>substr. incertum</i> , ?Belgium
DAOM 193713	<i>P. stoloniferum</i> Thom	ex-type	decaying bolete, Connecticut, USA
DAOM 214776	<i>P. brevicompactum</i> Dierckx		decaying mushroom, Denmark
DAOM 215331	<i>P. brevicompactum</i> Dierckx		spruce lumber, Quebec
DAOM 215332	<i>P. brevicompactum</i> Dierckx		on <i>Picea</i> , Quebec
DAOM 215335	<i>P. brevicompactum</i> Dierckx		spruce lumber, Quebec



**FIGURE 5-2.** Locations of primers used to amplify polymorphic regions in *P. brevicompactum*.

**Table 5-2:** Primers sequences employed in this study

---

<b>Beta-tubulin (benA)</b>			
Source:	Glass & Donaldson, 1995		
Fwd primer 5'-3':	GGT AAC CAA ATC GGT GCT GCT TTC		(Bt2a)
Rvs primer 5'-3':	ACC CTC AGT GTA GTG ACC CTT GGC		(Bt2b)
<b>Nuclear rDNA ITS regions</b>			
Source:	White et al., 1990, fwd; Untereiner et al., 1995, rvs		
Fwd primer 5'-3':	GGA AGT AAA AGT CGT AAC AAG G		(ITS5)
Rvs primer 5'-3':	TAT GCT TAA GTT CAG CGG		(WNL1)
<b>Histone 4 (H41)</b>			
Source:	Glass & Donaldson, 1995		
Fwd primer 5'-3':	GCT ATC CGC CGT CTC GCT		(H41a)
Rvs primer 5'-3':	GGT ACG GCC CTG GCG CTT		(H41b)

---

Partition Homogeneity Test (PHT). The PHT has been subject to recent criticism for its performance in determining sequence congruence (Barker and Lutzoni, 2000). Certain datasets which have been demonstrably congruent have not been reported so using this test. As such, the PHT should only be used as a guideline and not an absolute determinant of congruence; however, it remains widely used for this purpose and is offered as a best available assessment of congruence in the present study. These problems are considered in greater detail in the discussion section of this chapter.

Phylogenetic analyses were carried out using the Clustal X and PAUP\* software packages (PAUP\* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts) using the Neighbor-Joining method. The data were re-sampled by 1000 bootstrap replicates, and the proportion of Neighbor-Joining trees possessing each particular internal branch is indicated to express its level of support. Phylogenetic trees were generated using the TreeView software package, version 1.5.2 for Microsoft Windows 32 bit (Roderick Page, Oxford University), and formatted using Corel Draw version 8.232 (Corel Corporation, Ottawa).

## **RESULTS**

Collection locations of house dust isolates are shown in Figure 5-1. Isolates of *P. brevicompactum* were obtained from 54 of the 369 houses examined (15 %). Six of these houses were in rural locations (i.e. outside the town limits). In total, 72 isolates were examined, 54 of which originated from urban locations and the remainder (18) from rural locations.

### HETERODUPLEX MOBILITY ASSAY

The genotypes of house dust *P. brevicompactum* isolates are summarized in Table 5-3. The lowest degree of allelic variation was observed in the histone 4 locus (2 alleles) whereas the highest variation (6 alleles) was seen in the beta-tubulin locus (*see* Table 5-4). The three most commonly observed haplotypes were present in 57 %, 17 % and 16 % of isolates. The remaining minor haplotypes occurred in 4 % or fewer isolates. Mixed populations of two-or more genotypes were observed in two thirds of houses from which multiple isolates of *P. brevicompactum* were obtained suggesting the stable co-existence of multiple genotypes within individual houses.

### DNA SEQUENCE ANALYSIS

DNA sequences were obtained for representatives of each allele for the *benA* and ITS loci. Difficulties were encountered in obtaining unambiguous sequence for the histone 4 locus in house dust isolates and voucher strains. Further attempts to resolve these difficulties were not made due to the low allelic variation in this locus, and it was excluded from sequence analyses.

Sequence alignments of partial beta-tubulin and ITS sequences are give in Appendix F. Figure 5-3 shows the results of a Partition Homogeneity Test (PHT) conducted on a combined alignment of beta-tubulin and ITS sequences including representative isolates of all house dust genotypes and voucher strains (listed in Table 5-1). The PHT produced a p-value = 0.0943, indicating that sequence data from these two genetic loci were congruent and could be combined. A distance tree produced from the combined *benA*-ITS dataset with PAUP\* using the Neighbor-Joining method and rooted to *P. chrysogenum* (DAOM 193710 T) is shown in Figure 5-4c. Branch support is given as the percentage of 1000 bootstrap replications. Two well supported clades were observed. Clade 1 contained authentic strains of *P. brevicompactum* and *P.*

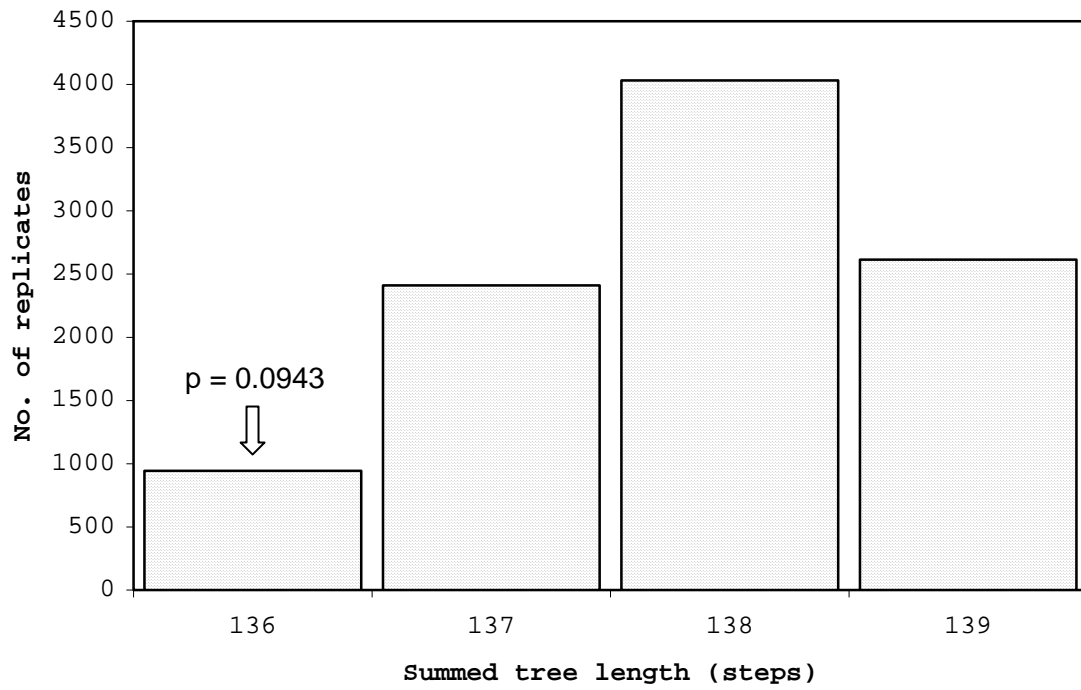


**Table 5-3:** Summary of haplotypes of *P. brevicompactum* isolates

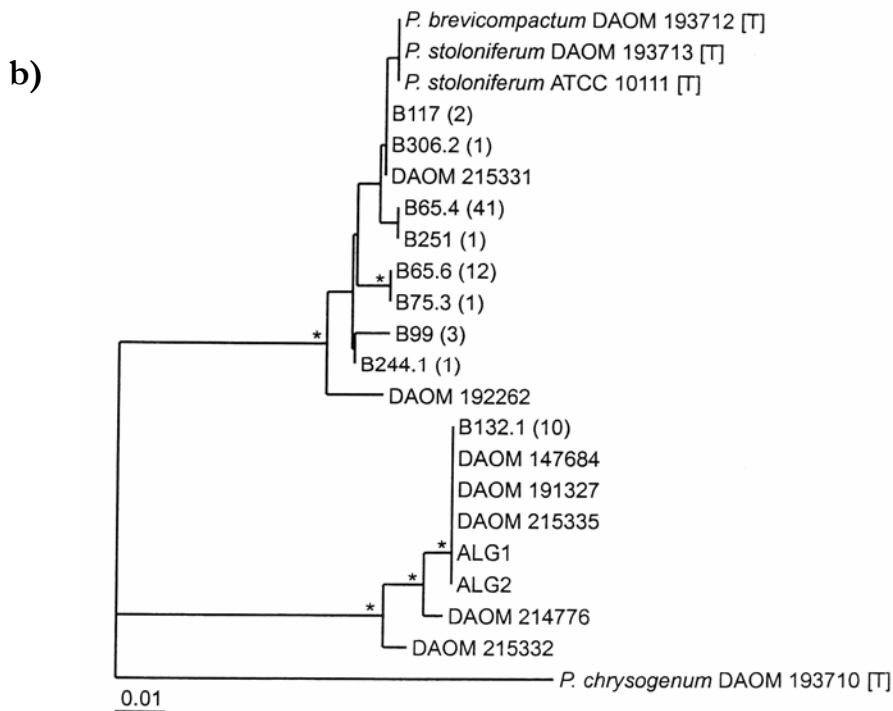
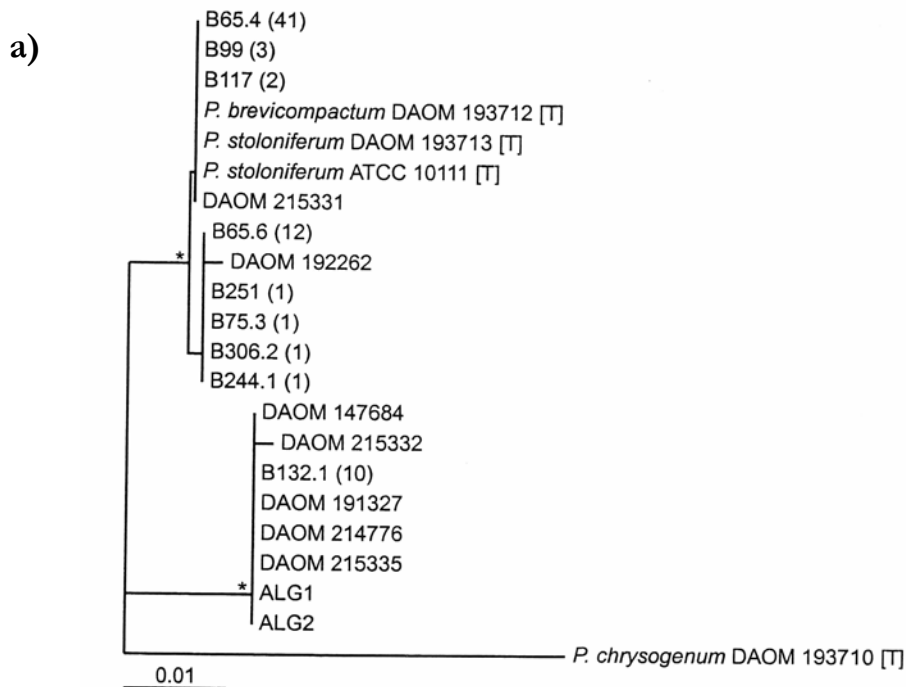
Isolate #	LOCUS			Isolate #	LOCUS		
	benA	his4	ITS		benA	his4	ITS
42.1	A	A	A	132.2	B	B	C
45.1	B	B	C	136	A	A	A
45.2	B	B	C	165	A	A	A
62	A	A	A	166	A	A	A
65.1	A	A	A	170.1	A	A	A
65.3	A	A	A	183	D	A	A
65.4	A	A	A	185	A	A	A
65.5	B	B	C	189	A	A	A
65.6	C	A	B	192.1	A	A	A
67.2	A	A	A	192.2	A	A	A
67.3	A	A	A	201	A	A	A
67.4	A	A	A	204	C	A	B
67.5	C	A	B	217.2	A	A	A
67.6	B	B	C	228.1	C	A	B
67.7	A	A	A	233.1	B	B	C
70.4	A	A	A	233.2	C	A	B
72	A	A	A	240	A	A	A
74.1	A	A	A	244.1	F	A	B
75.1	A	A	A	244.3	A	A	A
75.2	C	A	B	245.2	E	A	A
75.3	C	A	D	251	A	A	B
79	A	A	A	259	A	A	A
81.1	A	A	A	263.1	A	A	A
87	C	A	B	264	D	A	A
91	B	B	C	266	A	A	A
98	A	A	A	273	A	A	A
99	D	A	A	274	A	A	A
100.2	A	A	A	280	A	A	A
109.1	C	A	B	306.2	E	A	B
109.2	A	A	A	319	A	A	A
112	C	A	B	322	A	A	A
114	C	A	B	325	C	A	B
117	E	A	A	340	B	B	C
119.1	A	A	A	353.1	B	B	C
119.2	A	A	A	373	A	A	A
132.1	B	B	C	374	C	A	B

**Table 5-4:** Haplotype frequencies for *P. brevicompactum* isolates

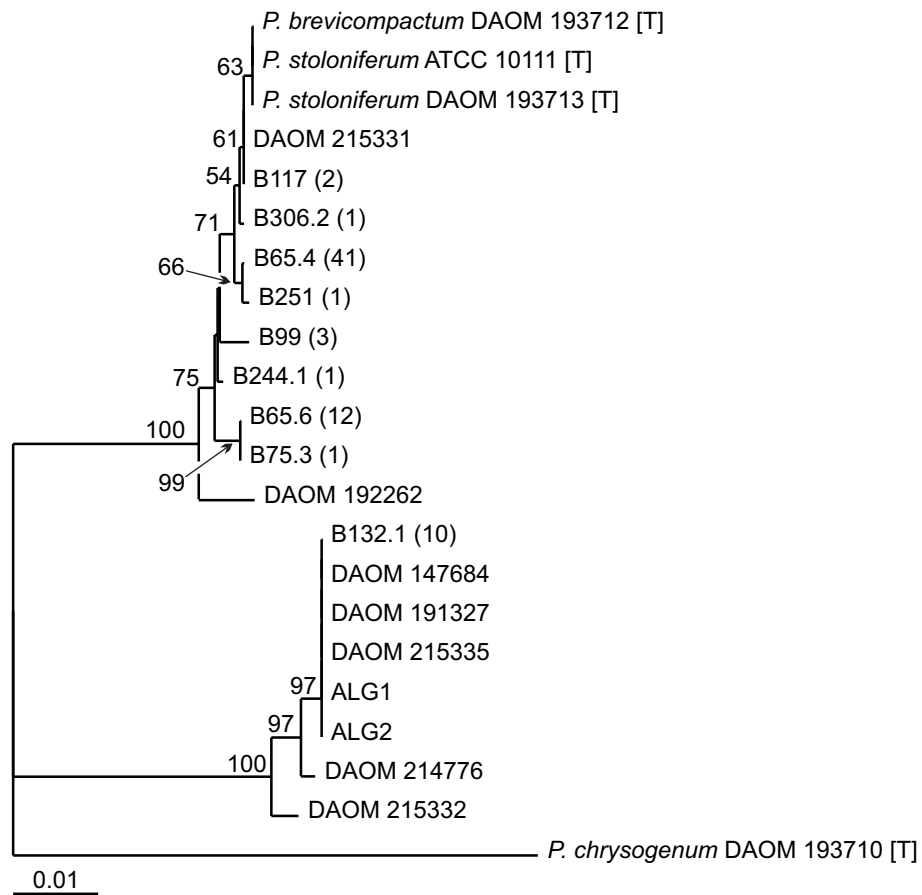
Representative Isolate	LOCUS			Frequency
	Bt2	H41	ITS	
B65.4	A	A	A	0.569
B65.6	C	A	B	0.167
B132.1	B	B	C	0.139
B99	D	A	A	0.042
B117	E	A	A	0.028
B251	A	A	B	0.014
B75.3	C	A	D	0.014
B306.2	E	A	B	0.014
B244	F	A	B	0.014



**FIGURE 5-3.** Results of Partition Homogeneity Test for combined *benA* and ITS sequence data for *P. brevicompactum*. Bars show the distribution of the total summed branch lengths of 10,000 trees generated from data sampled randomly across partitioned gene sequences (*benA* and ITS) using PAUP\* 4.0b4a (Swofford, 1999). Summed branch length for the observed MPT is indicated by the arrow.



**FIGURE 5-4A, B:** Neighbour-Joining trees of *Penicillium brevicompactum* isolates based on a) ITS dataset, and b) Bt2 dataset, rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Asterisks indicate bootstrap support greater than 90% based on 1000 replications.

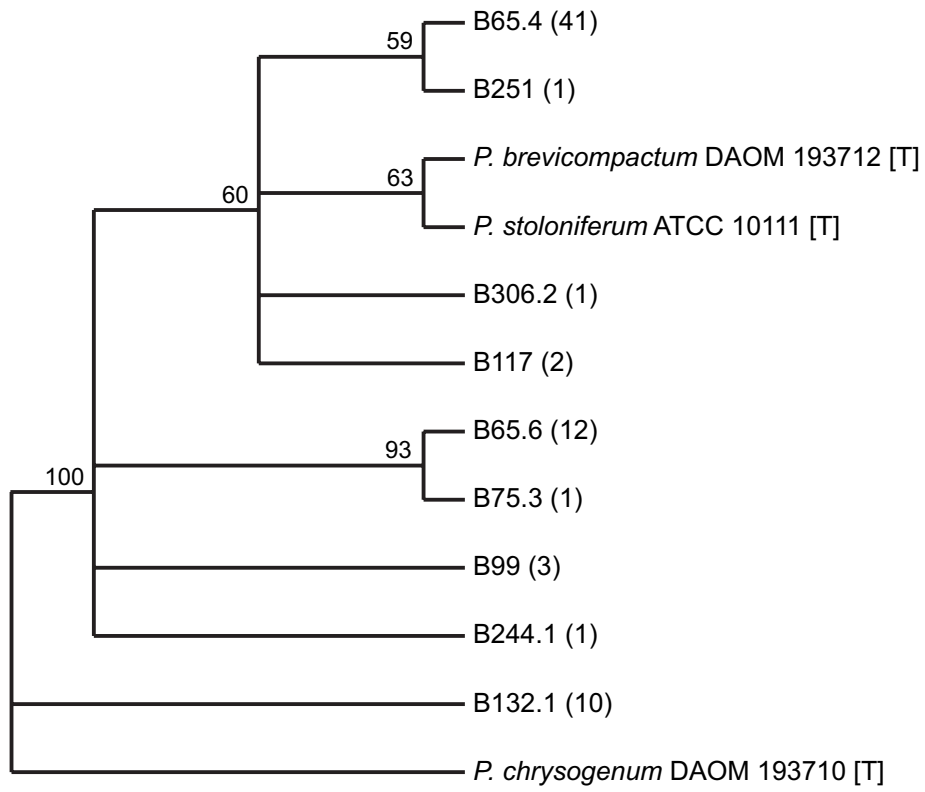


**FIGURE 5-4C.** Neighbour-Joining tree to *Penicillium brevicompactum* isolates based on combined ITS-benA data rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Asterisks indicate bootstrap support greater than 90% based on 1000 replications.

*stoloniferum* as well as 62 of the Wallaceburg house dust isolates and two DAOM strains (DAOM 192262 from urea formaldehyde foam insulation in Ottawa and DAOM 215331 from spruce lumber in Quebec). The synonymy of the *P. stoloniferum* with *P. brevicompactum* proposed initially by Pitt (1979) is supported. Within this clade, the house dust isolates clustered centrally, showing less than 1 % genetic distance between any pair of isolates. Isolate DAOM 215331 (*ex Picea* lumber, Quebec) was closest to B117, B306.2, B65.4, B251, B99 and B244.1, respectively, comprising 68 % of the isolates obtained from Wallaceburg. Sister to this group was a well supported clade containing 18 % of Wallaceburg strains represented by B65.6 and B75.3. Isolate DAOM 192262 (*ex* UFFI, Ottawa) was at the base of Clade 1 on a well-supported branch.

Clade 2 contained the remaining Wallaceburg house dust isolates (14 %) represented by B132.1 that clustered on a well-supported branch with 5 voucher collections (DAOM 147684, DAOM 191327, DAOM 215335, ALG1 and ALG2), 4 of which were obtained from decaying macrofungi. Sister to this cluster was DAOM 214776, an isolate obtained from a decaying mushroom in Denmark. Isolate DAOM 215332 from spruce lumber in Quebec was at the base of clade 2 on a well-supported branch.

Following the elimination of sequences of voucher strains from the combined gene dataset, a parsimony analysis was conducted using PAUP\*. Sequences of authentic strains were retained in this analysis. This reduced dataset yielded 29 parsimony informative characters and produced 20 MTPs of 139 steps in length. A strict consensus tree produced from the 20 MPTs is shown in Figure 5-5 (L = 141 ,CI = 0.9433, RI = 0.8182, RC = 0.7718). Branch support is shown as the percentage of trees showing a particular branch in 1000 bootstrap replications. The branching



**FIGURE 5-5.** Strict consensus tree of 20 MPTs for *Penicillium brevicompactum* isolates based on combined ITS-benA data rooted to the authentic strain of *P. chrysogenum* (DAOM 193710 T). Bootstrap values based on 1000 replications are indicated for branches that demonstrated over 50% bootstrap support.

topology of this tree is not in conflict with the distance tree shown in Figure 5-4 and shows strong support for the same clades of indoor isolates resolved by the latter.

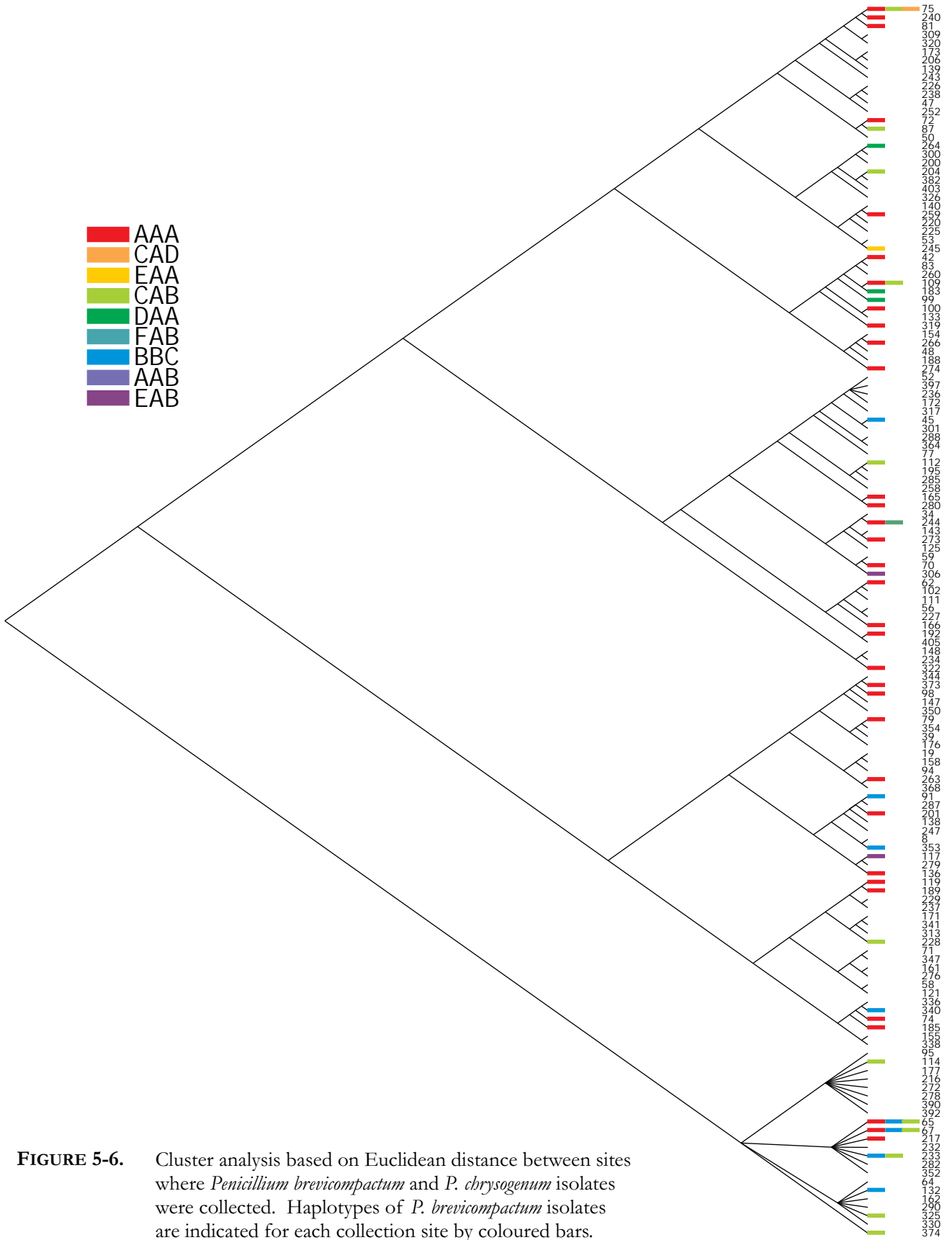
### **SPATIAL DISTRIBUTION**

A graphical summary of the distribution of isolate genotypes according to the proximity of source houses is shown in Figure 5-6. The only trend that is clearly evident is the disproportionate observation of clade 2-type isolates from rural locations (constrained at the base of the dendrogram). Eight percent of the houses sampled were from rural locations and accounted for one quarter of all isolates of the species examined. However, rural isolations provided half of all clade 2 genotypes. Overall, isolates with this genotype accounted for 9 % of urban isolates and 28 % of rural isolates.

### **DISCUSSION**

As methods of DNA sequencing improve and associated costs decrease, there has been a growing trend to infer phylogenies based on the analysis of multiple rather than single molecular datasets. Thus, approaches to analysing multiple datasets have received much recent discussion. Huelsenbeck and co-workers (1996) summarized and compared three fundamental strategies for dealing with multiple datasets: 1) Total evidence approach; 2) Separate Analysis and 3) Conditional Combination. The Total Evidence approach follows the assertion of Kluge (1989) that the inclusion of all available taxa (including both extant and extinct taxa) and all available characters favours convergence on the correct phylogenetic tree. Critics have argued that the demonstration of conditions under which parsimony fails to yield the correct branch topology given every informative character (*viz* Bull et al., 1993) counterindicates this approach (Huelsenbeck and Hillis, 1993). Miyamoto and Fitch (1995) advocated Separate Analysis of





**FIGURE 5-6.** Cluster analysis based on Euclidean distance between sites where *Penicillium brevicompactum* and *P. chrysogenum* isolates were collected. Haplotypes of *P. brevicompactum* isolates are indicated for each collection site by coloured bars.

multiple datasets, citing that the loss of independence of characters resulting from the combined analysis of multiple datasets weakens statistical support for phylogenetic inference. In contrast, these authors favoured multiple independent confirmation of phylogeny based upon the analysis of data partitions separately as a means to enhance accuracy and lend statistical support to the inferred pattern of descent. Several authors have proposed a middle-ground compromise to these conflicting viewpoints, offering that independent datasets may be analysed in combination when the data partitions can be shown to be congruent (Bull et al., 1993; Huelsenbeck et al., 1996; de Queiroz, 1993; Rodrigo et al., 1993). This approach of “Conditional Combination” mandates the prior demonstration of homogeneity of partitions. One favoured method to test sequence congruence has been the Partition Homogeneity test (PHT) (*viz.* PAUP\* software package by Swofford) also known as the Incongruence Length Difference (ILD) (*viz.* Farris et al., 1995) test, whereby separate datasets are randomly resampled across partitions without replacement, and these resampled data are used to generate trees by parsimony analysis. The sum of the branch lengths of the “best” tree obtained without resampling is then compared to the distribution of the sums of branch lengths taken from a set of trees inferred from randomly resampled data. These sums should be similar where datasets are congruent (the null hypothesis), and differ under incongruence (*see* Farris et al., 1995). This test is used widely to test congruence of partitioned datasets and has shown superior performance relative to other statistical tests used for this purpose (Cunningham, 1997). Barker and Lutzoni (2000), however, noted that the ILD test was susceptible to rejecting the null hypothesis of congruence erroneously when data partitions showed differing levels of homoplasy. This problem was similarly noted by Carbone and co-workers (1999). The PHT has been employed in the present study as a test of congruence of sequence data prior to combined analysis. However, the reader is cautioned that spurious rejection of partition homogeneity may be an issue.

The present study concerns *Penicillium brevicompactum*, which is a common colonist of water damaged indoor substrates, particularly drywall (Scott et al., 1999a; *also see* pg. 194). This species is also known from a number of outdoor substrates including decomposing fruiting bodies of macrofungi and other decaying organic matter (Pitt, 1979). However *P. brevicompactum* is poorly represented in outdoor air. Scott and colleagues (1999a) proposed that the differential removal of larger-spored fungi by mechanical and filtration effects (e.g. vacuum cleaning and elutriation in air conveyance systems), and the lengthy spore viabilities characteristic of anamorphs of the Trichocomaceae play a significant role in the artifactual concentration of propagules of these microfungi in indoor environments.

The present study identified two distinct lineages within *P. brevicompactum* (clades 1 & 2). Isolates from Clade 1 were distributed throughout the set of houses sampled, whereas Clade 2 isolates showed an increased prevalence in rural localities. Voucher isolates included in sequencing studies that clustered in Clade 2 demonstrated a substrate preference for decaying fungal fruit bodies. It is clear that the name *P. brevicompactum* applies to taxa included in Clade 1; however, based on the authentic isolates included in this study, there does not appear to be an available name for taxa in Clade 2. Seifert and Frisvad (2000) studied *Penicillium* species on solid wood products and reported two discrete micromorphologies for isolates of *P. brevicompactum*. In particular, certain *P. brevicompactum* isolates showed predominantly biverticillate branching and strongly apically inflated metulae in fresh cultures. These authors suggested that these cultural variants may represent distinct taxa. It is of interest to assess the use of these characters in separating the genetic lineages revealed in the present study. Furthermore, the genotypic markers employed in this study may help to elucidate Seifert and Frisvad's (2000) observation.

### ***PENICILLIUM STOLONIFERUM***

Thom (1910) described *Penicillium stoloniferum* based on an isolate obtained from a decaying mushroom in Connecticut. This species was reduced to synonymy with *P. brevicompactum* by Thom (1930) but later included in the *P. brevicompactum* series by Raper and Thom (1949), which included *P. brevicompactum*, *P. stoloniferum* and *P. paxilli*. Pitt (1979) suggested that isolates *P. stoloniferum* and *P. brevicompactum* showed a continuum of variation, and once again reduced *P. stoloniferum* to synonymy with *P. brevicompactum*. This synonymy is supported by the present study.

### ***PENICILLIUM PAXILLI***

The third species included by Raper and Thom (1949) in the *P. brevicompactum* series, *P. paxilli*, was described by Bainier (1907) from an isolate obtained from banana cultivated in the Paris Botanical Garden. This species was accepted by Thom (1930) and further characterized by Raper and Thom (1949) based on an isolate obtained from optical glass in Panama (NRRL 2008) due to the unavailability of authentic material. Pitt (1979) neotypified *P. paxilli* using this isolate (as Herb. IMI 40226), and noted morphological similarity of *P. paxilli* to isolates of *P. brevicompactum* in the production of apically inflated metulae. However, he justified the placement of *P. paxilli* in subgenus *Furcatum* based on the absence of rami in this taxon (Pitt, 1979), later noting that branching variation present in some isolates of *P. paxilli* might indicate the existence of two distinct species (Pitt, 1985). It is likely that the current concept of *P. paxilli* is inconsistent with *P. paxilli sensu* Bainier (1907) based on the dissimilarity of the habitat from which the neotype was obtained. In the present study, *P. paxilli* (NRRL 2008 T) clustered with the type strain of *P. sumatrense* (NRRL 779 T) on a well-supported branch that was sister to the clade that included ex-type strains of the divaricate taxa *P. canescens* (NRRL 2147 T), *P. waksmanii*

(NRRL 777 T) and *P. miczynskii* (NRRL 1077 T), the furcated taxon *Eu. shearii* (NRRL 715 T) and the monoverticillate taxon *P. roseopurpureum* (NRRL 2064 T) (see Chapter 4, Figure 4-6). This clade was distantly separated from the clade that included terverticillate taxa, the closest relatives of the *P. brevicompactum* group (see Figure 4-8). Despite some similarity in appearance of *P. paxilli* to the *P. brevicompactum* group, the former taxon is only distantly related. Nevertheless, it is possible that the recognition of a second species within the current circumscription of *P. paxilli* as suggested by Pitt (1985) may redistribute some isolates currently treated under this name to the *P. brevicompactum* group. However, the elucidation of this problem awaits the molecular characterization of multiple isolates of *P. paxilli*, including representatives from the originally described habitat (i.e. cultivated bananas).

#### **AFFILIATIONS OF *P. BREVICOMPACTUM***

During the First International *Penicillium* and *Aspergillus* Workshop (PAW-I) Williams and colleagues (1985) postulated that *P. brevicompactum* was derived from *P. aurantiogriseum* and that it represented a central evolutionarily lineage in the terverticillates. These authors depicted *P. brevicompactum* as a penultimate evolutionary step between *P. aurantiogriseum* (basal) and *P. olsonii* (derived) in a “nested trumpet” diagram (Williams et al., 1985). In discussion that followed the presentation of this paper, Samson (1985) further suggested that the immediate ancestor of *P. brevicompactum* may be *P. chrysogenum*. Neither of these hypotheses is supported by the present study. As shown in the ITS-based phylogeny presented in Chapter 4, isolates of *P. brevicompactum* including the ex-type of this species formed a basal clade that was sister to the terverticillate *Penicillia* (Figure 4-8), although bootstrap support for this branch was weak.

Ironically, the placement of *P. olsonii* by Williams and co-workers (1985) is in agreement with the position of this taxon inferred from the present molecular phylogeny based on ITS sequence (see Chapter 4, Figure 4-8). The type strain of *Penicillium olsonii* Bainier and Sartory (CBS 232.32 T) was situated on a long, weakly-supported branch that was sister to the type strain of *P. echinulatum* (NRRL 1151 T). In turn, this clade was basal to the clade that included the type strains of *P. aurantiogriseum* (NRRL 971 T), *P. polonicum* (NRRL 995 T) and *P. viridicatum* (NRRL 958 T). This inferred phylogeny suggests that *P. brevicompactum* (= *P. stoloniferum*) and *P. olsonii* represent distantly-related lineages which show convergent evolution of characters such as variously apically inflated metulae and compact, fan-shaped penicilli. Similarly, the elongated stipes reported from *P. stoloniferum* are reminiscent of those produced by *P. olsonii*. At present, however, I cannot exclude the possibility that the type strain of *P. olsonii* (CBS 232.32) included in this phylogeny was a specious isolate. As such, confirmation of this sequence using collections of the type strain from other culture collections is required to establish the proper phylogenetic position of *P. olsonii*.

## CONCLUSIONS

*Penicillium brevicompactum* as presently circumscribed consists of at least two lineages which may represent distinct species. One of these lineages, *P. brevicompactum* sensu stricto occurred commonly in broadloom dust in houses in southern Ontario. Members of the second lineage tended to occur predominantly as saprotrophs on the decaying fruit bodies of fleshy fungi, and were isolated rarely from indoor dust samples.

## CHAPTER 6. ASSESSMENT OF GENETIC VARIATION IN INDOOR ISOLATES OF *PENICILLIUM CHRYSOGENUM*<sup>9</sup>

### ABSTRACT

Isolates of *Penicillium chrysogenum* were examined from 369 houses in Wallaceburg, Ontario, Canada. In total, approximately 700 isolates of *P. chrysogenum* were obtained by serial dilution plating of broadloom dust samples, and identified based on standard criteria. From this collection, a subset of 198 isolates representing 109 houses was selected for genetic characterization based upon micromorphological and physiological uniformity on several carbon and nitrogen sources.

Multiple genetic loci spanning introns in structural and metabolic genes such as thioredoxin reductase (*trxB*), beta-tubulin (*benA*) and acetyl co-enzyme A synthase (*acuA*), as well as the internal transcribed spacer regions of the non-coding nuclear ribosomal sub-repeat (rDNA, ITS1-2) were compared using heteroduplex mobility assay. In this method, homologous PCR amplicons were pooled pairwise in equimolar proportion, thermally denatured and reannealed. Dissimilar amplicon pairs were resolved by the slower electrophoretic migration of heteroduplexed dsDNAs relative to homoduplexes on low-crosslinked polyacrylamide-agarose hybrid gels into which glycerol was incorporated as a mild denaturant.

---

<sup>9</sup> Parts of this work were presented as an invited symposium contribution at the IX International Congress of Mycology in Sydney, Australia, August 1999, as Scott, J.A., Straus, N. and Malloch, D. 1999. Molecular genetic characterization of variability in *Penicillium chrysogenum* from indoor environments. MOS5.6, IX International Union of Microbiological Societies (IUMS) Abstracts Book, p. 185.

Five unique multilocus haplotypes were revealed with no evidence of recombination, indicating clonal propagation. Two major genotypes were observed, which dominated the houses sampled, accounting for 88.6 % and 5.4 % of the sample, respectively. Three other multilocus motifs were observed at low frequency in several houses from which multiple isolates were obtained. Base sequencing of representatives of all groupings, including ex-type strains of *P. chrysogenum* and *P. notatum*, suggested that *P. chrysogenum* as currently circumscribed comprises three strongly supported lineages. Both ex-type strains clustered with the secondary genotype (7% of dust isolates), while the un-named, primary genotype (90%) included the notable laboratory contaminant isolated by Alexander Fleming in 1929. No nomenclatural types included in the present study clustered within the minor clade (4%).

The groups defined using the heteroduplex method were supported by three separate DNA fingerprinting methods: Two randomly amplified polymorphic DNA-type (RAPD) techniques using either the M13 core sequence or (GACA)<sub>4</sub> as a single primer; and a third method employing a primer pair of arbitrary sequence.

Extensive sampling of outdoor air in the study locality during the late summer 1995 failed to reveal *P. chrysogenum*. Outdoor air samples taken throughout the year at other localities in southern Ontario, Canada, have confirmed the rarity of this species complex in outdoor air.

## **INTRODUCTION**

Viable fungal spores occur in great numbers in household dust and indoor air. A large proportion of these spores typically arise outdoors in the phylloplane and are propagated indoors by mechanical means (e.g. upon air currents and contaminated footwear). In contrast,



the genera *Aspergillus* and *Penicillium* are among the most common indoor fungi, yet these moulds are relatively poorly represented in outdoor air. Thus, it is widely believed that they proliferate indoors, often cryptically, on various substrates including dust itself under conditions of low water activity.

*Penicillium chrysogenum* Thom is perhaps the most common of all *Penicillia* (Pitt, 1980; Raper and Thom, 1949), occurring as an agent of food spoilage (Samson et al., 1996) as well as a resident of household dust (Davies, 1960) and indoor air. *Penicillium chrysogenum* is also a well-known contaminant of damp building materials (Chang et al., 1995; Gravesen, 1999; Hunter and Lea, 1995) and indoor finishes (Adan and Samson, 1994). This species is one of the few terverticillate *Penicillia* that typically does not produce mycotoxins with significant mammalian toxicity (Dillon et al., 1996; Nielsen and Gravesen, 1999; Pitt and Cruikshank, 1990). However, *P. chrysogenum* has been identified as a significant allergen in the indoor environment (Cooley, 1999; Cooley et al., 1999; Fergusson et al., 1984) and as a rare causative agent of opportunistic human mycosis (Eschete et al., 1981; Hoffman et al., 1992).

Little is known about the distribution and variability of the *P. chrysogenum* group. Samson and co-workers (1977) applied a broad taxonomic interpretation of the variability they observed in this group, and elected to synonymize a number of later names with *P. chrysogenum*. *Penicillium chrysogenum* is thought to be a strictly asexual species, since no teleomorph has been identified. The putatively clonal nature of *P. chrysogenum* as well as its circumscription and the validity of proposed synonyms remains to be tested using modern molecular means. The present study will examine the extent of clonality within a core group of isolates from the *P. chrysogenum* group including representative authentic isolates, and test the suitability of current species concepts.

## MATERIALS AND METHODS

### ISOLATION AND IDENTIFICATION OF STRAINS

Over seven hundred isolates of *P. chrysogenum* were collected from 376 houses in Wallaceburg, Ontario, as described in Chapter 4. These isolates were grown for 14 days at room temperature on modified Leonian's agar (Malloch, 1981) and modified Creatine-Sucrose agar medium (Frisvad, 1993). A duplicate plate of each isolate was incubated at 37°C for 7 days. Based on the results of this preliminary examination, a subset of 198 micromorphologically and physiologically uniform isolates was selected for genetic characterization. Air sampling was conducted at 18 outdoor locations distributed evenly throughout the Wallaceburg study site during late summer, 1995, using a Reuter Centrifugal sampler (RCS) on Rose Bengal agar medium with a sampling volume of 80 L per sample. Colonies were incubated and identified as above.

The spatial relationship of participant houses is shown in Figure 6-1, in which houses are identified by arbitrary "house numbers" to protect occupant privacy. Sources of house dust isolates are summarized in Table 6-1, including houses from which multiple isolates were obtained. The observed condition of the house with respect to obvious mould damage at the time of site inspection is indicated. The number assigned to each fungal isolate is unique, and consists of the "house number" coupled with an incremental accession number reflective of the total number of isolates of *P. chrysogenum* obtained from that house.

Additional isolates included in sequencing studies consisted of authentic strains as well as a geographical range of voucher material (*see* Table 6-2).

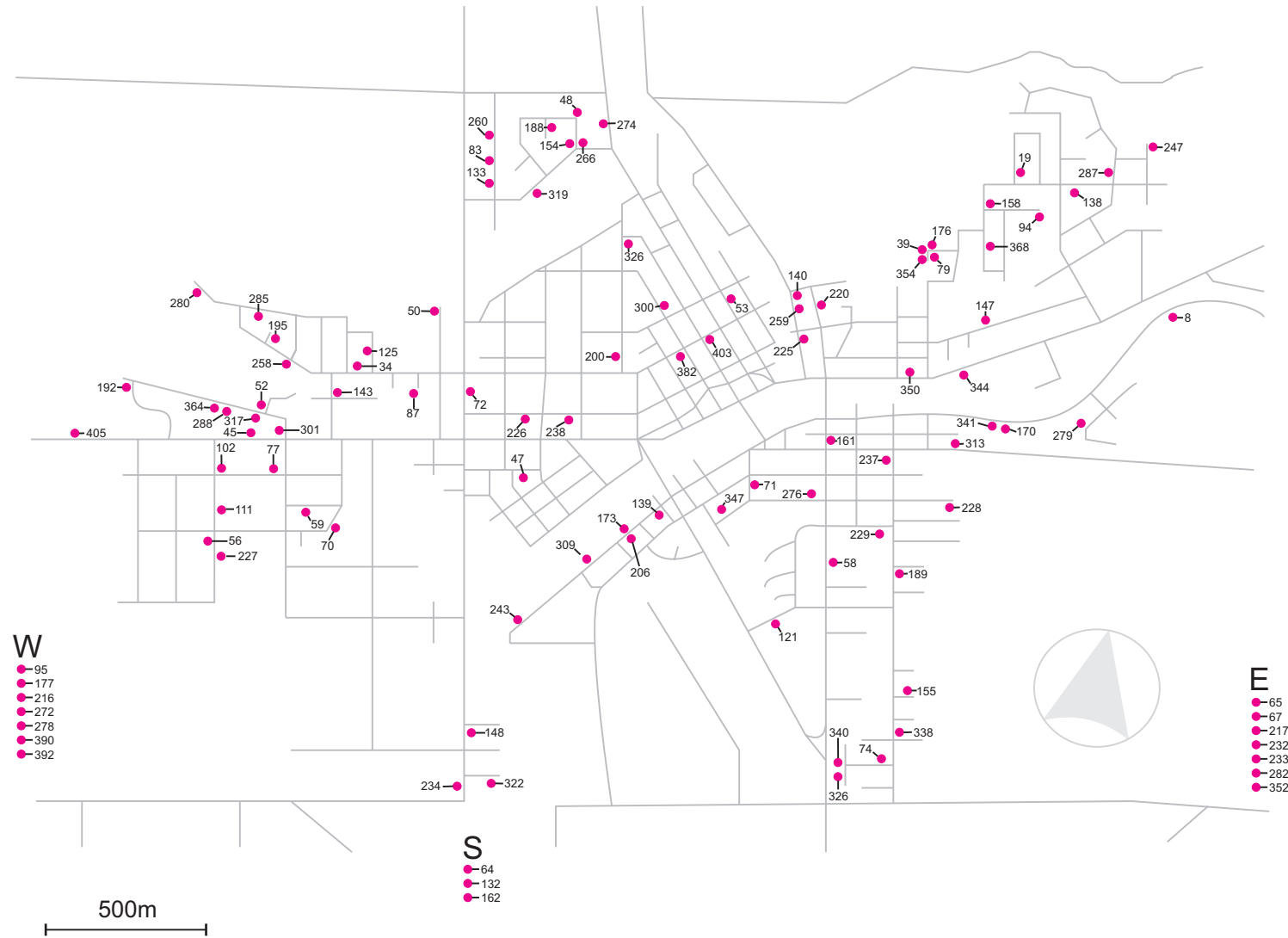


FIGURE 6-1. Street map of Wallaceburg, Ontario, indicating collection sites for *Penicillium chrysogenum* isolates used in this study.

**Table 6-1:** Sources of house dust isolates used in this study

House No.	No. of isolates	House No.	No. of isolates	House No.	No. of isolates
8	9	<b>* 154</b>	<b>2</b>	278	1
19	2	155	1	279	1
<b>* 34</b>	<b>2</b>	158	1	280	1
39	2	161	1	282	1
<b>* 45</b>	<b>5</b>	162	1	285	1
47	1	172	1	287	1
<b>* 48</b>	<b>5</b>	173	1	288	1
50	5	176	1	290	1
52	2	<b>* 177</b>	<b>3</b>	300	1
53	1	188	1	301	1
56	3	189	1	309	1
58	10	192	1	313	2
59	1	195	1	317	2
64	2	200	1	319	1
67	1	<b>* 206</b>	<b>1</b>	320	1
70	6	<b>* 216</b>	<b>1</b>	322	1
71	2	217	1	326	3
72	3	220	1	330	1
74	2	225	23	336	1
77	2	226	1	338	1
79	1	227	2	340	1
83	1	228	2	341	1
87	7	229	1	344	1
94	1	232	2	347	1
95	1	234	1	350	1
<b>* 102</b>	<b>1</b>	237	1	352	1
<b>* 111</b>	<b>1</b>	238	1	354	2
121	1	239	1	364	1
125	1	243	1	368	1
<b>* 132</b>	<b>1</b>	<b>* 247</b>	<b>1</b>	382	1
133	1	258	2	390	1
138	1	259	1	392	1
139	3	260	1	397	1
140	1	266	1	403	1
143	1	272	1	405	2
147	1	274	1		
148	1	<b>* 276</b>	<b>1</b>		

---

\*Houses showed visible mould growth on interior surfaces

**Table 6-2:** List of culture collection strains used in this study

Strain number	Identification	Status	Substratum
ATCC 10108	<i>Penicillium notatum</i> Westling	ex-type	branches of <i>Hysosopus</i> sp., Norway
CBS 484.84	<i>P. aethiopicum</i> Frisvad	ex-type	grains of <i>Hordeum vulgare</i> , Ethiopia
DAOM 155627	<i>P. chrysogenum</i> Thom		paper, Ottawa, Ontario
DAOM 155628	<i>P. chrysogenum</i> Thom		paper, Ottawa, Ontario
DAOM 155631	<i>P. chrysogenum</i> Thom		paper, Ottawa, Ontario
DAOM 167036	<i>P. chrysogenum</i> Thom		<i>Picea</i> forest soil, Quebec
DAOM 171025	<i>P. chrysogenum</i> Thom		salami, Ottawa, Ontario
DAOM 175157	<i>P. chrysogenum</i> Thom		walls of mouldy house, Niagara Falls, Ontario
DAOM 175176	<i>P. chrysogenum</i> Thom		<i>Lycopersicum esculentum</i> leaves, Prince Edward Island
DAOM 175758	<i>P. chrysogenum</i> Thom		office building, Quebec
DAOM 178623	<i>P. chrysogenum</i> Thom		<i>substr. et loc. incerta</i>
DAOM 190864	<i>P. chrysogenum</i> Thom		grains of <i>Hordeum</i> , Manitoba
DAOM 193710	<i>P. chrysogenum</i> Thom	ex-type	cheese, Connecticut, USA
DAOM 212031	<i>P. chrysogenum</i> Thom		wooden wall studs, Alberta
DAOM 215336	<i>P. chrysogenum</i> Thom		wooden wall studs, Alberta
DAOM 215337	<i>P. chrysogenum</i> Thom		hemlock lumber, British Columbia
DAOM 216700	<i>P. chrysogenum</i> Thom		grains of <i>Hordeum</i> , Canada
DAOM 216701	<i>P. chrysogenum</i> Thom		<i>Sesamum indicum</i> , Korea
DAOM 59494C	<i>P. chrysogenum</i> Thom		<i>substr. incert.</i> , Honduras
NRRL 13485	<i>P. dipodomyis</i> (Frisvad, Filtenborg & Wicklow) Banke, Frisvad & Rosendahl	ex-type	cheek pouch of <i>Dipodomyis spectabilis</i> , Arizona, USA
NRRL 13487	<i>P. dipodomyicola</i> (Frisvad, Filtenborg & Wicklow) Frisvad	ex-type	cheek pouch of <i>Dipodomyis spectabilis</i> , Arizona, USA
NRRL 824	<i>P. chrysogenum</i> Thom	Fleming strain	laboratory contaminant, London, England
NRRL 911	<i>P. nalgiovense</i> Laxa	ex-type	cheese, Nalzovy, Czech Republic

## **DNA PREPARATION AND HETERODUPLEX ANALYSIS**

DNA isolation, PCR and preparation of DNA heteroduplexes were performed according to the methods described in Chapter 4. Four polymorphic loci consisting of partial regions spanning introns in the genes encoding acetyl co-enzyme A synthase (*acuA*), beta-tubulin (*benA*), thioredoxin reductase (*trxB*) and the region spanning the internal transcribed spacers (ITS1 to ITS2) of nuclear ribosomal DNA (rDNA) were PCR-amplified using the primer sequences given in Table 6-3, employing the methods described in Chapter 4. Figure 6-2 shows the locations of primers used for PCR amplification and sequencing. Heteroduplexing reactions were set up in the manner described in Chapter 4, whereby isolates with adjacent numbers were pooled, pairwise in overlapped combinations, so as to encompass the entire set. Subsequent rounds of heteroduplexing were performed in which distinctive isolates were compared until the entire collection was completely characterized.

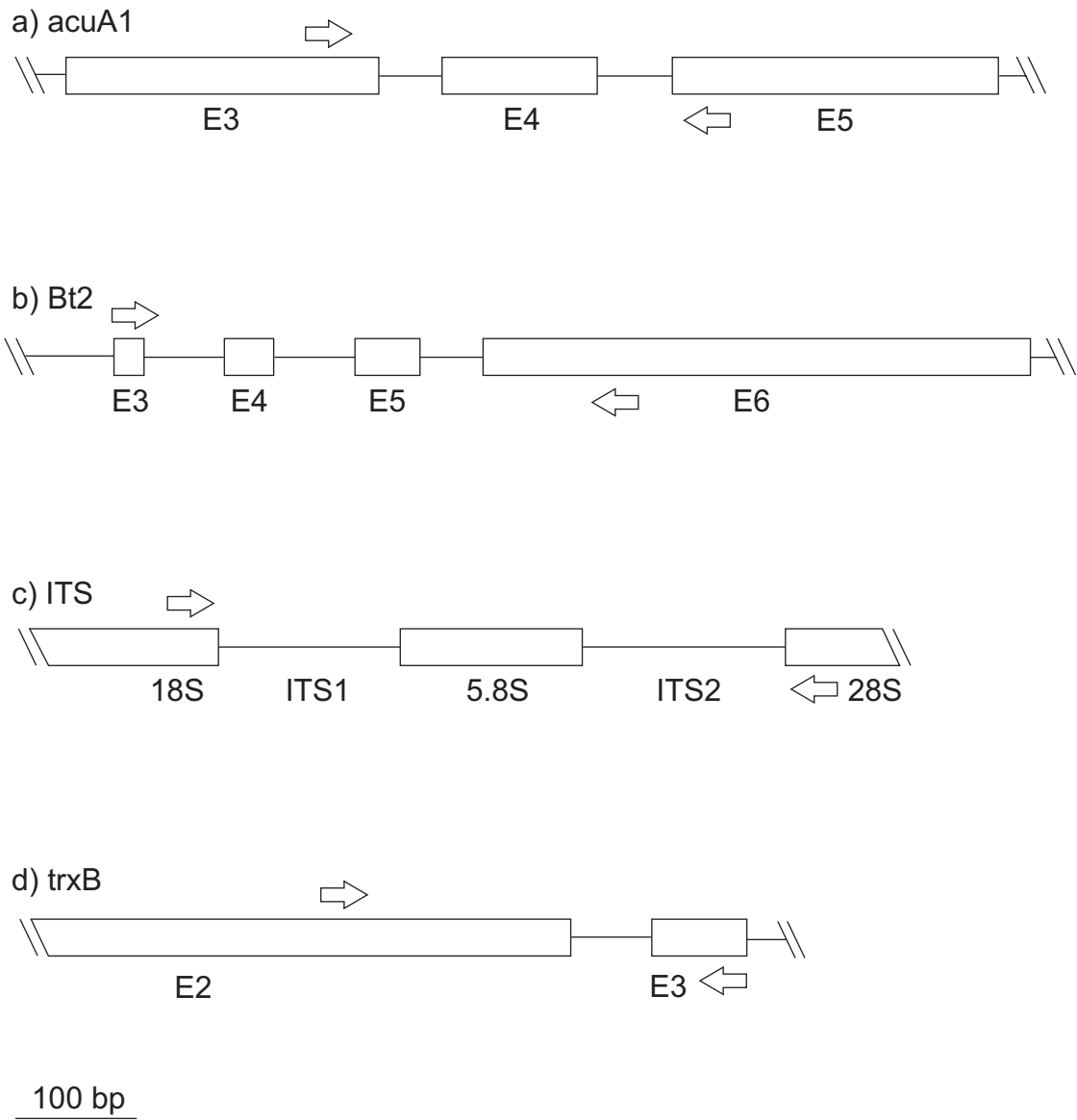
Electrophoresis and imaging of HMA reactions was conducted using the vertical method of electrophoresis described in Chapter 4.

## **PCR FINGERPRINTING<sup>10</sup>**

A subset of 40 isolates including representation of all observed multilocus haplotypes was selected for fingerprinting analysis. All minor multilocus haplotypes were included, and representative major haplotypes were randomly selected for inclusion. Two oligonucleotides, (GACA)<sub>4</sub>, and the core sequence of the wild-type phage M13 (5'-GAG GGT GGC GGT TTG T-3'), both minisatellite-specific primers were used as single primers in a PCR containing 25 ng

---

<sup>10</sup> This work was conducted as a collaboration with Dr. Wieland Meyer, Department of Medicine, University of Sydney, Australia



**FIGURE 6-2.** Locations of primers used to amplify polymorphic regions in *P. chrysogenum* in this study.

**Table 6-3:** Primers sequences employed in this study**Acetyl-CoA synthetase (acuA)**

Source: Genbank L09598, +2102 - 2452, spanning introns 3 & 4  
**Fwd primer 5'-3':** ACC GTG TGG GGT GCC CAC AAG CGT TAC ATG (acuA-2F)  
**Rvs primer 5'-3':** GGT CAG CTC GTC GGC AAT ACC AAC GAC AGC (acuA-1R)

**Beta-tubulin (benA)**

Source: Glass & Donaldson, 1995  
**Fwd primer 5'-3':** GGT AAC CAA ATC GGT GCT GCT TTC (Bt2a)  
**Rvs primer 5'-3':** ACC CTC AGT GTA GTG ACC CTT GGC (Bt2b)

**Nuclear rDNA ITS regions**

Source: White et al., 1990, fwd; Untereiner et al., 1995, rvs  
**Fwd primer 5'-3':** GGA AGT AAA AGT CGT AAC AAG G (ITS5)  
**Rvs primer 5'-3':** TAT GCT TAA GTT CAG CGG (WNL1)

**Thioredoxin reductase (trxB)**

Source: EMBL X76119, +801 - 1153, spanning intron 2  
**Fwd primer 5'-3':** AAC GCG GAG GAG GTC GTT GAG GCT AAC GGT (trxB-1F)  
**Rvs primer 5'-3':** TTA GAG CAC AGG CTT TGC CTC CTG GTG AGT (trxB-1R)



template, 250  $\mu$ M each of dATP, dCTP, dGTP, dTTP, 300  $\mu$ M magnesium acetate, 150  $\mu$ M magnesium chloride, 5 mM potassium chloride, 1mM Tris-HCl pH 8.3, 200  $\mu$ M primer and 1 unit of AmpliTaq (Perkin Elmer Corp.), brought to a total volume of 50  $\mu$ L with sterile deionized water, overlaid with one drop of sterile, light mineral oil. Reactions were submitted to 35 cycles of the following thermal incubation: 94 °C for 20 sec denaturation, 50 °C for 1 min annealing, 72 °C for 20 sec extension, with a final extension of 6 min at 72 °C.

Products of PCR were electrophoresed on a 1.4 % agarose gel (containing 1x TBE [10.8 g/L Tris-base, 5.5 g/L boric acid, 2mM EDTA pH 8.0] with 200  $\mu$ g/L ethidium bromide), in 1x TBE at a field strength of 2 V/cm, and visualized by ultraviolet light transillumination at 302 nm. A 1 kbp DNA ladder (Pharmacia) was loaded in several lanes for reference. This method follows the protocol described by Weising and co-workers (1995).

#### **RANDOM PRIMER-PAIR FINGERPRINTING<sup>11</sup>**

The random-sequence oligonucleotides 5SOR (5'-ATG GGA ATA CGA CGT GCT GTA A-3') and MYC1 (5'-GAG GAA GGT GGG GAT GAC GT-3') were used as a primer pair in a PCR containing 10 ng template, 200  $\mu$ M each of dATP, dCTP, dGTP, dTTP, 200 mM ammonium sulphate, 15 mM magnesium chloride, 5 mM potassium chloride, 750mM Tris-HCl pH 8.8, 5 pM of each primer and 1 unit of Taq DNA polymerase (Advanced Biotechnology, Surrey, UK), 0.1 % Tween 20 brought to a total volume of 25  $\mu$ L with sterile deionized water, and overlaid with one drop of sterile, light mineral oil. Following an initial denaturation of 3 min at 93 °C, reactions were submitted to 10 initial cycles of the following low-stringency thermal incubation:

---

<sup>11</sup> This work was conducted as a collaboration with Dr. Wieland Meyer, Department of Medicine, University of Sydney, Australia

93 °C for 1 min denaturation, 35 °C for 1 min annealing, 72 °C for 1 min extension, with a final extension of 6 min at 72 °C; this profile was followed by 20 cycles of high stringency thermal incubation: 1 min denaturation at 93 °C, 1 min annealing at 55 °C and an extension of 1 min at 72 °C.

Following PCR, products were electrophoresed on a 10 % polyacrylamide gel (1x TBE [10.8 g/L Tris-base, 5.5 g/L boric acid, 2mM EDTA pH 8.0] polymerised by free-radical method by the addition of 0.7 % ammonium persulfate and catalysed by the addition of 6.6 mM TEMED) at a field strength of 10 V/cm in 1x TBE until the bromophenol dye front was 3 cm from the bottom of the gel. A *Hae*III restriction digest of the plasmid  $\Phi$ X174 was used as a size marker. Gels were silver stained using a method modified from Bassam and Caetano-Anollés (*see* Weising et al., 1995) in a solution of 0.1 % silver nitrate and 0.07 % (w/w) formaldehyde for 30 min at room temperature. Following staining, gels were rinsed twice in distilled water and developed in a solution of 3 % sodium carbonate, 0.003 % sodium thiosulphate and 1.5 % formaldehyde. Development was stopped by the addition of 10 % acetic acid, prior to the drying of gels at 80 °C for 30 min on 3M Whatman paper. Gel bands were scored using the Gelcompar II software package (Applied Maths).

### **CLUSTER ANALYSIS**

Cluster analyses of all fingerprinting data were analysed using the Neighbor-Joining method and outgrouped using *P. polonicum* and *P. thomii* (Wallaceburg isolates no. 170 and 236, respectively) (*see* Weising et al., 1995).

## DNA SEQUENCING

PCR templates were purified using QIAquick PCR purification kit (Qiagen, Inc., Valencia, Calif.). PCR templates were sequenced using the Taq DyeDeoxy cycle sequencing kit (Applied Biosystems, Inc., Foster City, Calif.) and extension products were analysed on an ABI50 fluorescent automated sequencer (Applied Biosystems, Inc.). Sequences were determined on both sense and anti-sense strands using the same primers that were used for amplification (*see* Table 6-3).

## SEQUENCE ANALYSIS

Alignments of all sequences were performed using Clustal X software package version 1.8 (*see* Jeanmougin et al., 1998; Thompson et al., 1997) and adjusted by visual inspection using a text editor. Phylogenetic analyses were carried out by the Neighbor-Joining method using Clustal X and PAUP\* (PAUP\* version 4.0b4a for 32 bit Microsoft Windows, Sinauer Associates, Inc., Sunderland, Massachusetts). In all cases, the data were re-sampled by 1000 bootstrap replicates and the proportion of Neighbor-Joining trees possessing each internal branch was indicated to express its level of support. *Penicillium dipodomyis* was selected as an outgroup taxon on the basis of the ITS phylogeny presented in Chapter 4, Figure 4-9.

Data for *trxB* were further analysed using the maximum parsimony method in PAUP\*. Most-parsimonious trees (MPTs) were identified by exhaustive heuristic searches, upon which strict consensus tree were constructed.

Prior to combining sequence datasets, sequence alignments were analysed using the PHT within PAUP\* to determine the congruence of sequences. Results of the PHT were reproduced

graphically using Microsoft Excel, of the Microsoft Office 2000 software package (Microsoft Corp.). The limitations of the PHT are discussed in Chapter 5.

### **SPATIAL ANALYSIS**

Euclidean distances between all possible pairs of participating Wallaceburg houses were calculated from transformed x-y coordinates of all properties as plotted on a scale street map, and compiled in a distance matrix. The Neighbor-Joining method was used to cluster the house numbers according to the Euclidean distances between locations using the “Neighbor” module of PHYLIP.

### **DENDROGRAM CONSTRUCTION**

Dendrograms were generated using the TreeView software package, version 1.5.2 for 32 bit Microsoft Windows (Roderick Page, University of Glasgow), and formatted using Corel Draw version 8.232 (Corel Corporation).

### **RESULTS**

Isolates of *P. chrysogenum* were obtained from 109 of the 369 houses examined (30 %). Seventeen of these houses were in rural locations (i.e. outside the town limits). No isolates of *Penicillium* were obtained from the 18 outdoor air samples taken in Wallaceburg.

### **HETERODUPLEX ANALYSIS**

Multilocus genotypes identified by heteroduplex analysis for all loci are listed for all isolates in Table 6-4, and summarized in Table 6-5. The multilocus haplotype AAAA (acuA, bt2, ITS and trxB, respectively), represented by the isolate C8.12, was the most commonly observed

**Table 6-4:** Summary of haplotypes of *P. chrysogenum* isolates

Isolate	acuA	benA	ITS	trxB	Isolate	acuA	benA	ITS	trxB
8.1	A	A	A	A	58.13	A	A	A	A
8.4	A	A	A	A	58.14	A	A	A	A
8.8	A	A	A	A	58.15	A	C	B	C
8.12	A	A	A	A	58.16	A	A	A	A
8.14	A	A	A	A	59.2	A	A	A	A
8.16	A	A	A	A	64.1	A	A	A	A
8.18	A	C	B	C	64.2	A	A	A	A
8.19	A	A	A	A	67.3	B	B	B	B
8.24	B	B	B	B	70.1	A	A	A	A
19.2	A	A	A	A	70.3	B	B	B	B
19.3	A	A	A	A	70.5	A	A	A	A
34.4	B	B	B	B	70.6	A	A	A	A
34.10	A	A	A	A	70.7	A	A	A	A
39.1	A	A	A	A	70	A	A	A	A
39.4	A	A	A	A	71.1	C	B	B	B
45.2	A	A	A	A	71.2	A	A	A	A
45.3	A	A	A	A	72.1	B	B	B	B
45.5	A	A	A	A	72.2	B	B	B	B
45.6	A	A	A	A	72.3	A	A	A	A
45.7	A	A	A	A	74.1*	D	D	D	D
47	B	B	B	B	74.2	A	A	A	A
48.2	A	A	A	A	74.3	A	A	A	A
48.3	A	A	A	A	77.1	A	A	A	A
48.8	A	A	A	A	77.2	A	C	B	C
48.11	A	A	A	A	79	A	A	A	A
48.12	A	A	A	A	83	A	A	A	A
50.3	A	A	A	A	87.1	A	A	A	A
50.5	A	A	A	A	87.2	A	A	A	A
50.7	A	A	A	A	87.3	A	A	A	A
50.9	A	A	A	A	87.4	A	A	A	A
50.10	A	A	A	A	87.5	A	A	A	A
52.1	A	A	A	A	87.6	A	A	A	A
52.2	A	A	A	A	87.7	A	A	A	A
53	A	A	A	A	94	B	B	B	B
56.3	A	A	A	A	95	A	A	A	A
56.4	A	A	A	A	102	A	A	A	A
56.5	A	A	A	A	111	A	A	A	A
58.3	A	A	A	A	121.4	A	A	A	A
58.4	A	A	A	A	125	A	A	A	A
58.7	B	B	B	B	132	A	A	A	A
58.8	A	A	A	A	133	A	A	A	A
58.11	A	A	A	A	138	A	A	A	A
58.12	A	A	A	A	139.1	A	A	A	A

**Table 6-4:** Summary of haplotypes of *P. chrysogenum* isolates

Isolate	acuA	benA	ITS	trxB	Isolate	acuA	benA	ITS	trxB
139.2	A	A	A	A	225.19	A	A	A	A
139.3	A	A	A	A	225.20	A	A	A	A
140.1	A	A	A	A	225.22	A	A	A	A
143	A	A	A	A	225.23	A	A	A	A
147	A	A	A	A	225.25	A	A	A	A
148	A	A	A	A	225.26	A	A	A	A
154.1	A	A	A	A	225.30	A	A	A	A
154.2	A	A	A	A	225.31	A	A	A	A
155	A	A	A	A	226	A	A	A	A
158.2	A	A	A	A	227.1	A	A	A	A
161	A	A	A	A	227.2	A	A	A	A
162	A	A	A	A	228.2	A	A	A	A
170*	D	D	D	D	228.3	A	A	A	A
172	A	A	A	A	229.2	A	A	A	A
173	A	A	A	A	232.1	B	B	B	B
176	A	A	A	A	232.2	B	B	B	B
177.1	A	A	A	A	234	A	A	A	A
177.2	A	A	A	A	237.2	A	A	A	A
177.3	A	A	A	A	238	C	B	B	B
188	A	A	A	A	239	A	A	A	A
189	A	A	A	A	243	A	A	A	A
192	A	A	A	A	247	A	A	A	A
195	A	A	A	A	258.1	A	A	A	A
200	A	C	C	C	258.2	A	A	A	A
206	A	A	A	A	259	A	A	A	A
216	A	A	A	A	260	A	A	A	A
217	A	A	A	A	266	A	A	A	A
220	A	A	A	A	272	A	A	A	A
225.2	A	A	A	A	274	A	A	A	A
225.3	A	A	A	A	276.1	A	A	A	A
225.4	A	A	A	A	278	A	A	A	A
225.5	A	A	A	A	279.1	A	A	A	A
225.6	A	A	A	A	280.2	A	A	A	A
225.7	A	A	A	A	282	A	A	A	A
225.8	A	A	A	A	285	A	A	A	A
225.9	A	A	A	A	287	A	A	A	A
225.10	A	A	A	A	288	A	A	A	A
225.12	A	A	A	A	290	A	A	A	A
225.13	A	A	A	A	300	A	A	A	A
225.14	A	A	A	A	301.1	A	A	A	A
225.15	A	A	A	A	309	A	A	A	A
225.16	A	A	A	A	313.1	A	A	A	A
225.18	A	A	A	A	313.2	A	A	A	A

**Table 6-4:** Summary of haplotypes of *P. chrysogenum* isolates

<b>Isolate</b>	acuA	benA	ITS	trxB	<b>Isolate</b>	acuA	benA	ITS	trxB
317.1	A	C	B	C	347.1	A	A	A	A
317.2	A	C	B	C	350	A	A	A	A
319	A	A	A	A	352	A	A	A	A
320	A	A	A	A	354.1	A	A	A	A
322	A	A	A	A	354.2	A	A	A	A
326.1	A	A	A	A	364.1	A	A	A	A
326.2	A	A	A	A	368	A	A	A	A
326.4	A	A	A	A	382	A	A	A	A
330.1	A	A	A	A	390	A	A	A	A
336.1	A	A	A	A	392	A	A	A	A
338	A	A	A	A	397	A	A	A	A
340	A	A	A	A	403	A	A	A	A
341	A	A	A	A	405.1	A	A	A	A
344.1	A	A	A	A	405.2	A	A	A	A

\*isolates of *P. polonicum* included as reference

**Table 6-5:** Haplotype frequencies of *P. chrysogenum* isolates

Representative Isolate	LOCUS				Frequency
	acuA	Bt2	ITS	trxB	
C8.12	A	A	A	A	0.904
C317.1	A	C	B	C	0.025
C8.24	B	B	B	B	0.056
C238	C	B	B	B	0.010
C200	A	C	C	C	0.005



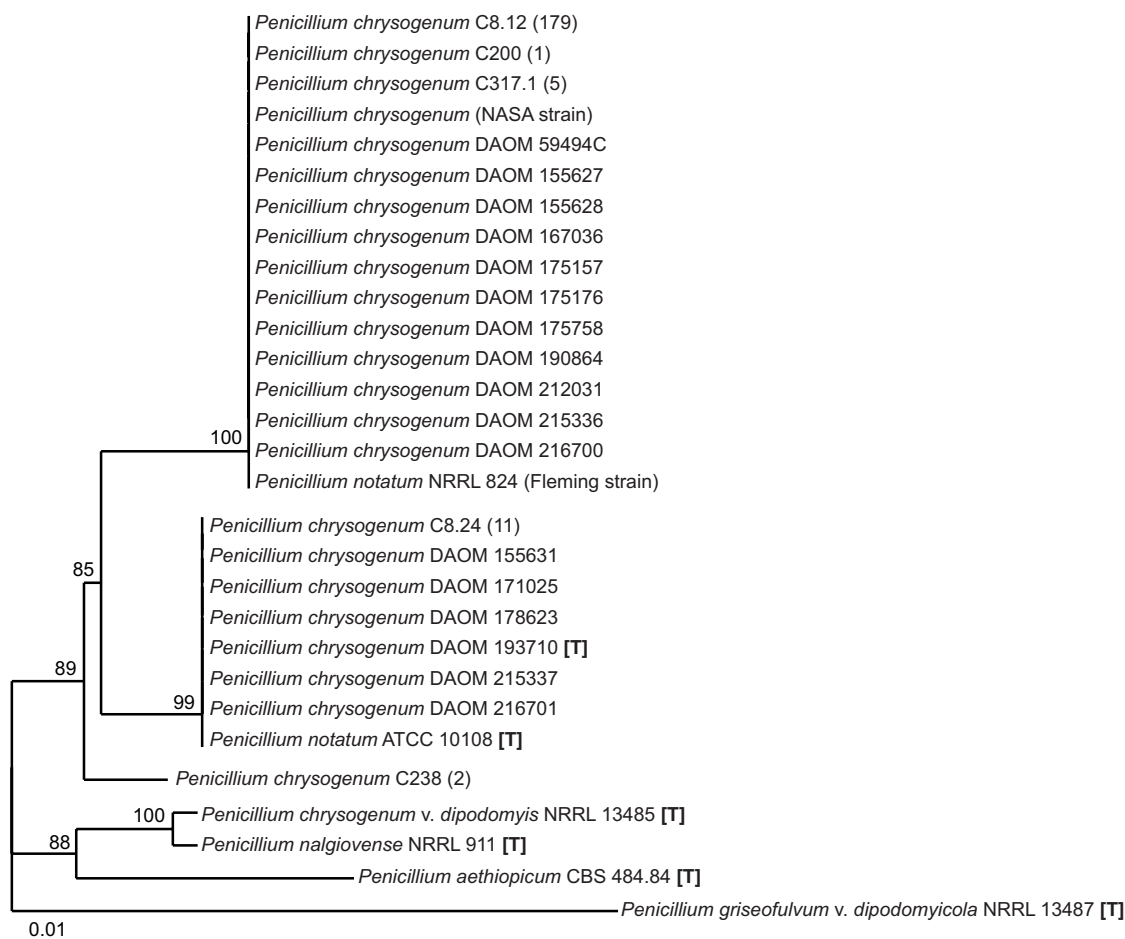
multilocus haplotype in the population and comprised over 90 % of all isolates. The second most common multilocus haplotype, BBBB, accounted for 5.6 % of the isolates studied and is represented by isolate C8.24 (the same house as the representative isolate used for AAAA, above). Three other minor multilocus haplotypes (ACBC, ACCC & CBBB) comprised the remainder of the isolate set. One or more characteristic isolates for each multilocus haplotype were sequenced for phylogenetic analysis.

### INDIVIDUAL DATA SETS

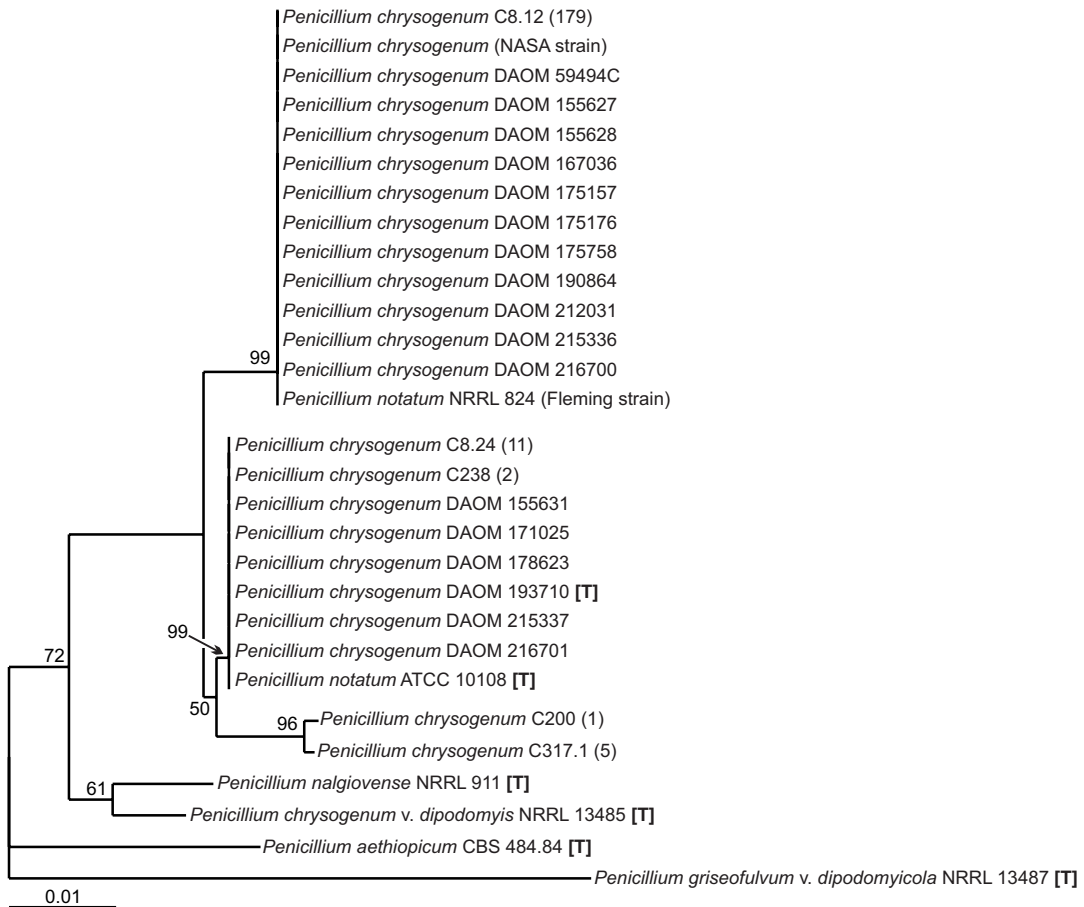
Distance trees for each of the four genetic loci, *acuA*, *benA*, ITS and *trxB*, are presented in Figures 6-3 to 6-6, respectively. Due to the lower degree of resolution in the ITS tree, it will be discussed separately. In the *acuA*, *benA* and *trxB* distance trees, the isolates were divided into two main groups. The first clade contained 179 or more of the 198 Wallaceburg isolates along with the strain of *P. chrysogenum* (as *P. notatum*) isolated in 1929 by Alexander Fleming (NRRL 824), and 11 DAOM voucher strains. This clade was supported by bootstrap values of 99 % or greater, and was dominated by the AAAA multilocus haplotype.

The second major clade was characterized by 13 Wallaceburg strains (11 with the multilocus genotype BBBB as determined by heteroduplex analyses, *see* Table 6-5), as well as the ex-type strains of *P. chrysogenum* (DAOM 193710) and *P. notatum* (ATCC 10108).

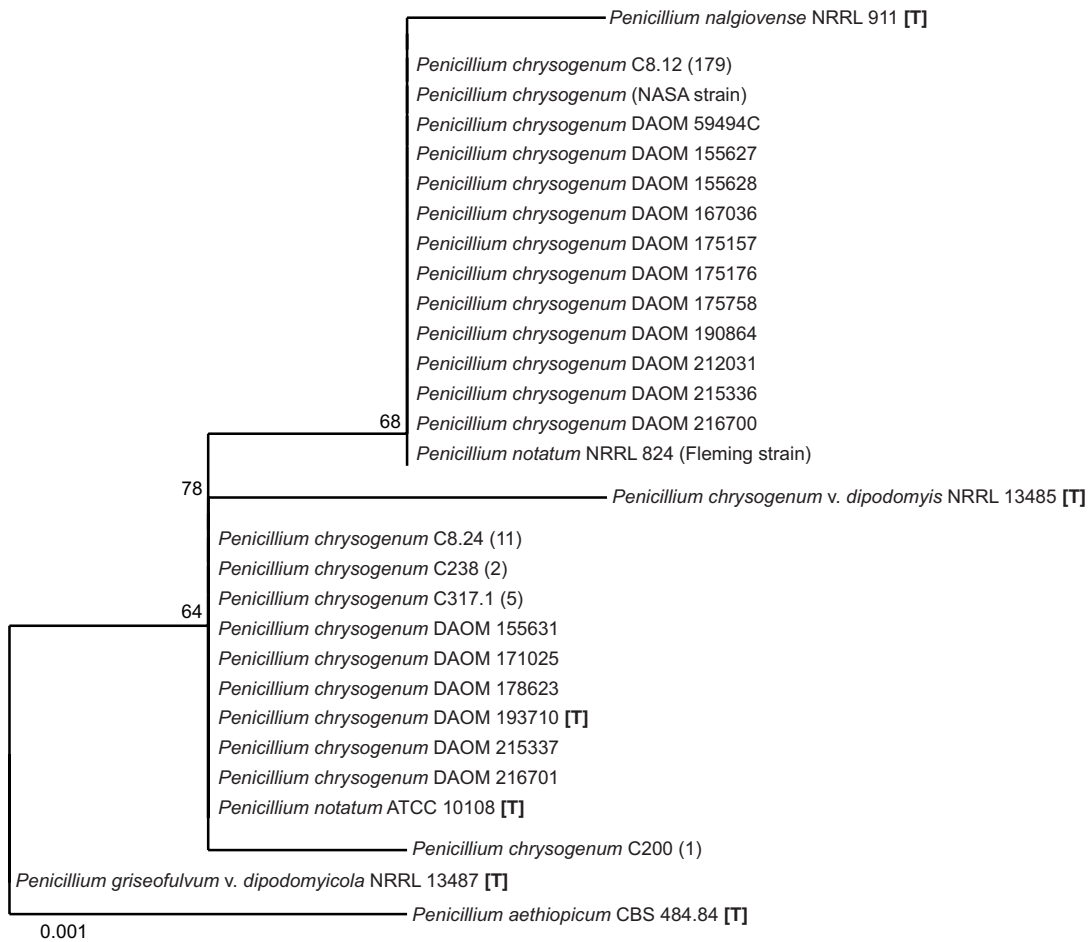
Several isolates showed re-assortment between *acuA*, *benA* and *trxB* trees. Notably, 6 isolates represented by C200 and C317.1 clustered in the first clade in the *acuA* tree, but were sister to the second clade in the *benA* and *trxB* trees (*see* Figures 6-3, 6-4 and 6-6). In addition, two



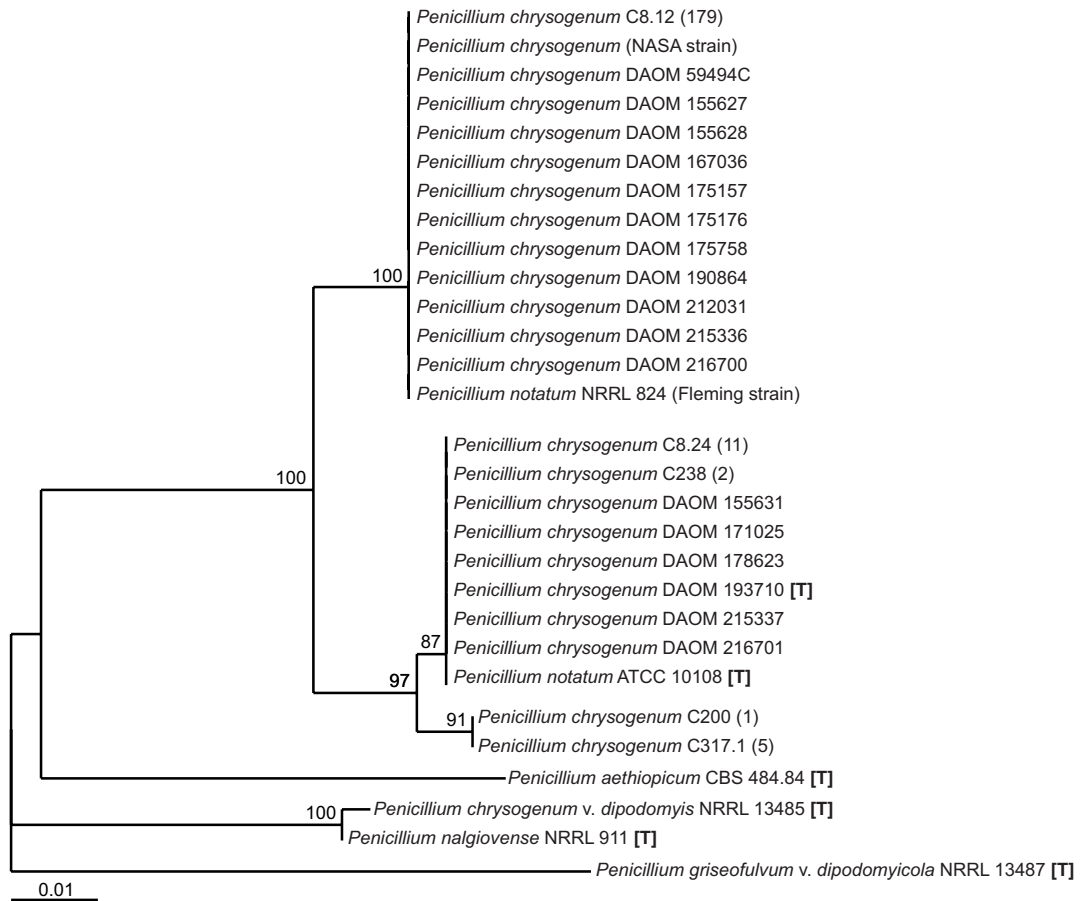
**FIGURE 6-3.** Neighbor-Joining tree of *P. chrysogenum* isolates based on partial *acuA* gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.



**FIGURE 6-4.** Neighbor-Joining tree of *P. chrysogenum* isolates based on partial *benA* gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.



**FIGURE 6-5.** Neighbor-Joining tree of *P. chrysogenum* isolates based on ITS1-5.8S-ITS2 data rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.



**FIGURE 6-6.** Neighbor-Joining tree of *P. chrysogenum* isolates based on partial *trxB* gene rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.

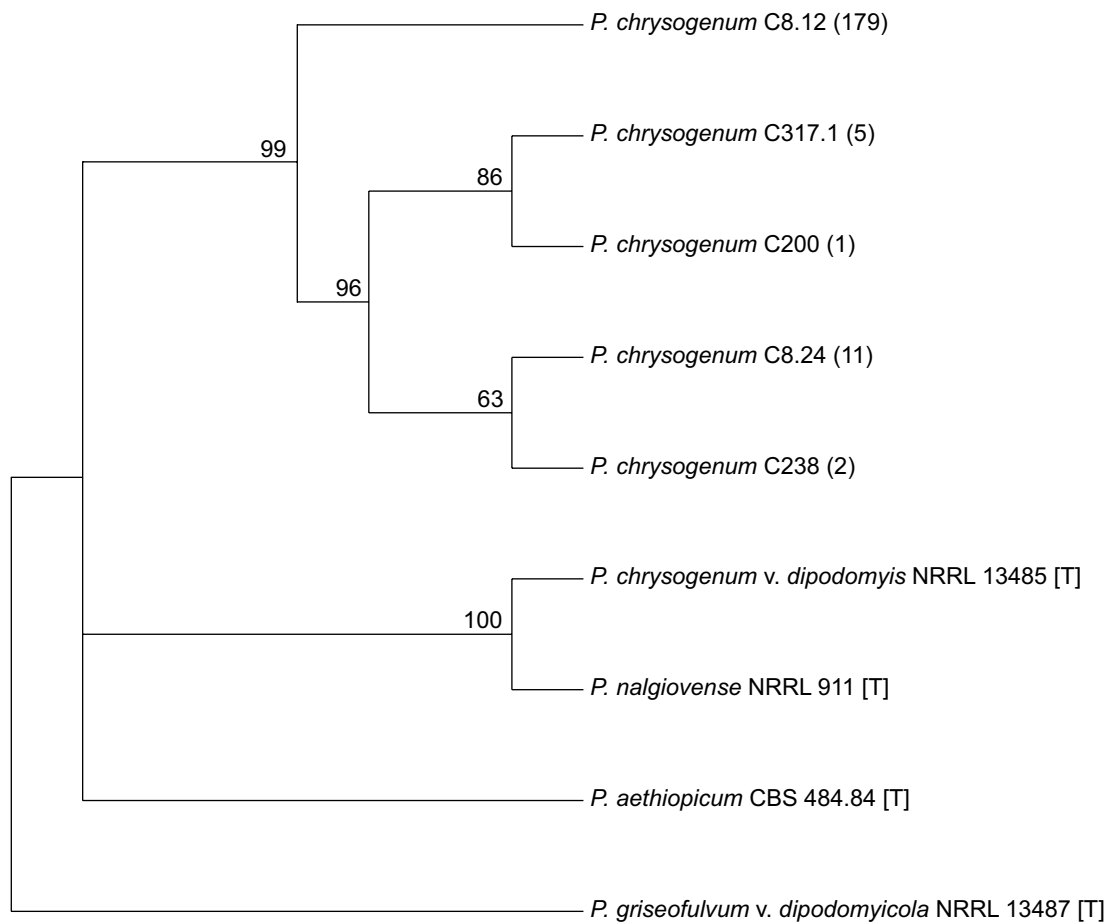
isolates represented by C238 clustered within the second clade in the *benA* and *trxB* trees, but formed a group that was sister to the two major *P. chrysogenum* clades in the *acuA* tree.

A distance tree based on ITS sequences (Figure 6-5) was similar in topology to the trees inferred from the other three loci; but, it resolved the two major clades of *P. chrysogenum* at a lower level of support.

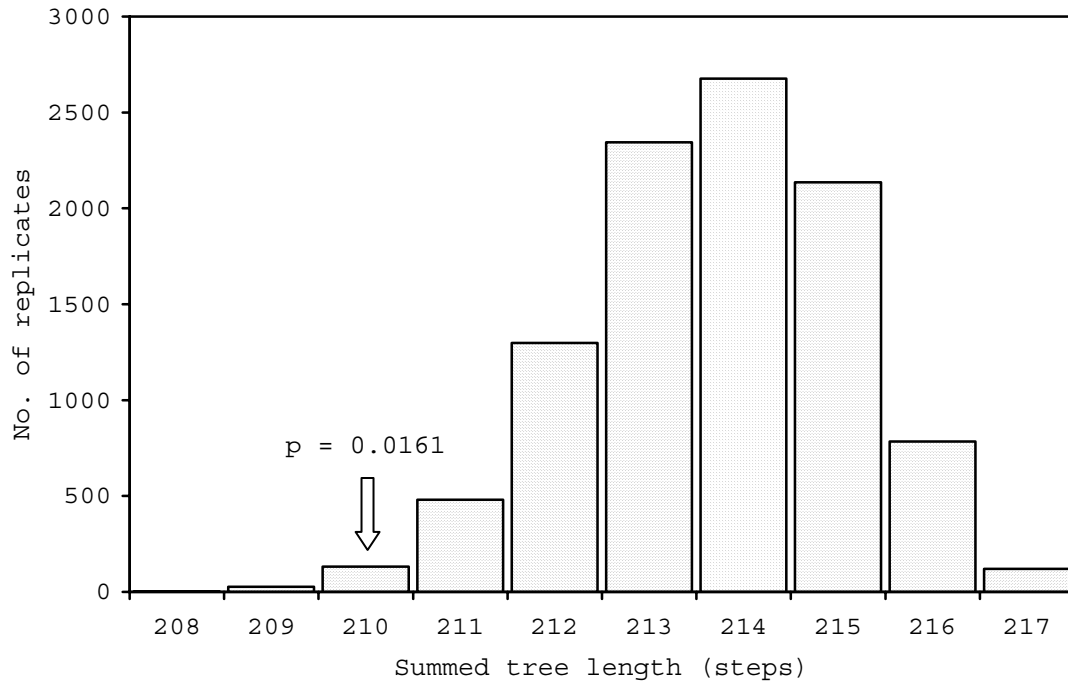
Parsimony analysis of the *trxB* dataset consisted of 306 bases of which 35 were parsimony-informative. An exhaustive search of this dataset yielded produced two MPTs 79 steps in length (L) with a consistency index (CI) of 0.8734, a retention index (RI) of 0.8305, and a re-scaled consistency index (RC) of 0.7354 (*see* Figure 6-7). The topology of this tree was similar to the tree produced by distance methods using this locus (Figure 6-6), as well as to those based on the other loci (Figures 6-3, 6-4 & 6-5). This analysis yielded a well-supported clade (bootstrap support of 99 %) that included representative isolates of the major groups of *P. chrysogenum*. The topology of this tree was similar to that produced by distance methods using this locus, and also to distance trees produced using other loci.

#### **COMBINED SEQUENCE DATA**

Sequence data from all genetic loci from representative Wallaceburg isolates, as well as culture collection strains (as summarized in Table 6-2) were pooled and subjected to PHT. Ten thousand trees were generated from this dataset and the summed branch lengths of these trees were depicted as a histogram (Figure 6-8). In this histogram the sum of branch lengths for the actual MPT (L = 210), is indicated by an arrow, and showed significance at  $p = 0.0161$ . This  $p$ -value indicates that the data sets produce significantly different topologies and therefore cannot



**FIGURE 6-7.** Strict consensus of two MPTs produced from partial *trxB* sequence rooted to the authentic strain of *P. griseofulvum* var. *dipodomyicola* (NRRL 13487 T). Bootstrap values based on 1000 replicates are indicated for branches which demonstrated over 50% bootstrap support.



**FIGURE 6-8.** Results of partition homogeneity test. Bars show the distribution of the total summed branch lengths of 10,000 trees generated from data sampled randomly across partitioned gene sequences (*acuA*, *benA*, ITS & *trxB*) using PAUP\* 4.0b4a (Swofford, 1999). Summed branch length for the observed single most parsimonious tree is indicated by the arrow.



be combined. One possible explanation for the incongruence of this data set is the inclusion in it of more than one biological species.

A second PHT was conducted on a subsample of isolates that included representatives of the Wallaceburg multilocus haplotypes as well as authentic material of *P. chrysogenum* (DAOM 193710), *P. notatum* (ATCC 10108), and the Alexander Fleming strain (NRRL 824) deposited under the latter name. The ITS data were eliminated from the partitioned dataset since no parsimony-informative characters were provided by this locus in the reduced panel of isolates (see Table 6-6). Furthermore, as shown in Table 6-6, elimination of the ITS data from this dataset reduced by two steps the total length of the MPT, from 35 to 33 steps. Results of this PHT are shown in Figure 6-9. The total branch length of the actual MPT fell within the 90<sup>th</sup> percentile of all tree lengths ( $L = 33$ ,  $p = 1$ ) based on random subsampling across partitions. The position of the actual MPT is indicated by an arrow in Figure 6-9. This result demonstrates that the three loci examined (*acuA*, *benA* and *trxB*) produce congruent topologies and that these sequence data may be combined. Furthermore, this result suggests that the isolates sampled have been propagated by strictly clonal means, in absence of recombination.

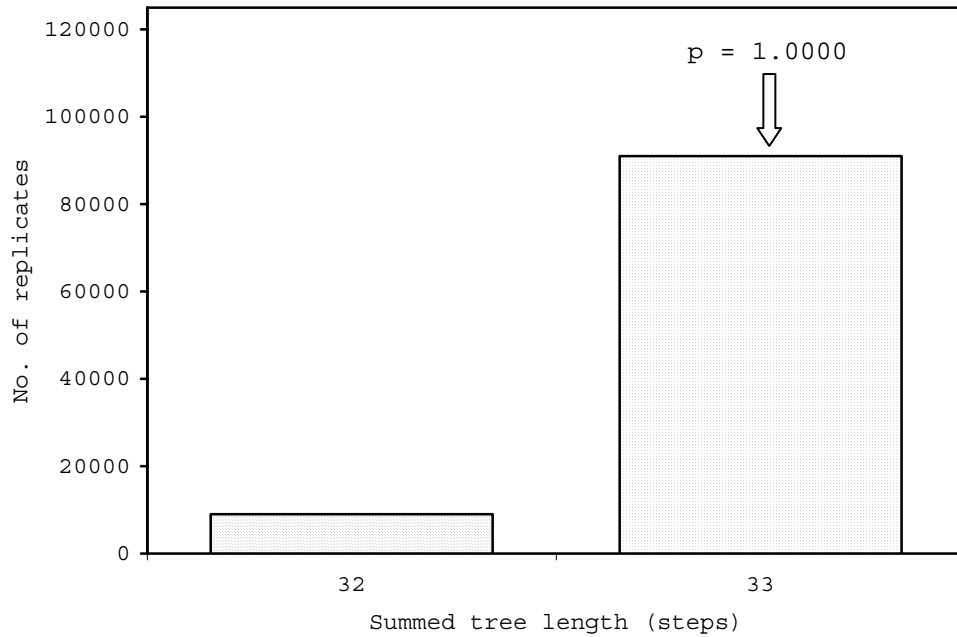
Analysis of the dataset that included sequences for the *acuA*, *benA* and *trxB* loci produced a single MPT ( $L = 33$ ,  $CI = 0.9333$ ,  $RI = 0.9286$ ,  $RC = 0.9004$ ) (Figure 6-10). The Wallaceburg *P. chrysogenum* isolates were divided among three well-supported clades and this tree showed essentially the same topology as the distance trees derived from analysis of individual genes. The first of these clades contained ex-type strains of *P. chrysogenum* and *P. notatum* along with 13 of the Wallaceburg isolates. The second clade was limited to 6 Wallaceburg isolates and the third clade contains 179 of 198 Wallaceburg isolates along with the Fleming strain (NRRL 824).

**Table 6-6:** Summary of MPTs produced from each of 4 loci examined

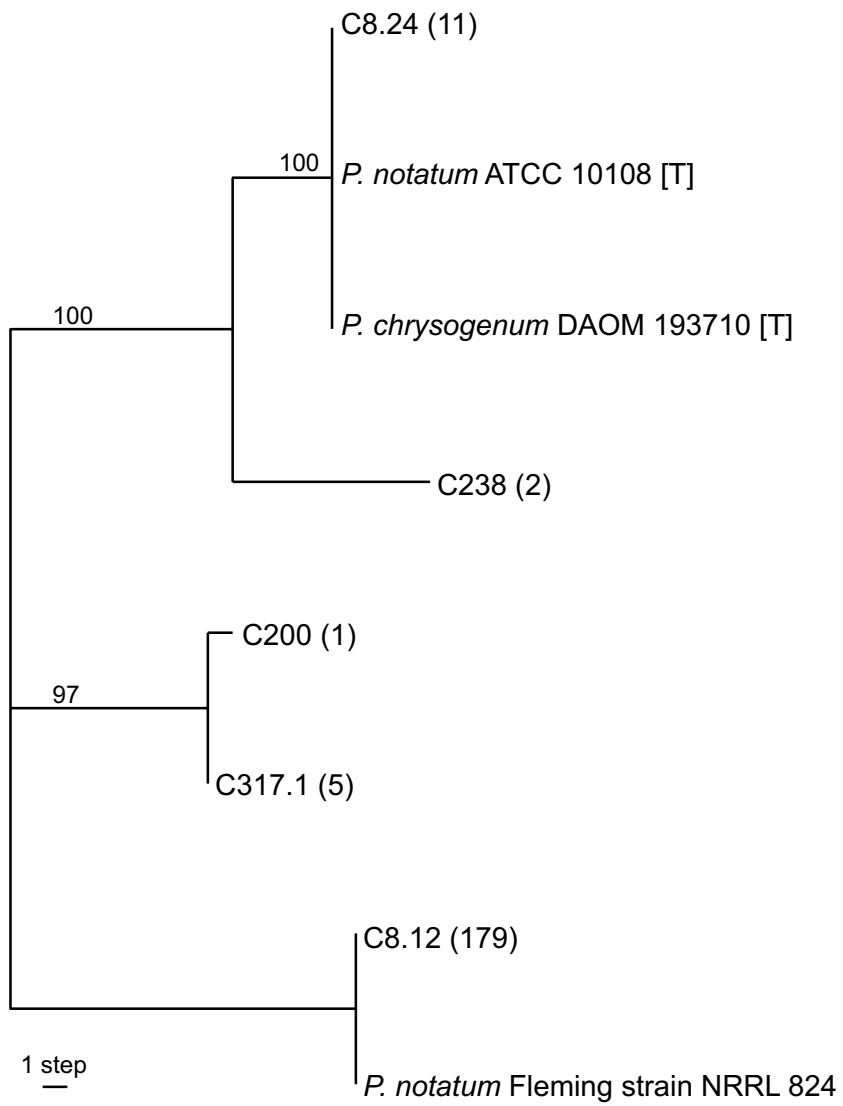
<b>Locus</b>	<b>No. of MPTs</b>	<b>No. of steps</b>	<b>CI*</b>	<b>PI** chars</b>	<b>Total chars</b>	<b>Constant chars</b>
acuA	3	14	1.0000	6	291	277
benA	3	9	0.8333	5	431	423
ITS	15	2	0/0	0	546	544
trxB	1	10	1.0000	3	306	296
all 4 loci	1	35	0.9333	14	1,580	1,546
all (w/o ITS)	1	33	0.9333	14	1,028	996

\*CI = Consistency index

\*\*PI = Parsimony-informative



**FIGURE 6-9.** Results of partition homogeneity test of *acuA*, *benA* & *trxB* sequence data for Wallaceburg dust isolates, including authentic material for *P. chrysogenum* (DAOM 193710), *P. notatum* (ATCC 10108) and the Fleming strain (NRRL 824). Bars show the distribution of the total summed branch lengths of 100,000 trees generated from data sampled randomly across partitioned gene sequences using PAUP\* 4.0b4a (Swofford, 1999). Summed branch length for the observed single most parsimonious tree is indicated by the arrow.



**FIGURE 6-10.** Unrooted MPT produced from combined *acuA*, *benA* and *trxB* sequences, including representative dust isolates and authentic strains ( $L=33$ ,  $CI=0.9333$ ,  $RI=0.9286$ ,  $RC=0.9004$ ).

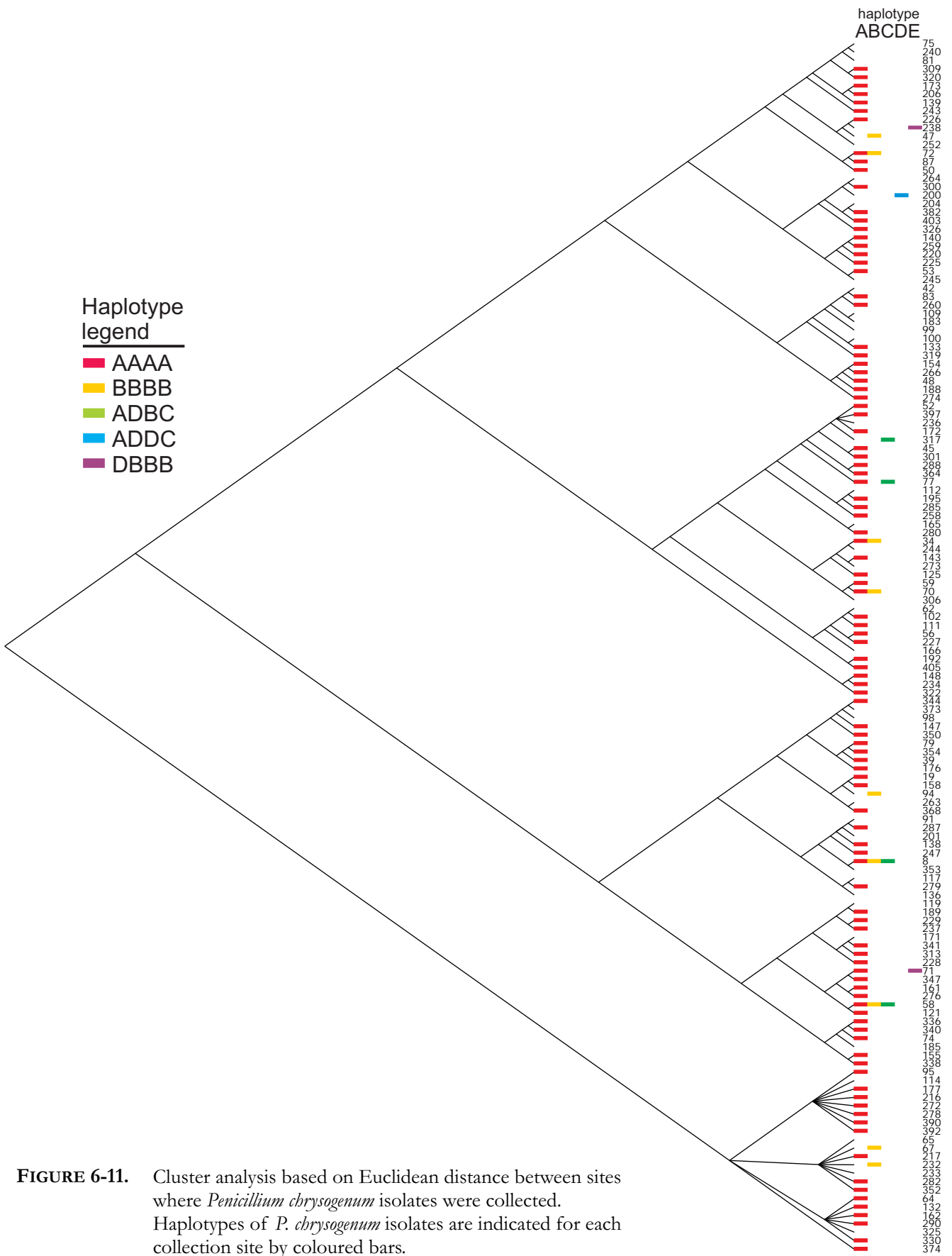
### **SPATIAL ANALYSIS**

Figure 6-11 shows a dendrogram of Wallaceburg house numbers used in this study that have been clustered by UPGMA analysis of geographic proximity. The array of multilocus haplotypes obtained from each house is mapped on this dendrogram. Visual inspection of these graphical data fail to reveal any obvious pattern of geographic distribution of genotypes. This may be due mainly to the strong dominance of a single genotype throughout the study site, as well as to the relatively low number of sites from which multiple isolates were obtained (*see* Table 6-1).

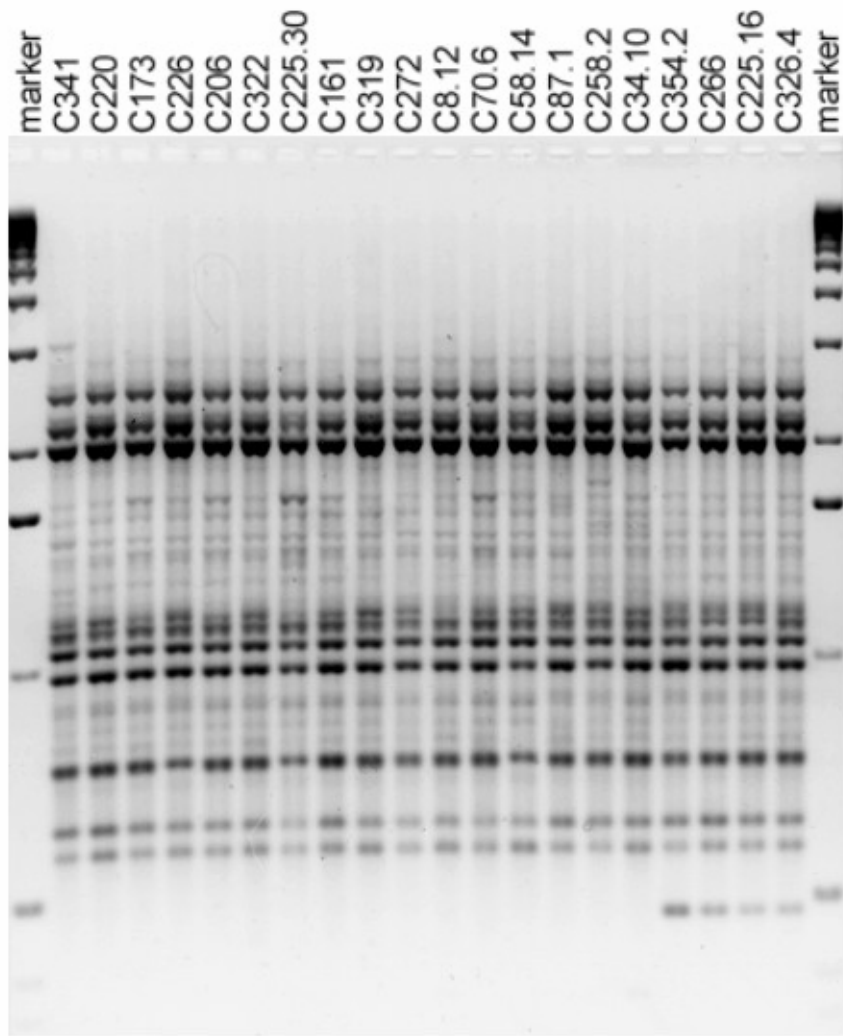
### **PCR FINGERPRINTING**

Photographs of electrophoresis gels based on M13-primed PCR amplifications are shown in Figures 12a & b. The isolates shown were arranged according to similarity following preliminary electrophoresis of the PCR products. Used as a single primer, the core M13 primer generated DNA products ranging in size from 0.9 to 4.1 kbp. Cluster analysis of M13 PCR fingerprint data separated the *P. chrysogenum* complex isolates into three distinct groups (Figure 6-13) that corresponded to the major clades revealed by parsimony analysis of the combined *acuA*-*benA*-*trxB* dataset shown in Figure 6-10.

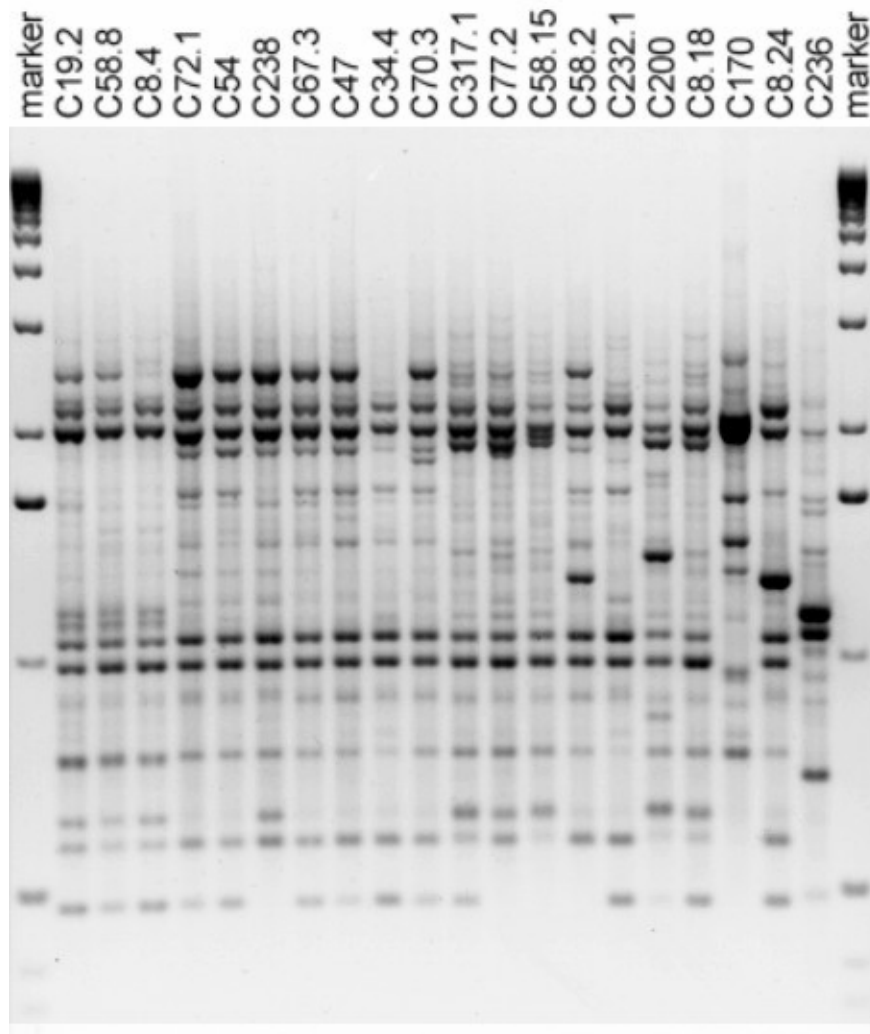
Products of PCR generated using (GACA)<sub>4</sub> as a single primer are shown in Figures 6-14a & b and are arranged based on a preliminary assessment of similarity. The PCR products generated by this primer ranged in size from approximately 1.2 to 3.8 kbp. Cluster analysis of band variation demonstrated the same major clades observed using the M13 and (GACA)<sub>4</sub> primers; but, minor variation in branch topology was observed in the dendrograms based on analyses of these primers (Figure 6-15).



**FIGURE 6-11.** Cluster analysis based on Euclidean distance between sites where *Penicillium chrysogenum* isolates were collected. Haplotypes of *P. chrysogenum* isolates are indicated for each collection site by coloured bars.

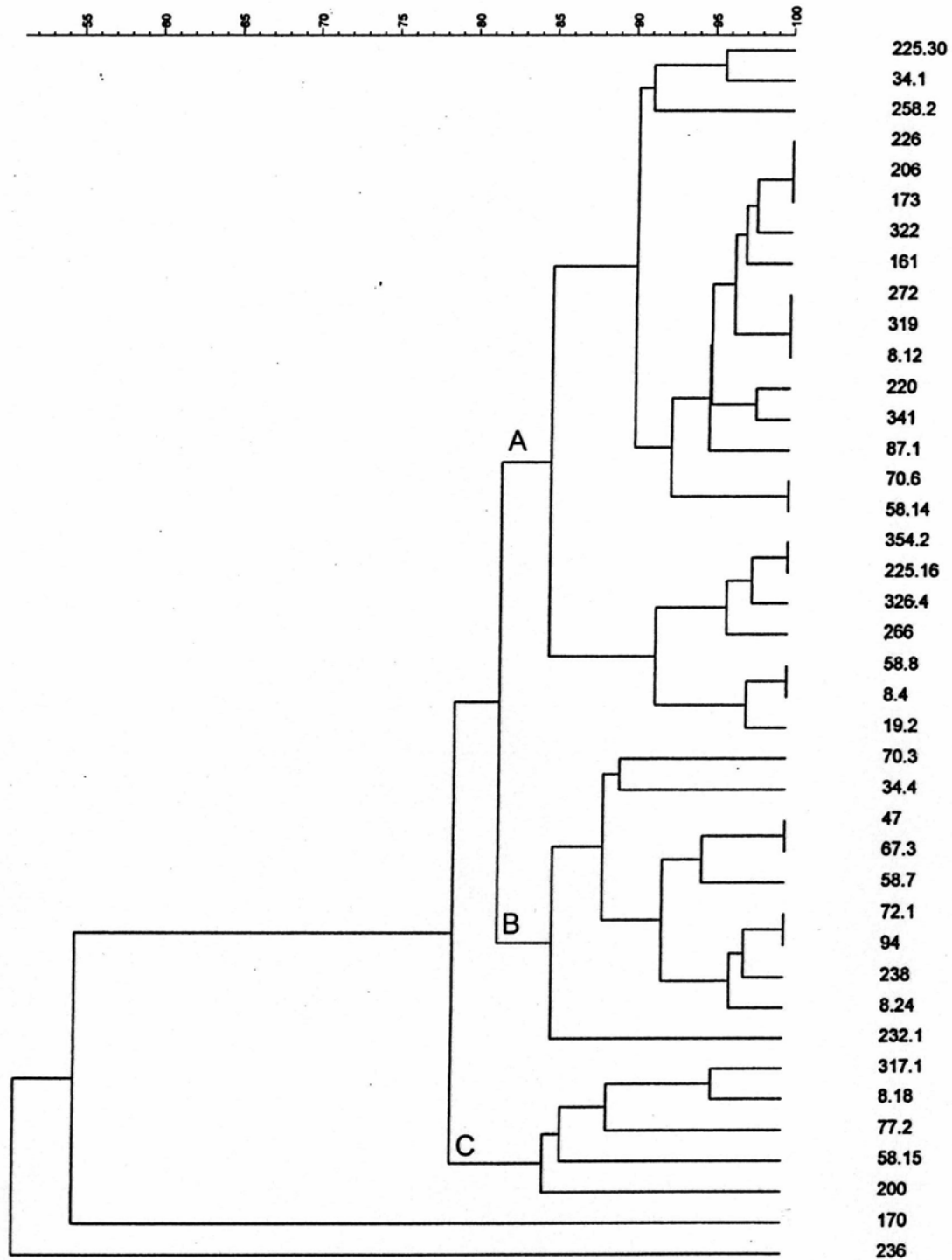


**FIGURE 6-12a.** DNA fingerprinting gel based on single-primer PCR using the M13 core sequence. Isolate numbers indicated above respective gel lanes.

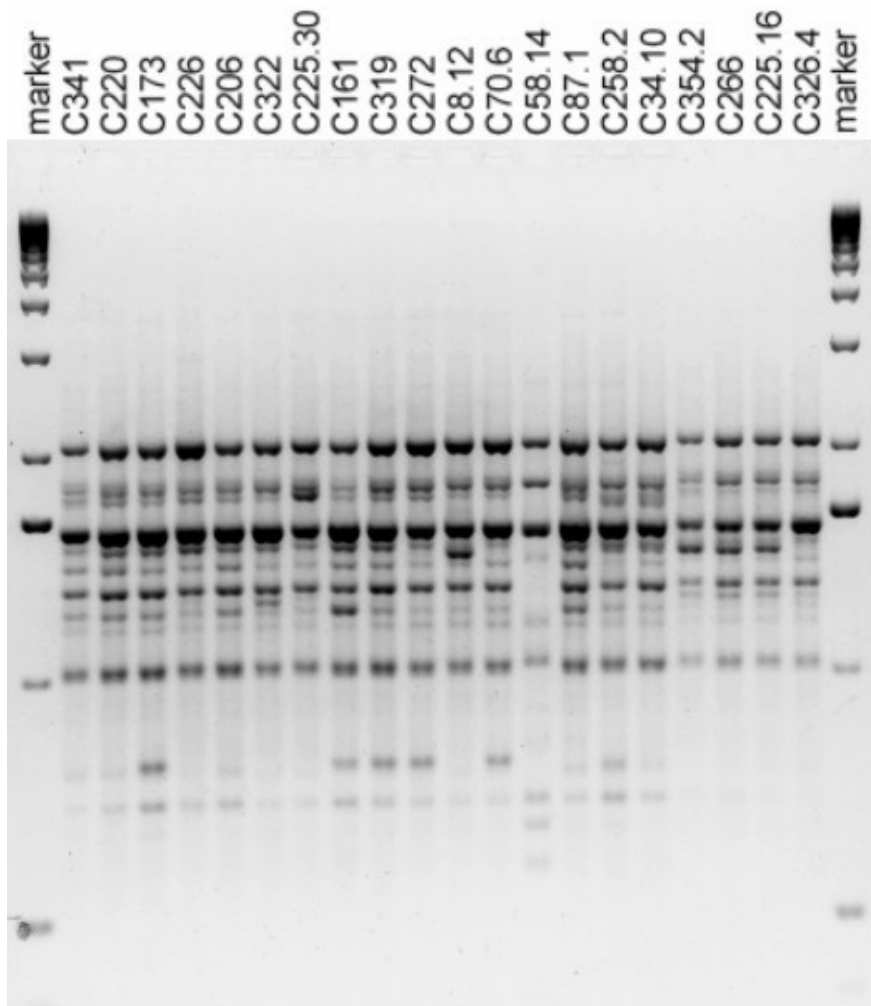


**FIGURE 6-12b.** DNA fingerprinting gel based on single-primer PCR using the M13 core sequence. Isolate numbers indicated above respective gel lanes

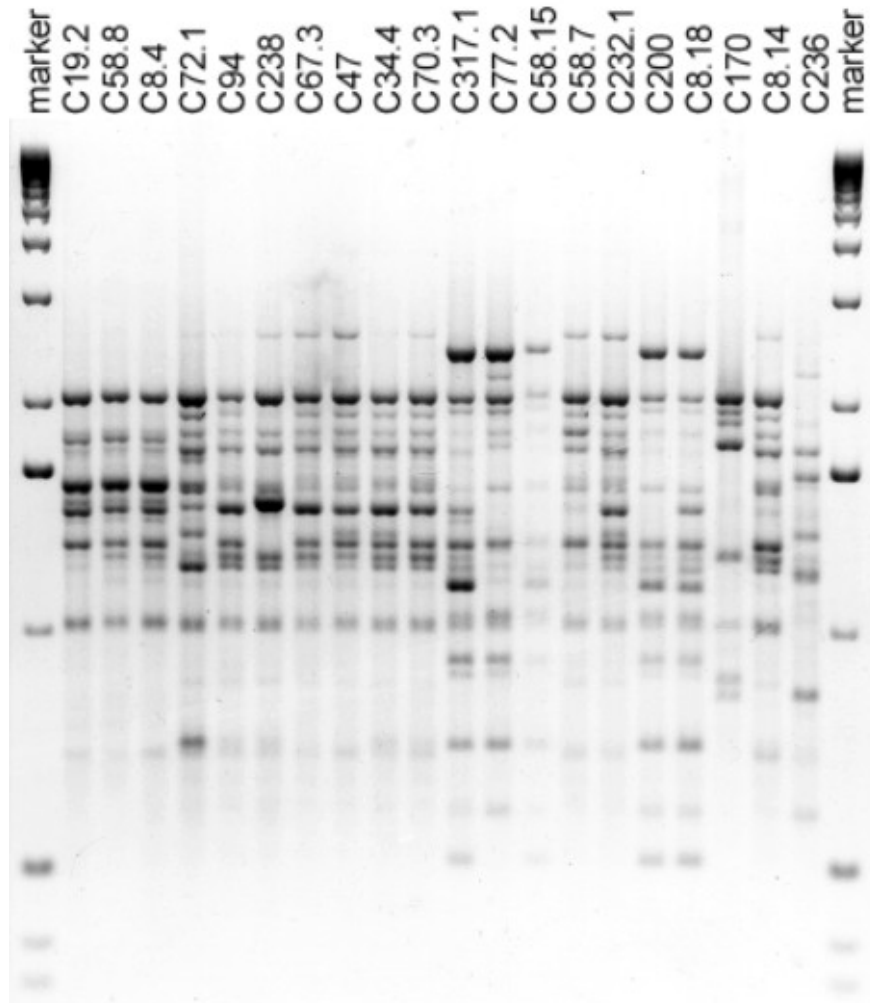




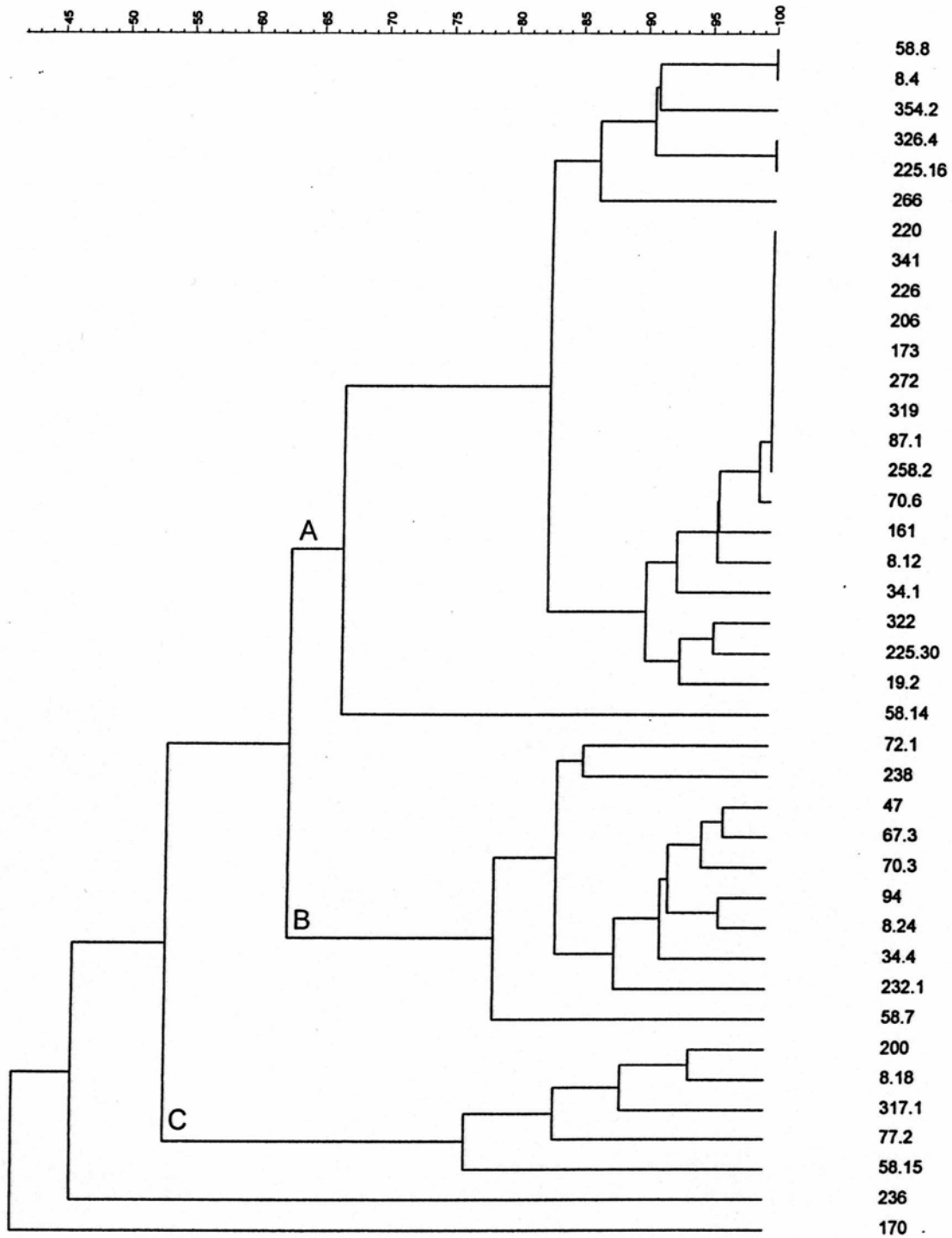
**FIGURE 6-13.** Neighbour-Joining cluster analysis based on band similarity of single-primer PCR products using M13 core sequence. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).



**FIGURE 6-14a.** Electrophoresis gel of PCR products amplified using the oligonucleotide (GACA)<sub>4</sub> in single-primer PCR. Isolate numbers indicated above respective lanes.



**FIGURE 6-14B.** Electrophoresis gel of PCR products amplified using the oligonucleotide  $(GACA)_4$  in single-primer PCR. Isolate numbers indicated above respective lanes.



**FIGURE 6-15.** Neighbour-Joining cluster analysis based on band similarity of single-primer PCR products using the oligonucleotide (GACA)<sub>4</sub>. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).

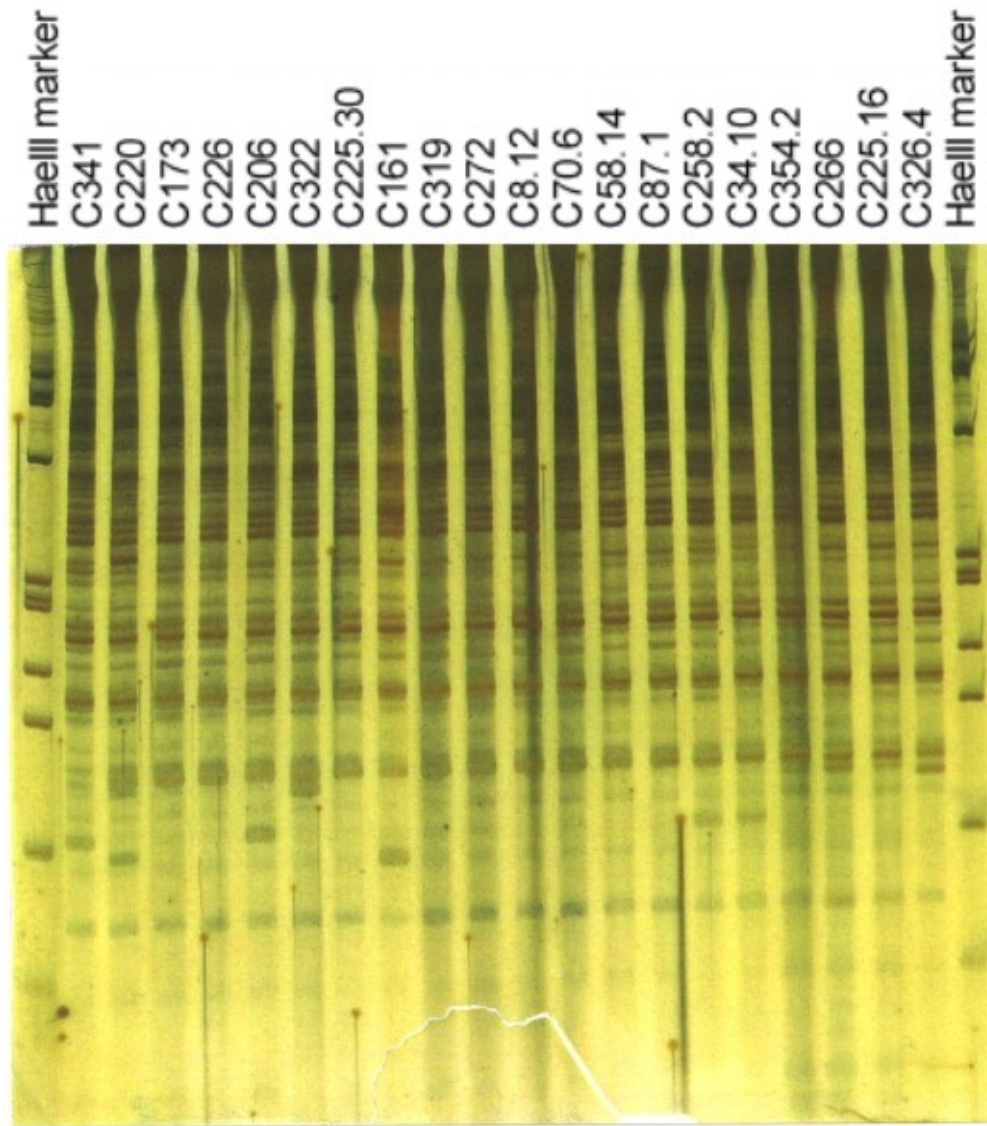
## RANDOM PRIMER FINGERPRINTING

Photographs of silver-stained polyacrylamide gels showing PCR products of the random-primer pair 5SOR & MYC1 are reproduced in Figures 6-16a & b. Amplified DNA products ranged in size from 80 to 1,300 bp and showed 30-40 discrete bands per isolate. Cluster analysis of the banding patterns is shown in Figure 6-17. Overall variation observed using the 5SOR and MYC1 primer pair was greater than for the single primer loci. While the three principal clades observed in this analysis corresponded to those inferred from the single-primer datasets, the pattern of terminal branching within the clades differed.

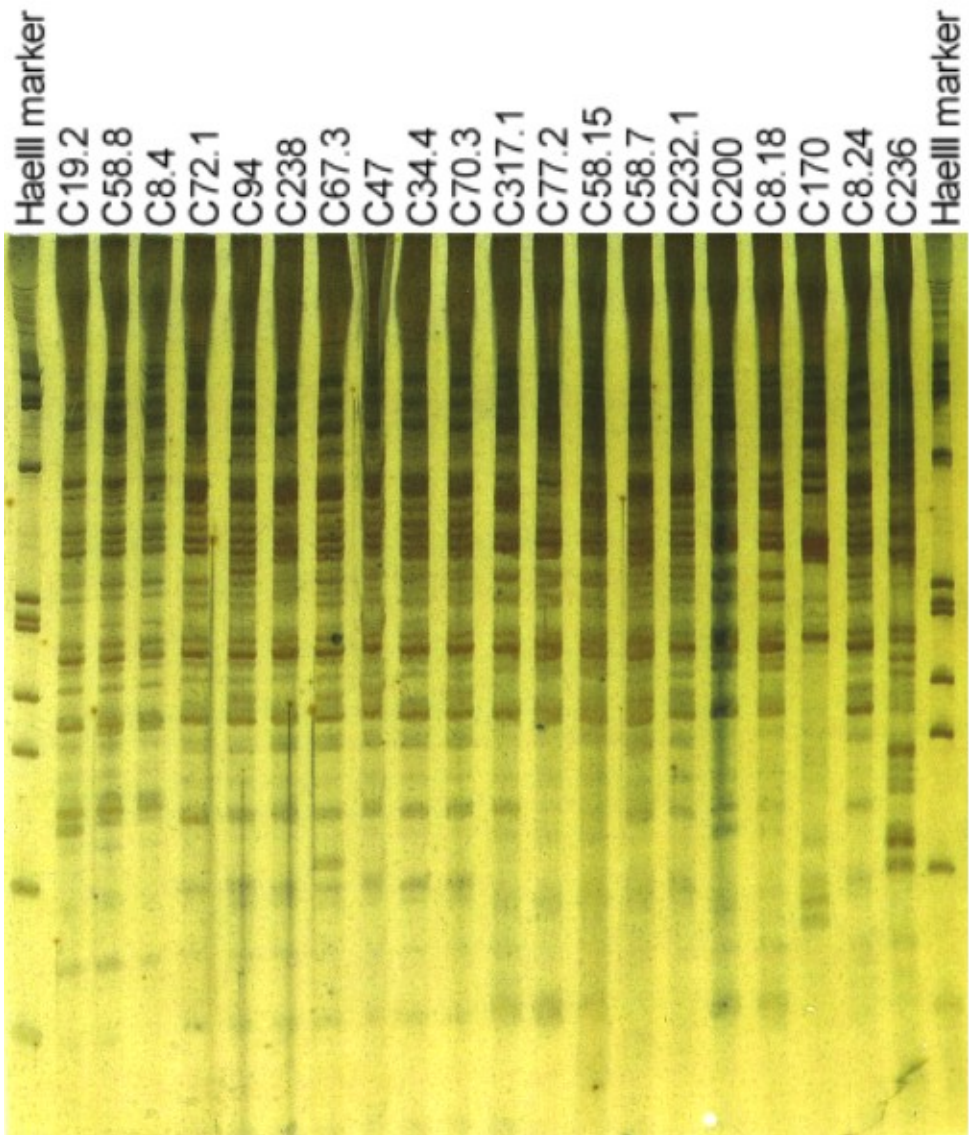
A cluster analysis of the combined fingerprinting data (M13 + GACA<sub>4</sub> + 5SOR/MYC1) is shown in Figure 6-18. Again, the major branches corresponded to principal clades identified in the sequence-based phylogeny. The branches supporting the principal clades were reinforced in the combined dataset relative to individual datasets (*see* Table 6-6). As well, the boundary similarity (minimum level of similarity shared by all members of a clade) of Clade A increased in the combined dataset (*see* Table 6-6).

Figure 6-19 shows a comparison between the combined fingerprint data tree (left) and the unrooted MPT based on combined *acuA*, *benA* and *trxB* sequence data (*viz* Figure 6-10) (right). Overall, the fingerprinting methods revealed the same strongly supported clades observed in the sequence-based phylogenies. The shared clades (A-C) are highlighted by colored rectangles.

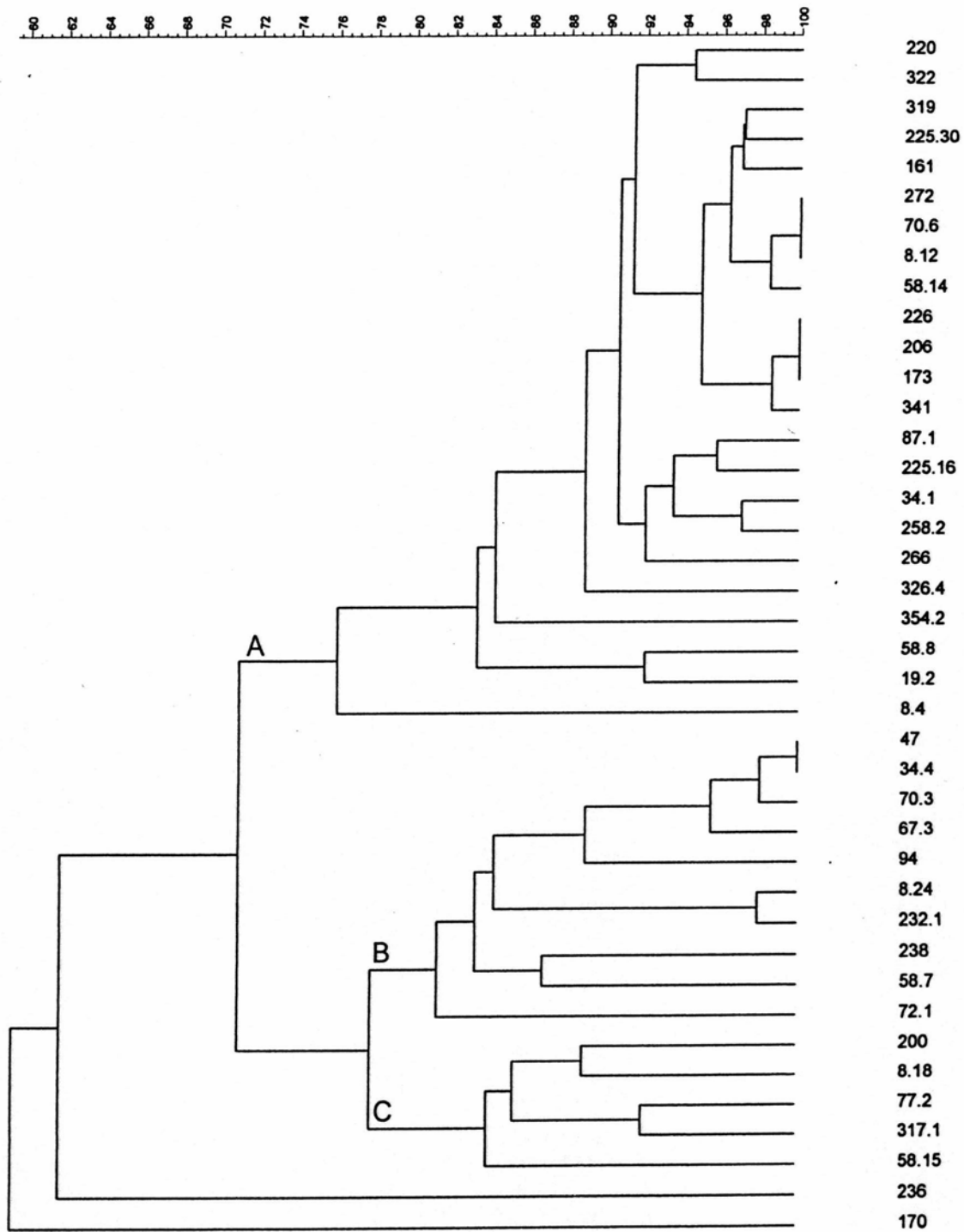
Although ex-type isolates were not included in the fingerprinting studies, the exact agreement of these data with sequence data suggests that the ex-type of *P. chrysogenum* and *P. notatum* should be situated in clade B whereas the Fleming strain should be found in clade A.



**FIGURE 6-16a.** Electrophoresis gel of PCR products amplified using the oligonucleotide primer pair 5SOR/MYC1. Isolate numbers indicated above respective lanes.

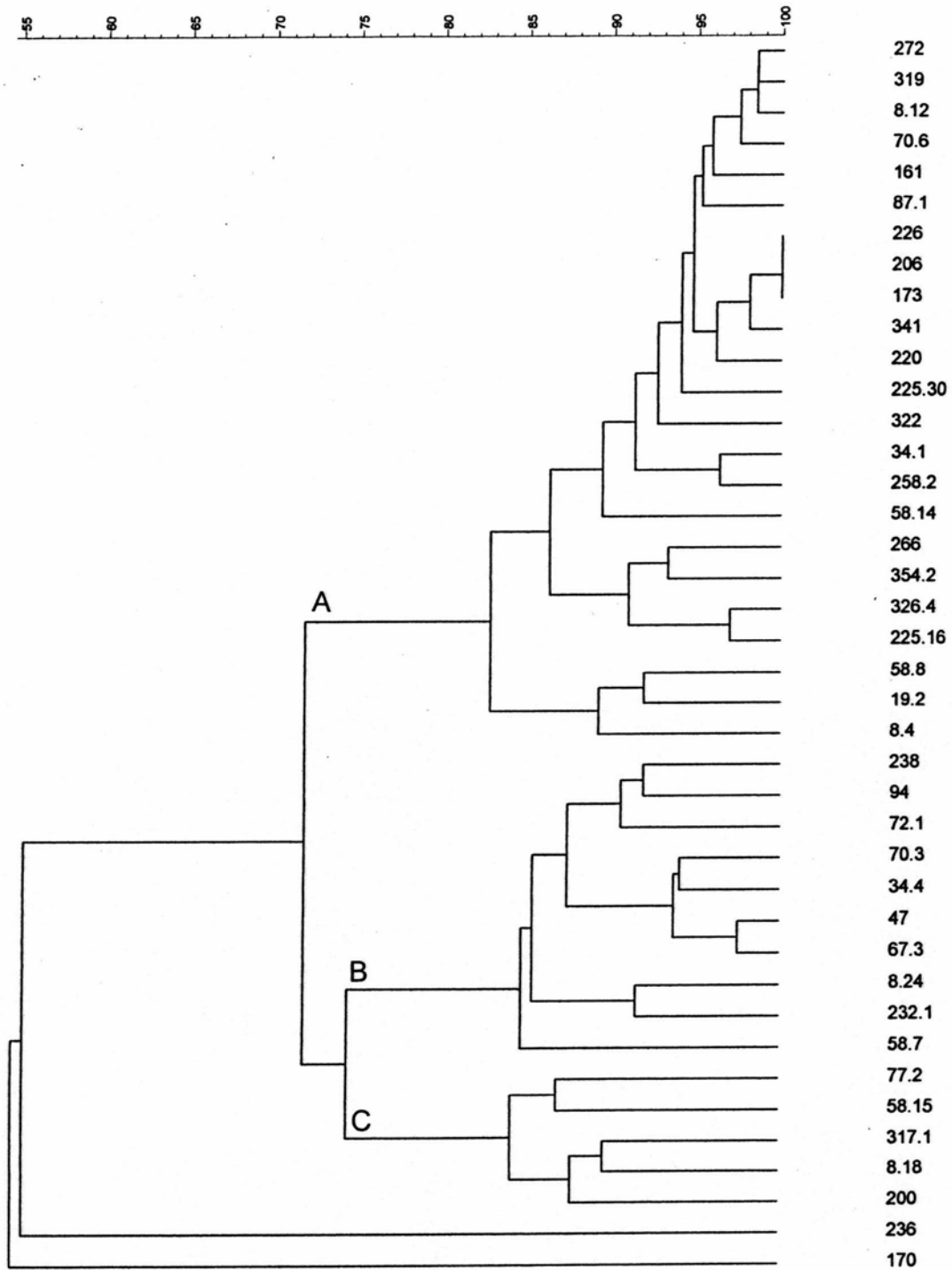


**FIGURE 6-16B.** Electrophoresis gel of PCR products amplified using the oligonucleotide primer pair 5SOR/MYC1. Isolate numbers indicated above respective lanes.

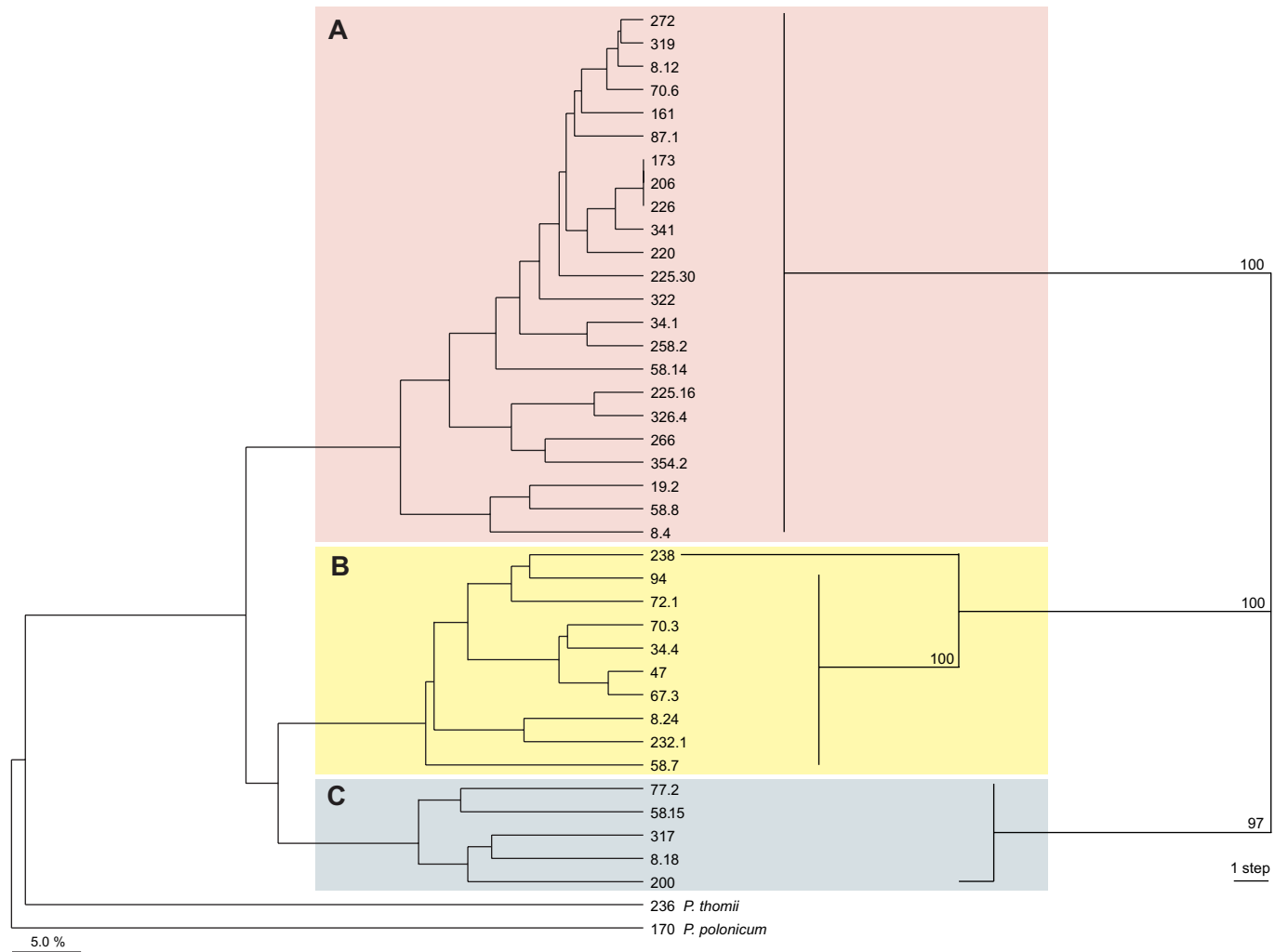


**FIGURE 6-17.** Neighbour-Joining cluster analysis based on band similarity of banding patterns of PCR products of the oligonucleotide primer pair 5SOR/ MYC1. . Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).





**FIGURE 6-18.** Neighbour-Joining cluster analysis based on band similarity of combined banding patterns of PCR products from three independent loci: the single primers M13 and  $(GACA)_4$  and the oligonucleotide primer pair 5SOR/ MYC1. Letters (A-C) indicate branches that correspond to major clades revealed in sequencing studies (*see* Fig. 6-10, p. 154).



**FIGURE 6-19.** Comparison of combined fingerprint data (*left*) and the single MPT produced from combined gene sequences of *acuA*, *benA* and *trxB* genes (*from* FIG. 6-10) (*right*).

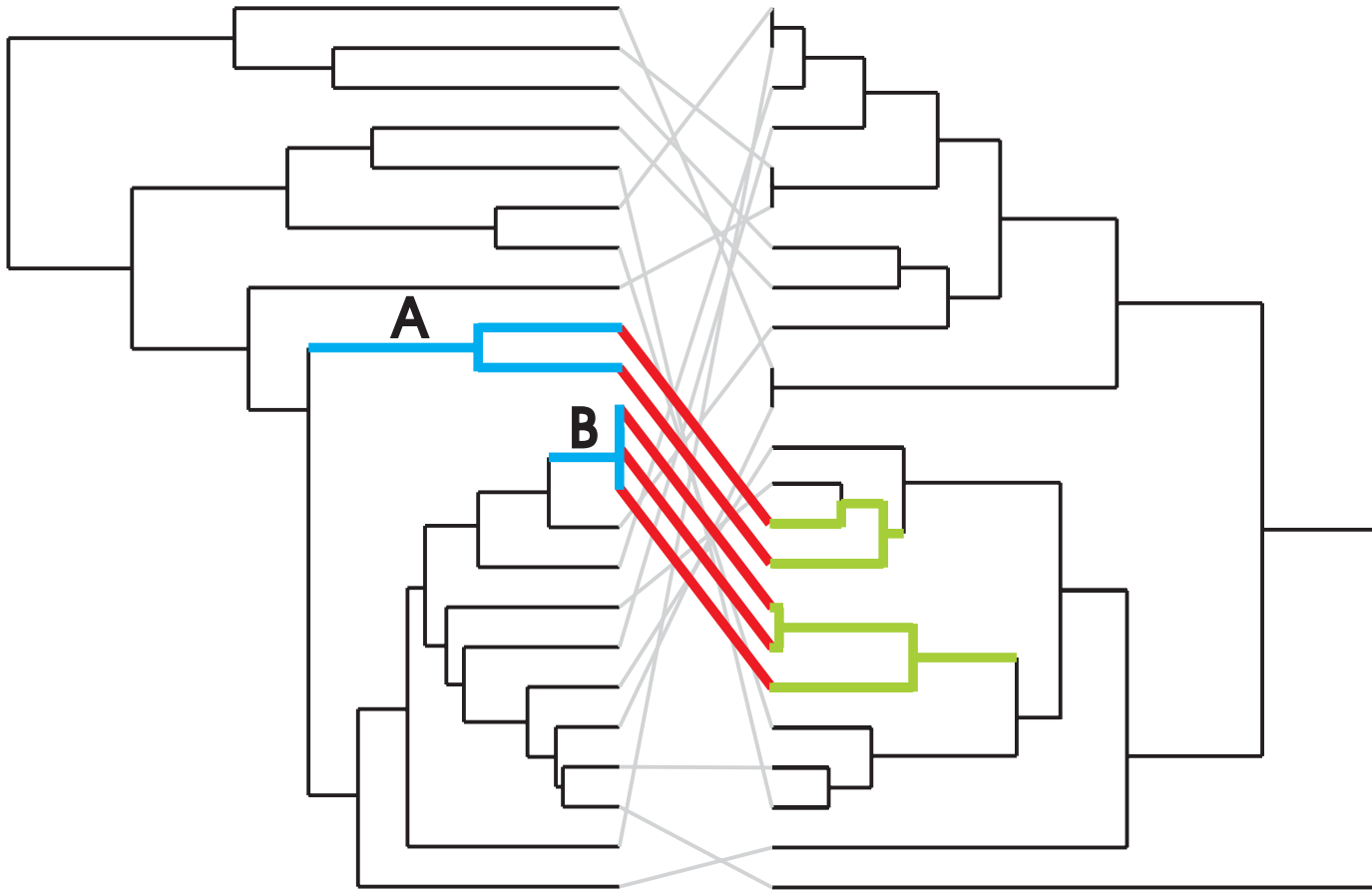
Figure 6-20 shows the correlation between genotype, as revealed by comparing clade A of combined fingerprinting method (from Figure 6-18) (left), geographic proximity of the houses from which isolates were obtained (right). The house numbers in clade A were 34 and 258. Similarly, the houses in clade B were 173, 206 and 226. The physical locations of these houses are shown in Figure 6-1.

## DISCUSSION

The combined sequence-based phylogeny revealed three strongly supported groups within the *P. chrysogenum* complex. The same major groups were revealed by three, independent DNA fingerprint datasets. A PHT of the sequence data for the core isolates comprising the *P. chrysogenum* clade showed that the independent loci were highly congruent, suggesting an absence of recombinatory signal in the present dataset (Geiser et al., 1998). This conclusion is in contrast to work by Rosendahl (1999) who reported recombination in a local population of *P. chrysogenum* using 50 isolates obtained from within and outside a single building on the campus of the University of Copenhagen (Rosendahl, pers. comm.). Their study examined a total of 6 polymorphic markers using SSCP (number of identified alleles shown in parentheses), including acetyl co-enzyme A synthase (*acuA*) (3), gamma-actin (*act*) (3), glutamine amido transferase (*trpC*) (4), orotidine-5'-phosphate decarboxylase (*pyrG*) (4), phosphoglycerate kinase (*pgk*) (7), and xylanase (*xyl*) (3) (Rosendahl, pers. comm.).

## FINGERPRINT DATA

Despite the strong correlation of the three principal clades by all fingerprinting methods, little consistency was observed in terminal branching of the trees obtained using these different methods. Inspection of the gel photographs (Figures 6-12a,b; 6-14a,b; & 6-16a,b) suggests that



**FIGURE 6-20.** Comparison of combined fingerprint data (*left*) and collection location (*right*) based on Neighbor-Joining cluster analysis of distance matrix of linear distances between collection sites.

the contribution of densely staining bands to the datasets may account for the deep branches which form the backbone of the dendrograms, while the less intensely staining banding may produce the fine branches. Thus, a likely explanation for the poor correlation of fine branch topology between loci is the ambiguous nature of faint bands, and the unreliability of their scoring due to lack of intensity. If this is the case, a comparison of terminal branching topology between clades should produce relative incongruence. In graphical terms, this incongruence is reflected in a loss of a robust dichotomous resolution, producing instead a stepped branching topology. This shift in branching topology is correlated to an increase in singlet terminal taxa, as well as an increase in the number of intermediate nodes along the longest path from root to terminal OTU. In other words, the number of intermediate nodes in the path from the root of a clade to a tip of the longest branch increases when such datasets are combined. This trend was observed in the present data, whereby the number of nodes in the longest path to a terminal OTU in Clade #1 was 8, 7, 9 and 11 for M13, GACA<sub>4</sub>, 5SOR/MYC1 and the combined data, respectively (*see* Table 6-7). As well, the relative number of singlet terminal OTUs increased in the combined dataset (*see* Table 6-7).

#### **MORPHOLOGICAL AND PHYSIOLOGICAL VARIATION**

Thom (1930) reported color variation during 22 years of cultivation of the type strain of *P. chrysogenum*. However, the authentic strain of *P. chrysogenum* used in the present study was robust and produced growth patterns and physiological responses that were highly comparable to descriptions provided by Raper and Thom (1949) and Pitt (1979). The variation in colony coloration reported by Thom (1930) may have been related to variations in copper and zinc content of the culture media. Copper and zinc co-factors facilitate melanin biosynthesis via the pentaketide pathway (Hughes and Poole, 1989; Williamson, 1997). Deficiency of these metals in

**Table 6-7:** Comparison of “Clade A” in all fingerprinting cluster analyses

Comparative Parameter	Fingerprint primer(s)			
	M13	GACA <sub>4</sub>	5SOR/MYC1	Combined
Similarity	85 %	67 %	76 %	83 %
N*	0.38 (8/21)	0.38 (7/21)	0.43 (9/21)	0.52 (11/21)
OTUR	0.30 (7/23)	0.35 (8/23)	0.30 (7/23)	0.44 (10/23)

**N\*** = ratio of number of nodes in longest branch (n) to total number of hypothetical internal nodes in the clade ( $N_T = \text{number of taxa} - 2$ ).

**OUTR** = ratio of terminal unpaired OTUs ( $t'$ ) to the total number of taxa ( $t_T$ ).

growth media was first suggested by Frisvad (published from a round table discussion *In PAW-I*, p. 101) to produce unusual colony pigmentation. Frisvad's observation has since served as justification for the supplementation of growth media with these metals to ensure consistency in colonial appearance (Samson et al., 1996). Similar variation has been noted in secondary metabolite profiles according to trace metal availability (Filtenborg et al., 1990). Indeed, much earlier Knight and Frazier (1945) hypothesized that the presence of trace minerals in corn steep liquor was partly responsible for the stimulatory effect of this compound on penicillin production in early industrial production of the antibiotic.

#### **HISTORY OF *P. CHRYSOGENUM***

Charles Thom (1910) described *P. chrysogenum* as a contaminant from cheese. The authentic strain of this taxon is deposited as NRRL 807 (from Thom #26), ATCC 10107, DAOM 193710 and CBS 306.48. This species was characterized by loosely branched smooth terverticillate conidiophores and smooth ellipsoidal conidia. The original description considered radially furrowed, velvety colonies with heavy sporulation, the production of yellow guttation and a yellow reverse pigment to be definitive characters (Thom, 1910). Raper and Thom (1949) concluded that the taxa described by Dierckx (1901) and Biourge (1923) were allied with their "*P. chrysogenum* Series" (*sensu* Raper & Thom, 1949 p.355. *nom. inval. Arts 21 & 36* = Series *Chrysogena* Raper & Thom *ex* Stolk & Samson, PAW-I, p. 180) and that they represented variant isolates along a continuum of variation. They proposed that the compliment of this variation could be better accommodated within 4 species: *P. chrysogenum* Thom, *P. meleagrinum* Biourge, *P. notatum* Westling and *P. cyaneo-fulvum* Biourge.

Samson and co-workers (1977) regarded *P. citreoroseum* and *P. brunneorubrum* as uncertain since Biourge's redescrptions of these taxa were based solely upon the drawings and unpublished notes of Dierckx and authentic material was unavailable for these species (Hennebert, 1985; Samson et al., 1977). These authors also considered *P. griseoroseum* as doubtful despite the availability of an authentic strain (as Dierckx Culture No. 3). Pitt (1979) "lectotypified" *P. chrysogenum* with a dried culture of IMI 24314 (as Herb. IMI 24314). However, this specimen must correctly be considered a neotype since the use of a living ex-type that has been maintained in culture cannot be assumed to have remained consistent with the original collection despite its heritage. Furthermore, the original author did not examine the specimen designated. In his examination of this strain and various voucher collections, Pitt (1979) noted that these isolates appeared to be floccose variants of *P. chrysogenum* that produced biverticillate to irregularly terverticillate penicillia, and classified *P. griseoroseum* in subgenus *Furcatum*. However, Cruickshank and Pitt (1987) showed support for the conspecificity of *P. chrysogenum* and *P. griseoroseum* on the basis of isozyme electrophoretic patterns. Although the stability of these markers in *Penicillium* taxonomy was later questioned by Samson (1991), empirical studies have demonstrated that isozyme methods can provide robust taxonomic separation within subgenus *Penicillium* under a range of experimental conditions (Paterson, 1993). Frisvad and Filtenborg (1989) similarly grouped *P. griseoroseum* with *P. chrysogenum* on the basis of mycotoxin profiles.

#### **NOMENCLATURAL STABILITY OF *P. CHRYSOGENUM***

Samson and co-workers (1977) considered the three Dierckxian species (*P. citreoroseum*, *P. brunneorubrum* and *P. griseoroseum*) as doubtful and placed them in synonymy with *P. chrysogenum*. They based this decision on their inability to locate authentic material (*vide* Hennebert, 1985) and the inadequacy of the descriptions provided by Biourge (1923). Furthermore, Samson and co-



workers (1977) noted that an authentic strain of *P. griseoroseum* had been examined by Raper and Thom (1949), who considered it a synonym of *P. notatum*. Pitt (1979) similarly examined an extant culture of *P. griseoroseum* (as IMI 92220, *fide* Hennebert, 1985) and lectotypified [sic] (a neotypification, see above discussion) the taxon based on a dried culture of Dierckx' original isolate (Pitt, 1980; Hennebert, 1985). The pedigree of this isolate of *P. griseoroseum* selected by Pitt (1979) (IMI 92220) was seven transfers removed from the original collection (e.g. Dierckx #3 (original) > Inst. Pasteur 85 > Biourge 29 > Thom 4733.70 > LSHB P39-1930 > CMI 1962 > IMI 92220). Pitt's decision to retain this taxon which he clearly considered to be close to *P. chrysogenum* was doubtlessly sentimental, since this Dierckx isolate is the oldest laboratory-maintained culture of the genus known (Pitt, 1979). Subsequent examinations of *P. griseoroseum* have suggested that it is conspecific with *P. chrysogenum* (Cruickshank and Pitt, 1987; Bridge et al., 1989). Interestingly, numerical analysis of morphological and physiological data by Bridge et al. (1989) excluded Thom's strain of *P. chrysogenum* (Cluster 7) from the core of isolates of this species, which included the authentic culture of *P. griseoroseum* (Clusters 7 and 14, respectively). These authors rationalized the position of the ex-type culture of *P. chrysogenum* (IMI 24314) by suggesting that it was an attenuated strain (Bridge et al., 1989). However, investigations of the *P. chrysogenum* type strain by other authors have not demonstrated any significant cultural deterioration (Pitt, 1980; Pitt and Samson, 1993). Indeed, Raper and Thom (1949) noted that during 40 years of continuous cultivation, the ex-type strain of *P. chrysogenum* remained stable.

Conspecificity of *P. griseoroseum* and *P. chrysogenum* is supported in the present study, in which isolate NRRL 820 clustered with the type cultures of *P. chrysogenum* (NRRL 807) and *P. notatum* (NRRL 821) (*see* Chapter 4, Figure 4-9, clade A). As such, *P. chrysogenum* is a later synonym, since *P. griseoroseum* has priority based on earlier publication.

The nomenclatural instability of *P. chrysogenum* and the clear industrial importance of this fungus prompted a recommendation for conservation of the name (Frisvad et al., 1990a, b). In fact, Frisvad and colleagues (1990a) went so far as to recommend broad conservation of *P. chrysogenum* as “the species name for the principal producer of penicillin”. This recommendation was advanced on the basis that the association between the name “*Penicillium chrysogenum*” and the biochemical characteristic of penicillin biosynthesis was of paramount industrial importance (Lowe and Elander, 1983), despite that this metabolite is known from other filamentous fungi (Abraham and Newton, 1967; Samson et al., 1996). Frisvad (PAW-I, p. 159) reported that he obtained identical secondary metabolite profiles for 150 isolates of *P. chrysogenum* that he examined. Frisvad and colleagues (1990a) included Westling’s (1911) species, *P. notatum*, as a synonym in their conservation recommendation despite that *P. chrysogenum* has nomenclatural priority in this case. A textual refinement of this article was advanced later as a formal proposal to conserve the name *P. chrysogenum* against earlier names (Kozakiewicz et al., 1992), stating that the conspecificity of *P. griseoroseum* and *P. chrysogenum* was “firmly established” by Bridge and co-workers (1989).

The present study suggests that the current concept of *P. chrysogenum* comprises three lineages which likely represent distinct species. There do not appear to be any available names which can be applied to the un-named clades. The erection of new species to accommodate these lineages is not in conflict with the nomenclatural conservation of *P. chrysogenum* (Frisvad et al., 1990a; Kozakiewicz et al., 1992). However, since it is clear that Frisvad and colleagues (1990a) intended to conserve *P. chrysogenum* upon biochemical- rather than taxonomic grounds, the erection of segregate species within the *P. chrysogenum* group might be an unpopular undertaking. At present, the delineation of sibling species from *P. chrysogenum* awaits the identification of stable, readily

observable morphological and/or physiological characters that reliably separate the members of these lineages.

#### SYNONYMS OF *P. CHRYSOGENUM*

The following synonymy of *P. chrysogenum* is based on an examination of existing taxonomic literature in addition to several authentic strains included in the present study.

*Penicillium chrysogenum* Thom in U.S. Dept. Agr. Bur. Anim. Ind., Bul. 118, 1910. pp. 58-60, fig. 20. NT: Herb. IMI 24314 Pitt Gen. *Penicillium* 1980, Pitt & Samson, Reg. Veg. **128**: 41. 1993., *nom. cons. prop.* Kozakiewicz et al., *Taxon* **41**: 109-110, 1992.

- = *Penicillium citreoroseum* Dierckx, *Annls. Soc. Scient. Brux.* **25**: 86. 1901, *syn. fide* Samson et al., 1977., *prop. nom. rej.* Kozakiewicz et al., *Taxon* **41**: 109-110, 1992.
- = *P. brunneorubrum* Dierckx, *Annls. Soc. Scient. Brux.* **25**: 88. 1901, *syn. fide* Samson et al., 1977., *prop. nom. rej.* Kozakiewicz et al., *Taxon* **41**: 109-110, 1992.
- = *P. griseoroseum* Dierckx, *Annls. Soc. Scient. Brux.* **25**: 89. 1901, *syn. fide* Samson et al., 1977., LT: IMI 92220i *ex* CMI 1962 Pitt, 1980, *prop. nom. rej.* Kozakiewicz et al., *Taxon* **41**: 109-110, 1992.
- = *P. baculatum* Westling, *Svensk Botanisk Tidskrift* **4**: 139-145, figs. 1-3. 1910, *syn. fide* Raper & Thom 1949.
- = *P. notatum* Westling, *Ark. Bot.* **11**: 55. 1911, *syn. fide* Samson et al., 1977; Pitt, 1980.
- = *P. chlorophaeum* Biourge, *Monogr., La Cellule* **33**: fasc. 1, pp. 271-273. Pls. VIII & XIII, fig. 78. 1923, *syn. fide* Raper & Thom 1949.
- = *P. rubens* Biourge, *Monogr. La Cellule* **33**: fasc. 1, p. 265. Pls. XI & XIX, fig. 111. 1923, *syn. fide* Raper & Thom 1949.
- = *P. flavidomarginatum* Biourge, *Monogr., La Cellule* **33**: fasc. 1, p. 150. 1923, *syn. fide* Pitt 1980.
- = *P. fluorescens* Laxa, *Zentbl. f. Bakt. &c. (II)* **86**: 164-165. 1932, *nom. nud. fide* Raper & Thom 1949.
- = *P. roseocitreum* Biourge *Monogr., La Cellule* **33**: fasc. 1, pp. 184-186. Pls. IV & VII, fig. 39. 1923, *syn. fide* Raper & Thom 1949.

- = *P. meleagrinum* Biourge, Monogr. La Cellule **33**: fasc. 1, p. 184. 1923 *syn. fide* Samson et al., 1977.
- = *P. cyaneofulvum* Biourge, Monogr. La Cellule **33**: fasc. 1, p. 171. 1923 *syn. fide* Samson et al., 1977.
- = *P. camerunense* Heim, Nouvel & Saccas, Bull. Acad. Belg. Cl. Sci., Ser 5, **35**: 52. 1949, *syn. fide* Samson et al., 1977.
- = *P. chrysogenum* Thom var. *brevisterigma* Forster, Brit. Pat. 691: 242. 1953, *nom. nud. fide* Samson et al., 1977.
- = *P. aromaticum* Sopp forma *microsporum* Romankova (Zap. Lenin. Univ. Zhdanov **191**: 102. 1955) *fide* Samson et al., 1977.
- = *P. harmonense* Baghdadi, Nov. Sist. niz. Rast. **5**: 102. 1968, *syn. fide* Pitt 1980.
- = *P. verrucosum* var. *cyclopium* strain *ananas-olens* Ramírez, Man. & Atl. Penicillia. 1982, *syn. fide* Stolk et al., in Modern concepts in *Penicillium* and *Aspergillus* classification. 1990. p. 126.

Recently, Banke and co-workers (1997) described *P. flavigenum*, a segregate species of *P. chrysogenum*, based on isozyme profiles. These workers examined 17 isolates which they assigned to this species. Two of these isolates were obtained from *Hordeum* grain from Canada. It is not clear if these isolates were obtained from the DAOM collection. At present the DAOM on-line catalogue lists two isolates of *P. chrysogenum* from *Hordeum* from Canada both of which were examined in the present study and clustered with the Fleming isolate of *P. notatum*. If these isolates represent *P. flavigenum sensu* Banke and co-workers (1997), then this name may be available for the clade containing the Fleming isolate. Examination of authentic material of *P. flavigenum* is necessary to make this determination.

#### ***PENICILLIUM CHRYSOGENUM* AND THE INDOOR ENVIRONMENT**

Raper and Thom (1949) observed that contamination of foods with *P. chrysogenum* resulted in sufficient content of penicillin to prevent the growth of *Clostridium*. Indeed, it is interesting to

note that *P. chrysogenum* is one of only a few species in subgenus *Penicillium* not known to produce metabolites of significant toxicity to animals (Dillon et al., 1996; Samson et al., 1996). Similar attenuated toxicity has been noted for mycotoxin-producing species of *Aspergillus* associated with the seed caches of burrowing rodents (D. Wicklow, pers. comm.). It is conceivable that the reduced mycotoxicity of *P. chrysogenum* coupled with its predominance relative to other *Penicillia* in human-associated habitats reflect a similar adaptation to the human environment. This being the case, the production of penicillin, a potent antibacterial metabolite with negligible mammalian toxicity, would clearly be an adaptive advantage, particularly given that the fungus in question is a frequent contaminant of foodstuffs. Similarly, the ubiquity of *P. chrysogenum* in indoor environments has led to speculation that exposure to this penicillin-producing species may be a factor in the development of allergy to this antibiotic, however, such a link so far has not been demonstrated (Gravesen, 1979).

## CONCLUSIONS

*Penicillium chrysogenum* is one of the most prevalent species in the indoor environment. Spores of this mould occur commonly in indoor dusts often at considerably high CFU per gram-mass concentration. To date, there has been little investigation into the level of genotypic diversity within this species. The present study supports the existence of a *P. chrysogenum* complex which consists of as many as three species propagated clonally in absence of recombination.

*Penicillium notatum* is a valid synonym of *P. chrysogenum*. Formal description of the two un-named clades as separate species awaits the identification of defining phenotypic characters (e.g. micro-morphology and/or physiology).

## Genotypic variation in *Penicillium chysogenum* from indoor environments

James Scott<sup>1</sup>

Department of Public Health Sciences, University of  
Toronto, Toronto, Ontario, M5T 1R4; and  
Sporometrics Inc., 219 Dufferin St., Suite G20C,  
Toronto, Ontario, M6K 1Y9

Wendy A. Untereiner

Botany Department, Brandon University, Brandon,  
Manitoba, R7A 6A9

Bess Wong

Neil A. Straus

David Malloch

Department of Botany, University of Toronto, Toronto,  
Ontario, M5S 3B2

**Abstract:** We examined 198 isolates of *P. chysogenum* recovered from 109 houses in Wallaceburg, Ontario, and 25 culture collection isolates including seven ex-type strains. Multilocus genotypes were determined by heteroduplex mobility assay of regions spanning introns in acetyl co-enzyme A synthase, beta-tubulin, thioredoxin reductase and the internal transcribed spacer regions of the nuclear ribosomal subrepeat. Five unique multilocus haplotypes were revealed without evidence of recombination, indicating strictly clonal population structures. Phylogenetic analysis of allele sequences using maximum parsimony resolved three strongly supported lineages. The dominant clade included more than 90% of house isolates in addition to the notable laboratory contaminant isolated by Alexander Fleming in 1929 in Britain. A second clade contained more than 5% of house isolates clustered with the ex-type strains of *P. chysogenum* and *P. notatum*. Follow-up sampling of outdoor air in the locality failed to reveal *P. chysogenum*, confirming the rarity of this fungus in outdoor air.

**Key words:** DNA sequence analysis, dust biology, fungal population genetics, heteroduplex mobility assay, indoor air quality, indoor molds

### INTRODUCTION

Viable fungal spores occur in great numbers in household dust and indoor air. Many of these spores

typically arise outdoors in the phylloplane and are carried indoors on air currents and contaminated footwear. Other genera, such as *Aspergillus* Fr.:Fr. and *Penicillium* Link, are poorly represented in outdoor air in contrast to their indoor frequency. Thus, it is widely believed that these molds proliferate indoors, often cryptically, on various substrates including dust itself under dry conditions.

*Penicillium chysogenum* Thom is perhaps the most common of all *Penicillia* (Pitt 1980, Raper and Thom 1949), occurring as an agent of food spoilage (Samson et al 1996) as well as a resident of household dust (Davies 1960) and indoor air. *Penicillium chysogenum* is also a well-known contaminant of damp building materials (Chang et al 1995, Gravesen 1999, Hunter and Lea 1995) and indoor finishes (Adan and Samson 1994). This species is one of the few terverticillate *Penicillia* that typically does not produce mycotoxins of significant mammalian toxicity (Dillon et al 1996, Nielsen and Gravesen 1999, Pitt and Cruikshank 1990). However, *P. chysogenum* has been identified as an important allergen in the indoor environment (Cooley 1999, Cooley et al 1999, Fergusson et al 1984) and as a rare causative agent of opportunistic mycosis in humans (Eschete et al 1981, Hoffman et al 1992).

Charles Thom (1910) described *P. chysogenum* as a contaminant from cheese. The authentic strain of this taxon is deposited as NRRL 807 (Thom's culture No. 26 = ATCC 10107, CBS 306.48 and DAOM 193710). Thom named *P. chysogenum* fundamentally based on the production of yellow guttation droplets on the colony surface, a characteristic he observed consistently during cultivation on a range of growth media. Thom discussed several strains that produced yellow guttation but varied in colony morphology to some degree, and he interpreted *P. chysogenum* in a broad sense to include these variant "races" (Thom 1910). Raper and Thom (1949) later expanded this already broad concept to include several taxa described by Dierckx (1901) and Biourge (1923), noting that these authors described taxa based largely on the examination of single strains that represented contrasting forms of *P. chysogenum*. However, they chose to maintain *P. cyaneo-fulvum* Biourge, *P. meleagrinum* Biourge and *P. notatum* Westling to accommodate the variation they observed in examinations

of hundreds of isolates of the *P. chysogenum* "series". Raper and Thom (1949) considered *P. griseoroseum* Dierckx to be a synonym of *P. notatum*. Samson and co-workers (1977) reinforced the broad concept of *P. chysogenum* by further reducing *P. cyaneofulvum*, *P. meleagrinum* and *P. notatum* to synonymy with *P. chysogenum*.

Pitt (1980) neotypified *P. chysogenum* with a dried culture of IMI 24314 (as Herb. IMI 24314). Although, in his designation, Pitt referred to the specimen as a lectotype, it formally must be considered a neotype because the designated specimen was not examined by the original author (Article 9.2, ICBN) and the use of a living ex-type that has been maintained in culture cannot be assumed to have remained consistent with the original collection despite its pedigree. In his examination of authentic isolates from the *P. chysogenum* group, Pitt (1980) noted that *P. griseoroseum* produced a floccose colony morphology and biverticillate to irregularly terverticillate penicillia. On this basis, Pitt (1980) reclassified *P. griseoroseum* in *Penicillium* subgenus *Furcatum* and neotypified it with a dried culture at least seven transfers removed from the original isolate (Dierckx 3 > Inst. Pasteur 85 > Biourge 29 > Thom 4733.70 > LSHB P39-1930 > CMI 1962 > IMI 92220) (Hennebert 1985). Despite this subgeneric separation, Pitt (1980) considered *P. griseoroseum* to be close to *P. chysogenum*. In part, his decision to retain the former taxon might have been influenced by the historical significance of the strain in question, which is the oldest laboratory-maintained culture of the genus known (Pitt 1980, p. 7). Cruickshank and Pitt (1987) later supported the conspecificity of *P. chysogenum* and *P. griseoroseum* on the basis of isozyme electrophoretic patterns and reduced *P. griseoroseum* into synonymy with the former. Frisvad and Filtenborg (1989) further supported this conclusion by the comparison of mycotoxin profiles. In contrast, the numerical analysis of morphological and physiological data by Bridge et al (1989) excluded Thom's strain of *P. chysogenum* (Cluster 7) from the core of isolates of this species, which included the authentic culture of *P. griseoroseum* (Cluster 14). These authors rationalized the position of the ex-type culture of *P. chysogenum* (IMI 24314) by suggesting that it was an attenuated strain (Bridge et al 1989). However, investigations of *P. chysogenum* ex-type strains by other authors have not demonstrated any significant cultural deterioration (Pitt 1980, Pitt and Samson 1993). Indeed, Raper and Thom (1949) noted that during 40 years of continuous cultivation, the ex-type strain of *P. chysogenum* remained stable.

The modern concept of *P. chysogenum* includes rapidly growing isolates with loosely branched

smooth terverticillate conidiophores and smooth ellipsoidal conidia. The production of yellow guttation and yellow diffusible pigment is also characteristic but varies from isolate to isolate. *Penicillium chysogenum* generally is thought to be strictly asexual because no teleomorph has been identified for this species. However, the clonal nature of *P. chysogenum* has not been tested systematically using a modern molecular genetic approach. Several additional taxa recently have been described that appear to be allied with *P. chysogenum*, specifically *P. aethiopicum* Frisvad, *P. dipodomys* Frisvad, Filtenborg & Wicklow, *P. flavigenum* Frisvad & Sampson. The placement of these taxa relative to *P. chysogenum* similarly has not been investigated using molecular phylogenetic methods.

In the present study, we examined the extent of clonality within a core group of isolates from the *P. chysogenum* group and representative authentic isolates of related taxa and tested the phylogenetic validity of the current species concept of *P. chysogenum* based on the analysis of multilocus haplotype and DNA sequence data.

#### MATERIALS AND METHODS

*Isolation and identification of strains.*—More than 700 isolates of *P. chysogenum* were collected from 376 houses in Wallaceburg, Ontario, in 1994. These isolates were grown 14 d at room temperature on modified Leonian's agar (Malloch 1981) and modified Creatine-Sucrose agar medium (CSA) (Frisvad 1993). A duplicate plate of each isolate was incubated 7 d at 37 °C. A subset of 198 micromorphologically and physiologically uniform isolates was selected for genetic characterization based on the hypothesis that these isolates represented a single phylogenetic species. Air sampling was conducted at 18 outdoor locations distributed evenly throughout Wallaceburg during late summer 1995, using a Reuter Centrifugal sampler (RCS) (Biotest, Dreieich, Germany) on Rose Bengal agar medium (Malloch 1981) with a sampling volume of 80 L per sample. Growth media were incubated and colonies analyzed as above.

The number assigned to each fungal isolate is unique and consists of an arbitrary "house number" coupled with an incremental accession number reflective of the total number of isolates of *P. chysogenum* obtained from that house. Additional isolates included in sequencing studies consisted of authentic strains as well as a geographical range of voucher isolates (TABLE I).

*DNA isolation.*—Fungal isolates were inoculated centrally on a Petri plate of Weitzman and Silva-Hutner's agar (WSHA) (Weitzman and Silva-Hutner 1967), and grown 7 d at room temperature under 12 h artificial daylight. The plates were flooded with 2 mL of 95% ethanol, and the conidia and mycelium were suspended by gently scraping the surface of the colonies with a sterile bent glass rod. Conidial suspensions were collected in microcentrifuge tubes, centrifuged at 12 000 rpm, and the supernatant was

TABLE I. Strains examined in this study

Species	Strain no.	Status	Substratum and locality
<i>Penicillium aethiopicum</i> Frisvad	CBS 484.84	ex-type	grains of <i>Hordeum vulgare</i> , Ethiopia
<i>P. chrysogenum</i> Thom	C8.12		house dust, Wallaceburg, ON, Canada
<i>P. chrysogenum</i>	C8.24		house dust, Wallaceburg, ON, Canada
<i>P. chrysogenum</i>	C200		house dust, Wallaceburg, ON, Canada
<i>P. chrysogenum</i>	C238		house dust, Wallaceburg, ON, Canada
<i>P. chrysogenum</i>	C317.1		house dust, Wallaceburg, ON, Canada
<i>P. chrysogenum</i>	DAOM 155627		paper, Ottawa, ON, Canada
<i>P. chrysogenum</i>	DAOM 155628		paper, Ottawa, ON, Canada
<i>P. chrysogenum</i>	DAOM 155631		paper, Ottawa, ON, Canada
<i>P. chrysogenum</i>	DAOM 167036		<i>Picea</i> forest soil, QC, Canada
<i>P. chrysogenum</i>	DAOM 171025		salami, Ottawa, ON, Canada
<i>P. chrysogenum</i>	DAOM 175157		walls of mouldy house, Niagara Falls, ON, Canada
<i>P. chrysogenum</i>	DAOM 175176		<i>Lycopersicum esculentum</i> leaves, PEI, Canada
<i>P. chrysogenum</i>	DAOM 175758		office building, OC, Canada
<i>P. chrysogenum</i>	DAOM 178623		substr. et loc. incert.
<i>P. chrysogenum</i>	DAOM 190864		grains of <i>Hordeum</i> , MB, Canada
<i>P. chrysogenum</i>	DAOM 193710	ex-type	cheese, CT, USA
<i>P. chrysogenum</i>	DAOM 212031		wooden wall studs, AB, Canada
<i>P. chrysogenum</i>	DAOM 215336		wooden wall studs, AB, Canada
<i>P. chrysogenum</i>	DAOM 215337		hemlock lumber, BC, Canada
<i>P. chrysogenum</i>	DAOM 216700		grains of <i>Hordeum</i> , Canada
<i>P. chrysogenum</i>	DAOM 216701		<i>Sesamum indicum</i> , Korea
<i>P. chrysogenum</i>	DAOM 59494C		substr. incert., Honduras
<i>P. chrysogenum</i>	NRRL 824		laboratory contaminant, London, England
<i>P. dipodomyis</i> (Frisvad et al) Banke et al	NRRL 1485	ex-type	cheek pouch of <i>Dipodomyis spectabilis</i> , AZ, USA
<i>P. flavigenum</i> Frisvad & Samson	CBS 419.89	ex-type	flour, Lyngby, Denmark
<i>P. flavigenum</i>	IMI 321909		substr. et loc. incert.
<i>P. nalgiovense</i> Laxa	NRRL 911	ex-type	cheese, Nalzozy, Czech Republic
<i>P. notatum</i> Westling	ATCC 10108	ex-type	branches of <i>Hyssopus</i> sp., Norway

discarded. The pellets were dried 30 min in a vacuum concentrator centrifuge. This protocol yielded approximately 15 mg of pelleted conidia per vial. Each vial was sufficient for a single DNA isolation.

Approximately 15 mg of sterile, acid-cleaned Dicalite 1400 (diatomaceous earth-based swimming pool filter, Grefco Inc., Torrance, California) was added to each tube of dry, pelleted, ethanol-killed conidia (Scott et al 1999). After the addition of 10  $\mu$ L of 70% EtOH, the mixture was ground with a sterile glass rod 1 min and suspended in 600  $\mu$ L of lysis buffer containing 1.4 M NaCl, 2% w/v CTAB, 200 mM Tris-HCl (pH 8.0) and 20 mM EDTA (Weising et al 1995). Tubes were incubated at 65 C for 1 h and were mixed by inversion at 30 min intervals.

After extraction, the tubes were cooled to room temperature and centrifuged at 10 000 rpm for 1 min. The supernatant liquid was extracted twice with chloroform:isoamyl alcohol (24:1), and the DNA was precipitated with 100% isopropanol at  $-80$  C for 10 min. The pellets were rinsed with 70% ethanol, air-dried and resuspended in 200  $\mu$ L TE (pH 8.0) (Sambrook et al 1989). Ribonuclease A was added to the DNA at a final concentration of 0.2  $\mu$ g/ $\mu$ L and incubated at 37 C for 30 min. The DNA was extracted with chloroform:isoamyl alcohol and precipitated with 0.3 M sodium acetate and an equal volume of 100% ethanol at  $-80$  C. DNA pellets were rinsed with 70% ethanol, air-dried and

resuspended in 100  $\mu$ L TE (pH 8.0). DNA concentration was adjusted to 60 ng/ $\mu$ L based on spectrophotometry.

*DNA preparation and heteroduplex mobility assay (HMA).*—Four polymorphic loci consisting of partial regions spanning introns in the genes encoding acetyl co-enzyme A synthase (*acuA*), beta-tubulin (*benA*), thioredoxin reductase (*trxB*) and the region spanning the internal transcribed spacer (ITS1-5.8S-ITS2) of the nuclear ribosomal RNA gene (rDNA) were PCR-amplified using the primers listed in TABLE II. PCR mixtures consisted of 1 unit of *Taq* DNA polymerase (Boehinger Mannheim, Laval, QC), 50 mM KCl, 2.0 mM  $MgCl_2$ , 250  $\mu$ M of each dNTP, 0.2 mM of each primer and 60 ng of template DNA in a total reaction volume of 50  $\mu$ L overlaid with a drop of sterile mineral oil. Reactions were carried out in a PTC-100 thermocycler (MJ Research, Reno, Nevada). Cycling conditions consisted of 30 cycles of 94 C for 30 s, 58 C for 30 s and 72 C for 30 s with a final extension at 72 C for 2 min. Yield was quantified based on ethidium bromide staining and UV visualization after electrophoresis on 1.2% agarose gels.

Heteroduplexing reactions pooled homologous PCR products pairwise in overlapped combinations (pairs comprised numerically adjacent isolates in a sequentially numbered series of PCRs and the first and last isolate of each series) to encompass the entire set. For each locus exam-



TABLE II. Primers sequences employed in this study

<b>Acetyl-CoA synthetase (acuA)</b>	
<b>Source:</b> this study, Genbank L09598, +2102-2452, spanning introns 3 and 4	
acuA-2F (fwd)	5'-ACC GTG TGG GGT GCC CAC AAG CGT TAC ATG-3'
acuA-1R (rvs)	5'-GGT CAG CTC GTC GGC AAT ACC AAC GAC AGC-3'
<b>Beta-tubulin (benA)</b>	
<b>Source:</b> Glass and Donaldson (1995)	
Bt2A (fwd)	5'-GGT AAC CAA ATC GGT GCT GCT TTC-3'
Bt2b (rvs)	5'-ACC CTC AGT GTA GTG ACC CTT GGC-3'
<b>Nuclear ribosomal DNA ITS1, 5.8S and ITS2 region (ITS)</b>	
<b>Source:</b> White et al (1990), fwd; Untereiner et al (1995), rvs	
ITS5 (fwd)	5'-GGA AGT AAA AGT CGT AAC AAG G-3'
WNLI (rvs)	5'-TAT GCT TAA GTT CAG CGG-3'
<b>Thioredoxin reductase (trxB)</b>	
<b>Source:</b> this study, EMBL X76119, +801-1153, spanning intron 2	
trxB-1F (fwd)	5'-AAC GCG GAG GAG GTC GTT GAG GCT AAC GGT-3'
trxB-1R (rvs)	5'-TTA GAG CAC AGG CTT TGC CTC CTG GTG AGT-3'

ined, PCRs were diluted to 50% of the original concentration with 4 mM EDTA and 50 mM KCl, combined in equimolar proportion in a total volume of 10  $\mu$ L and overlaid with a drop of sterile mineral oil. Reactions were heated to boiling for 4 min and immediately annealed at 65 C for 6 min. Products of HMA reactions were separated by electrophoresis in gels consisting of 12% acrylamide, 0.2% bisacrylamide and 0.04% ammonium persulfate in 1  $\times$  TBE. Immediately before casting, 0.5% agarose and 0.2% TEMED were added to the degassed solution. Gels were cast in a BioRad Protean electrophoresis apparatus (La Jolla, California) at 1 mm thick, allowed to polymerize 4–5 h and run on a vertical electrophoresis apparatus (Protean II, BioRad) at 10 V/cm, 12 C for up to 20 h. Gels were stained for 2 h in ethidium bromide (250 ng/mL) and destained in dH<sub>2</sub>O 3–4 h before imaging.

Using HMA, like pairs of isolates were reduced to a single “proxy” strain by transitive property of equality (Scott et al 1999, Scott et al 2000). Subsequent rounds of HMA compared proxy isolates ultimately reducing the entire population to a set of genotypically distinct alleles represented by a minimum number of proxy isolates for each locus tested. One or more isolates for each multilocus genotype identified by heteroduplex analysis were sequenced for phylogenetic analysis.

**DNA sequencing and analysis.**—PCR templates were purified using QIAquick PCR purification kit (Qiagen Inc., Valencia, California) and sequenced using a *Taq* DyeDeoxy cycle sequencing kit (Applied Biosystems Inc., Foster City, California) and the same primers employed for amplification. Extension products were run on an ABI50 fluorescent automated sequencer (Applied Biosystems Inc.).

Alignments of sequences were performed using Clustal X software version 1.64b (Thompson et al 1997) and adjusted by visual inspection. Phylogenetic relationships were inferred from aligned sequences using the maximum par-

simony (MP) method found in PAUP\* (beta version 4.0b10) (Swofford 2003).

An heuristic search of the *benA* dataset (29 taxa, 434 bp, gaps treated as missing) was performed employing tree bisection-reconstruction (TBR) branch swapping with MulTrees and steepest descent options activated. We also performed exhaustive searches of individual datasets consisting of sequences of *P. chysogenum* (DAOM 193710 ex-type, NRRL 824 Fleming strain), *P. notatum* (ATCC 10108 ex-type) and representatives of the Wallaceburg multilocus haplotypes (*P. chysogenum* C8.24, C8.12, C200, C238, C317.1) for each of the four genetic loci (*acuA* 291 bp, *benA* 430 bp, ITS 546 bp, *trxB* 306 bp). In addition, the ITS dataset was expanded to include the sequence of the ex-type strain of *P. griseoeseum* (NRRL 820). Phylogenies of the eight-taxon dataset also were generated from exhaustive searches of a combined three-locus (*acuA*, *benA*, *trxB*) and four-locus datasets. A single multibase indel in the *benA* dataset was rescored as a single gap, and gaps were treated as a fifth character in analyses of the pruned datasets that included sequences for this locus. Taxa use as outgroups included *P. nalgiovense* NRRL 911 and *P. dipodomys* NRRL 13485 (29-taxon *benA* dataset) and *P. chysogenum* NRRL 824 (eight-taxon dataset).

Bootstrap support (Felsenstein 1985) for internal branches was evaluated from 1000 heuristic searches, and groups with a frequency of greater than 50% were retained in the bootstrap consensus trees. Congruence between the three (*acuA*, *benA*, *trxB*) and four loci for eight taxa was measured based on 10 000 heuristic searches (TBR branch swapping with MulTrees and steepest descent options activated) using the partition-homogeneity test (PHT) included in PAUP\*.

## RESULTS

*Penicillium chysogenum* was observed in 52% of houses investigated. Isolates of *P. chysogenum* were re-

TABLE III. Haplotype frequencies of indoor *P. chrysogenum* isolates

Proxy isolate	Locus				No. of isolates	Frequency
	acuA	benA	ITS	trxB		
C8.12	A	A	A	A	179	0.904
C317.1	A	C	B	C	5	0.025
C8.24	B	B	B	B	11	0.056
C238	C	B	B	B	2	0.010
C200	A	C	C	C	1	0.005

tained from a subset of houses investigated (109/369 houses), yielding a total of 198 isolates. Multiple isolates were obtained from 30 houses. *Penicillium chrysogenum* was not observed in the 18 outdoor air samples taken throughout Wallaceburg during August 1995.

Haplotypes of house dust isolates identified by heteroduplex analysis are given in TABLE III. The multilocus haplotype AAAA (acuA, benA, ITS and trxB,

respectively), represented by the isolate C8.12, was the most commonly observed haplotype in the population and represented more than 90% of all isolates. The second most common multilocus haplotype, BBBB, accounted for 5.6% of the isolates studied and is represented by isolate C8.24 (the same house as the representative isolate used for AAAA, above). Three minor multilocus haplotypes (ACBC, ACCC and CBBB) accommodated the remainder of the isolates. Multiple genotypes were recovered from 27% of houses where multiple isolates were obtained. Allele identities were confirmed by the sequencing of proxy isolates. Genbank accession numbers for these and other sequences used in this study are given in TABLE IV.

Phylogenetic relationships of species in the *P. chrysogenum* group were inferred from an heuristic analysis of partial sequences of the beta-tubulin (benA) gene. This dataset included 29 taxa and consisted of a 434 bp region spanning introns 3–5. MP analysis yielded four MPTs 48 steps in length (L) with a con-

TABLE IV. Sequences used or developed in this study

Identification	Strain no.	GenBank accession numbers			
		acuA	benA	ITS	trxB
<i>P. aethiopicum</i>	CBS 484.84	AY371577	AY371605	AY371635	AY371663
<i>P. chrysogenum</i>	C8.12	AY371550	AY371578	AY371608	AY371637
<i>P. chrysogenum</i>	C8.24	AY371552	AY371579	AY371610	AY371640
<i>P. chrysogenum</i>	C200	AY371555	AY371580	AY371614	AY371639
<i>P. chrysogenum</i>	C238	AY371556	AY371581	AY371613	AY371642
<i>P. chrysogenum</i>	C317.1	AY371554	AY371582	AY371612	AY371638
<i>P. chrysogenum</i>	DAOM 155627	AY371561	AY371584	AY371619	AY371647
<i>P. chrysogenum</i>	DAOM 155628	AY371562	AY371585	AY371620	AY371648
<i>P. chrysogenum</i>	DAOM 155631	AY371563	AY371586	AY371629	AY371657
<i>P. chrysogenum</i>	DAOM 167036	AY371564	AY371587	AY371621	AY371649
<i>P. chrysogenum</i>	DAOM 171025	AY371565	AY371588	AY371630	AY371658
<i>P. chrysogenum</i>	DAOM 175157	AY371566	AY371589	AY371622	AY371650
<i>P. chrysogenum</i>	DAOM 175176	AY371567	AY371590	AY371623	AY371651
<i>P. chrysogenum</i>	DAOM 175758	AY371568	AY371591	AY371624	AY371652
<i>P. chrysogenum</i>	DAOM 178623	AY371569	AY371592	AY371631	AY371659
<i>P. chrysogenum</i>	DAOM 190864	AY371570	—	AY371625	AY371653
<i>P. chrysogenum</i>	DAOM 193710	AY371553	AY371594	AY371611	AY371641
<i>P. chrysogenum</i>	DAOM 212031	AY371571	AY371595	AY371626	AY371654
<i>P. chrysogenum</i>	DAOM 215336	AY371572	AY371596	AY371627	AY371655
<i>P. chrysogenum</i>	DAOM 215337	AY371573	AY371597	AY371632	AY371660
<i>P. chrysogenum</i>	DAOM 216700	AY371574	AY371598	AY371628	AY371656
<i>P. chrysogenum</i>	DAOM 216701	AY371575	AY371599	AY371633	AY371661
<i>P. chrysogenum</i>	DAOM 59494C	AY371560	AY371583	AY371618	AY371646
<i>P. chrysogenum</i>	NRRL 824	AY371551	AY371600	AY371609	AY371636
<i>P. dipodomys</i>	NRRL 13485	AY371557	AY371602	AY371615	AY371644
<i>P. flavigenum</i>	CBS 419.89	—	AY371607	—	—
<i>P. flavigenum</i>	IMI 321909	—	AY371606	—	—
<i>P. griseoroseum</i>	NRRL 820	—	—	AF034857	—
<i>P. nalgiovense</i>	NRRL 911	AY371559	AY371601	AY371617	AY371645
<i>P. notatum</i>	ATCC 10108	AY371576	AY371604	AY371634	AY371662

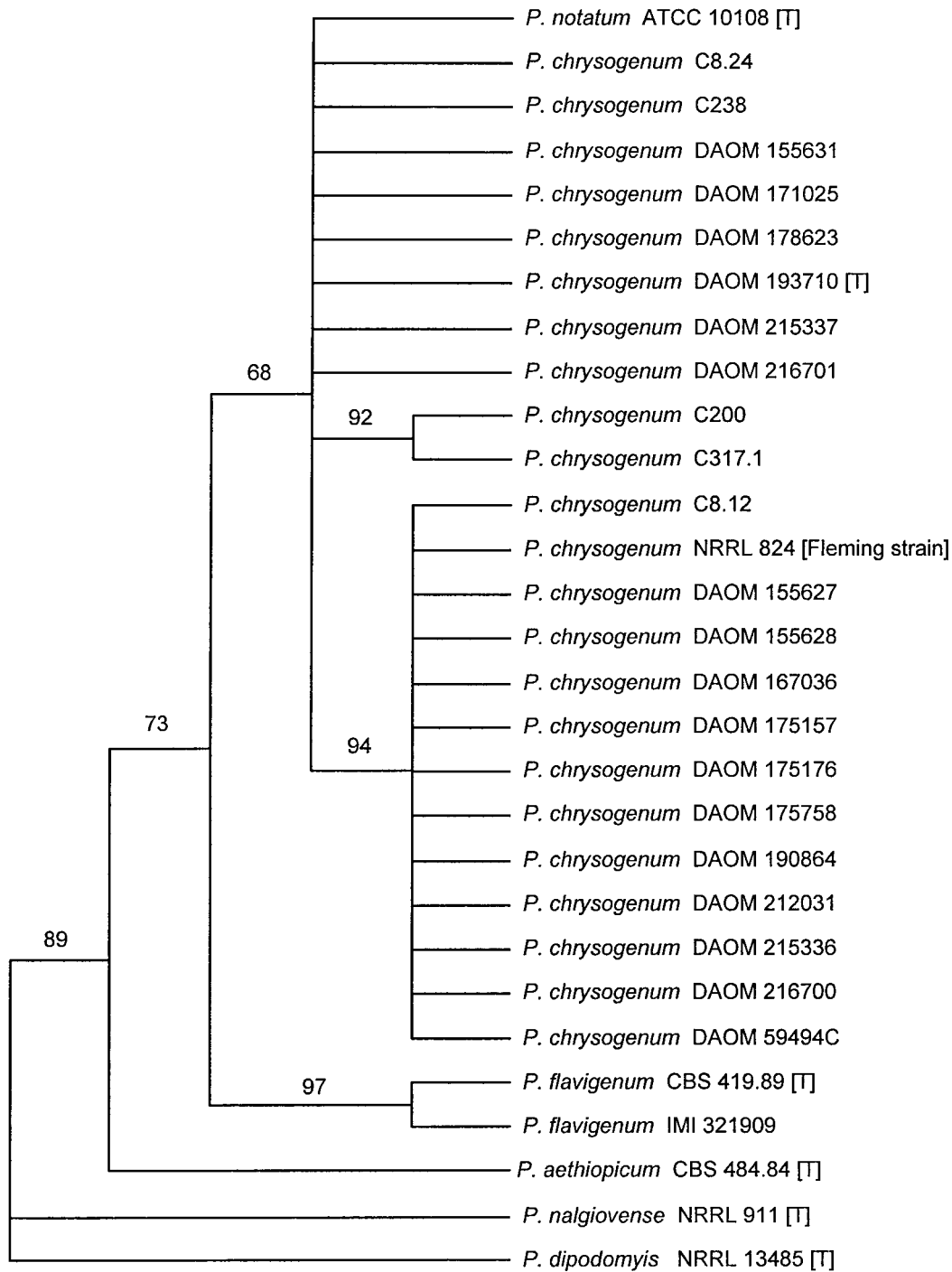


FIG. 1. Phylogenetic relationships of members of the *P. chrysogenum* group inferred from partial beta-tubulin gene sequences. This is a strict consensus of 4 MPTs ( $L = 48$ ,  $CI = 0.878$ ,  $RI = 0.918$ ) generated from a heuristic analysis of 434 bp for 29 taxa. Bootstrap values greater than 50% calculated from 1000 replicates are indicated above the branches. The outgroup taxon are *P. dipodomysis* NRRL 13485 and *P. nalgiovensis* NRRL 911.

sistency index (CI) and a retention index (RI) of 0.878 and 0.918, respectively. The strict consensus of these trees (FIG. 1) shows a large well supported lineage (bootstrap support of 73% in 1000 replicates) that corresponds to the *P. chrysogenum*-*P. flavigenum*

clade (TreeBase SN1793-5703). In this phylogeny, *P. chrysogenum sensu lato* (bootstrap support of 68%) comprised two well supported lineages as well as representative isolates from Canada (British Columbia and Ontario), Norway (ATCC 10108), South Korea

TABLE V. Summary of MPTs produced from each of 4 loci examined

Locus	Number of MPTs	Length (steps)	CI	RI	Total chrs	PI chrs
acuA	1	14	1.000	1.000	291	10
benA	1	12	0.833	0.846	432	10
ITS	1	2	1.000	1.000	546	1
trxB	1	10	1.000	1.000	306	10
4 loci	1	38	0.947	0.962	1575	31
3 loci (w/o ITS)	1	36	0.944	0.961	1029	30

(DAOM 216701) and the United States (DAOM 178623, DAOM 193710). The larger of these clades (bootstrap support of 94%) contained isolates from Canada (including Alberta, Manitoba, Ontario, Prince Edward Island and Quebec), Honduras (DAOM 59494C) and the United Kingdom (NRRL 824). The smaller clade (bootstrap support of 94%) included six isolates obtained from Wallaceburg house dust.

Analysis of individual data from partial acuA, benA and trxB sequences resulted in 10 parsimony-informative characters for each locus (TABLE V). Analysis of ITS data yielded only a single parsimony-informative character (TABLE V). MPTs generated from individual locus datasets showed identical or compatible topologies, supporting the analysis of these datasets in combination (data not shown). Results of 10 000 heuristic searches implementing the PHT ( $P = 1.0$ ) also demonstrated that these topologies are congruent and that sequences from the four different loci may be combined.

Combined analysis of data from partial acuA, benA, ITS and trxB sequences included eight taxa comprising the core of the *P. chysogenum* group. An exhaustive search of the combined dataset (1575 bp, 31 parsimony-informative characters) produced a single MPT ( $L = 38$ ,  $CI = 0.947$ ,  $RI = 962$ ) dividing *P. chysogenum sensu lato* into four well-supported clades (bootstraps 98% or higher) (FIG. 2) (TreeBase SN1793-5704). Clade 1 included the ex-type strains of *P. chysogenum* (DAOM 193710), *P. notatum* (ATCC 10108) and 11 (5.6%) isolates from Wallaceburg house dust (represented in FIG. 2 by C8.24). This lineage was sister of Clade 2, a group that contained two Wallaceburg isolates (1.0% of isolates). Clade 3 consisted of six Wallaceburg isolates (3.0%). The majority of Wallaceburg *P. chysogenum* isolates (179/198, 90.4%) clustered in Clade 4 with the British strain isolated by Alexander Fleming (NRRL 824).

The single dataset MPT based on ITS sequences divided *P. chysogenum sensu lato* into two lineages corresponding to Clades 1/2/3 and Clade 4 from the combined analysis (data not shown) (TreeBase SN1793-5705). The ex-type strain of *P. griseoroseum*

(NRRL 820, GenBank AF034857) grouped with the ex-type strains of *P. chysogenum* and *P. notatum*, but this clade was not strongly supported (data not shown).

#### DISCUSSION

Five unique multilocus haplotypes were revealed without evidence of recombination, indicating strictly clonal population structures in these lineages. Our results support the conclusions of Banke et al (1997) that *P. chysogenum*, *P. flavigenum*, *P. nalgiovense* and *P. dipodomys* are distinct species and that the former two taxa are sister groups. Banke et al (1997) noted a high degree of infraspecific variability in *P. flavigenum* and suggested that this species might consist of several subgroups. Our analysis showed two strains of *P. flavigenum* to be closely related, however these isolates did not share complete sequence homology for the region of beta-tubulin gene examined. Further work is necessary to resolve the phylogenetic structure of this species.

The phylogeny based on partial beta-tubulin sequence showed lineages in *P. chysogenum sensu lato* to be represented across Canada and from a broad geographic range extending to localities in North and Central America, Europe/Scandinavia and Asia (FIG. 1). Our analysis of four gene regions yielded three topologically compatible trees revealing three well supported clonal lineages within *P. chysogenum sensu lato*. Applying the phylogenetic species concept advocated by Taylor et al (2000) on the basis of concordance of multiple gene genealogies, these lineages represent distinct phylogenetic species. These lineages collectively may be called the *P. chysogenum* species complex. Our study showed *P. chysogenum sensu stricto* (Clade 1) to be uncommon in the indoor dust mycobiota relative to isolates of Clade 4. Culture collection strains positioned within Clade 1 were isolated as contaminants from raw wood, paper and proteinaceous foods (e.g., sausage, cheese). In contrast, strains clustering with Clade 4 isolates originated from cereals, paper, soil, construction materials and indoor environments, and included the strain isolat-

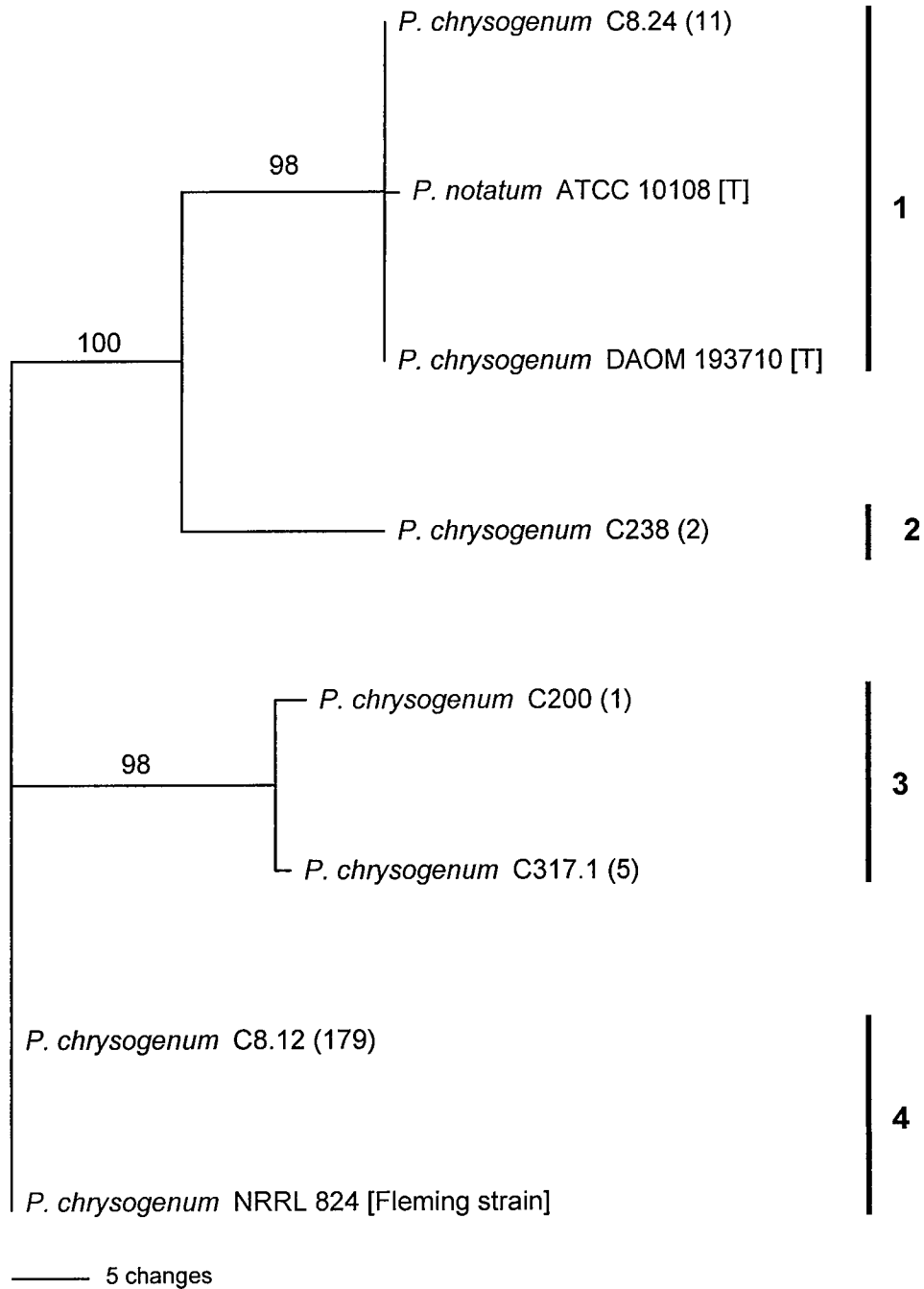


FIG 2. Single MPT inferred from an exhaustive search of the combined *acuA*, *benA*, ITS and *trxB* sequences of authentic or type strains of *P. chrysogenum* strains and Wallaceburg house dust isolates (1575 bp, L = 38, CI = 0.947, RI = 962; 1537 characters are constant, five variable characters are parsimony-uninformative, 31 characters are parsimony-informative). Bootstrap values greater than 50% calculated from 1000 replicates are indicated above the branches. The numbers of Wallaceburg isolates of identical multilocus haplotype are indicated in parentheses.

ed by Alexander Fleming in 1929 as a laboratory plate contaminant (Fleming 1929). The abundance of isolates assigned to Clade 4 suggests that this lineage may have a competitive advantage over other lineages to exploit human-associated indoor niches, although support for this hypothesis would require

the investigation of distribution patterns of members of this group in other geographic regions.

The absence of members of the *P. chrysogenum* species complex in outdoor air in comparison to the abundance of this group in indoor dust is intriguing. Two competing hypotheses could explain this observation:

(i) Members of the *P. chysogenum* complex form autochthonous populations (i.e., true populations) in household dust and/or on other indoor materials in the presence of superfluous moisture. Consequently, growth and sporulation (amplification) of these fungi indoors over time leads to their quantitative predominance in the dust mycoflora (Bronswijk 1981).

(ii) Viable indoor spores of the *P. chysogenum* complex originate from few airborne members of these taxa in the phylloplane and simply accumulate indoors faster than spores of other taxa as a consequence of their disproportionately longer viability and relatively inefficient removal. It is known that the asexual spores of members of the Trichocomaceae retain viability for a long time under dry conditions (Sussman 1968). Indeed, reculture of dust samples used in this project after a period of 5 yr in dry storage yielded only members of the Trichocomaceae and *Aureobasidium pullulans* (data not shown). In this manner, the number of *P. chysogenum* complex in indoor dust might relate in part to the “removal” of other taxa due to attenuated viability. Mechanical factors relating to size distribution also might be important. The spores of members of the *P. chysogenum* complex and related trichocomaceous anamorphs are small in relation to the majority of mitosporic taxa that quantitatively dominate dust in building interiors (e.g., *Cladosporium*, *Alternaria*, *Ulocladium*). These small-spored species might be inefficiently removed from the indoor environment by filtration systems in vacuum cleaners and forced-air heating systems. Stetzenbach et al (1999) reported this effect in relation to consumer market vacuum-cleaning devices. Combined, these effects of longer viability and less efficient removal might result in the emergence of an indoor allochthonous population (i.e., pseudo populations) whose constituent elements arise episodically in the phylloplane.

The conspecificity of *P. griseoroseum* and *P. chysogenum* is supported in the present study, in which the ex-type isolate (NRRL 820) clustered with the ex-type cultures of *P. chysogenum* (NRRL 807) and *P. notatum* (NRRL 821) based on the analysis of ITS sequences (data not shown). *Penicillium chysogenum* is thus a later synonym of *P. griseoroseum* based on priority of publication. This conclusion is not surprising because Banke et al (1997) obtained highly similar secondary metabolite profiles for 18 isolates of *P. chysogenum* including the ex-type strain of *P. griseoroseum*. Their proposed conspecificity of *P. chysogenum* with *P. griseoroseum* led Frisvad and co-workers (1990) to recommend conservation of the name due to the industrial importance of this species. They recommended the conservation of *P. chysogenum* as “the

species name for the principal producer of penicillin” on the basis that the association between the name “*Penicillium chysogenum*” and the biochemical characteristic of penicillin biosynthesis was of paramount industrial importance (Frisvad et al 1990a, Lowe and Elander 1983). However, penicillin is known from a range of filamentous fungi (Abraham and Newton 1967, Samson et al 1996) and is speculated to have originated in fungi by horizontal gene transfer from a penicillin-producing actinomycete (Rosewich and Kistler 2000). Kozakiewicz et al (1992) later made a formal proposal to conserve the name *P. chysogenum*. From a nomenclatural standpoint, there do not appear to be existing species or varietal names that can be applied to our clades 3 and 4. Moreover, the erection of new taxa to accommodate these lineages would not conflict with the nomenclatural conservation of *P. chysogenum* and should be pursued. The phylogenetic positions of the major penicillin-producing strains of *P. chysogenum sensu lato* in relation to these new species have not been investigated.

#### ACKNOWLEDGMENTS

We are grateful to Carolyn Babcock (CCFC, Agriculture Canada, Ottawa) and Dr Stephen W. Peterson (ARS Culture Collection, USDA, Peoria Illinois) for providing isolates used in this study. Financial support for this work was provided by an NSERC Doctoral Postgraduate Scholarship (PGS-B) to JS, an NSERC Strategic grant to DM and NAS, and an NSERC Discovery Grant to WAU.

#### LITERATURE CITED

- Abraham EP, Newton GGF. 1967. Penicillins and Cephalosporins. In: Gottlieb D, Shaw PD, eds. Antibiotics: biosynthesis. Vol. 2. New York: Springer-Verlag. p 1–16.
- Adan OCG, Samson RA. 1994. Fungal disfigurement of interior finishes. In: Singh J, ed. Building mycology: management of decay and health in buildings. London: Chapman & Hall. p 130–158.
- Anonymous. 1985. Round table discussion. In: Samson RA, Pitt JI, eds. Modern concepts in *Penicillium* and *Aspergillus* classification. New York: Plenum Press. p 101.
- Banke S, Frisvad JC, Rosendahl S. 1997. Taxonomy of *Penicillium chysogenum* and related xerophilic species, based on isozyme analysis. Mycol Res 101:617–624.
- Biourge P. 1923. Les moisissures du groupe *Penicillium* Link. Etude monographique. La Cellule (Louvain) 33: 1–322.
- Bridge PD, Hawksworth DL, Kozakiewicz Z, Onions AHS, Paterson RRM, Sackin MJ, Sneath PHA. 1989. A reappraisal of the terverticillate *Penicillia* using biochemical, physiological and morphological features. 1. Numerical taxonomy. J Gen Microbiol 135:2941–2966.

- Bronswijk JEMH v. 1981. House dust biology. Zoelmond, The Netherlands: NIB Publishers. 316 p.
- Chang JCS, Foarde KK, Vanosdell DW. 1995. Growth evaluation of fungi on ceiling tiles. *Atmosph Environ* 29: 2331–2337.
- Cooley JD. 1999. The role of *Penicillium chrysogenum* conidia in sick building syndrome and an asthma-like animal model. [Doctoral Thesis]. Graduate School of Biomedical Sciences, Texas Technical University Health Sciences Center.
- , Wong WC, Jumper CA, Straus DC. 1999. Cellular and humoral responses in an animal model inhaling *Penicillium chrysogenum* spores. In: Johanning E, ed. *Bioaerosols, fungi and mycotoxins*. Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23–25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. p 403–410.
- Cruickshank RH, Pitt JI. 1987. Identification of species in *Penicillium* subgenus *Penicillium* by enzyme electrophoresis. *Mycologia* 79:614–620.
- Davies RR. 1960. Viable moulds in house dust. *Trans Brit Mycol Soc* 43:617–630.
- Dierckx F. 1901. Essai de revision du genre *Penicillium* Link. Note préliminaire. *Ann Soc Sci Brux* 25:83–88.
- Dillon HK, Heinsohn PA, Miller JD, eds. 1996. Field guide for the determination of biological contaminants in environmental samples. Fairfax, Virginia: American Industrial Hygiene Association. 174 p.
- Eschete ML, King JW, West BC, Oberle A. 1981. *Penicillium chrysogenum* endophthalmitis. First reported case. *Mycopathol* 74:125–127.
- Felsenstein J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39:783–791.
- Fergusson RJ, Milne LRJ, Crompton GK. 1984. *Penicillium* allergic alveolitis: faulty installation of central heating. *Thorax* 39:294–298.
- Fleming A. 1929. On the antibacterial action of cultures of a *Penicillium*, with special reference to their use in the isolation of *B. influenzae*. *Br J Exp Pathol* 10:226–236.
- Frisvad JC. 1993. Modifications on media based on creatine for use in *Penicillium* and *Aspergillus* taxonomy. *Lett Appl Microbiol* 16:154–157.
- Frisvad JC, Filtenborg O. 1989. Terverticillate *Penicillia*: chemotaxonomy and mycotoxin production. *Mycologia* 81:837–861.
- , Hawksworth DL, Kozakiewicz Z, Pitt JI, Samson RA, Stolk AC. 1990. Proposals to conserve important species names in *Aspergillus* and *Penicillium*. In: Samson RA, Pitt JI, eds. *Modern concepts in Penicillium and Aspergillus classification*. New York: Plenum Press. p 83–90.
- Gravesen S. 1999. Microfungal contamination of damp buildings. In: Johanning E, ed. *Bioaerosols, fungi and mycotoxins*. Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23–25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. p 505–511.
- Hennebert GL. 1985. Dierckx' contribution to the genus *Penicillium*. In: Samson RA, Pitt JI, eds. *Modern concepts in Penicillium and Aspergillus classification*. New York: Plenum Press. p 9–21.
- Hoffman M, Bash E, Berger SA, Burke M, Yust I. 1992. Fatal necrotizing esophagitis due to *Penicillium chrysogenum* in a patient with acquired immunodeficiency syndrome. *Europ J Clin Microbiol Infec Dis* 11:1158–1160.
- Hunter CA, Lea RG. 1995. The airborne fungal population of representative British homes. *Air Qual Monogr* 2: 141–153.
- Kozakiewicz Z, Frisvad JC, Hawksworth DL, Pitt JI, Samson RA, Stolk AC. 1992. Proposal for nomina specifica conservanda and rejicienda in *Aspergillus* and *Penicillium*. *Taxon* 41:109–113.
- Lowe DA, Elander RP. 1983. Contribution of mycology to the antibiotic industry. *Mycologia* 75:361–373.
- Malloch DW. 1981. Moulds: their isolation, cultivation and identification. Toronto: University of Toronto Press. 97 p.
- Nielsen KF, Gravesen S. 1999. Production of mycotoxins on water damaged building materials. In: Johanning E, ed. *Bioaerosols, fungi and mycotoxins*. Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23–25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. p 423–431.
- Pitt JI. 1980. The genus *Penicillium* and its teleomorphic states *Eupenicillium* and *Talaromyces*. New York: Academic Press. 634 p.
- , Cruickshank RH. 1990. Speciation and synonymy in *Penicillium* subgenus *Penicillium*—toward a definitive taxonomy. In: Samson RA, Pitt JI, eds. *Modern concepts in Penicillium and Aspergillus classification*. New York: Plenum Press. p 103–119.
- , Samson RA. 1993. Species names in current use in the Trichocomaceae. In: Greuter W, ed. *Names in current use in the families Trichocomaceae, Cladoniaceae, Pinaceae and Lemnaceae (NCU-2)*. *Reg Veg* 128:13–57.
- Raper KB, Thom C. 1949. A manual of the Penicillia. Baltimore, Maryland: Williams and Wilkins. 875 p.
- Rosewich UL, Kistler HC. 2000. Role of horizontal gene transfer in the evolution of fungi. *Ann Rev Phytopathol* 38:325–363.
- Sambrook J, Fritsch EF, Maniatis T. 1989. Molecular cloning. A laboratory manual. 2nd ed. Vols 1–3. New York: Cold Spring Harbor Laboratory Press.
- Samson RA, Hadlok R, Stolk AC. 1977. A taxonomic study of the *Penicillium chrysogenum* series. *Antonie van Leeuwenhoek* 43:169–175.
- , Hoekstra ES, Frisvad JC, Filtenborg O. 1996. Introduction to food-borne fungi. 5th ed. Baarn, The Netherlands: Centraalbureau voor Schimmelcultures. 322 p.
- Scott JA, Straus, N and Wong B. 1999. Heteroduplex DNA fingerprinting of *Penicillium brevicompactum* from house dust. In: Johanning E, ed. *Bioaerosols, fungi and mycotoxins: health effects, assessment, prevention and control*. Albany, New York: Eastern New York Occupational and Environmental Health Center. p 335–342.

- , Malloch D, Wong B, Sawa T, Straus N. 2000. DNA heteroduplex fingerprinting in *Penicillium*. In: Samson RA, Pitt JI, eds. Integration of modern taxonomic methods for *Penicillium* and *Aspergillus* classification. Amsterdam: Harwood Academic Publishers, p 225–236.
- Stetzenbach LD, Buttner MP, Cruz-Perez P. 1999. Fungal spores aerosolized from contaminated flooring materials. (Abstract No. 243). American Industrial Hygiene Association Conference, Toronto, Ontario, June 5–11, 1999.
- Sussman AS. 1968. Longevity and survivability of fungi. In: Ainsworth GC, Sussman AS, eds. The fungi: an advanced treatise. Vol. 3. New York: Academic Press. p 447–486.
- Swofford DL. 2003. PAUP\*. Phylogenetic analysis using parsimony (\*and other methods). Version 4. Sunderland, Massachusetts: Sinauer Associates.
- Taylor JW, Jacobson DJ, Kroken S, Kasuga T, Geiser DM, Hibbett DS, Fisher MC. 2000. Phylogenetic species recognition and species concepts in Fungi. *Fungal Gen Biol* 31:21–32.
- Thom C. 1910. Cultural studies of species of *Penicillium*. Bureau of Animal Industry, Bulletin No. 118. Washington, D.C.: USDA. 108 p.
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. 1997. The Clustal X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24:4876–4882.
- Weising K, Nybom H, Wolff K, Meyer W. 1995. DNA fingerprinting in plants and fungi. Boca Raton: CRC Press. 322 p.
- Weitzman I, Silva-Hutner M. 1967. Nonkeratinous agar media as substrates for the ascigerous state in certain members of the Gymnoascaceae pathogenic for man and animals. *Sabouraudia* 5:335–340.



**DAOM accession numbers for *Penicillium chrysogenum* group cultures\***

**CLADE 1**

*Penicillium chrysogenum*

DAOM 238886 (C8.24)

DAOM 238887 (C34.4)

DAOM 238888 (C47)

DAOM 238889 (C58.7)

DAOM 238893 (C67.3)

DAOM 238895 (C72.1)

DAOM 238896 (C72.2)

DAOM 238898 (C94)

DAOM 238902 (C232.1)

**CLADE 2**

*Penicillium* sp. nov. 1

DAOM 238894 (C71.1)

DAOM 238903 (C238)

**CLADE 3**

*Penicillium* sp. nov. 2

DAOM 238885 (C8.18)

DAOM 238892 (C58.15)

DAOM 238897 (C77.2)

DAOM 238900 (C200)

DAOM 238904 (C317.1)

**CLADE 4**

*Penicillium* sp. nov. 3

DAOM 238883 (C8.4)

DAOM 238884 (C8.12)

DAOM 238890 (C58.8)

DAOM 238891 (C58.14)

DAOM 238899 (C161)

DAOM 238901 (C225.30)

DAOM 238905 (C326.4)

DAOM 238906 (C354.2)

---

\*Clades after Scott et al (2004) [updated April 3, 2007]

## CHAPTER 7. CONCLUSIONS AND GENERAL SUMMARY

The impact of indoor fungal contamination on human health has received ever-increasing attention since the early 1970s. Despite evidence that such problems have existed throughout recorded history, the present involvement of fungi as agents of declining IAQ and structural compromise is comparably recent and lacks historical precedent. I propose that the occurrence of three protracted events during the last century have collectively precipitated the present fungal epinostic in North America. These include:

1. The shift from a mainly industrial- to a white collar labor force
2. The development of an economy dependent upon access to Middle-Eastern reserves of fossil fuels
3. The movement to design and construct energy efficient buildings following the 1973 oil crisis

This hypothesis supports the view that the exploitation of indoor niches formed by water incursion on structural elements or indoor finishes by the ecological group of fungi collectively known as “domicile fungi” is a contemporary phenomenon. Despite that various of the fungal taxa involved in the contamination of human environments may to some extent have been pre-adapted to these habitats, principally as agents of food spoilage, I shall briefly outline a course of events in recent social history that refutes an hypothesis that these fungi have co-evolved with humans principally as contaminants of domestic structures.

The construction of houses for human habitation is thought to have coincided with the Agricultural Revolution 8,000 to 10,000 years ago, which was marked by a gradual shift from a primarily nomadic, hunter-gather lifestyle to a more sedentary life of agriculture (Childe, 1950; Grigg, 1974). The first observation of airborne spores may be credited to the Roman philosopher Lucretius of the first century BC, who remarked on the shimmering clouds of fine particles made visible by the passage of rays of sunlight through the air (Lucretius, *ca.* 50 BC). Although Lucretius incorrectly interpreted these particles as evidence of “thin images” that he hypothesized were perpetually radiated by all objects permitting their perception, the fact that he was able to visualize particles whose minute size rendered them otherwise imperceptible to the unaided eye was because of the “Tyndall effect” which was not elucidated until nearly two millennia later by Faraday (Considine, 1976).

#### **FUNGAL DECAY IN EARLY STRUCTURES**

Perhaps the earliest clearly attributable description of indoor fungal contamination comes from the Old Testament book of Leviticus, which provided a convincing account of the timber dry-rot fungi, *Serpula lacrimans* (Wulfen: Fr.) Schröeter and *S. incrassata* (Berk. & M.A. Curtis) Donk. This passage cautioned against structural rot in which the walls of a house develop “hollow strakes, greenish or reddish” (Lev. 14:37) or manifest as “a bright spot” (Lev. 14:56). Leviticus instructed that an affected house shall be sealed up for seven days after which it shall be examined to determine if the growth is active, in which case a series of remedies were proposed of increasing fervour. The goal of these procedures was the ultimate removal and disposal of affected materials with care not to risk contaminating other houses.

“...take away the stones in which the plague is, and... cast them into an unclean place without the city... cause the house to be scraped within round about, and... pour out the dust... without the city and into an unclean place.

(Lev. 14:40-41)

If remedial efforts failed, destruction of the house was recommended.

“...break down the house, the stones of it, and the timber thereof, and all the mortar of the house; and... carry them forth out of the city into an unclean place.

(Lev. 14:45)

In his seminal work on wood decay fungi, Bondartsev (1953) characterized dry rot of timber by the production of “...slightly noticeable discolorations... followed later by white spots and depressions”. Dolenko and colleagues (1981) similarly noted that dry rot infections begins as:

“thin, silky-gray mycelium with patches of yellow, or as a fan-shaped, lilac-colored mycelial mat. Characteristic thick strands, which are brown to black, may develop on the wood... In time the conk becomes rusty red as a result of myriads of spores produced.

The mycelium of *Serpula* produces aggressive rhizomorphs that can penetrate masonry and stone walls, often travelling long distances over concrete surfaces or plumbing to colonize more wood (Ellis and Ellis, 1990; Singh, 1994). Ginns (1986) reported this fungus as a frequent agent of brown rot of timbers in Canada, but noted that it was unknown from natural habitats. Similarly, the occurrence of this fungus in Europe appears limited to woods in service (Buczacki, 1989; Gray, 1956; Singh, 1994). Indeed the most natural habitat for this fungus worldwide is perhaps best described by its Swedish common name, *hussvamp*, literally house-mushroom (Ryman and Holmåsen, 1998). Dry rot is undeniably the most common agent of decay of wooden structure worldwide (Singh, 1994) and there is little doubt that this is the organism described in Leviticus.

## VENTILATION

Aurora (1986) suggested that the practice of occluding exterior house vents in Europe during WWII contributed to the extent of problems posed to British housing by dry rot. Indeed, archaeological evidence indicates that the ancients deliberately included structural features in their buildings to promote ventilation and prevent the build-up of indoor contaminants, including dampness (Janssen, 1999). The goal of most early ventilation was the removal of

smoke from heating and cooking fires (Spengler and Samet, 1991); however, ventilation was also used for disease prevention in ancient Egypt following the observation that stone carvers who worked in tightly enclosed buildings experienced a greater incidence of lung disease than those working in tents or outdoors (Woods, 1988). Later, in the Middle Ages, overcrowding of indoor environments and poor ventilation were recognized as factors for the transmission of communicable diseases (Janssen, 1999).

### **EARLY HOUSING AND URBANIZATION**

During the vast stretch of time from the Neolithic to the 13<sup>th</sup> century AD, few improvements were made to the construction of basic European housing (Bronswijk, 1981). Typical human dwellings consisted of elongate structures of wooden poles bound with twigs and thatched with reeds and loam, in which the interior space was generally divided up with the central third used for habitation while the front and back thirds provided grain storage and shelter for livestock (ibid.). This practice, and the widespread use of straw as a flooring material almost certainly contributed to IAQ-related problems, particularly dander allergies and contagious diseases (Pope et al., 1993).

In the late 17<sup>th</sup> century, the amateur Dutch optics experimenter Antonie van Leeuwenhoek was first to observe microscopic arthropods in dust collected from his home (Bronswijk, 1981). By this time, European urbanization had reached a sufficient density to cause significant levels of outdoor air pollution resulting from the consumption of coal and wood for fuel (Spengler and Samet, 1991). The British diarist John Evelyn wrote of its effects:

“It is this horrid smoke, which obscures our churches and makes our palaces look old, which fouls our clothes and corrupts the water so that the very rain and refreshing dews which fall in the several seasons precipitate this impure vapour,

which with its black and tenacious quality, spots and contaminates whatever is exposed to it.

(Evelyn, 1661 *vide* Spengler and Samet, 1991)

At the arrival of the Industrial Revolution in the middle of the 18<sup>th</sup> century, there was already widespread acknowledgement that declining outdoor air quality negatively influenced human respiratory health (Spengler and Samet, 1991). The dramatic shift in the workforce from agriculture to industry had the further effect of redistributing large segments of the population throughout Europe. In the period from the beginning to the end of the 19<sup>th</sup> century, the proportion of the world population who lived in towns of 20,000 or more inhabitants rose from 2.5 to 10 % (Davis, 1965). Matossian (1989) suggested that advances in agricultural practices, notably the introduction of the potato into Europe by the Spanish (Simpson and Ogorzaly, 1986), facilitated this population explosion. Her argument centred on the fact that the potato offered more caloric value than grain as a function of cultivated acreage, and that the potato was healthier, being less prone to the insidious mycotoxin contamination that so plagued stored cereals, particularly rye (Matossian, 1989). Nevertheless, increased urbanization meant a sharp increase in the proportion of the world's population that relied on food provided through commercial agriculture (Schlebeker, 1960). The gradual movement away from an agriculture-centred society marked by the Industrial Revolution was similarly correlated to the rapid build-up of urban centres at pivotal points along burgeoning trade routes by a large influx of working class population (Engels, 1845). Living conditions were grim, buildings were “badly planned, badly built, and kept in the worst condition, badly ventilated, damp, and unwholesome” (ibid.).

## **MODERN ERA**

The formal study of airborne fungi began with the work of the French microbiologist Louis Pasteur. In his landmark work which ultimately razed the Theory of Spontaneous Generation,

Pasteur collected microscopic airborne fungi in broth medium contained in swan-necked flasks from the air at numerous sites in and around Paris (Pasteur, 1861). Pasteur's work demonstrated that minute fungal propagules are carried upon air currents. It was this invisible microbial burden of air, he proposed, and not spontaneous generation that was responsible for microbial problems ranging from the spoilage of foods to human infections (Drouhet, 1999). Pierre Miquel, a student of Pasteur, documented in his 1883 dissertation the fungal content of air in homes and hospitals. He was first to propose an airborne route of exposure to fungal spores as an important factor in the establishment of nosocomial and opportunistic pulmonary mycotic infections (Drouhet, 1999).

Legislation of formalized building codes in Europe during the late 19<sup>th</sup> and early 20<sup>th</sup> centuries brought about an end to 6 millennia of *ad hoc* residential construction using sod, branches and clay (Bronswijk, 1981); although the concept of a standardized building practice was not new and examples of such directives are known from ancient Babylonia ca. 2000 BC (DeGrace, 1960) and the Bible. Canada however did not formalize a national building code until 1941 (Payne, 1981).

The large-scale emergence of health complaints due to IAQ problems began in the early 1970s and continues to the present day (Marbury and Woods, 1991). One factor contributing to the current problem is the increased exposure potential from the tendency of modern society to spend more and more of its time indoors (Singh, 1994). In addition, continued efforts have been made to improve building engineering and design to maximize thermal energy retention, thereby reducing heating costs. These same design improvements have brought about drastic reductions in dilution ventilation, and facilitated the build-up of indoor airborne contaminants

(Pope et al., 1993). This stringent concern about cost of heating fuel is a new phenomenon, since much of western civilization developed in an economic climate where fuel was relatively inexpensive and the inefficient use of fuel was tolerated. Prior to this time, the fungus-related building problem was structural, with the primary agent being *Serpula*, the dry rot fungus. The move to build tighter buildings and the awareness of IAQ problems that it precipitated was influenced by a number of social and technological developments.

### **THE CHANGING URBAN LANDSCAPE**

Following the Second World War, the western world experienced an unprecedented boom in economic prosperity. The arrival of the information age was marked in 1956 when, for the first time in US history, the majority of jobs were non-labor (Bloom, 1995). The shift away from a primarily industrial economy had a further effect of changing the urban landscape. Because a greater proportion of wage-earners were office-based, rather than factory workers, proximity to shipping and rail ports dwindled in importance. Workspace and residential accommodation necessary for a growing white-collar labor force were at a premium in growing urban centres during this post-war boom (Fishman, 1987). The skyscraper began as a novelty experiment by Massachusetts engineer William Le Baron Jenney in the late 19<sup>th</sup> century to optimise space by building on a primarily vertical, rather than horizontal axis (Fargis and Bykofsky, 1989). During the first 50 years of the 20<sup>th</sup> century this architectural form had been greatly developed in urban centres across North America. The continuing construction of high-rise structures was instrumental in providing office and commercial space in the growing post-war economy.



## **SUBURBAN LIFE**

Addressing of the post-war housing shortage required innovation, since the North American cultural preference was for detached homes (Warner, 1995). In part, the automobile which had become an ubiquitous symbol of freedom and status was crucial to the resolution of this problem since widespread automobile ownership permitted the decentralization of urban populations by dividing work and home between the city and suburb, respectively (*ibid.*). Indeed over the 20 years from 1950 to 1970, population growth in suburban America exceeded inner-city growth by nearly a factor of ten, and accounted for over three-quarters of new jobs in the manufacturing and retail sectors (Fishman, 1987). By 1970 the proportion of the US population living in suburbs had exceeded that in city cores or rural areas (37.6 %, 31.4% and 31.0%, respectively) (*ibid.*). The shortage of residential and institutional buildings was also partly addressed by the adoption of industrialized building techniques which involved the large-scale production and installation of pre-fabricated buildings with cost as the primary optimisation criterion (Payne, 1981; Testa, 1990).

## **NORTH AMERICAN DEPENDENCE ON PETROLEUM**

Along with changing architecture, transportation underwent a gradual yet profound transformation. The railway system that had figured so prominently in the settlement of North America steadily yielded to overland trucking as a means of freight transport, and the light gauge railways of urban streetcar systems slowly gave way to diesel buses (Bothwell, 1986). One theory on the impetus for this change was advanced in 1974 by US anti-trust attorney Bradford Snell (Slater, 1997). Snell's theory held that the American industrial giant, General Motors Corporation, had repeatedly allied with oil and rubber interests collectively fronted by shell companies operating as local public transit competitors in order to acquire control of local

streetcar transit systems, dismantle them and replace them with diesel buses (*ibid.*). Although Snell's ideas have been widely criticized (e.g. Bottles, 1987), the fact remains that GM and others had prospered on defence contracts during the First- and Second World Wars and when faced with post-war uncertainty in the defence sector, sought to exploit other markets.

At the same time, there was a shift to petroleum as a fuel for residential heating. Until the early 1950s, home heating had relied mostly on coal or wood to fuel central stoves or recirculated hot water systems. The use of oil as a home heating fuel became increasingly popular because of its ease of use, as well as its greater availability and comparative low cost (Nash, 1968).

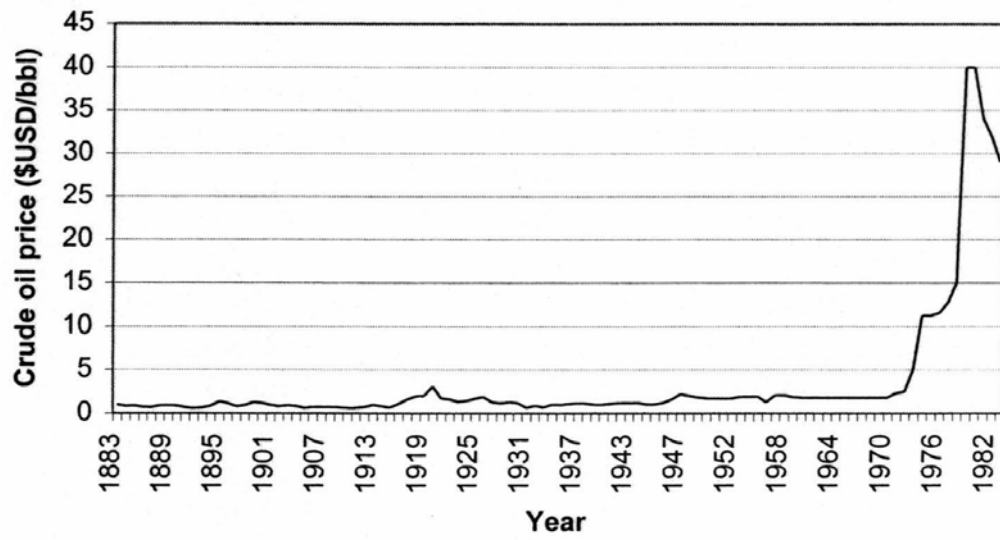
#### **THE ENERGY CRISIS AND THE SICK BUILDING**

The rapid expansion of North American oil markets over the 30 years following WWII approximated a mounting gluttony for petroleum driven by favourable economics and insatiable consumer appetite for the automobile. The so-called "oil crisis" of the 1970's began during a protracted period of political uncertainty in key Middle East oil-producing nations. The alliance of the United States with Israel during the "Yom Kippur War" of 1973 brought about a temporary embargo on US oil exports by Arab oil-producers. Shortly afterwards, a general strike in the Iranian oil fields preceded the eruption of full-scale political revolution in the Middle East, bringing a temporary halt to crude oil production and export. Dwindling reserves and uncertainty about future availability prompted the Organization of Petroleum Exporting Countries (OPEC) to implement a sharp increase in the minimum reference price of crude oil to protect remaining reserves (Nash, 1968). Within a few years, the base price of crude oil surged from its century-long average of around \$2 USD per barrel to over \$40 USD (*see* Figure 7-1). The dependence of North America on petroleum that had grown gradually in the years

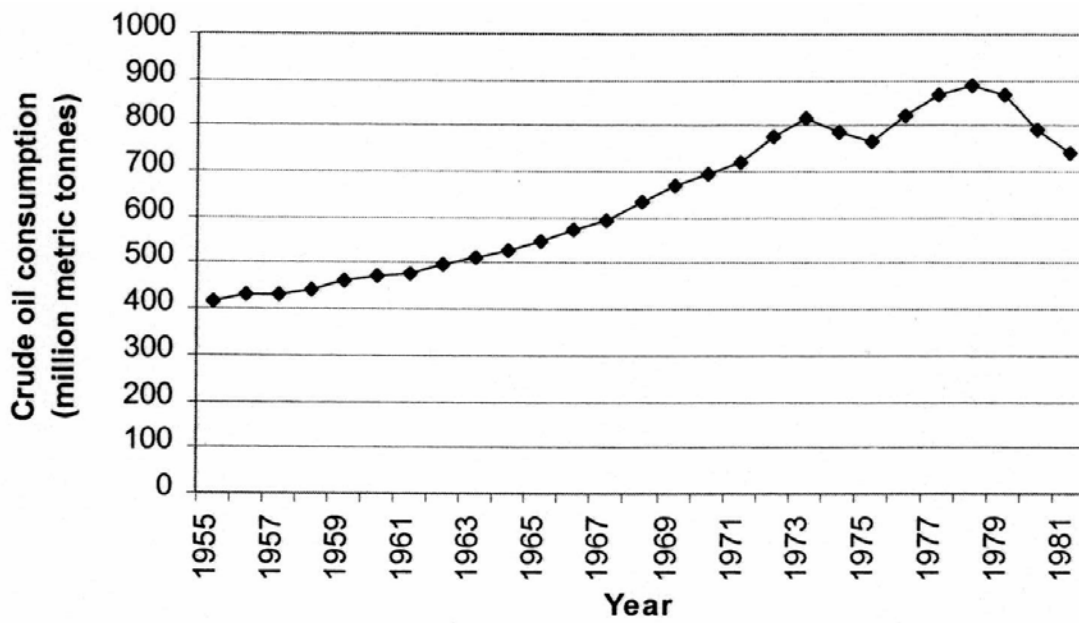
following WWII (*see* Figure 7-2) posed economically disastrous consequences if means could not be found to stem consumption.

## HEATING AND VENTILATION

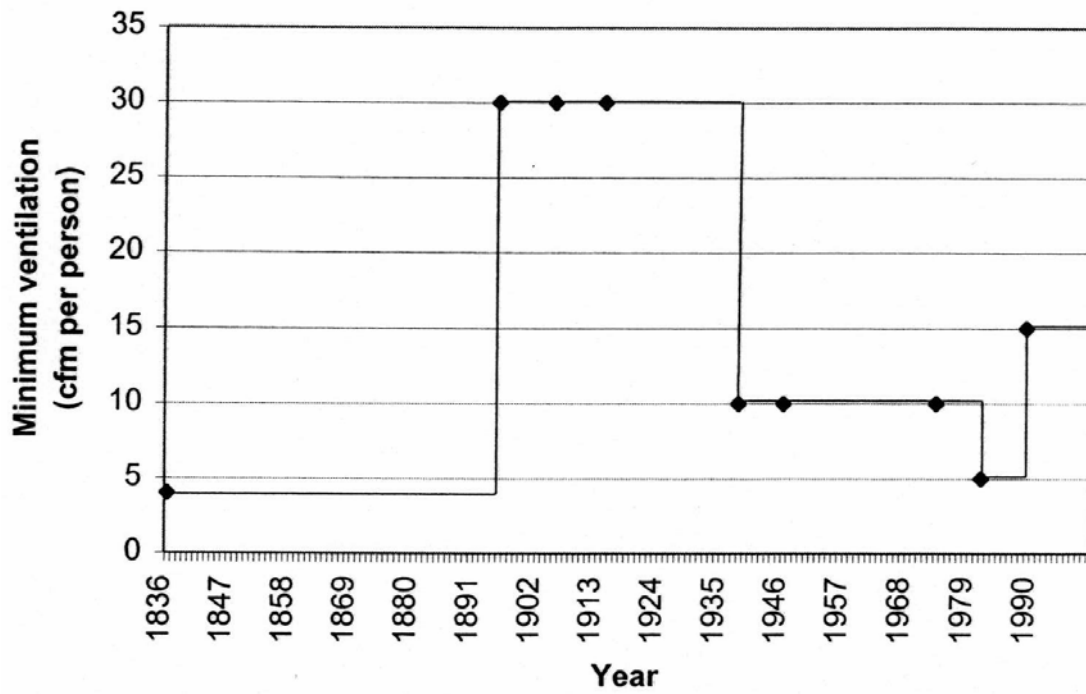
Klauss and colleagues (1970) credited Cornish mining engineer Thomas Tredgold with the first formal calculation of a minimal ventilation requirement, in this case 4 CFM per person, based on the physiological needs of miners. Workers at the beginning of the 20<sup>th</sup> century adopted ventilation rates of 30 CFM per person for workplace environments including hospitals to reduce the potential for disease spread and comfort issues such as minimizing odour generation (Janssen, 1999). Based on considerable empirical data regarding perception thresholds for body odour, Yaglou (1938) reduced the minimum ventilation requirement to 10 CFM per person. Subsequent standards published by the American Standards Association (ASA) and the American Society for Heating and Refrigeration Engineers (ASHRAE) maintained the minimum ventilation requirement at this level, where it remained until 1981 when unabating financial constraints on fuel use prompted ASHRAE to reduce the requirement further to 5 CFM per person (Janssen, 1999). ASHRAE Standard 62-1989 increased this to 15 CFM per person where it remains today based on confirmation of Yaglou's work (Berg-Munch et al., 1984; Cain, 1983). Although not formally included as a rationale for increasing the minimum ventilation rate, the groundswell of IAQ related complaints following ASHRAE 62-1981 undoubtedly played a role in this decision. Figure 7-3 shows a graphical history of changes in recommended minimum indoor ventilation rates. A decrease in the minimum ventilation level in the early 1980s coincided closely with a sharp surge in oil prices (*see* Figure 7-1), marking the beginning of the modern era of sick building syndrome.



**FIGURE 7-1.** Year-end reference price per barrel of crude oil from 1883 to 1981 (in 1981 USD). Source: Jenkins, G. 1983. *Oil Economists' Handbook*. New York: Applied Science Publishers. pp. 19, 50, 51 & 94.



**FIGURE 7-2.** Break-down of crude oil consumption from 1955 to 1981. SOURCE: Jenkins, G. 1983. *Oil Economists' Handbook*. New York: Applied Science Publishers. pp. 19, 50, 51 & 94.



**FIGURE 7-3.** Minimum prescribed ventilation rates from 1836 to the present.  
 SOURCE: Janssen (1999)

## CONSTRUCTION PRACTICES<sup>12</sup>

Besides influencing prescribed ventilation rates, rising fuel costs also drove changes in construction practices. Modern residential construction employs a tightly sealed building envelope design, with a vapour retardant membrane on the warm side- and an air barrier membrane on the cold side of a highly insulated wall assembly (Kesik et al., 1997). This wall construction deliberately restricts the infiltration of outdoor air, often permitting the accumulation of indoor pollutants including emission products from building products or furnishings, moisture and moulds (Flannigan and Morey, 1996).

Fungal contamination by dry rot fungi tends to dominate in buildings constructed prior to the 1920s (Koch, 1994). The introduction of many new building materials has both increased the potential for water damage and the biodiversity of ensuing fungal growth. In particular, many contemporary materials used for exterior sheathing are composites of wood or paper products bound together using a variety of resins, especially phenol-formaldehyde compounds (Mullins and McKnight, 1981). In Ontario, these products commonly include oriented strand boards (OSBs) and wafer boards, mostly made from chipped poplar. Composite products are lighter and less expensive to produce than solid wood or laminated wood products (such as plywood); however, they exhibit a greater potential for water absorption according to the vast, effective surface areas of these products (i.e. the total additive surface areas of individual chips). This tendency leads to greater susceptibility to fungal contamination.

---

<sup>12</sup> The following two sections contain considerable information of an anecdotal nature that draws upon personal experience studying fungal contamination within buildings. These observations remain largely subjective and have not been substantiated by systematic research. However, they are presented as a context for the work done in the thesis, and as a basis to determine logical directions for future research.

## GYPSUM-BASED WALLBOARD PRODUCTS

Perhaps the most common fungal problem affecting modern buildings results from the use of another highly susceptible building material, “drywall” or “gypsum board”, a wallboard panel made of gypsum plaster with a covering of paper (CMHC, 1982). *Stachybotrys chartarum* is a principal colonist of this material following water damage (Straus et al., 1999; Tsai et al., 1999). Leaks resulting from building envelope failures are the most common factors that cause water damage and lead to contamination. Drywall is used commonly as an interior finishing board, but may occasionally be used on the exterior side of a wall assembly as a fire retardant or an air barrier (Kesik and Lio, 1997) where it is susceptible to water damage and mould growth<sup>13</sup>. Mould damage on gypsum drywall is often limited to exterior walls and frequently occurs **1)** following water infiltration through exterior walls, beneath windows or mechanical penetrations in exterior walls, especially basements; **2)** in the interior of wall assemblies as a result of condensation on cold cavity elements of the wall assembly following exfiltration of humid room air (especially on leeward walls in wintertime); **3)** due to pipe leaks (often sanitary returns) or dripping condensation from uninsulated cold water pipes; and, **4)** at wall base behind baseboard due to saturation by mop water. Conversely, fungal disfigurement of the interior finished surfaces of exterior walls is often due to condensation, in which case *Stachybotrys* is rarely involved. The fungi most frequently encountered as agents of surface disfigurement are: *Cladosporium cladosporioides* and *Cl. sphaerospermum*, *Alternaria*, *Ulocladium*, *Aspergillus versicolor*,

---

<sup>13</sup> Recurrent water penetration often establishes a vertical moisture gradient whereby the lower extent of a wall remains saturated and the water diminishes at increasing vertical distance from the sill plate. *Stachybotrys chartarum* is both hydrophilic and strongly cellulolytic, and tends to proliferate on the lower extent of gypsum wallboard where the surface is buffered to intermittent drying (e.g. interior of the wall cavity, beneath baseboards, etc.). Microarthropods, primarily mites, are common in this region as active grazers of *Stachybotrys* conidia, as evidenced by the often exclusive content of these spores in their fecal pellets. *Acremonium* (resembling of *A. butyri*) frequently co-occurs in this region, and in addition is a common colonist of mite fecal pellets. At increasing distance from the water-damaged area hydrophilic species give way to mesophilic and xerophilic moulds such as *Aspergillus ustus*, *A. versicolor* and several species of *Penicillium* including *P. brevicompactum*.



*Penicillium chrysogenum*, *P. griseofulvum* and *P. spinulosum* (Adan and Samson, 1994). These problems are common where furnishings are placed directly against cool exterior walls, producing static air pockets which result in condensation on wall surfaces and fungal growth which often affects a dramatically large area, reciprocal in outline to the furnishing, and thus resembles a “shadow”.

### **THE DAWN OF “SICK BUILDING SYNDROME”**

The disease that heralded current awareness of IAQ as an influence on health was of bacterial etiology, namely Legionnaire's Disease, and its eponymous causative agent, *Legionella pneumophila*. Legionellosis was first recognized in 1976 during a convention of the American Legion in Cincinnati, Ohio, at which several hundred participants presented with symptoms of pneumonia. After an exhaustive search to attempt to identify the infectious agent and route of exposure, investigators identified the HVAC system of the host complex. Humidification units were found to contain stagnant water containing the disease causing agent, which was aspirated into the ventilation system and inhaled by the building occupants. In all, 34 deaths were recorded in this initial outbreak (Yu, 2000). To date, the earliest recorded outbreak of *Legionella pneumonia* determined by retrospective studies occurred in 1957 in meat-packing plant in Austin, Minnesota, 78 people were hospitalised (Mulazimoglu and Yu, 1998; Yu, 2000). The elucidation of Legionnaire's Disease began a continuing awareness of buildings as sources for potentially harmful biological aerosols.

### **ECOLOGY OF DUST-BORNE FUNGI**

Household dust is host to a great variety of microfungi that originate from diverse sources. Principally, dust functions as an accumulator of biological particles that settle out from the ambient air. Much of this spora originates from outdoor sources, such as the phylloplane, and

enters the indoor environment passively through open doors and windows. Another common contributor to the indoor airborne spore-load comes from indoor substrates manifesting fungal spoiling, including construction materials, furnishings and foodstuffs. The influx of spores from these sources into house dust effectively builds a microfungal “seed-bank”, in which fungal propagules accumulate over time, remaining dormant unless suitable conditions permit germination and growth. Many common house-cleaning practices do less to remove dust than they do to aerosolize and redistribute it. As such, asthmatic children typically show an increase in respiratory symptom prevalence following house-cleaning procedures (Clark et al., 1976). This disruption of dust-bound spores by housekeeping practices is particularly true for the vacuum-cleaning of broadloom (Stetzenbach et al., 1999). Association analysis of the mycoflora of broadloom dust shown in Chapter 2 of this study identified three distinct ecological assemblages which correspond well to the hypothesized primary sources of indoor mycoflora that ultimately contribute to dust formation.

#### **ASSOCIATION ANALYSIS OF DUST-BORNE FUNGI**

The first and most obvious dust-borne fungal assemblage consists of phylloplane fungi. Species identified in the present study that belonged to this ecological group included *Alternaria alternata*, *Aureobasidium pullulans*, *Cladosporium cladosporioides* and *Epicoccum nigrum*. All of these taxa are well-known from outdoor habitats, particularly on decaying vegetation during the growing season in northern temperate climates (*see* Domsch et al., 1980). However, it cannot be assumed that the growth of these fungi is necessarily limited to the phylloplane and that their presence in building interiors is exclusively from extralimital sources. Clearly the majority of construction materials employed in small-scale residential construction are based on plant fibre products, including dimensional lumber, laminates, oriented strand boards and paper products (Kesik and Lio, 1997;

Mullins and McKnight, 1981). Thus, it is not unexpected that in the event of water damage, these same fungi are common colonists of wood-based construction materials, which serve as intrinsic sources of fungal propagules in indoor air and subsequently in dust. Species of *Cladosporium* are of particular interest in this regard, since they are frequent colonists of indoor surfaces incurring intermittent wetting, such as winter-time condensation on exterior walls (see Chapter 2). Similarly *Alternaria* occurs commonly on wooden window sills, and *Aureobasidium pullulans* may be found on bathroom surfaces such as shower curtains, bath mats and tile grout (Domsch et al., 1980; Samson et al., 1996; Singh, 1994). Hence, the interpretation of typical “phylloplane” species as such depends upon the exclusion of significant indoor amplifiers of these taxa.

A second important contributor to the dust mycobiota indicated in the present study arises from the importation of soil fungi into indoor environments on soiled footwear. Based on these data, putative “indicator species” of this group include *Trichoderma viride*, *Penicillium citreonigrum*, and possibly *Rhizopus oryzae* and *Mucor plumbeus*. In my experience, these taxa are less prone to colonize indoor substrates under conditions of water damage than phylloplane taxa, but all are known as occasional foodborne contaminants (Domsch et al., 1980; Samson et al., 1996). Pitt and Hocking (1999) questioned the identification of foodborne *Trichoderma* isolates, and suggested that most isolates referred in the literature to *T. viride* are likely misidentified isolates of *T. harzianum*. Indoors, species of *Trichoderma* have been reported from urea formaldehyde foam insulation (Bissett, 1987); however, use of this material has been banned in Canada due to adverse health effects from formaldehyde release during deterioration of the product. The presence of *Trichoderma* and other typical soil fungi in household dust is most likely from passive entry on footwear and from implements contaminated by soil fomites.

A third source of allochthonous dust mycobiota likely arises from the growth of fungi on food materials indoors. Many typical food spoilage fungi are tolerant of low water activity and some species, such as *Aspergillus versicolor* and *Wallemia sebi* are highly xerophilic (Pitt and Hocking, 1999). The principal indicator species from this ecological group observed in the present study were *As. versicolor*, *Eurotium herbariorum* and *W. sebi*. As well, the most common species of *Penicillium* observed in Wallaceburg dust samples were *P. aurantiogriseum-viridicatum* group, *P. brevicompactum*, *P. chrysogenum*, *P. commune*, *P. corylophilum*, *P. expansum* and *P. spinulosum*. All of these species, particularly the first three, are well-known food contaminants and spoilage agents (Pitt and Hocking, 1999; Samson et al., 1996). Although their principal indoor niche may be foodstuffs, many of these species are also known as contaminants of building materials, interior finishes and furnishings following water damage (Domsch et al., 1980; Adan and Samson, 1994). This trend is not limited to the Penicillia. As discussed in Chapter 2, many fungi that are adventitious colonists of foodstuffs appear similarly to have diversified into other indoor niches, given suitable conditions (e.g. *As. versicolor*, *As. ustus*, *Chaetomium globosum*, *P. aurantiogriseum*, *P. brevicompactum*, *P. chrysogenum* and *Stachybotrys chartarum*). Within the group of indoor fungi characterized by this ecological group, there are considerable taxonomic difficulties, especially in the genus *Penicillium*. A second aspect of this thesis involved the examination of the taxonomy of two commonly occurring dust-borne Penicillia, *P. brevicompactum* and *P. chrysogenum*, presented in Chapters 5 and 6, respectively, using molecular genetic characters derived from multiple genetic loci.

### ***PENICILLIUM BREVICOMPACTUM***

The heteroduplex mobility assay (HMA) was used to identify alleles in PCR-amplified regions of the beta-tubulin-encoding gene, *benA*, the gene encoding histone 4 (*his4*) and the internal

transcribed spacer region of nuclear ribosomal RNA including the 5.8S region (rDNA ITS1-5.8S-ITS2). Nine multilocus haplotypes were observed in 75 isolates of *P. brevicompactum* collected from 50 houses. These haplotypes showed a strong association of alleles, suggesting clonal propagation in absence of recombination in the set of isolates examined. Representative alleles were sequenced for the *benA* and ITS loci (the histone locus was not included in sequencing studies due to difficulties in obtaining clean sequence). Sequence data from these two loci were combined for phylogenetic analyses based on the congruence of these data sets as demonstrated by the Partition Homogeneity Test (PHT). Two well-supported, highly divergent clades were resolved. The principal clade contained 86% of the isolates obtained from house dust samples. This clade included the type strains of *P. brevicompactum* and *P. stoloniferum*. As such, *P. brevicompactum* is the correct name for this taxon, since *P. stoloniferum* is a later epithet, and phylogenetic analyses presented in Chapter 5 supported the synonymy of the two taxa. The second clade contained 14% of house dust isolates, and was sufficiently divergent from the principal clade to warrant recognition as a distinct species. Several voucher collections deposited in the DAOM under the name *P. brevicompactum* clustered within this clade. Interestingly, the habitats for these voucher isolates tended to be the decomposing fruit bodies of fleshy fungi. The majority of house dust isolates from this clade were obtained from houses at rural addresses (extralimital to the municipal boarder of the Town of Wallaceburg), further suggesting that this presently unrecognized species is affiliated with more natural conditions, such as forested areas or other localities where macrofungi fruit in high density. No isolates of nomenclatural standing that were included in the present study clustered within this clade. The microscopic morphology of this taxon appears indistinguishable from *P. brevicompactum* in which metulae show considerable apical swelling, producing a characteristically aspergilloid conidiophore appearance. It is unlikely that this taxon can be accommodated in any currently recognized taxa, given that

this morphology is of limited distribution within subgenus *Penicillium*. A review of existing taxonomic literature on *Penicillium* failed to yield morphologically similar taxa described from fungicolous habitats. A future goal of research shall be the evaluation of multiple phenotypic characters such as carbon and nitrogen utilization patterns as well as morphometric analyses in an attempt to identify reliable characters upon which this new species may be based.

Inclusion of ITS sequences of these taxa within a larger sample of terverticillate *Penicillia* indicated that the clade containing members of the *P. brevicompactum* complex formed a monophyletic group situated on a long branch that was sister to the core of the terverticillate *Penicillia*, in the basal position (*see* Chapter 4, FIG. 4-8). In their phylogeny of the terverticillate *Penicillia*, Skouboe and colleagues (1999) did not include representatives of *P. brevicompactum*, and rDNA sequences are presently not available for this taxon on GenBank. Thus, the current study appears to be the first investigation of the phylogenetic placement of *P. brevicompactum* using modern phylogenetic methods.

#### ***PENICILLIUM CHRYSOGENUM***

An investigation of genotypic diversity in 198 isolates of *P. chrysogenum* obtained from broadloom dust from 109 houses was presented in Chapter 6. This study employed HMA to determine the allelic diversity of 4 polymorphic genetic loci amplified by PCR from genes encoding acetyl coenzyme-A synthase gene (*acuA*), beta-tubulin (*benA*), and thioredoxin reductase (*trxB*), as well as the non-coding internal transcribed spacer regions of nuclear ribosomal DNA encompassing the 5.8S region (ITS1-5.8S-ITS2), as above. Two of these loci (*acuA* and *trxB*) were developed during the course of the present investigation. Three unique alleles were observed for each locus examined, grouping the isolates into five multilocus haplotypes in which

a strictly clonal pattern of inheritance was observed, indicating the absence of recombination in the isolates tested.

Representative isolates of all alleles for each locus were sequenced, and the sequence data were combined for analysis based on congruence of the data as demonstrated by the PHT. Sequence data for ITS regions of rDNA were excluded from final analyses due to the absence of parsimony-informative characters at this locus (*see* Table 6-6). Parsimony analysis of the combined *acuA*-*benA*-*trxB* dataset divided the set of 198 dust isolates of *P. chrysogenum* into three well-supported lineages, containing 90%, 7% and 3% of Wallaceburg isolates, respectively. These principal lineages were in agreement with the major groups resolved by cluster analyses of electrophoretic banding patterns obtained from PCR amplification products primed using the core sequence of M13 phage DNA, the repeated sequence (GACA)<sub>4</sub>, as well as the arbitrary primer pair 5SOR/ MYC1 (*see* Chapter 6, Table 6-3). Considerably greater fine resolution was observed in terminal branches of cluster analyses of fingerprint data. However, this fine resolution may be the result of difficulties in scoring low intensity bands, and may be uninformative.

The primary well-supported lineage of dust-borne isolates included the original penicillin-producing strain collected by Alexander Fleming in 1929 (identified as *P. rubrum*). No isolates of nomenclatural standing clustered within this clade, suggesting that it may represent a distinct species within the *P. chrysogenum* species complex. The recognition of this species awaits the identification of stable phenotypic characters by which it can be separated from *P. chrysogenum sensu stricto*. A preliminary plate assay for penicillin production examining the inhibition of a penicillin-sensitive strain of *Staphylococcus aureus* demonstrated a general inhibitory effect of *P.*

*chrysogenum* on *S. aureus*, but failed to reveal patterns of antibiosis that correlated to the genetic groupings observed (data not presented). Future investigations shall assess patterns of carbon and nitrogen utilization, growth rates at different temperature regimens and tolerance to low water activity in an effort to identify distinguishing phenotypic characters. A third well-supported clade contained 6 house dust isolates. None of the isolates of nomenclatural status clustered within this clade, and it may represent a second undescribed taxon within the *P. chrysogenum* species complex. Preliminary investigations of isolates from this clade show increased sporulation and generally more robust growth relative to members of the other two clades when grown on Creatine-sucrose agar. This medium may prove useful in the delimitation of this species.

Type isolates of other closely related taxa including *P. aethiopicum*, *P. chrysogenum* v. *dipodomyis*, *P. griseofulvum* v. *dipodomyis* and *P. nalgiovense* were sequenced for all loci, facilitating the examination of species concepts within this broader group of smooth-stiped terverticillate *Penicillia*. These results supported the synonymy between *P. notatum* and *P. chrysogenum*, in which the latter name has nomenclatural priority (and has been proposed as *nomen conservandum* by Kozakiewicz and colleagues, 1992). *Penicillium chrysogenum* v. *dipodomyis* clustered as sister to *P. nalgiovense*, outside of the *P. chrysogenum* clade, and warrants transfer to avoid paraphyly in *P. chrysogenum*.

## SUMMARY

For millennia, fungi have occurred commonly in the indoor environments within which humans live and work. Their presence has influenced both human disease and structural decay. Until the early 20<sup>th</sup> century, the principal agent of structural decay worldwide has been dry rot caused mainly by species of the basidiomycete, *Serpula*. The construction of tighter buildings due to



higher constraints on thermal energy retention, and the greater use of processed wood products in place of solid wood has brought about an increase in problems related to indoor fungal contamination, and simultaneously a shift in the fungal taxa responsible. Presently, many of the fungi responsible for structural contamination originate as dustborne moulds or food spoilage agents. Relative to *Serpula*, contamination by these fungi may pose less structural risk; however, many of the taxa involved produce mycotoxins, and may present a relatively greater hazard to building occupants.

The present study examined fungi in house dust from 369 houses in Wallaceburg, Ontario, Canada. A total of 256 fungal taxa were observed, which followed a Raunkaier-type distribution. Three distinct ecological assemblages were observed in dust-borne species: phylloplane fungi, soil fungi and food-spoilage/ xerophilic fungi. It is likely that these habitats serve as the major sources of the culturable fungal propagules that accumulate in house dust where indoor amplifiers are absent.

Allelic variability was assessed for multiple PCR-amplified polymorphic regions in conserved structural and metabolic genes from isolates of *P. brevicompactum* and *P. chrysogenum* using heteroduplex mobility assay. Allele identities were confirmed by sequencing and phylogenetic analyses were conducted on representative sequences of all alleles. Both *P. brevicompactum* and *P. chrysogenum* as currently circumscribed appear to consist of species complexes containing multiple cryptic species.

*Penicillium stoloniferum* is recognized as a synonym of *P. brevicompactum*. This lineage is a common inhabitant of house dust and indoor air. A second related lineage occurs occasionally in

household dust but is primarily associated with the decaying fruit bodies of fleshy fungi outdoors. At present, this lineage lacks an available name.

*Penicillium notatum* is recognized as a synonym of *P. chrysogenum*. This lineage is an occasional inhabitant of household dust. A second more commonly occurring dust-borne lineage includes the original penicillin-producing isolate obtained by Alexander Fleming in 1929. There is presently no available name for this lineage.

Further investigation is necessary to determine the taxonomic level at which the un-named lineages in *P. brevicompactum* and *P. chrysogenum* should be recognized, and suitable phenotypic characters by which they may be defined.

## LITERATURE CITED

- Abdel-Hafez, S.I.I. and A.A.M. Shoreit. 1985. Mycotoxins producing fungi and mycoflora of air-dust from Taif, Saudi Arabia. *Mycopathol.* 92: 65-71.
- Abdel-Hafez, S.I.I., A.A.M. Shoreit A.I.I. Abdel-Hafez and O.M.O.E-. Maghraby. 1986. Mycoflora and mycotoxin-producing fungi of air dust particles from Egypt. *Mycopathol.* 93: 25-32.
- Abdel-Hafez, S.I.I., H. Abdel-Aal, H. Mobasher and A. Barakat. 1993. Seasonal variations of fungi if outdoor air and sedimented dust at Assiut regoin, Upper Egypt. *Grana* 32: 115-121.
- Abraham, E.P. and Newton, G.G.F. 1967. Penicillins and Cephalosporins. *In Antibiotics: Biosynthesis* v.2 D. Gottlieb and P.D. Shaw (eds). New York: Springer-Verlag. pp. 1-16.
- Adan, O.C.G. and Samson, R.A. 1994. Fungal disfigurement of interior finishes. *In Building Mycology: Management of Decay and Health in Buildings.* J. Singh (ed.). London: Chapman & Hall. pp. 130-158.
- Agrawak, O.P., S. Dhawan, K.L. Garg, F. Shaheen, N. Pathak and A. Misra. 1988. Study of biodeterioration of the ajanta wall paintings. *International Biodeterioration* 24: 121-129.
- Ainsworth, P.J., Surh, L.C. and Coulter-Mackie, M.B. 991). Diagnostic single strand conformation polymorphism, (SSCP): a simplified non-radioisotopic method as applied to a Tay-Sachs B1 variant. *Nucleic Acids Res.* 19: 405-406.
- Al-Doory, Y. 1984. Airborne fungi. pp. 27-40. *In Mould allergy.* Y. Al-Doory and J.F. Domson (eds.). Lea and Febiger, Philadelphia. 278 pp.
- American Industrial Hygiene Association (AIHA). 1996. *Field Guide for the Determination of Biological Contamination in Environmental Samples.* Dillon, H.K., Heinsohn, P.A. and Miller, J.D. (eds). Fairfax, Virginia: AIHA Publications. 174 pp. (see Dillon et al., 1996)
- American Society for Heating, Refrigeration and Air Conditioning Engineers (ASHRAE). 1995. *HVAC Applications Handbook.* Atlanta: ASHRAE.
- Anderson, J.B. and Kohn, L.M. 1995. Clonality in soilborne, plant-pathogenic fungi. *Ann. Rev. Phytopathol.* 33: 369-391.
- Arx, J.A. v. 1970. *The Genera of Fungi Sporulating in Pure Culture.* J. Cramer, Vaduz, 2nd ed. 315 pp.
- Aurora, D. 1986. *Mushrooms Demystified.* 2<sup>nd</sup> ed. Berkeley: Ten Speed Press. 959 pp.
- Ayliffe, M.A., Lawrence, G.J., Ellis, J.G. and Pryor, A.J. (1994). Heteroduplex molecules formed between allelic sequences cause nonparental RAPD bands. *Nucleic Acids Res.* 22: 1632-1636.
- Bachmann, M.H., Delwart, E.L., Shpaer, E.G., Lingenfelter, P., Singal, R., Mullins, J.I. and WHO Network for HIV Isolation and Characterization. 1994. Rapid genetic characterization of HIV Type 1 strains from four World Health Organization-sponsored vaccine evaluation sites using a heteroduplex mobility assay. *AIDS Research and Human Retroviruses* 10: 1245-1353.
- Bainier, G. 1907. Mycothèque de l'École de Pharmacie. Partie XIII. *Soc. Mycol. Fr., Bull. Trimestr.* 23: 94-97, Pl. X.

- Banke, S., Frisvad, J.C. and Rosendahl, S. 1997. Taxonomy of *Penicillium chrysogenum* and related xerophilic species, based on isozyme analysis. *Mycol. Res.* 101: 617-624.
- Barker, F.K. and Lutzoni, F. 2000. Spurious rejection of partition homogeneity by the ILD test: a simulation study. Annual Meeting of the Mycological Society of America, Burlington, Vermont. [Abstract]
- Barnett, H.L. and B.B. Hunter. 1986. *Illustrated Genera of Fungi Imperfecti*. MacMillan Co., New York. 218 pp.
- Barron, G.L. 1968. *The Genera of Hyphomycetes from Soil*. Williams and Wilkins, Baltimore. 364 pp.
- Beaumont, F., H.F. Kauffman, H.J. Sluiter and K. de Vries. 1984. A volumetric-aerobiologic study of seasonal fungus prevalence inside and outside dwellings of asthmatic patients living in Northeast Netherlands. *Ann. Allergy* 53: 486-492.
- Beaumont, F., H.F. Kauffman, H.J. Sluiter and K. de Vries. 1985. Volumetric aerobiological survey of conidial fungi in the North-East Netherlands. II. Comparison of aerobiological data and skin tests with mould extracts in an asthmatic population. *Allergy* 40: 181-186.
- Bellomy, G.R. & Record, T.M. Jr. 1989. A method for horizontal polyacrylamide slab gel electrophoresis. *BioFeedback* 7: 16, 19-21.
- Berg-Munch, B., Clausen, P. and Fanger, P.O. 1984. Ventilation requirements for the control of body odor in spaces occupied by women. *Proc. 3<sup>rd</sup> Int. Conf. IAQ, Stockholm*, v. 5.
- Berk, S., H. Ebert and L. Teitell. 1957. Utilization of plasticizers and related organic compounds by fungi. *Industr. Eng. Chem.* 49: 1115-1124.
- Bielawski, J.P., Noack, K. and Pumo, D.E. 1995. Reproducible amplification of RAPD markers from vertebrate DNA. *BioTechniques* 18: 856-857.
- Bissett, J. 1987. Fungi associated with urea-formaldehyde foam insulation in Canada. *Mycopathol.* 99: 47-56.
- Blackley, C.H. 1873. *Exp. Researches of Catarrhus aestivus*. London, *see* Nilsby (1949).
- Blaszyk, H., Hartmann, A., Schroeder, J.J., McGovern, R.M., Sommer, S.S. and Kovach, J.S. 1995. Rapid and efficient screening for p53 gene-mutations by dideoxy fingerprinting. *BioTechniques* 18: 256-260.
- Bleas, M.J., De Grandis, S.A., Lee, H. and Trevors, J.T. 1998. Amplified fragment length polymorphism (AFLP): a review of the procedure and its applications. *J. Industr. Microbiol. Biotechnol.* 21: 99-114.
- Bloom, H. 1995. *The Lucifer Principle*. New York: Atlantic Monthly Press. 466 pp.
- Bondartsev, A.S. 1971. *The Polyporaceae of the European USSR and Caucasia*. Z. Shapiro (Transl.) and E. Rabinovitz (Ed). Springfield, Virginia: USDA and National Science Foundation, Washington D.C.
- Börjesson, T. Stöllman, U., Adamek, P., and A. Kaspersson. 1989. Analysis of volatile compounds for detection of molds in stored cereals. *Cereal Chem.* 66: 300-304.
- Börjesson, T. Stöllman and J. Schnürer. 1990. Volatile metabolites and other indicators of *Penicillium aurantiogriseum* growth on different substrates. *Appl. Environ. Microbiol.* 56: 3705-3710.
- Börjesson, T. Stöllman and J. Schnürer. 1992. Volatile metabolites produced by six fungal species compared with other indicators of fungal growth on stored cereals. *Appl. Environ. Microbiol.* 58: 2599-2605.

- Börjesson, T. Stöllman and J. Schnürer. 1993. Off-odorous compounds produced by molds on oatmeal agar: identification and relations to other growth characteristics. *J. Agric. Food Chem.* 41: 2104-2111.
- Bothwell, R. 1986. *A Short History of Ontario*. Edmonton: Hurtig. 222 pp.
- Bottles, S.L. 1987. *Los Angeles and the Automobile: The Making of the Modern City*. Los Angeles: University of California Press.
- Braak, C.J.F. ter. 1992. CANOCO - a FORTRAN program for canonical community ordination. Microcomputer Power. Ithaca, New York, USA. 95+35 pp.
- Bronswijk, J.E.M.H. v. 1981. *House Dust Biology; for Allergists, Acarologists and Mycologists*. Zoelmond: Published by the author. 316 pp.
- Bronswijk, J.E.M.H., Rijckaert, G, and van de Lustgraaf, B. 1986. Indoor fungi. distribution and allergenicity. *Acta Bot. Neerl.* 35: 329-345.
- Brown, L. (Ed) 1993. *New Shorter Oxford English Dictionary*. Oxford: Clarendon Press.
- Bruford, M.W. & Wayne, R.K. 1993. Microsatellites and their application to population genetic studies. *Curr. Opin. Genet. Dev.* 3: 939-943.
- Brunekreef, B., D.W. Droekery, F.E. Speozer, J.H. Ware, J.D. Spengler and B.G. Ferris. 1989. Home dampness and respiratory morbidity in children. *Am. Rev. Respir. Dis.* 140: 1363-1367.
- Buczacki, S. 1989. *Fungi of Britain and Europe*. London: Collins. 321 pp.
- Bull, J.J., Huelsenbeck, J.P., Cunningham, C.W., Swofford, D.L. and Waddell, P.J. 1993. Partitioning and combining data in phylogenetic analysis. *Syst. Biol.* 42: 384-397.
- Bunnag, C., B. Dhorranintra and A. Plangpatanapanichya. 1982. A comparative study of the incidence of indoor and outdoor mold spores an Bangkok, Thailand. *Ann. Allergy* 48: 333-339.
- Burg, W.R., O.L. Shotwell and B.E. Saltzman. 1982. Measurements of airborne aflatoxins during the handling of 1979 contaminated corn. *Am. J. Hyg. Assoc. J.* 43: 580-586.
- Burge, H.A. 1989. Indoor air and infectious disease. *Occup. Med. State of the Art Reviews* 4: 713-721.
- Burge, H.A. 1990. Bioaerosols: prevalence and health effects in indoor environments. *J. Allergy Clin. Immunol.* 86: 687-703.
- Burge, H.A. and Ammann, H.M. 1999. Fungal toxins and beta-(1-3)-D-glucans *In Bioaerosols: Assessment and Control*. J. Macher (Ed.) Cincinnati: American Conference of Governmental Industrial Hygienists. pp. 24.1-24.13.
- Burge, H.A. and Otten, J.A. 1999. Fungi. *In Bioaerosols: Assessment and Control*. J. Macher (Ed.) Cincinnati: American Conference of Governmental Industrial Hygienists. pp. 19.1-19.13.
- Burge, H.A., W.R. Solomon and M.L. Mulenberg. 1982. Indoor plantings as allergen exposure sources. *J. Allergy Clin. Immunol.* 70: 101-108.
- Burr, M.L., J. Mullins, T.G. Merrett and N.C.H. Stott. 1988. Indoor moulds and asthma. *J. R. Soc. Health* 108: 99-101.

- Buscot, F. 1996. DNA polymorphism in morels: PCR/RFLP analysis of the ribosomal DNA spacers and microsatellite-primed PCR. *Mycol. Res.* 100: 63-71.
- Buscot, F., Wipf, D., Di Battista, C., Munch, J.-C., Botton, B. and Martin, F. 1996. DNA polymorphism in morels: PCR/RFLP analysis of the ribosomal DNA spacers and microsatellite-primed PCR. *Mycol. Res.* 100: 63-71.
- Caetano-Anollés, G., Brassam, B.J. and Gresshoff, P.M. 1992. Primer-template interactions during DNA amplification fingerprinting with single arbitrary oligonucleotides. *Mol. Gen. Genet.* 235: 157-165.
- Cai, S.-P., Eng, B., Kan, Y.W. and Chui, H.K. 1991. A rapid and simple electrophoretic method for the detection of mutations involving small insertion or deletion: application to  $\beta$ -thalassemia. *Hum. Genet.* 87: 728-730.
- Cain, W.S. 1983. Ventilation requirements in buildings. *Atmosph. Environ.* 17(6).
- Calvo, M.A., J. Guarro, G. Suarez and C. Ramirez. 1980. Airborne fungi in the air of Barcelona, Spain. IV. Studies of the spore content of air in dwellings. *Ann. Allergy* 44: 228-234.
- Calvo, M.A., M.A. Dronda and R. Castello. 1982. Fungal spores in house dust. *Ann. Allergy* 49: 213-219.
- Campbell, N.J.H., Harriss, F.C., Elphinstone, M.S. and Baverstock, P.R. 1995. Outgroup heteroduplex analysis using temperature-gradient gel-electrophoresis: high resolution, large-scale screening of DNA variation in the mitochondrial control region. *Molec. Ecol.* 4: 407-418.
- Carbone, I., Anderson, J.B. and Kohn, L.M. 1999. Patterns of descent in clonal lineages and their multilocus fingerprints are resolved with combined gene genealogies *Evolution* 53: 11-21.
- Carmichael, J.W. 1955. Lacto-fuchsin: A new medium for mounting fungi. *Mycologia* 47: 611.
- Carmichael, J.W., W.B. Kendrick, I.L. Connors and L. Sigler. 1980. *Genera of Hyphomycetes*. University of Alberta Press, Edmonton. 386 pp.
- Causton, D.R. 1988. *An Introduction to Vegetation Analysis*. London: Unwin Hyman. 342 pp.
- Cha, R.S. and Thilly W.G. 1993. Specificity, efficiency and fidelity of PCR. *PCR Methods Appl.* 3: S30-S37.
- Chang, J.C.S., Foarde, K.K. and Vanosdell, D.W. 1995. Growth evaluation of fungi on ceiling tiles. *Atmosph. Environ.* 29: 2331-2337.
- Cheng, J., Kasuga, T., Mitchelson, K.R., Lightly, E.R.T., Watson, N.D., Martin, W.J. and Atkinson, D. 1994. Polymerase chain reaction heteroduplex polymorphism analysis by entangled solution capillary electrophoresis. *J. Chromatogr.* 667: 169-177.
- Childe, V.G. 1950. The urban revolution. *Town Planning Review* 21: 3-17.
- Chowdhury, V., Olds, R.J., Lane, D.A., Conard, J., Pabinger, I., Ryan, K., Bauer, K.A., Bhavnani, M., Abildgaard, U., Finazzi, G., Castaman, G., Mannucci, P.M. and Thein, S.L. 1993. Identification of nine novel mutations in type I antithrombin deficiency by heteroduplex screening. *Brit. J. Haematol.* 84: 656-661.
- Clark, R.P., Cordon-Nesbitt, D.C., Malka, S., Preston, T.D. and Sinclair, L. 1976. The size of airborne dust particles precipitating bronchospasm in house dust sensitive children. *J. Hygiene*, 77: 321-325.

- CMHC. 1982. *Glossary of Housing Terms*. Ottawa: CMHC. 110 pp.
- Cohen, M.B., T. Nelson and B.H. Reinarz. 1935. Observations of the nature of the house dust allergens. *J. Allergy* 6: 517-520.
- Collins, R.P. 1976. Terpenes and odoriferous materials from micro-organisms. *Lloydia* 39: 20-24.
- Collins, R.P. 1979. The production of volatile compounds by filamentous fungi. *Dev. Ind. Microbiol.* 20: 239-245.
- Considine, D.M. (ed). 1976. *Van Nostrand's Scientific Encyclopedia*, 5<sup>th</sup> ed. New York: Van Nostrand Reinhold. 2370 pp.
- Cooley, J.D. 1999. *The Role of Penicillium chrysogenum Conidia in Sick Building Syndrome and an Asthma-Like Animal Model*. PhD Thesis, Graduate School of Biomedical Sciences, Texas Technical University Health Sciences Center.
- Cooley, J.D., Wong, W.C., Jumper, C.A, and Straus, D.C. 1999. Cellular and humoral responses in an animal model inhaling *Penicillium chrysogenum* spores. In *Bioaerosols, Fungi and Mycotoxins*. E. Johannig (ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 403-410.
- Cotton, R.G.H. 1993. Current methods of mutation detection. *Mutation Res.* 285: 125-144.
- Cox, C.S. and Wathes, C.M. (eds) 1995. *Bioaerosols Handbook*. Boca Raton: Lewis Publishers. 621 pp.
- Croft, W.A., B.B. Jarvis and C.S. Yatawara. 1986. Airborne outbreak of trichothecene toxicosis. *Atmos. Environ.* 20: 549-552.
- Dales, R., H. Zwanenburg, R. Burnett and C.A. Franklin. 1991a. Respiratory health effects of home dampness and molds among Canadian children. *Am. J. Epidemiol.* 134: 196-203.
- Dales, R., R. Burnett and H. Zwanenburg. 1991b. Adverse health effects in adults exposed to home dampness and molds. *Am. Rev. Respir. Dis.* 143: 505-509.
- D'Amato, M. and Sorrentino, R. 1994. A simple and economical DRB1 typing procedure combining group-specific amplification, DNA heteroduplex and enzyme restriction analysis. *Tissue Antigens* 43: 295-301.
- D'Amato, M. and Sorrentino, R. 1995. Short insertions in the partner strands greatly enhance the discriminating power of DNA heteroduplex analysis: resolution of HLA-DQB1 polymorphisms. *Nucleic Acids Res.* 23: 2078-2079.
- Dams, E., L. Hendriks, Y. van de Peer, J.-M. Neefs, G. Smits, I. Vandembrempt and R. de Wachter. 1988. Compilation of small ribosomal subunit RNA sequences. *Nucleic Acids Res.* 16 (suppl.): r87-r173.
- Daubenmire, R. 1968. *Plant Communities: A Textbook of Plant Synecology*. New York: Harper & Row. 300 pp.
- Davies, R.R. 1960. Viable moulds in house dust. *Trans. Brit. Mycol. Soc.* 43: 617-630.
- Davin-Regli, A., Abed, Y., Charrel, R.N., Bollet, C. and de Micco, P. 1995. Variations in DNA concentrations significantly affect the reproducibility of RAPD fingerprint patterns. *Res. Microbiol.* 146: 561-568.
- Davis, K. 1965. The urbanization of the human population. *Sci. Amer.* 213(3).

- Davis, T.M., Yu, H., Haigis, K.M. and McGowan, P.J. 1995. Template mixing: a method of enhancing detection and interpretation of codominant RAPD markers. *Theor. Appl. Genet.* 91: 582-588.
- Dean, M. and Gerrard, B. 1991. Helpful hints for the detection of single-stranded conformation polymorphisms. *BioTechniques* 10: 332-333.
- DeGrace, R.F. 1960. Facts about building codes that every supplier should know. *For. Prod. J.* 10(10): 538.
- Dekker, C., R. Dales, S. Bartlett, B. Brunekreef and H. Zwanenburg. 1991. Child asthma and the indoor environment. *Chest* 100: 922-926.
- Delwart E.L., Shpaer E.G., Louwagie J., McCutchan F.E., Grez M., Rubsamen-Waigmann H. and Mullins J.I. 1993. Genetic relationships determined by a DNA heteroduplex mobility assay: analysis of HIV-1 env genes. *Science* 262: 1257-1261.
- Delwart, E.L., Sheppard, H.W., Walker, B.D., Goudsmit, J. and Mullins, J.I. 1994. Human immunodeficiency virus type 1 evolution in vivo tracked by DNA heteroduplex mobility assays. *J. Virol.* 68: 6672-6683.
- de Queiroz, A. 1993. For consensus (sometimes). *Syst. Biol.* 42: 368-372.
- Dieffenbach, C.W., Lowe, T.M.J. and Dveksler, G.S. 1993. General concepts for PCR primer design. *PCR Methods Appl.* 3: S30-S37.
- Dillon, H.K., Heinsohn, P.A. and Miller, J.D. (eds) 1996. *Field Guide for the Determination of Biological Contaminants in Environmental Samples*. Fairfax, Virginia: American Industrial Hygiene Association. 174 pp. (see American Industrial Hygiene Association, 1996)
- Dockhorn-Dworniczak, B., Dworniczak, B., Brommelkamp, L., Bulles, J., Horst, J. and Bocker, W.W. 1991. Non-isotopic detection of single-strand conformation polymorphism (PCR-SSCP): a rapid and sensitive technique in the diagnosis of phenylketonuria. *Nucleic Acids Res.* 19: 2500.
- Dodson, L.A. and Kant, J.A. 1991. Two-temperature PCR and heteroduplex detection: application to rapid cystic fibrosis screening. *Molec. Cell. Probes* 5: 21-25.
- Doherty, T., Connell, J., Stoerker, J., Markham, N., Shroyer, A.L. and Shroyer, K.R. (1995). Analysis of clonality by polymerase chain reaction for phosphoglycerate kinase-I: heteroduplex generator. *Diagnostic Molec. Pathol.* 4: 182-190.
- Dolenko, A.J., Shields, J.K., King, F.W., Roff, J.W. and Ostaff, D. 1981. Wood Protection. In *Canadian Woods, Their Properties and Uses*. 3<sup>rd</sup> ed. J. Mullins and T.S. McKnight (eds). Toronto: University of Toronto Press. pp. 177-223.
- Domsch, K. H., W. Gams and T. H. Anderson. 1980. *Compendium of Soil Fungi*. Vol. 1. London: Academic Press. 859 pp.
- Don, R.H., Cox, P.T., Wainwright, B.J., Baker, K. and Mattick, J.S. 1991. 'Touchdown' PCR to circumvent spurious priming during gene amplification. *Nucleic Acids Res.* 19: 4008.
- Donaldson, G.C., Ball, L.A., Axelrod, P.E. and Glass, N.L. 1995. Primer sets developed to amplify conserved genes from filamentous ascomycetes are useful in differentiating *Fusarium* species associated with conifers. *Appl. Environ. Microbiol.* 61: 1331-1340.



- Drouhet, E. 1999. Louis Pasteur, ses disciples et la mycologie. Publication Trimestrielle de l' Association des Anciens Elèves de l'Institut Pasteur 41(158): 2-10.
- Ebner, M.R., K. Haselwandter and A. Frank. 1992. Indoor and outdoor incidence of airborne fungal allergens at low- and high-altitude alpine environments. *Mycol. Res.* 96: 117-124.
- El-Borai, M.H., D'Alfonso, S., Mazzola, G. and Fasano, M.E. 1994. A practical approach to HLA-DR genomic typing by heteroduplex analysis and a selective cleavage at position 86. *Human Immunol.* 40: 41-50.
- Ellegren, H., Mikko, S., Wallin, K. and Andersson, L. 1996. Limited polymorphism at major histocompatibility complex (MHC) loci in the Swedish moose, *A. alces*. *Molec. Ecol.* 5: 3-9.
- Ellis, M.B. 1971. *Dematiaceous Hyphomycetes*. Commonwealth Mycological Institute, C.A.B. Kew, Surrey. 608 pp.
- Ellis, M.B. 1976. *More Dematiaceous Hyphomycetes*. Commonwealth Mycological Institute, C.A.B. Kew, Surrey. 507 pp.
- Ellis, M.B. and Ellis, J.P. 1990. *Fungi Without Gills (Hymenomycetes and Gasteromycetes): An Identification Handbook*. London: Chapman & Hall. 329 pp.
- Ellison, J., Squires, G., Crutchfield, C. and Goldman, D. 1994. Detection of mutations and polymorphisms using fluorescence-based dideoxy fingerprinting (F-ddF). *BioTechniques* 17: 742.
- Ellsworth, D.L., Rittenhouse, K.D., Honeycutt, R.L. 1993. Artfactual variation in randomly amplified polymorphic DNA banding patterns. *BioTechniques* 14: 214-217.
- Engels, F. 1845. *The Conditions of the Working Class in England in 1844* (Excerpt) *In The City Reader*. 2<sup>nd</sup> ed., R.T. LeGates and F. Stout (eds). 2000. London: Routledge. pp. 47-55.
- Eschete, M.L., King, J.W., West, B.C. and Oberle, A. 1981. *Penicillium chrysogenum* endophthalmitis. First reported case. *Mycopathol.* 74: 125-127.
- Fargis, P. and Bykofsky, S. (eds). 1989. *The New York Public Library Desk Reference*. New York: Webster.
- Farr, D.F., Bills, G.F., Chamuris, G.P. and Rossman, A.Y. 1989. *Fungi on Plants and Plant Products in the United States*. St. Paul, Minnesota: American Phytopathological Society. 1252 pp.
- Farris, J.S., Kallersjo, M. and Kluge, A.G. 1994. Testing significance of incongruence. *Cladistics* 10: 315-319.
- Fauci, A.S., Braunwald, E., Isselbacher, K.J., Wilson, J.D., Martin, J.B., Kasper, D.L., Hauser, S.L. and Longo, D.L. (eds). 1998. *Harrison's Principles of Internal Medicine*, 14<sup>th</sup> ed. McGraw Hill: New York. 2569 pp.
- Felmlee, T.A., Liu, Q., Whelen, A.C., Williams, D., Sommer, S.S. and Persing, D.H. 1995. Genotypic detection of *Mycobacterium tuberculosis*-rifampin resistance: comparison of single-strand conformation polymorphism and dideoxy fingerprinting. *J. Clin. Microbiol.* 33: 1617-1623.
- Fergusson, R.J., Milne, L.R.J. and Crompton, G.K. 1984. *Penicillium* allergic alveolitis: faulty installation of central heating. *Thorax* 39: 294-298.
- Filtborg, O., Frisvad, J.C. and Thrane, U. 1990. The significance of yeast extract composition on metabolite production in *Penicillium*. *In Modern Concepts in Penicillium and Aspergillus Classification*. R.A. Samson and J.I. Pitt (eds). New York: Plenum Press. pp 433-441.

- Fisher, S.G. and Lerman, L.S., 1983. DNA fragments differing by single base-pair substitutions are separated in denaturing-gradient gels: correspondence with melting theory. *Proc. Natl. Acad. Sci. USA* 80: 1579-1583.
- Fishman, R. 1987. *Bourgeois Utopias: The Rise and Fall of Suburbia*. New York: Harper-Collins.
- Flannigan, B., E.M. McCabe and F. McGarry. 1991. Allergic and toxigenic micro-organisms in houses. *J. Appl. Bacteriol.* 70 (suppl.): 61s-73s.
- Flannigan, B. and Miller, J.D. 1994. Health implications of fungi in indoor environments - an overview. *In Health Implications of Fungi in Indoor Environments*. R.A. Samson, B. Flannigan, M.E. Flannigan, A.P. Verhoeff, O.C.G. Adan and E.S. Hoekstra (eds). Air Quality Monographs 2. Amsterdam: Elsevier. pp. 3-28.
- Flannigan, B. and Morey, P.R. 1996. *Control of Moisture Problems Affecting Biological Indoor Air Quality*. International Society for Indoor Air Quality and Climate (ISIAQ) Guideline TFI-1996. Ottawa: ISIAQ. 70 pp.
- Fleming, A. 1929. On the antibacterial action of cultures of a *Penicillium*, with special reference to their use in the isolation of *B. influenzae*. *Brit. J. Exp. Pathol.* 10: 226-236.
- Flood, C.A. 1931. Observations on the sensitivity to dust fungi in patients with asthma. *JAMA* 96: 2094.
- Fox, S.A., Lareu, R.R. and Swanson, N.R. 1995. Rapid genotyping of hepatitis-c virus isolates by dideoxy fingerprinting. *J. Virological Meth.* 53: 1-9.
- Frisvad, J.C. 1985. Creatine-sucrose agar, a differential medium for mycotoxin producing *Penicillium* species. *Letters in Appl. Microbiol.* 1: 109-113.
- Frisvad, J.C. 1993. Modifications on media based on creatine for use in *Penicillium* and *Aspergillus* taxonomy. *Lett. Appl. Microbiol.* 16: 154-157.
- Frisvad, J.C. and Gravesen, S. 1994. *Penicillium* and *Aspergillus* from Danish homes and working places with indoor air problems: identification and mycotoxin determination. *In Health Implications of Fungi in Indoor Environments*. R.A. Samson, B. Flannigan, M.E. Flannigan, A.P. Verhoeff, O.C.G. Adan and E.S. Hoekstra (eds). Air Quality Monographs 2. Amsterdam: Elsevier. pp. 281-290.
- Fuller, S.J., Mather, P.B. and Wilson, J.C. 1996. Limited genetic differentiation among wild *Oryctolagus cuniculus* (rabbit) populations in arid eastern Australia. *Heredity* 77: 138-145.
- Gaidano, G., Ballerini, P., Gong, J.Z., Inghirami, G., Neri, A., Newcomb, E.W., Magrath, I.T., Knowles, D.M. and Della-Favera, R. 1991. p53 mutations in human lymphoid malignancies: Association with Burkitt lymphoma and chronic lymphocytic leukemia. *Proc. Natl. Acad. Sci. USA.* 88: 5413-5417.
- Ganguly, A., Rock, M.J. & Prockop, D.J. 1993. Conformation-sensitive gel electrophoresis for rapid detection of single-base differences in double-stranded PCR products and DNA fragments: evidence for solvent-induced bends in DNA heteroduplexes. *Proc. Natl. Acad. Sci. USA* 90: 10325-10329.
- Gardes, M., White, T.J., Fortin, J.A., Bruns, T.D. and Taylor, J.W. 1991. Identification of indigenous and introduced symbiotic fungi in ectomycorrhizae by amplification of nuclear and mitochondrial DNA. *Canad. J. Bot.* 69: 180-190.
- Gargas, A. and DePriest, P.T. 1996. A nomenclature for fungal PCR primers with examples from intron-containing SSU rDNA. *Mycologia* 88: 745-748.

- Garrison, R. and L. Robertson. 1989. A comparative aeromycological survey of the atmospheric vs. in-home fungal population of thirty-one homes in Fort Worth, Texas (abstr.). *J. Allergy Clin. Immunol.* 83: 265.
- Geiser, D.M., Pitt, J.I. and Taylor, J.W. 1998. Cryptic speciation and recombination in the aflatoxin-producing fungus *Aspergillus flavus*. *Proc. Natl. Acad. Sci. USA* 95: 388-393.
- Giddings, M.J. 1986. Occupational health problems due to air exposure to fungal contamination. In: Significance of fungi in indoor air: Report of a working group. Health and Welfare Canada Working Group on Fungi and Indoor Air. 16 pp.
- Ginns, J.H. 1986. Compendium of plant disease and decay fungi in Canada, 1960-1980. Agriculture Canada Publ. No. 1813. Ottawa: Canadian Government Publishing Centre. 416 pp.
- Glass, N.L. and Donaldson, G.C. 1995. Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Appl. Environ. Microbiol.* 61: 1323-1330.
- Good, I.J. 1953. The population frequencies of species and the estimation of population parameters. *Biometrika* 40: 237-264.
- Grace, M.B., Buzard, G.S. and Weintraub, B.D. 1995. Allele-specific associated polymorphism analysis: novel modification of SSCP for mutation detection in heterozygous alleles using the paradigm of resistance to thyroid hormone. *Human Mutation* 6: 232-242.
- Grant, C., C.A. Hunter, B. Flannigan and A.F. Bravery. 1989. The moisture requirements of moulds isolated from domestic dwellings. *Int. Biodeter.* 25: 259-284.
- Gravesen, S. 1978a. Identification and prevalence of culturable mesophilic microfungi in house dust from 100 Danish homes. Comparison between airborne and dust-bound fungi. *Allergy* 33: 268-272.
- Gravesen, S. 1978b. Microfungi in private homes. *Allergy* 33: 328.
- Gravesen, S. 1979. Fungi as a cause of allergic disease. *Allergy* 34: 135-154.
- Gravesen, S. 1999. Microfungal contamination of damp buildings. In *Bioaerosols, Fungi and Mycotoxins*. E. Johannig (ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 505-511.
- Gray, W.D. 1959. *The Relation of Fungi to Human Affairs*. New York: Holt-Dryden. 510 pp.
- Greig-Smith, P. 1964. *Quantitative Plant Ecology*. 2nd ed., Butterworths, London, 256 pp.
- Gretch, D.R., Polyak, S.J., Wilson, J.J., Carithers, R.L., Perkins, J.D. and Corey, L. 1996. Tracking hepatitis-C virus quasi-species major and minor variants in symptomatic and asymptomatic liver-transplant recipients. *J. Virol.* 70: 7622-7631.
- Grigg, D.B. 1974. *The Agricultural Systems of the World: An Evolutionary Approach*. Avon, Great Britain: Cambridge University Press. 358 pp.
- Groppe, K., Sanders, I., Wiemken, A. and Boller, T. 1995. A microsatellite marker for studying the ecology and diversity of fungal endophytes (*Epicblöe* spp.) in grasses. *Appl. Environ. Microbiol.* 61: 3943-3949.

- Gross, R. and Nilsson, J. 1995. Application of heteroduplex analysis for detecting variation within the growth hormone 2 gene in *Salmo trutta* L. (brown trout). *Heredity* 74: 286-295.
- Gutell, R.R. and G.E. Fox. 1988. A compilation of large subunit RNA sequences presented in structural format. *Nucleic Acids Res.* 16 (suppl.): r175-r269.
- Guyton, A.C. 1982. *Human Physiology and Mechanisms of Disease*. Philadelphia: Wm. Saunders. 709 pp.
- Hallden, C., Hansen, M., Nilsson, N.O., Hjerdin, A. and Sall, T. 1996. Competition as a source of errors in RAPD analysis. *Theor. Appl. Genet.* 93: 1185-1192.
- Hamada, N. and A. Yamada. 1991. Seasonal change in the fungal flora of house dust. *Trans. Mycol. Soc. Japan* 32: 45-53.
- Hamlin, A.F., J.A. Narcisco and R.P. Collins. 1975. Odorous constituents of *Penicillium decumbens*. *Mycol.* 67: 1158-1165.
- Hanahan, D. 1985. Techniques for transformation of *E. coli*. In *DNA Cloning*, Vol. 1, *A Practical Approach*. D.M.Glover (ed). IRL Press, Oxford. pp. 109-135.
- Hanlin, R.T. 1990. *Illustrated genera of Ascomycetes*. APS Press, St. Paul, Minnesota. 263 pp.
- Hare, R. 1970. *The Birth of Penicillin and the Disarming of Microbes*. London: George Allen and Unwin.
- Harvey, P. and R. May. 1990. Matrimony, mattresses and mites. *New Scientist* 3: 48-49.
- Harving, H., J. Korsgaard and R. Dahl. 1993. House-dust mites and associated environmental conditions in Danish homes. *Allergy* 48: 106-109.
- Hatcher, S.L., Lambert, Q.T., Teplitz, R.L. and Carlson, J.R. 1993. Heteroduplex formation: a potential source of genotyping error from PCR products. *Prenatal Diagnosis* 13: 171-177.
- Hawksworth, D.L., Kirk, P.M., Sutton, B.C. and Pegler, D.N. 1995. *Ainsworth & Bisby's Dictionary of the Fungi*. 8<sup>th</sup> ed. Cambridge: CAB International.
- Hay, D.B., B.J. Hart and A.E. Douglas. 1992a. Evidence refuting the contribution of the fungus *Aspergillus penicillioides* to the allergenicity of the house dust mite *Dermatophagoides pteronyssinus*. *Int. Arch. Allergy Immunol.* 97: 86-88.
- Hay, D.B., B.J. Hart, R.B. Peirce, Z. Kozakiewicz and A.E. Douglas. 1992b. How relevant are house dust mite-fungal interactions in laboratory culture to the natural dust system? *Exp. Appl. Acarol.* 16: 37-47.
- Hayashi, K. 1991. PCR-SSCP: a simple and sensitive method for detection of mutations in the genomic DNA. *PCR Methods Appl.* 1: 34-38.
- Hayashi, K. 1992. PCR-SSCP: a method for detection of mutations. *Genet. Analysis: Techniques Applic.* 9: 73-79.
- He, Q., Viljanen, M. and Mertsola, J. 1994. Effects of thermocyclers and primers on the reproducibility of banding patterns in randomly amplified polymorphic DNA analysis. *Mol. Cell Probes* 8: 155-160.
- Hedrick, P. 1992. Population genetics: shooting the RAPDs. *Nature* 355: 679-680.

- Hennebert, G.L. 1985. Dierckx' contribution to the genus *Penicillium*. In *Advances in Penicillium and Aspergillus Systematics*. R.A. Samson and J.I. Pitt (eds). NATO ASI Series A, Vol. 102. New York: Plenum Press. pp. 9-21.
- Hill, J.L., Hocking, A.D. and Whitfield, F.B. 1995. The role of fungi in the production of chloroanisoles in general purpose freight containers. *Food Chem.* 54: 161-166.
- Hintikka, E.-L. 1978. Human stachybotryotoxicosis. In: *Mycotoxic Fungi, Mycotoxins, Mycotoxicoses*. Vol. 3. T.D. Wyllie and L.G. Morehouse (eds). Marcel Dekker Inc., New York. pp. 87-89.
- Ho, M.H.-M., Castañeda, R., Dugan, F.M. and Jong, S.C. 1999. *Cladosporium* and *Cladophialophora* in culture: descriptions and an expanded key. *Mycotaxon*: 72: 115-157.
- Hoekstra, E.S., Samson, R.A. and Verhoef, A.P. 1994. Fungal propagules in house dust: a qualitative assessment. In *Health Implications of Fungi in Indoor Environments*. R.A. Samson, B. Flannigan, M.E. Flannigan, A.P. Verhoeff, O.C.G. Adan and E.S. Hoekstra (eds). Air Quality Monographs 2. Amsterdam: Elsevier. pp. 169-177.
- Hoffman, M., Bash, E., Berger, S.A., Burke, M. and Yust, I. 1992. Fatal necrotizing esophagitis due to *Penicillium chrysogenum* in a patient with acquired immunodeficiency syndrome. *Europ. J. Clin. Microbiol. Infect. Dis.* 11: 1158-1160.
- Hoffmann, R.J. 1986. Variation in contributions of asexual reproduction to the genetic structure of populations of the sea anemone *Metridium senile*. *Evolution* 40: 357-365.
- Holmgren, P.K., Holmgren, N.H. and Barnett, L.C. (eds). 1990. *Index Herbariorum. Part I. The Herbaria of the World*. 8<sup>th</sup> ed. *Regnum Vegetabile* 120: 1-693.
- Hopkins, J.G., Benham, R.W., and Kesten, B.M. 1930. Asthma due to a fungus -- *Alternaria*. *JAMA* 94: 6-10.
- Howard, D.H. 1994. The miracle at The Radcliffe Infirmary. How a son of Adelaide and a mould changed the world. *J. Med. Vet. Mycol.* 32 (Suppl. 1): 9-16.
- Huelsensbeck, J.P., Bull, J.J. and Cunningham, C.W. 1996. Combining data in phylogenetic analysis. *Trends Ecol. Evol.* 11: 152-158.
- Huelsensbeck, J.P. and Hillis, D.M. 1993. Success of phylogenetic methods in the four-taxon case. *Syst. Biol.* 42: 247-264.
- Hughes, M.N. and Poole, R.K. 1989. *Metals and Micro-organisms*. London: Chapman and Hall. 412 pp.
- Hunninghake, G.W. and Richardson, H.B. 1998. Hypersensitivity pneumonitis and eosinophilic pneumonias. In *Harrison's Principles of Internal Medicine*, 14<sup>th</sup> Ed., Chap. 253. pp 1426-1429. New York: McGraw-Hill.
- Hunter, C.A., and Lea, R.G. 1995. The airborne fungal population of representative British homes. *Air Qual. Monogr.* 2: 141-153.
- Huysmans, E. and R. de Wachter. 1986. Compilation of small ribosomal subunit RNA sequences. *Nucleic Acids Res.* 14 (suppl.): r73-r118.
- Hyppel, A. 1984. Fingerprint of a mould odor. In: *Indoor air*. Vol. 3. *Sensory and Hyperactivity Reactions to Sick Buildings*. B. Berglund, T. Lindvall and J. Sundell (eds). Swedish Council for Building Research, Stockholm, Sweden. pp. 443-447.

- Ingold, C.T. 1965. *Spore liberation*. Oxford: Clarendon Press. 210 pp.
- Ishii, A., M. Takaoka, M. Ichinoe, Y. Kabasawa and T. Ouchi. 1979. Mite fauna and fungal flora in house dust from homes of asthmatic children. *Allergy* 34: 379-387.
- Jacob, R.L., C.P. Andrews and F.O. Jacobs. 1989. Hypersensitivity pneumonitis treated with an electrostatic dust filter. *Ann. Intern. Med.* 110: 115-118.
- Janssen, J.E. 1999. The history of ventilation and temperature control. *ASHRAE Journal* 41(10): 47-52
- Jarvis, B. 1986. Potential indoor air pollution problems due to air exposure to fungal contamination. *In: Significance of Fungi in Indoor Air: Report of a Working Group*. Health and Welfare Canada Working Group on Fungi and Indoor Air. 24 pp.
- Jeannmougin, F., Thompson, J.D., Gouy, M., Higgins, D.G. and Gibson, T.J. 1998. Multiple sequence alignment with Clustal X. *Trends Biochem. Sci.* 23: 403-405.
- Jefferies, A.J. 1987. Highly variable minisatellites and DNA fingerprints. *Biochem Soc. Trans.* 15: 309-317.
- Jefferies, A.J., Wilson, V. and Thein, S.L. 1985a. Individual-specific 'fingerprints' of human DNA. *Nature* 316: 76-79.
- Jefferies, A.J., Wilson, V. and Thien, S.L. 1985b. Hypervariable 'minisatellite' regions in human DNA. *Nature* 314: 67-73.
- Jelks, M. 1994. *Allergy Plants*. New York: World Publications. 64 pp.
- Jensen, M.A. and N. Straus. 1993. Effect of PCR conditions on the formation of heteroduplex and single-stranded DNA products in the amplification of bacterial ribosomal DNA spacer regions. *PCR Meth. Appl.* 3: 186-194.
- Katzis, G. 1977. Zierpflanzen-Hydrokulturen im Krankenhaus als mögliches Reservoir für Hospitalismus-Nasskeime. *Mitt Österr Sanitätsverwaltung* 78: 193-197.
- Keen, J., Lester, D., Inglehearn, C., Curtis, A. and Bhattacharya, S. 1991. Rapid detection of single base mismatches in heteroduplexes on hydrolink gels. *Trends Genet.* 7: 5.
- Kelly, A., Alcalá-Jiménez, A.R., Bainbridge, B.W., Heale, J.B., Pérez-Artés, E. and Jiménez-Díaz, R.M. 1994. Use of genetic fingerprinting and random amplified polymorphic DNA to characterize pathotypes of *Fusarium oxysporum* f. sp. *ciceris* infecting chickpea. *Phytopathology* 84: 1293-1298.
- Kendrick, W.B. 1992. *The Fifth Kingdom*. 2<sup>nd</sup> ed. Waterloo, Ontario: Mycologue. 406 pp.
- Kent, M., and P. Coker. 1992. *Vegetation Description and Analysis: A Practical Approach*. CRC Press, Boca Raton, 363 pp.
- Kesik, T.J. and Lio, M. 1997. *Canadian Wood-Frame House Construction*. Ottawa: Canada Mortgage and Housing Corporation (CMHC). 303 pp.
- Klauss, A.K., Tull, R.H. Roots, L.M. and Pfafflin, J.R. 1970. History of changing concepts of ventilation requirements. *ASHRAE Journal* 12(6).

- Kluge, A.G. 1989. A concern for evidence and a phylogenetic hypothesis of relationships among *Epicurates* (Boidae, Serpentes). *Syst. Zool.* 38: 7-25.
- Knight, S.G. and Frazier, W.C. 1945. The effect of corn steep liquor ash on penicillin production. *Science* 102: 617-618.
- Koch, A.P. 1994. Fungal problems in buildings: the Danish experience. *In Building Mycology: Management of Decay and Health in Buildings*. J. Singh (ed.). London: Chapman & Hall. pp. 280-294.
- Koren, H.S., Graham, D.E., and Devlin, R.B. 1992. Exposure of humans to a volatile organic mixture. Inflammatory response, III. *Arch. Environ. Health* 47: 39-44.
- Kumeda, Y. and Asao, T. 1996. Single-strand conformation polymorphism analysis of PCR-amplified ribosomal DNA internal transcribed spacers to differentiate species of *Aspergillus* section *Flavi*. *Appl. Environ. Microbiol.* 62: 2947-2952.
- Latgé, J.P. and Paris, S. 1991. The fungal spores: reservoir of allergens. *In The Fungal Spores and Disease Initiation in Plants and Animals*. G.T. Cole and H.C. Hoch (eds). New York: Plenum Press. pp. 379-401.
- Law, H.-Y., Ong, J., Yoon, C.-S., Cheng, H., Tan, C.-L. and Ng, I. 1994. Rapid antenatal diagnosis of  $\beta$ -thalassemia in Chinese caused by the common 4-bp deletion in codons 41/42 using high resolution agarose electrophoresis and heteroduplex detection. *Biochem. Med. Metabol. Biol.* 53: 149-151.
- Li, D.-W. 1994. *Studies on Aeromycota in Kitchener-Waterloo, Ontario, Canada*. PhD Thesis, University of Waterloo. 218 pp.
- Li, D.-W. and W.B. Kendrick. 1994. Functional relationships between airborne fungal spores and environmental factors in Kitchener-Waterloo, Ontario, as detected by canonical correspondence analysis. *Grana* 33:166-176.
- Li, D.-W. and W.B. Kendrick. 1995. A year-round study on functional relationships of airborne fungi with meteorological factors. *Int. J. Biometeorol.* 39: 74-80.
- Licorish, K., H.S. Novey, P. Kozak, R.D. Fairshter and A.H. Wilson. 1985. Role of *Alternaria* and *Penicillium* spores in the pathogenesis of asthma. *J. Allergy Clin. Immunol.* 76: 819-825.
- Lin, J.-J., Kuo, J. and Ma, J. 1996. A PCR-based DNA fingerprinting technique: AFLP for molecular typing of bacteria. *Nucleic Acids Res.* 24: 3649-3650.
- Liu, Q. and Sommer, S.S. 1995. Restriction-endonuclease fingerprinting: a sensitive method for screening mutations in long, contiguous segments of DNA. *BioTechniques* 18: 470-477.
- Lobuglio, K.F., Pitt, J.I. and Taylor, J.W. 1993. Phylogenetic analysis of two ribosomal DNA regions indicates multiple independent losses of a sexual *Talaromyces* state among asexual *Penicillium* species in subgenus *Biverticillium*. *Mycol.* 85: 592-604.
- Louwagie, J., Delwart, E.L., Mullins, J.I., McCutchan, F.E., Eddy, G. and Burke, D.S. 1994. Genetic analysis of HIV-1 isolates from Brazil reveals presence of two distinct genetic subtypes. *AIDS Research and Human Retroviruses* 10: 561-567.
- Lowe, D.A. and Elander, R.P. 1983. Contribution of mycology to the antibiotic industry. *Mycol.* 75: 361-373.

- Lucretius, ca. 50 BC. *De rerum natura* [On the Nature of the Universe]. Translation by R. Melville. 1997. Oxford: Clarendon Press. 275 pp.
- Lustgraaf, B.v.d. and J.E.M.H. van Bronswijk. 1977. Fungi living in house dust. *Ann. Allergy* 39: 152.
- MacFarlane, G. 1979. *Howard Florey*. Oxford: Oxford University Press.
- MacFarlane, G. 1984. *Alexander Fleming. The Man and the Myth*. London: Chatto & Windus.
- MacPherson, J.M., Eckstein, P.E., Scoles, G.J. and Gajadhar, A.A. 1993. Variability of the random amplified polymorphic DNA assay among thermocyclers, and effects of primer and DNA concentration. *Mol. Cell Probes* 7: 293-299.
- Majer, D., Mithen, R., Lewis, B.G., Vos, P. and Oliver, R.P. 1996. The use of AFLP fingerprinting for the detection of genetic-variation in fungi. *Mycol. Res.* 100: 1107-1111.
- Makino, R., Sekiya, T. and Hayashi, K. 1992. F-SSCP: Fluorescence-based polymerase chain reaction-single-strand conformation polymorphism (PCR-SSCP) analysis. *PCR Methods Appl.* 2: 10-13.
- Mulazimoglu, L. and V.L. Yu. 1998. Legionella infection. In *Harrison's Principles of Internal Medicine*, 14<sup>th</sup> Ed., Chap. 153. pp 928-933. New York: McGraw-Hill.
- Mallea, M., M. Renard and J. Charpin. 1982. La flore fongique des habitations. *Rev. Fr. Mal. Resp.* 10: 121-130.
- Malloch, D.W. 1981. *Moulds: Their Isolation, Cultivation and Identification*. University of Toronto Press, Toronto, Canada. 97 pp.
- Marbuy, M.C. and Woods, J.E. 1991. Building-related illnesses. In *Indoor Air Pollution: A Health Perspective*. Samet, J.M. and Spengler, J.D. (eds) Baltimore: Johns Hopkins University Press. pp. 306-322.
- Marshal, R.D., Koontz, J. and Sklar, J. 1995. Detection of mutations by cleavage of DNA heteroduplexes with bacteriophage resolvases. *Nature Genet.* 9: 177-183.
- Martinelli, G., Trabetti, E., Farabegoli, P., Buzzi, M., Zaccaria, A., Testoni, N., Amabile, M., Casartelli, A., Devivo, A., Pignatti, P.F. and Tura, S. 1996. Fingerprinting of HLA-DQA by polymerase chain reaction and heteroduplex analysis. *Molec. Cell. Probes* 10: 123-127.
- Mashiyama, S., Sekiya, T. and Hayashi, K. 1990. Screening of multiple DNA samples for detection of sequence changes. *Technique* 2: 304-306.
- Matossian, M.K. 1989. *Poisons of the Past: Molds, Epidemics and History*. New Haven: Yale University Press. 190 pp.
- Maxam, A.M. & Gilbert, W. 1980. Sequencing end-labelled DNA with base-specific chemical cleavages. *Meth. Enzymol.* 65: 499-560.
- McGinnis, M.C. and L. Pasarell. 1992. Viability of fungal cultures maintained at -70°C. *J. Clin. Microbiol.* 30: 1000-1004.
- Meunier, J.-R. and Grimont, P.A.D. 1993. Factors affecting reproducibility of random amplified polymorphic DNA fingerprinting. *Res. Microbiol.* 144: 373-379.



- Meyer, W., Liecktfeldt, T., Kayser, T., Nürnberg, P., Epplen, J.T. and Börner, T. 1992. Fingerprinting fungal genomes with phage M13 DNA and oligonucleotide probes specific for simple repetitive DNA sequences. *Adv. Mol. Gen.* 5: 241-253.
- Miyamoto, M.M. and Fitch, W.M. 1995. Testing species phylogenies and phylogenetic methods with congruence. *Syst. Biol.* 44: 64-76.
- Micheli, M.R., Bove, R., Calissano, P. and D'Ambrosio, E. 1993. Random amplified polymorphic DNA fingerprinting using combinations of oligonucleotide primers. *BioTechniques* 15: 388-390.
- Miller, J.D. 1992. Fungi as contaminants in indoor air. *Atmospheric Environment, part A*, 26: 2163-2172.
- Miller, J.D., A.M. LaFlamme, Y. Sobel, P. Lafontaine and R. Greenblagh. 1988. Fungi and fungal products in Canadian homes. *Int. J. Biodeterioration* 74: 1115-1123.
- Miquel, P. 1883. Des organismes vivants de l'atmosphère. Thèse Fac. Méd. Paris.
- Mishra, S.K., L. Ajello, D.G. Ahern, H.A. Burge, V.P. Kurup, D.L. Pierson, D.L. Price, R.A. Samson, R.S. Sandhu, B. Shelton, R.B. Simmons and K.F. Switzer. 1992. Environmental mycology and its importance to public health. *J. Med. Veterin. Mycol.* 30 (suppl. 1): 287-305.
- Miyamoto, T., S. Oshima, K. Mizuno, M. Sasa and T. Ishizaki. 1969. Cross-antigenicity among six species of dust mites and house dust antigens. *J. Allergy.* 44: 228-238.
- Mohabeer, J.A., Hiti, A.L. and Martin, W.J. 1991. Non-radioactive single strand conformation polymorphism (SSCP) using the Pharmacia 'PhastSystem'. *Nucleic Acids Res.* 19: 3154.
- Moore, W.E.C. and L.V. Holdeman. 1974. Human fecal flora: the normal flora of 20 Japanese-Hawaiians. *Appl. Microbiol.* 27: 961-969.
- Morey, P.R. 1990. Practical aspects of sampling for organic dusts and microorganisms. *Am. J. Ind. Med.* 18: 273-278.
- Morgante, M. and Olivieri, A.M. 1993. PCR-amplified microsatellites as markers in plant genetics. *Plant J.* 3: 175-182.
- Moriyama, Y., N. Nawata, T. Tsuda and M. Nitta. 1992. Occurrence of moulds in Japanese bathrooms. *Internat. Biodet. Biodegrad.* 30: 47-55.
- Mueller, U.G., Lipari, S.E., Milgroom, M.G. 1996. Amplified fragment length polymorphism (AFLP) fingerprinting of symbiotic fungi cultured by the fungus-growing ant *Cyphomyrmex minutus*. *Molecular Ecology* 5: 119-122.
- Mullins, J. and McKnight, T.S. (eds). 1981. *Canadian Woods, Their Properties and Used*. 3<sup>rd</sup> ed. Toronto: University of Toronto Press.
- Mullis, K.B. 1990. Process for amplifying, detecting, and/or cloning nucleic acid sequences using a thermostable enzyme. US Patent 4,965,188.
- Muralidharan, K. and Wakeland, E.K. 1993. Concentration of primer and template qualitatively affects products in randomly-amplified polymorphic DNA PCR. *BioTechniques* 14: 362-364.

- Myers, R.M., Fischer, S.G., Maniatis, T. and Lerman, L.S. 1985. Nearly all single base substitutions in DNA fragments joined to a GC-clamp can be detected by denaturing gradient gel electrophoresis. *Nucleic Acids Res.* 13: 3111-3129.
- Nagamine, C.M., Chan, K. and Lau, Y-F.C. 1989. A PCR artifact: generation of heteroduplexes. *Am. J. Hum. Genet.* 45: 337-339.
- Nash, G.D. 1968. *United States Oil Policy, 1890-1964*. Pittsburgh: University of Pittsburgh Press. 286 pp.
- Nielsen, K.F. and Gravesen, S. 1999. Production of mycotoxins on water damaged building materials. In *Bioaerosols, Fungi and Mycotoxins*. E. Johannig (ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 423-431.
- Nilsby, I. 1949. Allergy to moulds in Sweden. *Acta Allergol.* 2: 57-90.
- Norbäck, D., M. Torgén and C. Edling. 1990. Volatile organic compounds, respirable dust and personal factors related to prevalence and incidence of sick building syndrome in primary schools. *Br. J. Ind. Med.* 47: 733-741.
- Offermans, M.T.C., Struyk, L., Degeus, B., Breedveld, F.C., Vandenelsen, P.J. and Rozing, J. 1996. Direct assessment of junctional diversity in rearranged t-cell receptor-beta chain encoding genes by combined heteroduplex and single-strand conformation polymorphism (SSCP) analysis. *J. Immunol. Meth.* 191: 21-31.
- Oka, T., Matsunaga, H., Tokunaga, K., Mitsunaga, S., Juji, T. and Yamane, A. 1994. A simple method for detecting single base substitutions and its application to HLA-DPB1 typing. *Nucleic Acids Res.* 22: 1541-1547.
- Orita, M., Iwahana, H., Kanazawa, H., Hayashi, K. and Sekiya, T. 1989a Detection of polymorphisms of human DNA by gel electrophoresis as single-strand conformation polymorphisms. *Proc. Natl. Acad. Sci. USA* 86: 2766-2770.
- Orita, M., Suzuki, Y., Sekiya, T. and Hayashi, K. 1989b Rapid and sensitive detection of point mutations and DNA polymorphisms using the polymerase chain reaction. *Genomics* 5: 874-879.
- Ostrowski, R. 1999. *Exposure Assessment of Moulds in Indoor Environments in Relation to Chronic Respiratory Diseases*. Doctoral Thesis, Aachen, Germany.
- Park, H.-S., Jung, K.-S., Kim, S.O. and Kim, S.J. 1994. Hypersensitivity pneumonitis induced by *Penicillium expansum* in a home environment. *Clin. Exp. Allergy* 24: 383-385.
- Pasteur, L. 1861. Mémoire sur les corpuscules organisés qui existent dans l'atmosphère. Examen de la doctrine des générations spontanées. *Ann. Sci. Nat. Paris* 4(16): 5-98.
- Payne, R. 1981. Houses and structures. In *Canadian Woods, Their Properties and Uses*. 3<sup>rd</sup> Ed. Mullins, J. and McKnight, T.S. (eds). Toronto: University of Toronto Press. pp. 265-284.
- Penner, G.A., Bush, A., Wise, R., Kim, W., Domier, L., Kasha, K., Laroche, A., Scoles, G., Molnar, S.J. and Fedak, G. 1993. Reproducibility of random amplified polymorphic DNA (RAPD) analysis among laboratories. *PCR Methods Appl.* 2: 341-345.
- Pepys, J. 1969. Hypersensitivity diseases of the lungs due to fungal and organic dusts. *Monographs in Allergy*, Vol. 4.

- Peterson, S.W. 2000. Phylogenetic analysis of *Penicillium* species based on ITS and LSU-rDNA nucleotide sequences. pp. 163-178. In *Integration of Modern Taxonomic Methods for Penicillium and Aspergillus Classification*. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers.
- Pitt, J.I. 1979. *The Genus Penicillium and its Teleomorphic States Eupenicillium and Talaromyces*. New York: Academic Press. 634 pp.
- Pitt, J.I. 1985. Inherent problems in *Penicillium* taxonomy. In *Advances in Penicillium and Aspergillus Systematics*. R.A. Samson and J.I. Pitt (eds). New York: Plenum Press. pp 155-161.
- Pitt, J.I. 1988. *A Laboratory Guide to Common Penicillium Species*. North Ryde, N.S.W.: Commonwealth Scientific and Industrial Research Organization, Division of Food Processing. 187 pp.
- Pitt, J.I. and A.D. Hocking. 1999. *Fungi and Food Spoilage*. 2<sup>nd</sup> Edn. Gaithersburg, Maryland: Chapman and Hall. 593 pp.
- Pitt, J.I. and Cruikshank, R.H. 1990. Speciation and synonymy in *Penicillium* subgenus *Penicillium* -- towards a definitive taxonomy. In *Modern Concepts in Penicillium and Aspergillus classification*. R.A. Samson and J.I. Pitt (eds). New York: Plenum Press. pp 103-119.
- Pitt, J.I. and R.A. Samson. 1993. Species names in current use in the Trichocomaceae. In *Names in Current Use in the Families Trichocomaceae, Cladoniaceae, Pinaceae and Lemnaceae (NCU-2)*. W. Greuter (Ed). Regnum Vegetabile 128: 13-57.
- Platt, S.D., C.J. Martin, S.M. Hunt and C.W. Lewis. 1989. Damp housing, mould growth and symptomatic health state. Br. Med. J. 298: 1673-1678.
- Pope, A.M., Patterson, R. and Burge, H. (eds.). 1993. *Indoor Allergens: Assessing and Controlling Adverse Health Effects*. Committee on the Health Effects of Indoor Allergens. Division of Health Promotion and Disease Prevention. Institute of Medicine. Washington D.C.: National Academy Press. 308 pp.
- Prosser, J. 1993. Detecting single base mutations. Trends. Biol. Technol. 11: 238-246.
- Pulyaeva, H., Zakharov, S.F., Garner, M.M. and Chrambach, A. 1994. Detection of a single base mismatch in double-stranded DNA by electrophoresis on uncrosslinked polyacrylamide gel. Electrophoresis 15: 1095-1100.
- Raper, K.B., and Thom, C. 1949. *A Manual of the Penicillia*. Baltimore, Maryland: Williams and Wilkins. 875 pp.
- Raunkiaer, C. 1934. *The Life Forms of Plants and Statistical Plant Geography*. Oxford: Oxford University Press. 632 pp.
- Ravniklavac, M., Glavac, D. and Dean, M. 1994. Sensitivity of single-strand conformational polymorphism and heteroduplex method for mutation detection in the cystic fibrosis gene. Human Molec. Genet. 3: 801-807.
- Reymann, F. and M. Schwartz. 1947. Home dust and fungus allergy. Acta Pathol. Microbiol. Scand. 24: 76-85.
- Richards, M. 1954. Atmospheric mold spores in and out of doors. J. Allergy 25: 429-439.
- Riedy, M.F., Hamilton W.J. III and Aquadro, C.F. 1992. Excess of non-parental bands in offspring from known primate pedigrees assayed using RAPD PCR. Nucleic Acids Res. 20: 918.

- Ripe, E. 1962. Mold allergy. I. An investigation of the airborne fungal spores in Stockholm, Sweden. *Acta Allergol.* 18: 130-159.
- Rodricks, J., Hesseltine, C.W. and Mehlman, M.A. 1977. *Mycotoxins in human and animal health*. Park Forest South, Illinois: Pathotox Publishers, 807 pp.
- Rodrigo, A.G., Kellyborges, M., Bergquist, P.R. and Bergquist, P.L. 1993. A randomisation test of the null hypothesis that two cladograms are sample estimated of a parametric phylogenetic tree. *New Zealand J. Bot.* 31: 257-268.
- Rosendahl, S. 1999. Population structure of clonal fungi (Abstract MOP4.2) 9<sup>th</sup> Congress of the International Union of Microbiological Societies, Sydney, Australia, August 16-20, 1999.
- Rylander, R. 1999. Effects after mold exposure -- which are the causative agents? In *Bioaerosols, Fungi and Mycotoxins*. E. Johannig (Ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp. 28-32
- Ryman, S. and Holmåsen, I. 1998. *Svampar, En fälthandbok*. Stockholm: Interpublishing. 718 pp.
- Ryskov, A.P. 1999. Multilocus DNA fingerprinting in the genetic studies of biodiversity. *Mol. Biol.* 33: 880-892.
- Saad, R.R. and A.A. El-Gindy. 1990. Fungi of the house dust in Riyadh, Saudi Arabia. *Zentralbl. Mikrobiol.* 145: 65-68.
- Saiki, R.K., Gelfand, D.H., Stoffel, S., Scharf, S.J., Higuchi, R., Hory, G.T., Mullis, K.B. and Erlich, H.A. 1988. Primer directed enzymatic amplification of DNA with a thermostable DNA polymerase. *Science* 239: 487-491.
- Saiki, R.K., Scharf, S., Faloona, F., Mullis, K.B., Horn, G.T., Erlich, H.A. and Arnheim, N. 1985. Enzymatic amplification of beta-globulin genomic sequences and restriction site analysis for diagnosis of sickle cell anemia. *Science* 230: 1350-1354.
- Sakamoto, T., A. Urisu, M. Yamada, Y. Matsuda, K. Tanaka and S. Torii. 1989. Studies on the osmophilic fungus *Wallemia sebi* as an allergen evaluated by the skin prick test and radioallergosorbent test. *Int. Arch. Allergy Appl. Immunol.* 90: 368-372.
- Sambrook, J., E.F. Fritsch and T. Maniatis. 1989. *Molecular Cloning. A Laboratory Manual*. 2nd ed. Cold Spring Harbor Laboratory Press, New York. Vols 1-3.
- Samet, J.M., M.C. Marbury and J.D. Spengler. 1988. Health effects and sources of indoor air pollution. Part II. *Am. Rev. Respir. Dis.* 137: 221-242.
- Samet, J.M. and Spengler, J.D. (eds) 1991. *Indoor Air Pollution: A Health Perspective*. Baltimore: Johns Hopkins University Press. 407 pp.
- Samson, R.A. 1985. Dialogue following paper presented by Williams et al. The closely related species of subgenus *Penicillium* - a phylogenic exploration. In *Advances in Penicillium and Aspergillus Systematics*. R.A. Samson and J.I. Pitt (eds). New York: Plenum Press. p. 127.
- Samson, R.A., Flannigan, B., Flannigan, M.E., Verhoeff, A.P., Adan, O.C.G. and Hoekstra, E.S. (eds). 1994. Recommendations. In *Health Implications of Fungi in Indoor Environments*. Air Quality Monographs 2. Amsterdam: Elsevier. pp. 531-538.

- Samson, R.A., Hadlok, R. and Stolk, A.C. 1977. A taxonomic study of the *Penicillium chrysogenum* series. *Antonie van Leeuwenhoek* 43: 169-175.
- Samson, R.A., Hoekstra, E.S., Frisvad, J.C. and Filtenborg, O. 1996. *Introduction to Food-Borne Fungi*. 5<sup>th</sup> Edn. Baarn, The Netherlands: Centraalbureau voor Schimmelcultures. 322 pp.
- Samson, R.A. and B.v.d. Lustgraaf. 1978. *Aspergillus penicilloides* and *Eurotium halophilicum* in association with house-dust mites. *Mycopathol.* 64: 13-16.
- Samson, R.A. and E.S. van Reenen-Hoekstra. 1988. *Introduction to Food-Borne Fungi*. 3rd ed., Baarn, The Netherlands: Centraalbureau voor Schimmelcultures.
- Sanger, F., Nicklen, S. & Coulson, A.R. 1977. DNA sequencing with chain terminating inhibitors. *Proc. Natl. Acad. Sci. USA* 74: 5463-5467.
- Savage, D.A., Wood, N.A.P., Bidwell, J.L., Fitches, A., Old, J.M. and Hui, K.M. 1995. Detection of beta-thalassemia mutations using DNA heteroduplex generator molecules. *Brit. J. Haematol.* 90: 564-571.
- Savelkoud, P.H., Aarts, H.J., de Haas, J., Dijkshoorn, L., Duim, B., Otsen, M., Rademaker, J.L., Schouls, L. and Lenstra, J.A. 1999. Amplified-fragment length polymorphism analysis: the state of an art. *J. Clin. Microbiol.* 37: 3083-3091.
- Savolainen, J., Viander, R., Einarsson, R. and Koivikko, A. 1990. Immunoblotting analysis of concanavalin A isolated allergens of *Candida albicans*. *Allergy* 45: 40-46.
- Schiefer, H.B. 1986. Health effects from mycotoxins (volatile or absorbed to particulates): a review of the relevant data in animal experiments. In: Significance of fungi in indoor air: Report of a working group. Health and Welfare Canada Working Group on Fungi and Indoor Air. 18 pp.
- Schierwater, B. and Ender, A. 1993. Different DNA polymerases may amplify different RAPD products. *Nucleic Acids Res.* 21: 4647-4648.
- Schober, G. 1991. Fungi in carpeting and furniture dust. *Allergy* 46: 639-643.
- Schönian, G., Meunsel, O., Tietz, H.-J., Meyer, W., Gräser, Y., Tausch, I., Presber, W. and Mitchell, T.G. 1993. Identification of clinical strains of *Candida albicans* by DNA fingerprinting with polymerase chain reaction. *Mycoses* 36: 171-179.
- Schlebeker, J.T. 1960. The world metropolis and the history of American agriculture. *J. Econom. Hist.* 20: 187-208.
- Scott, J.A. and Straus, N.A. 2000. A review of current methods in DNA fingerprinting. pp. 209-224. *In Integration of Modern Taxonomic Methods for Penicillium and Aspergillus Classification*. R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers.
- Scott, J.A., Straus, N.A. and Wong, B. 1999a. Heteroduplex fingerprinting of *Penicillium brevicompactum* from house dust. *In Bioaerosols, Fungi and Mycotoxins*. E. Johannig (Ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 335-342.
- Scott, J.A., Straus, N.A. and Malloch, D. 1999b. Molecular genetic characterization of variability in *Penicillium chrysogenum* from indoor environments. (Abstract MOS5.6) 9<sup>th</sup> Congress of the International Union of Microbiological Societies, Sydney, Australia, August 16-20, 1999.

- Scott, R. 1968. Blue veined cheese. *Proc. Biochem.* 3: 11.
- Seifert, K.A. and Frisvad, J.C. 2000. *Penicillium* on wood products. pp. 285-298 *In Integration of Modern Taxonomic Methods for Penicillium and Aspergillus Classification.* R.A. Samson and J.I. Pitt (eds). Amsterdam: Harwood Academic Publishers.
- Selwyn, S. 1980. The discovery and evolution of penicillins and cyclosporins. *In The Beta-lactam Antibiotics Penicillins and Cephalosporins in Perspective.* S. Selwyn (Ed.). pp 1-55. London: Hodder and Straughton.
- Sheffield, V.C., Beck, J.S. and Stone, E.M. 1992. A simple and efficient method for attachment of a 40-base pair GC-rich sequence to PCR-amplified DNA. *Biofeedback* 12: 386-387.
- Sheffield, V.C., Beck, J.S., Kwitek, A.E., Sandstrom, D.W. and Stone, E.M. 1993. The sensitivity of single-strand conformation polymorphism analysis for the detection of single-base substitutions. *Genomics* 16: 325-332.
- Sheffield, V.C., Cox, D.R., Lerman, L.S. and Myers, R.M. 1989. Attachment of a 40-base-pair G+C-rich sequence (GC-clamp) to genomic DNA fragments by the polymerase chain reaction results in improved detection of single-base changes. *Proc. Natl. Acad. Sci. USA* 86: 232-236.
- Sherman, H. and D. Merksamer. 1964. Skin test reactions to mold sensitive patients in relation to presence of molds in their homes. *New York State J. Med.* 64: 2533-2535.
- Shields, G.F. and Straus, N.A. 1975. DNA-DNA hybridization studies of birds. *Evolution* 29: 159-166.
- Simpson, B.B. and Ogorzaly, M.C. 1986. *Economic Botany: Plants in our World.* New York: McGraw-Hill. 640 pp.
- Singh, J. (ed.). 1994. *Building Mycology: Management of Decay and Health in Buildings.* London: Chapman & Hall. 326 pp.
- Sinha, R.N., J.E.M.H. van Bronswijk and H.A.H. Wallace. 1970. House dust mites and their fungal associations. *Can. Med. Assoc. J.* 103: 300-301.
- Skouboe, P., Frisvad, J.C., Taylor, J.W., Lauritsen, D., Boysen, M. and Rossen, L. 1999. Phylogenetic analysis of nucleotide sequences from the ITS region of terverticillate *Penicillium* species. *Mycol. Res.* 103: 873-881.
- Slater, C. 1997. General Motors ad the demise of streetcars. *Transportation Quarterly* 51: 45-66.
- Smith, V., Streifel, A., Rhame, F.S. and Juni, B. 1988. Potted plant fungal spores shedding (Abstr.). *Ann. Meeting Amer. Soc. Microbiol.* p. 414.
- Smouse, P.E. and Chevillon, C. 1998. Analytical aspects of population-specific DNA fingerprinting for individuals. *J. Hered.* 89: 143-150.
- Sohn, U.-I., Rothfels, K.H. and Straus, N.A. 1975. DNA:DNA hybridization studies in black flies. *J. Molec. Evol.* 5: 75-85.
- Soll, D.R. 2000. The ins and outs of DNA fingerprinting the infectious fungi. *Clin. Microbiol. Rev.* 13: 332-370.
- Sorenson, W.G., D.G. Frazer, B.B. Jarvis, J. Simpson and V.A. Robinson. 1987. Trichothecene mycotoxins in aerosolized conidia of *Stachybotrys atra*. *Appl. Environ. Microbiol.* 53: 1270-1375.

- Soto, D. and Sukumar, S. 1992. Improved detection of mutations in the p53 gene human tumors as single-stranded conformation polymorphisms and double-stranded heteroduplex DNA. *PCR Methods Appl.* 2: 96-98.
- Spinardi, L., Mazars, R. and Theillet, C. 1991. Protocols for an improved detection of point mutations by SSCP. *Nucleic Acids Res.* 19: 4009.
- Stetzenbach, L., Buttner, M. and Cruz-Perez, P. 1999. Fungal spores aerosolised from contaminated flooring materials. (Abstr #243). American Industrial Hygiene Association Conference, Toronto, Ontario, June 5-11, 1999.
- Stotzky, G. and S. Schenck. 1976. Volatile organic compounds and microorganisms. *CRC Critical Rev. Microbiol.* 4: 333-382.
- Strachan, D.P. 1988. Damp housing and childhood asthma: validation of reporting symptoms. *Brit. Med. J.* 297: 1223-1226.
- Strachan, D.P., B. Flannigan, E.M. McCabe and F. McGarry. 1990. Quantification of airborne moulds in the homes of children with and without wheeze. *Thorax*: 382-387.
- Stratakis, C.A., Orban, Z., Burns, A.L., Vottero, A., Mitsiades, C.S., Marx, S.J., Abbassi, V. and Chrousos, G.P. 1996. Dideoxyfingerprinting (ddf) analysis of the type-x collagen gene (col10a1) and identification of a novel mutation (s671p) in a kindred with schmid metaphyseal chondrodysplasia. *Biochem. Molec. Med.* 59: 112-117.
- Straus, N.A., Scott, J.A. and Wong, B. 1999. The trichodiene synthase gene from *Stachybotrys chartarum*. A potential diagnostic indicator of indoor contamination. In *Bioaerosols, Fungi and Mycotoxins*. E. Johanning (Ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 343-350.
- Su, H.J., A. Rotnitzky, H.A. Burge and J. Spengler. 1992. Examination of fungi in domestic interiors by using factor analysis: correlations and associations with home factors. *Appl. Environ. Microbiol.* 58: 181-186.
- Summerbell, R.C. 1998. Taxonomy and ecology of *Aspergillus* species associated with colonizing infections of the respiratory tract. *Immunol. Allergy Clin. N. Amer.* 18: 549-573.
- Summerbell, R.C., Staib, F., Dales, R., Nolard, N., Kane, J., Zwanenburg, H., Burnett, R., Krajdén, S., Fung, D. and Leong, D. 1992. Ecology of fungi in human dwellings. *J. Med. Veterin. Mycol.* 30 (suppl. 1):279-285.
- Summerbell, R.C., Krajdén, S. and Kane, J. 1989. Potted plants in hospitals as reservoirs of pathogenic fungi. *Mycopathol.* 106: 13-22.
- Sunesson, A.-L., Vaes, W.H.J., Nilsson, C.-A., Blomquist, G., Andersson, B. and Carlson, R. 1995. Identification of volatile metabolites from five fungal species cultivated on two media. *Appl. Environ. Microbiol.* 61: 2911-2918.
- Sussman, A.S. 1968. Longevity and survivability of fungi. In *The Fungi: An Advanced Treatise*. G.C. Ainsworth and A.S. Sussman (eds). New York: Academic Press. pp. 447-476.
- Suzuki, Y., Orita, M., Shiraishi, M., Hayashi, K. and Sekiya, T. 1990. Detection of *ras* gene mutations in human lung cancers by single-strand conformation polymorphism analysis of polymerase chain reaction products. *Oncogene* 5: 1037-1043.

- Swaeby, M.A. and C.M. Christensen. 1952. Molds in house dust, furniture stuffing, and in the air within homes. *J. Allergy* 23: 370-374.
- Takishima, Y., Shimura, J. Udagawa, Y and Sugawara, A. 1989. *Guide to World Data Center on Microorganisms with a List of Culture Collections in the World*. Saitama, Japan.
- Taylor, J.W., Jacobson, D.J. and Fisher, M.C. 1999. The evolution of asexual fungi: reproduction, speciation and classification. *Ann. Rev. Phytopathol.* 37: 197-246.
- Testa, C. 1990. Indoor air pollution: Remedies and pitfalls. *In Indoor Air '90*, Proceedings of the 5<sup>th</sup> International Conference on Indoor Air Quality and Climate, Toronto, Ontario, July 29-August 3, 1990. D.S. Walkinshaw (ed). pp. 325-327.
- Thom, C. 1910. Cultural studies of species of *Penicillium*. Bureau of Animal Industry, Bulletin No. 118. Washington, D.C.: USDA. 108 pp.
- Thom, C. 1930. *The Penicillia*. Baltimore: Williams and Willkins. 643 pp.
- Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F. and Higgins, D.G. 1997. The Clustal X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24: 4876-4882.
- Tobin, R.S., E. Baranowski, A.P. Gilman, T. Kuiper-Goodman, J.D. Miller and M. Giddings. 1987. Significance of fungi in indoor air: report of a working group. *Can. J. Public Health* 78 (suppl.): s1-s14.
- Tommerup, I.C., Barton, J.E., O'Brien, P.A. 1995. Reliability of RAPD fingerprinting of three basidiomycete fungi *Laccaria*, *Hydnangium*, and *Rhizogtonia*. *Mycol. Res.* 99: 179-186.
- Tovey, R.E., Chapman, M.D., Wells, C.W. and Platts-Mills, T. 1981. The distribution of dust mite allergen in the houses of patients with asthma. *Amer. Rev. Resp. Dis.* 124: 630-635.
- Tsai, S.M., Yang, C.S. and Heinsohn, P. 1999. Comparative studies of fungal media for the recovery of *Stachybotrys chartarum* from environmental samples. *In Bioaerosols, Fungi and Mycotoxins*. E. Johanning (Ed.). Proceedings of the Third International Conference on Fungi, Mycotoxins and Bioaerosols. Saratoga Springs, New York. September 23-25, 1998. Albany, New York: Eastern New York Occupational and Environmental Health Center. pp 330-334.
- Untereiner, W.A., N.A. Straus and D.W. Malloch. 1995. A molecular-morphotaxonomic approach to the systematics of the Herpotrichiellaceae and allied black yeasts. *Mycol. Res.* 99: 897-913.
- Verhoeff, A.P., Wijnen, J.H. van, Reenen-Hoekstra, E.S. van, Samson, R.A., Strein, R.T. van and Brunekreef, B. 1994 Fungal propagules in house dust. II. Relation with residential characteristics and respiratory symptoms. *Allergy* 49: 540-547.
- Vilgalys, R., and Hester, M. 1990. Rapid generic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *J. Bacteriol.* 172: 4238-4246.
- Vos, P., Hojers, R., Bleeker, M., Reijans, M., van de Lee, T., Hornes, M., Frijters, A., Pot, J., Peleman, J., Kuiper, M. and Zabeau, M. 1995. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res.* 23: 4407-4414.



- Wack, A., Montagna, D., Dellabona, P. and Casorati, G. 1996. An improved PCR-heteroduplex method permits high-sensitivity detection of clonal expansions in complex t-cell populations. *J. Immunol. Meth.* 196: 181-192.
- Wang, Y.-H., Barker, P. and Griffith, J. 1992. Visualization of diagnostic heteroduplex DNAs from cystic fibrosis deletion heterozygotes provides an estimate of the kinking of DNA by bulged bases. *J. Biol. Chem.* 267: 4911-4915.
- Warner, S.B. 1995. *The Urban Wilderness: A History of the American City*. Berkeley: University of California Press.
- Weising, K., Nybom, H., Wolff, K. and Meyer, W. 1995. DNA fingerprinting in plants and fungi. CRC Press, Boca Raton. 322 pp.
- Weissman, D.N. and M.R. Schuyler. 1991. Biological agents and allergic diseases. *In: Indoor Air Pollution: a Health Perspective*. J.M. Stamets and J.D. Spengler (eds.). Johns Hopkins University Press, Baltimore. pp. 285-306.
- Weitzman, I., and M. Silva-Hutner. 1967. Non-keratinous agar media as substrates for the ascigerous state in certain members of the Gymnoascaceae pathogenic for man and animals. *Sabouraudia* 5: 335-340.
- Welsh, J. and McClelland, M. 1990. Fingerprinting genomes using PCR with arbitrary primers. *Nucleic Acids Res.* 18: 7213-7218.
- Welsh, J. and McClelland, M. 1991. Genomic fingerprinting using arbitrary primers PCR and a matrix of pairwise combinations of primers. *Nucleic Acids Res.* 19: 5275-5279.
- Westling, R. 1911. Über die grünen Spezies der Gattung *Penicillium*. *Ark. Bot.* 11: 1-156.
- White, M.B., Carvalho, M., Derse, D., O'Brien, S.J. and Dean, M. 1992. Detecting single-base substitutions as heteroduplex polymorphisms. *Genomics* 12: 301-306.
- White, T.J., Arnheim, N. and Erlich, H.A. 1989. The polymerase chain reaction. *Trends Genet.* 5: 185-189.
- White, T.J., T. Bruns, S. Lee and J. Taylor. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. *In: PCR Protocols. A Guide to Methods and Applications*. M.A. Innis, D.H. Gelfand, J.J. Sninsky and T.J. White (eds.). Academic Press, San Diego. pp. 315-324.
- Wickman M., S. Gravesen, S.L. Nordvall, G. Pershagen and J. Sundell. 1992. Indoor viable dust-bound microfungi in relation to residential characteristics, living habits, and symptoms in atopic and control children. *J. Allergy Clin. Immunol.* 89: 752-759.
- Williams, A.P., Pitt, J.I. and Hocking, A.D. 1985. The closely related species of subgenus *Penicillium* - a phylogenetic exploration. *In: Advances in Penicillium and Aspergillus Systematics*. R.A. Samson and J.I. Pitt (eds). New York: Plenum Press. pp. 121-128.
- Williams, J.G.K., Kubelik, A.R., Livak, K.J., Rafalski, J.A. and Tingey, S.V. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Res.* 18: 6531-6535.
- Williams, T.I. 1984. *Howard Florey. Penicillin and After*. Oxford: Oxford University Press.
- Williamson, P.R. 1997. Laccase and melanin in the pathogenesis of *Cryptococcus neoformans*. *Frontiers in Bioscience* 2, e99-107.

- Wilson, J.J., Polyak, S.J., Day, T.D. and Gretch, D.R. 1995. Characterization of simple and complex hepatitis C virus quasispecies by heteroduplex gel shift analysis: correlation with nucleotide sequencing. *J. Gen. Virol.* 76: 1763-1771.
- Winter, E., Yamamoto, F., Almoguera, C. and Perucho, M. 1985. A method to detect and characterize point mutations in transcribed genes: Amplification and overexpression of the mutant c-Ki-*ras* allele in human tumor cells. *Proc. Natl. Acad. Sci. USA.* 82: 7575-7579.
- Wood, N., Standen, G., Hows, J., Bradley, B. and Bidwell, J. 1993. Diagnosis of sickle-cell disease with a universal heteroduplex generator. *Lancet* 342: 1519-1520.
- Woods, J.E. 1988. "Air Quality" *In Encyclopedia of Architectures: Design Engineering and Construction.* Vol 1. New York: Wiley & Sons.
- Wyllie, T.D. and L.G. Morehouse (eds.). 1977. *Mycotoxic Fungi, Mycotoxins and Mycotoxicoses. An Encyclopedic Handbook.* Marcel Dekker, Inc., New York.
- Xing, Y., Wells, R.L. & Elking, M.M. 1996. Nonradioisotopic PCR heteroduplex analysis: a rapid, reliable method of detecting minor gene mutations. *BioTechniques* 21: 186-187.
- Yaglou, C.P.E., Riley, C. and Coggins, D.I. 1936. Ventilation requirements. *ASHVE Trans.* 42.
- Yu, K. and Pauls, K.P. 1992. Optimization of the PCR program for RAPD analysis. *Nucleic Acids Res.* 20: 2606.
- Yu, V.L. 2000. *Legionella pneumophila* (Legionnaire's Disease). *In Principles and Practice of Infectious Disease.* Mandell, G.L., Bennett, J.E. and R.Dolin (eds.), Chap. 221, pp 2424-2435. Philadelphia: Churchill Livingstone.
- Zabeau, M. and Vos, P. 1993. Selective restriction fragment amplification: a general method for DNA fingerprinting. European Patent Office, publication 0 534 858 A1.
- Zakharov, S.F. and Chrambach, A. 1994. The relative separation efficiencies of highly concentrated, uncrosslinked or low-crosslinked polyacrylamide gels compared to conventional gels of moderate concentration and crosslinking. *Electrophoresis* 15: 1101-1103.
- Zhang, Q.J. and Minoda, K. 1996. Detection of congenital color-vision defects using heteroduplex-SSCP analysis. *Japanese J. Ophthalmol.* 40: 79-85.

## **APPENDICES**

## **APPENDIX A**

### **SUMMARY OF RESULTS OF BROADLOOM DUST CULTURES FROM WALLACEBURG HOUSES**

---

HN indicates "house number"

G+/- indicates the presence/ absence of 10% glycerol in the isolation medium

Viable fungal levels are expressed as CFU/g dust

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
1	Alternaria alternata	2830		3	Penicillium citrinum	1415	
1	Alternaria tenuissima	1603	+	3	Penicillium corylophilum	471	
1	Alternaria tenuissima	471		3	Penicillium spinulosum	471	
1	Aspergillus niger	47	+	3	Phoma herbarum	943	
1	Aspergillus sydowii	471		3	Phoma sp.	943	
1	Aureobasidium pullulans	1886		3	Trichoderma viride	1415	
1	Chaetomium globosum	471		3	Ulocladium chartarum	943	+
1	Epicoccum nigrum	6603		3	unknown	9905	
1	Epicoccum nigrum	2358	+	3	unknown	5660	+
1	Mucor racemosus	235	+	3	yeast	147169	
1	Penicillium corylophilum	471	+	4	Alternaria alternata	50471	
1	Penicillium expansum	1462	+	4	Alternaria alternata	471	+
1	Penicillium sp. #1	2358		4	Aspergillus candidus	471	
1	Penicillium sp. #13	47	+	4	Aspergillus flavus	943	+
1	Penicillium spinulosum	1509	+	4	Aspergillus flavus	471	
1	Penicillium spinulosum	471		4	Aspergillus glaucus	471	+
1	Penicillium viridicatum	518	+	4	Aspergillus niger	4245	+
1	Penicillium viridicatum	471		4	Aspergillus niger	3301	
1	Pithomyces chartarum	471		4	Epicoccum nigrum	1886	
1	Pithomyces chartarum	471	+	4	Epicoccum nigrum	943	+
1	unknown	4716		4	Eurotium herbariorum	3301	+
1	unknown	3301	+	4	Eurotium sp.	471	+
1	yeast	9433		4	Fusarium sp.	471	
2	Alternaria alternata	7075		4	Fusarium sp.	471	+
2	Alternaria alternata	141	+	4	Mucor circinelloides	471	
2	Alternaria sp.	1415		4	Mucor hiemalis	471	
2	Alternaria tenuissima	3537	+	4	Mucor plumbeus	471	
2	Aspergillus glaucus	1179	+	4	Mucor racemosus	471	
2	Aureobasidium pullulans	2830		4	Penicillium chrysogenum	2830	+
2	Aureobasidium pullulans	566	+	4	Penicillium citrinum	471	
2	Curvularia protuberata	471	+	4	Penicillium expansum	471	+
2	Epicoccum nigrum	1886		4	Penicillium sp. #1	471	
2	Penicillium atramentosum	94	+	4	Penicillium sp. #26	471	
2	Penicillium chrysogenum	1037	+	4	Penicillium spinulosum	10377	+
2	Penicillium chrysogenum	471		4	Penicillium spinulosum	6132	
2	Penicillium citrinum	471		4	Phoma herbarum	471	
2	Phoma herbarum	1415		4	Rhizopus oryzae	943	
2	Ulocladium chartarum	566	+	4	Stemphylium solani	943	+
2	unknown	7547		4	unknown	2358	
2	unknown	2783	+	4	unknown	471	+
2	yeast	3773		4	yeast	15094	
3	Alternaria alternata	1415		5	Alternaria alternata	1415	
3	Alternaria alternata	943	+	5	Alternaria sp.	943	
3	Alternaria sp.	1415		5	Alternaria tenuissima	1886	+
3	Aspergillus candidus	471	+	5	Aspergillus glaucus	471	+
3	Aspergillus flavus	943		5	Aspergillus niger	1415	
3	Aspergillus fumigatus	8962	+	5	Aspergillus sydowii	943	+
3	Aspergillus fumigatus	3301		5	Aureobasidium pullulans	18396	
3	Aspergillus glaucus	471	+	5	Aureobasidium pullulans	8018	+
3	Aspergillus ochraceus	943	+	5	Chrysosporium sp.	2358	+
3	Aspergillus terreus	2358	+	5	Cladosporium cladosporioides	471	
3	Aspergillus terreus	943		5	Cladosporium sp.	943	
3	Aureobasidium pullulans	3773		5	Epicoccum nigrum	471	
3	Aureobasidium pullulans	2358	+	5	Eurotium herbariorum	471	
3	Chrysosporium sp.	3773		5	Eurotium herbariorum	471	+
3	Chrysosporium sp.	471	+	5	Eurotium sp.	471	+
3	Cladosporium cladosporioides	471		5	Mucor plumbeus	471	
3	Mucor racemosus	471	+	5	Penicillium atramentosum	471	
3	Penicillium atramentosum	471	+	5	Penicillium atramentosum	471	+
3	Penicillium chrysogenum	1415	+	5	Penicillium citrinum	471	
3	Penicillium chrysogenum	471		5	Penicillium commune	1415	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
5	Penicillium corylophilum	1415	+	8	Penicillium aurantiogriseum	4743	+
5	Penicillium expansum	3773	+	8	Penicillium chrysogenum	15685	
5	Penicillium expansum	943		8	Penicillium chrysogenum	9505	+
5	Penicillium sp. #26	943		8	Penicillium decumbens	9523	+
5	Penicillium sp. #26	471	+	8	Penicillium decumbens	3796	
5	Penicillium spinulosum	1886	+	8	Penicillium spinulosum	476	
5	Penicillium spinulosum	943		8	Phoma herbarum	474	
5	Phoma herbarum	471		8	unknown	28553	+
5	Pithomyces chartarum	471	+	8	yeast	6185	
5	Scopulariopsis brevicaulis	471	+	10	Acremonium sp.	4901	
5	unknown	4245	+	10	Alternaria alternata	4970	
5	unknown	1415		10	Alternaria tenuissima	4901	+
5	yeast	8962		10	Aspergillus sp.	4901	
6	Alternaria alternata	4725	+	10	Aspergillus versicolor	4901	
6	Aspergillus fumigatus	4672	+	10	Aureobasidium pullulans	4901	
6	Aspergillus versicolor	4672	+	10	Aureobasidium pullulans	4901	+
6	Aureobasidium pullulans	9345	+	10	basidiomycete	24509	+
6	Cladosporium chlorocephalum	9345	+	10	basidiomycete	4970	
6	Cladosporium macrocarpum	7556		10	Chrysosporium sp.	14774	+
6	Cladosporium sp.	4672	+	10	Chrysosporium sp.	4970	
6	Cladosporium sphaerospermum	51931	+	10	Cladosporium sphaerospermum	19812	+
6	Epicoccum nigrum	4725		10	Diplococcium spicatum	24850	
6	Epicoccum nigrum	4725	+	10	Epicoccum nigrum	24850	
6	Eurotium herbariorum	9398	+	10	Epicoccum nigrum	19744	+
6	Paecilomyces variotii	14018		10	Exophiala jeanselmei	49701	+
6	Penicillium expansum	9345	+	10	Exophiala jeanselmei	14910	
6	Phoma herbarum	4672	+	10	Fusarium sp.	9872	
6	unknown	79704	+	10	Geomyces pannorum	14910	+
6	unknown	18797		10	Geomyces pannorum	9803	
6	Wallemia sebi	4672	+	10	Hortaea werneckii	14910	
6	yeast	37701		10	Monascus ruber	9803	
7	Alternaria alternata	52228		10	Penicillium chrysogenum	19676	
7	Alternaria alternata	458	+	10	Penicillium citreonigrum	24646	
7	Aspergillus niger	458		10	Penicillium citreonigrum	19880	+
7	Aspergillus versicolor	2752		10	Penicillium commune	4901	
7	Cladosporium herbarum	910	+	10	Penicillium corylophilum	4970	
7	Eurotium herbariorum	6860	+	10	Penicillium expansum	54330	+
7	Eurotium herbariorum	455		10	Penicillium implicatum	4970	
7	Penicillium aurantiogriseum	458	+	10	Penicillium miczynskii	4901	+
7	Penicillium brevicompactum	455		10	Penicillium spinulosum	14705	+
7	Penicillium chrysogenum	3663	+	10	Phoma herbarum	19812	
7	Penicillium chrysogenum	1369		10	Phoma herbarum	9940	+
7	Penicillium commune	1376	+	10	Pyrenochaeta sp.	24850	
7	Penicillium commune	455		10	Stemphylium solani	9940	+
7	Penicillium expansum	3642	+	10	Trichoderma harzianum	4901	
7	Penicillium expansum	2286		10	Trichoderma viride	24850	
7	Penicillium simplicissimum	458	+	10	Trichoderma viride	24782	+
7	Penicillium sp. #1	458		10	unknown	74279	+
7	unknown	1831		10	unknown	34723	
7	unknown	458	+	10	yeast	84015	
7	Verticillium sp.	914	+	11	Acremonium butyri	15387	
7	yeast	35291		11	Alternaria alternata	2418	+
8	Aspergillus niveus	4743	+	11	Aspergillus versicolor	1456	+
8	Aspergillus ochraceus	10104		11	Aspergillus versicolor	485	
8	Aspergillus paradoxus	1897		11	Aureobasidium pullulans	14940	+
8	Aspergillus sp.	4743	+	11	Chaetomium globosum	954	
8	Aspergillus versicolor	2851		11	Cladosporium cladosporioides	1916	+
8	Eurotium chevalieri	474		11	Cladosporium sp.	477	+
8	Eurotium herbariorum	38041	+	11	Cladosporium sphaerospermum	1933	+
8	Hormonema dematioides	18975	+	11	Epicoccum nigrum	3373	+
8	Myrothecium cinctum	474		11	Eurotium herbariorum	962	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
11 Fusarium oxysporum	962		15 Cladosporium chlorocephalum	2369	+
11 Fusarium oxysporum	954	+	15 Cladosporium cladosporioides	3431	+
11 Penicillium chrysogenum	970	+	15 Cladosporium sp.	1470	
11 Penicillium commune	1908		15 Cladosporium sp.	960	+
11 Penicillium expansum	3373	+	15 Cladosporium sphaerospermum	939	+
11 Penicillium expansum	1456		15 Epicoccum nigrum	3390	+
11 Penicillium sp. #26	18773		15 Epicoccum nigrum	490	
11 Penicillium sp. #26	8646	+	15 Eurotium herbariorum	8150	+
11 Penicillium viridicatum	1916	+	15 Eurotium herbariorum	1470	
11 Phoma herbarum	485	+	15 Humicola fuscoatra	980	
11 Pithomyces chartarum	485	+	15 Oidiodendron sp.	469	
11 unknown	4318		15 Paecilomyces variotii	939	
11 unknown	1941	+	15 Penicillium brevicompactum	490	
11 yeast	6746		15 Penicillium brevicompactum	490	+
12 Aspergillus sp.	13368	+	15 Penicillium chrysogenum	3350	+
12 Aspergillus sydowii	17825	+	15 Penicillium chrysogenum	2390	
12 Aspergillus versicolor	8912	+	15 Penicillium corylophilum	980	+
12 Aureobasidium pullulans	36816	+	15 Penicillium purpurogenum	939	
12 Epicoccum nigrum	4844		15 Penicillium sp.	469	+
12 Epicoccum nigrum	4456	+	15 Penicillium spinulosum	1920	+
12 Fusarium sp.	4844		15 Penicillium spinulosum	469	
12 Mucor racemosus	18602		15 Phoma herbarum	469	+
12 Mucor racemosus	4844	+	15 Scopulariopsis candida	3431	
12 Penicillium commune	9301		15 Trichoderma viride	939	
12 Penicillium expansum	70342	+	15 Trichoderma viride	469	+
12 Penicillium expansum	37982		15 unknown	5189	
12 Penicillium sp. #26	13368	+	15 unknown	2880	+
12 Phialophora fastigiata	4844		15 yeast	939	
12 Pithomyces sp.	4456		16 Aspergillus candidus	495741	
12 Rhizopus oryzae	4844	+	16 Aspergillus candidus	184177	+
12 Scopulariopsis brevicaulis	4844		16 Aspergillus sp.	56818	+
12 Trichoderma viride	8912		16 Aspergillus ustus	4708	
12 unknown	23447		16 Aspergillus versicolor	94161	+
12 unknown	4456	+	16 Aspergillus versicolor	56711	
12 Wallemia sebi	66274	+	16 Aureobasidium pullulans	4734	+
12 yeast	53294		16 Cladosporium sp.	4734	+
13 Alternaria alternata	972	+	16 Cladosporium sphaerospermum	9442	+
13 Aspergillus sp.	499	+	16 Epicoccum nigrum	4708	
13 Aspergillus versicolor	11135		16 Eurotium herbariorum	37771	+
13 Aureobasidium pullulans	3441	+	16 Mucor racemosus	23540	+
13 Cladosporium cladosporioides	2917	+	16 Mucor racemosus	4734	
13 Eurotium herbariorum	1970	+	16 Penicillium aurantiogriseum	42372	
13 Eurotium sp.	499	+	16 Penicillium chrysogenum	94161	+
13 Penicillium brevicompactum	473	+	16 Penicillium chrysogenum	84933	
13 Penicillium chrysogenum	2891	+	16 Penicillium echinulatum	4708	
13 Penicillium citrinum	473	+	16 Penicillium expansum	123106	+
13 Penicillium corylophilum	998	+	16 Penicillium sp. #1	4708	
13 Penicillium spinulosum	972		16 Penicillium sp. #26	4708	
13 Scopulariopsis brevicaulis	499		16 Penicillium sp. #26	4708	+
13 unknown	972	+	16 Penicillium spinulosum	4734	
13 unknown	499		16 unknown	9469	
13 yeast	18990		17 Alternaria alternata	2341	+
15 Alternaria alternata	3330	+	17 Alternaria alternata	462	
15 Aspergillus candidus	40843		17 Alternaria sp.	489	+
15 Aspergillus candidus	469	+	17 Alternaria tenuissima	952	
15 Aspergillus fumigatus	3431		17 Aspergillus versicolor	1851	
15 Aspergillus niger	490	+	17 Aspergillus versicolor	1388	+
15 Aspergillus versicolor	490		17 Aureobasidium pullulans	8054	+
15 Aureobasidium pullulans	10601	+	17 Aureobasidium pullulans	489	
15 Aureobasidium pullulans	2839		17 Cladosporium cladosporioides	2935	+
15 Botrytis sp.	469	+	17 Cladosporium macrocarpum	1388	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
17 Cladosporium macrocarpum	952		20 Penicillium corylophilum	160791	+
17 Epicoccum nigrum	978	+	20 Penicillium purpurogenum	28324	
17 Eurotium herbariorum	952	+	20 Penicillium raistrickii	4761	+
17 Geotrichum candidum	2419		20 Phoma herbarum	4761	+
17 Mucor plumbeus	489		20 Trichoderma viride	4761	
17 Penicillium commune	489	+	20 unknown	37724	
17 Penicillium expansum	462		22 Alternaria alternata	2882	
17 Penicillium verrucosum	462		22 Alternaria alternata	1926	+
17 Rhizopus oryzae	462		22 Aspergillus candidus	2879	
17 unknown	462	+	22 Aspergillus fumigatus	2406	
17 yeast	10037		22 Aspergillus fumigatus	961	+
18 Alternaria alternata	5303		22 Aspergillus niger	481	
18 Alternaria alternata	294	+	22 Aspergillus ochraceus	963	
18 Aspergillus niger	98		22 Aspergillus versicolor	39428	+
18 Aureobasidium pullulans	3331	+	22 Aspergillus versicolor	26456	
18 Aureobasidium pullulans	581		22 Aureobasidium pullulans	25972	+
18 Cladosporium cladosporioides	757	+	22 Aureobasidium pullulans	4804	
18 Coniothyrium sp.	884	+	22 Cladosporium cladosporioides	481	+
18 Penicillium chrysogenum	98		22 Cladosporium sphaerospermum	2404	+
18 Penicillium commune	286		22 Epicoccum nigrum	1445	
18 Penicillium corylophilum	98		22 Epicoccum nigrum	961	+
18 Penicillium expansum	769		22 Eurotium herbariorum	3846	+
18 Penicillium expansum	577	+	22 Penicillium chrysogenum	1923	
18 Penicillium sp. #35	98	+	22 Penicillium chrysogenum	1443	+
18 Penicillium viridicatum	470	+	22 Penicillium commune	1924	
18 Phoma herbarum	491		22 Penicillium expansum	7206	+
18 Rhizopus oryzae	98	+	22 Penicillium purpurogenum	4804	
18 unknown	98		22 Penicillium spinulosum	481	+
18 unknown	94	+	22 Penicillium viridicatum	1923	+
18 yeast	1047		22 Penicillium viridicatum	959	
19 Alternaria alternata	1351	+	22 unknown	10076	
19 Alternaria alternata	1297		22 unknown	3358	+
19 Aureobasidium pullulans	7207	+	22 Wallemia sebi	1443	
19 Aureobasidium pullulans	900		22 Wallemia sebi	479	+
19 Cochliobolus sativus	1801	+	22 yeast	42311	
19 Epicoccum nigrum	450		24 Alternaria alternata	34929	
19 Epicoccum nigrum	450	+	24 Alternaria alternata	34212	+
19 Mucor plumbeus	450		24 Alternaria tenuissima	3409	
19 Penicillium chrysogenum	2252	+	24 Aspergillus ochraceus	1072	
19 Penicillium citrinum	450	+	24 Aspergillus sp.	3218	+
19 Penicillium expansum	1801		24 Aureobasidium pullulans	10037	+
19 Penicillium expansum	1351	+	24 Aureobasidium pullulans	9090	
19 Phoma herbarum	12612	+	24 Cladosporium cladosporioides	5681	+
19 Phoma herbarum	900		24 Cladosporium sp.	4545	
19 unknown	1351	+	24 Cladosporium sp.	1136	+
19 unknown	900		24 Epicoccum nigrum	9027	
19 yeast	3153		24 Epicoccum nigrum	3282	+
20 Alternaria alternata	9400		24 Eurotium herbariorum	4418	+
20 Alternaria alternata	4761	+	24 Geomyces sp.	1136	
20 Aspergillus ochraceus	9523	+	24 Penicillium restrictum	1072	
20 Aspergillus ochraceus	4761		24 Penicillium sp. #38	2272	+
20 Aureobasidium pullulans	75200		24 Penicillium spinulosum	3218	+
20 Aureobasidium pullulans	66171	+	24 Penicillium variabile	1072	+
20 Cladosporium sphaerospermum	28076	+	24 Penicillium viridicatum	1072	
20 Epicoccum nigrum	9523	+	24 Phoma herbarum	5555	+
20 Epicoccum nigrum	9276		24 Scopulariopsis brevicaulis	1136	
20 Eurotium herbariorum	4638	+	24 Trichoderma viride	1136	
20 Hortaea werneckii	9523		24 Trichothecium roseum	1136	
20 Penicillium citrinum	4638	+	24 Ulocladium chartarum	2272	
20 Penicillium commune	4761		24 unknown	4291	
20 Penicillium corylophilum	174582		24 yeast	2209	



HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
25	Alternaria alternata	5684		27	Eurotium herbariorum	464	+
25	Alternaria alternata	1438	+	27	Mucor racemosus	464	+
25	Aspergillus candidus	475	+	27	Paecilomyces variotii	942	
25	Aspergillus niger	481	+	27	Penicillium commune	478	+
25	Aspergillus ochraceus	475	+	27	Penicillium commune	464	
25	Aspergillus versicolor	481	+	27	Penicillium corylophilum	464	+
25	Aureobasidium pullulans	44361		27	Penicillium expansum	464	+
25	Aureobasidium pullulans	34001	+	27	Penicillium sp.	464	+
25	Cladosporium cladosporioides	481	+	27	Penicillium viridicatum	478	
25	Cladosporium sp.	11445	+	27	Phoma herbarum	464	+
25	Cladosporium sp.	481		27	Rhizopus oryzae	464	+
25	Cladosporium sphaerospermum	475	+	27	Ulocladium chartarum	464	+
25	Epicoccum nigrum	1425	+	27	yeast	13184	
25	Epicoccum nigrum	963		28	Alternaria alternata	13865	
25	Penicillium citrinum	475	+	28	Alternaria alternata	13751	+
25	Penicillium digitatum	2376	+	28	Aspergillus niger	1467	
25	Penicillium digitatum	1438		28	Aspergillus niger	1467	+
25	Penicillium implicatum	481	+	28	Aureobasidium pullulans	4927	+
25	Penicillium sp. #44	475	+	28	Aureobasidium pullulans	3957	
25	Penicillium sp. #87	1901		28	Cladosporium cladosporioides	489	+
25	Penicillium sp. #87	1432	+	28	Cladosporium sp.	498	+
25	Penicillium spinulosum	3821		28	Cladosporium sphaerospermum	498	+
25	Penicillium spinulosum	1920	+	28	Epicoccum nigrum	987	+
25	Rhizopus oryzae	8079	+	28	Epicoccum nigrum	489	
25	Rhizopus oryzae	2851		28	Penicillium chrysogenum	1485	+
25	Trichoderma viride	1438		28	Penicillium commune	489	
25	unknown	13905	+	28	Penicillium oxalicum	4438	+
25	unknown	2402		28	Penicillium simplicissimum	489	+
26	Alternaria alternata	945	+	28	Penicillium variable	489	
26	Aspergillus ochraceus	474		28	Penicillium viridicatum	1467	
26	Aspergillus versicolor	5692	+	28	Penicillium vulpinum	489	
26	Aspergillus versicolor	3313		28	unknown	978	
26	Aureobasidium pullulans	34001		28	yeast	997483	
26	Aureobasidium pullulans	19816	+	29	Alternaria alternata	475	+
26	Chaetomium globosum	474	+	29	Aspergillus niger	947	+
26	Chaetomium globosum	470		29	Aspergillus versicolor	4258	+
26	Cladosporium cladosporioides	3309	+	29	Aspergillus versicolor	475	
26	Cladosporium sp.	474		29	Aureobasidium pullulans	6159	+
26	Cladosporium sphaerospermum	474	+	29	Aureobasidium pullulans	2840	
26	Epicoccum nigrum	2368		29	Cladosporium herbarum	475	+
26	Eurotium herbariorum	5667	+	29	Eurotium herbariorum	1423	+
26	Geotrichum candidum	470		29	Penicillium chrysogenum	2368	+
26	Penicillium aurantiogriseum	941		29	Penicillium chrysogenum	1423	
26	Penicillium aurantiogriseum	941	+	29	Penicillium spinulosum	475	+
26	Penicillium brevicompactum	474	+	29	Scopulariopsis chartarum	950	
26	Penicillium commune	1419		29	Scopulariopsis fusca	475	+
26	Penicillium variable	474	+	29	Scopulariopsis sp.	472	
26	Penicillium viridicatum	941		29	Ulocladium chartarum	475	
26	Phoma herbarum	1419	+	29	Ulocladium chartarum	475	+
26	unknown	7590		29	unknown	1895	
26	unknown	470	+	29	unknown	947	+
26	yeast	1423		29	yeast	104508	
27	Alternaria alternata	6626		30	Alternaria alternata	20000	
27	Alternaria alternata	1885	+	30	Alternaria alternata	482	+
27	Alternaria sp.	929	+	30	Aspergillus niger	98	+
27	Aspergillus sydowii	478		30	Aspergillus niger	94	
27	Aspergillus versicolor	464		30	Aspergillus ochraceus	470	+
27	Aureobasidium pullulans	9851	+	30	Aspergillus ochraceus	282	
27	Aureobasidium pullulans	929		30	Aspergillus sp.	98	+
27	Cladosporium cladosporioides	2363	+	30	Aureobasidium pullulans	1529	+
27	Epicoccum nigrum	464	+	30	Aureobasidium pullulans	772	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
30	Cladosporium cladosporioides	196	+	34	Aspergillus versicolor	466	
30	Cladosporium cladosporioides	98		34	Aureobasidium pullulans	2858	+
30	Epicoccum nigrum	94	+	34	Aureobasidium pullulans	952	
30	Fusarium oxysporum	294	+	34	Chaetomium globosum	466	
30	Penicillium atramentosum	94		34	Cladosporium cladosporioides	486	+
30	Penicillium aurantiogriseum	384	+	34	Cladosporium sphaerospermum	486	
30	Penicillium aurantiogriseum	98		34	Cladosporium sphaerospermum	466	+
30	Penicillium brevicompactum	376		34	Epicoccum nigrum	2818	+
30	Penicillium brevicompactum	94	+	34	Epicoccum nigrum	466	
30	Penicillium citrinum	98		34	Eurotium herbariorum	19362	+
30	Penicillium commune	94	+	34	Paecilomyces variotii	486	
30	Penicillium roquefortii	98		34	Penicillium chrysogenum	1945	
30	Penicillium sp.	294		34	Penicillium commune	2878	+
30	Penicillium sp. #26	98		34	Penicillium commune	1439	
30	Penicillium sp. #52	282	+	34	Penicillium corylophilum	4724	
30	Penicillium spinulosum	192		34	Penicillium corylophilum	3751	+
30	Penicillium verrucosum	384	+	34	Penicillium crustosum	486	
30	Penicillium verrucosum	98		34	Penicillium expansum	952	+
30	Penicillium vulpinum	196	+	34	Penicillium sp. #1	1419	
30	Scopulariopsis brevicaulis	98		34	Penicillium sp. #1	486	+
30	Trichoderma viride	94		34	Penicillium spinulosum	1905	
30	Ulocladium chartarum	98		34	Penicillium spinulosum	952	+
30	unknown	388		34	Scopulariopsis brevicaulis	486	
30	unknown	196	+	34	Ulocladium chartarum	486	+
30	yeast	19220		34	Ulocladium sp.	466	
31	Alternaria alternata	1177		34	unknown	3791	+
31	Alternaria alternata	1084	+	34	unknown	466	
31	Aspergillus fumigatus	97		34	yeast	17457	
31	Aspergillus niger	97	+	35	Alternaria alternata	7138	
31	Aspergillus sp.	197	+	35	Alternaria alternata	2380	+
31	Aspergillus versicolor	97		35	Aspergillus versicolor	471	+
31	Aureobasidium pullulans	589	+	35	Aureobasidium pullulans	50568	
31	Cladosporium cladosporioides	97	+	35	Aureobasidium pullulans	46312	+
31	Drechslera sp.	97	+	35	Cladosporium cladosporioides	471	+
31	Emericella sp.	97	+	35	Cladosporium sp.	3356	+
31	Epicoccum nigrum	592		35	Cladosporium sphaerospermum	482	+
31	Epicoccum nigrum	97	+	35	Epicoccum nigrum	1436	+
31	Monascus ruber	97	+	35	Epicoccum nigrum	943	
31	Mucor plumbeus	197	+	35	Eurotium herbariorum	7612	+
31	Penicillium chrysogenum	296	+	35	Eurotium herbariorum	954	
31	Penicillium chrysogenum	198		35	Mucor racemosus	482	+
31	Penicillium corylophilum	99	+	35	Penicillium chrysogenum	471	
31	Pithomyces chartarum	97	+	35	Penicillium chrysogenum	471	+
31	unknown	589		35	Penicillium corylophilum	954	+
31	yeast	1287		35	Penicillium sp. #1	1919	
33	Aureobasidium pullulans	8474		35	Penicillium spinulosum	943	+
33	Aureobasidium pullulans	1878	+	35	Penicillium variable	471	
33	Cladosporium cladosporioides	939	+	35	Phoma herbarum	1415	+
33	Cladosporium sp.	465	+	35	Ulocladium chartarum	1426	
33	Eurotium herbariorum	12231	+	35	unknown	1930	+
33	Penicillium expansum	931	+	35	unknown	1886	
33	Penicillium spinulosum	946	+	35	yeast	2358	
33	Penicillium spinulosum	465		36	Alternaria alternata	5254	
33	Phoma herbarum	473	+	36	Alternaria alternata	1431	+
33	Trichoderma viride	473		36	Aspergillus niger	469	+
33	Ulocladium chartarum	465	+	36	Aspergillus ochraceus	947	+
33	unknown	6099		36	Aspergillus ochraceus	477	
33	yeast	237673		36	Aureobasidium pullulans	68619	
34	Alternaria alternata	4242		36	Aureobasidium pullulans	23220	+
34	Alternaria alternata	3771	+	36	Cladosporium cladosporioides	1416	+
34	Aspergillus fumigatus	466		36	Cladosporium sp.	954	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
36 Cladosporium sphaerospermum	469	+	40 Aureobasidium pullulans	470	
36 Epicoccum nigrum	1424		40 Coniothyrium sp.	468	+
36 Epicoccum nigrum	469	+	40 Epicoccum nigrum	1883	+
36 Eurotium herbariorum	469	+	40 Eurotium herbariorum	1407	+
36 Mucor plumbeus	477		40 Mucor racemosus	1877	+
36 Mucor racemosus	477		40 Penicillium miczynskii	2343	+
36 Penicillium brevicompactum	469		40 Penicillium sp. #26	7993	+
36 Penicillium citrinum	939	+	40 Penicillium sp. #26	5165	
36 Penicillium coprophilum	469		40 Penicillium viridicatum	4702	+
36 Penicillium corylophilum	469	+	40 Penicillium viridicatum	468	
36 Penicillium expansum	13749	+	40 Penicillium vulpinum	468	+
36 Penicillium expansum	947		40 Phialophora sp.	470	
36 Penicillium purpurogenum	1409		40 Rhizopus oryzae	470	
36 Penicillium simplicissimum	7113	+	40 Sphaeropsis sp.	1404	
36 Penicillium simplicissimum	3339		40 Sphaeropsis sp.	468	+
36 Penicillium sp. #26	1431		40 Trichoderma viride	5636	
36 Penicillium spinulosum	21767	+	40 Trichoderma viride	4221	+
36 Penicillium spinulosum	17089		40 unknown	22556	
36 Phoma herbarum	477	+	40 unknown	6580	+
36 unknown	3303		40 yeast	1883	
36 unknown	1879	+	41 Alternaria alternata	196	+
36 yeast	14653		41 Aspergillus sydowii	1084	+
39 Alternaria alternata	4726		41 Aspergillus versicolor	4698	
39 Alternaria alternata	1420	+	41 Aspergillus versicolor	196	+
39 Aspergillus niger	476	+	41 Aureobasidium pullulans	1475	
39 Aspergillus sp.	949		41 Aureobasidium pullulans	983	+
39 Aspergillus sp.	476	+	41 Eurotium herbariorum	98	+
39 Aspergillus sydowii	476	+	41 Exophiala sp.	1572	
39 Aspergillus versicolor	473	+	41 Exophiala sp.	392	+
39 Aureobasidium pullulans	1896	+	41 Penicillium aurantiogriseum	2262	+
39 Aureobasidium pullulans	946		41 Penicillium aurantiogriseum	393	
39 Cladosporium cladosporioides	476	+	41 Penicillium coprophilum	98	
39 Cladosporium sp.	946	+	41 Penicillium miczynskii	98	
39 Cladosporium sp.	476		41 Penicillium simplicissimum	98	+
39 Cladosporium sphaerospermum	946		41 Penicillium spinulosum	294	
39 Cladosporium sphaerospermum	476	+	41 Penicillium spinulosum	196	+
39 Epicoccum nigrum	1420		41 unknown	98	+
39 Epicoccum nigrum	473	+	41 yeast	2267	
39 Eurotium herbariorum	476		42 Alternaria alternata	14775	
39 Eurotium herbariorum	473	+	42 Alternaria alternata	4854	+
39 Penicillium chrysogenum	1423	+	42 Aspergillus ochraceus	24443	+
39 Penicillium chrysogenum	473		42 Aspergillus restrictus	9765	
39 Penicillium corylophilum	476		42 Aspergillus restrictus	4911	+
39 Penicillium echinulatum	476	+	42 Aspergillus sp.	4854	+
39 Penicillium spinulosum	6639	+	42 Aspergillus tamarii	4854	+
39 Penicillium spinulosum	5224		42 Aspergillus versicolor	4911	
39 Penicillium vulpinum	2375	+	42 Aureobasidium pullulans	82810	+
39 Penicillium vulpinum	473		42 Aureobasidium pullulans	19417	
39 Scopulariopsis candida	476	+	42 Chaetomium globosum	4854	
39 Scopulariopsis sp.	476	+	42 Cladosporium cladosporioides	9708	+
39 Ulocladium chartarum	473		42 Cladosporium cladosporioides	9708	
39 unknown	3325		42 Cladosporium sphaerospermum	39063	+
39 unknown	949	+	42 Epicoccum nigrum	4911	+
39 yeast	2370		42 Eurotium herbariorum	9765	+
40 Acremonium sp.	48842	+	42 Penicillium brevicompactum	9765	+
40 Acremonium sp.	8945		42 Penicillium chrysogenum	4854	+
40 Alternaria alternata	1409	+	42 Penicillium citrinum	4911	
40 Alternaria alternata	470		42 Penicillium citrinum	4911	+
40 Aspergillus fumigatus	470		42 Penicillium commune	9765	+
40 Aspergillus versicolor	941	+	42 Penicillium commune	4911	
40 Aspergillus versicolor	468		42 Penicillium echinulatum	4854	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
42	Penicillium expansum	4854	+	45	Wallemia sebi	47787	+
42	Penicillium vulpinum	14677	+	45	yeast	33508	
42	Trichoderma viride	4854		47	Alternaria alternata	318458	
42	unknown	73044	+	47	Alternaria alternata	2429	+
42	unknown	4854		47	Aspergillus niger	485	
42	Wallemia sebi	4854	+	47	Aspergillus sp.	1457	+
42	yeast	359738		47	Aureobasidium pullulans	10690	+
43	Alternaria alternata	135869		47	Aureobasidium pullulans	7288	
43	Alternaria alternata	23228	+	47	Cladosporium sphaerospermum	2430	+
43	Aspergillus penicilloides	4708	+	47	Cladosporium sphaerospermum	486	
43	Aureobasidium pullulans	18416		47	Coniothyrium sp.	2914	
43	Aureobasidium pullulans	14124	+	47	Coniothyrium sp.	2427	+
43	Chrysosporium sp.	9416		47	Epicoccum nigrum	970	
43	Cladosporium cladosporioides	9208	+	47	Fusarium oxysporum	1458	+
43	Cladosporium sp.	13812	+	47	Mucor racemosus	485	
43	Cladosporium sphaerospermum	9416	+	47	Penicillium brevicompactum	1458	
43	Epicoccum nigrum	4708	+	47	Penicillium chrysogenum	485	+
43	Penicillium aurantiogriseum	4708	+	47	Penicillium citreonigrum	486	+
43	Penicillium brevicompactum	4708		47	Penicillium corylophilum	971	+
43	Penicillium citreonigrum	4708		47	Penicillium corylophilum	486	
43	Penicillium commune	14020		47	Penicillium vulpinum	485	
43	Penicillium corylophilum	4708		47	Pithomyces chartarum	485	
43	Penicillium spinulosum	9416		47	Trichoderma viride	485	
43	Penicillium spinulosum	4604	+	47	unknown	4859	+
43	Phoma herbarum	4708		47	unknown	2913	
43	Pithomyces chartarum	27728		47	yeast	6798	
43	Syncephalastrum verruculosum	4604		48	Aspergillus sp.	1949	+
43	Trichoderma harzianum	9416	+	48	Aureobasidium pullulans	4377	
43	Trichoderma viride	4708		48	Aureobasidium pullulans	2916	+
43	unknown	1146721		48	Cladosporium sp.	974	
43	unknown	879686	+	48	Cladosporium sphaerospermum	974	+
43	yeast	9208		48	Epicoccum nigrum	483	+
45	Alternaria alternata	9372		48	Eurotium herbariorum	483	+
45	Alternaria alternata	9328	+	48	Fusarium oxysporum	982	+
45	Aspergillus fumigatus	77490	+	48	Fusarium oxysporum	483	
45	Aspergillus fumigatus	4664		48	Geomyces pannorum	483	+
45	Aureobasidium pullulans	43695		48	Humicola fuscoatra	491	
45	Aureobasidium pullulans	13992	+	48	Penicillium chrysogenum	5372	+
45	Cladosporium cladosporioides	4664	+	48	Penicillium chrysogenum	2924	
45	Cladosporium sp.	4664		48	Penicillium citreonigrum	483	
45	Cladosporium sphaerospermum	9614	+	48	Penicillium citrinum	483	+
45	Epicoccum nigrum	9614	+	48	Penicillium coprophilum	483	+
45	Eurotium herbariorum	4950	+	48	Penicillium corylophilum	491	
45	Penicillium brevicompactum	9328	+	48	Penicillium sp. #64	491	
45	Penicillium chrysogenum	38745	+	48	Penicillium spinulosum	491	+
45	Penicillium chrysogenum	19229		48	Penicillium vulpinum	483	
45	Penicillium citreonigrum	4664		48	Trichoderma viride	491	
45	Penicillium commune	38745	+	48	unknown	5372	+
45	Penicillium corylophilum	9614		48	unknown	2924	
45	Penicillium echinulatum	4950		48	yeast	3891	
45	Penicillium expansum	4664	+	49	Alternaria alternata	6300	
45	Penicillium viridicatum	9328		49	Alternaria alternata	1992	+
45	Penicillium viridicatum	4664	+	49	Aureobasidium pullulans	996	+
45	Pestalotiopsis sp.	4664	+	49	Botrytis sp.	978	
45	Phoma herbarum	27985		49	Cladosporium cladosporioides	1494	+
45	Rhizopus oryzae	4950	+	49	Cladosporium sphaerospermum	498	+
45	Trichoderma viride	28844		49	Epicoccum nigrum	498	
45	Ulocladium chartarum	9614	+	49	Epicoccum nigrum	498	+
45	Ulocladium chartarum	9328		49	Penicillium brevicompactum	480	
45	unknown	139842	+	49	Penicillium chrysogenum	498	
45	unknown	67302		49	Penicillium decumbens	498	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
49	Penicillium raistrickii	1442		52	Alternaria alternata	4752	+
49	Penicillium raistrickii	978	+	52	Aspergillus sydowii	4770	+
49	Penicillium spinulosum	2953	+	52	Aureobasidium pullulans	114345	
49	Penicillium spinulosum	1940		52	Cladosporium cladosporioides	9523	+
49	unknown	1940	+	52	Cladosporium sphaerospermum	4752	+
49	unknown	1494		52	Geotrichum candidum	4752	+
49	yeast	28815		52	Mucor racemosus	4770	+
50	Alternaria alternata	11791		52	Paecilomyces variotii	9505	+
50	Alternaria alternata	6334	+	52	Penicillium chrysogenum	9523	
50	Alternaria sp.	488	+	52	Penicillium commune	47619	
50	Aspergillus niger	488		52	Penicillium digitatum	19029	
50	Aspergillus versicolor	1461	+	52	Penicillium digitatum	4770	+
50	Aureobasidium pullulans	19016		52	Penicillium expansum	28589	+
50	Aureobasidium pullulans	15596	+	52	Penicillium spinulosum	4752	+
50	Botrytis cinerea	488		52	Penicillium viridicatum	52335	+
50	Cladosporium cladosporioides	486		52	Penicillium viridicatum	42848	
50	Cladosporium cladosporioides	486	+	52	Phoma herbarum	4752	+
50	Cladosporium sp.	486	+	52	unknown	14312	+
50	Cladosporium sphaerospermum	1461	+	52	unknown	9523	
50	Epicoccum nigrum	1949		52	yeast	9505	
50	Eurotium herbariorum	486	+	53	Alternaria alternata	171918	
50	Mucor racemosus	6332		53	Alternaria alternata	951	+
50	Mucor racemosus	3410	+	53	Aspergillus niger	941	+
50	Penicillium chrysogenum	5840	+	53	Aspergillus niger	480	
50	Penicillium chrysogenum	3896		53	Aspergillus ochraceus	480	
50	Penicillium citrinum	976	+	53	Aspergillus sp.	470	+
50	Penicillium corylophilum	1459	+	53	Aspergillus sydowii	951	+
50	Penicillium expansum	974	+	53	Aureobasidium pullulans	1432	+
50	Penicillium sp. #1	488	+	53	Chryso sporium sp.	480	
50	Phoma herbarum	488	+	53	Eurotium herbariorum	470	+
50	Trichoderma sp.	488	+	53	Mucor plumbeus	470	
50	Ulocladium chartarum	488		53	Mucor racemosus	3335	
50	unknown	4379		53	Mucor racemosus	2354	+
50	unknown	2920	+	53	Penicillium aurantiogriseum	3816	
50	yeast	1461		53	Penicillium aurantiogriseum	1412	+
51	Alternaria alternata	1450	+	53	Penicillium chrysogenum	470	
51	Alternaria alternata	483		53	Penicillium commune	1893	
51	Aureobasidium pullulans	39046		53	Penicillium commune	1412	+
51	Aureobasidium pullulans	10537	+	53	Penicillium expansum	480	
51	Cladosporium cladosporioides	948		53	Penicillium sp.	1923	+
51	Cladosporium sphaerospermum	967	+	53	Penicillium spinulosum	951	
51	Eurotium herbariorum	1450	+	53	Penicillium viridicatum	6160	+
51	Mucor plumbeus	9998		53	Penicillium vulpinum	2844	+
51	Mucor plumbeus	9059	+	53	Penicillium vulpinum	1903	
51	Mucor racemosus	483		53	Rhizopus oryzae	1923	+
51	Paecilomyces variotii	967	+	53	unknown	951	
51	Penicillium aurantiogriseum	4306	+	53	unknown	941	+
51	Penicillium aurantiogriseum	1925		53	yeast	10958	
51	Penicillium citrinum	957		54	Alternaria alternata	14793	+
51	Penicillium citrinum	474	+	54	Aureobasidium pullulans	34246	+
51	Penicillium expansum	12425		54	Aureobasidium pullulans	5373	
51	Penicillium expansum	10537	+	54	Cladosporium cladosporioides	24461	+
51	Penicillium spinulosum	483	+	54	Cladosporium sp.	9900	+
51	Penicillium spinulosum	474		54	Penicillium citrinum	4892	
51	Phoma herbarum	1897	+	54	Penicillium corylophilum	19627	+
51	Rhizopus oryzae	474		54	Penicillium corylophilum	4950	
51	Rhodotorula sp.	5264		54	Penicillium islandicum	4892	
51	unknown	6723		54	Penicillium sp. #26	4950	
51	unknown	2371	+	54	Penicillium spinulosum	24752	+
51	Wallemia sebi	474	+	54	Penicillium spinulosum	4892	
51	yeast	19825		54	Penicillium verrucosum	4950	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
54	Trichoderma harzianum	4950		57	Aureobasidium pullulans	43069	
54	Trichoderma viride	98370	+	57	Cladosporium cladosporioides	4826	+
54	Trichoderma viride	44438		57	Eurotium herbariorum	23837	+
54	Ulocladium chartarum	9784		57	Ophiostoma tenellum	9505	
54	unknown	29412	+	57	Paecilomyces variotii	14405	
54	yeast	14677		57	Paecilomyces variotii	4752	+
55	Aspergillus niger	492	+	57	Penicillium brevicompactum	4752	
55	Aspergillus niger	481		57	Penicillium citreonigrum	4752	+
55	Aspergillus parasiticus	492		57	Penicillium corylophilum	4752	
55	Aspergillus sp.	984	+	57	Penicillium restrictum	4826	
55	Aspergillus versicolor	492	+	57	Penicillium sp. #26	9505	
55	Aureobasidium pullulans	12136		57	Penicillium spinulosum	143539	+
55	Cladosporium sp.	28167	+	57	Penicillium spinulosum	62227	
55	Cladosporium sphaerospermum	17560	+	57	Scopulariopsis candida	4826	
55	Cladosporium sphaerospermum	492		57	Trichoderma sp.	14405	+
55	Eurotium herbariorum	9727	+	57	Trichoderma viride	14258	
55	Geomyces pannorum	2952		57	unknown	47968	
55	Paecilomyces sp.	984		58	Alternaria alternata	38380	
55	Penicillium chrysogenum	973		58	Aspergillus sp.	4743	+
55	Penicillium citrinum	973		58	Aspergillus sydowii	4743	+
55	Penicillium commune	3434	+	58	Chaetomium funicola	4743	+
55	Penicillium coprophilum	1947	+	58	Cladosporium sphaerospermum	4743	
55	Rhodotorula sp.	1926	+	58	Penicillium chrysogenum	42749	
55	Rhodotorula sp.	963		58	Penicillium chrysogenum	38169	+
55	Scopulariopsis candida	492		58	Scopulariopsis candida	4798	
55	unknown	492		58	unknown	33316	+
55	Wallemia sebi	133261		58	unknown	23719	
56	Acremonium sclerotigenum	440283		58	yeast	42694	
56	Alternaria alternata	1960	+	59	Alternaria alternata	490	+
56	Alternaria alternata	998		59	Aspergillus versicolor	491	+
56	Aspergillus niger	487		59	Aureobasidium pullulans	1472	
56	Aureobasidium pullulans	1960	+	59	Chrysosporium sp.	491	
56	Cladosporium cladosporioides	986	+	59	Penicillium chrysogenum	1960	
56	Cladosporium sphaerospermum	974	+	59	Penicillium commune	2451	+
56	Epicoccum nigrum	499	+	59	Penicillium expansum	2942	
56	Eurotium herbariorum	487	+	59	Penicillium viridicatum	9321	+
56	Mucor plumbeus	487		59	Penicillium viridicatum	4906	
56	Penicillium brevicompactum	2483	+	59	Ulocladium chartarum	490	+
56	Penicillium brevicompactum	986		59	unknown	2451	+
56	Penicillium chrysogenum	2935	+	59	unknown	1472	
56	Penicillium chrysogenum	986		59	yeast	7847	
56	Penicillium citrinum	3956	+	61	Aspergillus sp.	25474	
56	Penicillium citrinum	499		61	Coniothyrium fuckelii	478	+
56	Penicillium commune	499	+	61	Fusarium sp.	473	
56	Penicillium expansum	974		61	Mucor racemosus	946	
56	Penicillium miczynskii	499		61	Mucor racemosus	946	+
56	Penicillium sp. #26	986	+	61	Penicillium corylophilum	473	
56	Penicillium spinulosum	2471	+	61	Penicillium corylophilum	473	+
56	Penicillium spinulosum	499		61	Penicillium expansum	473	
56	Penicillium viridicatum	499	+	61	Penicillium viridicatum	1424	
56	Scopulariopsis brevicaulis	499	+	61	Penicillium viridicatum	951	+
56	Scopulariopsis brevicaulis	487		61	Trichoderma viride	478	+
56	Trichoderma viride	974		61	unknown	5240	+
56	Ulocladium chartarum	2958	+	61	unknown	1898	
56	Ulocladium chartarum	986		61	yeast	956	
56	unknown	2947	+	62	Aureobasidium pullulans	20651	
56	unknown	998		62	Aureobasidium pullulans	4807	+
56	Wallemia sebi	986	+	62	Eurotium herbariorum	92676	+
56	yeast	10826		62	Eurotium herbariorum	4807	
57	Acremonium sp.	24432		62	Mucor racemosus	43269	
57	Alternaria alternata	4752	+	62	Mucor racemosus	24038	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
62	Oidiodendron sp.	4807		65	Penicillium sp. #26	489	
62	Penicillium brevicompactum	19629		65	Penicillium sp. #26	481	+
62	Penicillium brevicompactum	9881	+	65	Penicillium spinulosum	4372	+
62	Penicillium corylophilum	4940		65	Penicillium spinulosum	2927	
62	Penicillium corylophilum	4807	+	65	Phialophora fastigiata	481	
62	Penicillium restrictum	4940		65	Trichoderma viride	1460	+
62	Penicillium spinulosum	9881	+	65	Trichoderma viride	978	
62	Penicillium spinulosum	4940		65	unknown	130811	
62	Penicillium viridicatum	9881	+	65	unknown	124589	+
62	Penicillium viridicatum	4807		65	yeast	12667	
62	Phoma herbarum	1976284		67	Alternaria alternata	48288	+
62	Phoma herbarum	1976284	+	67	Aureobasidium pullulans	23808	+
62	Trichoderma viride	24171		67	Aureobasidium pullulans	20207	
62	unknown	135945		67	Cladosporium cladosporioides	14374	+
62	yeast	264271		67	Cladosporium macrocarpum	4716	+
64	Alternaria alternata	3324	+	67	Cladosporium sp.	4940	+
64	Aspergillus niger	14893		67	Cladosporium sphaerospermum	9657	+
64	Aspergillus sp.	4781	+	67	Eurotium herbariorum	4940	
64	Aspergillus sp.	941		67	Eurotium herbariorum	4940	+
64	Aspergillus versicolor	485		67	Penicillium brevicompactum	33466	+
64	Aureobasidium pullulans	3324	+	67	Penicillium brevicompactum	4940	
64	Aureobasidium pullulans	1456		67	Penicillium chrysogenum	9657	+
64	Cladosporium herbarum	470	+	67	Penicillium chrysogenum	9433	
64	Cladosporium sphaerospermum	970	+	67	Penicillium spinulosum	24032	+
64	Epicoccum nigrum	970	+	67	Penicillium spinulosum	9657	
64	Epicoccum nigrum	470		67	Trichoderma harzianum	63334	+
64	Eurotium amstelodami	2427		67	Trichoderma harzianum	24032	
64	Eurotium herbariorum	5266	+	67	Trichoderma koningii	9433	
64	Mucor plumbeus	470	+	67	Trichoderma viride	102188	
64	Penicillium atramentosum	970	+	67	unknown	58393	+
64	Penicillium atramentosum	485		67	unknown	19315	
64	Penicillium chrysogenum	1897	+	67	yeast	9433	
64	Penicillium corylophilum	6722		70	Alternaria alternata	64044	
64	Penicillium corylophilum	3810	+	70	Alternaria alternata	1980	+
64	Penicillium echinulatum	485	+	70	Aspergillus sp.	1459	
64	Penicillium sp. #26	1897		70	Aspergillus versicolor	9345	+
64	Pestalotiopsis sp.	470		70	Aspergillus versicolor	1968	
64	Phoma chrysanthemicola	5339	+	70	Aureobasidium pullulans	8373	+
64	Phoma herbarum	470		70	Aureobasidium pullulans	2466	
64	unknown	956		70	Epicoccum nigrum	972	
64	unknown	470	+	70	Epicoccum nigrum	498	+
64	yeast	956		70	Eurotium herbariorum	2478	+
65	Alternaria alternata	3386	+	70	Geomyces pannorum	486	
65	Aspergillus sp.	489	+	70	Mucor plumbeus	486	+
65	Aspergillus versicolor	489	+	70	Penicillium brevicompactum	5419	+
65	Aureobasidium pullulans	12617		70	Penicillium chrysogenum	996	
65	Aureobasidium pullulans	970	+	70	Penicillium citrinum	498	+
65	Epicoccum nigrum	2423	+	70	Penicillium corylophilum	984	+
65	Epicoccum nigrum	481		70	Penicillium expansum	5431	
65	Eurotium herbariorum	481	+	70	Penicillium viridicatum	498	+
65	Mucor racemosus	1445	+	70	Rhizopus oryzae	498	
65	Paecilomyces sp.	978	+	70	Scopulariopsis candida	486	+
65	Paecilomyces sp.	481		70	unknown	7377	
65	Penicillium brevicompactum	3402	+	70	unknown	3462	+
65	Penicillium citreonigrum	489		70	yeast	11835	
65	Penicillium coprophilum	481		71	Alternaria alternata	8287	
65	Penicillium decumbens	481		71	Alternaria alternata	1431	+
65	Penicillium implicatum	963		71	Aspergillus ochraceus	23359	+
65	Penicillium implicatum	489	+	71	Aspergillus ochraceus	15744	
65	Penicillium miczynskii	2920	+	71	Aspergillus versicolor	950	+
65	Penicillium miczynskii	1941		71	Aureobasidium pullulans	25752	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
71	Cladosporium sp.	478	+	73	Trichoderma viride	9689	
71	Cladosporium sphaerospermum	478	+	73	yeast	47438	
71	Eurotium herbariorum	956	+	74	Alternaria alternata	31870	
71	Mucor racemosus	475	+	74	Alternaria alternata	4874	+
71	Mucor sp.	478		74	Aspergillus versicolor	8255	+
71	Penicillium chrysogenum	2387	+	74	Aspergillus versicolor	5897	
71	Penicillium chrysogenum	953		74	Aureobasidium pullulans	3486	+
71	Penicillium citrinum	1431		74	Cladosporium cladosporioides	1939	+
71	Penicillium citrinum	475	+	74	Cladosporium sp.	2988	+
71	Penicillium corylophilum	478	+	74	Cladosporium sphaerospermum	471	+
71	Penicillium islandicum	5719		74	Eurotium herbariorum	2490	+
71	Penicillium islandicum	953	+	74	Penicillium brevicompactum	943	
71	Penicillium spinulosum	478	+	74	Penicillium brevicompactum	471	+
71	Penicillium spinulosum	475		74	Penicillium chrysogenum	12318	+
71	Phoma herbarum	475		74	Penicillium chrysogenum	3852	
71	unknown	27719	+	74	Penicillium digitatum	498	
71	unknown	1903		74	Penicillium viridicatum	498	+
71	Wallemia sebi	3340	+	74	Phoma herbarum	471	+
71	yeast	98403		74	unknown	5976	
72	Alternaria alternata	11915		74	unknown	5870	+
72	Alternaria alternata	478	+	74	yeast	62953	
72	Aspergillus niger	1467		75	Alternaria alternata	23140	
72	Aspergillus niger	489	+	75	Aspergillus ochraceus	485	
72	Aspergillus ochraceus	489		75	Aspergillus versicolor	5354	+
72	Aspergillus versicolor	957	+	75	Aspergillus versicolor	485	
72	Aureobasidium pullulans	957	+	75	Aureobasidium pullulans	20416	+
72	Cladosporium cladosporioides	478	+	75	Candida sp.	1460	
72	Cladosporium sphaerospermum	1467	+	75	Cladosporium cladosporioides	6813	+
72	Epicoccum nigrum	1447	+	75	Cladosporium sphaerospermum	487	
72	Eurotium herbariorum	13075	+	75	Cladosporium sphaerospermum	485	+
72	Penicillium brevicompactum	489	+	75	Epicoccum nigrum	974	+
72	Penicillium chrysogenum	2914	+	75	Eurotium herbariorum	3403	+
72	Penicillium chrysogenum	2904		75	Mucor plumbeus	487	
72	Penicillium coprophilum	489	+	75	Penicillium brevicompactum	3889	+
72	Penicillium spinulosum	489		75	Penicillium brevicompactum	485	
72	Penicillium variabile	478		75	Penicillium chrysogenum	1458	+
72	Penicillium viridicatum	2435	+	75	Penicillium chrysogenum	974	
72	Penicillium viridicatum	978		75	Penicillium coprophilum	487	+
72	Phoma herbarum	478		75	Penicillium coprophilum	485	
72	Phoma herbarum	478	+	75	Penicillium expansum	2434	+
72	Trichoderma viride	478		75	Penicillium raistrickii	4378	+
72	unknown	2904	+	75	Penicillium sp. #26	487	+
72	unknown	2415		75	Penicillium spinulosum	1460	
72	yeast	11077		75	Penicillium spinulosum	974	+
73	Alternaria alternata	9588	+	75	Penicillium viridicatum	485	
73	Alternaria alternata	7679		75	Phoma herbarum	970	
73	Aspergillus candidus	4844		75	Phoma leveillei	45234	+
73	Aureobasidium pullulans	14332		75	unknown	19972	+
73	Aureobasidium pullulans	9588	+	75	unknown	5347	
73	Chrysosporium sp.	4743	+	75	yeast	159465	
73	Cladosporium sp.	23921	+	76	Alternaria alternata	73569	
73	Cladosporium sphaerospermum	4743	+	76	Aspergillus niger	469	
73	Eurotium herbariorum	9588	+	76	Aspergillus ochraceus	469	+
73	Penicillium chrysogenum	19278		76	Aspergillus sp.	482	+
73	Penicillium commune	28867	+	76	Aspergillus versicolor	482	+
73	Penicillium commune	23820		76	Aureobasidium pullulans	2870	
73	Penicillium sp. #26	24022	+	76	Aureobasidium pullulans	952	+
73	Penicillium sp. #26	14534		76	Botrytis sp.	482	+
73	Penicillium spinulosum	4743		76	Cladosporium sp.	965	+
73	Penicillium vulpinum	24123	+	76	Penicillium citreonigrum	1879	
73	Trichoderma viride	14332	+	76	Penicillium citreonigrum	1409	+



HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
76	Penicillium commune	12383	+	79	Aspergillus ustus	1467	+
76	Penicillium commune	9563		79	Aspergillus ustus	990	
76	Penicillium crustosum	469	+	79	Aspergillus versicolor	30518	+
76	Penicillium echinulatum	4280	+	79	Aspergillus versicolor	6424	
76	Penicillium raistrickii	3314	+	79	Penicillium brevicompactum	984	
76	Penicillium raistrickii	469		79	Penicillium chrysogenum	2463	
76	Penicillium sp.	1905	+	79	Penicillium citreonigrum	978	+
76	Penicillium sp. #26	939		79	Penicillium commune	2958	
76	Penicillium sp. #26	469	+	79	Penicillium commune	1467	+
76	Penicillium sp. #64	3810		79	Penicillium digitatum	6895	
76	Penicillium spinulosum	3810	+	79	Penicillium digitatum	4950	+
76	Penicillium spinulosum	939		79	Penicillium oxalicum	984	
76	Pithomyces chartarum	482	+	79	Penicillium sp. #84	3942	+
76	yeast	4280		79	Penicillium sp. #84	3453	
77	Alternaria alternata	1424		79	unknown	27094	
77	Alternaria alternata	1418	+	80	Alternaria alternata	959	+
77	Aureobasidium pullulans	1895	+	80	Aspergillus versicolor	5878	
77	Aureobasidium pullulans	1425		80	Aspergillus versicolor	479	+
77	Chrysosporium sp.	470		80	Aureobasidium pullulans	7153	+
77	Cladosporium cladosporioides	477		80	Aureobasidium pullulans	1900	
77	Epicoccum nigrum	477	+	80	Cladosporium sphaerospermum	3333	+
77	Epicoccum nigrum	470		80	Cladosporium sphaerospermum	479	
77	Eurotium herbariorum	477	+	80	Eurotium herbariorum	473	+
77	Exophiala jeanselmei	470		80	Mucor plumbeus	1433	+
77	Hortaea werneckii	477		80	Mucor plumbeus	473	
77	Penicillium chrysogenum	1425	+	80	Penicillium citrinum	2386	+
77	Penicillium commune	3320		80	Penicillium commune	953	
77	Penicillium commune	2354	+	80	Penicillium commune	479	+
77	Penicillium corylophilum	2850	+	80	Penicillium corylophilum	479	+
77	Penicillium corylophilum	941		80	Penicillium expansum	479	+
77	Penicillium glandicola	470	+	80	Phoma herbarum	479	
77	Penicillium islandicum	947		80	unknown	16756	+
77	Pithomyces chartarum	1412	+	80	unknown	3358	
77	Sphaeropsis sp.	470	+	80	Wallemia sebi	47984	+
77	Trichoderma viride	954		80	yeast	121088	
77	Ulocladium chartarum	477		81	Alternaria alternata	1449	+
77	unknown	17621	+	81	Aspergillus niger	99589	
77	unknown	7112		81	Aspergillus niger	94	+
77	yeast	18945		81	Aureobasidium pullulans	377	+
78	Alternaria alternata	18593		81	Cochliobolus sativus	94	+
78	Alternaria alternata	3924	+	81	Eurotium herbariorum	289	+
78	Aspergillus candidus	497	+	81	Mucor plumbeus	194	
78	Aspergillus niger	479	+	81	Mucor plumbeus	194	+
78	Aspergillus ochraceus	497	+	81	Penicillium brevicompactum	477	+
78	Aureobasidium pullulans	8243	+	81	Penicillium brevicompactum	94	
78	Aureobasidium pullulans	3838		81	Penicillium chrysogenum	1427	+
78	Chrysosporium sp.	497		81	Penicillium chrysogenum	286	
78	Cladosporium sp.	479	+	81	Penicillium corylophilum	383	+
78	Cladosporium sphaerospermum	1473	+	81	Rhizopus oryzae	94	
78	Epicoccum nigrum	976		81	Trichoderma viride	97	
78	Hortaea werneckii	497		81	unknown	383	
78	Mucor racemosus	1439	+	81	unknown	383	+
78	Rhizopus oryzae	959		81	yeast	377	
78	Scopulariopsis brevicaulis	497	+	82	Aspergillus sp.	24460	
78	Sporotrichum pruinosum	497		82	Aspergillus sp.	19305	+
78	Trichoderma viride	1491		82	Aspergillus versicolor	189930	+
78	unknown	1936		82	Aspergillus versicolor	175025	
78	yeast	57962		82	Aureobasidium pullulans	4911	+
79	Alternaria alternata	495	+	82	Cladosporium cladosporioides	4826	+
79	Aspergillus flavipes	7364		82	Eurotium herbariorum	4911	+
79	Aspergillus sp.	2475	+	82	Penicillium brevicompactum	4826	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
82	Penicillium chrysogenum	24472		86	Aureobasidium pullulans	4578	
82	Penicillium chrysogenum	19475	+	86	Chrysonilia sp.	14258	+
82	Penicillium coprophilum	14478	+	86	Chrysosporium sp.	4752	+
82	Penicillium corylophilum	24301	+	86	Cladosporium sp.	13910	+
82	Penicillium decumbens	19475		86	Cladosporium sp.	4578	
82	Penicillium decumbens	19305	+	86	Cladosporium sphaerospermum	88215	+
82	Penicillium sp. #26	9652		86	Cladosporium sphaerospermum	4578	
82	Penicillium sp. #87	4826	+	86	Eurotium herbariorum	60916	+
82	Trichoderma viride	24301		86	Eurotium herbariorum	4578	
82	Trichoderma viride	4826	+	86	Penicillium citrinum	4578	
82	unknown	130735		86	Penicillium corylophilum	9331	
82	Wallemia sebi	9652		86	Penicillium griseofulvum	9157	+
83	Alternaria alternata	952	+	86	Penicillium raistrickii	4752	+
83	Aureobasidium pullulans	3330	+	86	Penicillium sp.	4752	+
83	Cladosporium sp.	475	+	86	Penicillium viridicatum	9157	
83	Gilmaniella humicola	146542		86	Rhizopus oryzae	4752	
83	Mucor plumbeus	5229		86	Talaromyces flavus	4578	
83	Mucor racemosus	10474	+	86	Trichoderma viride	4752	+
83	Mucor racemosus	4758		86	unknown	4578	+
83	Paecilomyces variotii	952		86	Wallemia sebi	13910	+
83	Penicillium chrysogenum	10479		86	yeast	125715	
83	Penicillium citrinum	1427	+	87	Alternaria alternata	5455	+
83	Penicillium citrinum	475		87	Aspergillus niger	422116	
83	Penicillium commune	2857		87	Aspergillus niger	1379	+
83	Penicillium commune	2380	+	87	Aspergillus sp.	452	+
83	Penicillium sp. #64	1902		87	Aspergillus versicolor	3232	+
83	Penicillium viridicatum	2858	+	87	Aspergillus versicolor	1811	
83	Penicillium viridicatum	477		87	Aureobasidium pullulans	1379	
83	Trichoderma viride	477		87	Aureobasidium pullulans	452	+
83	unknown	952		87	Chaetomium sp.	946	
83	yeast	13826		87	Cladosporium sphaerospermum	19309	+
85	Alternaria alternata	1899		87	Epicoccum nigrum	905	+
85	Alternaria alternata	480	+	87	Eurotium herbariorum	1852	+
85	Aspergillus niger	471	+	87	Mucor plumbeus	473	+
85	Aureobasidium pullulans	17144	+	87	Mucor racemosus	473	
85	Aureobasidium pullulans	480		87	Penicillium brevicompactum	946	+
85	Cladosporium sp.	943	+	87	Penicillium chrysogenum	2779	
85	Cladosporium sphaerospermum	471	+	87	Penicillium chrysogenum	452	+
85	Emericella nidulans	471	+	87	Penicillium corylophilum	452	
85	Mucor plumbeus	480		87	Penicillium crustosum	3643	+
85	Mucor racemosus	471		87	Penicillium crustosum	3623	
85	Mucor racemosus	471	+	87	Penicillium griseofulvum	8296	+
85	Penicillium corylophilum	1415	+	87	Penicillium griseofulvum	1811	
85	Penicillium corylophilum	480		87	Penicillium raistrickii	1358	+
85	Penicillium sp. #26	943		87	Penicillium sp. #26	946	+
85	Penicillium spinulosum	2376	+	87	Penicillium sp. #26	905	
85	Penicillium viridicatum	3800	+	87	Rhizopus oryzae	452	
85	Penicillium viridicatum	2358		87	Scopulariopsis sp.	9799	
85	Pithomyces chartarum	471		87	Scopulariopsis sp.	1832	+
85	Rhizopus oryzae	471		87	Sphaeropsis sp.	452	+
85	Trichoderma viride	1442		87	Ulocladium chartarum	473	+
85	unknown	2385		87	unknown	38269	+
85	unknown	943	+	87	unknown	10540	
85	yeast	23149		87	Wallemia sebi	13175	+
86	Acremonium kiliense	34583		87	yeast	7925	
86	Acremonium kiliense	4752	+	88	Alternaria alternata	936	+
86	Acremonium sp.	9157	+	88	Aspergillus ochraceus	472	+
86	Alternaria alternata	4752	+	88	Aspergillus sclerotiorum	4111	
86	Aspergillus ochraceus	9505	+	88	Aureobasidium pullulans	2826	+
86	Aspergillus ochraceus	4752		88	Aureobasidium pullulans	940	
86	Aureobasidium pullulans	18489	+	88	Chaetomium globosum	468	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
88	Cladosporium sp.	472	+	91	Penicillium commune	4621	
88	Cladosporium sphaerospermum	936	+	91	Penicillium expansum	9438	+
88	Eurotium herbariorum	2349	+	91	Penicillium sp.	9438	
88	Penicillium commune	468		91	Penicillium sp. #26	4621	+
88	Penicillium expansum	6594	+	91	Penicillium sp. #87	4816	+
88	Penicillium expansum	1413		91	Penicillium verrucosum	4816	+
88	Penicillium sp. #26	1881		91	Penicillium viridicatum	4621	+
88	Penicillium sp. #26	945	+	91	Phoma leveillei	4816	
88	Penicillium waksmanii	945		91	Trichoderma viride	23497	
88	Scopulariopsis brevicaulis	472		91	Trichoderma viride	4621	+
88	Scopulariopsis brumptii	472	+	91	unknown	9438	+
88	Ulocladium chartarum	472	+	91	yeast	19267	
88	unknown	940		92	Alternaria alternata	478	+
88	unknown	940	+	92	Aspergillus sp.	478	+
88	yeast	4712		92	Aureobasidium pullulans	956	+
89	Alternaria alternata	3772		92	Epicoccum nigrum	478	+
89	Alternaria alternata	1926	+	92	Fusarium sp.	478	
89	Aspergillus niger	481	+	92	Penicillium aurantiogriseum	3346	
89	Aspergillus ochraceus	481	+	92	Penicillium aurantiogriseum	957	+
89	Aspergillus sp.	481	+	92	Penicillium expansum	1912	
89	Aureobasidium pullulans	5780	+	92	Penicillium hirsutum	3830	
89	Aureobasidium pullulans	1926		92	Penicillium hirsutum	478	+
89	Chrysosporium sp.	963		92	Penicillium miczynskii	478	
89	Cladosporium cladosporioides	963	+	92	Penicillium miczynskii	478	+
89	Cladosporium herbarum	963	+	92	Penicillium viridicatum	2391	
89	Cladosporium sp.	963	+	92	unknown	956	+
89	Cladosporium sphaerospermum	1445	+	92	unknown	478	
89	Epicoccum nigrum	1445		92	yeast	191387	
89	Epicoccum nigrum	481	+	94	Alternaria alternata	464	+
89	Eurotium herbariorum	963	+	94	Alternaria sp.	467	+
89	Penicillium brevicompactum	3371	+	94	Aspergillus fumigatus	21959	
89	Penicillium citrinum	7707	+	94	Aspergillus fumigatus	2798	+
89	Penicillium corylophilum	1445		94	Aspergillus niger	1396	+
89	Penicillium echinulatum	481	+	94	Aspergillus ochraceus	2333	
89	Penicillium spinulosum	2408	+	94	Aureobasidium pullulans	931	
89	Penicillium spinulosum	1926		94	Chrysosporium sp.	464	
89	Penicillium variabile	481	+	94	Cladosporium sp.	464	+
89	Trichoderma viride	481		94	Cladosporium sphaerospermum	931	+
89	unknown	1445		94	Epicoccum nigrum	934	
89	unknown	1445	+	94	Eurotium herbariorum	2795	+
89	Wallemia sebi	481	+	94	Mucor plumbeus	934	+
89	yeast	96339		94	Mucor racemosus	464	
90	Alternaria alternata	18298		94	Paecilomyces variotii	21892	+
90	Alternaria sp.	927		94	Paecilomyces variotii	467	
90	Aureobasidium pullulans	4223	+	94	Penicillium chrysogenum	934	+
90	Eurotium herbariorum	2807	+	94	Penicillium commune	464	
90	Fusarium oxysporum	476		94	Penicillium corylophilum	467	
90	Penicillium commune	3283	+	94	Trichoderma harzianum	467	
90	Penicillium commune	1391		94	Trichoderma viride	931	
90	Penicillium raistrickii	476	+	94	Trichoderma viride	467	+
90	unknown	463	+	94	unknown	931	
90	Wallemia sebi	61539	+	94	yeast	101822	
90	yeast	168194		95	Acremonium sp.	154440	
91	Absidia sp.	18150		95	Alternaria alternata	14204	+
91	Alternaria alternata	4621	+	95	Alternaria alternata	4612	
91	Aspergillus niger	4816	+	95	Aspergillus glaucus	18450	+
91	Aureobasidium pullulans	38339	+	95	Aspergillus niger	14204	+
91	Aureobasidium pullulans	9633		95	Aspergillus niger	9347	
91	Cladosporium sp.	4621	+	95	Aspergillus ochraceus	4734	+
91	Penicillium brevicompactum	4621	+	95	Aspergillus ochraceus	4612	
91	Penicillium commune	4816	+	95	Aspergillus ustus	23185	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
95 Aspergillus ustus	9225		98 Aureobasidium pullulans	44466	+
95 Aspergillus versicolor	18450		98 Cladosporium cladosporioides	339174	+
95 Aspergillus versicolor	4734	+	98 Cladosporium cladosporioides	4940	
95 Aspergillus wentii	14082		98 Cladosporium sphaerospermum	923594	+
95 Aureobasidium pullulans	65920	+	98 Cladosporium sphaerospermum	779704	
95 Aureobasidium pullulans	9225		98 Epicoccum nigrum	4743	
95 Cladosporium macrocarpum	18572	+	98 Eurotium herbariorum	57910	+
95 Cladosporium sp.	27675	+	98 Penicillium brevicompactum	44269	
95 Cladosporium sphaerospermum	79147	+	98 Penicillium brevicompactum	14822	+
95 Coniothyrium fuckelii	4734		98 Penicillium commune	48619	+
95 Epicoccum nigrum	13959		98 Penicillium commune	9684	
95 Eurotium herbariorum	37389	+	98 Phoma sp.	4743	
95 Moniliella sp.	9347		98 Scopulariopsis candida	4940	
95 Penicillium chrysogenum	37267		98 unknown	24703	
95 Penicillium chrysogenum	13837	+	98 Wallemia sebi	974145	+
95 Penicillium citrinum	4612	+	99 Alternaria alternata	79949	
95 Penicillium corylophilum	14082	+	99 Alternaria alternata	5517	+
95 Penicillium crustosum	4734		99 Aspergillus oryzae	1121	
95 Penicillium crustosum	4612	+	99 Aspergillus versicolor	42723	+
95 Penicillium decumbens	18817	+	99 Aspergillus versicolor	39506	
95 Penicillium decumbens	13959		99 Aureobasidium pullulans	19738	
95 Trichoderma viride	4612		99 Aureobasidium pullulans	18705	+
95 unknown	305319	+	99 Epicoccum nigrum	3275	
95 unknown	37022		99 Epicoccum nigrum	1091	+
95 Wallemia sebi	112413	+	99 Eurotium herbariorum	17731	+
95 Wardomyces humicola	4734		99 Penicillium brevicompactum	3275	
95 yeast	145068		99 Penicillium chrysogenum	11093	+
96 Alternaria alternata	2814	+	99 Penicillium chrysogenum	4484	
96 Aspergillus fumigatus	117739		99 Penicillium expansum	5517	
96 Aspergillus fumigatus	474	+	99 Penicillium expansum	4425	+
96 Aspergillus niger	474		99 Penicillium spinulosum	2183	
96 Aspergillus sp.	1423	+	99 Penicillium spinulosum	1091	+
96 Aspergillus versicolor	1423	+	99 Phoma sp.	2183	
96 Aureobasidium pullulans	77946	+	99 unknown	9854	
96 Aureobasidium pullulans	943		100 Alternaria alternata	9076	
96 Cladosporium cladosporioides	469	+	100 Alternaria alternata	3340	+
96 Drechslera sp.	469	+	100 Aspergillus niger	495	
96 Epicoccum nigrum	943	+	100 Aspergillus niger	495	+
96 Mucor plumbeus	943		100 Aureobasidium pullulans	3835	
96 Mucor racemosus	7094	+	100 Aureobasidium pullulans	1948	+
96 Mucor racemosus	7083		100 Chrysosporium sp.	463	
96 Penicillium citreonigrum	948	+	100 Cladosporium sp.	2845	+
96 Penicillium citrinum	943	+	100 Cladosporium sphaerospermum	958	+
96 Penicillium sp.	474		100 Epicoccum nigrum	990	
96 Penicillium spinulosum	4743	+	100 Epicoccum nigrum	463	+
96 Penicillium spinulosum	938		100 Penicillium atramentosum	495	+
96 Penicillium viridicatum	9930	+	100 Penicillium brevicompactum	4361	+
96 Penicillium viridicatum	4253		100 Penicillium commune	495	
96 Trichoderma viride	2830		100 Penicillium corylophilum	1886	+
96 unknown	2361	+	100 Penicillium janthinellum	495	+
96 unknown	469		100 Penicillium miczynskii	495	
96 yeast	63614		100 Penicillium simplicissimum	8875	
98 Acremonium sp.	48397		100 Penicillium sp. #26	958	
98 Alternaria alternata	143280	+	100 Penicillium sp. #64	927	
98 Alternaria alternata	9881		100 Penicillium spinulosum	2876	
98 Aspergillus ochraceus	154755		100 Penicillium spinulosum	1422	+
98 Aspergillus ochraceus	68185	+	100 Pithomyces chartarum	990	
98 Aspergillus sp.	4743		100 Trichoderma viride	1948	
98 Aspergillus versicolor	288961		100 unknown	5784	+
98 Aspergillus versicolor	102179	+	100 unknown	4825	
98 Aureobasidium pullulans	472339		100 yeast	11042	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
101	Alternaria alternata	12102		104	Alternaria alternata	4476	
101	Alternaria alternata	9699	+	104	Alternaria alternata	1886	+
101	Aspergillus ochraceus	296474		104	Apiospora montagnei	471	
101	Aspergillus ochraceus	254723	+	104	Apiospora sp.	510	
101	Aspergillus sp.	6578	+	104	Aspergillus sp.	1925	+
101	Aspergillus versicolor	19399	+	104	Aspergillus sp.	471	
101	Aspergillus versicolor	3289		104	Aureobasidium pullulans	510	
101	Cladosporium cladosporioides	488360	+	104	Cladosporium herbarum	510	+
101	Cladosporium cladosporioides	371794		104	Cladosporium herbarum	471	
101	Cladosporium sp.	3289	+	104	Cladosporium sp.	4437	+
101	Cladosporium sphaerospermum	19399	+	104	Cladosporium sp.	2474	
101	Coniothyrium sp.	19230		104	Epicoccum nigrum	2358	+
101	Eurotium herbariorum	9699	+	104	Epicoccum nigrum	1453	
101	Penicillium chrysogenum	6494	+	104	Epicoccum sp.	471	
101	Penicillium chrysogenum	6410		104	Eurotium herbariorum	1453	+
101	Phoma sp.	3205		104	Eurotium sp.	510	+
101	Rhizopus oryzae	3205		104	Microsphaeropsis sp.	1886	
101	Trichoderma viride	6410		104	Penicillium griseofulvum	3022	+
101	unknown	1234817		104	Penicillium griseofulvum	1415	
101	unknown	221406	+	104	Penicillium implicatum	471	+
102	Alternaria alternata	85802		104	Penicillium sp.	510	
102	Aspergillus ochraceus	2873		104	Penicillium sp. #26	471	+
102	Aureobasidium pullulans	148881		104	Penicillium spinulosum	1453	
102	Aureobasidium pullulans	95798	+	104	Penicillium spinulosum	981	+
102	Cladosporium cladosporioides	35997	+	104	Penicillium viridicatum	471	
102	Cladosporium cladosporioides	3378		104	Sphaeropsis sp.	3340	
102	Cladosporium sphaerospermum	12503		104	unknown	2512	
102	Epicoccum nigrum	5747		104	unknown	1925	+
102	Epicoccum nigrum	2873	+	104	yeast	943	
102	Penicillium aurantiogriseum	6251	+	105	Aspergillus versicolor	2258	
102	Penicillium chrysogenum	22639		105	Eurotium herbariorum	1744	+
102	Penicillium chrysogenum	9630	+	105	Humicola fuscoatra	338	
102	Penicillium corylophilum	14367	+	105	Mucor racemosus	371	
102	Penicillium corylophilum	2873		105	Penicillium atramentosum	169	
102	Penicillium spinulosum	2873		105	Penicillium aurantiogriseum	1066	
102	Phoma sp.	174161		105	Penicillium aurantiogriseum	355	+
102	Phoma sp.	161657	+	105	Penicillium chrysogenum	2438	+
102	Trichoderma viride	5747		105	Penicillium chrysogenum	1219	
102	unknown	2873		105	Penicillium commune	557	+
102	unknown	2873	+	105	Penicillium corylophilum	185	
103	Alternaria alternata	684		105	Penicillium raistrickii	1301	+
103	Alternaria alternata	684	+	105	Penicillium raistrickii	169	
103	Aspergillus glaucus	342	+	105	Penicillium simplicissimum	847	+
103	Aspergillus sp.	684	+	105	Penicillium simplicissimum	727	
103	Aureobasidium pullulans	1712	+	105	Penicillium sp. #26	169	
103	Aureobasidium pullulans	342		105	Penicillium spinulosum	1033	+
103	Cladosporium sp.	342		105	Penicillium spinulosum	169	
103	Cladosporium sp.	342	+	105	Scopulariopsis brevicaulis	338	+
103	Epicoccum nigrum	684		105	unknown	355	
103	Epicoccum nigrum	342	+	105	Wallemia sebi	4871	+
103	Eurotium herbariorum	1027	+	105	yeast	28511	
103	Penicillium commune	342		106	Alternaria alternata	63375	+
103	Penicillium commune	342	+	106	Alternaria alternata	28209	
103	Penicillium expansum	1027		106	Aureobasidium pullulans	179081	
103	Penicillium spinulosum	1369		106	Aureobasidium pullulans	126600	+
103	Penicillium spinulosum	684	+	106	Cladosporium cladosporioides	4921	
103	Penicillium viridicatum	342		106	Cladosporium sphaerospermum	34448	+
103	Phoma fimeti	342	+	106	Epicoccum nigrum	57852	+
103	unknown	1369		106	Epicoccum nigrum	33847	
103	unknown	684	+	106	Eurotium herbariorum	19083	+
103	yeast	1369		106	Fusarium sp.	14763	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
106	Mucor racemosus	24155	+	109	Pestalotiopsis sp.	946	+
106	Penicillium chrysogenum	76636		109	unknown	1419	
106	Penicillium chrysogenum	43840	+	109	yeast	2366	
106	Penicillium oxalicum	14763		110	Alternaria alternata	5127	+
106	Penicillium oxalicum	9541	+	110	Alternaria alternata	1612	
106	Penicillium vulpinum	19685		110	Aureobasidium pullulans	22207	+
106	Penicillium vulpinum	19384	+	110	Aureobasidium pullulans	15337	
106	Phoma herbarum	9541		110	Cladosporium cladosporioides	2272	+
106	Trichoderma viride	48761		110	Cladosporium herbarum	566	+
106	unknown	9842	+	110	Cladosporium sphaerospermum	572	
106	unknown	4921		110	Eurotium herbariorum	12513	+
106	Wallemia sebi	38167	+	110	Fusarium sp.	572	+
107	Alternaria alternata	2946		110	Paecilomyces sp.	572	+
107	Alternaria alternata	1476	+	110	Penicillium chrysogenum	2272	
107	Aureobasidium pullulans	30482		110	Penicillium chrysogenum	566	+
107	Aureobasidium pullulans	17681	+	110	Penicillium implicatum	1711	
107	Cladosporium cladosporioides	493		110	Penicillium miczynskii	5122	
107	Cladosporium sphaerospermum	493	+	110	Penicillium miczynskii	3416	+
107	Epicoccum nigrum	1963		110	Scopulariopsis brumptii	572	
107	Epicoccum nigrum	1473	+	110	unknown	5694	
107	Eurotium herbariorum	493	+	110	unknown	2277	+
107	Penicillium commune	2946		110	yeast	1133	
107	Penicillium commune	983	+	111	Alternaria alternata	6195	+
107	Penicillium griseofulvum	493		111	Alternaria alternata	3916	
107	Penicillium viridicatum	1476	+	111	Aspergillus niger	478	
107	Penicillium viridicatum	493		111	Aspergillus niger	476	+
107	Stachybotrys chartarum	490		111	Aspergillus ochraceus	2862	+
107	Ulocladium chartarum	490	+	111	Aspergillus ochraceus	2380	
108	Alternaria alternata	982		111	Aspergillus versicolor	2389	
108	Alternaria alternata	490	+	111	Aureobasidium pullulans	9066	
108	Aspergillus versicolor	490		111	Aureobasidium pullulans	8119	+
108	Aureobasidium pullulans	45637		111	Cladosporium cladosporioides	952	+
108	Aureobasidium pullulans	28954	+	111	Cladosporium sphaerospermum	478	+
108	Cladosporium cladosporioides	980	+	111	Cladosporium sphaerospermum	476	
108	Eurotium herbariorum	2945	+	111	Epicoccum nigrum	3820	
108	Fusarium sp.	491		111	Epicoccum nigrum	478	+
108	Paecilomyces variotii	6866		111	Eurotium herbariorum	478	+
108	Paecilomyces variotii	490	+	111	Mucor plumbeus	957	+
108	Penicillium citrinum	1962		111	Penicillium chrysogenum	4302	+
108	Penicillium citrinum	1471	+	111	Penicillium chrysogenum	2862	
108	Penicillium decumbens	3926		111	Penicillium raistrickii	478	
108	Penicillium raistrickii	19626	+	111	Penicillium spinulosum	478	
108	Penicillium raistrickii	12757		111	Penicillium spinulosum	478	+
108	Phoma herbarum	491		111	unknown	3341	
108	Ulocladium chartarum	491	+	112	Alternaria alternata	13301	+
108	unknown	1960		112	Alternaria alternata	9398	
108	yeast	2452		112	Aspergillus niger	550	
109	Alternaria alternata	8756		112	Aureobasidium pullulans	2759	+
109	Alternaria alternata	945	+	112	Cladosporium cladosporioides	7715	+
109	Aspergillus niger	473		112	Cladosporium cladosporioides	2759	
109	Aspergillus niger	472	+	112	Epicoccum nigrum	3322	+
109	Aureobasidium pullulans	1892	+	112	Epicoccum nigrum	2214	
109	Botrytis allii	1420	+	112	Mucor sp.	550	+
109	Cladosporium cladosporioides	473		112	Nigrospora sphaerica	550	
109	Cladosporium cladosporioides	472	+	112	Penicillium brevicompactum	1107	
109	Epicoccum nigrum	473		112	Penicillium sp. #26	550	+
109	Mucor plumbeus	472	+	112	Penicillium spinulosum	556	
109	Paecilomyces variotii	473		112	Penicillium viridicatum	1113	
109	Penicillium brevicompactum	473	+	112	Penicillium viridicatum	556	+
109	Penicillium brevicompactum	472		112	Sphaeropsis sp.	1107	
109	Penicillium spinulosum	472		112	unknown	3310	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
112 unknown	2759		117 Chaetomium nozdrenkoae	94	
112 Wallemia sebi	556	+	117 Penicillium brevicompactum	92	
112 yeast	11625		117 Penicillium commune	185	+
114 Alternaria alternata	6858		117 Penicillium corylophilum	278	+
114 Alternaria alternata	2914	+	117 Penicillium expansum	375	+
114 Aspergillus niger	969	+	117 Penicillium expansum	189	
114 Aspergillus versicolor	2426	+	117 Penicillium implicatum	658	+
114 Aureobasidium pullulans	20875	+	117 Penicillium implicatum	189	
114 Aureobasidium pullulans	13559		117 Penicillium restrictum	94	
114 Cladosporium sphaerospermum	2418	+	117 Penicillium simplicissimum	94	+
114 Epicoccum nigrum	976		117 Penicillium sp.	92	
114 Epicoccum nigrum	488	+	117 Rhizopus oryzae	94	+
114 Eurotium herbariorum	488	+	117 Trichoderma viride	282	
114 Mucor racemosus	488		117 Trichoderma viride	94	+
114 Penicillium brevicompactum	480		118 Alternaria alternata	959	
114 Penicillium citrinum	1953		118 Alternaria alternata	479	+
114 Penicillium corylophilum	1930	+	118 Aureobasidium pullulans	3358	
114 Penicillium corylophilum	1449		118 Aureobasidium pullulans	1439	+
114 Phoma herbarum	2892		118 Chaetomium globosum	478	+
114 unknown	2907		118 Epicoccum nigrum	478	+
114 yeast	1464		118 Eurotium herbariorum	478	+
115 Alternaria alternata	5261	+	118 Microsphaeropsis olivaceus	2390	
115 Alternaria alternata	2868		118 Microsphaeropsis sp.	2869	
115 Aspergillus ochraceus	492	+	118 Microsphaeropsis sp.	957	+
115 Aureobasidium pullulans	16395		118 Paecilomyces variotii	1435	
115 Aureobasidium pullulans	16361	+	118 Paecilomyces variotii	957	+
115 Cladosporium cladosporioides	2426	+	118 Penicillium echinulatum	1917	+
115 Cladosporium sphaerospermum	984		118 Penicillium echinulatum	479	
115 Epicoccum nigrum	492		118 Penicillium glandicola	478	
115 Mucor plumbeus	475		118 Penicillium raistrickii	479	
115 Mucor racemosus	475	+	118 Penicillium raistrickii	478	+
115 Penicillium brevicompactum	475	+	118 unknown	5267	
115 Penicillium islandicum	492		118 unknown	1439	+
115 Penicillium oxalicum	475		118 Wallemia sebi	479	+
115 Penicillium spinulosum	37085	+	118 yeast	6234	
115 Penicillium spinulosum	32500		119 Alternaria alternata	24452	+
115 Scopulariopsis candida	492	+	119 Alternaria alternata	6320	
115 Ulocladium chartarum	492		119 Aspergillus glaucus	9804	+
115 unknown	3835		119 Aspergillus sp.	4921	+
115 yeast	475		119 Aspergillus versicolor	19608	+
116 Alternaria alternata	1081		119 Cladosporium cladosporioides	4921	
116 Aspergillus niger	382		119 Cladosporium cladosporioides	4921	+
116 Aspergillus niger	285	+	119 Cladosporium sp.	9842	
116 Aspergillus ustus	96		119 Cladosporium sp.	9842	+
116 Aspergillus versicolor	94	+	119 Epicoccum nigrum	4882	
116 Cylindrocarpon sp.	94		119 Epicoccum sp.	4882	
116 Eurotium herbariorum	94	+	119 Epicoccum sp.	4882	+
116 Fusarium sp.	94	+	119 Eurotium herbariorum	34295	+
116 Mucor racemosus	760		119 Penicillium brevicompactum	9765	+
116 Mucor racemosus	668	+	119 Penicillium brevicompactum	4882	
116 Paecilomyces variotii	96		119 Penicillium commune	24529	
116 Penicillium chrysogenum	763	+	119 Penicillium commune	4882	+
116 Penicillium citrinum	189	+	119 unknown	568597	+
116 Penicillium funiculosum	94		119 yeast	29527	
116 unknown	380		120 Alternaria alternata	676	+
116 yeast	571		120 Aspergillus niger	714212	
117 Alternaria alternata	189	+	120 Aspergillus niger	75	+
117 Aspergillus niger	94		120 Aspergillus versicolor	834	+
117 Aspergillus ochraceus	94	+	120 Chaetomium globosum	75	
117 Aspergillus ochraceus	92		120 Cladosporium cladosporioides	834	+
117 Aspergillus versicolor	379	+	120 Cladosporium herbarum	75	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
120	Cladosporium sphaerospermum	759	+	122	Eurotium herbariorum	388	+
120	Emericella nidulans	759	+	122	Leptosphaerulina australis	76	
120	Eurotium herbariorum	909	+	122	Penicillium brevicompactum	76	+
120	Fusarium flocciferum	151		122	Penicillium chrysogenum	3398	
120	Fusarium oxysporum	759	+	122	Penicillium chrysogenum	546	+
120	Lecythophora hoffmannii	759	+	122	Penicillium commune	76	+
120	Paecilomyces sp.	227		122	Penicillium oxalicum	79	+
120	Paecilomyces variotii	75		122	Penicillium sp.	229	
120	Penicillium citreonigrum	834	+	122	Penicillium spinulosum	792	
120	Penicillium commune	75		122	Phoma herbarum	79	+
120	Penicillium commune	75	+	122	Ulocladium chartarum	153	
120	Penicillium crustosum	150	+	122	unknown	766	
120	Penicillium crustosum	75		122	unknown	699	+
120	Penicillium expansum	75	+	122	Wallemia sebi	232	+
120	Penicillium raistrickii	759	+	122	yeast	1890	
120	Penicillium simplicissimum	1518	+	123	Alternaria alternata	525	
120	Penicillium sp.	759	+	123	Aspergillus niger	64	
120	Penicillium sp.	150		123	Aspergillus versicolor	2566	+
120	Penicillium spinulosum	75	+	123	Chaetomium globosum	649	+
120	Penicillium variabile	75		123	Cochliobolus sativus	64	
120	Phoma medicaginis	75	+	123	Eurotium herbariorum	2566	+
120	Scopulariopsis brevicaulis	1058		123	Mucor plumbeus	63	
120	Scopulariopsis brevicaulis	984	+	123	Mucor racemosus	633	+
120	Torula herbarum	759	+	123	Penicillium atramentosum	1283	+
120	Trichoderma viride	75		123	Penicillium aurantiogriseum	1949	+
120	Trichoderma viride	75	+	123	Penicillium corylophilum	128	
120	unknown	1668	+	123	Penicillium crustosum	649	+
120	Wallemia sebi	150	+	123	Penicillium crustosum	129	
120	yeast	454		123	Penicillium echinulatum	649	+
121	Alternaria alternata	10725	+	123	Penicillium expansum	649	+
121	Alternaria alternata	682		123	Penicillium expansum	190	
121	Aspergillus niger	8190	+	123	Penicillium sp. #1	63	
121	Aspergillus niger	5832		123	Penicillium viridicatum	1933	+
121	Aspergillus sydowii	494	+	123	Penicillium vulpinum	649	+
121	Aspergillus sydowii	478		123	Rhizopus oryzae	64	
121	Aspergillus versicolor	972	+	123	Scopulariopsis candida	64	
121	Aspergillus versicolor	478		123	Trichoderma koningii	64	
121	Aureobasidium pullulans	19377		123	Trichoderma viride	649	+
121	Aureobasidium pullulans	5370	+	123	Wallemia sebi	1283	+
121	Epicoccum nigrum	494	+	123	yeast	833	
121	Eurotium herbariorum	4908	+	125	Acremonium rutilum	3947	
121	Penicillium aurantiogriseum	478		125	Alternaria alternata	482	+
121	Penicillium chrysogenum	19297	+	125	Aspergillus ochraceus	97	+
121	Penicillium chrysogenum	14946		125	Cladosporium sphaerospermum	96	+
121	Penicillium citreonigrum	494		125	Epicoccum nigrum	193	+
121	Penicillium italicum	5338		125	Eurotium herbariorum	97	+
121	Penicillium italicum	1482	+	125	Paecilomyces sp.	96	+
121	Penicillium spinulosum	2868	+	125	Penicillium chrysogenum	290	+
121	Penicillium spinulosum	2868		125	Penicillium crustosum	97	+
121	unknown	7840		125	Penicillium expansum	97	
121	unknown	1466	+	125	Pestalotiopsis palustris	96	+
121	yeast	8254		125	Pithomyces chartarum	193	+
122	Alternaria alternata	9362		125	Rhizopus oryzae	289	
122	Alternaria alternata	314	+	125	Rhizopus oryzae	96	+
122	Aspergillus niger	792		125	Stachybotrys parvispora	291	
122	Aspergillus versicolor	79	+	125	Torula herbarum	97	+
122	Aspergillus versicolor	76		125	unknown	97	+
122	Aureobasidium pullulans	311	+	125	yeast	872	
122	Chaetomium globosum	536		126	Aspergillus niger	477	+
122	Emericella nidulans	549	+	126	Aspergillus ochraceus	2831	+
122	Emericella sp.	792		126	Aspergillus ochraceus	567	



HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
126 Aspergillus paradoxus	3339	+	129 Aspergillus fumigatus	477	+
126 Aspergillus paradoxus	470		129 Aspergillus fumigatus	477	
126 Aspergillus versicolor	6139		129 Aspergillus niger	191	
126 Aspergillus versicolor	3791	+	129 Aspergillus ochraceus	96	+
126 Cladosporium sphaerospermum	1908		129 Aspergillus oryzae	96	+
126 Cladosporium sphaerospermum	470	+	129 Aspergillus restrictus	96	+
126 Emericella varicolor	470	+	129 Cochliobolus geniculatus	95	+
126 Eurotium herbariorum	1889	+	129 Drechslera biseptata	95	+
126 Eurotium rubrum	470	+	129 Epicoccum nigrum	96	
126 Gliomastix murorum var. felina	7081		129 Paecilomyces inflatus	670	
126 Penicillium aurantiogriseum	1425		129 Paecilomyces variotii	96	
126 Penicillium commune	947	+	129 Penicillium commune	191	+
126 Penicillium corylophilum	941		129 Penicillium corylophilum	95	
126 Penicillium decumbens	941		129 Penicillium expansum	191	
126 Penicillium decumbens	470	+	129 Penicillium simplicissimum	479	+
126 Penicillium expansum	477	+	129 Penicillium simplicissimum	96	
126 Penicillium variabile	477		129 Penicillium spinulosum	192	
126 Phoma herbarum	470		129 Pithomyces chartarum	95	
126 Scolecobasidium constrictum	470		129 Pithomyces chartarum	95	+
126 Scopulariopsis brevicaulis	470		129 Pythium sp.	96	
126 Scopulariopsis chartarum	1425	+	129 Scopulariopsis brevicaulis	96	+
126 Scopulariopsis chartarum	470		129 Scopulariopsis candida	96	
126 Sporobolomyces sp.	954		129 Ulocladium atrum	96	+
126 Stachybotrys chartarum	2385		129 Ulocladium chartarum	95	+
126 Trichoderma viride	1412		129 unknown	477	+
126 unknown	941	+	129 unknown	384	
126 unknown	470		130 Alternaria alternata	766	
126 Wallemia sebi	941	+	130 Alternaria alternata	377	+
126 yeast	2366		130 Aspergillus niger	384	+
127 Alternaria alternata	485	+	130 Chaetomium globosum	96	
127 Aspergillus niger	978		130 Epicoccum nigrum	93	+
127 Aspergillus niger	485	+	130 Eurotium herbariorum	283	+
127 Fusarium oxysporum	485		130 Fusarium oxysporum	93	
127 Mucor plumbeus	493	+	130 Penicillium chrysogenum	571	+
127 Penicillium sp. #64	3914	+	130 Penicillium chrysogenum	96	
127 Penicillium sp. #64	493		130 Penicillium commune	93	
127 Penicillium spinulosum	2920	+	130 Penicillium viridicatum	384	
127 Penicillium spinulosum	2450		130 Scopulariopsis brevicaulis	387	
127 Pestalotiopsis palustris	485	+	130 Talaromyces trachyspermus var. macrocarpus	96	
128 Alternaria alternata	2946	+	130 yeast	280	
128 Aspergillus niger	3925	+	132 Alternaria alternata	2366	+
128 Aspergillus niger	2455		132 Alternaria alternata	861	
128 Aspergillus versicolor	491		132 Aspergillus fumigatus	463	+
128 Chaetomium circinatum	491		132 Aspergillus ochraceus	1855	
128 Cladosporium cladosporioides	487	+	132 Aspergillus ochraceus	463	+
128 Eurotium herbariorum	491	+	132 Aspergillus terreus	1391	+
128 Mucor racemosus	487	+	132 Aspergillus versicolor	2806	+
128 Penicillium corylophilum	5890	+	132 Aspergillus versicolor	1855	
128 Penicillium corylophilum	4416		132 Aureobasidium pullulans	3851	+
128 Penicillium expansum	487		132 Aureobasidium pullulans	3781	
128 Penicillium expansum	487	+	132 Cunninghamella sp.	10069	
128 Penicillium spinulosum	3426	+	132 Cunninghamella sp.	5683	+
128 Penicillium spinulosum	487		132 Eurotium herbariorum	3851	+
128 Phoma herbarum	982	+	132 Geomyces sp.	1902	
128 Scopulariopsis candida	491	+	132 Penicillium brevicompactum	4779	+
128 Stachybotrys chartarum	487	+	132 Penicillium chrysogenum	2923	
128 unknown	974	+	132 Penicillium chrysogenum	2389	+
128 Wallemia sebi	45048	+	132 Penicillium commune	463	+
128 yeast	6358		132 Penicillium spinulosum	6611	
129 Alternaria alternata	95	+	132 Penicillium spinulosum	4732	+
129 Alternaria sp.	95	+	132 Phoma sp.	1461	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
132 Trichoderma viride	463	+	136 Penicillium viridicatum	478	+
132 unknown	9488		136 Phoma herbarum	470	+
132 unknown	1949	+	136 unknown	2832	+
132 Wallemia sebi	487	+	136 Wallemia sebi	2846	+
132 yeast	9535		136 yeast	10972	
133 Alternaria alternata	465	+	137 Alternaria alternata	467	+
133 Aspergillus niger	4703		137 Alternaria sp.	467	+
133 Aspergillus niger	4668	+	137 Cladosporium cladosporioides	3347	
133 Aspergillus ochraceus	469		137 Cladosporium cladosporioides	2386	+
133 Eurotium herbariorum	4189	+	137 Eurotium herbariorum	467	+
133 Mucor plumbeus	4211	+	137 Mucor racemosus	3838	+
133 Mucor plumbeus	3276		137 Mucor racemosus	2386	
133 Mucor racemosus	11721		137 Penicillium spinulosum	467	
133 Mucor racemosus	5608	+	137 Penicillium viridicatum	3788	+
133 Penicillium aurantiogriseum	3276		137 Penicillium viridicatum	1906	
133 Penicillium aurantiogriseum	469	+	137 Penicillium vulpinum	479	
133 Penicillium chrysogenum	17264	+	137 unknown	2374	
133 Penicillium chrysogenum	4203		137 unknown	1426	+
133 Penicillium janthinellum	469		137 yeast	1894	
133 Penicillium sp.	931		138 Alternaria alternata	391	+
133 Penicillium sp. #26	2349		138 Alternaria sp.	393	
133 Phoma herbarum	3759	+	138 Aspergillus sydowii	98	+
133 yeast	7492		138 Aspergillus versicolor	194	
134 Alternaria alternata	9398		138 Aspergillus versicolor	97	+
134 Alternaria alternata	4621	+	138 Aureobasidium pullulans	1865	
134 Aspergillus restrictus	4621	+	138 Aureobasidium pullulans	1566	+
134 Aureobasidium pullulans	9398		138 Chaetomium globosum	584	
134 Epicoccum nigrum	4621	+	138 Cladosporium sphaerospermum	97	+
134 Eurotium herbariorum	23183	+	138 Eurotium herbariorum	983	+
134 Mucor racemosus	9320	+	138 Fusarium sp.	98	+
134 Penicillium aurantiogriseum	4621	+	138 Fusarium sp.	97	
134 Penicillium citrinum	4621	+	138 Mucor plumbeus	97	+
134 Penicillium commune	18718	+	138 Paecilomyces variotii	97	+
134 Penicillium commune	13941		138 Penicillium aurantiogriseum	196	
134 Wallemia sebi	4206739	+	138 Penicillium chrysogenum	1171	+
134 yeast	23261		138 Penicillium chrysogenum	683	
135 Alternaria alternata	37825		138 Penicillium corylophilum	98	
135 Alternaria alternata	4210	+	138 Penicillium spinulosum	195	
135 Aureobasidium pullulans	2342		138 Penicillium spinulosum	194	+
135 Epicoccum nigrum	2814	+	138 Scopulariopsis candida	393	
135 Penicillium corylophilum	469		138 unknown	881	+
135 Penicillium raistrickii	2809	+	138 unknown	687	
135 Phoma herbarum	938		138 yeast	583	
135 Phoma herbarum	935	+	139 Aspergillus glaucus	641	+
135 Scopulariopsis brevicaulis	469	+	139 Aspergillus niger	627	+
135 unknown	938	+	139 Aspergillus niger	387	
135 Wallemia sebi	7001	+	139 Chaetomium globosum	64	
135 Wallemia sebi	469		139 Eurotium herbariorum	7639	+
135 yeast	1404		139 Fusarium oxysporum	190	
136 Chaetomium funicola	4699		139 Penicillium aurantiogriseum	1208	
136 Cochliobolus geniculatus	478	+	139 Penicillium chrysogenum	2524	+
136 Epicoccum nigrum	470		139 Penicillium chrysogenum	253	
136 Eurotium herbariorum	470	+	139 Penicillium crustosum	62	
136 Mucor mucedo	470		139 Penicillium spinulosum	1909	+
136 Mucor racemosus	478	+	139 Penicillium spinulosum	252	
136 Penicillium brevicompactum	470	+	139 Phoma herbarum	627	+
136 Penicillium canescens	1412		139 Pithomyces chartarum	1883	+
136 Penicillium commune	5207	+	139 Scopulariopsis candida	7639	+
136 Penicillium commune	3795		139 Scopulariopsis candida	2151	
136 Penicillium corylophilum	948	+	139 unknown	62	
136 Penicillium italicum	478	+	140 Mucor plumbeus	10842	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
140 Penicillium chrysogenum	108229	+	146 yeast	1337	
140 Penicillium chrysogenum	9881		147 Alternaria alternata	1464	+
140 Penicillium commune	19646	+	147 Alternaria alternata	491	
140 Penicillium corylophilum	4940		147 Aspergillus niger	976	+
140 Penicillium decumbens	19675	+	147 Aspergillus niger	491	
140 Penicillium decumbens	9823		147 Aureobasidium pullulans	2450	+
140 Penicillium expansum	4911		147 Cladosporium cladosporioides	488	+
140 Penicillium griseofulvum	88466		147 Epicoccum nigrum	2441	
140 Penicillium spinulosum	4940		147 Paecilomyces variotii	976	
140 Trichoderma viride	4940	+	147 Penicillium brevicompactum	491	
140 unknown	9823		147 Penicillium chrysogenum	1961	
143 Alternaria alternata	15236		147 Penicillium commune	2935	
143 Alternaria alternata	2358	+	147 Penicillium commune	2450	+
143 Aspergillus versicolor	51482	+	147 Penicillium corylophilum	6362	+
143 Aspergillus versicolor	34472		147 Penicillium corylophilum	5385	
143 Aureobasidium pullulans	2830	+	147 Penicillium raistrickii	39648	+
143 Aureobasidium pullulans	943		147 Penicillium raistrickii	976	
143 Cladosporium cladosporioides	472	+	147 Rhizopus oryzae	488	+
143 Eurotium herbariorum	2361	+	147 unknown	3917	
143 Penicillium chrysogenum	4251	+	147 unknown	2946	+
143 Penicillium citreonigrum	471	+	147 yeast	2452	
143 Penicillium corylophilum	1415		148 Acremonium sp.	2952	
143 Penicillium spinulosum	3776		148 Alternaria alternata	2468	+
143 Penicillium spinulosum	945	+	148 Aspergillus clavatus	487	
143 Wallemia sebi	2361	+	148 Aspergillus fumigatus	498	
143 Wallemia sebi	472		148 Aspergillus niger	3919	+
143 yeast	6132		148 Aspergillus niger	487	
145 Acremonium sp.	3769		148 Aspergillus ochraceus	498	+
145 Alternaria alternata	1409	+	148 Aspergillus versicolor	974	
145 Aspergillus versicolor	17750	+	148 Aspergillus versicolor	498	+
145 Aspergillus versicolor	14530		148 Aureobasidium pullulans	498	+
145 Cladosporium sphaerospermum	473	+	148 Cladosporium cladosporioides	487	
145 Eurotium herbariorum	2335	+	148 Lecythophora hoffmannii	974	
145 Penicillium chrysogenum	925	+	148 Mucor racemosus	498	
145 unknown	3272	+	148 Paecilomyces inflatus	498	
145 unknown	1409		148 Penicillium aurantiogriseum	13752	+
145 yeast	1388		148 Penicillium citreonigrum	498	+
146 Alternaria alternata	5774		148 Penicillium commune	1472	+
146 Alternaria alternata	467	+	148 Penicillium commune	974	
146 Aspergillus versicolor	276		148 Penicillium sp. #26	498	
146 Aureobasidium pullulans	276	+	148 Penicillium spinulosum	1959	+
146 Chaetomium globosum	98		148 Penicillium viridicatum	498	+
146 Cladosporium cladosporioides	92		148 unknown	498	
146 Epicoccum nigrum	92		148 yeast	10774	
146 Eurotium herbariorum	197	+	149 Aspergillus niger	9299	
146 Fusarium sp.	98		149 Aspergillus niger	478	+
146 Penicillium brevicompactum	92	+	149 Aspergillus ochraceus	472	
146 Penicillium commune	369	+	149 Aspergillus versicolor	3318	+
146 Penicillium commune	92		149 Aspergillus versicolor	472	
146 Penicillium corylophilum	197	+	149 Aureobasidium pullulans	1890	+
146 Penicillium crustosum	757		149 Chaetomium cochliodes	1423	
146 Penicillium crustosum	474	+	149 Cladosporium sphaerospermum	945	+
146 Penicillium decumbens	289	+	149 Eurotium herbariorum	2846	+
146 Penicillium decumbens	191		149 Penicillium chrysogenum	2857	+
146 Penicillium glandicola	197	+	149 Penicillium chrysogenum	950	
146 Penicillium raistrickii	184		149 Phoma fimeti	472	
146 Penicillium raistrickii	92	+	149 Pithomyces chartarum	472	+
146 Penicillium viridicatum	289	+	149 unknown	956	+
146 Penicillium vulpinum	98	+	149 yeast	1895	
146 Penicillium vulpinum	92		150 Acremonium sp.	5695	
146 unknown	184	+	150 Alternaria alternata	979	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
150 Aspergillus fumigatus	654		153 Cladosporium cladosporioides	4412	
150 Aspergillus niger	125	+	153 Epicoccum nigrum	1962	
150 Aspergillus ochraceus	128	+	153 Epicoccum nigrum	491	+
150 Aspergillus restrictus	627		153 Eurotium herbariorum	489	+
150 Aspergillus sp.	627		153 Penicillium citrinum	4410	
150 Aspergillus versicolor	17983		153 Penicillium citrinum	3430	+
150 Aspergillus versicolor	646	+	153 Penicillium purpurogenum	2941	+
150 Aureobasidium pullulans	7532		153 Penicillium purpurogenum	1473	
150 Chaetomium globosum	627		153 Penicillium sp.	489	+
150 Epicoccum nigrum	627		153 Penicillium verrucosum	980	+
150 Eurotium herbariorum	1470	+	153 Scopulariopsis brevicaulis	2941	
150 Geomyces pannorum	62	+	153 Scopulariopsis brevicaulis	489	+
150 Penicillium citreonigrum	627		153 Scopulariopsis fusca	489	
150 Penicillium expansum	4475		153 Trichoderma viride	491	
150 Penicillium expansum	578	+	153 unknown	8340	
150 Penicillium variabile	627		153 unknown	3919	+
150 Penicillium variabile	130	+	153 yeast	10788	
150 Phoma herbarum	1255		154 Alternaria alternata	114	+
150 Scopulariopsis candida	4394		154 Aspergillus fumigatus	23647	
150 Trichoderma viride	1255		154 Aspergillus ochraceus	345	+
150 unknown	10970		154 Aspergillus ochraceus	114	
150 unknown	2188	+	154 Aspergillus sydowii	115	
150 Wallemia sebi	627		154 Aspergillus versicolor	114	
150 Wallemia sebi	62	+	154 Chaetomium cochliodes	115	
150 yeast	21831		154 Eurotium rubrum	230	+
151 Alternaria alternata	1456		154 Exophiala jeanselmei	115	
151 Aspergillus candidus	99	+	154 Mucor mucedo	343	
151 Aspergillus ochraceus	289		154 Mucor plumbeus	114	
151 Aspergillus ochraceus	95	+	154 Mucor racemosus	228	+
151 Aspergillus versicolor	190	+	154 Penicillium chrysogenum	459	+
151 Epicoccum nigrum	476		154 Penicillium chrysogenum	114	
151 Eurotium herbariorum	289	+	154 Penicillium citrinum	229	
151 Paecilomyces variotii	99	+	154 Penicillium oxalicum	229	+
151 Penicillium citrinum	95	+	154 Trichoderma viride	343	+
151 Penicillium corylophilum	194	+	154 Trichoderma viride	115	
151 Penicillium glandicola	95		154 unknown	115	
151 Penicillium viridicatum	1058		154 unknown	114	+
151 Penicillium viridicatum	289	+	154 yeast	1154	
151 Pithomyces chartarum	190	+	155 Alternaria alternata	515	
151 Pithomyces chartarum	95		155 Alternaria alternata	96	+
151 yeast	860		155 Aspergillus oryzae	94	
152 Acremonium sp.	93		155 Aspergillus versicolor	191	
152 Alternaria alternata	93	+	155 Aureobasidium pullulans	290	
152 Aspergillus sydowii	93		155 Aureobasidium pullulans	288	+
152 Aspergillus ustus	93		155 Eurotium herbariorum	964	+
152 Cochliobolus geniculatus	93		155 Mucor plumbeus	96	
152 Eurotium herbariorum	93	+	155 Penicillium chrysogenum	2109	
152 Fusarium sp.	93		155 Penicillium chrysogenum	1057	+
152 Penicillium viridicatum	751		155 Penicillium corylophilum	288	
152 Penicillium viridicatum	187	+	155 Penicillium corylophilum	191	+
152 Phoma eupyrena	93		155 Scopulariopsis brevicaulis	667	
152 Phoma herbarum	187		155 Trichoderma viride	96	
152 Scopulariopsis brevicaulis	93	+	155 unknown	1627	
152 Trichoderma koningii	93		155 unknown	484	+
152 unknown	93	+	155 Wallemia sebi	288	+
152 yeast	1970		155 yeast	3726	
153 Alternaria alternata	5882	+	156 Acremonium strictum	289	
153 Alternaria alternata	3923		156 Alternaria alternata	96	
153 Aspergillus fumigatus	491	+	156 Aspergillus ochraceus	95	+
153 Aureobasidium pullulans	7854		156 Aspergillus sydowii	95	+
153 Cladosporium cladosporioides	4905	+	156 Blastobotrys sp.	289	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
156	<i>Epicoccum nigrum</i>	191		162	<i>Dothiorella</i> sp.	476	
156	<i>Eurotium herbariorum</i>	191	+	162	<i>Eurotium herbariorum</i>	1953	+
156	<i>Penicillium spinulosum</i>	575		162	<i>Mucor plumbeus</i>	1904	+
156	<i>Penicillium spinulosum</i>	95	+	162	<i>Mucor plumbeus</i>	476	
156	<i>Penicillium viridicatum</i>	286	+	162	<i>Penicillium chrysogenum</i>	488	
156	<i>Penicillium viridicatum</i>	95		162	<i>Penicillium commune</i>	488	
156	unknown	95		162	<i>Penicillium corylophilum</i>	1464	
156	yeast	1150		162	<i>Penicillium corylophilum</i>	488	+
157	<i>Alternaria alternata</i>	1324	+	162	<i>Penicillium expansum</i>	488	+
157	<i>Alternaria alternata</i>	862		162	<i>Penicillium italicum</i>	976	
157	<i>Aspergillus niger</i>	1231	+	162	<i>Penicillium</i> sp. #26	488	
157	<i>Aspergillus niger</i>	483		162	<i>Trichoderma viride</i>	964	
157	<i>Penicillium citreonigrum</i>	96	+	162	<i>Trichoderma viride</i>	476	+
157	<i>Penicillium citrinum</i>	284		162	unknown	1452	+
157	<i>Penicillium oxalicum</i>	290	+	162	unknown	476	
157	<i>Penicillium</i> sp. #26	96		162	yeast	7739	
157	<i>Penicillium spinulosum</i>	383		163	<i>Alternaria alternata</i>	1328	
157	<i>Trichoderma viride</i>	93		163	<i>Alternaria alternata</i>	525	+
157	<i>Ulocladium chartarum</i>	93		163	<i>Aspergillus versicolor</i>	3320	
157	unknown	958	+	163	<i>Aspergillus versicolor</i>	592	+
157	unknown	93		163	<i>Aureobasidium pullulans</i>	259	+
157	<i>Wallemia sebi</i>	2403	+	163	<i>Epicoccum nigrum</i>	194	+
157	yeast	2417		163	<i>Eurotium herbariorum</i>	651	+
158	<i>Alternaria alternata</i>	2122		163	<i>Fusarium</i> sp.	66	+
158	<i>Alternaria alternata</i>	384	+	163	<i>Penicillium chrysogenum</i>	13835	
158	<i>Aureobasidium pullulans</i>	947	+	163	<i>Penicillium chrysogenum</i>	2163	+
158	<i>Aureobasidium pullulans</i>	192		163	<i>Penicillium corylophilum</i>	194	+
158	<i>Cladosporium cladosporioides</i>	94		163	<i>Penicillium vulpinum</i>	585	+
158	<i>Eurotium herbariorum</i>	959	+	163	<i>Phoma herbarum</i>	664	
158	<i>Geotrichum candidum</i>	94		163	unknown	15936	
158	<i>Mucor plumbeus</i>	1055		163	unknown	7955	+
158	<i>Mucor plumbeus</i>	288	+	163	yeast	6485	
158	<i>Penicillium chrysogenum</i>	951	+	165	<i>Alternaria alternata</i>	2291	+
158	<i>Penicillium chrysogenum</i>	671		165	<i>Alternaria alternata</i>	1091	
158	<i>Penicillium commune</i>	94		165	<i>Aspergillus ochraceus</i>	546	
158	<i>Penicillium commune</i>	94	+	165	<i>Aspergillus ochraceus</i>	545	+
158	<i>Penicillium spinulosum</i>	94		165	<i>Aureobasidium pullulans</i>	1745	+
158	<i>Trichoderma viride</i>	94		165	<i>Cladosporium sphaerospermum</i>	54	+
158	unknown	572		165	<i>Epicoccum nigrum</i>	1745	+
158	yeast	1977		165	<i>Eurotium herbariorum</i>	54	+
160	<i>Aspergillus niger</i>	4423		165	<i>Fusarium oxysporum</i>	1635	
160	<i>Aspergillus ochraceus</i>	92	+	165	<i>Fusarium oxysporum</i>	545	+
160	<i>Eurotium herbariorum</i>	92	+	165	<i>Hainesia lythri</i>	546	
160	<i>Mucor plumbeus</i>	184		165	<i>Mucor racemosus</i>	545	+
160	<i>Mucor plumbeus</i>	92	+	165	<i>Paecilomyces inflatus</i>	545	
160	<i>Nigrospora sphaerica</i>	92		165	<i>Paecilomyces variotii</i>	545	
160	<i>Penicillium spinulosum</i>	277		165	<i>Penicillium aurantiogriseum</i>	1090	
160	<i>Penicillium spinulosum</i>	92	+	165	<i>Penicillium aurantiogriseum</i>	654	+
160	<i>Scopulariopsis brevicaulis</i>	184		165	<i>Penicillium brevicompactum</i>	54	+
160	unknown	92		165	<i>Penicillium corylophilum</i>	599	+
160	yeast	2125		165	<i>Penicillium oxalicum</i>	1090	+
161	<i>Aspergillus cervinus</i>	75	+	165	<i>Penicillium viridicatum</i>	546	
161	<i>Aspergillus oryzae</i>	75	+	165	<i>Pestalotiopsis</i> sp.	545	
161	<i>Aspergillus versicolor</i>	519		165	<i>Phoma herbarum</i>	1091	
161	<i>Chaetomium globosum</i>	79	+	165	<i>Phoma herbarum</i>	545	+
161	<i>Chaetomium globosum</i>	75		165	<i>Pithomyces chartarum</i>	546	
161	<i>Penicillium chrysogenum</i>	79	+	165	<i>Scopulariopsis candida</i>	545	
161	<i>Penicillium citrinum</i>	159	+	165	<i>Sphaeropsis</i> sp.	1254	+
161	yeast	51034		165	<i>Trichoderma viride</i>	163	+
162	<i>Alternaria alternata</i>	1464	+	165	<i>Ulocladium chartarum</i>	54	+
162	<i>Aspergillus niger</i>	14420		165	unknown	1145	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
165 unknown	546		169 Penicillium raistrickii	2033	+
165 yeast	7639		169 Penicillium spinulosum	386	+
166 Alternaria alternata	7572	+	169 Penicillium spinulosum	290	
166 Alternaria alternata	2855		169 Rhizopus oryzae	97	+
166 Aureobasidium pullulans	950	+	169 Trichoderma viride	97	
166 Epicoccum nigrum	469		169 unknown	193	+
166 Fusarium oxysporum	1415		169 yeast	289	
166 Mucor racemosus	475	+	170 Alternaria alternata	3853	+
166 Penicillium aurantiogriseum	1420		170 Aspergillus oryzae	64	
166 Penicillium brevicompactum	3770	+	170 Aspergillus sp.	64	
166 Penicillium corylophilum	9489	+	170 Aspergillus versicolor	642	+
166 Penicillium corylophilum	475		170 Cladosporium sp.	660	+
166 Penicillium decumbens	1901		170 Cladosporium sphaerospermum	2640	+
166 Penicillium sp.	475		170 Eurotium herbariorum	72859	+
166 Penicillium spinulosum	3791	+	170 Fusarium sp.	1302	+
166 Penicillium spinulosum	1885		170 Penicillium brevicompactum	1320	+
166 Trichoderma viride	6578	+	170 Penicillium brevicompactum	770	
166 Trichoderma viride	4736		170 Penicillium commune	1284	+
166 unknown	1420		170 Penicillium commune	385	
166 yeast	1890		170 Penicillium verrucosum	2586	+
167 Alternaria alternata	6867		170 Scopulariopsis brevicaulis	132	
167 Alternaria alternata	384	+	170 Talaromyces flavus	132	
167 Cladosporium cladosporioides	388	+	170 unknown	26064	+
167 Fusarium sp.	98	+	170 Wallemia sebi	68149	+
167 Penicillium brevicompactum	784	+	171 Alternaria alternata	1446	+
167 Penicillium brevicompactum	194		171 Aureobasidium pullulans	11508	+
167 Penicillium commune	98	+	171 Aureobasidium pullulans	2394	
167 Penicillium spinulosum	192		171 Chaetomium globosum	478	
167 Penicillium spinulosum	96	+	171 Fusarium sp.	957	+
167 Trichoderma viride	292	+	171 Mucor plumbeus	967	+
167 Trichoderma viride	290		171 Penicillium brevicompactum	1924	+
168 Aspergillus candidus	95		171 Penicillium corylophilum	478	+
168 Aspergillus fumigatus	482		171 Penicillium raistrickii	7685	+
168 Aspergillus niger	1359		171 unknown	5286	+
168 Aspergillus niger	1345	+	171 unknown	1436	
168 Chaetomium globosum	95		171 yeast	1920	
168 Chaetomium subspirale	98		171 Zetiaspizna heteromorpha	957	
168 Eurotium herbariorum	95	+	172 Alternaria alternata	10424	
168 Mucor mucedo	98	+	172 Alternaria alternata	9345	+
168 Mucor mucedo	95		172 Aspergillus niger	4816	+
168 Penicillium aurantiogriseum	383		172 Aspergillus ochraceus	28613	
168 Penicillium oxalicum	98		172 Aspergillus ochraceus	18691	+
168 Penicillium oxalicum	95	+	172 Aspergillus sydowii	4816	+
168 Penicillium sp. #26	95	+	172 Aspergillus versicolor	14306	
168 Penicillium sp. #64	98		172 Aspergillus versicolor	14018	+
168 Penicillium sp. #87	98	+	172 Aureobasidium pullulans	110357	
168 Penicillium spinulosum	390		172 Aureobasidium pullulans	28037	+
168 Penicillium viridicatum	778	+	172 Botrytis cinerea	4816	+
168 unknown	98		172 Chaetomium sp.	247663	
168 yeast	3168		172 Chaetomium sp.	127608	+
169 Alternaria alternata	579	+	172 Cladosporium cladosporioides	70093	+
169 Alternaria alternata	388		172 Cladosporium cladosporioides	14162	
169 Aspergillus glaucus	1061		172 Cladosporium sphaerospermum	4672	+
169 Aspergillus niger	97		172 Eurotium herbariorum	4672	+
169 Aureobasidium pullulans	7439	+	172 Penicillium chrysogenum	14306	
169 Aureobasidium pullulans	582		172 Penicillium chrysogenum	14306	+
169 Cladosporium cladosporioides	290	+	172 Penicillium spinulosum	9489	+
169 Eurotium herbariorum	290	+	172 Penicillium spinulosum	4816	
169 Mucor plumbeus	96	+	172 Penicillium viridicatum	38103	+
169 Penicillium commune	967	+	172 Penicillium viridicatum	33286	
169 Penicillium commune	291		172 Phoma sp.	14450	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
172 unknown	23940		176 Eurotium herbariorum	2839	+
172 unknown	4672	+	176 Paecilomyces variotii	472	
173 Alternaria alternata	24529	+	176 Penicillium aurantiogriseum	1890	+
173 Aspergillus niger	4911	+	176 Penicillium chrysogenum	473	+
173 Aspergillus ochraceus	186515	+	176 Penicillium corylophilum	9933	
173 Aspergillus ochraceus	63698		176 Penicillium purpurogenum	2838	
173 Aspergillus sp.	14734	+	176 Penicillium sp.	473	
173 Aspergillus sp.	4901		176 Penicillium viridicatum	473	
173 Aspergillus sydowii	161957	+	176 unknown	1417	
173 Aspergillus versicolor	49019		176 yeast	473	
173 Aureobasidium pullulans	1487220	+	177 Aspergillus niger	166	+
173 Aureobasidium pullulans	63812		177 Chaetomium cochliodes	10298	
173 Chaetomium globosum	4901		177 Eurotium herbariorum	221	+
173 Cladosporium sphaerospermum	1256616	+	177 Penicillium chrysogenum	2219	
173 Penicillium chrysogenum	9823		177 Penicillium chrysogenum	499	+
173 Penicillium raistrickii	137428	+	177 Penicillium corylophilum	1400	+
173 Penicillium raistrickii	4911		177 Penicillium sp. #26	554	
173 Penicillium sp. #64	107958	+	177 Penicillium sp. #26	110	+
173 Penicillium spinulosum	9803	+	177 Penicillium spinulosum	1664	
173 unknown	39215	+	177 Penicillium spinulosum	166	+
173 unknown	4911		177 Penicillium waksmanii	55	+
173 Wallemia sebi	4901	+	177 yeast	4905725	
173 yeast	29411		178 Acremonium sclerotigenum	4032186	
174 Alternaria alternata	4770	+	178 Acremonium sclerotigenum	78	+
174 Aspergillus niger	4770		178 Aspergillus niger	77	
174 Aspergillus versicolor	28855	+	178 Aspergillus ochraceus	77	
174 Aspergillus versicolor	14450		178 Aspergillus sydowii	9411	
174 Cladosporium herbarum	4816	+	178 Aspergillus sydowii	1013	+
174 Cladosporium sphaerospermum	62344	+	178 Aspergillus versicolor	2587	+
174 Emericella nidulans	4770	+	178 Aspergillus versicolor	2508	
174 Eurotium herbariorum	19221	+	178 Eurotium herbariorum	312	+
174 Mucor plumbeus	4770	+	178 Penicillium aurantiogriseum	784	
174 Penicillium aurantiogriseum	4816	+	178 Penicillium aurantiogriseum	233	+
174 Penicillium commune	14404	+	178 Penicillium citrinum	77	
174 Trichoderma viride	62114	+	178 Penicillium commune	233	
174 Trichoderma viride	19267		178 Penicillium corylophilum	626	+
174 unknown	52802	+	178 Penicillium glandicola	77	
175 Absidia corymbifera	95		178 Penicillium miczynskii	78	+
175 Alternaria alternata	97		178 Penicillium raistrickii	77	
175 Chaetomium globosum	95		178 Penicillium sp. #1	78	+
175 Mucor plumbeus	288	+	178 Phialophora sp.	77	
175 Mucor plumbeus	194		178 Phoma herbarum	784	
175 Penicillium chrysogenum	772		178 Scopulariopsis chartarum	784	
175 Penicillium chrysogenum	673	+	178 Scopulariopsis chartarum	625	+
175 Penicillium roquefortii	95	+	178 Scopulariopsis sp.	32941	
175 Penicillium spinulosum	95		178 Scopulariopsis sp.	78	+
175 Penicillium spinulosum	95	+	178 unknown	2352	
175 Penicillium viridicatum	194		178 yeast	16218	
175 Rhizopus oryzae	95	+	180 Alternaria alternata	462	+
175 Sporothrix sp.	287		180 Alternaria alternata	92	
175 Trichoderma viride	291		180 Aspergillus niger	92	+
175 unknown	577		180 Aspergillus ochraceus	92	+
175 unknown	97	+	180 Aureobasidium pullulans	5833	+
175 yeast	6271		180 Eurotium herbariorum	92	+
176 Aspergillus glaucus	473	+	180 Mucor plumbeus	462	+
176 Aspergillus niger	764		180 Mucor plumbeus	370	
176 Aspergillus niger	473	+	180 Penicillium commune	3888	+
176 Aspergillus versicolor	5202		180 Penicillium commune	1666	
176 Aspergillus versicolor	473	+	180 unknown	277	+
176 Chaetomium cochliodes	1420		180 yeast	1296	
176 Chaetomium cochliodes	946	+	182 Alternaria alternata	4752	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
182 Aspergillus niger	477810	+	187 Cladosporium herbarum	958	+
182 Aspergillus niger	19531		187 Cladosporium sphaerospermum	1917	+
182 Aspergillus versicolor	81968	+	187 Cladosporium sphaerospermum	483	
182 Aureobasidium pullulans	4752	+	187 Eurotium herbariorum	1442	+
182 Eurotium herbariorum	9635	+	187 Fusarium sp.	950	
182 Penicillium citreonigrum	33789	+	187 Fusarium sp.	475	+
182 Penicillium citreonigrum	33529		187 Paecilomyces variotii	483	
182 Penicillium corylophilum	4752	+	187 Penicillium commune	1434	
182 Trichoderma viride	57684		187 Penicillium commune	475	+
182 Trichoderma viride	28906	+	187 Penicillium spinulosum	1425	
182 unknown	333999		187 Penicillium spinulosum	475	+
183 Alternaria alternata	23789	+	187 Phoma herbarum	483	+
183 Aspergillus versicolor	14222	+	187 Phoma sp.	1442	
183 Aureobasidium pullulans	9567	+	187 unknown	2392	
183 Cladosporium sphaerospermum	4655	+	188 Alternaria alternata	3845	+
183 Fusarium sp.	9823	+	188 Alternaria alternata	2857	
183 Oidiodendron sp.	116826		188 Aspergillus versicolor	4419	
183 Penicillium brevicompactum	4911	+	188 Aspergillus versicolor	3378	+
183 Trichoderma viride	9823		188 Aureobasidium pullulans	12723	
183 Trichoderma viride	4911	+	188 Aureobasidium pullulans	1922	+
183 unknown	38524	+	188 Cladosporium cladosporioides	2470	
183 unknown	24301		188 Cladosporium cladosporioides	467	+
185 Aspergillus niger	287	+	188 Emericella nidulans	988	
185 Aspergillus ochraceus	191	+	188 Epicoccum nigrum	1401	
185 Aureobasidium pullulans	382	+	188 Epicoccum nigrum	467	+
185 Chaetomium globosum	154193		188 Eurotium herbariorum	467	+
185 Eurotium herbariorum	191	+	188 Penicillium chrysogenum	3324	+
185 Penicillium brevicompactum	191	+	188 Penicillium chrysogenum	2857	
185 Penicillium commune	667	+	188 Penicillium commune	494	
185 Penicillium commune	189		188 Penicillium spinulosum	4833	+
185 Penicillium expansum	954	+	188 Penicillium spinulosum	3404	
185 Penicillium expansum	94		188 Phoma herbarum	2803	
185 Scopulariopsis brevicaulis	95		188 Phoma herbarum	467	+
185 Ulocladium chartarum	94	+	188 unknown	5794	+
185 unknown	191		188 unknown	2857	
185 Wallemia sebi	15509	+	188 yeast	5714	
185 yeast	2004		189 Alternaria alternata	10764	
186 Acremonium strictum	387		189 Alternaria alternata	7383	+
186 Acremonium strictum	98	+	189 Aspergillus niger	498	+
186 Aspergillus niger	99	+	189 Aureobasidium pullulans	8790	
186 Aspergillus ustus	99		189 Aureobasidium pullulans	4438	+
186 Aspergillus versicolor	197	+	189 Cladosporium cladosporioides	498	
186 Aspergillus versicolor	98		189 Cladosporium cladosporioides	498	+
186 Eurotium herbariorum	99	+	189 Cladosporium sp.	967	+
186 Fusarium oxysporum	196	+	189 Epicoccum nigrum	1450	
186 Paecilomyces variotii	99		189 Epicoccum nigrum	483	+
186 Penicillium aurantiogriseum	396		189 Eurotium herbariorum	2944	+
186 Penicillium chrysogenum	395		189 Penicillium brevicompactum	498	+
186 Penicillium sp. #64	98		189 Penicillium chrysogenum	3911	+
186 Penicillium spinulosum	98	+	189 Penicillium chrysogenum	3428	
186 unknown	593		189 Penicillium corylophilum	483	
186 yeast	891		189 Penicillium spinulosum	1948	
187 Acremonium sp.	1925		189 Phoma herbarum	498	
187 Alternaria alternata	1450		189 Rhizopus oryzae	483	+
187 Alternaria alternata	967	+	189 Trichoderma viride	4482	
187 Aspergillus niger	483		189 unknown	4864	
187 Aspergillus versicolor	2384	+	189 unknown	2446	+
187 Aspergillus versicolor	967		189 yeast	28393	
187 Aureobasidium pullulans	15858	+	190 Alternaria alternata	8822	
187 Aureobasidium pullulans	13899		190 Alternaria alternata	2346	+
187 Cladosporium cladosporioides	483	+	190 Eurotium herbariorum	1881	+



HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
190 Myrothecium cinctum	1407		193 Penicillium chrysogenum	4807	+
190 Penicillium brevicompactum	941		193 Phoma herbarum	4807	
190 Penicillium roquefortii	938	+	193 Stachybotrys chartarum	4807	
190 Penicillium spinulosum	6120	+	193 unknown	39292	+
190 Penicillium spinulosum	2824		193 unknown	19334	
190 Scopulariopsis brevicaulis	938	+	193 Wallemia sebi	576998	+
190 unknown	4697	+	193 yeast	111096	
190 unknown	2346		194 Alternaria alternata	151337	
190 Wallemia sebi	938		194 Alternaria alternata	479	+
190 yeast	2354		194 Aspergillus niger	479	
191 Alternaria alternata	2435	+	194 Aspergillus sp.	494	
191 Aspergillus fumigatus	484	+	194 Aspergillus sp.	494	+
191 Aspergillus niger	3424		194 Aspergillus sydowii	44970	
191 Aspergillus niger	1957	+	194 Aspergillus sydowii	22993	+
191 Aureobasidium pullulans	26289	+	194 Aureobasidium pullulans	6760	
191 Aureobasidium pullulans	2946		194 Aureobasidium pullulans	2964	+
191 Cladosporium cladosporioides	3391	+	194 Cladosporium cladosporioides	2879	+
191 Cladosporium sphaerospermum	491	+	194 Cladosporium cladosporioides	479	
191 Eurotium herbariorum	491	+	194 Epicoccum nigrum	479	
191 Fusarium sp.	2442	+	194 Eurotium herbariorum	3430	+
191 Geomyces pannorum	484		194 Penicillium chrysogenum	3444	
191 Graphium sp.	982		194 Penicillium chrysogenum	2413	+
191 Microsphaeropsis olivaceus	484	+	194 Penicillium corylophilum	1453	
191 Paecilomyces sp.	484		194 Penicillium corylophilum	494	+
191 Penicillium brevicompactum	1944	+	194 Penicillium simplicissimum	959	+
191 Penicillium brevicompactum	1466		194 Penicillium spinulosum	973	+
191 Penicillium commune	484		194 Penicillium spinulosum	494	
191 Penicillium corylophilum	982	+	194 Scopulariopsis candida	973	+
191 unknown	2422	+	194 Scopulariopsis candida	494	
191 unknown	1944		194 unknown	959	
191 yeast	4858		194 yeast	1947	
192 Alternaria alternata	2409	+	195 Alternaria alternata	1369	+
192 Aspergillus versicolor	479	+	195 Aspergillus terreus	769	+
192 Aureobasidium pullulans	10221	+	195 Aspergillus versicolor	198570	
192 Cladosporium cladosporioides	2440	+	195 Aspergillus versicolor	3076	+
192 Epicoccum nigrum	490	+	195 Aureobasidium pullulans	29430	
192 Fusarium oxysporum	12181		195 Aureobasidium pullulans	23097	+
192 Penicillium brevicompactum	2440		195 Cladosporium cladosporioides	7702	+
192 Penicillium brevicompactum	980	+	195 Cladosporium sphaerospermum	2307	
192 Penicillium chrysogenum	970		195 Paecilomyces variotii	2739	
192 Penicillium spinulosum	15582	+	195 Penicillium chrysogenum	769	+
192 Penicillium spinulosum	4901		195 Penicillium citrinum	2992	
192 Phoma sp.	490		195 Penicillium commune	2139	
192 Rhizopus stolonifer	2910	+	195 Penicillium commune	1369	+
192 unknown	1940	+	195 Phoma herbarum	4362	
192 unknown	1460		195 Phoma herbarum	684	+
192 Wallemia sebi	490	+	195 Phoma sp.	6849	
192 yeast	2930		195 Trichoderma viride	2992	
193 Acremonium murorum var. felina	4807		195 Trichoderma viride	769	+
193 Alternaria alternata	4911	+	195 Ulocladium chartarum	2054	+
193 Aspergillus sp.	28846	+	195 unknown	11801	+
193 Botryotrichum piluliferum	24038	+	195 unknown	6417	
193 Botryotrichum piluliferum	9823		195 yeast	11464	
193 Chaetomium globosum	14630		197 Alternaria alternata	2890	+
193 Chaetomium globosum	4911	+	197 Aspergillus niger	468	+
193 Cladosporium cladosporioides	24557	+	197 Aureobasidium pullulans	29129	+
193 Cladosporium sphaerospermum	34069	+	197 Aureobasidium pullulans	19890	
193 Eurotium herbariorum	9719	+	197 Cladosporium cladosporioides	2874	+
193 Geomyces pannorum	4807		197 Cladosporium cladosporioides	468	
193 Humicola fuscoatra	4807		197 Epicoccum nigrum	468	
193 Penicillium chrysogenum	14526		197 Mucor plumbeus	3326	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
197 Mucor racemosus	2357	+	200 Eurotium herbariorum	9842	+
197 Phoma sp.	1872	+	200 Penicillium chrysogenum	58487	+
197 unknown	1420		200 Penicillium chrysogenum	29300	
197 yeast	4278		200 Penicillium implicatum	39370	
198 Alternaria alternata	4302		200 Penicillium implicatum	33880	+
198 Alternaria alternata	3851	+	200 Trichoderma viride	19344	
198 Aspergillus niger	476	+	200 Trichoderma viride	14763	+
198 Aspergillus ochraceus	476		200 unknown	63749	
198 Aspergillus sp.	476		200 unknown	34335	+
198 Aspergillus versicolor	968		201 Alternaria alternata	5412	
198 Aureobasidium pullulans	41259	+	201 Alternaria alternata	977	+
198 Aureobasidium pullulans	15872		201 Aureobasidium pullulans	36293	+
198 Cladosporium cladosporioides	1436	+	201 Aureobasidium pullulans	8797	
198 Cladosporium cladosporioides	484		201 Cladosporium cladosporioides	486	
198 Coniothyrium sp.	3391		201 Eurotium herbariorum	977	+
198 Coniothyrium sp.	968	+	201 Exophiala sp.	491	
198 Epicoccum nigrum	968	+	201 Penicillium brevicompactum	491	+
198 Epicoccum nigrum	968		201 Penicillium chrysogenum	2446	
198 Eurotium herbariorum	1904	+	201 Penicillium chrysogenum	977	+
198 Fusarium sp.	1921		201 Penicillium purpurogenum	2937	
198 Fusarium sp.	968	+	201 Penicillium sp. #26	977	
198 Hyalodendron sp.	476		201 Penicillium sp. #26	491	+
198 Mucor racemosus	484	+	201 Penicillium spinulosum	486	+
198 Mucor racemosus	476		201 Phoma sp.	6866	
198 Penicillium expansum	1445	+	201 Phoma sp.	982	+
198 Penicillium simplicissimum	968	+	201 Trichophyton tonsurans	972	
198 Penicillium spinulosum	1436		201 Ulocladium sp.	972	+
198 Penicillium variable	960		201 unknown	3914	
198 Phoma herbarum	1436		201 yeast	3929	
198 Phoma medicaginis	5238		202 Alternaria alternata	1428	
198 unknown	4786		202 Alternaria alternata	1428	+
198 unknown	1428	+	202 Aspergillus ochraceus	952	
198 yeast	5797		202 Aspergillus sydowii	476	+
199 Alternaria alternata	6302	+	202 Aspergillus versicolor	957	+
199 Alternaria alternata	2004		202 Aspergillus versicolor	476	
199 Aspergillus sydowii	477		202 Aureobasidium pullulans	19639	
199 Aspergillus versicolor	1146		202 Aureobasidium pullulans	13859	+
199 Aureobasidium pullulans	69621	+	202 Cladosporium cladosporioides	1434	+
199 Aureobasidium pullulans	18904		202 Cladosporium cladosporioides	952	
199 Cladosporium cladosporioides	5156	+	202 Cladosporium sphaerospermum	476	+
199 Cladosporium sphaerospermum	954		202 Epicoccum nigrum	476	
199 Cladosporium sphaerospermum	954	+	202 Eurotium herbariorum	1926	+
199 Epicoccum nigrum	477		202 Geomyces sp.	1434	
199 Geomyces pannorum	1431		202 Gliocladium sp.	476	
199 Mucor racemosus	1146		202 Microsphaeropsis olivaceus	7148	
199 Mucor racemosus	573	+	202 Microsphaeropsis olivaceus	1921	+
199 Penicillium aurantiogriseum	6014	+	202 Mucor plumbeus	963	+
199 Penicillium commune	8592	+	202 Mucor racemosus	476	+
199 Penicillium commune	1720		202 Penicillium citreonigrum	952	+
199 Penicillium simplicissimum	9839	+	202 Penicillium citreonigrum	476	
199 Penicillium spinulosum	2674		202 Penicillium commune	6229	+
199 Phoma sp.	1146		202 Penicillium commune	1915	
199 Sporobolomyces sp.	1431		202 Penicillium expansum	952	+
199 Trichoderma viride	1050		202 Penicillium verrucosum	1434	
199 unknown	11069		202 Phoma glomerata	481	
199 yeast	3532		202 Phoma herbarum	2890	
200 Acremonium sp.	169117		202 Thamnidium elegans	963	
200 Aspergillus sp.	9842		202 Thamnidium elegans	952	+
200 Aureobasidium pullulans	39142		202 Ulocladium chartarum	963	
200 Aureobasidium pullulans	4807	+	202 Ulocladium sp.	963	
200 Cladosporium sphaerospermum	4921	+	202 yeast	3853	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
204	Alternaria alternata	3924		212	Alternaria alternata	7219	
204	Alternaria alternata	2467	+	212	Alternaria alternata	6191	+
204	Aspergillus candidus	489	+	212	Aspergillus niger	9630	+
204	Aspergillus glaucus	500		212	Aspergillus niger	8601	
204	Aspergillus niger	14349	+	212	Aspergillus ochraceus	472	+
204	Aspergillus niger	6946		212	Aspergillus sp.	1417	
204	Aspergillus ochraceus	489	+	212	Aspergillus versicolor	484	
204	Aspergillus sydowii	500	+	212	Aureobasidium pullulans	36158	
204	Aspergillus ustus	1000		212	Aureobasidium pullulans	6250	+
204	Aspergillus versicolor	500	+	212	Chaetomium globosum	2362	
204	Aureobasidium pullulans	33440	+	212	Cladosporium cladosporioides	1429	+
204	Aureobasidium pullulans	11892		212	Cladosporium cladosporioides	472	
204	Cladosporium cladosporioides	4424	+	212	Eurotium herbariorum	3804	+
204	Cladosporium sphaerospermum	1989		212	Mucor plumbeus	484	+
204	Cladosporium sphaerospermum	500	+	212	Mucor racemosus	484	
204	Epicoccum nigrum	1000		212	Penicillium brevicompactum	472	
204	Eurotium herbariorum	989	+	212	Penicillium chrysogenum	20984	+
204	Fusarium sp.	1467		212	Penicillium chrysogenum	17735	
204	Fusarium sp.	489	+	212	Penicillium italicum	3367	
204	Mucor plumbeus	500		212	Penicillium italicum	1937	+
204	Penicillium brevicompactum	489		212	Penicillium sp. #26	1417	
204	Penicillium simplicissimum	3924	+	212	Penicillium sp. #26	968	+
204	Penicillium simplicissimum	2456		212	Phoma herbarum	1890	+
204	Penicillium spinulosum	978	+	212	Phoma herbarum	945	
204	Penicillium spinulosum	489		212	unknown	945	
204	Phoma sp.	3000	+	212	yeast	4797	
206	Acremonium sp.	466		213	Aspergillus niger	530	
206	Alternaria alternata	6154		213	Aspergillus ustus	3162	
206	Alternaria alternata	4801	+	213	Aspergillus ustus	1586	+
206	Aspergillus ochraceus	3310		213	Mucor plumbeus	2117	+
206	Aspergillus ochraceus	955	+	213	Mucor plumbeus	1050	
206	Aspergillus versicolor	3424		213	Mucor racemosus	3162	
206	Aspergillus versicolor	3424	+	213	Paecilomyces variotii	525	+
206	Aureobasidium pullulans	16895	+	213	Penicillium chrysogenum	7917	+
206	Aureobasidium pullulans	8248		213	Penicillium chrysogenum	4229	
206	Cladosporium cladosporioides	7064	+	213	Penicillium corylophilum	13152	+
206	Cladosporium cladosporioides	932		213	Penicillium corylophilum	6347	
206	Cladosporium sphaerospermum	1865	+	213	Rhizopus oryzae	1055	+
206	Eurotium herbariorum	6780	+	213	Syncephalastrum racemosum	3162	+
206	Paecilomyces variotii	1422		213	Syncephalastrum racemosum	2642	
206	Paecilomyces variotii	466	+	213	Syncephalastrum sp.	1050	
206	Penicillium chrysogenum	9977	+	214	Aspergillus glaucus	948	
206	Penicillium chrysogenum	3333		214	Aspergillus glaucus	941	+
206	Penicillium corylophilum	5244		214	Eurotium herbariorum	5200	+
206	Penicillium corylophilum	978	+	214	Paecilomyces variotii	478	
206	Phoma herbarum	1934		214	Paecilomyces variotii	470	+
206	Trichoderma viride	978		214	Penicillium corylophilum	3310	
206	Ulocladium sp.	3731	+	214	Penicillium corylophilum	941	+
206	unknown	4311		214	Penicillium decumbens	1426	+
206	unknown	2377	+	214	Penicillium glandicola	17607	
206	Wallemia sebi	4403	+	214	Penicillium implicatum	948	
206	yeast	3287		214	Penicillium implicatum	948	+
209	Alternaria alternata	4921		214	Penicillium sp. #26	5200	+
209	Aspergillus versicolor	73731		214	Penicillium viridicatum	30861	+
209	Aureobasidium pullulans	4911	+	214	Penicillium viridicatum	20403	
209	Cladosporium sphaerospermum	4921		214	Rhizopus oryzae	470	
209	Cladosporium sphaerospermum	4921	+	214	unknown	2846	
209	Epicoccum nigrum	4921		215	Alternaria alternata	2899	+
209	Penicillium chrysogenum	186785		215	Aspergillus niger	486	
209	Penicillium chrysogenum	118003	+	215	Aspergillus niger	482	+
209	Penicillium commune	4911		215	Aspergillus sp.	482	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
215 Aspergillus versicolor	2420	+	217 Penicillium chrysogenum	6910	+
215 Aureobasidium pullulans	4852	+	217 Penicillium corylophilum	2961	+
215 Aureobasidium pullulans	2413		217 Penicillium griseofulvum	3453	
215 Cladosporium cladosporioides	486	+	217 Penicillium simplicissimum	493	+
215 Cladosporium sp.	1455	+	217 Penicillium sp.	494	+
215 Eurotium herbariorum	482	+	217 Penicillium sp. #26	2468	+
215 Mucor racemosus	9686		217 Penicillium sp. #26	1974	
215 Mucor racemosus	3389	+	217 Penicillium spinulosum	1480	
215 Penicillium chrysogenum	486	+	217 Pithomyces sp.	987	+
215 Penicillium chrysogenum	482		217 Pithomyces sp.	493	
215 Penicillium commune	969		217 unknown	7406	
215 Penicillium commune	965	+	217 unknown	5923	+
215 Penicillium sp.	482		217 Wallemia sebi	2468	+
215 Penicillium sp. #26	486	+	217 yeast	3944	
215 unknown	486		220 Aureobasidium pullulans	6100	
216 Acremonium furcatum	1444		220 Eurotium herbariorum	2047	+
216 Alternaria alternata	9645	+	220 Gliomastix murorum	194	
216 Alternaria alternata	3865		220 Paecilomyces variotii	98	
216 Aspergillus clavatus	478		220 Penicillium chrysogenum	687	+
216 Aspergillus niger	487		220 Penicillium chrysogenum	195	
216 Aspergillus ochraceus	487		220 Penicillium citreonigrum	293	
216 Aspergillus ustus	487		220 Penicillium citreonigrum	98	+
216 Cladosporium cladosporioides	3386	+	220 Penicillium spinulosum	195	
216 Cladosporium macrocarpum	6268	+	220 Penicillium spinulosum	97	+
216 Epicoccum nigrum	974	+	220 Scopulariopsis candida	97	
216 Fusarium sp.	1445		220 unknown	196	
216 Fusarium sp.	478	+	220 unknown	195	+
216 Microsphaeropsis olivaceus	22324	+	220 yeast	15225	
216 Microsphaeropsis olivaceus	3394		223 Alternaria alternata	2846	+
216 Mucor racemosus	966	+	223 Aspergillus fumigatus	473	+
216 Penicillium chrysogenum	957		223 Aspergillus versicolor	473	+
216 Penicillium echinulatum	3377	+	223 Aureobasidium pullulans	473	+
216 Penicillium echinulatum	1436		223 Cladosporium cladosporioides	2851	+
216 Penicillium expansum	957		223 Cladosporium herbarum	2484	
216 Penicillium implicatum	487		223 Cladosporium herbarum	2372	+
216 Penicillium italicum	1445		223 Cladosporium sp.	3322	+
216 Penicillium spinulosum	4360		223 Coniothyrium fuckelii	476	
216 Penicillium spinulosum	966	+	223 Fusarium sp.	3322	
216 Phoma eupyrena	14535		223 Fusarium sp.	476	+
216 Pithomyces sp.	487	+	223 Penicillium implicatum	476	
216 Rhizopus oryzae	487		223 Penicillium oxalicum	476	
216 Trichoderma polysporum	487		223 Penicillium oxalicum	473	+
216 unknown	8250		223 Pithomyces chartarum	473	+
216 unknown	4335	+	223 unknown	7594	+
216 yeast	7251		223 unknown	6176	
217 Alternaria alternata	11600		223 yeast	6642	
217 Alternaria alternata	987	+	225 Absidia corymbifera	19150	
217 Aspergillus versicolor	1975	+	225 Alternaria alternata	138	
217 Aureobasidium pullulans	494		225 Alternaria alternata	132	+
217 Cladosporium cladosporioides	9376	+	225 Aspergillus glaucus	404	+
217 Cladosporium cladosporioides	1973		225 Aspergillus niger	132	
217 Cladosporium sphaerospermum	9881		225 Aspergillus ornatus	138	+
217 Cladosporium sphaerospermum	8389	+	225 Aspergillus oryzae	132	
217 Emericella varicolor	3946		225 Aspergillus ustus	138	
217 Emericella varicolor	1972	+	225 Aspergillus versicolor	2163	+
217 Eurotium herbariorum	3453	+	225 Aspergillus versicolor	1340	
217 Fusarium oxysporum	494		225 Chaetomium globosum	132	
217 Mucor plumbeus	1482	+	225 Cladosporium cladosporioides	138	
217 Mucor plumbeus	987		225 Eurotium herbariorum	542	+
217 Penicillium brevicompactum	1480		225 Fusarium oxysporum	138	
217 Penicillium brevicompactum	986	+	225 Paecilomyces variotii	265	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
225 Penicillium atramentosum	542	+	228 Cladosporium sphaerospermum	29206	+
225 Penicillium atramentosum	271		228 Cladosporium sphaerospermum	4780	
225 Penicillium chrysogenum	3508		228 Eurotium herbariorum	82445	+
225 Penicillium chrysogenum	3498	+	228 Penicillium brevicompactum	24557	
225 Penicillium corylophilum	276		228 Penicillium brevicompactum	14734	+
225 Penicillium implicatum	941		228 Penicillium chrysogenum	144981	+
225 Penicillium sp. #26	537		228 Penicillium chrysogenum	87751	
225 Penicillium spinulosum	265	+	228 Penicillium citrinum	29206	+
225 Penicillium spinulosum	138		228 Penicillium citrinum	4911	
225 Penicillium verrucosum	404		228 Penicillium corylophilum	29206	+
225 Phoma exigua	276		228 Penicillium corylophilum	19251	
225 Phoma herbarum	138		228 Penicillium echinulatum	58018	
225 Syncephalastrum racemosum	132	+	228 Penicillium funiculosum	9823	
225 Trichoderma sp.	271	+	228 Penicillium sp.	33460	
225 Trichoderma viride	132		228 Penicillium sp. #26	19383	
225 unknown	2711		228 Penicillium variabile	4911	
225 unknown	1074	+	228 Rhizopus oryzae	33723	+
225 yeast	956		228 Rhizopus oryzae	14340	
226 Alternaria alternata	196		228 unknown	265930	
226 Aspergillus versicolor	127		228 unknown	86567	+
226 Aureobasidium pullulans	4029	+	228 yeast	23900	
226 Aureobasidium pullulans	253		229 Alternaria alternata	1182	+
226 Chaetomium aureum	255		229 Aspergillus niger	19908	
226 Cladosporium cladosporioides	191	+	229 Aspergillus niger	132	+
226 Eurotium herbariorum	316	+	229 Aspergillus ustus	130	
226 Fusarium sp.	128		229 Aureobasidium pullulans	16983	+
226 Penicillium chrysogenum	127		229 Aureobasidium pullulans	8294	
226 Penicillium commune	446	+	229 Cladosporium cladosporioides	4476	+
226 Penicillium commune	127		229 Eurotium herbariorum	526	+
226 Penicillium sp. #26	256	+	229 Geomyces pannorum	263	
226 Penicillium sp. #26	64		229 Mucor racemosus	394	+
226 Penicillium spinulosum	63	+	229 Penicillium chrysogenum	3680	+
226 Phoma herbarum	63		229 Penicillium chrysogenum	658	
226 Scopulariopsis candida	256	+	229 Penicillium commune	261	
226 Ulocladium chartarum	63	+	229 Penicillium spinulosum	1449	+
226 unknown	63		229 Penicillium spinulosum	655	
226 Wallemia sebi	63	+	229 unknown	919	
226 yeast	3647		229 yeast	264	
227 Acremonium sp.	3858	+	230 Alternaria alternata	1130	
227 Alternaria alternata	467		230 Alternaria alternata	499	+
227 Aspergillus glaucus	467		230 Aspergillus glaucus	1482	+
227 Aspergillus versicolor	1903		230 Aspergillus niger	998	
227 Aspergillus versicolor	934	+	230 Aspergillus niger	499	+
227 Eurotium herbariorum	968		230 Aspergillus sydowii	1497	
227 Penicillium aurantiogriseum	951		230 Aspergillus ustus	484	+
227 Penicillium chrysogenum	1903	+	230 Coniothyrium fuckelii	499	
227 Penicillium chrysogenum	1886		230 Emericella nidulans	499	
227 Penicillium citreonigrum	2855	+	230 Epicoccum nigrum	499	
227 Penicillium citreonigrum	1869		230 Eurotium herbariorum	1482	+
227 Penicillium commune	467	+	230 Fusarium sp.	998	
227 Penicillium corylophilum	1903	+	230 Lecythophora sp.	1497	
227 Penicillium implicatum	484	+	230 Lecythophora sp.	499	+
227 Pestalotiopsis sp.	467		230 Mucor racemosus	1952	
227 unknown	4274	+	230 Paecilomyces variotii	499	
227 unknown	484		230 Penicillium citrinum	499	+
228 Alternaria alternata	8268		230 Penicillium corylophilum	2451	
228 Aspergillus glaucus	4780	+	230 Penicillium griseofulvum	5900	+
228 Aspergillus sydowii	9823		230 Penicillium oxalicum	1467	
228 Aspergillus versicolor	77139	+	230 Penicillium simplicissimum	3405	+
228 Aspergillus versicolor	53633	+	230 Penicillium sp. #26	968	
228 Aureobasidium pullulans	9823	+	230 Penicillium spinulosum	1482	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
230 unknown	4931	+	234 Penicillium echinulatum	473	
230 unknown	3449		234 Penicillium oxalicum	485	
230 yeast	3919		234 Penicillium sp. #26	958	+
231 Alternaria alternata	13183		234 Penicillium sp. #26	473	
231 Aspergillus niger	4743		234 Trichocladium asperum	485	
231 Aspergillus niger	4743	+	234 unknown	3835	
231 Aureobasidium pullulans	104671	+	234 unknown	970	+
231 Aureobasidium pullulans	4761		235 Alternaria alternata	3327	
231 Gliocladium sp.	9523	+	235 Aspergillus niger	486	+
231 Penicillium echinulatum	4761		235 Aspergillus oryzae	486	
231 Penicillium spinulosum	4761	+	235 Aspergillus restrictus	2418	+
231 Phoma herbarum	4761	+	235 Aspergillus ustus	1931	+
231 Trichoderma viride	9505		235 Aspergillus versicolor	1931	+
231 yeast	14231		235 Aureobasidium pullulans	958	
232 Alternaria alternata	32191		235 Aureobasidium pullulans	945	+
232 Alternaria alternata	2878	+	235 Cladosporium cladosporioides	486	+
232 Aspergillus niger	704	+	235 Curvularia prasadii	2431	+
232 Aspergillus ustus	72		235 Eurotium herbariorum	1445	+
232 Epicoccum nigrum	70		235 Fusarium sp.	472	+
232 Penicillium chrysogenum	2134	+	235 Penicillium chrysogenum	1445	+
232 Penicillium chrysogenum	72		235 Penicillium miczynskii	3363	+
232 Pithomyces chartarum	1409	+	235 Penicillium miczynskii	472	
232 Pithomyces chartarum	211		235 Penicillium restrictum	1945	+
232 Syncephalastrum racemosum	72		235 Penicillium spinulosum	958	
232 yeast	281		235 Phoma sp.	7254	
233 Alternaria alternata	10133	+	235 Trichoderma viride	9061	
233 Aspergillus candidus	480		235 Trichoderma viride	2362	+
233 Aspergillus versicolor	2418		235 unknown	10131	
233 Aspergillus versicolor	968	+	235 unknown	7212	+
233 Aureobasidium pullulans	24612	+	235 Wallemia sebi	486	+
233 Aureobasidium pullulans	9171		235 yeast	3822	
233 Cladosporium cladosporioides	961	+	236 Aspergillus versicolor	3802	
233 Exophiala sp.	480		236 Aspergillus versicolor	1873	+
233 Fusarium sp.	480	+	236 Aureobasidium pullulans	467	+
233 Gliocladium virens	480		236 Cladosporium cladosporioides	938	+
233 Mucor racemosus	1934	+	236 Cladosporium cladosporioides	467	
233 Mucor racemosus	968		236 Epicoccum nigrum	467	
233 Penicillium aurantiogriseum	6287	+	236 Eurotium herbariorum	7053	+
233 Penicillium aurantiogriseum	1442		236 Penicillium chrysogenum	25886	
233 Penicillium brevicompactum	961	+	236 Penicillium chrysogenum	22597	+
233 Penicillium chrysogenum	961		236 Sporobolomyces sp.	181092	
233 Penicillium chrysogenum	484	+	236 Sporobolomyces sp.	99532	+
233 Penicillium corylophilum	480		236 unknown	1406	+
233 Penicillium echinulatum	2415		236 unknown	467	
233 Penicillium implicatum	968	+	237 Aspergillus versicolor	4708	+
233 Penicillium roquefortii	7737	+	237 Eurotium herbariorum	9451	+
233 Penicillium roquefortii	1926		237 Mortierella ramanniana var. autotrophica	4725	
233 Trichoderma viride	3387		237 Mucor mucedo	14159	
233 Trichoderma viride	2403	+	237 Mucor mucedo	4708	+
233 unknown	2906		237 Mucor plumbeus	28319	+
233 unknown	1930	+	237 Mucor plumbeus	23611	
233 Wallemia sebi	449873	+	237 Mucor racemosus	42461	+
234 Alternaria alternata	4794	+	237 Penicillium chrysogenum	47205	+
234 Aspergillus versicolor	3386	+	237 Penicillium chrysogenum	32992	
234 Aureobasidium pullulans	42486	+	237 Penicillium citrinum	14177	+
234 Aureobasidium pullulans	2390		237 Penicillium restrictum	4708	
234 Cladosporium cladosporioides	1917	+	237 Rhizopus oryzae	66126	
234 Eurotium herbariorum	24991	+	237 Trichoderma viride	4725	+
234 Mucor racemosus	946	+	237 Trichoderma viride	4708	
234 Mucor racemosus	485		237 unknown	23576	
234 Penicillium chrysogenum	970	+	237 yeast	51842	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
238 Aspergillus niger	954	+	241 Aureobasidium pullulans	30256	+
238 Aspergillus ochraceus	9927		241 Aureobasidium pullulans	6702	
238 Aspergillus versicolor	478	+	241 Cladosporium cladosporioides	1937	+
238 Aureobasidium pullulans	17636	+	241 Epicoccum nigrum	1425	
238 Aureobasidium pullulans	13358		241 Eurotium herbariorum	950	+
238 Cladosporium cladosporioides	954	+	241 Mucor racemosus	475	+
238 Eurotium herbariorum	950	+	241 Paecilomyces variotii	962	
238 Mucor plumbeus	475	+	241 Paecilomyces variotii	475	+
238 Penicillium chrysogenum	478	+	241 Penicillium chrysogenum	2412	+
238 Penicillium chrysogenum	475		241 Penicillium corylophilum	8188	
238 Penicillium implicatum	950		241 Penicillium corylophilum	4837	+
238 Penicillium spinulosum	475		241 Penicillium viridicatum	10053	
238 Penicillium viridicatum	3805	+	241 Penicillium viridicatum	8627	+
238 Penicillium viridicatum	950		241 Phoma herbarum	487	
238 Ulocladium chartarum	478	+	241 Rhizopus oryzae	487	
238 unknown	4277		241 unknown	3862	
238 unknown	2390	+	241 yeast	19023	
238 yeast	2873		243 Alternaria alternata	93	+
239 Alternaria alternata	3359		243 Aspergillus niger	1994	
239 Alternaria alternata	2884	+	243 Aureobasidium pullulans	4890	
239 Aureobasidium pullulans	47051		243 Aureobasidium pullulans	3610	+
239 Aureobasidium pullulans	16269	+	243 Cladosporium sphaerospermum	93	+
239 Cladosporium cladosporioides	2852	+	243 Mucor plumbeus	292	+
239 Cladosporium cladosporioides	480		243 Mucor racemosus	195	
239 Cladosporium sphaerospermum	474	+	243 Penicillium aurantiogriseum	390	
239 Epicoccum nigrum	2403		243 Penicillium chrysogenum	2291	+
239 Epicoccum nigrum	1423	+	243 Penicillium chrysogenum	186	
239 Fusarium sp.	474		243 Penicillium citrinum	190	
239 Mucor plumbeus	474		243 Penicillium citrinum	97	+
239 Penicillium chrysogenum	8615		243 Penicillium italicum	279	
239 Penicillium chrysogenum	6224	+	243 Penicillium italicum	93	+
239 Penicillium corylophilum	2871	+	243 Scopulariopsis candida	186	+
239 Penicillium restrictum	1442		243 unknown	1047	
239 Penicillium sp. #26	1910	+	244 Alternaria alternata	4689	
239 Phoma herbarum	24519		244 Alternaria alternata	3652	+
239 unknown	2865		244 Aspergillus niger	524	
239 yeast	8077		244 Aspergillus ustus	1556	
240 Alternaria alternata	487	+	244 Aspergillus versicolor	524	
240 Aspergillus versicolor	965		244 Aureobasidium pullulans	1037	+
240 Aureobasidium pullulans	16006	+	244 Cladosporium sp.	2598	+
240 Aureobasidium pullulans	13120		244 Cladosporium sp.	1037	
240 Cladosporium cladosporioides	1457	+	244 Cladosporium sphaerospermum	1566	+
240 Epicoccum nigrum	487	+	244 Cladosporium sphaerospermum	1037	
240 Mucor racemosus	487		244 Eurotium herbariorum	1048	+
240 Mucor racemosus	487	+	244 Exophiala jeanselmei	6245	
240 Penicillium brevicompactum	3401	+	244 Fusarium equiseti	2090	
240 Penicillium commune	9671		244 Fusarium sp.	1042	+
240 Penicillium commune	7262	+	244 Gliocladium roseum	5727	
240 Penicillium expansum	1949		244 Penicillium brevicompactum	3652	
240 Penicillium sp.	487		244 Penicillium brevicompactum	3652	+
240 Penicillium spinulosum	1935		244 Penicillium commune	1566	+
240 Penicillium vulpinum	6780		244 Penicillium echinulatum	1561	+
240 unknown	4863		244 Phoma herbarum	524	+
240 unknown	1939	+	244 Pithomyces chartarum	3128	
240 yeast	5308		244 Trichoderma viride	524	
241 Alternaria alternata	962	+	244 Truncatella angustata	3663	
241 Alternaria alternata	487		244 unknown	6775	+
241 Aspergillus fumigatus	475		244 unknown	4695	
241 Aspergillus niger	475		244 Wallemia sebi	1048	+
241 Aspergillus versicolor	1949		244 yeast	20402	
241 Aspergillus versicolor	475	+	245 Alternaria alternata	8955	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
245 Aspergillus niger	485		247 unknown	24331	
245 Aureobasidium pullulans	94747		247 yeast	19646	
245 Aureobasidium pullulans	64706	+	248 Alternaria alternata	961	
245 Cladosporium cladosporioides	24990	+	248 Alternaria alternata	480	+
245 Cladosporium cladosporioides	478		248 Aspergillus niger	482	
245 Cladosporium sphaerospermum	4316		248 Aspergillus sp.	480	
245 Epicoccum nigrum	963		248 Aspergillus versicolor	480	+
245 Eurotium herbariorum	2897	+	248 Aureobasidium pullulans	27422	
245 Mucor racemosus	956	+	248 Aureobasidium pullulans	18781	+
245 Penicillium brevicompactum	3353		248 Cladosporium cladosporioides	2405	+
245 Penicillium brevicompactum	1456	+	248 Cladosporium cladosporioides	1446	
245 Penicillium corylophilum	1441	+	248 Cladosporium herbarum	7239	+
245 Penicillium corylophilum	478		248 Cladosporium sphaerospermum	480	
245 Penicillium vulpinum	3368		248 Mucor plumbeus	480	+
245 Penicillium vulpinum	956	+	248 Penicillium chrysogenum	5778	+
245 Phoma herbarum	7222		248 Penicillium chrysogenum	4815	
245 Trichoderma sp.	1434		248 Penicillium spinulosum	965	+
245 Ulocladium chartarum	485		248 Penicillium spinulosum	482	
245 unknown	1456	+	248 Phoma sp.	3848	
245 unknown	1441		248 Trichoderma viride	480	
245 yeast	2890		248 unknown	2886	+
246 Alternaria alternata	7721		248 unknown	1928	
246 Aspergillus ochraceus	490		248 yeast	965	
246 Aspergillus sp.	487		249 Aspergillus versicolor	968	+
246 Aureobasidium pullulans	11231		249 Aureobasidium pullulans	484	+
246 Aureobasidium pullulans	4403	+	249 Cladosporium cladosporioides	2403	+
246 Cladosporium cladosporioides	1949		249 Cladosporium sp.	479	+
246 Cladosporium cladosporioides	974	+	249 Cladosporium sphaerospermum	4327	+
246 Cladosporium sphaerospermum	980		249 Eurotium herbariorum	2403	+
246 Eurotium herbariorum	1952	+	249 Mucor plumbeus	479	+
246 Penicillium citreonigrum	1957		249 Myrothecium roridum	484	
246 Penicillium commune	1464	+	249 Penicillium implicatum	968	+
246 Penicillium crustosum	6845	+	249 Penicillium implicatum	964	
246 Penicillium crustosum	4403		249 Penicillium variabile	1928	
246 Penicillium raistrickii	2445		249 Penicillium variabile	964	+
246 Penicillium raistrickii	1955	+	249 Penicillium viridicatum	1444	
246 Penicillium vulpinum	977		249 Penicillium viridicatum	1439	+
246 Ulocladium chartarum	487		249 Phoma exigua	968	
246 unknown	3422	+	249 Phoma exigua	484	+
246 unknown	1955		249 Scopulariopsis brevicaulis	484	
246 yeast	974		249 Trichoderma viride	479	
247 Acremonium sp.	4798		249 unknown	484	+
247 Alternaria alternata	4911		249 yeast	2902	
247 Aspergillus sydowii	4798		250 Alternaria alternata	3378	
247 Aspergillus versicolor	14508		250 Alternaria alternata	482	+
247 Aspergillus versicolor	4911	+	250 Aspergillus versicolor	1447	
247 Aureobasidium pullulans	330933	+	250 Aureobasidium pullulans	8687	+
247 Aureobasidium pullulans	110704		250 Aureobasidium pullulans	3861	
247 Cladosporium sphaerospermum	14621		250 Cladosporium cladosporioides	1447	+
247 Cladosporium sphaerospermum	9823	+	250 Eurotium herbariorum	482	+
247 Epicoccum nigrum	4798		250 Mucor racemosus	482	+
247 Fusarium sp.	9823	+	250 Penicillium citreonigrum	3861	
247 Mucor racemosus	9710	+	250 Penicillium citreonigrum	1447	+
247 Penicillium chrysogenum	43525	+	250 Penicillium commune	482	
247 Penicillium chrysogenum	24218		250 Penicillium spinulosum	482	
247 Penicillium expansum	43638	+	250 Ulocladium chartarum	482	+
247 Penicillium expansum	24331		250 unknown	1930	
247 Penicillium spinulosum	24218	+	250 yeast	13996	
247 Penicillium spinulosum	9710		251 Alternaria alternata	4793	
247 Ulocladium chartarum	9823		251 Alternaria alternata	473	+
247 unknown	29017	+	251 Aureobasidium pullulans	36056	+



HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
251 Aureobasidium pullulans	28450		258 Aureobasidium pullulans	8179	
251 Cladosporium cladosporioides	2374	+	258 Aureobasidium pullulans	2890	+
251 Cladosporium cladosporioides	473		258 Cladosporium sphaerospermum	493	
251 Epicoccum nigrum	475		258 Coniothyrium sp.	481	
251 Penicillium brevicompactum	475		258 Eurotium herbariorum	974	+
251 Penicillium commune	475	+	258 Mucor racemosus	493	+
251 Penicillium italicum	475	+	258 Penicillium chrysogenum	7843	
251 Phoma herbarum	2369		258 Penicillium chrysogenum	3887	+
251 Sporobolomyces sp.	4277		258 Penicillium crustosum	974	
251 unknown	946		258 Penicillium crustosum	481	+
251 unknown	473	+	258 unknown	481	
251 Wallemia sebi	1420	+	258 yeast	481	
253 Alternaria alternata	14404		259 Alternaria alternata	1879	
253 Alternaria alternata	2398	+	259 Alternaria alternata	469	+
253 Aspergillus ochraceus	472	+	259 Aspergillus candidus	961	
253 Aureobasidium pullulans	14816		259 Aspergillus flavus	480	
253 Aureobasidium pullulans	8589	+	259 Aspergillus niger	1431	+
253 Chrysonilia sitophila	957	+	259 Aspergillus niger	469	
253 Cladosporium cladosporioides	9630	+	259 Aspergillus versicolor	480	+
253 Cladosporium cladosporioides	968		259 Aspergillus versicolor	469	
253 Epicoccum nigrum	2422		259 Cladosporium cladosporioides	469	
253 Epicoccum nigrum	472	+	259 Cladosporium sphaerospermum	950	
253 Eurotium herbariorum	3355	+	259 Eurotium herbariorum	1420	+
253 Penicillium commune	472		259 Gliocladium sp.	469	
253 Penicillium hirsutum	1453		259 Mucor racemosus	939	+
253 Penicillium hirsutum	484	+	259 Mucor racemosus	469	
253 Penicillium sp. #64	7656	+	259 Paecilomyces variotii	1442	
253 Penicillium sp. #64	7243		259 Penicillium brevicompactum	950	
253 unknown	4336		259 Penicillium brevicompactum	469	+
256 Alternaria alternata	4854	+	259 Penicillium chrysogenum	1879	
256 Aspergillus ochraceus	21761		259 Penicillium citreonigrum	480	
256 Aspergillus ochraceus	19455	+	259 Penicillium citrinum	1431	
256 Aspergillus sp.	555906		259 Penicillium islandicum	480	
256 Aspergillus sp.	414939	+	259 Penicillium miczynskii	469	
256 Aspergillus sydowii	73195	+	259 Penicillium restrictum	480	
256 Aspergillus sydowii	73119		259 Penicillium viridicatum	9409	
256 Aureobasidium pullulans	199713	+	259 Penicillium viridicatum	480	+
256 Aureobasidium pullulans	73119		259 Phoma herbarum	469	
256 Eurotium herbariorum	4854	+	259 unknown	950	+
256 Penicillium oxalicum	24347		259 unknown	469	
256 Penicillium oxalicum	14639	+	259 yeast	93963	
256 unknown	4892		260 Alternaria alternata	21486	
256 yeast	4854		260 Aspergillus glaucus	485	
257 Alternaria alternata	5328		260 Aspergillus sydowii	21844	
257 Alternaria alternata	955	+	260 Aspergillus versicolor	17541	+
257 Aspergillus versicolor	2371		260 Aspergillus versicolor	8774	
257 Aspergillus versicolor	474	+	260 Aureobasidium pullulans	7789	+
257 Cladosporium cladosporioides	474	+	260 Epicoccum nigrum	485	+
257 Cladosporium sphaerospermum	474	+	260 Eurotium herbariorum	2926	+
257 Hormonema dematioides	474		260 Mucor sp.	488	
257 Mucor racemosus	5769	+	260 Penicillium chrysogenum	15582	
257 Penicillium corylophilum	955	+	260 Penicillium chrysogenum	13155	+
257 Penicillium spinulosum	474		260 Penicillium glandicola	1461	+
257 Pithomyces chartarum	474		260 Penicillium glandicola	970	
257 Rhizopus oryzae	7692		260 Penicillium sp. #26	1456	
257 Rhizopus oryzae	474	+	260 Penicillium sp. #26	488	+
257 unknown	1429	+	260 Phoma herbarum	488	
257 unknown	474		260 Trichoderma viride	485	+
257 Wallemia sebi	1423	+	260 unknown	2438	
257 yeast	1423		260 unknown	1953	+
258 Alternaria alternata	481	+	260 yeast	26838	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
261 Alternaria alternata	22879		264 unknown	1945	+
261 Alternaria alternata	478	+	264 unknown	1939	
261 Aureobasidium pullulans	8679		264 yeast	106191	
261 Aureobasidium pullulans	7706	+	265 Aspergillus niger	149594	
261 Cladosporium cladosporioides	478	+	265 Aspergillus niger	62659	+
261 Penicillium chrysogenum	478	+	265 Aureobasidium pullulans	72424	
261 Penicillium oxalicum	486		265 Aureobasidium pullulans	38499	+
261 Penicillium purpurogenum	964		265 Cladosporium cladosporioides	19305	+
261 Penicillium sp.	1945		265 Penicillium sp. #26	4854	
261 Penicillium viridicatum	1450	+	265 Phoma sp.	9652	+
261 Penicillium vulpinum	2398		265 Stemphylium sp.	4854	+
261 Phoma herbarum	478		265 unknown	9596	
261 Phoma sp.	486		266 Aspergillus versicolor	4970	
261 unknown	478		266 Aureobasidium pullulans	88376	
261 yeast	964		266 Aureobasidium pullulans	72379	+
262 Alternaria alternata	284		266 Cladosporium cladosporioides	33704	
262 Aureobasidium pullulans	1442		266 Cladosporium cladosporioides	28734	+
262 Aureobasidium pullulans	853	+	266 Cladosporium sphaerospermum	9940	
262 Cladosporium sp.	94	+	266 Epicoccum nigrum	4970	
262 Eurotium herbariorum	96	+	266 Mucor racemosus	4752	
262 Penicillium citreonigrum	189	+	266 Penicillium brevicompactum	4752	
262 Penicillium commune	191		266 Penicillium chrysogenum	14910	+
262 Penicillium commune	94	+	266 Penicillium chrysogenum	9940	
262 Penicillium raistrickii	287	+	266 Penicillium sp. #26	4970	
262 Penicillium raistrickii	191		266 Penicillium spinulosum	19446	+
262 Penicillium vulpinum	289		266 Penicillium spinulosum	9940	
262 Scopulariopsis brevicaulis	189		266 unknown	19663	+
262 unknown	382		266 unknown	19011	
263 Alternaria alternata	575		267 Alternaria alternata	2869	+
263 Aspergillus ochraceus	96		267 Alternaria alternata	2389	
263 Aspergillus versicolor	381		267 Aspergillus niger	477	
263 Aspergillus versicolor	189	+	267 Aspergillus versicolor	478	
263 Aureobasidium pullulans	2094		267 Aspergillus versicolor	478	+
263 Aureobasidium pullulans	1244	+	267 Aureobasidium pullulans	16263	
263 Cladosporium cladosporioides	378	+	267 Aureobasidium pullulans	12912	+
263 Cladosporium sphaerospermum	192	+	267 Cladosporium cladosporioides	956	
263 Cladosporium sphaerospermum	96		267 Cladosporium cladosporioides	477	+
263 Curvularia senegalensis	94		267 Epicoccum nigrum	1436	
263 Epicoccum nigrum	189		267 Eurotium herbariorum	1910	+
263 Eurotium herbariorum	94	+	267 Geomyces sp.	477	
263 Mucor racemosus	96	+	267 Penicillium decumbens	954	
263 Penicillium brevicompactum	763	+	267 Penicillium expansum	2392	+
263 Penicillium brevicompactum	287		267 Penicillium expansum	478	
263 Penicillium raistrickii	671	+	267 Penicillium sp. #26	477	+
263 Penicillium raistrickii	665		267 Ulocladium chartarum	478	
263 Penicillium spinulosum	94		267 unknown	477	
263 Penicillium viridicatum	94		267 yeast	2389	
263 Scopulariopsis candida	96		269 Alternaria alternata	1911	+
263 Sordaria sp.	192		269 Alternaria alternata	1909	
264 Alternaria alternata	2424		269 Aureobasidium pullulans	29525	+
264 Alternaria alternata	1457	+	269 Aureobasidium pullulans	24252	
264 Aspergillus ochraceus	484		269 Cladosporium cladosporioides	3325	+
264 Aspergillus versicolor	970		269 Cladosporium sp.	2846	+
264 Aureobasidium pullulans	95935		269 Epicoccum nigrum	957	
264 Aureobasidium pullulans	2916	+	269 Fusarium sp.	474	
264 Eurotium herbariorum	1455	+	269 Mucor racemosus	474	
264 Mucor racemosus	486		269 Penicillium crustosum	30040	
264 Penicillium brevicompactum	486	+	269 Penicillium crustosum	27623	+
264 Penicillium spinulosum	486	+	269 Penicillium echinulatum	2381	
264 Phoma herbarum	486		269 Penicillium griseofulvum	478	
264 Trichoderma viride	486		269 Penicillium viridicatum	2394	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
269 Penicillium viridicatum	953		272 Cladosporium herbarum	2462	
269 Phoma herbarum	957		272 Cladosporium herbarum	493	+
269 Phoma sp.	948	+	272 Cladosporium sphaerospermum	493	
269 Phoma sp.	474		272 Cladosporium sphaerospermum	493	+
269 Ulocladium chartarum	478		272 Eurotium herbariorum	2450	+
269 unknown	2855		272 Mucor racemosus	490	
270 Alternaria alternata	6713		272 Penicillium chrysogenum	2952	+
270 Alternaria alternata	3838	+	272 Penicillium chrysogenum	493	
270 Aspergillus niger	479	+	272 Penicillium citrinum	983	
270 Aureobasidium pullulans	15405	+	272 Penicillium spinulosum	980	
270 Aureobasidium pullulans	14919		272 Penicillium spinulosum	490	+
270 Cladosporium cladosporioides	5303	+	272 Phoma sp.	980	+
270 Cladosporium sphaerospermum	1442	+	272 Phoma sp.	493	
270 Epicoccum nigrum	1442		272 Stachybotrys chartarum	490	
270 Eurotium herbariorum	479	+	272 unknown	1969	
270 Penicillium aurantiogriseum	482		273 Alternaria alternata	17974	
270 Penicillium brevicompactum	482	+	273 Alternaria alternata	8544	+
270 Penicillium commune	7696		273 Aspergillus niger	951	
270 Penicillium commune	7222	+	273 Aureobasidium pullulans	23318	+
270 Penicillium miczynskii	479	+	273 Aureobasidium pullulans	15636	
270 Penicillium spinulosum	962	+	273 Cladosporium cladosporioides	6140	+
270 Penicillium spinulosum	479		273 Cladosporium sphaerospermum	1422	
270 Phoma sp.	1447		273 Epicoccum nigrum	961	
270 unknown	1445		273 Eurotium herbariorum	480	+
270 yeast	962		273 Paecilomyces variotii	470	+
271 Alternaria alternata	11318	+	273 Penicillium brevicompactum	470	+
271 Alternaria alternata	8966		273 Penicillium coprophilum	480	+
271 Aureobasidium pullulans	134512		273 Penicillium digitatum	2864	
271 Aureobasidium pullulans	65948	+	273 Penicillium expansum	6671	
271 Cladosporium cladosporioides	1869	+	273 Penicillium expansum	4737	+
271 Cladosporium cladosporioides	950		273 Penicillium spinulosum	1913	
271 Cladosporium sphaerospermum	934		273 Penicillium vulpinum	1893	+
271 Cladosporium sphaerospermum	475	+	273 Penicillium vulpinum	1432	
271 Epicoccum nigrum	5196		273 Phoma herbarum	470	+
271 Epicoccum nigrum	1885	+	273 Phoma sp.	2824	+
271 Fusarium sp.	3802		273 Scopulariopsis brevicaulis	480	
271 Gliocladium sp.	1885		273 unknown	1432	
271 Mucor plumbeus	475	+	274 Alternaria alternata	1466	+
271 Mucor racemosus	1417	+	274 Alternaria alternata	976	
271 Mucor racemosus	475		274 Aspergillus sp.	489	+
271 Penicillium corylophilum	3287		274 Aureobasidium pullulans	2443	+
271 Penicillium oxalicum	2851		274 Cladosporium cladosporioides	978	
271 Penicillium viridicatum	3794	+	274 Cladosporium cladosporioides	489	+
271 Penicillium viridicatum	942		274 Emericella nidulans	488	
271 Phoma herbarum	4229		274 Epicoccum nigrum	977	
271 Trichoderma sp.	475	+	274 Mucor plumbeus	1466	
271 unknown	2827	+	274 Mucor plumbeus	489	+
271 unknown	1869		274 Penicillium brevicompactum	489	+
271 yeast	3778		274 Penicillium chrysogenum	1465	+
272 Alternaria alternata	4417	+	274 Rhizopus stolonifer	489	+
272 Alternaria alternata	2944		274 unknown	2444	
272 Aspergillus niger	493	+	274 unknown	1956	+
272 Aspergillus sp.	490		274 yeast	8311	
272 Aspergillus sydowii	493		276 Acremonium sp.	21596	
272 Aspergillus sydowii	490	+	276 Alternaria alternata	9505	
272 Aspergillus versicolor	986		276 Aspergillus versicolor	4798	+
272 Aspergillus versicolor	490	+	276 Aureobasidium pullulans	807200	+
272 Aureobasidium pullulans	25530	+	276 Aureobasidium pullulans	114524	
272 Aureobasidium pullulans	17194		276 Cladosporium cladosporioides	4752	+
272 Cladosporium cladosporioides	3440	+	276 Eurotium herbariorum	19057	+
272 Cladosporium cladosporioides	1470		276 Mucor plumbeus	4798	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
276	Mucor plumbeus	4798	+	281	Alternaria alternata	5803	+
276	Penicillium chrysogenum	14304	+	281	Alternaria alternata	4843	
276	Penicillium chrysogenum	9596		281	Aspergillus ochraceus	479	
276	Penicillium restrictum	4752	+	281	Aspergillus versicolor	33401	
276	Penicillium sp. #26	4798		281	Aspergillus versicolor	22327	+
276	yeast	23992		281	Aureobasidium pullulans	27943	+
278	Alternaria alternata	3358	+	281	Aureobasidium pullulans	10638	
278	Alternaria alternata	1921		281	Cladosporium cladosporioides	1949	+
278	Aspergillus niger	478		281	Cladosporium cladosporioides	974	
278	Aureobasidium pullulans	17814	+	281	Cladosporium sphaerospermum	479	+
278	Aureobasidium pullulans	12524		281	Epicoccum nigrum	974	+
278	Cladosporium cladosporioides	957	+	281	Epicoccum nigrum	487	
278	Cladosporium cladosporioides	484		281	Eurotium herbariorum	479	+
278	Cladosporium sphaerospermum	478		281	Microsphaeropsis olivaceus	1919	+
278	Cladosporium sphaerospermum	478	+	281	Mucor plumbeus	487	
278	Epicoccum nigrum	2884		281	Penicillium corylophilum	1941	
278	Penicillium chrysogenum	1442	+	281	Penicillium digitatum	974	+
278	Penicillium chrysogenum	963		281	Penicillium digitatum	479	
278	Penicillium islandicum	957	+	281	Scopulariopsis candida	479	
278	Penicillium islandicum	478		281	Ulocladium chartarum	479	+
278	Penicillium oxalicum	963		281	unknown	959	+
278	Phoma herbarum	11015		281	unknown	479	
278	Phoma sp.	478	+	281	yeast	3891	
278	unknown	963	+	282	Alternaria alternata	23713	
278	unknown	484		282	Alternaria alternata	494	+
278	yeast	1921		282	Aspergillus sydowii	491	
279	Alternaria alternata	14734		282	Aureobasidium pullulans	19684	+
279	Alternaria alternata	4911	+	282	Candida sp.	8399	
279	Aureobasidium pullulans	44204	+	282	Cladosporium cladosporioides	494	+
279	Aureobasidium pullulans	14734		282	Cladosporium cladosporioides	491	
279	Cladosporium cladosporioides	29241	+	282	Cladosporium sphaerospermum	982	
279	Epicoccum nigrum	4911	+	282	Epicoccum nigrum	2467	
279	Epicoccum nigrum	4835		282	Eurotium herbariorum	491	+
279	Penicillium chrysogenum	272161	+	282	Mucor plumbeus	491	+
279	Penicillium chrysogenum	267705		282	Penicillium chrysogenum	5408	+
279	Penicillium glandicola	9671		282	Penicillium glandicola	4423	
279	unknown	24405		282	Penicillium implicatum	988	
280	Alternaria alternata	968		282	Penicillium spinulosum	2952	+
280	Aspergillus sp.	484	+	282	Phoma sp.	988	+
280	Aspergillus versicolor	2862	+	282	unknown	1970	
280	Aspergillus versicolor	2389		282	Wallemia sebi	3929	+
280	Aureobasidium pullulans	2378		282	yeast	191530	
280	Cladosporium cladosporioides	484	+	283	Alternaria alternata	474	+
280	Eurotium herbariorum	3380	+	283	Alternaria citri	183241	
280	Gliomastix murorum var. murorum	8071		283	Aspergillus sp.	1430	+
280	Mucor plumbeus	473	+	283	Aspergillus sp.	481	
280	Paecilomyces variotii	484	+	283	Aureobasidium pullulans	7210	+
280	Paecilomyces variotii	473		283	Cladosporium cladosporioides	2379	+
280	Penicillium aurantiogriseum	2895		283	Cladosporium herbarum	2393	+
280	Penicillium aurantiogriseum	484	+	283	Curvularia prasadii	2408	
280	Penicillium brevicompactum	957	+	283	Epicoccum nigrum	481	
280	Penicillium chrysogenum	1453	+	283	Eurotium herbariorum	2401	+
280	Penicillium chrysogenum	1420		283	Paecilomyces variotii	474	
280	Penicillium citrinum	484		283	Penicillium aurantiogriseum	10502	
280	Penicillium citrinum	484	+	283	Penicillium aurantiogriseum	474	+
280	Penicillium purpurogenum	484		283	Penicillium brevicompactum	948	+
280	Penicillium sp. #26	4294		283	Penicillium brevicompactum	481	
280	Penicillium sp. #26	2884	+	283	Penicillium chrysogenum	4269	
280	unknown	5252	+	283	Penicillium commune	14311	+
280	unknown	4316		283	Penicillium commune	2401	
280	yeast	10119		283	Penicillium corylophilum	956	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
283 Penicillium glandicola	1926		287 Aspergillus fumigatus	480	+
283 Penicillium glandicola	474	+	287 Aspergillus versicolor	481	+
283 Penicillium hirsutum	4306	+	287 Aureobasidium pullulans	18297	+
283 Penicillium hirsutum	4291		287 Aureobasidium pullulans	9625	
283 Penicillium implicatum	1430	+	287 Cladosporium cladosporioides	481	
283 Penicillium raistrickii	956	+	287 Cladosporium cladosporioides	481	+
283 Penicillium simplicissimum	963		287 Penicillium chrysogenum	14929	+
283 Penicillium sp. #87	2379		287 Penicillium chrysogenum	10587	
283 Phoma sp.	474		287 Penicillium sp. #26	1445	
283 Pithomyces sp.	948	+	287 Penicillium sp. #26	480	+
283 Rhizopus oryzae	481	+	287 Penicillium viridicatum	7704	
283 unknown	7174	+	287 Penicillium viridicatum	5779	+
283 unknown	3824		287 Sporobolomyces sp.	480	
283 yeast	10487		287 unknown	2888	
284 Alternaria alternata	20365		287 yeast	480	
284 Alternaria alternata	9784	+	288 Acremonium sp.	478	
284 Aureobasidium pullulans	53392		288 Alternaria alternata	3356	
284 Aureobasidium pullulans	48584	+	288 Alternaria alternata	966	+
284 Cladosporium cladosporioides	29269	+	288 Aspergillus sydowii	956	+
284 Cladosporium sphaerospermum	14507	+	288 Aspergillus versicolor	29477	+
284 Epicoccum nigrum	4807	+	288 Aspergillus versicolor	27585	
284 Paecilomyces variotii	4892		288 Aureobasidium pullulans	11209	+
284 Penicillium commune	9784		288 Aureobasidium pullulans	8696	
284 Penicillium spinulosum	9615		288 Cladosporium cladosporioides	1912	+
284 Penicillium spinulosum	4892	+	288 Cladosporium sphaerospermum	478	+
284 Phoma medicaginis	14592		288 Emericella nidulans	478	
284 Trichoderma viride	4807		288 Emericella nidulans	478	+
284 unknown	33992		288 Epicoccum nigrum	478	
284 unknown	14592	+	288 Eurotium herbariorum	11574	+
284 Wallemia sebi	44031	+	288 Fusarium sp.	4322	
284 yeast	33738		288 Fusarium sp.	1434	+
285 Alternaria alternata	9655	+	288 Penicillium chrysogenum	5777	
285 Aspergillus versicolor	4743	+	288 Penicillium chrysogenum	1444	+
285 Aureobasidium pullulans	48792		288 Penicillium citreonigrum	488	+
285 Aureobasidium pullulans	14399	+	288 Penicillium sp. #26	3865	
285 Mucor plumbeus	4743		288 Penicillium sp. #26	478	+
285 Penicillium aurantiogriseum	29301		288 Penicillium spinulosum	1464	+
285 Penicillium aurantiogriseum	4743	+	288 Penicillium viridicatum	488	+
285 Penicillium chrysogenum	96050	+	288 Phoma sp.	956	
285 Penicillium chrysogenum	77578		288 yeast	966	
285 Penicillium spinulosum	19310	+	289 Alternaria alternata	3036	+
285 Penicillium spinulosum	9655		289 Alternaria alternata	1016	
285 unknown	14567		289 Aspergillus niger	502	
285 yeast	4911		289 Aspergillus niger	502	+
286 Alternaria alternata	5698		289 Aspergillus ochraceus	514	+
286 Alternaria alternata	1914	+	289 Cladosporium cladosporioides	3049	+
286 Aspergillus sydowii	479		289 Fusarium sp.	514	+
286 Aureobasidium pullulans	7641		289 Leptosphaerulina australis	1016	
286 Aureobasidium pullulans	7129	+	289 Leptosphaerulina australis	514	+
286 Doratomyces microsporus	2399		289 Paecilomyces fulva	514	+
286 Epicoccum nigrum	1425	+	289 Penicillium citrinum	502	
286 Eurotium herbariorum	475	+	289 Penicillium echinulatum	1004	+
286 Fusarium sp.	1901		289 Penicillium implicatum	1016	+
286 Penicillium glandicola	479		289 Penicillium implicatum	514	
286 Penicillium griseofulvum	22438	+	289 Phoma eupyrena	2032	+
286 Penicillium griseofulvum	16703		289 Phoma glomerata	1028	+
286 Penicillium roquefortii	1919		289 Trichoderma viride	514	
286 Trichoderma sp.	475	+	289 unknown	5571	+
286 Trichoderma viride	475		289 unknown	5559	
286 yeast	18152		289 yeast	1518	
287 Alternaria alternata	11041		290 Aspergillus versicolor	489	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
290 Emericella nidulans	46661		294 Aspergillus ochraceus	481	+
290 Emericella nidulans	973	+	294 Aspergillus ustus	969	+
290 Eurotium herbariorum	973	+	294 Aureobasidium pullulans	487	+
290 Penicillium chrysogenum	1458		294 Penicillium chrysogenum	487	
290 Penicillium chrysogenum	484	+	294 Penicillium spinulosum	11084	+
290 Penicillium citreonigrum	3909	+	294 Penicillium spinulosum	5780	
290 Penicillium citreonigrum	1467		294 Penicillium viridicatum	1450	+
290 Trichoderma viride	489	+	294 unknown	487	+
290 unknown	2921	+	294 unknown	481	
290 unknown	1458		294 yeast	29020	
290 yeast	5367		296 Alternaria alternata	1945	
291 Alternaria alternata	1920		296 Coniothyrium sporulosum	16924	
291 Alternaria alternata	976	+	296 Coniothyrium sporulosum	11121	+
291 Aureobasidium pullulans	18864	+	296 Eurotium herbariorum	957	+
291 Aureobasidium pullulans	16556		296 Fusarium sp.	478	
291 Cladosporium cladosporioides	1431	+	296 Paecilomyces variotii	483	
291 Cladosporium herbarum	965	+	296 Penicillium griseofulvum	967	+
291 Cladosporium herbarum	477		296 Pestalotiopsis sp.	483	+
291 Epicoccum nigrum	488		296 Scytalidium sp.	1441	
291 Eurotium herbariorum	1442	+	296 unknown	6760	
291 Geomyces pannorum	3350		296 unknown	962	+
291 Mucor racemosus	2929	+	296 Wallemia sebi	483	+
291 Mucor racemosus	2419		296 yeast	478	
291 Penicillium citrinum	477		297 Aureobasidium pullulans	52859	
291 Penicillium corylophilum	488		297 Aureobasidium pullulans	4761	+
291 Penicillium corylophilum	488	+	297 Cladosporium cladosporioides	4761	+
291 Penicillium sp. #64	976	+	297 Coniothyrium sp.	90476	+
291 Penicillium sp. #64	477		297 Coniothyrium sp.	71428	
291 Phoma chrysanthemicola	9553	+	297 Penicillium vulpinum	4761	
291 Phoma chrysanthemicola	954		297 Penicillium vulpinum	4761	+
291 Phoma herbarum	954		297 Trichoderma viride	4761	+
291 unknown	3373		297 unknown	423809	+
291 unknown	477	+	298 Aspergillus ochraceus	473	
291 yeast	1953		298 Aspergillus ustus	475	+
292 Acremonium sp.	2859		298 Aureobasidium pullulans	1422	
292 Alternaria alternata	1910		298 Penicillium chrysogenum	475	
292 Alternaria alternata	974	+	298 Penicillium corylophilum	2371	+
292 Aspergillus niger	474		298 Penicillium corylophilum	948	
292 Aspergillus ochraceus	2410	+	298 Penicillium sp. #26	473	+
292 Aspergillus ochraceus	1936		298 Penicillium spinulosum	475	+
292 Aspergillus sp.	487	+	298 Phoma herbarum	946	+
292 Aspergillus sp.	474		298 unknown	473	
292 Aspergillus sydowii	487		298 yeast	147781	
292 Aspergillus sydowii	487	+	299 Alternaria alternata	14186	+
292 Aspergillus versicolor	2436		299 Aspergillus sp.	16620	
292 Aspergillus versicolor	474	+	299 Aureobasidium pullulans	4716	+
292 Aureobasidium pullulans	41250		299 Cladosporium sp.	4752	
292 Aureobasidium pullulans	40456	+	299 Cladosporium sp.	4752	+
292 Cladosporium cladosporioides	1436	+	299 Eurotium herbariorum	4752	+
292 Eurotium herbariorum	1423	+	299 Graphium sp.	4752	+
292 Mucor plumbeus	487		299 Oidiodendron rhodogenum	14258	
292 Penicillium griseofulvum	18811	+	299 Ophiostoma sp.	18867	
292 Penicillium griseofulvum	7680		299 Penicillium aurantiogriseum	9469	
292 Penicillium sp. #26	1461		299 Penicillium vulpinum	18939	
292 Penicillium sp. #26	487	+	299 Penicillium vulpinum	9433	+
292 Penicillium spinulosum	2410		299 Phoma chrysanthemicola	4716	
292 Penicillium spinulosum	1461	+	299 unknown	28445	+
292 Rhizopus oryzae	474	+	299 unknown	18903	
292 unknown	974	+	299 yeast	9469	
292 unknown	487		300 Alternaria alternata	15235	
292 yeast	2885		300 Alternaria alternata	2435	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
300	Aspergillus ustus	488		304	Aspergillus sp.	478	+
300	Aspergillus versicolor	1462	+	304	Aspergillus versicolor	957	
300	Aureobasidium pullulans	486		304	Aureobasidium pullulans	8177	
300	Aureobasidium pullulans	486	+	304	Aureobasidium pullulans	5284	+
300	Cladosporium cladosporioides	1949		304	Cladosporium cladosporioides	3371	+
300	Cladosporium cladosporioides	1462	+	304	Cladosporium sphaerospermum	1442	+
300	Cladosporium herbarum	972	+	304	Eurotium herbariorum	3366	+
300	Cladosporium sphaerospermum	1945	+	304	Fusarium sp.	1439	
300	Cladosporium sphaerospermum	1459		304	Microsphaeropsis olivaceus	960	
300	Epicoccum nigrum	1949	+	304	Microsphaeropsis olivaceus	481	+
300	Oidiodendron sp.	972		304	Mucor plumbeus	481	
300	Penicillium chrysogenum	976	+	304	Penicillium chrysogenum	963	+
300	Penicillium corylophilum	1951	+	304	Penicillium corylophilum	481	+
300	Penicillium corylophilum	976		304	Penicillium spinulosum	481	+
300	Penicillium sp.	486		304	Sordaria sp.	960	
300	Scopulariopsis candida	488		304	Trichoderma viride	963	
300	Trichoderma viride	1459		304	unknown	1442	+
300	unknown	2437	+	304	unknown	478	
300	unknown	2435		304	Wallemia sebi	25480	+
300	yeast	10706		304	yeast	21618	
301	Alternaria alternata	32180		305	Alternaria alternata	15891	
301	Alternaria alternata	14832	+	305	Alternaria alternata	14258	+
301	Aspergillus glaucus	4970	+	305	Aspergillus sydowii	9881	+
301	Aspergillus versicolor	4892	+	305	Aspergillus sydowii	4752	
301	Eurotium herbariorum	9862	+	305	Aspergillus versicolor	29268	
301	Penicillium brevicompactum	4970		305	Aspergillus versicolor	14822	+
301	Penicillium chrysogenum	4970	+	305	Cladosporium cladosporioides	4940	
301	Penicillium chrysogenum	4892		305	Cladosporium sp.	4752	+
301	Penicillium spinulosum	9940	+	305	Phoma sp.	9505	
301	Phoma sp.	4970		305	Pithomyces chartarum	4940	
301	Pithomyces chartarum	4892		305	unknown	14258	
301	Rhizopus oryzae	19647		305	unknown	14258	+
302	Alternaria alternata	22998		305	yeast	9505	
302	Alternaria alternata	10037	+	306	Acremonium rutilum	477	
302	Aspergillus fumigatus	958		306	Alternaria alternata	1431	
302	Aspergillus niger	471		306	Alternaria alternata	477	+
302	Aspergillus ornatus	3331	+	306	Aspergillus niger	477	+
302	Aspergillus ornatus	486		306	Aspergillus sydowii	959	+
302	Aspergillus sp.	471	+	306	Aureobasidium pullulans	1924	+
302	Aspergillus sydowii	486		306	Cladosporium cladosporioides	3350	+
302	Aureobasidium pullulans	29170		306	Cladosporium sphaerospermum	1436	+
302	Aureobasidium pullulans	16788	+	306	Epicoccum nigrum	477	
302	Cladosporium cladosporioides	7178	+	306	Eurotium herbariorum	1913	+
302	Cladosporium cladosporioides	1930		306	Mucor racemosus	482	
302	Cladosporium herbarum	471		306	Paecilomyces inflatus	954	
302	Cladosporium sphaerospermum	486		306	Penicillium aurantiogriseum	959	+
302	Epicoccum nigrum	4289		306	Penicillium brevicompactum	959	+
302	Epicoccum nigrum	1444	+	306	Penicillium brevicompactum	482	
302	Eurotium herbariorum	7148	+	306	Penicillium commune	2879	
302	Penicillium aurantiogriseum	1916	+	306	Penicillium expansum	2402	+
302	Penicillium aurantiogriseum	958		306	Penicillium sp.	482	
302	Penicillium spinulosum	2844		306	Penicillium spinulosum	3827	
302	Penicillium spinulosum	471	+	306	Penicillium spinulosum	959	+
302	Phoma herbarum	486		306	Penicillium viridicatum	959	
302	Phoma herbarum	486	+	306	Penicillium viridicatum	477	+
302	unknown	958		306	Phoma sp.	89762	
302	yeast	2844		306	Phoma sp.	53088	+
304	Alternaria alternata	3371		306	Trichoderma viride	2402	
304	Alternaria alternata	2394	+	306	Trichoderma viride	2402	+
304	Aspergillus glaucus	478		306	unknown	5275	+
304	Aspergillus ochraceus	481		306	unknown	2879	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
306	Wallemia sebi	965	+	311	Cladosporium cladosporioides	3405	+
306	yeast	6690		311	Cladosporium cladosporioides	1941	
307	Alternaria alternata	1457		311	Cladosporium sphaerospermum	986	
307	Aspergillus versicolor	490		311	Cladosporium sphaerospermum	986	+
307	Aureobasidium pullulans	13739		311	Epicoccum nigrum	493	
307	Aureobasidium pullulans	490	+	311	Eurotium herbariorum	4368	+
307	Cladosporium cladosporioides	1470		311	Fusarium oxysporum	1456	
307	Epicoccum nigrum	1470	+	311	Fusarium sp.	1972	
307	Epicoccum nigrum	491		311	Fusarium sp.	493	+
307	Eurotium herbariorum	981	+	311	Paecilomyces variotii	485	
307	Penicillium spinulosum	981	+	311	Penicillium corylophilum	2457	+
307	Phoma herbarum	491		311	Penicillium expansum	978	+
307	Sphaeropsis sp.	491		311	Phoma sp.	4384	
307	unknown	980		311	Phoma sp.	1463	+
307	unknown	490	+	311	Rhizopus oryzae	493	
307	yeast	3436		311	Scopulariopsis brevicaulis	970	+
309	Alternaria alternata	33358		311	Ulocladium chartarum	493	+
309	Alternaria alternata	4743	+	312	Alternaria alternata	2614	
309	Aspergillus niger	4734		312	Aspergillus versicolor	1307	
309	Aureobasidium pullulans	9487	+	312	Aspergillus versicolor	663	+
309	Cladosporium herbarum	4743		312	Aureobasidium pullulans	14494	
309	Cladosporium herbarum	4734	+	312	Aureobasidium pullulans	8489	+
309	Cladosporium sp.	4734		312	Cladosporium herbarum	1989	+
309	Cladosporium sp.	4734	+	312	Fusarium sp.	663	+
309	Cladosporium sphaerospermum	9469	+	312	Mucor racemosus	1288	
309	Epicoccum nigrum	4743	+	312	Mucor racemosus	663	+
309	Epicoccum nigrum	4734		312	Penicillium aurantiogriseum	3922	+
309	Fusarium oxysporum	4743		312	Penicillium aurantiogriseum	1951	
309	Fusarium oxysporum	4743	+	312	unknown	1326	
309	Myrothecium sp.	4743		313	Alternaria alternata	496	
309	Penicillium chrysogenum	4743	+	313	Aspergillus niger	992	+
309	Penicillium expansum	4743		313	Aspergillus sp.	497	
309	Penicillium spinulosum	9469		313	Aspergillus ustus	992	+
309	Penicillium spinulosum	4734	+	313	Aspergillus ustus	496	
309	Phoma sp.	9487		313	Aspergillus versicolor	993	
309	unknown	14231		313	Aspergillus versicolor	497	+
309	yeast	56872		313	Aureobasidium pullulans	496	
310	Alternaria alternata	56526		313	Cladosporium cladosporioides	496	
310	Alternaria alternata	4403	+	313	Eurotium herbariorum	1491	+
310	Aspergillus candidus	489	+	313	Mucor plumbeus	2481	
310	Aspergillus versicolor	489	+	313	Mucor plumbeus	1491	+
310	Aureobasidium pullulans	49653		313	Penicillium chrysogenum	19365	+
310	Aureobasidium pullulans	42886	+	313	Penicillium chrysogenum	11918	
310	Cladosporium cladosporioides	2408	+	313	Penicillium commune	2483	+
310	Cladosporium cladosporioides	1445		313	Penicillium sp.	496	
310	Cladosporium sphaerospermum	970	+	313	Penicillium spinulosum	1490	
310	Cladosporium sphaerospermum	963		313	Penicillium spinulosum	992	+
310	Fusarium sp.	481	+	313	unknown	1490	
310	Penicillium expansum	3409	+	315	Alternaria alternata	978	
310	Penicillium expansum	489		315	Alternaria alternata	484	+
310	Rhizopus oryzae	970		315	Aspergillus candidus	978	+
310	unknown	1445		315	Aspergillus fumigatus	988	+
310	yeast	5374		315	Aspergillus sp.	494	+
311	Alternaria alternata	13114		315	Aspergillus sydowii	1482	
311	Alternaria alternata	5339	+	315	Aspergillus versicolor	1966	+
311	Aspergillus cervinus	1957	+	315	Aureobasidium pullulans	4854	
311	Aspergillus ochraceus	1456		315	Aureobasidium pullulans	484	+
311	Aspergillus terreus	986		315	Eurotium herbariorum	494	+
311	Aspergillus versicolor	3891	+	315	unknown	494	
311	Aureobasidium pullulans	89325		315	unknown	484	+
311	Aureobasidium pullulans	34718	+	315	yeast	153767	



HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
316 Alternaria alternata	478	+	319 Epicoccum nigrum	1915	
316 Aspergillus flavus	2403	+	319 Eurotium herbariorum	962	+
316 Aspergillus fumigatus	92371		319 Mucor plumbeus	478	+
316 Aspergillus sydowii	2884		319 Penicillium brevicompactum	2896	
316 Aspergillus sydowii	480	+	319 Penicillium chrysogenum	8671	
316 Aspergillus versicolor	480	+	319 Penicillium chrysogenum	8188	+
316 Cladosporium cladosporioides	478	+	319 Penicillium islandicum	483	+
316 Epicoccum nigrum	1439		319 Phoma herbarum	967	
316 Eurotium herbariorum	1914	+	319 Phoma herbarum	478	+
316 Mucor racemosus	480	+	319 Trichoderma viride	483	
316 Penicillium chrysogenum	1439	+	319 unknown	1920	
316 Penicillium citreonigrum	1917		320 Acremonium sp.	961	+
316 Penicillium citreonigrum	958	+	320 Alternaria alternata	5329	
316 Penicillium commune	4791	+	320 Alternaria alternata	1459	+
316 Penicillium commune	2398		320 Aspergillus niger	480	
316 Penicillium decumbens	1917	+	320 Aspergillus ochraceus	480	+
316 Pithomyces chartarum	956		320 Aureobasidium pullulans	6370	
316 Pithomyces chartarum	480	+	320 Aureobasidium pullulans	6336	+
316 Trichoderma viride	3829		320 Cladosporium herbarum	1476	
316 Trichoderma viride	1439	+	320 Cladosporium sphaerospermum	498	+
316 unknown	1917		320 Epicoccum nigrum	1476	+
316 yeast	3357		320 Eurotium herbariorum	1940	+
317 Alternaria alternata	4716	+	320 Eurotium herbariorum	498	
317 Aspergillus ustus	14150	+	320 Paecilomyces variotii	978	
317 Aspergillus ustus	9671		320 Penicillium chrysogenum	1459	
317 Aspergillus versicolor	42808	+	320 Phoma herbarum	1923	
317 Aspergillus versicolor	18867		320 Phoma sp.	996	
317 Cladosporium cladosporioides	9433	+	320 unknown	978	
317 Epicoccum nigrum	9433	+	320 yeast	978	
317 Penicillium chrysogenum	19105		322 Alternaria alternata	4801	
317 Penicillium chrysogenum	14269	+	322 Alternaria alternata	3327	+
317 Penicillium expansum	9433		322 Aspergillus sp.	1133	
317 unknown	9433		322 Aspergillus sp.	542	+
318 Alternaria alternata	1391	+	322 Aspergillus ustus	542	
318 Aspergillus versicolor	3561	+	322 Aspergillus versicolor	1651	+
318 Aspergillus versicolor	1002		322 Aureobasidium pullulans	1626	
318 Cladosporium cladosporioides	1391	+	322 Aureobasidium pullulans	542	+
318 Cladosporium sp.	501	+	322 Cladosporium cladosporioides	3327	+
318 Cladosporium sp.	389		322 Cladosporium cladosporioides	566	
318 Cladosporium sphaerospermum	1279	+	322 Cladosporium herbarum	1109	
318 Cladosporium sphaerospermum	501		322 Epicoccum nigrum	1626	
318 Eurotium herbariorum	389	+	322 Epicoccum nigrum	542	+
318 Mucor racemosus	389		322 Fusarium sp.	2169	+
318 Penicillium italicum	389		322 Fusarium sp.	1133	
318 Phoma sp.	389		322 Mucor racemosus	566	+
318 Stemphylium sp.	1168	+	322 Myrothecium sp.	1084	
318 Ulocladium chartarum	501		322 Paecilomyces variotii	2218	+
318 unknown	1669		322 Penicillium brevicompactum	566	+
318 unknown	1503	+	322 Penicillium chrysogenum	1109	
318 yeast	3338		322 Penicillium chrysogenum	1109	+
319 Alternaria alternata	11555		322 Penicillium citrinum	566	+
319 Alternaria alternata	1450	+	322 Scopulariopsis candida	1084	
319 Aspergillus ochraceus	483	+	322 unknown	3352	
319 Aspergillus ochraceus	478		322 unknown	2242	+
319 Aspergillus versicolor	1446		322 yeast	21592	
319 Aureobasidium pullulans	19770		323 Alternaria alternata	19255	
319 Aureobasidium pullulans	7220	+	323 Aspergillus restrictus	73964	+
319 Cladosporium cladosporioides	478	+	323 Aspergillus restrictus	4882	
319 Cladosporium herbarum	478		323 Aureobasidium pullulans	64102	+
319 Cladosporium sphaerospermum	483	+	323 Cladosporium herbarum	4930	+
319 Cladosporium sphaerospermum	478		323 Epicoccum nigrum	19723	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
323 Eurotium herbariorum	9861	+	328 Sporobolomyces sp.	490	
323 Penicillium islandicum	4882		328 Ulocladium chartarum	490	+
323 Trichoderma viride	4882		328 unknown	497	
323 unknown	63476		329 Alternaria alternata	23320	
323 unknown	34516	+	329 Alternaria alternata	4835	+
323 Wallemia sebi	14792	+	329 Aspergillus ochraceus	9699	+
323 yeast	659179		329 Aspergillus sp.	4863	
325 Alternaria alternata	420053		329 Aspergillus versicolor	4863	+
325 Alternaria alternata	11730	+	329 Aspergillus versicolor	4835	
325 Aureobasidium pullulans	2912	+	329 Aureobasidium pullulans	160251	
325 Aureobasidium pullulans	1941		329 Aureobasidium pullulans	77567	+
325 Cladosporium cladosporioides	6357		329 Cladosporium cladosporioides	4863	+
325 Cladosporium cladosporioides	4429	+	329 Cladosporium herbarum	14591	+
325 Cladosporium herbarum	10739	+	329 Cladosporium sphaerospermum	4835	
325 Epicoccum nigrum	1948		329 Epicoccum nigrum	4835	+
325 Epicoccum nigrum	977	+	329 Eurotium herbariorum	9699	+
325 Eurotium herbariorum	485	+	329 Fusarium sp.	14506	
325 Fusarium sp.	1948	+	329 Mucor racemosus	4835	+
325 Fusarium sp.	492		329 Penicillium citreonigrum	9699	+
325 Mucor plumbeus	492	+	329 Penicillium citreonigrum	4863	
325 Oidiodendron sp.	492	+	329 Penicillium decumbens	4863	
325 Penicillium aurantiogriseum	977		329 Phoma herbarum	9671	
325 Penicillium brevicompactum	6377	+	329 Phoma sp.	4863	
325 Penicillium brevicompactum	5400		329 Ulocladium chartarum	4863	
325 Penicillium commune	2932	+	329 unknown	4835	
325 Penicillium commune	1948		330 Acremonium sp.	478	
325 Phoma herbarum	984		330 Acremonium sp.	477	+
325 Rhizopus oryzae	492		330 Alternaria alternata	5729	+
325 Trichoderma viride	485		330 Alternaria alternata	4775	
325 unknown	6337		330 Aureobasidium pullulans	52511	
325 unknown	2440	+	330 Aureobasidium pullulans	27691	+
325 yeast	7321		330 Cladosporium herbarum	13846	+
326 Alternaria alternata	7614		330 Cladosporium herbarum	6202	
326 Aspergillus candidus	4681		330 Cladosporium sphaerospermum	3346	
326 Aspergillus versicolor	323033		330 Epicoccum nigrum	1433	
326 Aspergillus versicolor	14044	+	330 Epicoccum nigrum	1433	+
326 Aureobasidium pullulans	135767	+	330 Eurotium herbariorum	2385	
326 Aureobasidium pullulans	117041		330 Eurotium herbariorum	1431	+
326 Cladosporium cladosporioides	224719	+	330 Fusarium sp.	477	
326 Cladosporium cladosporioides	84269		330 Mucor racemosus	478	+
326 Eurotium herbariorum	650749	+	330 Paecilomyces variotii	8595	
326 Penicillium chrysogenum	1413857		330 Paecilomyces variotii	4776	+
326 Penicillium chrysogenum	964419	+	330 Penicillium chrysogenum	3817	+
326 yeast	23408		330 Penicillium chrysogenum	1432	
328 Alternaria alternata	16019		330 Penicillium corylophilum	478	
328 Alternaria alternata	1981	+	330 Penicillium decumbens	478	
328 Aspergillus cervinus	497		330 Penicillium decumbens	477	+
328 Aureobasidium pullulans	70017		330 Penicillium raistrickii	955	
328 Aureobasidium pullulans	46385	+	330 Phoma herbarum	956	
328 Cladosporium cladosporioides	3955		330 Phoma sp.	1431	
328 Cladosporium cladosporioides	497	+	330 Trichocladium asperum	956	
328 Cladosporium sphaerospermum	980	+	330 Ulocladium chartarum	478	
328 Mucor plumbeus	2471	+	330 unknown	2388	+
328 Mucor plumbeus	987		330 unknown	956	
328 Paecilomyces variotii	2485		331 Alternaria alternata	9689	
328 Paecilomyces variotii	2450	+	331 Aureobasidium pullulans	399342	+
328 Penicillium expansum	14283	+	331 Aureobasidium pullulans	317256	
328 Penicillium expansum	9347		331 Cladosporium herbarum	4844	
328 Phoma herbarum	497		331 Cladosporium sphaerospermum	4844	
328 Phoma sp.	2450		331 Penicillium viridicatum	4798	
328 Phoma sp.	994	+	331 Penicillium viridicatum	4798	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
331 Phoma herbarum	33914		336 Cladosporium herbarum	4356	+
331 Phoma herbarum	19240	+	336 Epicoccum nigrum	488	+
332 Alternaria alternata	9161		336 Epicoccum nigrum	480	
332 Alternaria alternata	6783	+	336 Fusarium sp.	480	+
332 Aureobasidium pullulans	12120		336 Penicillium chrysogenum	480	+
332 Aureobasidium pullulans	12114	+	336 yeast	480	
332 Cladosporium cladosporioides	972	+	337 Alternaria alternata	5219	+
332 Cladosporium cladosporioides	483		337 Alternaria alternata	477	
332 Cladosporium herbarum	969	+	337 Aspergillus sp.	950	
332 Cladosporium herbarum	483		337 Aspergillus sp.	477	+
332 Cladosporium sphaerospermum	483	+	337 Aspergillus versicolor	1420	+
332 Epicoccum nigrum	1456		337 Aureobasidium pullulans	4763	+
332 Epicoccum nigrum	486	+	337 Aureobasidium pullulans	1897	
332 Eurotium herbariorum	967	+	337 Cladosporium cladosporioides	477	+
332 Mucor racemosus	1456	+	337 Cladosporium herbarum	2844	+
332 Penicillium commune	38786	+	337 Eurotium herbariorum	473	+
332 Penicillium commune	30070		337 Fusarium sp.	473	+
332 Penicillium viridicatum	483	+	337 Penicillium chrysogenum	3332	+
332 Phoma herbarum	483	+	337 Penicillium chrysogenum	1424	
332 unknown	969	+	337 Penicillium citrinum	473	+
332 yeast	1450		337 Penicillium griseofulvum	946	+
333 Alternaria alternata	2262	+	337 Trichoderma viride	7633	+
333 Aspergillus versicolor	1146	+	337 Trichoderma viride	1908	
333 Aureobasidium pullulans	3348	+	337 unknown	7629	
333 Cladosporium herbarum	18225	+	337 unknown	3325	+
333 Cladosporium herbarum	2718		337 Wallemia sebi	950	+
333 Epicoccum nigrum	7935	+	337 yeast	10452	
333 Epicoccum nigrum	2293		338 Alternaria alternata	7124	
333 Penicillium commune	5703		338 Alternaria alternata	2375	+
333 Penicillium commune	4525	+	338 Aspergillus candidus	2860	+
333 Phoma sp.	2262		338 Aspergillus candidus	1903	
333 unknown	2262	+	338 Aspergillus niger	478	
333 Wallemia sebi	1146	+	338 Aspergillus ornatus	478	
333 yeast	15717		338 Aspergillus versicolor	478	
335 Alternaria alternata	7609		338 Aureobasidium pullulans	3308	
335 Alternaria alternata	4762	+	338 Aureobasidium pullulans	2848	+
335 Aspergillus versicolor	484		338 Cladosporium cladosporioides	951	+
335 Aureobasidium pullulans	44467		338 Epicoccum nigrum	2381	+
335 Aureobasidium pullulans	24461	+	338 Fusarium sp.	957	
335 Cladosporium cladosporioides	2401	+	338 Myrothecium olivaceum	478	
335 Cladosporium cladosporioides	484		338 Penicillium chrysogenum	2848	+
335 Cladosporium herbarum	1453	+	338 Penicillium chrysogenum	957	
335 Cladosporium sphaerospermum	2782		338 Penicillium janthinellum	472	
335 Cladosporium sphaerospermum	1391	+	338 Phoma sp.	4253	
335 Epicoccum nigrum	1855		338 Phoma sp.	478	+
335 Epicoccum nigrum	1391	+	338 Rhizopus oryzae	1890	+
335 Eurotium herbariorum	4195	+	338 Rhizopus oryzae	472	
335 Eurotium sp.	1412		338 unknown	19861	+
335 Penicillium expansum	1917	+	338 unknown	4278	
335 Penicillium expansum	484		338 yeast	14304	
335 Penicillium italicum	968	+	339 Alternaria alternata	2413	+
335 unknown	6153	+	339 Alternaria alternata	1446	
335 unknown	3731		339 Aspergillus glaucus	474	+
335 yeast	2906		339 Aspergillus ochraceus	488	
336 Alternaria alternata	11235		339 Aspergillus ochraceus	474	+
336 Alternaria alternata	2884	+	339 Aspergillus sydowii	962	
336 Aureobasidium pullulans	9202	+	339 Aspergillus sydowii	488	+
336 Aureobasidium pullulans	8263		339 Aspergillus versicolor	488	
336 Cladosporium cladosporioides	1449		339 Aureobasidium pullulans	3808	
336 Cladosporium cladosporioides	976	+	339 Aureobasidium pullulans	2846	+
336 Cladosporium herbarum	4364		339 Cladosporium cladosporioides	1925	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
339	Cladosporium herbarum	7631	+	341	Penicillium chrysogenum	478	
339	Cladosporium herbarum	976		341	unknown	482	
339	Epicoccum nigrum	1437	+	341	unknown	482	+
339	Epicoccum nigrum	474		341	yeast	16836	
339	Eurotium herbariorum	5859	+	342	Alternaria alternata	20257	
339	Mucor plumbeus	488		342	Alternaria alternata	8290	+
339	Mucor plumbeus	488	+	342	Aspergillus fumigatus	1467	
339	Mucor racemosus	488		342	Aspergillus fumigatus	980	+
339	Mucor racemosus	474	+	342	Aspergillus ustus	980	
339	Penicillium expansum	4827	+	342	Aureobasidium pullulans	25358	
339	Penicillium expansum	3850		342	Aureobasidium pullulans	23434	+
339	Penicillium oxalicum	488		342	Cladosporium cladosporioides	1461	+
339	Penicillium oxalicum	474	+	342	Cladosporium herbarum	980	+
339	Penicillium waksmanii	1450		342	Cladosporium sp.	980	+
339	Scopulariopsis brevicaulis	474		342	Penicillium chrysogenum	1957	+
339	Sphaeropsis sp.	474		342	Penicillium chrysogenum	487	
339	Stachybotrys chartarum	474		342	Penicillium citreonigrum	490	
339	Trichoderma viride	1437		342	Penicillium spinulosum	490	+
339	unknown	5775		342	Penicillium spinulosum	487	
339	unknown	5748	+	342	Rhizopus oryzae	490	
339	Wallemia sebi	976	+	342	Tolypocladium sp.	36274	
339	yeast	6724		342	Tolypocladium sp.	977	+
340	Alternaria alternata	8680		342	Trichoderma viride	1464	
340	Alternaria alternata	4804	+	342	unknown	7825	+
340	Alternaria sp.	9223		342	unknown	5389	
340	Aspergillus versicolor	954		342	yeast	11251	
340	Aureobasidium pullulans	40201	+	344	Alternaria alternata	3248	
340	Aureobasidium pullulans	33663		344	Alternaria alternata	1407	+
340	Cladosporium cladosporioides	485	+	344	Aspergillus ustus	115	
340	Cladosporium herbarum	54010	+	344	Aspergillus versicolor	234	
340	Cladosporium herbarum	962		344	Aspergillus versicolor	119	+
340	Cladosporium sphaerospermum	1916	+	344	Aureobasidium pullulans	1280	+
340	Epicoccum nigrum	485		344	Cladosporium herbarum	465	+
340	Fusarium sp.	477		344	Cladosporium herbarum	115	
340	Mucor racemosus	485	+	344	Eurotium herbariorum	119	+
340	Paecilomyces variotii	477		344	Penicillium chrysogenum	2695	+
340	Penicillium brevicompactum	477		344	Penicillium chrysogenum	2092	
340	Penicillium chrysogenum	962	+	344	Penicillium simplicissimum	234	
340	Penicillium chrysogenum	477		344	Penicillium simplicissimum	115	+
340	Penicillium citreonigrum	477		344	unknown	699	+
340	Penicillium corylophilum	1447	+	344	unknown	465	
340	Penicillium corylophilum	962		344	yeast	2832	
340	Penicillium viridicatum	485		345	Alternaria alternata	4424	+
340	Penicillium viridicatum	477	+	345	Aspergillus versicolor	4713	
340	Phoma herbarum	954	+	345	Aspergillus versicolor	4424	+
340	Phoma herbarum	477		345	Epicoccum nigrum	4424	+
340	Phoma sp.	970	+	345	Penicillium sp.	4621	
340	unknown	2410		345	Rhizopus oryzae	4621	
341	Acremonium sp.	2396		345	unknown	22123	+
341	Alternaria alternata	478		345	unknown	18091	
341	Aspergillus niger	478		345	yeast	62732	
341	Aspergillus ochraceus	478	+	347	Alternaria alternata	125597	
341	Aspergillus sp.	478	+	347	Alternaria alternata	1037	+
341	Aureobasidium pullulans	4803	+	347	Aureobasidium pullulans	13935	
341	Aureobasidium pullulans	478		347	Aureobasidium pullulans	6724	+
341	Cladosporium sp.	2886	+	347	Cladosporium cladosporioides	525	+
341	Epicoccum nigrum	960	+	347	Cladosporium herbarum	1050	+
341	Epicoccum nigrum	478		347	Cladosporium sphaerospermum	525	+
341	Mucor plumbeus	478	+	347	Epicoccum nigrum	1037	+
341	Mucor racemosus	478	+	347	Eurotium herbariorum	1037	+
341	Myrothecium sp.	478		347	Penicillium chrysogenum	44035	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
347 Penicillium chrysogenum	32662		351 Penicillium citreonigrum	499	
347 unknown	4713		351 Penicillium oxalicum	2471	
348 Alternaria alternata	4808	+	351 Penicillium oxalicum	1485	+
348 Alternaria alternata	3064		351 Phoma herbarum	7984	
348 Aspergillus sp.	477	+	351 Trichoderma viride	7895	
348 Aureobasidium pullulans	3395	+	351 Trichoderma viride	5424	+
348 Aureobasidium pullulans	1449		351 unknown	499	
348 Cladosporium cladosporioides	477		351 yeast	499	
348 Epicoccum nigrum	2394		352 Alternaria alternata	4878	
348 Eurotium herbariorum	1449	+	352 Alternaria alternata	1409	+
348 Penicillium corylophilum	1431		352 Aspergillus oryzae	490	
348 Penicillium expansum	1440	+	352 Aspergillus versicolor	469	+
348 Penicillium expansum	477		352 Aureobasidium pullulans	10480	
348 Penicillium simplicissimum	1440		352 Aureobasidium pullulans	4330	+
348 Penicillium sp. #26	1440		352 Cladosporium herbarum	490	+
348 Penicillium spinulosum	2899	+	352 Cladosporium sphaerospermum	490	+
348 Penicillium spinulosum	1449		352 Eurotium herbariorum	960	+
348 Phoma sp.	477	+	352 Paecilomyces variotii	490	
348 unknown	9176	+	352 Penicillium chrysogenum	5229	+
348 unknown	963		352 Penicillium chrysogenum	490	
348 yeast	3816		352 Penicillium islandicum	490	
349 Alternaria alternata	9863		352 Penicillium janthinellum	4371	+
349 Aspergillus versicolor	5000	+	352 Penicillium janthinellum	2860	
349 Aureobasidium pullulans	5000		352 Penicillium spinulosum	939	
349 Cladosporium sp.	5000		352 Penicillium spinulosum	490	+
349 Dothichiza sp.	10000		352 Phoma herbarum	2860	
349 Epicoccum nigrum	15000		352 unknown	490	
349 Penicillium citreonigrum	5000		352 yeast	469	
349 yeast	1230000		353 Alternaria alternata	4301	
350 Alternaria alternata	55979		353 Alternaria alternata	4294	+
350 Alternaria alternata	979	+	353 Aspergillus versicolor	471	+
350 Aspergillus niger	482		353 Aureobasidium pullulans	37126	
350 Aureobasidium pullulans	1973		353 Aureobasidium pullulans	35052	+
350 Aureobasidium pullulans	497	+	353 Cladosporium cladosporioides	951	+
350 Cladosporium herbarum	6900	+	353 Cladosporium sphaerospermum	1439	
350 Cladosporium herbarum	497		353 Cladosporium sphaerospermum	479	+
350 Epicoccum nigrum	979	+	353 Epicoccum nigrum	471	
350 Eurotium herbariorum	2485	+	353 Eupenicillium ochrosalmonium	2391	
350 Fusarium oxysporum	1491		353 Eupenicillium ochrosalmonium	1894	+
350 Paecilomyces variotii	482		353 Eurotium herbariorum	2382	+
350 Penicillium chrysogenum	2967	+	353 Myrothecium olivaceum	1415	+
350 Penicillium chrysogenum	979		353 Penicillium brevicompactum	6701	+
350 Penicillium griseofulvum	1959	+	353 Penicillium brevicompactum	3326	
350 Pithomyces sp.	497		353 Penicillium commune	479	+
350 Pithomyces sp.	497	+	353 Penicillium spinulosum	1903	
350 unknown	2953	+	353 Penicillium spinulosum	479	+
350 unknown	994		353 Phoma herbarum	4741	
350 Wallemia sebi	1973	+	353 Phoma sp.	255278	
350 yeast	21155		353 Rhizopus oryzae	471	
351 Alternaria alternata	11689		353 Ulocladium chartarum	471	+
351 Alternaria alternata	2477	+	353 unknown	471	
351 Aspergillus niger	499		354 Alternaria alternata	2890	
351 Aspergillus niger	493	+	354 Alternaria alternata	2410	+
351 Aspergillus sydowii	499	+	354 Aspergillus ochraceus	9520	+
351 Aspergillus versicolor	992	+	354 Aspergillus ochraceus	9111	
351 Aureobasidium pullulans	12368		354 Aureobasidium pullulans	12951	
351 Aureobasidium pullulans	7431	+	354 Aureobasidium pullulans	8519	+
351 Cladosporium sphaerospermum	1497	+	354 Cladosporium cladosporioides	1450	+
351 Epicoccum nigrum	499	+	354 Cladosporium herbarum	939	+
351 Eurotium herbariorum	986	+	354 Epicoccum nigrum	939	
351 Paecilomyces fumosoroseus	499		354 Eurotium herbariorum	2450	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
354 Penicillium chrysogenum	7660		357 Epicoccum nigrum	1449	+
354 Penicillium chrysogenum	7620	+	357 Paecilomyces variotii	486	
354 Penicillium citrinum	960		357 Penicillium brevicompactum	2909	
354 Penicillium raistrickii	469		357 Penicillium brevicompactum	477	+
354 Penicillium spinulosum	960		357 Penicillium chrysogenum	1440	+
354 Penicillium spinulosum	960	+	357 Penicillium citrinum	1449	
354 Phoma herbarum	490		357 Penicillium glandicola	486	
354 Phoma herbarum	469	+	357 Phoma herbarum	972	
354 Scopulariopsis brevicaulis	469		357 Scopulariopsis candida	486	+
354 Scopulariopsis brevicaulis	469	+	357 unknown	486	
354 Stachybotrys chartarum	490		358 Alternaria alternata	5807	
354 unknown	4881	+	358 Alternaria alternata	2412	+
354 unknown	1920		358 Aspergillus niger	486	+
354 yeast	939		358 Aspergillus versicolor	2412	+
355 Alternaria alternata	13092	+	358 Aspergillus versicolor	959	
355 Alternaria alternata	2921		358 Aureobasidium pullulans	17878	+
355 Aspergillus candidus	495	+	358 Aureobasidium pullulans	14013	
355 Aureobasidium pullulans	24602	+	358 Cladosporium cladosporioides	1439	+
355 Aureobasidium pullulans	24188		358 Cladosporium cladosporioides	959	
355 Cladosporium cladosporioides	495	+	358 Cladosporium herbarum	11594	+
355 Cladosporium herbarum	1964	+	358 Cladosporium herbarum	486	
355 Cladosporium sphaerospermum	478		358 Cladosporium sphaerospermum	1925	+
355 Cladosporium sphaerospermum	478	+	358 Cladosporium sphaerospermum	486	
355 Epicoccum nigrum	3384		358 Epicoccum nigrum	8663	+
355 Eurotium herbariorum	1452	+	358 Epicoccum nigrum	7729	
355 Mucor plumbeus	478		358 Mucor plumbeus	966	
355 Mucor racemosus	1436		358 Mucor racemosus	486	+
355 Penicillium viridicatum	5381		358 Penicillium brevicompactum	966	+
355 Penicillium viridicatum	5348	+	358 Penicillium brevicompactum	966	+
355 Phoma herbarum	3847		358 Penicillium digitatum	4824	+
355 Phoma herbarum	1436	+	358 Penicillium digitatum	3398	
355 Trichoderma viride	478		358 Phoma herbarum	479	
355 unknown	1964		358 unknown	3851	
356 Alternaria alternata	6785		358 unknown	3391	+
356 Alternaria alternata	2892	+	359 Alternaria alternata	9480	+
356 Aspergillus versicolor	1446		359 Aureobasidium pullulans	47517	+
356 Aspergillus versicolor	481	+	359 Aureobasidium pullulans	28440	
356 Aureobasidium pullulans	4820	+	359 Cladosporium herbarum	4681	+
356 Aureobasidium pullulans	1446		359 Eurotium herbariorum	4798	+
356 Cladosporium cladosporioides	963		359 Myrothecium olivaceum	151681	
356 Cladosporium herbarum	1446	+	359 unknown	9596	
356 Epicoccum nigrum	2892	+	361 Alternaria alternata	162637	
356 Epicoccum nigrum	482		361 Alternaria alternata	9633	+
356 Eurotium herbariorum	482	+	361 Aspergillus versicolor	19323	
356 Penicillium corylophilum	964		361 Aspergillus versicolor	9633	+
356 Penicillium corylophilum	964	+	361 Aureobasidium pullulans	9671	+
356 Stachybotrys chartarum	963		361 Aureobasidium pullulans	4816	
356 unknown	4340	+	361 Cladosporium herbarum	14450	+
356 unknown	1928		361 Cladosporium sphaerospermum	4816	+
356 Verticillium sp.	481		361 Coniothyrium sp.	33811	
356 yeast	3861		361 Epicoccum nigrum	9671	+
357 Alternaria alternata	4330		361 Penicillium chrysogenum	4835	+
357 Alternaria alternata	1917	+	361 Penicillium corylophilum	4835	+
357 Aspergillus versicolor	1459	+	361 Phoma sp.	14469	
357 Aspergillus versicolor	954		361 Phoma sp.	4835	+
357 Aureobasidium pullulans	13882	+	361 Stachybotrys chartarum	4816	
357 Aureobasidium pullulans	10616		361 unknown	9652	
357 Cladosporium cladosporioides	3826	+	361 unknown	9652	+
357 Cladosporium herbarum	1459	+	361 yeast	19323	
357 Cladosporium herbarum	477		362 Alternaria alternata	24574	
357 Cladosporium sphaerospermum	1459	+	362 Alternaria alternata	1901	+

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
362 Aspergillus niger	475	+	364 Penicillium griseofulvum	499	
362 Aspergillus versicolor	470		364 Penicillium spinulosum	2465	
362 Aspergillus versicolor	470	+	364 Penicillium spinulosum	978	+
362 Aureobasidium pullulans	16047		364 Phoma herbarum	499	
362 Aureobasidium pullulans	7559	+	364 Phoma herbarum	499	+
362 Cladosporium cladosporioides	475		364 Scopulariopsis brevicaulis	499	
362 Cladosporium herbarum	470		364 unknown	2935	
362 Coniothyrium sp.	470	+	364 unknown	1477	+
362 Epicoccum nigrum	470	+	364 yeast	988	
362 Eurotium herbariorum	470	+	366 Acremonium sp.	497	
362 Fusarium sp.	475	+	366 Alternaria alternata	3458	
362 Penicillium expansum	4268	+	366 Alternaria alternata	1988	+
362 Penicillium expansum	941		366 Aspergillus sydowii	994	
362 Penicillium griseofulvum	5689	+	366 Aspergillus versicolor	980	
362 Penicillium griseofulvum	4268		366 Aureobasidium pullulans	16823	
362 Penicillium italicum	14213	+	366 Aureobasidium pullulans	5936	+
362 Penicillium italicum	4721		366 Cladosporium herbarum	5882	+
362 Phoma herbarum	66539		366 Eurotium herbariorum	3458	+
362 Phoma herbarum	14733	+	366 Penicillium chrysogenum	8884	+
362 Sphaeropsis sp.	475	+	366 Penicillium chrysogenum	5426	
362 Trichoderma viride	1421		366 Penicillium citrinum	5453	
362 Trichoderma viride	946	+	366 Penicillium citrinum	2471	+
362 unknown	470		366 Phoma herbarum	1960	
363 Alternaria alternata	3309		366 Phoma herbarum	497	+
363 Aspergillus cervinus	471	+	366 unknown	3438	
363 Aspergillus versicolor	943	+	368 Alternaria alternata	3907	
363 Aspergillus versicolor	471		368 Aspergillus versicolor	490	
363 Aureobasidium pullulans	9451	+	368 Aureobasidium pullulans	40514	
363 Aureobasidium pullulans	7075		368 Aureobasidium pullulans	18074	+
363 Cladosporium cladosporioides	471		368 Cladosporium herbarum	2932	+
363 Cladosporium herbarum	471		368 Cladosporium sphaerospermum	490	
363 Cladosporium herbarum	471	+	368 Cladosporium sphaerospermum	490	+
363 Fusarium sp.	471		368 Epicoccum nigrum	1470	
363 Mucor plumbeus	28355	+	368 Epicoccum nigrum	490	+
363 Mucor plumbeus	24101		368 Fusarium sp.	487	
363 Penicillium expansum	199902	+	368 Penicillium chrysogenum	11251	
363 Penicillium expansum	190451		368 Penicillium chrysogenum	9789	+
363 Penicillium simplicissimum	15121	+	368 Penicillium spinulosum	6355	
363 Penicillium simplicissimum	471		368 Penicillium spinulosum	1461	+
363 Trichoderma viride	471	+	368 Phoma herbarum	2442	
363 unknown	5197	+	368 Phoma herbarum	490	+
363 Wallemia sebi	182547	+	368 unknown	490	
364 Alternaria alternata	5420		368 yeast	974	
364 Alternaria alternata	3943	+	370 Aspergillus versicolor	73275	
364 Aspergillus ochraceus	1976		370 Aspergillus versicolor	68803	+
364 Aspergillus ochraceus	489	+	370 Aureobasidium pullulans	19647	
364 Aspergillus versicolor	1976	+	370 Aureobasidium pullulans	14716	+
364 Aureobasidium pullulans	15332		370 Cladosporium herbarum	24578	+
364 Aureobasidium pullulans	11839	+	370 Eurotium herbariorum	19647	+
364 Cladosporium cladosporioides	499		370 Penicillium brevicompactum	4930	
364 Cladosporium herbarum	14852	+	370 Penicillium expansum	24578	+
364 Cladosporium herbarum	6917		370 Penicillium expansum	19647	
364 Cladosporium sphaerospermum	4451	+	370 unknown	24348	+
364 Cladosporium sphaerospermum	489		370 unknown	4930	
364 Epicoccum nigrum	2495		370 yeast	44225	
364 Epicoccum nigrum	1956	+	372 Alternaria alternata	96249	
364 Eurotium herbariorum	2455	+	372 Aspergillus versicolor	950	
364 Geomyces pannorum	489	+	372 Aureobasidium pullulans	23492	
364 Mucor racemosus	489		372 Aureobasidium pullulans	12173	+
364 Penicillium chrysogenum	3453	+	372 Cladosporium herbarum	7991	+
364 Penicillium chrysogenum	2954		372 Cladosporium herbarum	1409	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
372 Cladosporium sphaerospermum	942	+	375 Penicillium chrysogenum	3935	
372 Epicoccum nigrum	1885	+	375 Penicillium chrysogenum	1485	+
372 Epicoccum nigrum	1401		375 Penicillium corylophilum	4875	+
372 Paecilomyces variotii	475	+	375 Penicillium corylophilum	1942	
372 Penicillium chrysogenum	20800	+	375 Penicillium miczynskii	2895	
372 Penicillium chrysogenum	7089		375 Phoma herbarum	9826	
372 Penicillium decumbens	934		375 Phoma herbarum	6410	+
372 Penicillium griseofulvum	4213		375 Rhizopus oryzae	482	
372 Penicillium griseofulvum	475	+	375 unknown	1460	
372 Penicillium oxalicum	467		376 Alternaria alternata	4733	
372 Penicillium spinulosum	475	+	376 Alternaria alternata	4262	+
372 Phoma herbarum	2851		376 Aspergillus niger	948	+
372 Rhizopus oryzae	475		376 Aspergillus niger	472	
372 Rhizopus oryzae	467	+	376 Aspergillus sp.	472	+
373 Alternaria alternata	4725	+	376 Aspergillus sydowii	472	
373 Aspergillus versicolor	12294		376 Aspergillus ustus	1897	
373 Aspergillus versicolor	4725	+	376 Aspergillus ustus	472	+
373 Aureobasidium pullulans	18876	+	376 Aspergillus versicolor	474	
373 Aureobasidium pullulans	9451		376 Aureobasidium pullulans	945	+
373 Cladosporium herbarum	18885	+	376 Cladosporium cladosporioides	1893	+
373 Cladosporium herbarum	14177		376 Cladosporium herbarum	472	+
373 Eurotium herbariorum	4725	+	376 Cladosporium sp.	472	+
373 Penicillium brevicompactum	4725		376 Epicoccum nigrum	2362	
373 Penicillium chrysogenum	4725	+	376 Epicoccum nigrum	474	+
373 Penicillium spinulosum	9433		376 Eurotium herbariorum	474	+
373 unknown	23602	+	376 Fusarium oxysporum	2840	
373 yeast	14168		376 Fusarium oxysporum	472	+
374 Alternaria alternata	5494	+	376 Penicillium brevicompactum	2368	+
374 Aspergillus sydowii	14928		376 Penicillium brevicompactum	1892	
374 Aspergillus versicolor	31789		376 Penicillium commune	474	
374 Aspergillus versicolor	5102	+	376 Phoma sp.	474	
374 Aureobasidium pullulans	5102		376 Rhizopus oryzae	472	+
374 Cladosporium cladosporioides	31789	+	376 Stachybotrys chartarum	946	
374 Cladosporium cladosporioides	5494		376 Trichoderma viride	948	+
374 Cladosporium herbarum	15698		376 Trichoderma viride	946	
374 Cladosporium herbarum	5102	+	376 unknown	946	+
374 Epicoccum nigrum	5102	+	376 unknown	472	
374 Eurotium herbariorum	5102	+	376 yeast	48248	
374 Penicillium brevicompactum	5494	+	377 Aspergillus ochraceus	4716	+
374 Penicillium spinulosum	5102	+	377 Aspergillus versicolor	30723	
374 Scopulariopsis brevicaulis	48665	+	377 Aureobasidium pullulans	191238	+
374 Scopulariopsis brevicaulis	10596		377 Aureobasidium pullulans	94339	
374 Trichoderma viride	10989	+	377 Cladosporium herbarum	4716	+
374 unknown	32967	+	377 Cladosporium sphaerospermum	4844	+
374 unknown	5494		377 Eurotium herbariorum	9689	+
374 yeast	41993		377 Penicillium chrysogenum	230510	+
375 Alternaria alternata	15067		377 Penicillium chrysogenum	61320	
375 Alternaria alternata	2413	+	377 Penicillium expansum	4716	
375 Aspergillus niger	1447	+	377 Phoma herbarum	4716	
375 Aspergillus versicolor	482		377 Trichoderma viride	96259	+
375 Aureobasidium pullulans	51657	+	377 unknown	9433	
375 Aureobasidium pullulans	24899		378 Alternaria alternata	10925	
375 Cladosporium cladosporioides	495	+	378 Alternaria alternata	1988	+
375 Cladosporium herbarum	1955	+	378 Aspergillus glaucus	497	+
375 Cladosporium herbarum	990		378 Aspergillus niger	497	
375 Cladosporium sphaerospermum	990	+	378 Aspergillus oryzae	497	
375 Epicoccum nigrum	977		378 Aureobasidium pullulans	16665	
375 Epicoccum nigrum	495	+	378 Aureobasidium pullulans	6958	+
375 Eurotium herbariorum	1460	+	378 Cladosporium cladosporioides	994	+
375 Geomyces pannorum	2462		378 Cladosporium cladosporioides	497	
375 Mucor racemosus	482	+	378 Cladosporium herbarum	497	



HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
378	Cladosporium herbarum	497	+	385	Penicillium corylophilum	1489	
378	Epicoccum nigrum	4892		385	Penicillium expansum	998	+
378	Epicoccum nigrum	994	+	385	Phoma sp.	1489	
378	Penicillium chrysogenum	1491		385	Phoma sp.	998	+
378	Penicillium spinulosum	241217		385	unknown	3461	+
378	Penicillium spinulosum	201581	+	385	unknown	990	
378	unknown	497		385	Wallemia sebi	2487	+
381	Alternaria alternata	14796	+	385	yeast	8966	
381	Aspergillus sydowii	5197	+	386	Alternaria alternata	6944	
381	Aureobasidium pullulans	13204		386	Alternaria alternata	2958	+
381	Cladosporium herbarum	15592	+	386	Aspergillus versicolor	497	+
381	Cladosporium sp.	5197	+	386	Aureobasidium pullulans	17825	
381	Epicoccum nigrum	14796		386	Aureobasidium pullulans	14843	+
381	Mucor racemosus	4401	+	386	Cladosporium cladosporioides	497	+
381	unknown	17605		386	Cladosporium herbarum	6441	+
381	unknown	15592	+	386	Cladosporium sphaerospermum	497	
381	yeast	13204		386	Epicoccum nigrum	497	+
382	Alternaria alternata	12731		386	Eurotium herbariorum	1491	+
382	Alternaria alternata	9357	+	386	Myrothecium olivaceum	6461	+
382	Aspergillus sp.	500	+	386	Myrothecium olivaceum	986	
382	Aspergillus versicolor	10857		386	Penicillium citreonigrum	1976	+
382	Aspergillus versicolor	10214	+	386	Penicillium citreonigrum	1972	
382	Aureobasidium pullulans	6428	+	386	Penicillium decumbens	3467	
382	Aureobasidium pullulans	3928		386	Penicillium decumbens	1483	+
382	Cladosporium herbarum	11119	+	386	Phoma herbarum	497	
382	Cladosporium herbarum	2428		386	Rhizopus oryzae	990	+
382	Emericella nidulans	1928		386	Trichoderma viride	497	
382	Emericella nidulans	500	+	386	unknown	1479	+
382	Epicoccum nigrum	1476		386	yeast	493	
382	Epicoccum nigrum	500	+	387	Acremonium sp.	5755	
382	Eurotium herbariorum	476	+	387	Alternaria alternata	14285	+
382	Fusarium oxysporum	500		387	Aspergillus glaucus	4892	
382	Fusarium sp.	2928	+	387	Aspergillus versicolor	4761	
382	Fusarium sp.	1452		387	Aureobasidium pullulans	219830	
382	Penicillium chrysogenum	1452		387	Aureobasidium pullulans	71689	+
382	Penicillium chrysogenum	1428	+	387	Cladosporium cladosporioides	9784	
382	Penicillium corylophilum	1952	+	387	Cladosporium cladosporioides	4892	+
382	Penicillium griseofulvum	476		387	Cladosporium herbarum	43639	+
382	Phialophora fastigiata	476		387	Cladosporium herbarum	19569	
382	Rhizopus oryzae	1904	+	387	Penicillium corylophilum	4761	
382	Rhizopus oryzae	476		387	Penicillium digitatum	9784	
382	Ulocladium chartarum	2452	+	387	Penicillium digitatum	4761	+
382	Ulocladium chartarum	500		387	Phoma herbarum	23809	
382	unknown	7380	+	387	Phoma sp.	9523	+
382	unknown	1928		387	unknown	68232	
382	Wallemia sebi	4833	+	387	yeast	14285	
382	yeast	6476		388	Alternaria alternata	76732	
385	Alternaria alternata	19319	+	388	Alternaria alternata	481	+
385	Alternaria alternata	4894		388	Aspergillus glaucus	481	
385	Alternaria sp.	499		388	Aureobasidium pullulans	124050	+
385	Aspergillus glaucus	499	+	388	Aureobasidium pullulans	65244	
385	Aspergillus niger	982	+	388	Cladosporium herbarum	15693	+
385	Aspergillus versicolor	982	+	388	Cladosporium herbarum	8138	
385	Aureobasidium pullulans	4443	+	388	Epicoccum nigrum	481	
385	Aureobasidium pullulans	499		388	Eurotium herbariorum	938	+
385	Cladosporium herbarum	6439	+	388	Mucor racemosus	2345	+
385	Cladosporium herbarum	1980		388	Penicillium chrysogenum	13817	
385	Epicoccum nigrum	982		388	Penicillium chrysogenum	11991	+
385	Eurotium herbariorum	491	+	388	Penicillium digitatum	938	+
385	Fusarium sp.	982		388	Phoma herbarum	469	
385	Penicillium commune	499		388	Phoma sp.	30487	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
388	Phoma sp.	22514	+	392	Stachybotrys chartarum	464	
388	Trichoderma viride	7504		392	Trichoderma sp.	464	+
388	Ulocladium chartarum	1926	+	392	Trichoderma viride	464	
388	unknown	481		392	Ulocladium chartarum	8846	
389	Epicoccum nigrum	4385	+	392	Ulocladium chartarum	6524	+
389	Phoma sp.	344339	+	392	unknown	2798	
389	Phoma sp.	344339		392	yeast	466	
389	unknown	23253	+	393	Alternaria alternata	2101	
389	unknown	4385		393	Alternaria alternata	573	+
389	yeast	27308		393	Aureobasidium pullulans	573	+
390	Alternaria alternata	4844	+	393	Cladosporium cladosporioides	595	+
390	Aureobasidium pullulans	111813	+	393	Cladosporium herbarum	1742	+
390	Aureobasidium pullulans	58329		393	Cladosporium herbarum	573	
390	Cladosporium cladosporioides	14629	+	393	Cladosporium sp.	1190	+
390	Cladosporium herbarum	29069	+	393	Cladosporium sp.	595	
390	Cladosporium herbarum	9689		393	Eurotium herbariorum	595	+
390	Epicoccum nigrum	9737		393	Mucor plumbeus	573	
390	Penicillium chrysogenum	4892		393	Penicillium aurantiogriseum	1168	
390	Penicillium chrysogenum	4844	+	393	Penicillium chrysogenum	2359	+
390	Phoma herbarum	29069		393	Penicillium sp.	573	
390	Phoma herbarum	14534	+	393	Penicillium spinulosum	573	
390	Sphaeropsis sp.	4844		393	Phoma sp.	1168	
390	unknown	14582		393	Phoma sp.	1168	+
391	Alternaria alternata	30569		393	Trichoderma viride	573	
391	Alternaria alternata	17582	+	393	unknown	10386	+
391	Aspergillus versicolor	1648	+	393	unknown	9327	
391	Aspergillus versicolor	1098		393	yeast	7055	
391	Eurotium herbariorum	1098	+	394	Alternaria alternata	8224	+
391	Mucor racemosus	8966	+	394	Alternaria alternata	7388	
391	Mucor racemosus	8966		394	Aspergillus versicolor	970	
391	Penicillium corylophilum	549	+	394	Aureobasidium pullulans	21732	
391	Penicillium melinii	1098	+	394	Aureobasidium pullulans	6282	+
391	Penicillium melinii	549		394	Cladosporium herbarum	5797	+
391	Phoma sp.	549		394	Cladosporium herbarum	970	
391	Scopulariopsis brevicaulis	549		394	Eurotium herbariorum	485	+
391	Scopulariopsis candida	1648		394	Penicillium aurantiogriseum	1941	
391	Scopulariopsis candida	549	+	394	Penicillium digitatum	4854	
391	yeast	1098		394	Rhizopus oryzae	1456	+
392	Acremonium sp.	466	+	394	Scopulariopsis brevicaulis	485	+
392	Alternaria alternata	5581	+	394	Stemphylium botryosum	970	+
392	Alternaria alternata	4197		394	Trichoderma viride	970	
392	Aspergillus candidus	466	+	394	unknown	76277	
392	Aureobasidium pullulans	37743	+	394	unknown	53574	+
392	Aureobasidium pullulans	20029		394	yeast	162207	
392	Cladosporium cladosporioides	4197		395	Alternaria alternata	178713	
392	Cladosporium cladosporioides	464	+	395	Alternaria alternata	3914	+
392	Cladosporium herbarum	6053	+	395	Aureobasidium pullulans	25017	+
392	Cladosporium herbarum	464		395	Aureobasidium pullulans	12257	
392	Cladosporium sphaerospermum	932	+	395	Cladosporium herbarum	7851	+
392	Cladosporium sphaerospermum	466		395	Cladosporium herbarum	492	
392	Epicoccum nigrum	931		395	Epicoccum nigrum	1470	
392	Epicoccum nigrum	464	+	395	Epicoccum nigrum	1464	+
392	Penicillium aurantiogriseum	932	+	395	Eurotium herbariorum	972	+
392	Penicillium chrysogenum	2323	+	395	Penicillium glandicola	1470	+
392	Penicillium chrysogenum	932		395	Penicillium griseofulvum	3925	
392	Penicillium corylophilum	3729	+	395	Penicillium griseofulvum	2443	+
392	Penicillium corylophilum	1862		395	Phoma herbarum	2460	+
392	Phoma herbarum	3261		395	Phoma herbarum	984	
392	Phoma herbarum	1397	+	395	Trichoderma viride	486	+
392	Pithomyces chartarum	932		395	Ulocladium chartarum	972	+
392	Sphaeropsis sp.	1395		395	unknown	2929	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
395	unknown	1962	+	399	Aspergillus versicolor	14506	
396	Alternaria alternata	19379		399	Aspergillus versicolor	4743	+
396	Aspergillus sp.	4844		399	Aureobasidium pullulans	4835	+
396	Aureobasidium pullulans	126994		399	Cladosporium cladosporioides	4835	+
396	Aureobasidium pullulans	53750	+	399	Cladosporium herbarum	19250	+
396	Cladosporium cladosporioides	9803	+	399	Cladosporium herbarum	4743	
396	Cladosporium cladosporioides	9689		399	Epicoccum nigrum	9487	+
396	Cladosporium herbarum	34142	+	399	Epicoccum nigrum	4743	
396	Cladosporium sphaerospermum	9746	+	399	Microsphaeropsis sp.	9671	
396	Epicoccum nigrum	4901	+	399	Myrothecium olivaceum	18975	
396	Penicillium miczynskii	34199	+	399	Myrothecium olivaceum	14415	+
396	Penicillium miczynskii	9803		399	Penicillium chrysogenum	4743	
396	Phoma exigua	9803	+	399	Penicillium coprophilum	4743	
396	Phoma herbarum	4901		399	Phoma sp.	175521	+
396	Phoma sp.	14534	+	399	Phoma sp.	118687	
396	Sphaeropsis sp.	4901		399	Pithomyces chartarum	9579	+
396	Ulocladium chartarum	4844	+	399	unknown	9487	+
396	unknown	29297		399	yeast	28921	
396	Wallemia sebi	43604	+	400	Alternaria alternata	50363	
397	Alternaria alternata	14801	+	400	Alternaria alternata	4277	+
397	Alternaria alternata	5730		400	Aspergillus sp.	2946	+
397	Aureobasidium pullulans	3345		400	Aspergillus versicolor	5321	
397	Aureobasidium pullulans	2863	+	400	Aspergillus versicolor	4359	+
397	Cladosporium herbarum	477	+	400	Aureobasidium pullulans	1944	
397	Coniothyrium sp.	1910		400	Aureobasidium pullulans	941	+
397	Coniothyrium sp.	955	+	400	Cladosporium cladosporioides	470	+
397	Epicoccum nigrum	1432		400	Cladosporium herbarum	1903	
397	Epicoccum nigrum	955	+	400	Cladosporium herbarum	941	+
397	Eurotium herbariorum	21967	+	400	Cladosporium sphaerospermum	470	
397	Mucor racemosus	477		400	Epicoccum nigrum	2845	
397	Penicillium chrysogenum	956		400	Epicoccum nigrum	941	+
397	Penicillium islandicum	954		400	Eurotium herbariorum	2354	+
397	Scopulariopsis brevicaulis	477		400	Mucor plumbeus	470	
397	unknown	1909	+	400	Mucor plumbeus	470	+
397	unknown	955		400	Mucor racemosus	1473	
397	yeast	32469		400	Mucor racemosus	491	+
398	Alternaria alternata	15787		400	Penicillium chrysogenum	2354	+
398	Alternaria alternata	2408	+	400	Penicillium chrysogenum	1944	
398	Aspergillus glaucus	487	+	400	Penicillium griseofulvum	2374	+
398	Aspergillus niger	487	+	400	Penicillium griseofulvum	1412	
398	Aureobasidium pullulans	117127	+	400	Penicillium sp.	470	+
398	Aureobasidium pullulans	98091		400	Rhizopus oryzae	941	
398	Cladosporium cladosporioides	3369	+	400	Rhizopus oryzae	470	+
398	Cladosporium herbarum	4330	+	400	Trichoderma viride	470	
398	Cladosporium herbarum	487		400	unknown	1903	
398	Cladosporium sphaerospermum	974	+	400	unknown	1903	+
398	Cladosporium sphaerospermum	487		400	Wallemia sebi	4257	
398	Epicoccum nigrum	1949		400	Wallemia sebi	941	+
398	Epicoccum nigrum	473	+	400	yeast	19977	
398	Penicillium brevicompactum	16126	+	401	Alternaria alternata	27483	
398	Penicillium brevicompactum	11837		401	Alternaria alternata	4699	+
398	Penicillium griseofulvum	7157		401	Aspergillus sydowii	4699	+
398	Penicillium griseofulvum	2840	+	401	Aspergillus versicolor	9398	
398	Penicillium spinulosum	2408		401	Aspergillus versicolor	4699	+
398	Penicillium spinulosum	487	+	401	Aureobasidium pullulans	19083	
398	Phoma herbarum	2408	+	401	Aureobasidium pullulans	14312	+
398	Phoma herbarum	946		401	Cladosporium herbarum	23783	+
398	unknown	946		401	Cladosporium herbarum	9398	
399	Alternaria alternata	9487	+	401	Cladosporium sphaerospermum	4699	+
399	Alternaria alternata	4835		401	Epicoccum nigrum	9470	+
399	Aspergillus niger	4835	+	401	Epicoccum nigrum	4770	

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
401	Penicillium chrysogenum	28554		409	Eurotium herbariorum	1887	+
401	Penicillium crustosum	4699		409	Fusarium sp.	473	
401	Penicillium griseofulvum	4770	+	409	Penicillium commune	467	
401	Penicillium spinulosum	28410	+	409	Penicillium decumbens	473	
401	Penicillium spinulosum	18940		409	Phoma herbarum	946	+
401	unknown	42580		409	unknown	2816	
402	Alternaria alternata	23558		409	yeast	1414	
402	Alternaria alternata	4761	+	411	Alternaria alternata	6612	
402	Aureobasidium pullulans	200354	+	411	Alternaria alternata	700	+
402	Aureobasidium pullulans	85841		411	Aspergillus sp.	101	+
402	Cladosporium herbarum	9541		411	Aureobasidium pullulans	98	+
402	Cladosporium herbarum	9523	+	411	Cladosporium sp.	98	+
402	Penicillium italicum	14303		411	Epicoccum nigrum	399	+
402	Penicillium italicum	14285	+	411	Epicoccum nigrum	196	
402	Phoma herbarum	4761		411	Eurotium herbariorum	602	+
402	Trichoderma viride	14285		411	Eurotium herbariorum	101	
402	unknown	9532		411	Mucor racemosus	101	
402	unknown	4770	+	411	Paecilomyces sp.	101	
402	yeast	548664		411	Penicillium citreonigrum	101	
403	Alternaria alternata	181788		411	Penicillium expansum	893	+
403	Alternaria alternata	1964	+	411	Penicillium expansum	504	
403	Aspergillus niger	478		411	unknown	497	
403	Aspergillus niger	478	+	411	unknown	203	+
403	Aureobasidium pullulans	14096		411	yeast	1877	
403	Aureobasidium pullulans	6802	+	412	Alternaria alternata	1782	
403	Chrysonilia sitophila	491		412	Aspergillus versicolor	482	+
403	Cladosporium cladosporioides	478		412	Aureobasidium pullulans	453	
403	Cladosporium cladosporioides	478	+	412	Chrysosporium sp.	453	+
403	Cladosporium herbarum	491	+	412	Cladosporium sphaerospermum	482	+
403	Epicoccum nigrum	982		412	Epicoccum nigrum	1361	
403	Epicoccum nigrum	478	+	412	Eurotium herbariorum	4652	+
403	Eurotium herbariorum	12672	+	412	Paecilomyces variotii	453	
403	Mucor racemosus	6704		412	Penicillium chrysogenum	2355	+
403	Mucor racemosus	4310	+	412	Penicillium chrysogenum	965	
403	Penicillium chrysogenum	4395	+	412	Penicillium corylophilum	965	
403	Penicillium chrysogenum	2443		412	Penicillium corylophilum	453	+
403	Penicillium commune	1964	+	412	Penicillium viridicatum	1447	+
403	Penicillium commune	491		412	unknown	1418	+
403	Penicillium decumbens	3438		412	yeast	91071	
403	Penicillium oxalicum	491		414	Alternaria alternata	4793	+
403	unknown	3389		414	Aspergillus niger	418	+
405	Aspergillus sp.	4854	+	414	Aspergillus versicolor	42407	
405	Aureobasidium pullulans	5836		414	Aspergillus versicolor	512	+
405	Cladosporium herbarum	9469	+	414	Cladosporium cladosporioides	2606	+
405	Cladosporium herbarum	4854		414	Cladosporium cladosporioides	2374	
405	Penicillium chrysogenum	392440	+	414	Epicoccum nigrum	418	+
405	Penicillium chrysogenum	230858		414	Eurotium herbariorum	1349	+
405	Rhizopus oryzae	4854	+	414	Mucor circinelloides	512	+
405	unknown	416473		414	Penicillium chrysogenum	1024	
405	unknown	43330	+	414	Penicillium islandicum	1862	+
405	Wallemia sebi	9469	+	414	Phoma sp.	418	+
405	yeast	57176		414	unknown	4793	
409	Alternaria alternata	46490		414	unknown	1349	+
409	Alternaria alternata	3283	+	414	yeast	7261	
409	Aspergillus niger	467		415	Alternaria alternata	63960	
409	Aureobasidium pullulans	11762		415	Alternaria alternata	53304	+
409	Aureobasidium pullulans	9389	+	415	Aureobasidium pullulans	81580	+
409	Cladosporium cladosporioides	1881		415	Aureobasidium pullulans	33581	
409	Cladosporium herbarum	940		415	Cladosporium cladosporioides	4930	+
409	Cladosporium sphaerospermum	467	+	415	Cladosporium herbarum	4930	
409	Epicoccum nigrum	473		415	Epicoccum nigrum	4930	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
415 Eurotium herbariorum	4930	+	420 yeast	5592	
415 Penicillium viridicatum	4743	+	424 Alternaria alternata	6226	
415 Phoma herbarum	18975	+	424 Aspergillus niger	467	+
415 Phoma herbarum	4930		424 Aspergillus sydowii	963	
415 Phoma sp.	28837		424 Aspergillus sydowii	948	+
415 unknown	39260		424 Aspergillus versicolor	481	
415 yeast	9674		424 Epicoccum nigrum	948	+
416 Alternaria alternata	3666	+	424 Eurotium herbariorum	948	+
416 Aspergillus versicolor	526		424 Fusarium sp.	467	
416 Aureobasidium pullulans	526		424 Penicillium chrysogenum	948	+
416 Cladosporium cladosporioides	508		424 Penicillium citrinum	1430	
416 Cladosporium sp.	526	+	424 Phoma sp.	948	
416 Epicoccum nigrum	2050		424 Ulocladium chartarum	948	
416 Epicoccum nigrum	1542	+	424 Ulocladium chartarum	948	+
416 Eurotium herbariorum	1034	+	424 unknown	1897	
416 Penicillium chrysogenum	508		424 unknown	467	+
416 Penicillium griseofulvum	526		424 Wallemia sebi	481	
416 Penicillium griseofulvum	526	+	424 yeast	3839	
416 Penicillium spinulosum	3103	+	425 Aspergillus versicolor	5163	
416 Penicillium spinulosum	1052		425 Aureobasidium pullulans	4595	+
416 Penicillium viridicatum	1542	+	425 Phoma sp.	4681	
416 Penicillium viridicatum	1016		425 Phoma sp.	4681	+
416 Stemphylium sp.	1052	+	425 Trichoderma viride	9277	+
416 unknown	1016	+	425 Trichoderma viride	4595	
416 unknown	508		425 yeast	189365	
416 yeast	17603		427 Alternaria alternata	139338	
417 Alternaria alternata	10403		427 Alternaria alternata	188	+
417 Alternaria alternata	1204	+	427 Aureobasidium pullulans	94	
417 Aspergillus clavatus	1078	+	427 Paecilomyces sp.	94	
417 Aspergillus niger	602		427 Paecilomyces variotii	188	+
417 Aspergillus sydowii	476	+	427 Penicillium chrysogenum	1968	+
417 Aureobasidium pullulans	2409	+	427 Penicillium chrysogenum	1168	
417 Aureobasidium pullulans	1428		427 Penicillium corylophilum	258	+
417 Chaetomium sp.	602		427 Penicillium corylophilum	172	
417 Chaetomium sp.	476	+	427 unknown	188	
417 Cladosporium cladosporioides	476	+	427 unknown	94	+
417 Cladosporium herbarum	602	+	427 yeast	23293	
417 Epicoccum nigrum	1078	+	429 Alternaria alternata	5027	
417 Eurotium herbariorum	2157	+	429 Aspergillus versicolor	9225	
417 Penicillium chrysogenum	602	+	429 Aspergillus versicolor	4604	+
417 Penicillium chrysogenum	476		429 Chrysonilia sp.	4604	
417 Penicillium implicatum	602		429 Cladosporium herbarum	9225	
417 unknown	1078		429 Trichoderma viride	4612	+
417 unknown	602	+	429 unknown	18424	
417 yeast	11193		429 unknown	9225	+
419 Alternaria alternata	551		431 Alternaria alternata	4737	+
419 Aureobasidium pullulans	1017	+	431 Alternaria alternata	488	
419 Cladosporium sphaerospermum	551	+	431 Cladosporium sp.	556	
419 Epicoccum nigrum	1569	+	431 Epicoccum nigrum	1113	
419 Epicoccum nigrum	551		431 Eurotium herbariorum	556	+
419 Eurotium herbariorum	551	+	431 Penicillium expansum	1533	+
419 Neosartorya sp.	551		431 Penicillium expansum	488	
419 Neosartorya sp.	551	+	431 Penicillium melinii	1045	+
419 Penicillium chrysogenum	1017	+	431 Penicillium oxalicum	488	+
419 unknown	1396	+	431 unknown	1113	
419 unknown	551		431 yeast	20404	
419 yeast	60543		432 Alternaria alternata	2505	
420 Alternaria alternata	10855	+	432 Alternaria alternata	97	+
420 Cladosporium herbarum	5592	+	432 Aspergillus clavatus	194	
420 unknown	16448	+	432 Aureobasidium pullulans	97	
420 unknown	14194		432 Epicoccum nigrum	203	+

HN	Identification	AVG CFU/g	G	HN	Identification	AVG CFU/g	G
432	<i>Epicoccum nigrum</i>	194		436	<i>Alternaria alternata</i>	3012	+
432	<i>Eurotium herbariorum</i>	203	+	436	<i>Aspergillus versicolor</i>	722	
432	<i>Penicillium chrysogenum</i>	106		436	<i>Aureobasidium pullulans</i>	2167	
432	<i>Penicillium chrysogenum</i>	106	+	436	<i>Aureobasidium pullulans</i>	722	+
432	<i>Stemphylium</i> sp.	97	+	436	<i>Cladosporium</i> sp.	2890	+
432	<i>Trichoderma viride</i>	106	+	436	<i>Cladosporium</i> sp.	722	
432	unknown	194		436	<i>Cladosporium sphaerospermum</i>	2228	+
432	unknown	106	+	436	<i>Cladosporium sphaerospermum</i>	722	
432	<i>Verticillium</i> sp.	203	+	436	<i>Epicoccum nigrum</i>	2289	
432	yeast	20328		436	<i>Eurotium herbariorum</i>	1506	+
433	<i>Alternaria alternata</i>	5613		436	<i>Penicillium chrysogenum</i>	783	
433	<i>Alternaria alternata</i>	4192	+	436	<i>Penicillium spinulosum</i>	1506	
433	<i>Alternaria</i> sp.	511		436	<i>Phoma</i> sp.	783	+
433	<i>Alternaria</i> sp.	452	+	436	unknown	6625	+
433	<i>Aspergillus versicolor</i>	511		436	unknown	783	
433	<i>Aspergillus versicolor</i>	452	+	436	yeast	6208	
433	<i>Aureobasidium pullulans</i>	452		437	<i>Alternaria alternata</i>	1596	
433	<i>Cladosporium cladosporioides</i>	2044	+	437	<i>Alternaria alternata</i>	444	+
433	<i>Cladosporium herbarum</i>	1928	+	437	<i>Aspergillus versicolor</i>	1318	+
433	<i>Cladosporium</i> sp.	452	+	437	<i>Aspergillus versicolor</i>	1304	
433	<i>Epicoccum nigrum</i>	4587	+	437	<i>Eurotium amstelodami</i>	430	
433	<i>Eurotium herbariorum</i>	5726	+	437	<i>Eurotium herbariorum</i>	430	+
433	<i>Fusarium</i> sp.	511	+	437	<i>Fusarium</i> sp.	1318	
433	<i>Penicillium corylophilum</i>	452	+	437	<i>Fusarium</i> sp.	430	+
433	<i>Penicillium spinulosum</i>	905	+	437	<i>Penicillium brevicompactum</i>	1721	+
433	<i>Phoma</i> sp.	511		437	<i>Penicillium citrinum</i>	888	
433	<i>Stemphylium</i> sp.	511	+	437	<i>Penicillium spinulosum</i>	430	+
433	unknown	8327	+	437	<i>Trichoderma viride</i>	430	
433	unknown	5156		437	unknown	2165	
433	yeast	14170		437	unknown	2165	+
434	<i>Alternaria alternata</i>	4919	+	437	yeast	16374	
434	<i>Alternaria alternata</i>	3331		438	<i>Alternaria alternata</i>	974	+
434	<i>Aspergillus niger</i>	487		438	<i>Aspergillus</i> sp.	28956	
434	<i>Aspergillus sydowii</i>	499		438	<i>Aspergillus</i> sp.	1441	+
434	<i>Aspergillus versicolor</i>	499		438	<i>Aspergillus versicolor</i>	467	
434	<i>Aureobasidium pullulans</i>	1984		438	<i>Aureobasidium pullulans</i>	20791	+
434	<i>Cladosporium herbarum</i>	2459	+	438	<i>Cladosporium sphaerospermum</i>	1441	+
434	<i>Epicoccum nigrum</i>	4444	+	438	<i>Epicoccum nigrum</i>	2028	+
434	<i>Epicoccum nigrum</i>	1485		438	<i>Epicoccum nigrum</i>	1481	
434	<i>Mucor plumbeus</i>	986		438	<i>Penicillium corylophilum</i>	507	+
434	<i>Penicillium raistrickii</i>	986	+	438	<i>Penicillium viridicatum</i>	1014	
434	<i>Penicillium</i> sp.	499		438	<i>Penicillium viridicatum</i>	507	+
434	<i>Penicillium spinulosum</i>	487	+	438	<i>Stachybotrys chartarum</i>	467	
434	<i>Phoma</i> sp.	487		438	unknown	467	
434	<i>Rhizopus oryzae</i>	487		438	<i>Wallemia sebi</i>	1869	
434	unknown	1972		438	yeast	19477	
434	unknown	499	+	439	<i>Alternaria alternata</i>	2658	+
434	yeast	8377		439	<i>Aspergillus</i> sp.	1046	
435	<i>Alternaria alternata</i>	310	+	439	<i>Aspergillus</i> sp.	523	+
435	<i>Aspergillus niger</i>	5101		439	<i>Aureobasidium pullulans</i>	544	+
435	<i>Aspergillus niger</i>	302	+	439	<i>Cladosporium herbarum</i>	544	+
435	<i>Aureobasidium pullulans</i>	499	+	439	<i>Epicoccum nigrum</i>	1590	
435	<i>Eurotium herbariorum</i>	514	+	439	<i>Eurotium herbariorum</i>	6406	+
435	<i>Mucor racemosus</i>	106	+	439	<i>Fusarium</i> sp.	544	
435	<i>Penicillium commune</i>	711	+	439	<i>Fusarium</i> sp.	523	+
435	<i>Penicillium commune</i>	196		439	<i>Mucor plumbeus</i>	523	+
435	<i>Penicillium spinulosum</i>	212	+	439	<i>Penicillium brevicompactum</i>	15513	+
435	<i>Trichoderma viride</i>	1226		439	<i>Penicillium chrysogenum</i>	1569	
435	unknown	294		439	<i>Penicillium chrysogenum</i>	544	+
435	unknown	106	+	439	<i>Penicillium corylophilum</i>	4357	+
435	yeast	7305		439	<i>Penicillium corylophilum</i>	1046	

HN Identification	AVG CFU/g	G	HN Identification	AVG CFU/g	G
439 Penicillium expansum	2135		446 Aspergillus versicolor	106	+
439 Penicillium viridicatum	3181		446 Aureobasidium pullulans	212	+
439 Ulocladium chartarum	2680		446 Epicoccum nigrum	712	+
439 unknown	7931		446 Epicoccum nigrum	95	
439 yeast	25840		446 Eurotium herbariorum	95	+
442 Alternaria alternata	556	+	446 Mucor plumbeus	191	
442 Alternaria alternata	432		446 Penicillium chrysogenum	298	+
442 Aspergillus niger	556	+	446 Penicillium chrysogenum	95	
442 Aspergillus tamarii	432		446 Penicillium commune	308	
442 Aspergillus versicolor	989		446 Penicillium commune	308	+
442 Aureobasidium pullulans	432	+	446 Penicillium sp.	106	
442 Cladosporium cladosporioides	1421		446 Rhizopus oryzae	106	+
442 Epicoccum nigrum	1421		446 Rhizopus oryzae	95	
442 Epicoccum nigrum	432	+	446 unknown	298	+
442 Eurotium herbariorum	2659		446 unknown	212	
442 Eurotium herbariorum	1546	+	446 yeast	13753	
442 Penicillium aurantiogriseum	865	+	447 Alternaria alternata	89	+
442 Penicillium aurantiogriseum	556		447 Epicoccum nigrum	510	+
442 Syncephalastrum sp.	556		447 Epicoccum nigrum	201	
442 Syncephalastrum sp.	556	+	447 Eurotium herbariorum	89	+
442 yeast	432		447 Penicillium corylophilum	461	+
443 Alternaria alternata	563		447 Penicillium corylophilum	356	
443 Alternaria alternata	563	+	447 Penicillium viridicatum	89	+
443 Aspergillus versicolor	1539	+	447 unknown	89	+
443 Aspergillus versicolor	488		447 yeast	5112	
443 Cladosporium sp.	488	+	448 Alternaria alternata	1075	+
443 Epicoccum nigrum	563		448 Aspergillus niger	486	+
443 Eurotium herbariorum	1126	+	448 Aspergillus versicolor	1510	+
443 Penicillium chrysogenum	2177		448 Aureobasidium pullulans	348	
443 Penicillium chrysogenum	1539	+	448 Cladosporium sp.	48	
443 Stemphylium sp.	488	+	448 Eurotium herbariorum	1459	+
443 yeast	70338		448 Fusarium sp.	53	
444 Acremonium sp.	446	+	448 Penicillium chrysogenum	1024	+
444 Alternaria alternata	3006	+	448 Penicillium chrysogenum	53	
444 Alternaria alternata	1448		448 Penicillium griseofulvum	2688	+
444 Aspergillus versicolor	1002		448 yeast	30578	
444 Aspergillus versicolor	892	+	449 Alternaria alternata	35675	
444 Cladosporium herbarum	892	+	449 Alternaria alternata	1355	+
444 Cladosporium sp.	1448		449 Alternaria sp.	896	
444 Epicoccum nigrum	1393		449 Aureobasidium pullulans	2251	+
444 Epicoccum nigrum	501	+	449 Cladosporium sphaerospermum	901	+
444 Eurotium herbariorum	2004	+	449 Eurotium herbariorum	1792	+
444 Mucor plumbeus	501		449 Penicillium corylophilum	6323	+
444 Mucor plumbeus	501	+	449 Penicillium corylophilum	2251	
444 Paecilomyces variotii	501		449 Phoma sp.	1803	+
444 Scopulariopsis candida	446	+	449 Pithomyces chartarum	4928	
444 unknown	7753		449 unknown	901	
444 unknown	4290	+	449 unknown	448	+
444 yeast	4628		449 yeast	204370	
445 Alternaria alternata	318	+	460 Alternaria alternata	998	+
445 Aspergillus versicolor	6890		460 Alternaria alternata	923	
445 Epicoccum nigrum	111	+	460 Aureobasidium pullulans	939	
445 Penicillium corylophilum	189		460 Epicoccum nigrum	499	
445 Phoma sp.	94	+	460 Penicillium chrysogenum	499	
445 unknown	206	+	460 Penicillium corylophilum	939	+
445 unknown	94		460 Penicillium verrucosum	499	+
445 Wallemia sebi	94	+	460 Phoma sp.	1879	
445 yeast	6767		460 Phoma sp.	939	+
446 Alternaria alternata	1359	+	460 Scopulariopsis candida	1879	+
446 Alternaria alternata	793		460 Stachybotrys chartarum	469	
446 Alternaria sp.	414		460 Ulocladium chartarum	968	

<b>HN Identification</b>	<b>AVG CFU/g</b>	<b>G</b>	<b>HN Identification</b>	<b>AVG CFU/g</b>	<b>G</b>
460 Ulocladium chartarum	939	+			
460 yeast	4815				
500 Alternaria alternata	833				
500 Alternaria alternata	463	+			
500 Aspergillus sp.	1250	+			
500 Aspergillus versicolor	463	+			
500 Cladosporium sphaerospermum	463	+			
500 Eurotium herbariorum	463	+			
500 Eurotium herbariorum	416				
500 Paecilomyces variotii	463				
500 Penicillium corylophilum	416				
500 Penicillium roquefortii	1391	+			
500 Penicillium roquefortii	463				
500 Penicillium simplicissimum	927	+			
500 Rhizopus oryzae	833				
500 Rhizopus oryzae	416	+			
500 yeast	5699				



## **APPENDIX B**

Chi square statistics for association analysis of dust-borne taxa

---

A+B+ indicates relevés in which taxa A & B were both observed

A+B- indicates relevés in which taxon A was present and taxon B was absent

A-B+ indicates relevés in which taxon A was absent and taxon B was present

A-B- indicates relevés in which taxa A & B were both absent

E(A+B+) indicates the expected number of relevés with both taxa present

Correlation (CORR) is indicated as positive (POS) or negative (NEG)

Statistical significance is given by p-value

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
ALTEALTE	2	ACRESP	1	POS	24	303	1	41	22.2	0.77	0.380
ALTESP	3	ACRESP	1	NEG	0	16	25	328	1.1	2.60	0.107
ALTESP	3	ALTEALTE	2	POS	16	0	311	42	14.2	1.13	0.288
ASPECAND	4	ACRESP	1	NEG	1	18	24	326	1.3	0.54	0.462
ASPECAND	4	ALTEALTE	2	POS	17	2	310	40	16.8	0.06	0.806
ASPECAND	4	ALTESP	3	POS	1	18	15	335	0.8	0.14	0.708
ASPEFUMI	5	ACRESP	1	POS	3	22	22	322	1.7	0.44	0.507
ASPEFUMI	5	ALTEALTE	2	POS	24	1	303	41	22.2	0.77	0.380
ASPEFUMI	5	ALTESP	3	POS	3	22	13	331	1.1	2.07	0.150
ASPEFUMI	5	ASPECAND	4	POS	5	20	14	330	1.3	9.07	0.003
ASPEGLAU	6	ACRESP	1	POS	3	22	22	322	1.7	0.44	0.507
ASPEGLAU	6	ALTEALTE	2	NEG	22	3	305	39	22.2	0.18	0.671
ASPEGLAU	6	ALTESP	3	POS	4	21	12	332	1.1	6.04	0.014
ASPEGLAU	6	ASPECAND	4	POS	3	22	16	328	1.3	1.29	0.256
ASPEGLAU	6	ASPEFUMI	5	NEG	1	24	24	320	1.7	0.97	0.325
ASPENIGE	7	ACRESP	1	NEG	7	119	18	225	8.5	0.79	0.374
ASPENIGE	7	ALTEALTE	2	POS	112	14	215	28	111.7	0.00	1.000
ASPENIGE	7	ALTESP	3	NEG	5	121	11	232	5.5	0.27	0.603
ASPENIGE	7	ASPECAND	4	POS	9	117	10	233	6.5	1.00	0.317
ASPENIGE	7	ASPEFUMI	5	POS	12	114	13	230	8.5	1.68	0.195
ASPENIGE	7	ASPEGLAU	6	POS	12	114	13	230	8.5	1.68	0.195
ASPEOCHR	8	ACRESP	1	POS	9	63	16	281	4.9	3.58	0.058
ASPEOCHR	8	ALTEALTE	2	NEG	62	10	265	32	63.8	0.91	0.340
ASPEOCHR	8	ALTESP	3	NEG	3	69	13	284	3.1	0.16	0.689
ASPEOCHR	8	ASPECAND	4	POS	6	66	13	284	3.7	1.14	0.286
ASPEOCHR	8	ASPEFUMI	5	POS	8	64	17	280	4.9	1.88	0.170
ASPEOCHR	8	ASPEGLAU	6	POS	5	67	20	277	4.9	0.04	0.841
ASPEOCHR	8	ASPENIGE	7	POS	34	38	92	205	24.6	6.10	0.014
ASPEORYZ	9	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
ASPEORYZ	9	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
ASPEORYZ	9	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
ASPEORYZ	9	ASPECAND	4	NEG	0	9	19	341	0.5	2.16	0.142
ASPEORYZ	9	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
ASPEORYZ	9	ASPEGLAU	6	POS	2	7	23	337	0.6	1.43	0.232
ASPEORYZ	9	ASPENIGE	7	POS	4	5	122	238	3.1	0.09	0.764
ASPEORYZ	9	ASPEOCHR	8	NEG	1	8	71	289	1.8	1.14	0.286
ASPESP	10	ACRESP	1	POS	6	61	19	283	4.5	0.27	0.603
ASPESP	10	ALTEALTE	2	NEG	58	9	269	33	59.4	0.63	0.427
ASPESP	10	ALTESP	3	NEG	0	67	16	286	2.9	5.10	0.024
ASPESP	10	ASPECAND	4	NEG	2	65	17	285	3.5	1.42	0.233
ASPESP	10	ASPEFUMI	5	POS	5	62	20	282	4.5	0.00	1.000
ASPESP	10	ASPEGLAU	6	NEG	3	64	22	280	4.5	1.20	0.273
ASPESP	10	ASPENIGE	7	POS	24	43	102	200	22.9	0.03	0.862
ASPESP	10	ASPEOCHR	8	POS	19	48	53	249	13.1	3.42	0.064
ASPESP	10	ASPEORYZ	9	NEG	1	66	8	294	1.6	0.99	0.320
ASPESYDO	11	ACRESP	1	POS	5	41	20	303	3.1	0.75	0.386
ASPESYDO	11	ALTEALTE	2	POS	44	2	283	40	40.8	1.84	0.175
ASPESYDO	11	ALTESP	3	POS	3	43	13	310	2.0	0.15	0.699
ASPESYDO	11	ASPECAND	4	NEG	2	44	17	306	2.4	0.38	0.538
ASPESYDO	11	ASPEFUMI	5	POS	4	42	21	302	3.1	0.06	0.806
ASPESYDO	11	ASPEGLAU	6	POS	6	40	19	304	3.1	2.23	0.135
ASPESYDO	11	ASPENIGE	7	POS	20	26	106	217	15.7	1.59	0.207
ASPESYDO	11	ASPEOCHR	8	POS	11	35	61	262	9.0	0.37	0.543
ASPESYDO	11	ASPEORYZ	9	NEG	0	46	9	314	1.1	2.75	0.097
ASPESYDO	11	ASPESP	10	POS	12	34	55	268	8.4	1.66	0.198
ASPEUSTU	12	ACRESP	1	POS	2	22	23	322	1.6	0.01	0.920
ASPEUSTU	12	ALTEALTE	2	NEG	19	5	308	37	21.3	3.39	0.066
ASPEUSTU	12	ALTESP	3	NEG	0	24	16	329	1.0	2.55	0.110
ASPEUSTU	12	ASPECAND	4	POS	2	22	17	328	1.2	0.06	0.806
ASPEUSTU	12	ASPEFUMI	5	NEG	1	23	24	321	1.6	0.89	0.345
ASPEUSTU	12	ASPEGLAU	6	POS	4	20	21	324	1.6	2.48	0.115
ASPEUSTU	12	ASPENIGE	7	POS	14	10	112	233	8.2	5.58	0.018

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
ASPEUSTU	12	ASPEOCHR	8	POS	5	19	67	278	4.7	0.01	0.920
ASPEUSTU	12	ASPEORYZ	9	POS	2	22	7	338	0.6	1.57	0.210
ASPEUSTU	12	ASPESP	10	POS	5	19	62	283	4.4	0.01	0.920
ASPEUSTU	12	ASPESYDO	11	POS	4	20	42	303	3.0	0.11	0.740
ASPEVERS	13	ACRESP	1	POS	17	179	8	165	13.3	1.79	0.181
ASPEVERS	13	ALTEALTE	2	POS	175	21	152	21	173.7	0.07	0.791
ASPEVERS	13	ALTESP	3	NEG	8	188	8	165	8.5	0.26	0.610
ASPEVERS	13	ASPECAND	4	POS	12	184	7	166	10.1	0.44	0.507
ASPEVERS	13	ASPEFUMI	5	POS	16	180	9	164	13.3	0.85	0.357
ASPEVERS	13	ASPEGLAU	6	NEG	13	183	12	161	13.3	0.10	0.752
ASPEVERS	13	ASPENIGE	7	NEG	64	132	62	111	66.9	0.57	0.450
ASPEVERS	13	ASPEOCHR	8	POS	41	155	31	142	38.2	0.35	0.554
ASPEVERS	13	ASPEORYZ	9	POS	7	189	2	171	4.8	1.35	0.245
ASPEVERS	13	ASPESP	10	POS	41	155	26	147	35.6	1.77	0.183
ASPEVERS	13	ASPESYDO	11	POS	30	166	16	157	24.4	2.56	0.110
ASPEVERS	13	ASPEUSTU	12	POS	15	181	9	164	12.8	0.55	0.458
AUREPULL	14	ACRESP	1	POS	21	272	4	72	19.9	0.11	0.740
AUREPULL	14	ALTEALTE	2	POS	270	23	57	19	259.7	15.94	0.000
AUREPULL	14	ALTESP	3	POS	14	279	2	74	12.7	0.25	0.617
AUREPULL	14	ASPECAND	4	NEG	15	278	4	72	15.1	0.12	0.729
AUREPULL	14	ASPEFUMI	5	POS	21	272	4	72	19.9	0.11	0.740
AUREPULL	14	ASPEGLAU	6	NEG	16	277	9	67	19.9	4.97	0.026
AUREPULL	14	ASPENIGE	7	NEG	95	198	31	45	100.1	2.27	0.132
AUREPULL	14	ASPEOCHR	8	POS	58	235	14	62	57.2	0.01	0.920
AUREPULL	14	ASPEORYZ	9	NEG	5	288	4	72	7.2	4.88	0.027
AUREPULL	14	ASPESP	10	POS	58	235	9	67	53.2	2.06	0.151
AUREPULL	14	ASPESYDO	11	POS	37	256	9	67	36.5	0.00	1.000
AUREPULL	14	ASPEUSTU	12	NEG	14	279	10	66	19.1	8.41	0.004
AUREPULL	14	ASPEVERS	13	NEG	154	139	42	34	155.6	0.30	0.584
CHAEGLOB	15	ACRESP	1	NEG	1	23	24	321	1.6	0.89	0.345
CHAEGLOB	15	ALTEALTE	2	NEG	20	4	307	38	21.3	1.38	0.240
CHAEGLOB	15	ALTESP	3	NEG	1	23	15	330	1.0	0.31	0.578
CHAEGLOB	15	ASPECAND	4	NEG	1	23	18	327	1.2	0.49	0.484
CHAEGLOB	15	ASPEFUMI	5	POS	3	21	22	323	1.6	0.54	0.462
CHAEGLOB	15	ASPEGLAU	6	POS	2	22	23	322	1.6	0.01	0.920
CHAEGLOB	15	ASPENIGE	7	POS	12	12	114	231	8.2	2.16	0.142
CHAEGLOB	15	ASPEOCHR	8	POS	7	17	65	280	4.7	0.94	0.332
CHAEGLOB	15	ASPEORYZ	9	POS	2	22	7	338	0.6	1.57	0.210
CHAEGLOB	15	ASPESP	10	POS	5	19	62	283	4.4	0.01	0.920
CHAEGLOB	15	ASPESYDO	11	POS	3	21	43	302	3.0	0.10	0.752
CHAEGLOB	15	ASPEUSTU	12	NEG	1	23	23	322	1.6	0.82	0.365
CHAEGLOB	15	ASPEVERS	13	POS	14	10	182	163	12.8	0.10	0.752
CHAEGLOB	15	AUREPULL	14	NEG	15	9	278	67	19.1	5.66	0.017
CHRSPMSP	16	ACRESP	1	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ALTEALTE	2	POS	14	0	313	42	12.4	0.88	0.348
CHRSPMSP	16	ALTESP	3	POS	3	11	13	342	0.6	6.41	0.011
CHRSPMSP	16	ASPECAND	4	POS	3	11	16	339	0.7	4.81	0.028
CHRSPMSP	16	ASPEFUMI	5	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ASPEGLAU	6	POS	2	12	23	332	1.0	0.36	0.549
CHRSPMSP	16	ASPENIGE	7	POS	6	8	120	235	4.8	0.17	0.680
CHRSPMSP	16	ASPEOCHR	8	POS	6	8	66	289	2.7	3.62	0.057
CHRSPMSP	16	ASPEORYZ	9	NEG	0	14	9	346	0.3	2.21	0.137
CHRSPMSP	16	ASPESP	10	POS	3	11	64	291	2.5	0.00	1.000
CHRSPMSP	16	ASPESYDO	11	POS	2	12	44	311	1.8	0.04	0.841
CHRSPMSP	16	ASPEUSTU	12	NEG	0	14	24	331	0.9	2.43	0.119
CHRSPMSP	16	ASPEVERS	13	NEG	3	11	193	162	7.4	7.26	0.007
CHRSPMSP	16	AUREPULL	14	POS	14	0	279	76	11.1	2.58	0.108
CHRSPMSP	16	CHAEGLOB	15	NEG	0	14	24	331	0.9	2.43	0.119
CLADCLAD	17	ACRESP	1	NEG	10	175	15	169	12.5	1.58	0.209
CLADCLAD	17	ALTEALTE	2	POS	177	8	150	34	163.9	16.95	0.000
CLADCLAD	17	ALTESP	3	NEG	8	177	8	176	8.0	0.07	0.791
CLADCLAD	17	ASPECAND	4	POS	12	173	7	177	9.5	0.87	0.351

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
CLADCLAD	17	ASPEFUMI	5	POS	16	169	9	175	12.5	1.51	0.219
CLADCLAD	17	ASPEGLAU	6	NEG	11	174	14	170	12.5	0.71	0.399
CLADCLAD	17	ASPENIGE	7	POS	66	119	60	124	63.2	0.26	0.610
CLADCLAD	17	ASPEOCHR	8	POS	38	147	34	150	36.1	0.14	0.708
CLADCLAD	17	ASPEORYZ	9	NEG	3	182	6	178	4.5	1.84	0.175
CLADCLAD	17	ASPESP	10	POS	34	151	33	151	33.6	0.00	1.000
CLADCLAD	17	ASPESYDO	11	NEG	21	164	25	159	23.1	0.65	0.420
CLADCLAD	17	ASPEUSTU	12	NEG	11	174	13	171	12.0	0.42	0.517
CLADCLAD	17	ASPEVERS	13	POS	104	81	92	92	98.3	1.19	0.275
CLADCLAD	17	AUREPULL	14	POS	168	17	125	59	146.9	28.14	0.000
CLADCLAD	17	CHAEGLOB	15	NEG	9	176	15	169	12.0	2.22	0.136
CLADCLAD	17	CHRSPMSP	16	NEG	5	180	9	175	7.0	1.88	0.170
CLADHERB	18	ACRESP	1	POS	7	80	18	264	5.9	0.09	0.764
CLADHERB	18	ALTEALTE	2	POS	84	3	243	39	77.1	6.11	0.013
CLADHERB	18	ALTESP	3	NEG	3	84	13	269	3.8	0.59	0.442
CLADHERB	18	ASPECAND	4	NEG	2	85	17	265	4.5	2.73	0.098
CLADHERB	18	ASPEFUMI	5	NEG	3	84	22	260	5.9	2.74	0.098
CLADHERB	18	ASPEGLAU	6	POS	6	81	19	263	5.9	0.04	0.841
CLADHERB	18	ASPENIGE	7	NEG	25	62	101	181	29.7	1.81	0.179
CLADHERB	18	ASPEOCHR	8	NEG	8	79	64	218	17.0	8.60	0.003
CLADHERB	18	ASPEORYZ	9	NEG	2	85	7	275	2.1	0.24	0.624
CLADHERB	18	ASPESP	10	POS	16	71	51	231	15.8	0.01	0.920
CLADHERB	18	ASPESYDO	11	NEG	10	77	36	246	10.9	0.25	0.617
CLADHERB	18	ASPEUSTU	12	NEG	5	82	19	263	5.7	0.33	0.566
CLADHERB	18	ASPEVERS	13	POS	49	38	147	135	46.2	0.32	0.572
CLADHERB	18	AUREPULL	14	POS	81	6	212	70	69.1	11.99	0.001
CLADHERB	18	CHAEGLOB	15	NEG	1	86	23	259	5.7	6.58	0.010
CLADHERB	18	CHRSPMSP	16	NEG	1	86	13	269	3.3	3.23	0.072
CLADHERB	18	CLADCLAD	17	POS	49	38	136	146	43.6	1.43	0.232
CLADSP	19	ACRESP	1	NEG	4	60	21	284	4.3	0.21	0.647
CLADSP	19	ALTEALTE	2	POS	59	5	268	37	56.7	0.60	0.439
CLADSP	19	ALTESP	3	POS	4	60	12	293	2.8	0.24	0.624
CLADSP	19	ASPECAND	4	POS	5	59	14	291	3.3	0.56	0.454
CLADSP	19	ASPEFUMI	5	POS	6	58	19	286	4.3	0.41	0.522
CLADSP	19	ASPEGLAU	6	NEG	4	60	21	284	4.3	0.21	0.647
CLADSP	19	ASPENIGE	7	POS	23	41	103	202	21.9	0.04	0.841
CLADSP	19	ASPEOCHR	8	POS	14	50	58	247	12.5	0.12	0.729
CLADSP	19	ASPEORYZ	9	NEG	1	63	8	297	1.6	0.89	0.345
CLADSP	19	ASPESP	10	POS	17	47	50	255	11.6	3.03	0.082
CLADSP	19	ASPESYDO	11	NEG	5	59	41	264	8.0	2.10	0.147
CLADSP	19	ASPEUSTU	12	POS	5	59	19	286	4.2	0.04	0.841
CLADSP	19	ASPEVERS	13	NEG	31	33	165	140	34.0	0.93	0.335
CLADSP	19	AUREPULL	14	POS	56	8	237	68	50.8	2.53	0.112
CLADSP	19	CHAEGLOB	15	NEG	3	61	21	284	4.2	0.86	0.354
CLADSP	19	CHRSPMSP	16	POS	8	56	6	299	2.4	13.32	0.000
CLADSP	19	CLADCLAD	17	NEG	32	32	153	152	32.1	0.03	0.862
CLADSP	19	CLADHERB	18	NEG	10	54	77	228	15.1	3.28	0.070
CLADSPHA	20	ACRESP	1	POS	13	128	12	216	9.6	1.58	0.209
CLADSPHA	20	ALTEALTE	2	POS	132	9	195	33	125.0	4.88	0.027
CLADSPHA	20	ALTESP	3	NEG	5	136	11	217	6.1	0.72	0.396
CLADSPHA	20	ASPECAND	4	POS	11	130	8	220	7.3	2.47	0.116
CLADSPHA	20	ASPEFUMI	5	NEG	8	133	17	211	9.6	0.77	0.380
CLADSPHA	20	ASPEGLAU	6	NEG	5	136	20	208	9.6	4.64	0.031
CLADSPHA	20	ASPENIGE	7	NEG	48	93	78	150	48.2	0.02	0.888
CLADSPHA	20	ASPEOCHR	8	POS	39	102	33	195	27.5	8.82	0.003
CLADSPHA	20	ASPEORYZ	9	NEG	2	139	7	221	3.4	1.81	0.179
CLADSPHA	20	ASPESP	10	POS	27	114	40	188	25.6	0.06	0.806
CLADSPHA	20	ASPESYDO	11	POS	18	123	28	200	17.6	0.00	1.000
CLADSPHA	20	ASPEUSTU	12	NEG	5	136	19	209	9.2	4.12	0.042
CLADSPHA	20	ASPEVERS	13	POS	83	58	113	115	74.9	2.67	0.102
CLADSPHA	20	AUREPULL	14	POS	128	13	165	63	112.0	16.95	0.000
CLADSPHA	20	CHAEGLOB	15	NEG	9	132	15	213	9.2	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
CLADSPHA	20	CHRSPMSP	16	POS	9	132	5	223	5.4	3.12	0.077
CLADSPHA	20	CLADCLAD	17	POS	86	55	99	129	70.7	10.07	0.002
CLADSPHA	20	CLADHERB	18	POS	37	104	50	178	33.2	0.68	0.410
CLADSPHA	20	CLADSP	19	POS	34	107	30	198	24.5	6.55	0.010
CONISP	21	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
CONISP	21	ALTEALTE	2	POS	9	1	318	41	8.9	0.13	0.718
CONISP	21	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
CONISP	21	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
CONISP	21	ASPEFUMI	5	POS	1	9	24	335	0.7	0.05	0.823
CONISP	21	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
CONISP	21	ASPENIGE	7	POS	4	6	122	237	3.4	0.00	1.000
CONISP	21	ASPEOCHR	8	POS	2	8	70	289	2.0	0.13	0.718
CONISP	21	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
CONISP	21	ASPESP	10	POS	3	7	64	295	1.8	0.32	0.572
CONISP	21	ASPESYDO	11	NEG	0	10	46	313	1.3	2.87	0.090
CONISP	21	ASPEUSTU	12	NEG	0	10	24	335	0.7	2.24	0.134
CONISP	21	ASPEEVERS	13	NEG	5	5	191	168	5.3	0.27	0.603
CONISP	21	AUREPULL	14	POS	9	1	284	75	7.9	0.20	0.655
CONISP	21	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
CONISP	21	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
CONISP	21	CLADCLAD	17	NEG	5	5	180	179	5.0	0.11	0.740
CONISP	21	CLADHERB	18	POS	3	7	84	275	2.4	0.01	0.920
CONISP	21	CLADSP	19	NEG	1	9	63	296	1.7	1.09	0.296
CONISP	21	CLADSPHA	20	POS	4	6	137	222	3.8	0.04	0.841
EMERNIDU	22	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
EMERNIDU	22	ALTEALTE	2	POS	9	1	318	41	8.9	0.13	0.718
EMERNIDU	22	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
EMERNIDU	22	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
EMERNIDU	22	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
EMERNIDU	22	ASPEGLAU	6	POS	1	9	24	335	0.7	0.05	0.823
EMERNIDU	22	ASPENIGE	7	POS	5	5	121	238	3.4	0.54	0.462
EMERNIDU	22	ASPEOCHR	8	NEG	0	10	72	287	2.0	3.93	0.047
EMERNIDU	22	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
EMERNIDU	22	ASPESP	10	POS	2	8	65	294	1.8	0.07	0.791
EMERNIDU	22	ASPESYDO	11	POS	2	8	44	315	1.3	0.06	0.806
EMERNIDU	22	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
EMERNIDU	22	ASPEEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
EMERNIDU	22	AUREPULL	14	NEG	6	4	287	72	7.9	3.74	0.053
EMERNIDU	22	CHAEGLOB	15	POS	2	8	22	337	0.7	1.22	0.269
EMERNIDU	22	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
EMERNIDU	22	CLADCLAD	17	NEG	4	6	181	178	5.0	0.94	0.332
EMERNIDU	22	CLADHERB	18	POS	3	7	84	275	2.4	0.01	0.920
EMERNIDU	22	CLADSP	19	NEG	1	9	63	296	1.7	1.09	0.296
EMERNIDU	22	CLADSPHA	20	POS	4	6	137	222	3.8	0.04	0.841
EMERNIDU	22	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
EPICNIGR	23	ACRESP	1	NEG	12	188	13	156	13.6	0.73	0.393
EPICNIGR	23	ALTEALTE	2	POS	193	7	134	35	177.2	25.22	0.000
EPICNIGR	23	ALTESP	3	POS	11	189	5	164	8.7	0.88	0.348
EPICNIGR	23	ASPECAND	4	POS	11	189	8	161	10.3	0.01	0.920
EPICNIGR	23	ASPEFUMI	5	POS	15	185	10	159	13.6	0.16	0.689
EPICNIGR	23	ASPEGLAU	6	POS	14	186	11	158	13.6	0.00	1.000
EPICNIGR	23	ASPENIGE	7	POS	69	131	57	112	68.3	0.00	1.000
EPICNIGR	23	ASPEOCHR	8	NEG	39	161	33	136	39.0	0.02	0.888
EPICNIGR	23	ASPEORYZ	9	NEG	3	197	6	163	4.9	2.59	0.108
EPICNIGR	23	ASPESP	10	POS	38	162	29	140	36.3	0.10	0.752
EPICNIGR	23	ASPESYDO	11	POS	29	171	17	152	24.9	1.27	0.260
EPICNIGR	23	ASPEUSTU	12	NEG	10	190	14	155	13.0	2.21	0.137
EPICNIGR	23	ASPEEVERS	13	NEG	100	100	96	73	106.2	1.99	0.158
EPICNIGR	23	AUREPULL	14	POS	178	22	115	54	158.8	23.32	0.000
EPICNIGR	23	CHAEGLOB	15	NEG	9	191	15	154	13.0	3.65	0.056
EPICNIGR	23	CHRSPMSP	16	POS	9	191	5	164	7.6	0.25	0.617
EPICNIGR	23	CLADCLAD	17	POS	118	82	67	102	100.3	12.96	0.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
EPICNIGR	23	CLADHERB	18	POS	59	141	28	141	47.2	7.80	0.005
EPICNIGR	23	CLADSP	19	POS	38	162	26	143	34.7	0.60	0.439
EPICNIGR	23	CLADSPHA	20	POS	91	109	50	119	76.4	9.16	0.002
EPICNIGR	23	CONISP	21	POS	6	194	4	165	5.4	0.00	1.000
EPICNIGR	23	EMERNIDU	22	NEG	5	195	5	164	5.4	0.35	0.554
EUROHERB	24	ACRESP	1	POS	19	226	6	118	16.6	0.70	0.403
EUROHERB	24	ALTEALTE	2	NEG	216	29	111	13	217.1	0.31	0.578
EUROHERB	24	ALTESP	3	POS	12	233	4	120	10.6	0.23	0.632
EUROHERB	24	ASPECAND	4	NEG	12	233	7	117	12.6	0.31	0.578
EUROHERB	24	ASPEFUMI	5	NEG	16	229	9	115	16.6	0.23	0.632
EUROHERB	24	ASPEGLAU	6	POS	20	225	5	119	16.6	1.62	0.203
EUROHERB	24	ASPENIGE	7	POS	86	159	40	84	83.7	0.18	0.671
EUROHERB	24	ASPEOCHR	8	POS	55	190	17	107	47.8	3.47	0.062
EUROHERB	24	ASPEORYZ	9	POS	6	239	3	121	6.0	0.12	0.729
EUROHERB	24	ASPESP	10	POS	48	197	19	105	44.5	0.74	0.390
EUROHERB	24	ASPESYDO	11	POS	34	211	12	112	30.5	0.97	0.325
EUROHERB	24	ASPEUSTU	12	NEG	14	231	10	114	15.9	1.18	0.277
EUROHERB	24	ASPEVERS	13	POS	144	101	52	72	130.1	8.71	0.003
EUROHERB	24	AUREPULL	14	NEG	193	52	100	24	194.5	0.31	0.578
EUROHERB	24	CHAEGLOB	15	POS	19	226	5	119	15.9	1.31	0.252
EUROHERB	24	CHRSPMSP	16	NEG	8	237	6	118	9.3	1.07	0.301
EUROHERB	24	CLADCLAD	17	POS	123	122	62	62	122.8	0.01	0.920
EUROHERB	24	CLADHERB	18	NEG	56	189	31	93	57.8	0.35	0.554
EUROHERB	24	CLADSP	19	POS	46	199	18	106	42.5	0.77	0.380
EUROHERB	24	CLADSPHA	20	POS	98	147	43	81	93.6	0.78	0.377
EUROHERB	24	CONISP	21	NEG	6	239	4	120	6.6	0.60	0.439
EUROHERB	24	EMERNIDU	22	POS	8	237	2	122	6.6	0.34	0.560
EUROHERB	24	EPICNIGR	23	NEG	130	115	70	54	132.8	0.53	0.467
FUSAOXYS	25	ACRESP	1	NEG	0	20	25	324	1.4	2.88	0.090
FUSAOXYS	25	ALTEALTE	2	NEG	17	3	310	39	17.7	0.78	0.377
FUSAOXYS	25	ALTESP	3	POS	1	19	15	334	0.9	0.17	0.680
FUSAOXYS	25	ASPECAND	4	NEG	0	20	19	330	1.0	2.53	0.112
FUSAOXYS	25	ASPEFUMI	5	NEG	0	20	25	324	1.4	2.88	0.090
FUSAOXYS	25	ASPEGLAU	6	POS	2	18	23	326	1.4	0.02	0.888
FUSAOXYS	25	ASPENIGE	7	POS	11	9	115	234	6.8	3.17	0.075
FUSAOXYS	25	ASPEOCHR	8	NEG	3	17	69	280	3.9	0.66	0.417
FUSAOXYS	25	ASPEORYZ	9	POS	1	19	8	341	0.5	0.00	1.000
FUSAOXYS	25	ASPESP	10	POS	5	15	62	287	3.6	0.27	0.603
FUSAOXYS	25	ASPESYDO	11	NEG	1	19	45	304	2.5	1.92	0.166
FUSAOXYS	25	ASPEUSTU	12	POS	3	17	21	328	1.3	1.25	0.264
FUSAOXYS	25	ASPEVERS	13	NEG	9	11	187	162	10.6	0.96	0.327
FUSAOXYS	25	AUREPULL	14	NEG	14	6	279	70	15.9	1.83	0.176
FUSAOXYS	25	CHAEGLOB	15	POS	5	15	19	330	1.3	8.90	0.003
FUSAOXYS	25	CHRSPMSP	16	NEG	0	20	14	335	0.8	2.30	0.129
FUSAOXYS	25	CLADCLAD	17	NEG	8	12	177	172	10.0	1.35	0.245
FUSAOXYS	25	CLADHERB	18	POS	5	15	82	267	4.7	0.01	0.920
FUSAOXYS	25	CLADSP	19	POS	4	16	60	289	3.5	0.00	1.000
FUSAOXYS	25	CLADSPHA	20	POS	8	12	133	216	7.6	0.00	1.000
FUSAOXYS	25	CONISP	21	POS	1	19	9	340	0.5	0.00	1.000
FUSAOXYS	25	EMERNIDU	22	POS	2	18	8	341	0.5	1.84	0.175
FUSAOXYS	25	EPICNIGR	23	POS	13	7	187	162	10.8	0.59	0.442
FUSAOXYS	25	EUROHERB	24	POS	14	6	231	118	13.3	0.01	0.920
FUSASP	26	ACRESP	1	POS	6	53	19	291	4.0	0.72	0.396
FUSASP	26	ALTEALTE	2	POS	57	2	270	40	52.3	3.55	0.060
FUSASP	26	ALTESP	3	POS	4	55	12	298	2.6	0.43	0.512
FUSASP	26	ASPECAND	4	POS	5	54	14	296	3.0	0.88	0.348
FUSASP	26	ASPEFUMI	5	NEG	2	57	23	287	4.0	1.99	0.158
FUSASP	26	ASPEGLAU	6	POS	5	54	20	290	4.0	0.08	0.777
FUSASP	26	ASPENIGE	7	NEG	17	42	109	201	20.2	1.19	0.275
FUSASP	26	ASPEOCHR	8	NEG	7	52	65	245	11.5	3.23	0.072
FUSASP	26	ASPEORYZ	9	POS	2	57	7	303	1.4	0.00	1.000
FUSASP	26	ASPESP	10	POS	12	47	55	255	10.7	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
FUSASP	26	ASPESYDO	11	POS	9	50	37	273	7.4	0.24	0.624
FUSASP	26	ASPEUSTU	12	POS	8	51	16	294	3.8	4.45	0.035
FUSASP	26	ASPEVERS	13	POS	37	22	159	151	31.3	2.16	0.142
FUSASP	26	AUREPULL	14	POS	47	12	246	64	46.9	0.01	0.920
FUSASP	26	CHAEGLOB	15	NEG	3	56	21	289	3.8	0.59	0.442
FUSASP	26	CHRSPMSP	16	NEG	1	58	13	297	2.2	1.67	0.196
FUSASP	26	CLADCLAD	17	POS	33	26	152	158	29.6	0.69	0.406
FUSASP	26	CLADHERB	18	POS	19	40	68	242	13.9	2.36	0.124
FUSASP	26	CLADSP	19	NEG	6	53	58	252	10.2	3.15	0.076
FUSASP	26	CLADSPHA	20	NEG	22	37	119	191	22.5	0.09	0.764
FUSASP	26	CONISP	21	POS	2	57	8	302	1.6	0.01	0.920
FUSASP	26	EMERNIDU	22	POS	3	56	7	303	1.6	0.62	0.431
FUSASP	26	EPICNIGR	23	POS	33	26	167	143	32.0	0.02	0.888
FUSASP	26	EUROHERB	24	NEG	36	23	209	101	39.2	1.22	0.269
FUSASP	26	FUSAOXYS	25	NEG	2	57	18	292	3.2	1.13	0.288
GEOMPANN	27	ACRESP	1	POS	2	10	23	334	0.8	0.64	0.424
GEOMPANN	27	ALTEALTE	2	NEG	10	2	317	40	10.6	1.10	0.294
GEOMPANN	27	ALTESP	3	NEG	0	12	16	341	0.5	2.16	0.142
GEOMPANN	27	ASPECAND	4	NEG	0	12	19	338	0.6	2.20	0.138
GEOMPANN	27	ASPEFUMI	5	POS	2	10	23	334	0.8	0.64	0.424
GEOMPANN	27	ASPEGLAU	6	NEG	0	12	25	332	0.8	2.35	0.125
GEOMPANN	27	ASPENIGE	7	POS	5	7	121	236	4.1	0.06	0.806
GEOMPANN	27	ASPEOCHR	8	NEG	2	10	70	287	2.3	0.39	0.532
GEOMPANN	27	ASPEORYZ	9	NEG	0	12	9	348	0.3	2.27	0.132
GEOMPANN	27	ASPESP	10	POS	6	6	61	296	2.2	6.39	0.011
GEOMPANN	27	ASPESYDO	11	NEG	1	11	45	312	1.5	0.78	0.377
GEOMPANN	27	ASPEUSTU	12	POS	1	11	23	334	0.8	0.11	0.740
GEOMPANN	27	ASPEVERS	13	POS	7	5	189	168	6.4	0.01	0.920
GEOMPANN	27	AUREPULL	14	POS	11	1	282	75	9.5	0.50	0.480
GEOMPANN	27	CHAEGLOB	15	POS	2	10	22	335	0.8	0.73	0.393
GEOMPANN	27	CHRSPMSP	16	POS	1	11	13	344	0.5	0.00	1.000
GEOMPANN	27	CLADCLAD	17	POS	7	5	178	179	6.0	0.08	0.777
GEOMPANN	27	CLADHERB	18	POS	3	9	84	273	2.8	0.05	0.823
GEOMPANN	27	CLADSP	19	NEG	2	10	62	295	2.1	0.20	0.655
GEOMPANN	27	CLADSPHA	20	POS	8	4	133	224	4.6	3.10	0.078
GEOMPANN	27	CONISP	21	NEG	0	12	10	347	0.3	2.22	0.136
GEOMPANN	27	EMERNIDU	22	NEG	0	12	10	347	0.3	2.22	0.136
GEOMPANN	27	EPICNIGR	23	POS	8	4	192	165	6.5	0.34	0.560
GEOMPANN	27	EUROHERB	24	POS	10	2	235	122	8.0	0.91	0.340
GEOMPANN	27	FUSAOXYS	25	POS	1	11	19	338	0.7	0.04	0.841
GEOMPANN	27	FUSASP	26	POS	2	10	57	300	1.9	0.11	0.740
MUCOPLUM	28	ACRESP	1	NEG	4	69	21	275	5.0	0.57	0.450
MUCOPLUM	28	ALTEALTE	2	POS	67	6	260	36	64.7	0.55	0.458
MUCOPLUM	28	ALTESP	3	POS	5	68	11	285	3.2	0.73	0.393
MUCOPLUM	28	ASPECAND	4	NEG	3	70	16	280	3.8	0.55	0.458
MUCOPLUM	28	ASPEFUMI	5	NEG	4	69	21	275	5.0	0.57	0.450
MUCOPLUM	28	ASPEGLAU	6	POS	6	67	19	277	5.0	0.08	0.777
MUCOPLUM	28	ASPENIGE	7	POS	34	39	92	204	24.9	5.58	0.018
MUCOPLUM	28	ASPEOCHR	8	POS	20	53	52	244	14.2	3.00	0.083
MUCOPLUM	28	ASPEORYZ	9	NEG	1	72	8	288	1.8	1.18	0.277
MUCOPLUM	28	ASPESP	10	POS	16	57	51	245	13.3	0.58	0.446
MUCOPLUM	28	ASPESYDO	11	POS	10	63	36	260	9.1	0.03	0.862
MUCOPLUM	28	ASPEUSTU	12	NEG	3	70	21	275	4.8	1.42	0.233
MUCOPLUM	28	ASPEVERS	13	NEG	37	36	159	137	38.8	0.35	0.554
MUCOPLUM	28	AUREPULL	14	POS	60	13	233	63	58.0	0.25	0.617
MUCOPLUM	28	CHAEGLOB	15	POS	5	68	19	277	4.8	0.02	0.888
MUCOPLUM	28	CHRSPMSP	16	POS	3	70	11	285	2.8	0.03	0.862
MUCOPLUM	28	CLADCLAD	17	POS	40	33	145	151	36.6	0.57	0.450
MUCOPLUM	28	CLADHERB	18	NEG	14	59	73	223	17.2	1.31	0.252
MUCOPLUM	28	CLADSP	19	NEG	9	64	55	241	12.7	2.06	0.151
MUCOPLUM	28	CLADSPHA	20	POS	29	44	112	184	27.9	0.03	0.862
MUCOPLUM	28	CONISP	21	NEG	0	73	10	286	2.0	3.98	0.046

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
MUCOPLUM	28	EMERNIDU	22	POS	3	70	7	289	2.0	0.18	0.671
MUCOPLUM	28	EPICNIGR	23	NEG	35	38	165	131	39.6	1.77	0.183
MUCOPLUM	28	EUROHERB	24	NEG	48	25	197	99	48.5	0.07	0.791
MUCOPLUM	28	FUSAOXYS	25	NEG	2	71	18	278	4.0	2.01	0.156
MUCOPLUM	28	FUSASP	26	NEG	10	63	49	247	11.7	0.60	0.439
MUCOPLUM	28	GEOMPANN	27	NEG	1	72	11	285	2.4	1.91	0.167
MUCORACE	29	ACRESP	1	NEG	5	86	20	258	6.2	0.64	0.424
MUCORACE	29	ALTEALTE	2	POS	82	9	245	33	80.6	0.11	0.740
MUCORACE	29	ALTESP	3	POS	6	85	10	268	4.0	0.85	0.357
MUCORACE	29	ASPECAND	4	POS	7	84	12	266	4.7	0.98	0.322
MUCORACE	29	ASPEFUMI	5	POS	8	83	17	261	6.2	0.41	0.522
MUCORACE	29	ASPEGLAU	6	NEG	5	86	20	258	6.2	0.64	0.424
MUCORACE	29	ASPENIGE	7	POS	36	55	90	188	31.1	1.27	0.260
MUCORACE	29	ASPEOCHR	8	POS	21	70	51	227	17.8	0.70	0.403
MUCORACE	29	ASPEORYZ	9	NEG	0	91	9	269	2.2	4.53	0.033
MUCORACE	29	ASPESP	10	POS	17	74	50	228	16.5	0.00	1.000
MUCORACE	29	ASPESYDO	11	POS	15	76	31	247	11.3	1.33	0.249
MUCORACE	29	ASPEUSTU	12	POS	7	84	17	261	5.9	0.08	0.777
MUCORACE	29	ASPEVERS	13	NEG	47	44	149	129	48.3	0.20	0.655
MUCORACE	29	AUREPULL	14	NEG	72	19	221	57	72.3	0.05	0.823
MUCORACE	29	CHAEGLOB	15	NEG	3	88	21	257	5.9	2.80	0.094
MUCORACE	29	CHRSPMSP	16	POS	4	87	10	268	3.5	0.00	1.000
MUCORACE	29	CLADCLAD	17	POS	49	42	136	142	45.6	0.48	0.488
MUCORACE	29	CLADHERB	18	NEG	18	73	69	209	21.5	1.27	0.260
MUCORACE	29	CLADSP	19	NEG	15	76	49	229	15.8	0.17	0.680
MUCORACE	29	CLADSPHA	20	POS	39	52	102	176	34.8	0.86	0.354
MUCORACE	29	CONISP	21	POS	5	86	5	273	2.5	2.29	0.130
MUCORACE	29	EMERNIDU	22	NEG	2	89	8	270	2.5	0.52	0.471
MUCORACE	29	EPICNIGR	23	POS	56	35	144	134	49.3	2.24	0.134
MUCORACE	29	EUROHERB	24	NEG	59	32	186	92	60.4	0.24	0.624
MUCORACE	29	FUSAOXYS	25	NEG	3	88	17	261	4.9	1.68	0.195
MUCORACE	29	FUSASP	26	POS	17	74	42	236	14.6	0.41	0.522
MUCORACE	29	GEOMPANN	27	POS	5	86	7	271	3.0	1.10	0.294
MUCORACE	29	MUCOPLUM	28	POS	25	66	48	230	18.0	3.88	0.049
PAECSP	30	ACRESP	1	NEG	0	8	25	336	0.5	2.20	0.138
PAECSP	30	ALTEALTE	2	NEG	7	1	320	41	7.1	0.44	0.507
PAECSP	30	ALTESP	3	NEG	0	8	16	345	0.4	2.21	0.137
PAECSP	30	ASPECAND	4	NEG	0	8	19	342	0.4	2.18	0.140
PAECSP	30	ASPEFUMI	5	POS	1	7	24	337	0.5	0.00	1.000
PAECSP	30	ASPEGLAU	6	NEG	0	8	25	336	0.5	2.20	0.138
PAECSP	30	ASPENIGE	7	POS	3	5	123	238	2.7	0.03	0.862
PAECSP	30	ASPEOCHR	8	NEG	1	7	71	290	1.6	0.92	0.337
PAECSP	30	ASPEORYZ	9	NEG	0	8	9	352	0.2	2.59	0.108
PAECSP	30	ASPESP	10	POS	3	5	64	297	1.5	0.94	0.332
PAECSP	30	ASPESYDO	11	NEG	0	8	46	315	1.0	2.63	0.105
PAECSP	30	ASPEUSTU	12	NEG	0	8	24	337	0.5	2.19	0.139
PAECSP	30	ASPEVERS	13	NEG	3	5	193	168	4.3	1.57	0.210
PAECSP	30	AUREPULL	14	NEG	6	2	287	74	6.4	0.57	0.450
PAECSP	30	CHAEGLOB	15	POS	1	7	23	338	0.5	0.00	1.000
PAECSP	30	CHRSPMSP	16	NEG	0	8	14	347	0.3	2.26	0.133
PAECSP	30	CLADCLAD	17	NEG	3	5	182	179	4.0	1.17	0.279
PAECSP	30	CLADHERB	18	POS	2	6	85	276	1.9	0.11	0.740
PAECSP	30	CLADSP	19	POS	2	6	62	299	1.4	0.01	0.920
PAECSP	30	CLADSPHA	20	POS	5	3	136	225	3.1	1.13	0.288
PAECSP	30	CONISP	21	NEG	0	8	10	351	0.2	2.49	0.115
PAECSP	30	EMERNIDU	22	POS	1	7	9	352	0.2	0.39	0.532
PAECSP	30	EPICNIGR	23	NEG	3	5	197	164	4.3	1.74	0.187
PAECSP	30	EUROHERB	24	POS	7	1	238	123	5.3	0.81	0.368
PAECSP	30	FUSAOXYS	25	POS	1	7	19	342	0.4	0.01	0.920
PAECSP	30	FUSASP	26	POS	2	6	57	304	1.3	0.05	0.823
PAECSP	30	GEOMPANN	27	POS	2	6	10	351	0.3	6.24	0.012
PAECSP	30	MUCOPLUM	28	NEG	0	8	73	288	1.6	3.49	0.062



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PAECSP	30	MUCORACE	29	POS	2	6	89	272	2.0	0.15	0.699
PAECVARI	31	ACRESP	1	POS	6	44	19	300	3.4	1.63	0.202
PAECVARI	31	ALTEALTE	2	POS	45	5	282	37	44.3	0.01	0.920
PAECVARI	31	ALTESP	3	POS	5	45	11	308	2.2	3.03	0.082
PAECVARI	31	ASPECAND	4	POS	3	47	16	303	2.6	0.00	1.000
PAECVARI	31	ASPEFUMI	5	POS	6	44	19	300	3.4	1.63	0.202
PAECVARI	31	ASPEGLAU	6	POS	4	46	21	298	3.4	0.00	1.000
PAECVARI	31	ASPENIGE	7	POS	18	32	108	211	17.1	0.02	0.888
PAECVARI	31	ASPEOCHR	8	NEG	7	43	65	254	9.8	1.56	0.212
PAECVARI	31	ASPEORYZ	9	POS	3	47	6	313	1.2	1.59	0.207
PAECVARI	31	ASPESP	10	NEG	4	46	63	256	9.1	4.84	0.028
PAECVARI	31	ASPESYDO	11	NEG	4	46	42	277	6.2	1.58	0.209
PAECVARI	31	ASPEUSTU	12	POS	6	44	18	301	3.3	1.92	0.166
PAECVARI	31	ASPEVERS	13	POS	27	23	169	150	26.6	0.00	1.000
PAECVARI	31	AUREPULL	14	NEG	36	14	257	62	39.7	2.50	0.114
PAECVARI	31	CHAEGLOB	15	POS	5	45	19	300	3.3	0.59	0.442
PAECVARI	31	CHRSPMSP	16	POS	2	48	12	307	1.9	0.10	0.752
PAECVARI	31	CLADCLAD	17	NEG	25	25	160	159	25.1	0.03	0.862
PAECVARI	31	CLADHERB	18	POS	12	38	75	244	11.8	0.01	0.920
PAECVARI	31	CLADSP	19	NEG	5	45	59	260	8.7	2.81	0.094
PAECVARI	31	CLADSPHA	20	POS	25	25	116	203	19.1	2.85	0.091
PAECVARI	31	CONISP	21	NEG	0	50	10	309	1.4	3.02	0.082
PAECVARI	31	EMERNIDU	22	POS	2	48	8	311	1.4	0.02	0.888
PAECVARI	31	EPICNIGR	23	NEG	26	24	174	145	27.1	0.24	0.624
PAECVARI	31	EUROHERB	24	POS	36	14	209	110	33.2	0.55	0.458
PAECVARI	31	FUSAOXYS	25	POS	6	44	14	305	2.7	3.51	0.061
PAECVARI	31	FUSASP	26	POS	10	40	49	270	8.0	0.39	0.532
PAECVARI	31	GEOMPANN	27	NEG	0	50	12	307	1.6	3.32	0.068
PAECVARI	31	MUCOPLUM	28	NEG	9	41	64	255	9.9	0.28	0.597
PAECVARI	31	MUCORACE	29	POS	14	36	77	242	12.3	0.17	0.680
PAECVARI	31	PAECSP	30	POS	2	48	6	313	1.1	0.19	0.663
PENIATRA	32	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIATRA	32	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
PENIATRA	32	ALTESP	3	POS	3	6	13	347	0.4	12.22	0.000
PENIATRA	32	ASPECAND	4	POS	1	8	18	342	0.5	0.00	1.000
PENIATRA	32	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENIATRA	32	ASPEGLAU	6	POS	4	5	21	339	0.6	15.06	0.000
PENIATRA	32	ASPENIGE	7	POS	6	3	120	240	3.1	2.98	0.084
PENIATRA	32	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIATRA	32	ASPEORYZ	9	POS	1	8	8	352	0.2	0.38	0.538
PENIATRA	32	ASPESP	10	POS	2	7	65	295	1.6	0.01	0.920
PENIATRA	32	ASPESYDO	11	NEG	1	8	45	315	1.1	0.40	0.527
PENIATRA	32	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIATRA	32	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIATRA	32	AUREPULL	14	NEG	6	3	287	73	7.2	1.89	0.169
PENIATRA	32	CHAEGLOB	15	POS	2	7	22	338	0.6	1.57	0.210
PENIATRA	32	CHRSPMSP	16	POS	3	6	11	349	0.3	14.54	0.000
PENIATRA	32	CLADCLAD	17	NEG	4	5	181	179	4.5	0.47	0.493
PENIATRA	32	CLADHERB	18	NEG	1	8	86	274	2.1	1.66	0.198
PENIATRA	32	CLADSP	19	POS	2	7	62	298	1.6	0.00	1.000
PENIATRA	32	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIATRA	32	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIATRA	32	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIATRA	32	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIATRA	32	EUROHERB	24	NEG	5	4	240	120	6.0	1.11	0.292
PENIATRA	32	FUSAOXYS	25	POS	2	7	18	342	0.5	2.28	0.131
PENIATRA	32	FUSASP	26	NEG	0	9	59	301	1.4	3.19	0.074
PENIATRA	32	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIATRA	32	MUCOPLUM	28	POS	3	6	70	290	1.8	0.37	0.543
PENIATRA	32	MUCORACE	29	POS	3	6	88	272	2.2	0.05	0.823
PENIATRA	32	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIATRA	32	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIAURA	33	ACRESP	1	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ALTEALTE	2	NEG	35	9	292	33	39.0	5.16	0.023
PENIAURA	33	ALTESP	3	NEG	1	43	15	310	1.9	1.23	0.267
PENIAURA	33	ASPECAND	4	POS	4	40	15	310	2.3	0.81	0.368
PENIAURA	33	ASPEFUMI	5	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ASPEGLAU	6	POS	3	41	22	303	3.0	0.09	0.764
PENIAURA	33	ASPENIGE	7	POS	19	25	107	218	15.0	1.39	0.238
PENIAURA	33	ASPEOCHR	8	POS	10	34	62	263	8.6	0.14	0.708
PENIAURA	33	ASPEORYZ	9	NEG	0	44	9	316	1.1	2.68	0.102
PENIAURA	33	ASPESP	10	POS	9	35	58	267	8.0	0.05	0.823
PENIAURA	33	ASPESYDO	11	POS	8	36	38	287	5.5	0.96	0.327
PENIAURA	33	ASPEUSTU	12	NEG	2	42	22	303	2.9	0.79	0.374
PENIAURA	33	ASPEVERS	13	NEG	23	21	173	152	23.4	0.08	0.777
PENIAURA	33	AUREPULL	14	NEG	31	13	262	63	34.9	3.11	0.078
PENIAURA	33	CHAEGLOB	15	POS	5	39	19	306	2.9	1.14	0.286
PENIAURA	33	CHRSPMSP	16	POS	2	42	12	313	1.7	0.02	0.888
PENIAURA	33	CLADCLAD	17	NEG	17	27	168	157	22.1	3.19	0.074
PENIAURA	33	CLADHERB	18	NEG	9	35	78	247	10.4	0.50	0.480
PENIAURA	33	CLADSP	19	NEG	5	39	59	266	7.6	1.77	0.183
PENIAURA	33	CLADSPHA	20	NEG	15	29	126	199	16.8	0.58	0.446
PENIAURA	33	CONISP	21	NEG	0	44	10	315	1.2	2.80	0.094
PENIAURA	33	EMERNIDU	22	NEG	1	43	9	316	1.2	0.47	0.493
PENIAURA	33	EPICNIGR	23	NEG	18	26	182	143	23.9	4.19	0.041
PENIAURA	33	EUROHERB	24	POS	32	12	213	112	29.2	0.60	0.439
PENIAURA	33	FUSAOXYS	25	POS	5	39	15	310	2.4	2.25	0.134
PENIAURA	33	FUSASP	26	NEG	5	39	54	271	7.0	1.23	0.267
PENIAURA	33	GEOMPANN	27	NEG	1	43	11	314	1.4	0.71	0.399
PENIAURA	33	MUCOPLUM	28	POS	11	33	62	263	8.7	0.52	0.471
PENIAURA	33	MUCORACE	29	POS	15	29	76	249	10.9	1.85	0.174
PENIAURA	33	PAECSP	30	NEG	0	44	8	317	1.0	2.57	0.109
PENIAURA	33	PAECVARI	31	POS	7	37	43	282	6.0	0.06	0.806
PENIAURA	33	PENIATRA	32	POS	3	41	6	319	1.1	2.21	0.137
PENIBREV	34	ACRESP	1	NEG	2	84	23	260	5.8	4.49	0.034
PENIBREV	34	ALTEALTE	2	POS	80	6	247	36	76.2	1.63	0.202
PENIBREV	34	ALTESP	3	NEG	1	85	15	268	3.7	3.81	0.051
PENIBREV	34	ASPECAND	4	NEG	4	82	15	268	4.4	0.27	0.603
PENIBREV	34	ASPEFUMI	5	NEG	4	82	21	262	5.8	1.30	0.254
PENIBREV	34	ASPEGLAU	6	NEG	5	81	20	263	5.8	0.42	0.517
PENIBREV	34	ASPENIGE	7	POS	32	54	94	189	29.4	0.31	0.578
PENIBREV	34	ASPEOCHR	8	POS	18	68	54	229	16.8	0.05	0.823
PENIBREV	34	ASPEORYZ	9	NEG	2	84	7	276	2.1	0.23	0.632
PENIBREV	34	ASPESP	10	POS	20	66	47	236	15.6	1.54	0.215
PENIBREV	34	ASPESYDO	11	NEG	5	81	41	242	10.7	5.38	0.020
PENIBREV	34	ASPEUSTU	12	NEG	5	81	19	264	5.6	0.30	0.584
PENIBREV	34	ASPEVERS	13	POS	48	38	148	135	45.7	0.20	0.655
PENIBREV	34	AUREPULL	14	POS	75	11	218	65	68.3	3.58	0.058
PENIBREV	34	CHAEGLOB	15	POS	7	79	17	266	5.6	0.20	0.655
PENIBREV	34	CHRSPMSP	16	NEG	3	83	11	272	3.3	0.24	0.624
PENIBREV	34	CLADCLAD	17	POS	55	31	130	153	43.1	7.86	0.005
PENIBREV	34	CLADHERB	18	NEG	15	71	72	211	20.3	2.81	0.094
PENIBREV	34	CLADSP	19	POS	15	71	49	234	14.9	0.02	0.888
PENIBREV	34	CLADSPHA	20	POS	40	46	101	182	32.9	2.83	0.093
PENIBREV	34	CONISP	21	NEG	1	85	9	274	2.3	1.93	0.165
PENIBREV	34	EMERNIDU	22	NEG	2	84	8	275	2.3	0.40	0.527
PENIBREV	34	EPICNIGR	23	POS	53	33	147	136	46.6	2.12	0.145
PENIBREV	34	EUROHERB	24	POS	59	27	186	97	57.1	0.13	0.718
PENIBREV	34	FUSAOXYS	25	POS	7	79	13	270	4.7	1.00	0.317
PENIBREV	34	FUSASP	26	POS	14	72	45	238	13.8	0.01	0.920
PENIBREV	34	GEOMPANN	27	NEG	2	84	10	273	2.8	0.81	0.368
PENIBREV	34	MUCOPLUM	28	POS	18	68	55	228	17.0	0.02	0.888
PENIBREV	34	MUCORACE	29	POS	22	64	69	214	21.2	0.01	0.920
PENIBREV	34	PAECSP	30	POS	2	84	6	277	1.9	0.09	0.764

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIBREV	34	PAECVARI	31	POS	12	74	38	245	11.7	0.00	1.000
PENIBREV	34	PENIATRA	32	NEG	2	84	7	276	2.1	0.23	0.632
PENIBREV	34	PENIAURA	33	POS	12	74	32	251	10.3	0.22	0.639
PENICHRY	35	ACRESP	1	POS	14	177	11	167	12.9	0.05	0.823
PENICHRY	35	ALTEALTE	2	NEG	166	25	161	17	169.3	1.52	0.218
PENICHRY	35	ALTESP	3	NEG	7	184	9	169	8.3	0.83	0.362
PENICHRY	35	ASPECAND	4	POS	11	180	8	170	9.8	0.10	0.752
PENICHRY	35	ASPEFUMI	5	POS	13	178	12	166	12.9	0.03	0.862
PENICHRY	35	ASPEGLAU	6	POS	14	177	11	167	12.9	0.05	0.823
PENICHRY	35	ASPENIGE	7	POS	66	125	60	118	65.2	0.00	1.000
PENICHRY	35	ASPEOCHR	8	NEG	33	158	39	139	37.3	1.57	0.210
PENICHRY	35	ASPEORYZ	9	POS	7	184	2	176	4.7	1.55	0.213
PENICHRY	35	ASPESP	10	POS	38	153	29	149	34.7	0.58	0.446
PENICHRY	35	ASPESYDO	11	NEG	21	170	25	153	23.8	1.09	0.296
PENICHRY	35	ASPEUSTU	12	POS	19	172	5	173	12.4	6.59	0.010
PENICHRY	35	ASPEVERS	13	POS	114	77	82	96	101.5	6.33	0.012
PENICHRY	35	AUREPULL	14	POS	155	36	138	40	151.7	0.53	0.467
PENICHRY	35	CHAEGLOB	15	POS	13	178	11	167	12.4	0.00	1.000
PENICHRY	35	CHRSPMSP	16	POS	8	183	6	172	7.3	0.02	0.888
PENICHRY	35	CLADCLAD	17	POS	96	95	89	89	95.8	0.00	1.000
PENICHRY	35	CLADHERB	18	POS	46	145	41	137	45.0	0.01	0.920
PENICHRY	35	CLADSP	19	NEG	28	163	36	142	33.1	2.40	0.121
PENICHRY	35	CLADSPHA	20	POS	80	111	61	117	73.0	1.95	0.163
PENICHRY	35	CONISP	21	POS	6	185	4	174	5.2	0.04	0.841
PENICHRY	35	EMERNIDU	22	POS	6	185	4	174	5.2	0.04	0.841
PENICHRY	35	EPICNIGR	23	NEG	99	92	101	77	103.5	1.10	0.294
PENICHRY	35	EUROHERB	24	POS	128	63	117	61	126.8	0.02	0.888
PENICHRY	35	FUSAOXYS	25	POS	12	179	8	170	10.4	0.28	0.597
PENICHRY	35	FUSASP	26	NEG	27	164	32	146	30.5	1.32	0.251
PENICHRY	35	GEOMANN	27	POS	8	183	4	174	6.2	0.57	0.450
PENICHRY	35	MUCOPLUM	28	POS	42	149	31	147	37.8	0.94	0.332
PENICHRY	35	MUCORACE	29	NEG	44	147	47	131	47.1	0.76	0.383
PENICHRY	35	PAECSP	30	NEG	4	187	4	174	4.1	0.21	0.647
PENICHRY	35	PAECVARI	31	POS	29	162	21	157	25.9	0.64	0.424
PENICHRY	35	PENIATRA	32	POS	5	186	4	174	4.7	0.01	0.920
PENICHRY	35	PENIAURA	33	NEG	21	170	23	155	22.8	0.53	0.467
PENICHRY	35	PENIBREV	34	NEG	40	151	46	132	44.5	1.53	0.216
PENICOMM	36	ACRESP	1	NEG	5	89	20	255	6.4	0.79	0.374
PENICOMM	36	ALTEALTE	2	POS	86	8	241	34	83.3	0.68	0.410
PENICOMM	36	ALTESP	3	POS	8	86	8	267	4.1	4.03	0.045
PENICOMM	36	ASPECAND	4	NEG	2	92	17	258	4.8	3.26	0.071
PENICOMM	36	ASPEFUMI	5	POS	9	85	16	259	6.4	1.03	0.310
PENICOMM	36	ASPEGLAU	6	NEG	6	88	19	256	6.4	0.17	0.680
PENICOMM	36	ASPENIGE	7	POS	40	54	86	189	32.1	3.48	0.062
PENICOMM	36	ASPEOCHR	8	POS	21	73	51	224	18.3	0.42	0.517
PENICOMM	36	ASPEORYZ	9	NEG	2	92	7	268	2.3	0.38	0.538
PENICOMM	36	ASPESP	10	NEG	17	77	50	225	17.1	0.03	0.862
PENICOMM	36	ASPESYDO	11	NEG	11	83	35	240	11.7	0.19	0.663
PENICOMM	36	ASPEUSTU	12	NEG	5	89	19	256	6.1	0.61	0.435
PENICOMM	36	ASPEVERS	13	NEG	47	47	149	126	49.9	0.67	0.413
PENICOMM	36	AUREPULL	14	POS	76	18	217	58	74.6	0.06	0.806
PENICOMM	36	CHAEGLOB	15	POS	10	84	14	261	6.1	2.69	0.101
PENICOMM	36	CHRSPMSP	16	POS	9	85	5	270	3.6	9.52	0.002
PENICOMM	36	CLADCLAD	17	POS	52	42	133	142	47.1	1.09	0.296
PENICOMM	36	CLADHERB	18	NEG	12	82	75	200	22.2	9.01	0.003
PENICOMM	36	CLADSP	19	POS	21	73	43	232	16.3	1.75	0.186
PENICOMM	36	CLADSPHA	20	POS	38	56	103	172	35.9	0.15	0.699
PENICOMM	36	CONISP	21	NEG	1	93	9	266	2.6	2.27	0.132
PENICOMM	36	EMERNIDU	22	POS	4	90	6	269	2.6	0.49	0.484
PENICOMM	36	EPICNIGR	23	NEG	50	44	150	125	51.0	0.12	0.729
PENICOMM	36	EUROHERB	24	POS	68	26	177	98	62.4	1.66	0.198
PENICOMM	36	FUSAOXYS	25	POS	6	88	14	261	5.1	0.05	0.823

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENICOMM	36	FUSASP	26	NEG	12	82	47	228	15.0	1.32	0.251
PENICOMM	36	GEOMPANN	27	POS	5	89	7	268	3.1	0.94	0.332
PENICOMM	36	MUCOPLUM	28	NEG	17	77	56	219	18.6	0.40	0.527
PENICOMM	36	MUCORACE	29	NEG	21	73	70	205	23.2	0.55	0.458
PENICOMM	36	PAECSP	30	POS	3	91	5	270	2.0	0.14	0.708
PENICOMM	36	PAECVARI	31	NEG	12	82	38	237	12.7	0.19	0.663
PENICOMM	36	PENIATRA	32	POS	4	90	5	270	2.3	0.87	0.351
PENICOMM	36	PENIAURA	33	POS	17	77	27	248	11.2	3.81	0.051
PENICOMM	36	PENIBREV	34	POS	31	63	55	220	21.9	5.90	0.015
PENICOMM	36	PENICHRY	35	NEG	39	55	152	123	48.7	5.90	0.015
PENICOPR	37	ACRESP	1	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ALTEALTE	2	NEG	7	3	320	39	8.9	5.68	0.017
PENICOPR	37	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENICOPR	37	ASPECAND	4	NEG	0	10	19	340	0.5	2.17	0.141
PENICOPR	37	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
PENICOPR	37	ASPENIGE	7	POS	5	5	121	238	3.4	0.54	0.462
PENICOPR	37	ASPEOCHR	8	POS	3	7	69	290	2.0	0.20	0.655
PENICOPR	37	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENICOPR	37	ASPESP	10	POS	4	6	63	296	1.8	1.96	0.162
PENICOPR	37	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENICOPR	37	ASPEUSTU	12	NEG	0	10	24	335	0.7	2.24	0.134
PENICOPR	37	ASPEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
PENICOPR	37	AUREPULL	14	POS	10	0	283	76	7.9	1.53	0.216
PENICOPR	37	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
PENICOPR	37	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
PENICOPR	37	CLADCLAD	17	POS	6	4	179	180	5.0	0.10	0.752
PENICOPR	37	CLADHERB	18	NEG	1	9	86	273	2.4	1.97	0.160
PENICOPR	37	CLADSP	19	POS	3	7	61	298	1.7	0.42	0.517
PENICOPR	37	CLADSPHA	20	POS	6	4	135	224	3.8	1.23	0.267
PENICOPR	37	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENICOPR	37	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENICOPR	37	EPICNIGR	23	POS	7	3	193	166	5.4	0.48	0.488
PENICOPR	37	EUROHERB	24	POS	9	1	236	123	6.6	1.59	0.207
PENICOPR	37	FUSAOXYS	25	POS	1	9	19	340	0.5	0.00	1.000
PENICOPR	37	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENICOPR	37	GEOMPANN	27	POS	2	8	10	349	0.3	4.51	0.034
PENICOPR	37	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENICOPR	37	MUCORACE	29	NEG	2	8	89	270	2.5	0.52	0.471
PENICOPR	37	PAECSP	30	POS	2	8	6	353	0.2	7.98	0.005
PENICOPR	37	PAECVARI	31	NEG	1	9	49	310	1.4	0.64	0.424
PENICOPR	37	PENIATRA	32	NEG	0	10	9	350	0.2	2.39	0.122
PENICOPR	37	PENIAURA	33	NEG	1	9	43	316	1.2	0.47	0.493
PENICOPR	37	PENIBREV	34	POS	6	4	80	279	2.3	5.78	0.016
PENICOPR	37	PENICHRY	35	POS	6	4	185	174	5.2	0.04	0.841
PENICOPR	37	PENICOMM	36	NEG	1	9	93	266	2.6	2.27	0.132
PENICORY	38	ACRESP	1	POS	9	99	16	245	7.3	0.29	0.590
PENICORY	38	ALTEALTE	2	NEG	94	14	233	28	95.7	0.63	0.427
PENICORY	38	ALTESP	3	POS	11	97	5	256	4.7	10.68	0.001
PENICORY	38	ASPECAND	4	NEG	5	103	14	247	5.6	0.30	0.584
PENICORY	38	ASPEFUMI	5	POS	9	99	16	245	7.3	0.29	0.590
PENICORY	38	ASPEGLAU	6	POS	12	96	13	248	7.3	3.63	0.057
PENICORY	38	ASPENIGE	7	POS	39	69	87	174	36.9	0.15	0.699
PENICORY	38	ASPEOCHR	8	NEG	20	88	52	209	21.1	0.21	0.647
PENICORY	38	ASPEORYZ	9	POS	3	105	6	255	2.6	0.01	0.920
PENICORY	38	ASPESP	10	POS	20	88	47	214	19.6	0.00	1.000
PENICORY	38	ASPESYDO	11	NEG	9	99	37	224	13.5	2.96	0.085
PENICORY	38	ASPEUSTU	12	NEG	6	102	18	243	7.0	0.50	0.480
PENICORY	38	ASPEVERS	13	NEG	56	52	140	121	57.4	0.18	0.671
PENICORY	38	AUREPULL	14	NEG	84	24	209	52	85.8	0.41	0.522
PENICORY	38	CHAEGLOB	15	NEG	7	101	17	244	7.0	0.06	0.806
PENICORY	38	CHRSPMSP	16	POS	10	98	4	257	4.1	10.47	0.001

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENICORY	38	CLADCLAD	17	NEG	49	59	136	125	54.2	1.67	0.196
PENICORY	38	CLADHERB	18	NEG	16	92	71	190	25.5	7.21	0.007
PENICORY	38	CLADSP	19	POS	19	89	45	216	18.7	0.00	1.000
PENICORY	38	CLADSPHA	20	POS	48	60	93	168	41.3	2.15	0.143
PENICORY	38	CONISP	21	POS	3	105	7	254	2.9	0.09	0.764
PENICORY	38	EMERNIDU	22	POS	3	105	7	254	2.9	0.09	0.764
PENICORY	38	EPICNIGR	23	POS	63	45	137	124	58.5	0.83	0.362
PENICORY	38	EUROHERB	24	POS	74	34	171	90	71.7	0.19	0.663
PENICORY	38	FUSAOXYS	25	POS	8	100	12	249	5.9	0.69	0.406
PENICORY	38	FUSASP	26	POS	19	89	40	221	17.3	0.15	0.699
PENICORY	38	GEOMPANN	27	POS	6	102	6	255	3.5	1.64	0.200
PENICORY	38	MUCOPLUM	28	POS	23	85	50	211	21.4	0.11	0.740
PENICORY	38	MUCORACE	29	POS	32	76	59	202	26.6	1.67	0.196
PENICORY	38	PAECSP	30	NEG	2	106	6	255	2.3	0.44	0.507
PENICORY	38	PAECVARI	31	POS	24	84	26	235	14.6	8.78	0.003
PENICORY	38	PENIATRA	32	POS	7	101	2	259	2.6	8.22	0.004
PENICORY	38	PENIAURA	33	POS	14	94	30	231	12.9	0.05	0.823
PENICORY	38	PENIBREV	34	POS	31	77	55	206	25.2	2.08	0.149
PENICORY	38	PENICHRY	35	POS	58	50	133	128	55.9	0.13	0.718
PENICORY	38	PENICOMM	36	NEG	26	82	68	193	27.5	0.28	0.597
PENICORY	38	PENICOPR	37	POS	3	105	7	254	2.9	0.09	0.764
PENICRUS	39	ACRESP	1	POS	1	13	24	331	1.0	0.24	0.624
PENICRUS	39	ALTEALTE	2	POS	13	1	314	41	12.4	0.01	0.920
PENICRUS	39	ALTESP	3	NEG	0	14	16	339	0.6	2.19	0.139
PENICRUS	39	ASPECAND	4	NEG	0	14	19	336	0.7	2.27	0.132
PENICRUS	39	ASPEFUMI	5	POS	1	13	24	331	1.0	0.24	0.624
PENICRUS	39	ASPEGLAU	6	POS	2	12	23	332	1.0	0.36	0.549
PENICRUS	39	ASPENIGE	7	POS	7	7	119	236	4.8	0.98	0.322
PENICRUS	39	ASPEOCHR	8	POS	4	10	68	287	2.7	0.28	0.597
PENICRUS	39	ASPEORYZ	9	NEG	0	14	9	346	0.3	2.21	0.137
PENICRUS	39	ASPESP	10	POS	3	11	64	291	2.5	0.00	1.000
PENICRUS	39	ASPESYDO	11	NEG	1	13	45	310	1.8	1.06	0.303
PENICRUS	39	ASPEUSTU	12	POS	1	13	23	332	0.9	0.21	0.647
PENICRUS	39	ASPEVERS	13	POS	8	6	188	167	7.4	0.00	1.000
PENICRUS	39	AUREPULL	14	NEG	9	5	284	71	11.1	3.11	0.078
PENICRUS	39	CHAEGLOB	15	POS	6	8	18	337	0.9	25.72	0.000
PENICRUS	39	CHRSPMSP	16	NEG	0	14	14	341	0.5	2.16	0.142
PENICRUS	39	CLADCLAD	17	NEG	5	9	180	175	7.0	1.88	0.170
PENICRUS	39	CLADHERB	18	NEG	2	12	85	270	3.3	1.34	0.247
PENICRUS	39	CLADSP	19	POS	3	11	61	294	2.4	0.00	1.000
PENICRUS	39	CLADSPHA	20	POS	8	6	133	222	5.4	1.45	0.229
PENICRUS	39	CONISP	21	POS	1	13	9	346	0.4	0.04	0.841
PENICRUS	39	EMERNIDU	22	POS	1	13	9	346	0.4	0.04	0.841
PENICRUS	39	EPICNIGR	23	POS	8	6	192	163	7.6	0.00	1.000
PENICRUS	39	EUROHERB	24	POS	11	3	234	121	9.3	0.48	0.488
PENICRUS	39	FUSAOXYS	25	POS	3	11	17	338	0.8	4.39	0.036
PENICRUS	39	FUSASP	26	NEG	2	12	57	298	2.2	0.30	0.584
PENICRUS	39	GEOMPANN	27	NEG	0	14	12	343	0.5	2.15	0.143
PENICRUS	39	MUCOPLUM	28	NEG	2	12	71	284	2.8	0.75	0.386
PENICRUS	39	MUCORACE	29	POS	4	10	87	268	3.5	0.00	1.000
PENICRUS	39	PAECSP	30	POS	2	12	6	349	0.3	5.01	0.025
PENICRUS	39	PAECVARI	31	POS	2	12	48	307	1.9	0.10	0.752
PENICRUS	39	PENIATRA	32	POS	1	13	8	347	0.3	0.08	0.777
PENICRUS	39	PENIAURA	33	POS	2	12	42	313	1.7	0.02	0.888
PENICRUS	39	PENIBREV	34	NEG	2	12	84	271	3.3	1.29	0.256
PENICRUS	39	PENICHRY	35	POS	8	6	183	172	7.3	0.02	0.888
PENICRUS	39	PENICOMM	36	POS	6	8	88	267	3.6	1.46	0.227
PENICRUS	39	PENICOPR	37	NEG	0	14	10	345	0.4	2.18	0.140
PENICRUS	39	PENICORY	38	POS	5	9	103	252	4.1	0.06	0.806
PENICTNG	40	ACRESP	1	POS	6	28	19	316	2.3	5.24	0.022
PENICTNG	40	ALTEALTE	2	POS	31	3	296	39	30.1	0.04	0.841
PENICTNG	40	ALTESP	3	NEG	1	33	15	320	1.5	0.74	0.390

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENICTNG	40	ASPECAND	4	NEG	1	33	18	317	1.8	1.04	0.308
PENICTNG	40	ASPEFUMI	5	POS	6	28	19	316	2.3	5.24	0.022
PENICTNG	40	ASPEGLAU	6	NEG	1	33	24	311	2.3	1.67	0.196
PENICTNG	40	ASPENIGE	7	NEG	11	23	115	220	11.6	0.18	0.671
PENICTNG	40	ASPEOCHR	8	NEG	6	28	66	269	6.6	0.27	0.603
PENICTNG	40	ASPEORYZ	9	NEG	0	34	9	326	0.8	2.41	0.121
PENICTNG	40	ASPESP	10	POS	11	23	56	279	6.2	4.08	0.043
PENICTNG	40	ASPESYDO	11	POS	5	29	41	294	4.2	0.02	0.888
PENICTNG	40	ASPEUSTU	12	NEG	2	32	22	313	2.2	0.27	0.603
PENICTNG	40	ASPEVERS	13	POS	23	11	173	162	18.1	2.57	0.109
PENICTNG	40	AUREPULL	14	NEG	27	7	266	69	27.0	0.05	0.823
PENICTNG	40	CHAEGLOB	15	NEG	2	32	22	313	2.2	0.27	0.603
PENICTNG	40	CHRSPMSP	16	POS	2	32	12	323	1.3	0.04	0.841
PENICTNG	40	CLADCLAD	17	NEG	17	17	168	167	17.1	0.04	0.841
PENICTNG	40	CLADHERB	18	NEG	5	29	82	253	8.0	2.22	0.136
PENICTNG	40	CLADSP	19	POS	8	26	56	279	5.9	0.58	0.446
PENICTNG	40	CLADSPHA	20	POS	14	20	127	208	13.0	0.04	0.841
PENICTNG	40	CONISP	21	POS	1	33	9	326	0.9	0.22	0.639
PENICTNG	40	EMERNIDU	22	POS	3	31	7	328	0.9	3.06	0.080
PENICTNG	40	EPICNIGR	23	NEG	18	16	182	153	18.4	0.11	0.740
PENICTNG	40	EUROHERB	24	POS	23	11	222	113	22.6	0.00	1.000
PENICTNG	40	FUSAOXYS	25	POS	3	31	17	318	1.8	0.27	0.603
PENICTNG	40	FUSASP	26	NEG	4	30	55	280	5.4	0.90	0.343
PENICTNG	40	GEOMPANN	27	POS	3	31	9	326	1.1	2.00	0.157
PENICTNG	40	MUCOPLUM	28	NEG	2	32	71	264	6.7	5.58	0.018
PENICTNG	40	MUCORACE	29	POS	11	23	80	255	8.4	0.78	0.377
PENICTNG	40	PAECSP	30	POS	3	31	5	330	0.7	4.75	0.029
PENICTNG	40	PAECVARI	31	POS	5	29	45	290	4.6	0.00	1.000
PENICTNG	40	PENIATRA	32	NEG	0	34	9	326	0.8	2.41	0.121
PENICTNG	40	PENIAURA	33	NEG	4	30	40	295	4.1	0.09	0.764
PENICTNG	40	PENIBREV	34	POS	8	26	78	257	7.9	0.03	0.862
PENICTNG	40	PENICHRY	35	NEG	15	19	176	159	17.6	1.25	0.264
PENICTNG	40	PENICOMM	36	POS	13	21	81	254	8.7	2.51	0.113
PENICTNG	40	PENICOPR	37	POS	2	32	8	327	0.9	0.41	0.522
PENICTNG	40	PENICORY	38	POS	10	24	98	237	10.0	0.03	0.862
PENICTNG	40	PENICRUS	39	POS	3	31	11	324	1.3	1.30	0.254
PENICTRM	41	ACRESP	1	NEG	3	49	22	295	3.5	0.37	0.543
PENICTRM	41	ALTEALTE	2	POS	47	5	280	37	46.1	0.04	0.841
PENICTRM	41	ALTESP	3	POS	4	48	12	305	2.3	0.84	0.359
PENICTRM	41	ASPECAND	4	POS	5	47	14	303	2.7	1.52	0.218
PENICTRM	41	ASPEFUMI	5	POS	4	48	21	296	3.5	0.00	1.000
PENICTRM	41	ASPEGLAU	6	POS	7	45	18	299	3.5	3.14	0.076
PENICTRM	41	ASPENIGE	7	POS	21	31	105	212	17.8	0.75	0.386
PENICTRM	41	ASPEOCHR	8	POS	15	37	57	260	10.2	2.70	0.100
PENICTRM	41	ASPEORYZ	9	NEG	1	51	8	309	1.3	0.56	0.454
PENICTRM	41	ASPESP	10	POS	12	40	55	262	9.4	0.64	0.424
PENICTRM	41	ASPESYDO	11	POS	8	44	38	279	6.5	0.21	0.647
PENICTRM	41	ASPEUSTU	12	POS	4	48	20	297	3.4	0.01	0.920
PENICTRM	41	ASPEVERS	13	POS	29	23	167	150	27.6	0.07	0.791
PENICTRM	41	AUREPULL	14	NEG	39	13	254	63	41.3	1.07	0.301
PENICTRM	41	CHAEGLOB	15	NEG	2	50	22	295	3.4	1.30	0.254
PENICTRM	41	CHRSPMSP	16	POS	4	48	10	307	2.0	1.43	0.232
PENICTRM	41	CLADCLAD	17	NEG	25	27	160	157	26.1	0.22	0.639
PENICTRM	41	CLADHERB	18	NEG	8	44	79	238	12.3	2.82	0.093
PENICTRM	41	CLADSP	19	POS	12	40	52	265	9.0	0.96	0.327
PENICTRM	41	CLADSPHA	20	POS	21	31	120	197	19.9	0.04	0.841
PENICTRM	41	CONISP	21	NEG	0	52	10	307	1.4	3.09	0.079
PENICTRM	41	EMERNIDU	22	NEG	1	51	9	308	1.4	0.70	0.403
PENICTRM	41	EPICNIGR	23	NEG	26	26	174	143	28.2	0.65	0.420
PENICTRM	41	EUROHERB	24	POS	36	16	209	108	34.5	0.10	0.752
PENICTRM	41	FUSAOXYS	25	NEG	2	50	18	299	2.8	0.76	0.383
PENICTRM	41	FUSASP	26	POS	9	43	50	267	8.3	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENICTRM	41	GEOMPANN	27	POS	4	48	8	309	1.7	2.33	0.127
PENICTRM	41	MUCOPLUM	28	POS	14	38	59	258	10.3	1.46	0.227
PENICTRM	41	MUCORACE	29	POS	19	33	72	245	12.8	3.88	0.049
PENICTRM	41	PAECSP	30	NEG	1	51	7	310	1.1	0.42	0.517
PENICTRM	41	PAECVARI	31	POS	11	41	39	278	7.1	2.28	0.131
PENICTRM	41	PENIATRA	32	POS	4	48	5	312	1.3	4.69	0.030
PENICTRM	41	PENIAURA	33	NEG	6	46	38	279	6.2	0.10	0.752
PENICTRM	41	PENIBREV	34	POS	14	38	72	245	12.1	0.24	0.624
PENICTRM	41	PENICHRY	35	POS	30	22	161	156	26.9	0.60	0.439
PENICTRM	41	PENICOMM	36	NEG	11	41	83	234	13.3	0.89	0.345
PENICTRM	41	PENICOPR	37	POS	3	49	7	310	1.4	1.01	0.315
PENICTRM	41	PENICORY	38	POS	20	32	88	229	15.2	1.98	0.159
PENICTRM	41	PENICRUS	39	NEG	1	51	13	304	2.0	1.33	0.249
PENICTRM	41	PENICTNG	40	NEG	4	48	30	287	4.8	0.45	0.502
PENIDECU	42	ACRESP	1	POS	2	17	23	327	1.3	0.04	0.841
PENIDECU	42	ALTEALTE	2	NEG	14	5	313	37	16.8	6.13	0.013
PENIDECU	42	ALTESP	3	NEG	0	19	16	334	0.8	2.34	0.126
PENIDECU	42	ASPECAND	4	NEG	0	19	19	331	1.0	2.48	0.115
PENIDECU	42	ASPEFUMI	5	NEG	1	18	24	326	1.3	0.54	0.462
PENIDECU	42	ASPEGLAU	6	POS	2	17	23	327	1.3	0.04	0.841
PENIDECU	42	ASPENIGE	7	NEG	5	14	121	229	6.5	0.98	0.322
PENIDECU	42	ASPEOCHR	8	POS	4	15	68	282	3.7	0.02	0.888
PENIDECU	42	ASPEORYZ	9	NEG	0	19	9	341	0.5	2.16	0.142
PENIDECU	42	ASPESP	10	POS	4	15	63	287	3.5	0.00	1.000
PENIDECU	42	ASPESYDO	11	NEG	1	18	45	305	2.4	1.78	0.182
PENIDECU	42	ASPEUSTU	12	NEG	1	18	23	327	1.2	0.49	0.484
PENIDECU	42	ASPEVERS	13	POS	12	7	184	166	10.1	0.44	0.507
PENIDECU	42	AUREPULL	14	NEG	14	5	279	71	15.1	0.85	0.357
PENIDECU	42	CHAEGLOB	15	NEG	1	18	23	327	1.2	0.49	0.484
PENIDECU	42	CHRSPMSP	16	NEG	0	19	14	336	0.7	2.27	0.132
PENIDECU	42	CLADCLAD	17	POS	10	9	175	175	9.5	0.00	1.000
PENIDECU	42	CLADHERB	18	POS	6	13	81	269	4.5	0.32	0.572
PENIDECU	42	CLADSP	19	NEG	1	18	63	287	3.3	3.02	0.082
PENIDECU	42	CLADSPHA	20	POS	8	11	133	217	7.3	0.01	0.920
PENIDECU	42	CONISP	21	NEG	0	19	10	340	0.5	2.17	0.141
PENIDECU	42	EMERNIDU	22	NEG	0	19	10	340	0.5	2.17	0.141
PENIDECU	42	EPICNIGR	23	POS	13	6	187	163	10.3	1.08	0.299
PENIDECU	42	EUROHERB	24	POS	15	4	230	120	12.6	0.88	0.348
PENIDECU	42	FUSAOXYS	25	NEG	1	18	19	331	1.0	0.30	0.584
PENIDECU	42	FUSASP	26	POS	5	14	54	296	3.0	0.88	0.348
PENIDECU	42	GEOMPANN	27	NEG	0	19	12	338	0.6	2.20	0.138
PENIDECU	42	MUCOPLUM	28	NEG	1	18	72	278	3.8	3.71	0.054
PENIDECU	42	MUCORACE	29	POS	6	13	85	265	4.7	0.20	0.655
PENIDECU	42	PAECSP	30	POS	1	18	7	343	0.4	0.02	0.888
PENIDECU	42	PAECVARI	31	POS	4	15	46	304	2.6	0.41	0.522
PENIDECU	42	PENIATRA	32	NEG	0	19	9	341	0.5	2.16	0.142
PENIDECU	42	PENIAURA	33	POS	3	16	41	309	2.3	0.03	0.862
PENIDECU	42	PENIBREV	34	POS	5	14	81	269	4.4	0.00	1.000
PENIDECU	42	PENICHRY	35	NEG	9	10	182	168	9.8	0.40	0.527
PENIDECU	42	PENICOMM	36	POS	6	13	88	262	4.8	0.13	0.718
PENIDECU	42	PENICOPR	37	POS	2	17	8	342	0.5	2.04	0.153
PENIDECU	42	PENICORY	38	POS	8	11	100	250	5.6	1.01	0.315
PENIDECU	42	PENICRUS	39	POS	2	17	12	338	0.7	0.92	0.337
PENIDECU	42	PENICTNG	40	POS	4	15	30	320	1.8	2.03	0.154
PENIDECU	42	PENICTRM	41	NEG	2	17	50	300	2.7	0.64	0.424
PENIDIGI	43	ACRESP	1	POS	1	9	24	335	0.7	0.05	0.823
PENIDIGI	43	ALTEALTE	2	POS	10	0	317	42	8.9	0.42	0.517
PENIDIGI	43	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENIDIGI	43	ASPECAND	4	POS	1	9	18	341	0.5	0.00	1.000
PENIDIGI	43	ASPEFUMI	5	NEG	0	10	25	334	0.7	2.26	0.133
PENIDIGI	43	ASPEGLAU	6	POS	2	8	23	336	0.7	1.10	0.294
PENIDIGI	43	ASPENIGE	7	NEG	3	7	123	236	3.4	0.38	0.538

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIDIGI	43	ASPEOCHR	8	POS	2	8	70	289	2.0	0.13	0.718
PENIDIGI	43	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENIDIGI	43	ASPESP	10	NEG	1	9	66	293	1.8	1.20	0.273
PENIDIGI	43	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENIDIGI	43	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
PENIDIGI	43	ASPEVERS	13	POS	7	3	189	170	5.3	0.58	0.446
PENIDIGI	43	AUREPULL	14	POS	9	1	284	75	7.9	0.20	0.655
PENIDIGI	43	CHAEGLOB	15	NEG	0	10	24	335	0.7	2.24	0.134
PENIDIGI	43	CHRSPMSP	16	NEG	0	10	14	345	0.4	2.18	0.140
PENIDIGI	43	CLADCLAD	17	POS	7	3	178	181	5.0	0.91	0.340
PENIDIGI	43	CLADHERB	18	POS	4	6	83	276	2.4	0.74	0.390
PENIDIGI	43	CLADSP	19	POS	2	8	62	297	1.7	0.04	0.841
PENIDIGI	43	CLADSPHA	20	POS	6	4	135	224	3.8	1.23	0.267
PENIDIGI	43	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENIDIGI	43	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENIDIGI	43	EPICNIGR	23	NEG	5	5	195	164	5.4	0.35	0.554
PENIDIGI	43	EUROHERB	24	NEG	5	5	240	119	6.6	2.11	0.146
PENIDIGI	43	FUSAOXYS	25	NEG	0	10	20	339	0.5	2.18	0.140
PENIDIGI	43	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENIDIGI	43	GEOMPANN	27	NEG	0	10	12	347	0.3	2.22	0.136
PENIDIGI	43	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENIDIGI	43	MUCORACE	29	POS	3	7	88	271	2.5	0.00	1.000
PENIDIGI	43	PAECSP	30	NEG	0	10	8	351	0.2	2.49	0.115
PENIDIGI	43	PAECVARI	31	POS	2	8	48	311	1.4	0.02	0.888
PENIDIGI	43	PENIATRA	32	NEG	0	10	9	350	0.2	2.39	0.122
PENIDIGI	43	PENIAURA	33	NEG	1	9	43	316	1.2	0.47	0.493
PENIDIGI	43	PENIBREV	34	POS	4	6	82	277	2.3	0.79	0.374
PENIDIGI	43	PENICHR	35	NEG	4	6	187	172	5.2	1.16	0.281
PENIDIGI	43	PENICOMM	36	NEG	2	8	92	267	2.6	0.59	0.442
PENIDIGI	43	PENICOPR	37	POS	1	9	9	350	0.3	0.20	0.655
PENIDIGI	43	PENICORY	38	NEG	2	8	106	253	2.9	1.01	0.315
PENIDIGI	43	PENICRUS	39	NEG	0	10	14	345	0.4	2.18	0.140
PENIDIGI	43	PENICTNG	40	POS	1	9	33	326	0.9	0.22	0.639
PENIDIGI	43	PENICTRM	41	NEG	1	9	51	308	1.4	0.70	0.403
PENIDIGI	43	PENIDECU	42	NEG	0	10	19	340	0.5	2.17	0.141
PENIECHI	44	ACRESP	1	NEG	0	17	25	327	1.2	2.66	0.103
PENIECHI	44	ALTEALTE	2	POS	16	1	311	41	15.1	0.12	0.729
PENIECHI	44	ALTESP	3	NEG	0	17	16	336	0.7	2.28	0.131
PENIECHI	44	ASPECAND	4	POS	2	15	17	335	0.9	0.49	0.484
PENIECHI	44	ASPEFUMI	5	NEG	1	16	24	328	1.2	0.41	0.522
PENIECHI	44	ASPEGLAU	6	NEG	1	16	24	328	1.2	0.41	0.522
PENIECHI	44	ASPENIGE	7	POS	9	8	117	235	5.8	1.99	0.158
PENIECHI	44	ASPEOCHR	8	POS	5	12	67	285	3.3	0.55	0.458
PENIECHI	44	ASPEORYZ	9	NEG	0	17	9	343	0.4	2.17	0.141
PENIECHI	44	ASPESP	10	POS	6	11	61	291	3.1	2.42	0.120
PENIECHI	44	ASPESYDO	11	NEG	2	15	44	308	2.1	0.22	0.639
PENIECHI	44	ASPEUSTU	12	POS	3	14	21	331	1.1	1.97	0.160
PENIECHI	44	ASPEVERS	13	POS	10	7	186	166	9.0	0.05	0.823
PENIECHI	44	AUREPULL	14	POS	14	3	279	73	13.5	0.00	1.000
PENIECHI	44	CHAEGLOB	15	POS	3	14	21	331	1.1	1.97	0.160
PENIECHI	44	CHRSPMSP	16	POS	1	16	13	339	0.6	0.04	0.841
PENIECHI	44	CLADCLAD	17	POS	9	8	176	176	8.5	0.00	1.000
PENIECHI	44	CLADHERB	18	NEG	2	15	85	267	4.0	2.15	0.143
PENIECHI	44	CLADSP	19	POS	7	10	57	295	3.0	5.43	0.020
PENIECHI	44	CLADSPHA	20	POS	8	9	133	219	6.5	0.26	0.610
PENIECHI	44	CONISP	21	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	EMERNIDU	22	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	EPICNIGR	23	NEG	9	8	191	161	9.2	0.13	0.718
PENIECHI	44	EUROHERB	24	NEG	11	6	234	118	11.3	0.17	0.680
PENIECHI	44	FUSAOXYS	25	NEG	0	17	20	332	0.9	2.43	0.119
PENIECHI	44	FUSASP	26	POS	5	12	54	298	2.7	1.46	0.227
PENIECHI	44	GEOMPANN	27	NEG	0	17	12	340	0.6	2.17	0.141



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIECHI	44	MUCOPLUM	28	NEG	2	15	71	281	3.4	1.35	0.245
PENIECHI	44	MUCORACE	29	POS	6	11	85	267	4.2	0.57	0.450
PENIECHI	44	PAECSP	30	NEG	0	17	8	344	0.4	2.19	0.139
PENIECHI	44	PAECVARI	31	NEG	1	16	49	303	2.3	1.71	0.191
PENIECHI	44	PENIATRA	32	POS	2	15	7	345	0.4	3.05	0.081
PENIECHI	44	PENIAURA	33	POS	3	14	41	311	2.0	0.13	0.718
PENIECHI	44	PENIBREV	34	POS	6	11	80	272	4.0	0.82	0.365
PENIECHI	44	PENICHRY	35	POS	9	8	182	170	8.8	0.02	0.888
PENIECHI	44	PENICOMM	36	NEG	4	13	90	262	4.3	0.22	0.639
PENIECHI	44	PENICOPR	37	NEG	0	17	10	342	0.5	2.16	0.142
PENIECHI	44	PENICORY	38	POS	7	10	101	251	5.0	0.69	0.406
PENIECHI	44	PENICRUS	39	POS	3	14	11	341	0.6	5.81	0.016
PENIECHI	44	PENICTNG	40	POS	2	15	32	320	1.6	0.00	1.000
PENIECHI	44	PENICTRM	41	POS	4	13	48	304	2.4	0.62	0.431
PENIECHI	44	PENIDECU	42	NEG	0	17	19	333	0.9	2.39	0.122
PENIECHI	44	PENIDIGI	43	NEG	0	17	10	342	0.5	2.16	0.142
PENIEXPA	45	ACRESP	1	NEG	3	66	22	278	4.7	1.33	0.249
PENIEXPA	45	ALTEALTE	2	NEG	60	9	267	33	61.2	0.48	0.488
PENIEXPA	45	ALTESP	3	POS	6	63	10	290	3.0	2.70	0.100
PENIEXPA	45	ASPECAND	4	POS	4	65	15	285	3.6	0.00	1.000
PENIEXPA	45	ASPEFUMI	5	POS	6	63	19	281	4.7	0.19	0.663
PENIEXPA	45	ASPEGLAU	6	POS	5	64	20	280	4.7	0.01	0.920
PENIEXPA	45	ASPENIGE	7	POS	28	41	98	202	23.6	1.23	0.267
PENIEXPA	45	ASPEOCHR	8	POS	18	51	54	246	13.5	1.85	0.174
PENIEXPA	45	ASPEORYZ	9	POS	2	67	7	293	1.7	0.03	0.862
PENIEXPA	45	ASPESP	10	POS	14	55	53	247	12.5	0.11	0.740
PENIEXPA	45	ASPESYDO	11	POS	10	59	36	264	8.6	0.13	0.718
PENIEXPA	45	ASPEUSTU	12	NEG	3	66	21	279	4.5	1.16	0.281
PENIEXPA	45	ASPEVERS	13	POS	38	31	158	142	36.7	0.05	0.823
PENIEXPA	45	AUREPULL	14	NEG	54	15	239	61	54.8	0.18	0.671
PENIEXPA	45	CHAEGLOB	15	POS	9	60	15	285	4.5	4.72	0.030
PENIEXPA	45	CHRSPMSP	16	POS	4	65	10	290	2.6	0.38	0.538
PENIEXPA	45	CLADCLAD	17	NEG	34	35	151	149	34.6	0.09	0.764
PENIEXPA	45	CLADHERB	18	NEG	11	58	76	224	16.3	3.29	0.070
PENIEXPA	45	CLADSP	19	POS	14	55	50	250	12.0	0.29	0.590
PENIEXPA	45	CLADSPHA	20	POS	29	40	112	188	26.4	0.34	0.560
PENIEXPA	45	CONISP	21	POS	3	66	7	293	1.9	0.27	0.603
PENIEXPA	45	EMERNIDU	22	NEG	1	68	9	291	1.9	1.27	0.260
PENIEXPA	45	EPICNIGR	23	POS	45	24	155	145	37.4	3.62	0.057
PENIEXPA	45	EUROHERB	24	POS	48	21	197	103	45.8	0.23	0.632
PENIEXPA	45	FUSAOXYS	25	POS	4	65	16	284	3.7	0.02	0.888
PENIEXPA	45	FUSASP	26	POS	14	55	45	255	11.0	0.81	0.368
PENIEXPA	45	GEOMPANN	27	POS	3	66	9	291	2.2	0.04	0.841
PENIEXPA	45	MUCOPLUM	28	POS	19	50	54	246	13.7	2.64	0.104
PENIEXPA	45	MUCORACE	29	POS	21	48	70	230	17.0	1.16	0.281
PENIEXPA	45	PAECSP	30	POS	3	66	5	295	1.5	0.85	0.357
PENIEXPA	45	PAECVARI	31	POS	10	59	40	260	9.4	0.00	1.000
PENIEXPA	45	PENIATRA	32	POS	2	67	7	293	1.7	0.03	0.862
PENIEXPA	45	PENIAURA	33	NEG	8	61	36	264	8.2	0.09	0.764
PENIEXPA	45	PENIBREV	34	NEG	16	53	70	230	16.1	0.03	0.862
PENIEXPA	45	PENICHRY	35	NEG	28	41	163	137	35.8	4.82	0.028
PENIEXPA	45	PENICOMM	36	POS	31	38	63	237	17.6	15.68	0.000
PENIEXPA	45	PENICOPR	37	POS	3	66	7	293	1.9	0.27	0.603
PENIEXPA	45	PENICORY	38	POS	23	46	85	215	20.2	0.46	0.498
PENIEXPA	45	PENICRUS	39	POS	4	65	10	290	2.6	0.38	0.538
PENIEXPA	45	PENICTNG	40	NEG	6	63	28	272	6.4	0.16	0.689
PENIEXPA	45	PENICTRM	41	POS	10	59	42	258	9.7	0.01	0.920
PENIEXPA	45	PENIDECU	42	NEG	3	66	16	284	3.6	0.40	0.527
PENIEXPA	45	PENIDIGI	43	POS	2	67	8	292	1.9	0.09	0.764
PENIEXPA	45	PENIECHI	44	POS	5	64	12	288	3.2	0.71	0.399
PENIGLAN	46	ACRESP	1	NEG	0	13	25	331	0.9	2.41	0.121
PENIGLAN	46	ALTEALTE	2	NEG	11	2	316	40	11.5	0.82	0.365

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIGLAN	46	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
PENIGLAN	46	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
PENIGLAN	46	ASPEFUMI	5	NEG	0	13	25	331	0.9	2.41	0.121
PENIGLAN	46	ASPEGLAU	6	POS	2	11	23	333	0.9	0.48	0.488
PENIGLAN	46	ASPENIGE	7	NEG	1	12	125	231	4.4	5.50	0.019
PENIGLAN	46	ASPEOCHR	8	NEG	2	11	70	286	2.5	0.55	0.458
PENIGLAN	46	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
PENIGLAN	46	ASPESP	10	NEG	1	12	66	290	2.4	1.86	0.173
PENIGLAN	46	ASPESYDO	11	POS	4	9	42	314	1.6	2.58	0.108
PENIGLAN	46	ASPEUSTU	12	NEG	0	13	24	332	0.9	2.37	0.124
PENIGLAN	46	ASPEVERS	13	NEG	5	8	191	165	6.9	1.85	0.174
PENIGLAN	46	AUREPULL	14	NEG	10	3	283	73	10.3	0.33	0.566
PENIGLAN	46	CHAEGLOB	15	POS	2	11	22	334	0.9	0.56	0.454
PENIGLAN	46	CHRSPMSP	16	POS	1	12	13	343	0.5	0.00	1.000
PENIGLAN	46	CLADCLAD	17	NEG	6	7	179	177	6.5	0.33	0.566
PENIGLAN	46	CLADHERB	18	NEG	3	10	84	272	3.1	0.14	0.708
PENIGLAN	46	CLADSP	19	NEG	0	13	64	292	2.3	4.22	0.040
PENIGLAN	46	CLADSPHA	20	NEG	2	11	139	217	5.0	4.06	0.044
PENIGLAN	46	CONISP	21	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	EPICNIGR	23	POS	11	2	189	167	7.1	3.83	0.050
PENIGLAN	46	EUROHERB	24	POS	11	2	234	122	8.6	1.25	0.264
PENIGLAN	46	FUSAOXYS	25	NEG	0	13	20	336	0.7	2.26	0.133
PENIGLAN	46	FUSASP	26	NEG	2	11	57	299	2.1	0.20	0.655
PENIGLAN	46	GEOMPANN	27	NEG	0	13	12	344	0.4	2.16	0.142
PENIGLAN	46	MUCOPLUM	28	NEG	1	12	72	284	2.6	2.16	0.142
PENIGLAN	46	MUCORACE	29	NEG	0	13	91	265	3.2	5.89	0.015
PENIGLAN	46	PAECOSP	30	NEG	0	13	8	348	0.3	2.30	0.129
PENIGLAN	46	PAECVARI	31	POS	5	8	45	311	1.8	5.10	0.024
PENIGLAN	46	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
PENIGLAN	46	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
PENIGLAN	46	PENIBREV	34	NEG	3	10	83	273	3.0	0.13	0.718
PENIGLAN	46	PENICHRY	35	NEG	6	7	185	171	6.7	0.48	0.488
PENIGLAN	46	PENICOMM	36	POS	4	9	90	266	3.3	0.01	0.920
PENIGLAN	46	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	PENICORY	38	POS	6	7	102	254	3.8	1.11	0.292
PENIGLAN	46	PENICRUS	39	POS	1	12	13	343	0.5	0.00	1.000
PENIGLAN	46	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
PENIGLAN	46	PENICTRM	41	POS	3	10	49	307	1.8	0.29	0.590
PENIGLAN	46	PENIDECU	42	POS	2	11	17	339	0.7	1.13	0.288
PENIGLAN	46	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
PENIGLAN	46	PENIECHI	44	POS	1	12	16	340	0.6	0.02	0.888
PENIGLAN	46	PENIEXPA	45	NEG	0	13	69	287	2.4	4.51	0.034
PENIGRIS	47	ACRESP	1	POS	2	21	23	323	1.6	0.00	1.000
PENIGRIS	47	ALTEALTE	2	POS	22	1	305	41	20.4	0.57	0.450
PENIGRIS	47	ALTESP	3	NEG	0	23	16	330	1.0	2.51	0.113
PENIGRIS	47	ASPECAND	4	NEG	0	23	19	327	1.2	2.69	0.101
PENIGRIS	47	ASPEFUMI	5	NEG	0	23	25	321	1.6	3.11	0.078
PENIGRIS	47	ASPEGLAU	6	POS	2	21	23	323	1.6	0.00	1.000
PENIGRIS	47	ASPENIGE	7	NEG	7	16	119	227	7.9	0.38	0.538
PENIGRIS	47	ASPEOCHR	8	NEG	3	20	69	277	4.5	1.17	0.279
PENIGRIS	47	ASPEORYZ	9	NEG	0	23	9	337	0.6	2.19	0.139
PENIGRIS	47	ASPESP	10	POS	6	17	61	285	4.2	0.55	0.458
PENIGRIS	47	ASPESYDO	11	POS	4	19	42	304	2.9	0.17	0.680
PENIGRIS	47	ASPEUSTU	12	NEG	1	22	23	323	1.5	0.76	0.383
PENIGRIS	47	ASPEVERS	13	NEG	12	11	184	162	12.2	0.10	0.752
PENIGRIS	47	AUREPULL	14	POS	20	3	273	73	18.3	0.43	0.512
PENIGRIS	47	CHAEGLOB	15	NEG	0	23	24	322	1.5	3.04	0.081
PENIGRIS	47	CHRSPMSP	16	POS	1	22	13	333	0.9	0.18	0.671
PENIGRIS	47	CLADCLAD	17	NEG	10	13	175	171	11.5	0.77	0.380
PENIGRIS	47	CLADHERB	18	POS	11	12	76	270	5.4	6.63	0.010
PENIGRIS	47	CLADSP	19	POS	5	18	59	287	4.0	0.08	0.777

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIGRIS	47	CLADSPHA	20	POS	9	14	132	214	8.8	0.02	0.888
PENIGRIS	47	CONISP	21	POS	1	22	9	337	0.6	0.03	0.862
PENIGRIS	47	EMERNIDU	22	POS	2	21	8	338	0.6	1.35	0.245
PENIGRIS	47	EPICNIGR	23	POS	16	7	184	162	12.5	1.72	0.190
PENIGRIS	47	EUROHERB	24	POS	18	5	227	119	15.3	1.03	0.310
PENIGRIS	47	FUSAOXYS	25	POS	3	20	17	329	1.3	1.42	0.233
PENIGRIS	47	FUSASP	26	POS	8	15	51	295	3.7	5.04	0.025
PENIGRIS	47	GEOMPANN	27	POS	1	22	11	335	0.8	0.09	0.764
PENIGRIS	47	MUCOPLUM	28	POS	5	18	68	278	4.6	0.00	1.000
PENIGRIS	47	MUCORACE	29	NEG	5	18	86	260	5.7	0.34	0.560
PENIGRIS	47	PAECSP	30	NEG	0	23	8	338	0.5	2.18	0.140
PENIGRIS	47	PAECVARI	31	POS	4	19	46	300	3.1	0.06	0.806
PENIGRIS	47	PENIATRA	32	NEG	0	23	9	337	0.6	2.19	0.139
PENIGRIS	47	PENIAURA	33	NEG	0	23	44	302	2.7	4.64	0.031
PENIGRIS	47	PENIBREV	34	NEG	3	20	83	263	5.4	2.12	0.145
PENIGRIS	47	PENICHRYS	35	POS	12	11	179	167	11.9	0.03	0.862
PENIGRIS	47	PENICOMM	36	NEG	2	21	92	254	5.9	4.64	0.031
PENIGRIS	47	PENICOPR	37	NEG	0	23	10	336	0.6	2.22	0.136
PENIGRIS	47	PENICORY	38	NEG	6	17	102	244	6.7	0.34	0.560
PENIGRIS	47	PENICRUS	39	POS	3	20	11	335	0.9	3.36	0.067
PENIGRIS	47	PENICTNG	40	NEG	0	23	34	312	2.1	3.80	0.051
PENIGRIS	47	PENICTRM	41	NEG	3	20	49	297	3.2	0.21	0.647
PENIGRIS	47	PENIDECU	42	POS	2	21	17	329	1.2	0.09	0.764
PENIGRIS	47	PENIDIGI	43	NEG	0	23	10	336	0.6	2.22	0.136
PENIGRIS	47	PENIECHI	44	NEG	1	22	16	330	1.1	0.33	0.566
PENIGRIS	47	PENIEXPA	45	NEG	2	21	67	279	4.3	2.39	0.122
PENIGRIS	47	PENIGLAN	46	POS	2	21	11	335	0.8	0.65	0.420
PENIIMPL	48	ACRESP	1	POS	3	16	22	328	1.3	1.29	0.256
PENIIMPL	48	ALTEALTE	2	NEG	15	4	312	38	16.8	3.01	0.083
PENIIMPL	48	ALTESP	3	NEG	0	19	16	334	0.8	2.34	0.126
PENIIMPL	48	ASPECAND	4	POS	2	17	17	333	1.0	0.31	0.578
PENIIMPL	48	ASPEFUMI	5	NEG	1	18	24	326	1.3	0.54	0.462
PENIIMPL	48	ASPEGLAU	6	POS	3	16	22	328	1.3	1.29	0.256
PENIIMPL	48	ASPENIGE	7	POS	7	12	119	231	6.5	0.00	1.000
PENIIMPL	48	ASPEOCHR	8	POS	5	14	67	283	3.7	0.22	0.639
PENIIMPL	48	ASPEORYZ	9	POS	1	18	8	342	0.5	0.00	1.000
PENIIMPL	48	ASPESP	10	POS	5	14	62	288	3.5	0.41	0.522
PENIIMPL	48	ASPESYDO	11	NEG	2	17	44	306	2.4	0.38	0.538
PENIIMPL	48	ASPEUSTU	12	POS	2	17	22	328	1.2	0.06	0.806
PENIIMPL	48	ASPEVERS	13	NEG	10	9	186	164	10.1	0.08	0.777
PENIIMPL	48	AUREPULL	14	NEG	13	6	280	70	15.1	2.27	0.132
PENIIMPL	48	CHAEGLOB	15	NEG	1	18	23	327	1.2	0.49	0.484
PENIIMPL	48	CHRSPMSP	16	POS	1	18	13	337	0.7	0.07	0.791
PENIIMPL	48	CLADCLAD	17	POS	12	7	173	177	9.5	0.87	0.351
PENIIMPL	48	CLADHERB	18	POS	5	14	82	268	4.5	0.00	1.000
PENIIMPL	48	CLADSP	19	POS	4	15	60	290	3.3	0.02	0.888
PENIIMPL	48	CLADSPHA	20	NEG	6	13	135	215	7.3	0.73	0.393
PENIIMPL	48	CONISP	21	NEG	0	19	10	340	0.5	2.17	0.141
PENIIMPL	48	EMERNIDU	22	NEG	0	19	10	340	0.5	2.17	0.141
PENIIMPL	48	EPICNIGR	23	NEG	8	11	192	158	10.3	1.75	0.186
PENIIMPL	48	EUROHERB	24	NEG	12	7	233	117	12.6	0.31	0.578
PENIIMPL	48	FUSAOXYS	25	NEG	1	18	19	331	1.0	0.30	0.584
PENIIMPL	48	FUSASP	26	POS	6	13	53	297	3.0	2.50	0.114
PENIIMPL	48	GEOMPANN	27	POS	1	18	11	339	0.6	0.02	0.888
PENIIMPL	48	MUCOPLUM	28	NEG	3	16	70	280	3.8	0.55	0.458
PENIIMPL	48	MUCORACE	29	NEG	3	16	88	262	4.7	1.43	0.232
PENIIMPL	48	PAECSP	30	POS	2	17	6	344	0.4	3.10	0.078
PENIIMPL	48	PAECVARI	31	POS	3	16	47	303	2.6	0.00	1.000
PENIIMPL	48	PENIATRA	32	POS	1	18	8	342	0.5	0.00	1.000
PENIIMPL	48	PENIAURA	33	POS	3	16	41	309	2.3	0.03	0.862
PENIIMPL	48	PENIBREV	34	NEG	4	15	82	268	4.4	0.27	0.603
PENIIMPL	48	PENICHRYS	35	POS	11	8	180	170	9.8	0.10	0.752

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIIMPL	48	PENICOMM	36	NEG	4	15	90	260	4.8	0.52	0.471
PENIIMPL	48	PENICOPR	37	POS	1	18	9	341	0.5	0.00	1.000
PENIIMPL	48	PENICORY	38	POS	7	12	101	249	5.6	0.24	0.624
PENIIMPL	48	PENICRUS	39	NEG	0	19	14	336	0.7	2.27	0.132
PENIIMPL	48	PENICTNG	40	POS	3	16	31	319	1.8	0.37	0.543
PENIIMPL	48	PENICTRM	41	NEG	2	17	50	300	2.7	0.64	0.424
PENIIMPL	48	PENIDECU	42	POS	2	17	17	333	1.0	0.31	0.578
PENIIMPL	48	PENIDIGI	43	POS	1	18	9	341	0.5	0.00	1.000
PENIIMPL	48	PENIECHI	44	POS	3	16	14	336	0.9	3.33	0.068
PENIIMPL	48	PENIEXPA	45	NEG	3	16	66	284	3.6	0.40	0.527
PENIIMPL	48	PENIGLAN	46	POS	3	16	10	340	0.7	5.47	0.019
PENIIMPL	48	PENIGRIS	47	NEG	1	18	22	328	1.2	0.44	0.507
PENIISLA	49	ACRESP	1	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ALTEALTE	2	POS	11	0	316	42	9.8	0.53	0.467
PENIISLA	49	ALTESP	3	NEG	0	11	16	342	0.5	2.16	0.142
PENIISLA	49	ASPECAND	4	POS	1	10	18	340	0.6	0.01	0.920
PENIISLA	49	ASPEFUMI	5	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ASPEGLAU	6	NEG	0	11	25	333	0.8	2.30	0.129
PENIISLA	49	ASPENIGE	7	NEG	3	8	123	235	3.8	0.66	0.417
PENIISLA	49	ASPEOCHR	8	POS	3	8	69	289	2.2	0.07	0.791
PENIISLA	49	ASPEORYZ	9	POS	1	10	8	350	0.3	0.21	0.647
PENIISLA	49	ASPESP	10	NEG	0	11	67	291	2.0	3.93	0.047
PENIISLA	49	ASPESYDO	11	NEG	0	11	46	312	1.4	3.01	0.083
PENIISLA	49	ASPEUSTU	12	NEG	0	11	24	334	0.7	2.28	0.131
PENIISLA	49	ASPEVERS	13	NEG	5	6	191	167	5.8	0.68	0.410
PENIISLA	49	AUREPULL	14	POS	9	2	284	74	8.7	0.03	0.862
PENIISLA	49	CHAEGLOB	15	NEG	0	11	24	334	0.7	2.28	0.131
PENIISLA	49	CHRSPMSP	16	POS	1	10	13	345	0.4	0.02	0.888
PENIISLA	49	CLADCLAD	17	POS	7	4	178	180	5.5	0.36	0.549
PENIISLA	49	CLADHERB	18	POS	4	7	83	275	2.6	0.43	0.512
PENIISLA	49	CLADSP	19	POS	2	9	62	296	1.9	0.11	0.740
PENIISLA	49	CLADSPHA	20	POS	6	5	135	223	4.2	0.67	0.413
PENIISLA	49	CONISP	21	POS	1	10	9	349	0.3	0.14	0.708
PENIISLA	49	EMERNIDU	22	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	EPICNIGR	23	POS	7	4	193	165	6.0	0.11	0.740
PENIISLA	49	EUROHERB	24	POS	8	3	237	121	7.3	0.02	0.888
PENIISLA	49	FUSAOXYS	25	NEG	0	11	20	338	0.6	2.20	0.138
PENIISLA	49	FUSASP	26	NEG	0	11	59	299	1.8	3.56	0.059
PENIISLA	49	GEOMPAN	27	NEG	0	11	12	346	0.4	2.19	0.139
PENIISLA	49	MUCOPLUM	28	NEG	2	9	71	287	2.2	0.27	0.603
PENIISLA	49	MUCORACE	29	POS	4	7	87	271	2.7	0.31	0.578
PENIISLA	49	PAECSP	30	NEG	0	11	8	350	0.2	2.41	0.121
PENIISLA	49	PAECVARI	31	POS	2	9	48	310	1.5	0.00	1.000
PENIISLA	49	PENIATRA	32	NEG	0	11	9	349	0.3	2.32	0.128
PENIISLA	49	PENIAURA	33	NEG	0	11	44	314	1.3	2.93	0.087
PENIISLA	49	PENIBREV	34	POS	3	8	83	275	2.6	0.00	1.000
PENIISLA	49	PENICHRY	35	POS	8	3	183	175	5.7	1.22	0.269
PENIISLA	49	PENICOMM	36	NEG	1	10	93	265	2.8	2.62	0.106
PENIISLA	49	PENICOPR	37	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	PENICORY	38	NEG	3	8	105	253	3.2	0.23	0.632
PENIISLA	49	PENICRUS	39	NEG	0	11	14	344	0.4	2.16	0.142
PENIISLA	49	PENICTNG	40	NEG	1	10	33	325	1.0	0.30	0.584
PENIISLA	49	PENICTRM	41	POS	3	8	49	309	1.6	0.70	0.403
PENIISLA	49	PENIDECU	42	NEG	0	11	19	339	0.6	2.18	0.140
PENIISLA	49	PENIDIGI	43	NEG	0	11	10	348	0.3	2.26	0.133
PENIISLA	49	PENIECHI	44	NEG	0	11	17	341	0.5	2.16	0.142
PENIISLA	49	PENIEXPA	45	NEG	0	11	69	289	2.1	4.03	0.045
PENIISLA	49	PENIGLAN	46	POS	1	10	12	346	0.4	0.03	0.862
PENIISLA	49	PENIGRIS	47	NEG	0	11	23	335	0.7	2.25	0.134
PENIISLA	49	PENIIMPL	48	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	ACRESP	1	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ALTEALTE	2	POS	10	1	317	41	9.8	0.06	0.806

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIITAL	50	ALTESP	3	NEG	0	11	16	342	0.5	2.16	0.142
PENIITAL	50	ASPECAND	4	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	ASPEFUMI	5	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ASPEGLAU	6	NEG	0	11	25	333	0.8	2.30	0.129
PENIITAL	50	ASPENIGE	7	POS	6	5	120	238	3.8	1.27	0.260
PENIITAL	50	ASPEOCHR	8	NEG	2	9	70	288	2.2	0.25	0.617
PENIITAL	50	ASPEORYZ	9	NEG	0	11	9	349	0.3	2.32	0.128
PENIITAL	50	ASPESP	10	NEG	1	10	66	292	2.0	1.41	0.235
PENIITAL	50	ASPESYDO	11	NEG	1	10	45	313	1.4	0.65	0.420
PENIITAL	50	ASPEUSTU	12	POS	1	10	23	335	0.7	0.07	0.791
PENIITAL	50	ASPEVERS	13	NEG	5	6	191	167	5.8	0.68	0.410
PENIITAL	50	AUREPULL	14	NEG	7	4	286	72	8.7	2.86	0.091
PENIITAL	50	CHAEGLOB	15	POS	1	10	23	335	0.7	0.07	0.791
PENIITAL	50	CHRSPMSP	16	NEG	0	11	14	344	0.4	2.16	0.142
PENIITAL	50	CLADCLAD	17	POS	6	5	179	179	5.5	0.00	1.000
PENIITAL	50	CLADHERB	18	POS	3	8	84	274	2.6	0.00	1.000
PENIITAL	50	CLADSP	19	NEG	1	10	63	295	1.9	1.30	0.254
PENIITAL	50	CLADSPHA	20	NEG	3	8	138	220	4.2	1.15	0.284
PENIITAL	50	CONISP	21	POS	1	10	9	349	0.3	0.14	0.708
PENIITAL	50	EMERNIDU	22	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	EPICNIGR	23	POS	6	5	194	164	6.0	0.08	0.777
PENIITAL	50	EUROHERB	24	NEG	7	4	238	120	7.3	0.27	0.603
PENIITAL	50	FUSAOXYS	25	NEG	0	11	20	338	0.6	2.20	0.138
PENIITAL	50	FUSASP	26	POS	2	9	57	301	1.8	0.05	0.823
PENIITAL	50	GEOMPANN	27	NEG	0	11	12	346	0.4	2.19	0.139
PENIITAL	50	MUCOPLUM	28	POS	3	8	70	288	2.2	0.06	0.806
PENIITAL	50	MUCORACE	29	POS	5	6	86	272	2.7	1.61	0.204
PENIITAL	50	PAECOSP	30	NEG	0	11	8	350	0.2	2.41	0.121
PENIITAL	50	PAECVARI	31	NEG	0	11	50	308	1.5	3.17	0.075
PENIITAL	50	PENIATRA	32	NEG	0	11	9	349	0.3	2.32	0.128
PENIITAL	50	PENIAURA	33	POS	2	9	42	316	1.3	0.03	0.862
PENIITAL	50	PENIBREV	34	POS	3	8	83	275	2.6	0.00	1.000
PENIITAL	50	PENICHRY	35	NEG	5	6	186	172	5.7	0.53	0.467
PENIITAL	50	PENICOMM	36	POS	3	8	91	267	2.8	0.05	0.823
PENIITAL	50	PENICOPR	37	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	PENICORY	38	NEG	2	9	106	252	3.2	1.34	0.247
PENIITAL	50	PENICRUS	39	NEG	0	11	14	344	0.4	2.16	0.142
PENIITAL	50	PENICTNG	40	NEG	1	10	33	325	1.0	0.30	0.584
PENIITAL	50	PENICTRM	41	NEG	1	10	51	307	1.6	0.85	0.357
PENIITAL	50	PENIDECU	42	NEG	0	11	19	339	0.6	2.18	0.140
PENIITAL	50	PENIDIGI	43	NEG	0	11	10	348	0.3	2.26	0.133
PENIITAL	50	PENIECHI	44	POS	1	10	16	342	0.5	0.00	1.000
PENIITAL	50	PENIEXPA	45	POS	4	7	65	293	2.1	1.28	0.258
PENIITAL	50	PENIGLAN	46	NEG	0	11	13	345	0.4	2.17	0.141
PENIITAL	50	PENIGRIS	47	POS	1	10	22	336	0.7	0.06	0.806
PENIITAL	50	PENIIMPL	48	POS	1	10	18	340	0.6	0.01	0.920
PENIITAL	50	PENIISLA	49	NEG	0	11	11	347	0.3	2.22	0.136
PENIMICZ	51	ACRESP	1	POS	2	12	23	332	1.0	0.36	0.549
PENIMICZ	51	ALTEALTE	2	POS	13	1	314	41	12.4	0.01	0.920
PENIMICZ	51	ALTESP	3	NEG	0	14	16	339	0.6	2.19	0.139
PENIMICZ	51	ASPECAND	4	POS	1	13	18	337	0.7	0.07	0.791
PENIMICZ	51	ASPEFUMI	5	POS	1	13	24	331	1.0	0.24	0.624
PENIMICZ	51	ASPEGLAU	6	NEG	0	14	25	330	1.0	2.47	0.116
PENIMICZ	51	ASPENIGE	7	POS	7	7	119	236	4.8	0.98	0.322
PENIMICZ	51	ASPEOCHR	8	NEG	1	13	71	284	2.7	2.35	0.125
PENIMICZ	51	ASPEORYZ	9	POS	1	13	8	347	0.3	0.08	0.777
PENIMICZ	51	ASPESP	10	POS	4	10	63	292	2.5	0.46	0.498
PENIMICZ	51	ASPESYDO	11	POS	2	12	44	311	1.8	0.04	0.841
PENIMICZ	51	ASPEUSTU	12	POS	1	13	23	332	0.9	0.21	0.647
PENIMICZ	51	ASPEVERS	13	POS	8	6	188	167	7.4	0.00	1.000
PENIMICZ	51	AUREPULL	14	POS	12	2	281	74	11.1	0.07	0.791
PENIMICZ	51	CHAEGLOB	15	NEG	0	14	24	331	0.9	2.43	0.119

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIMICZ	51	CHRSPMSP	16	POS	2	12	12	343	0.5	1.91	0.167
PENIMICZ	51	CLADCLAD	17	NEG	7	7	178	177	7.0	0.08	0.777
PENIMICZ	51	CLADHERB	18	NEG	3	11	84	271	3.3	0.26	0.610
PENIMICZ	51	CLADSP	19	NEG	1	13	63	292	2.4	1.93	0.165
PENIMICZ	51	CLADSPHA	20	POS	8	6	133	222	5.4	1.45	0.229
PENIMICZ	51	CONISP	21	POS	1	13	9	346	0.4	0.04	0.841
PENIMICZ	51	EMERNIDU	22	NEG	0	14	10	345	0.4	2.18	0.140
PENIMICZ	51	EPICNIGR	23	POS	9	5	191	164	7.6	0.25	0.617
PENIMICZ	51	EUROHERB	24	POS	10	4	235	120	9.3	0.01	0.920
PENIMICZ	51	FUSAOXYS	25	NEG	0	14	20	335	0.8	2.30	0.129
PENIMICZ	51	FUSASP	26	POS	4	10	55	300	2.2	0.88	0.348
PENIMICZ	51	GEOMPANN	27	POS	2	12	10	345	0.5	2.58	0.108
PENIMICZ	51	MUCOPLUM	28	NEG	1	13	72	283	2.8	2.41	0.121
PENIMICZ	51	MUCORACE	29	POS	4	10	87	268	3.5	0.00	1.000
PENIMICZ	51	PAECSP	30	POS	2	12	6	349	0.3	5.01	0.025
PENIMICZ	51	PAECVARI	31	NEG	1	13	49	306	1.9	1.24	0.265
PENIMICZ	51	PENIATRA	32	POS	1	13	8	347	0.3	0.08	0.777
PENIMICZ	51	PENIAURA	33	POS	4	10	40	315	1.7	2.37	0.124
PENIMICZ	51	PENIBREV	34	POS	5	9	81	274	3.3	0.64	0.424
PENIMICZ	51	PENICHRY	35	NEG	6	8	185	170	7.3	0.91	0.340
PENIMICZ	51	PENICOMM	36	POS	5	9	89	266	3.6	0.34	0.560
PENIMICZ	51	PENICOPR	37	POS	2	12	8	347	0.4	3.54	0.060
PENIMICZ	51	PENICORY	38	NEG	4	10	104	251	4.1	0.13	0.718
PENIMICZ	51	PENICRUS	39	NEG	0	14	14	341	0.5	2.16	0.142
PENIMICZ	51	PENICTNG	40	POS	3	11	31	324	1.3	1.30	0.254
PENIMICZ	51	PENICTRM	41	POS	3	11	49	306	2.0	0.17	0.680
PENIMICZ	51	PENIDECU	42	POS	1	13	18	337	0.7	0.07	0.791
PENIMICZ	51	PENIDIGI	43	NEG	0	14	10	345	0.4	2.18	0.140
PENIMICZ	51	PENIECHI	44	NEG	0	14	17	338	0.6	2.21	0.137
PENIMICZ	51	PENIEXPA	45	POS	3	11	66	289	2.6	0.01	0.920
PENIMICZ	51	PENIGLAN	46	POS	1	13	12	343	0.5	0.00	1.000
PENIMICZ	51	PENIGRIS	47	NEG	0	14	23	332	0.9	2.39	0.122
PENIMICZ	51	PENIIMPL	48	POS	3	11	16	339	0.7	4.81	0.028
PENIMICZ	51	PENIISLA	49	POS	1	13	10	345	0.4	0.02	0.888
PENIMICZ	51	PENIITAL	50	NEG	0	14	11	344	0.4	2.16	0.142
PENIOXAL	52	ACRESP	1	NEG	0	21	25	323	1.4	2.96	0.085
PENIOXAL	52	ALTEALTE	2	POS	20	1	307	41	18.6	0.40	0.527
PENIOXAL	52	ALTESP	3	NEG	0	21	16	332	0.9	2.42	0.120
PENIOXAL	52	ASPECAND	4	NEG	1	20	18	330	1.1	0.35	0.554
PENIOXAL	52	ASPEFUMI	5	POS	3	18	22	326	1.4	0.93	0.335
PENIOXAL	52	ASPEGLAU	6	POS	2	19	23	325	1.4	0.00	1.000
PENIOXAL	52	ASPENIGE	7	POS	8	13	118	230	7.2	0.02	0.888
PENIOXAL	52	ASPEOCHR	8	POS	5	16	67	281	4.1	0.05	0.823
PENIOXAL	52	ASPEORYZ	9	NEG	0	21	9	339	0.5	2.17	0.141
PENIOXAL	52	ASPESP	10	NEG	2	19	65	283	3.8	1.82	0.177
PENIOXAL	52	ASPESYDO	11	POS	5	16	41	307	2.6	1.64	0.200
PENIOXAL	52	ASPEUSTU	12	POS	2	19	22	326	1.4	0.01	0.920
PENIOXAL	52	ASPEVERS	13	NEG	8	13	188	160	11.2	2.71	0.100
PENIOXAL	52	AUREPULL	14	NEG	15	6	278	70	16.7	1.46	0.227
PENIOXAL	52	CHAEGLOB	15	POS	2	19	22	326	1.4	0.01	0.920
PENIOXAL	52	CHRSPMSP	16	NEG	0	21	14	334	0.8	2.33	0.127
PENIOXAL	52	CLADCLAD	17	NEG	10	11	175	173	10.5	0.21	0.647
PENIOXAL	52	CLADHERB	18	NEG	4	17	83	265	5.0	0.59	0.442
PENIOXAL	52	CLADSP	19	NEG	3	18	61	287	3.6	0.46	0.498
PENIOXAL	52	CLADSPHA	20	NEG	8	13	133	215	8.0	0.06	0.806
PENIOXAL	52	CONISP	21	NEG	0	21	10	338	0.6	2.19	0.139
PENIOXAL	52	EMERNIDU	22	POS	2	19	8	340	0.6	1.66	0.198
PENIOXAL	52	EPICNIGR	23	POS	12	9	188	160	11.4	0.00	1.000
PENIOXAL	52	EUROHERB	24	NEG	11	10	234	114	13.9	2.68	0.102
PENIOXAL	52	FUSAOXYS	25	NEG	1	20	19	329	1.1	0.40	0.527
PENIOXAL	52	FUSASP	26	POS	4	17	55	293	3.4	0.01	0.920
PENIOXAL	52	GEOMPANN	27	NEG	0	21	12	336	0.7	2.25	0.134

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIOXAL	52	MUCOPLUM	28	NEG	4	17	69	279	4.2	0.14	0.708
PENIOXAL	52	MUCORACE	29	POS	9	12	82	266	5.2	3.00	0.083
PENIOXAL	52	PAECSP	30	NEG	0	21	8	340	0.5	2.17	0.141
PENIOXAL	52	PAECVARI	31	POS	3	18	47	301	2.9	0.05	0.823
PENIOXAL	52	PENIATRA	32	NEG	0	21	9	339	0.5	2.17	0.141
PENIOXAL	52	PENIAURA	33	NEG	2	19	42	306	2.5	0.48	0.488
PENIOXAL	52	PENIBREV	34	NEG	4	17	82	266	4.9	0.55	0.458
PENIOXAL	52	PENICHRYS	35	NEG	10	11	181	167	10.9	0.38	0.538
PENIOXAL	52	PENICOMM	36	NEG	4	17	90	258	5.4	0.91	0.340
PENIOXAL	52	PENICOPR	37	NEG	0	21	10	338	0.6	2.19	0.139
PENIOXAL	52	PENICORY	38	NEG	3	18	105	243	6.2	3.24	0.072
PENIOXAL	52	PENICRUS	39	NEG	0	21	14	334	0.8	2.33	0.127
PENIOXAL	52	PENICTNG	40	POS	3	18	31	317	1.9	0.19	0.663
PENIOXAL	52	PENICTRM	41	POS	3	18	49	299	3.0	0.09	0.764
PENIOXAL	52	PENIDECU	42	POS	2	19	17	331	1.1	0.18	0.671
PENIOXAL	52	PENIDIGI	43	POS	1	20	9	339	0.6	0.01	0.920
PENIOXAL	52	PENIECHI	44	POS	1	20	16	332	1.0	0.25	0.617
PENIOXAL	52	PENIEXPA	45	NEG	2	19	67	281	3.9	1.96	0.162
PENIOXAL	52	PENIGLAN	46	NEG	0	21	13	335	0.7	2.28	0.131
PENIOXAL	52	PENIGRIS	47	POS	2	19	21	327	1.3	0.03	0.862
PENIOXAL	52	PENIIMPL	48	NEG	1	20	18	330	1.1	0.35	0.554
PENIOXAL	52	PENIISLA	49	POS	2	19	9	339	0.6	1.33	0.249
PENIOXAL	52	PENIITAL	50	NEG	0	21	11	337	0.6	2.21	0.137
PENIOXAL	52	PENIMICZ	51	NEG	0	21	14	334	0.8	2.33	0.127
PENIPURP	53	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIPURP	53	ALTEALTE	2	POS	8	1	319	41	8.0	0.26	0.610
PENIPURP	53	ALTESP	3	NEG	0	9	16	344	0.4	2.18	0.140
PENIPURP	53	ASPECAND	4	POS	2	7	17	343	0.5	2.51	0.113
PENIPURP	53	ASPEFUMI	5	POS	3	6	22	338	0.6	6.44	0.011
PENIPURP	53	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENIPURP	53	ASPENIGE	7	POS	4	5	122	238	3.1	0.09	0.764
PENIPURP	53	ASPEOCHR	8	POS	3	6	69	291	1.8	0.40	0.527
PENIPURP	53	ASPEORYZ	9	NEG	0	9	9	351	0.2	2.48	0.115
PENIPURP	53	ASPEP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENIPURP	53	ASPESYDO	11	NEG	0	9	46	314	1.1	2.75	0.097
PENIPURP	53	ASPEUSTU	12	NEG	0	9	24	336	0.6	2.21	0.137
PENIPURP	53	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIPURP	53	AUREPULL	14	POS	8	1	285	75	7.2	0.09	0.764
PENIPURP	53	CHAEGLOB	15	NEG	0	9	24	336	0.6	2.21	0.137
PENIPURP	53	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	CLADCLAD	17	POS	7	2	178	182	4.5	1.80	0.180
PENIPURP	53	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIPURP	53	CLADSP	19	POS	2	7	62	298	1.6	0.00	1.000
PENIPURP	53	CLADSPHA	20	POS	4	5	137	223	3.4	0.00	1.000
PENIPURP	53	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIPURP	53	EUROHERB	24	POS	8	1	237	123	6.0	1.19	0.275
PENIPURP	53	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENIPURP	53	FUSASP	26	NEG	0	9	59	301	1.4	3.19	0.074
PENIPURP	53	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIPURP	53	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENIPURP	53	MUCORACE	29	NEG	1	8	90	270	2.2	1.81	0.179
PENIPURP	53	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIPURP	53	PAECVARI	31	POS	3	6	47	313	1.2	1.59	0.207
PENIPURP	53	PENIATRA	32	NEG	0	9	9	351	0.2	2.48	0.115
PENIPURP	53	PENIAURA	33	POS	2	7	42	318	1.1	0.20	0.655
PENIPURP	53	PENIBREV	34	POS	4	5	82	278	2.1	1.25	0.264
PENIPURP	53	PENICHRYS	35	POS	6	3	185	175	4.7	0.32	0.572
PENIPURP	53	PENICOMM	36	NEG	2	7	92	268	2.3	0.38	0.538
PENIPURP	53	PENICOPR	37	POS	1	8	9	351	0.2	0.28	0.597
PENIPURP	53	PENICORY	38	POS	4	5	104	256	2.6	0.41	0.522

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIPURP	53	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	PENICTNG	40	NEG	0	9	34	326	0.8	2.41	0.121
PENIPURP	53	PENICTRM	41	POS	4	5	48	312	1.3	4.69	0.030
PENIPURP	53	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIPURP	53	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIPURP	53	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIPURP	53	PENIEXPA	45	POS	2	7	67	293	1.7	0.03	0.862
PENIPURP	53	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIPURP	53	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIPURP	53	PENIIMPL	48	NEG	0	9	19	341	0.5	2.16	0.142
PENIPURP	53	PENIISLA	49	NEG	0	9	11	349	0.3	2.32	0.128
PENIPURP	53	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIPURP	53	PENIMICZ	51	NEG	0	9	14	346	0.3	2.21	0.137
PENIPURP	53	PENIOXAL	52	POS	1	8	20	340	0.5	0.00	1.000
PENIRAIS	54	ACRESP	1	POS	2	24	23	320	1.8	0.04	0.841
PENIRAIS	54	ALTEALTE	2	POS	24	2	303	40	23.0	0.09	0.764
PENIRAIS	54	ALTESP	3	NEG	1	25	15	328	1.1	0.39	0.532
PENIRAIS	54	ASPECAND	4	NEG	0	26	19	324	1.3	2.86	0.091
PENIRAIS	54	ASPEFUMI	5	NEG	0	26	25	318	1.8	3.35	0.067
PENIRAIS	54	ASPEGLAU	6	NEG	1	25	24	319	1.8	1.04	0.308
PENIRAIS	54	ASPENIGE	7	POS	9	17	117	226	8.9	0.03	0.862
PENIRAIS	54	ASPEOCHR	8	POS	10	16	62	281	5.1	5.16	0.023
PENIRAIS	54	ASPEORYZ	9	NEG	0	26	9	334	0.6	2.24	0.134
PENIRAIS	54	ASPESP	10	POS	5	21	62	281	4.7	0.01	0.920
PENIRAIS	54	ASPESYDO	11	NEG	3	23	43	300	3.2	0.21	0.647
PENIRAIS	54	ASPEUSTU	12	NEG	0	26	24	319	1.7	3.27	0.071
PENIRAIS	54	ASPEVERS	13	NEG	12	14	184	159	13.8	0.89	0.345
PENIRAIS	54	AUREPULL	14	POS	23	3	270	73	20.6	0.87	0.351
PENIRAIS	54	CHAEGLOB	15	POS	5	21	19	324	1.7	5.37	0.020
PENIRAIS	54	CHRSPMSP	16	POS	1	25	13	330	1.0	0.27	0.603
PENIRAIS	54	CLADCLAD	17	NEG	12	14	173	170	13.0	0.39	0.532
PENIRAIS	54	CLADHERB	18	NEG	5	21	82	261	6.1	0.61	0.435
PENIRAIS	54	CLADSP	19	NEG	3	23	61	282	4.5	1.17	0.279
PENIRAIS	54	CLADSPHA	20	POS	11	15	130	213	9.9	0.06	0.806
PENIRAIS	54	CONISP	21	NEG	0	26	10	333	0.7	2.28	0.131
PENIRAIS	54	EMERNIDU	22	POS	1	25	9	334	0.7	0.07	0.791
PENIRAIS	54	EPICNIGR	23	NEG	14	12	186	157	14.1	0.06	0.806
PENIRAIS	54	EUROHERB	24	POS	19	7	226	117	17.3	0.28	0.597
PENIRAIS	54	FUSAOXYS	25	POS	2	24	18	325	1.4	0.01	0.920
PENIRAIS	54	FUSASP	26	NEG	4	22	55	288	4.2	0.13	0.718
PENIRAIS	54	GEOMPANN	27	NEG	0	26	12	331	0.9	2.38	0.123
PENIRAIS	54	MUCOPLUM	28	POS	6	20	67	276	5.1	0.03	0.862
PENIRAIS	54	MUCORACE	29	NEG	4	22	87	256	6.4	1.89	0.169
PENIRAIS	54	PAECSP	30	POS	1	25	7	336	0.6	0.01	0.920
PENIRAIS	54	PAECVARI	31	POS	6	20	44	299	3.5	1.38	0.240
PENIRAIS	54	PENIATRA	32	POS	1	25	8	335	0.6	0.03	0.862
PENIRAIS	54	PENIAURA	33	NEG	3	23	41	302	3.1	0.14	0.708
PENIRAIS	54	PENIBREV	34	POS	8	18	78	265	6.1	0.48	0.488
PENIRAIS	54	PENICHRY	35	NEG	10	16	181	162	13.5	2.60	0.107
PENIRAIS	54	PENICOMM	36	POS	12	14	82	261	6.6	5.18	0.023
PENIRAIS	54	PENICOPR	37	POS	1	25	9	334	0.7	0.07	0.791
PENIRAIS	54	PENICORY	38	POS	11	15	97	246	7.6	1.67	0.196
PENIRAIS	54	PENICRUS	39	POS	5	21	9	334	1.0	13.99	0.000
PENIRAIS	54	PENICTNG	40	POS	4	22	30	313	2.4	0.60	0.439
PENIRAIS	54	PENICTRM	41	POS	5	21	47	296	3.7	0.24	0.624
PENIRAIS	54	PENIDECU	42	POS	4	22	15	328	1.3	3.96	0.047
PENIRAIS	54	PENIDIGI	43	NEG	0	26	10	333	0.7	2.28	0.131
PENIRAIS	54	PENIECHI	44	POS	2	24	15	328	1.2	0.09	0.764
PENIRAIS	54	PENIEXPA	45	NEG	2	24	67	276	4.9	3.08	0.079
PENIRAIS	54	PENIGLAN	46	POS	4	22	9	334	0.9	8.13	0.004
PENIRAIS	54	PENIGRIS	47	POS	2	24	21	322	1.6	0.01	0.920
PENIRAIS	54	PENIIMPL	48	NEG	1	25	18	325	1.3	0.60	0.439



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIRAIS	54	PENIISLA	49	NEG	0	26	11	332	0.8	2.33	0.127
PENIRAIS	54	PENIITAL	50	NEG	0	26	11	332	0.8	2.33	0.127
PENIRAIS	54	PENIMICZ	51	POS	1	25	13	330	1.0	0.27	0.603
PENIRAIS	54	PENIOXAL	52	NEG	0	26	21	322	1.5	3.02	0.082
PENIRAIS	54	PENIPURP	53	POS	1	25	8	335	0.6	0.03	0.862
PENIREST	55	ACRESP	1	POS	2	7	23	337	0.6	1.43	0.232
PENIREST	55	ALTEALTE	2	NEG	7	2	320	40	8.0	2.46	0.117
PENIREST	55	ALTESP	3	NEG	0	9	16	344	0.4	2.18	0.140
PENIREST	55	ASPECAND	4	POS	1	8	18	342	0.5	0.00	1.000
PENIREST	55	ASPEFUMI	5	NEG	0	9	25	335	0.6	2.22	0.136
PENIREST	55	ASPEGLAU	6	NEG	0	9	25	335	0.6	2.22	0.136
PENIREST	55	ASPENIGE	7	NEG	3	6	123	237	3.1	0.17	0.680
PENIREST	55	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIREST	55	ASPEORYZ	9	POS	1	8	8	352	0.2	0.38	0.538
PENIREST	55	ASPESP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENIREST	55	ASPESYDO	11	NEG	0	9	46	314	1.1	2.75	0.097
PENIREST	55	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIREST	55	ASPEVERS	13	POS	5	4	191	169	4.8	0.04	0.841
PENIREST	55	AUREPULL	14	NEG	6	3	287	73	7.2	1.89	0.169
PENIREST	55	CHAEGLOB	15	NEG	0	9	24	336	0.6	2.21	0.137
PENIREST	55	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIREST	55	CLADCLAD	17	POS	6	3	179	181	4.5	0.44	0.507
PENIREST	55	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIREST	55	CLADSP	19	NEG	1	8	63	297	1.6	0.89	0.345
PENIREST	55	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIREST	55	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	EPICNIGR	23	NEG	2	7	198	162	4.9	5.24	0.022
PENIREST	55	EUROHERB	24	POS	7	2	238	122	6.0	0.14	0.708
PENIREST	55	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENIREST	55	FUSASP	26	POS	2	7	57	303	1.4	0.00	1.000
PENIREST	55	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIREST	55	MUCOPLUM	28	POS	3	6	70	290	1.8	0.37	0.543
PENIREST	55	MUCORACE	29	POS	3	6	88	272	2.2	0.05	0.823
PENIREST	55	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIREST	55	PAECVARI	31	POS	2	7	48	312	1.2	0.08	0.777
PENIREST	55	PENIATRA	32	NEG	0	9	9	351	0.2	2.48	0.115
PENIREST	55	PENIAURA	33	NEG	0	9	44	316	1.1	2.68	0.102
PENIREST	55	PENIBREV	34	POS	4	5	82	278	2.1	1.25	0.264
PENIREST	55	PENICHRY	35	POS	5	4	186	174	4.7	0.01	0.920
PENIREST	55	PENICOMM	36	NEG	1	8	93	267	2.3	1.93	0.165
PENIREST	55	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	PENICORY	38	POS	4	5	104	256	2.6	0.41	0.522
PENIREST	55	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIREST	55	PENICTNG	40	POS	2	7	32	328	0.8	0.61	0.435
PENIREST	55	PENICTRM	41	POS	2	7	50	310	1.3	0.05	0.823
PENIREST	55	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIREST	55	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIREST	55	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIREST	55	PENIEXPA	45	NEG	1	8	68	292	1.7	1.05	0.306
PENIREST	55	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIREST	55	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIREST	55	PENIIMPL	48	POS	1	8	18	342	0.5	0.00	1.000
PENIREST	55	PENIISLA	49	POS	1	8	10	350	0.3	0.21	0.647
PENIREST	55	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIREST	55	PENIMICZ	51	POS	2	7	12	348	0.3	4.19	0.041
PENIREST	55	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENIREST	55	PENIPURP	53	NEG	0	9	9	351	0.2	2.48	0.115
PENIREST	55	PENIRAIS	54	NEG	0	9	26	334	0.6	2.24	0.134
PENISIMP	56	ACRESP	1	NEG	0	20	25	324	1.4	2.88	0.090
PENISIMP	56	ALTEALTE	2	POS	19	1	308	41	17.7	0.32	0.572
PENISIMP	56	ALTESP	3	POS	1	19	15	334	0.9	0.17	0.680

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISIMP	56	ASPECAND	4	NEG	1	19	18	331	1.0	0.30	0.584
PENISIMP	56	ASPEFUMI	5	NEG	1	19	24	325	1.4	0.61	0.435
PENISIMP	56	ASPEGLAU	6	POS	2	18	23	326	1.4	0.02	0.888
PENISIMP	56	ASPENIGE	7	POS	11	9	115	234	6.8	3.17	0.075
PENISIMP	56	ASPEOCHR	8	POS	5	15	67	282	3.9	0.12	0.729
PENISIMP	56	ASPEORYZ	9	POS	1	19	8	341	0.5	0.00	1.000
PENISIMP	56	ASPESP	10	POS	5	15	62	287	3.6	0.27	0.603
PENISIMP	56	ASPESYDO	11	POS	5	15	41	308	2.5	1.95	0.163
PENISIMP	56	ASPEUSTU	12	POS	3	17	21	328	1.3	1.25	0.264
PENISIMP	56	ASPEVERS	13	POS	12	8	184	165	10.6	0.16	0.689
PENISIMP	56	AUREPULL	14	NEG	13	7	280	69	15.9	3.69	0.055
PENISIMP	56	CHAEGLOB	15	NEG	1	19	23	326	1.3	0.56	0.454
PENISIMP	56	CHRSPMSP	16	POS	1	19	13	336	0.8	0.10	0.752
PENISIMP	56	CLADCLAD	17	POS	11	9	174	175	10.0	0.05	0.823
PENISIMP	56	CLADHERB	18	POS	5	15	82	267	4.7	0.01	0.920
PENISIMP	56	CLADSP	19	NEG	3	17	61	288	3.5	0.35	0.554
PENISIMP	56	CLADSPHA	20	POS	8	12	133	216	7.6	0.00	1.000
PENISIMP	56	CONISP	21	POS	1	19	9	340	0.5	0.00	1.000
PENISIMP	56	EMERNIDU	22	POS	2	18	8	341	0.5	1.84	0.175
PENISIMP	56	EPICNIGR	23	POS	11	9	189	160	10.8	0.02	0.888
PENISIMP	56	EUROHERB	24	POS	14	6	231	118	13.3	0.01	0.920
PENISIMP	56	FUSAOXYS	25	POS	2	18	18	331	1.1	0.18	0.671
PENISIMP	56	FUSASP	26	POS	4	16	55	294	3.2	0.04	0.841
PENISIMP	56	GEOMPANN	27	POS	1	19	11	338	0.7	0.04	0.841
PENISIMP	56	MUCOPLUM	28	POS	4	16	69	280	4.0	0.07	0.791
PENISIMP	56	MUCORACE	29	POS	5	15	86	263	4.9	0.05	0.823
PENISIMP	56	PAECSP	30	POS	1	19	7	342	0.4	0.01	0.920
PENISIMP	56	PAECVARI	31	POS	5	15	45	304	2.7	1.45	0.229
PENISIMP	56	PENIATRA	32	POS	2	18	7	342	0.5	2.28	0.131
PENISIMP	56	PENIAURA	33	POS	5	15	39	310	2.4	2.25	0.134
PENISIMP	56	PENIBREV	34	POS	7	13	79	270	4.7	1.00	0.317
PENISIMP	56	PENICHR	35	NEG	7	13	184	165	10.4	3.14	0.076
PENISIMP	56	PENICOMM	36	POS	9	11	85	264	5.1	3.23	0.072
PENISIMP	56	PENICOPR	37	POS	2	18	8	341	0.5	1.84	0.175
PENISIMP	56	PENICORY	38	POS	11	9	97	252	5.9	5.51	0.019
PENISIMP	56	PENICRUS	39	POS	1	19	13	336	0.8	0.10	0.752
PENISIMP	56	PENICTNG	40	NEG	1	19	33	316	1.8	1.14	0.286
PENISIMP	56	PENICTRM	41	NEG	2	18	50	299	2.8	0.76	0.383
PENISIMP	56	PENIDECU	42	NEG	0	20	19	330	1.0	2.53	0.112
PENISIMP	56	PENIDIGI	43	NEG	0	20	10	339	0.5	2.18	0.140
PENISIMP	56	PENIECHI	44	NEG	0	20	17	332	0.9	2.43	0.119
PENISIMP	56	PENIEXPA	45	POS	8	12	61	288	3.7	4.92	0.027
PENISIMP	56	PENIGLAN	46	POS	1	19	12	337	0.7	0.07	0.791
PENISIMP	56	PENIGRIS	47	POS	2	18	21	328	1.3	0.06	0.806
PENISIMP	56	PENIIMPL	48	POS	2	18	17	332	1.0	0.24	0.624
PENISIMP	56	PENIISLA	49	NEG	0	20	11	338	0.6	2.20	0.138
PENISIMP	56	PENIITAL	50	NEG	0	20	11	338	0.6	2.20	0.138
PENISIMP	56	PENIMICZ	51	POS	2	18	12	337	0.8	0.80	0.371
PENISIMP	56	PENIOXAL	52	POS	2	18	19	330	1.1	0.13	0.718
PENISIMP	56	PENIPURP	53	POS	1	19	8	341	0.5	0.00	1.000
PENISIMP	56	PENIRAIS	54	POS	3	17	23	326	1.4	0.96	0.327
PENISIMP	56	PENIREST	55	POS	1	19	8	341	0.5	0.00	1.000
PENISP	57	ACRESP	1	NEG	1	28	24	316	2.0	1.27	0.260
PENISP	57	ALTEALTE	2	POS	28	1	299	41	25.7	1.20	0.273
PENISP	57	ALTESP	3	POS	2	27	14	326	1.3	0.05	0.823
PENISP	57	ASPECAND	4	NEG	1	28	18	322	1.5	0.76	0.383
PENISP	57	ASPEFUMI	5	POS	3	26	22	318	2.0	0.17	0.680
PENISP	57	ASPEGLAU	6	NEG	2	27	23	317	2.0	0.13	0.718
PENISP	57	ASPENIGE	7	POS	15	14	111	229	9.9	3.52	0.061
PENISP	57	ASPEOCHR	8	POS	6	23	66	274	5.7	0.01	0.920
PENISP	57	ASPEORYZ	9	NEG	0	29	9	331	0.7	2.29	0.130
PENISP	57	ASPESP	10	POS	8	21	59	281	5.3	1.26	0.262

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISP	57	ASPESYDO	11	POS	5	24	41	299	3.6	0.27	0.603
PENISP	57	ASPEUSTU	12	POS	2	27	22	318	1.9	0.09	0.764
PENISP	57	ASPEVERS	13	POS	18	11	178	162	15.4	0.66	0.417
PENISP	57	AUREPULL	14	POS	24	5	269	71	23.0	0.05	0.823
PENISP	57	CHAEGLOB	15	POS	2	27	22	318	1.9	0.09	0.764
PENISP	57	CHRSPMSP	16	POS	2	27	12	328	1.1	0.16	0.689
PENISP	57	CLADCLAD	17	POS	15	14	170	170	14.5	0.00	1.000
PENISP	57	CLADHERB	18	NEG	6	23	81	259	6.8	0.37	0.543
PENISP	57	CLADSP	19	POS	7	22	57	283	5.0	0.56	0.454
PENISP	57	CLADSPHA	20	NEG	8	21	133	207	11.1	2.03	0.154
PENISP	57	CONISP	21	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	EMERNIDU	22	POS	2	27	8	332	0.8	0.72	0.396
PENISP	57	EPICNIGR	23	NEG	14	15	186	154	16.0	0.74	0.390
PENISP	57	EUROHERB	24	NEG	18	11	227	113	19.3	0.52	0.471
PENISP	57	FUSAOXYS	25	POS	4	25	16	324	1.6	2.71	0.100
PENISP	57	FUSASP	26	NEG	0	29	59	281	4.6	7.35	0.007
PENISP	57	GEOMPANN	27	NEG	0	29	12	328	0.9	2.48	0.115
PENISP	57	MUCOPLUM	28	POS	9	20	64	276	5.7	1.80	0.180
PENISP	57	MUCORACE	29	POS	9	20	82	258	7.2	0.37	0.543
PENISP	57	PAECSP	30	POS	1	28	7	333	0.6	0.03	0.862
PENISP	57	PAECVARI	31	POS	4	25	46	294	3.9	0.06	0.806
PENISP	57	PENIATRA	32	POS	1	28	8	332	0.7	0.07	0.791
PENISP	57	PENIAURA	33	POS	7	22	37	303	3.5	3.30	0.069
PENISP	57	PENIBREV	34	POS	10	19	76	264	6.8	1.57	0.210
PENISP	57	PENICHR	35	NEG	14	15	177	163	15.0	0.34	0.560
PENISP	57	PENICOMM	36	POS	13	16	81	259	7.4	5.15	0.023
PENISP	57	PENICOPR	37	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	PENICORY	38	POS	9	20	99	241	8.5	0.00	1.000
PENISP	57	PENICRUS	39	POS	2	27	12	328	1.1	0.16	0.689
PENISP	57	PENICTNG	40	POS	3	26	31	309	2.7	0.01	0.920
PENISP	57	PENICTRM	41	POS	5	24	47	293	4.1	0.05	0.823
PENISP	57	PENIDECU	42	NEG	1	28	18	322	1.5	0.76	0.383
PENISP	57	PENIDIGI	43	NEG	0	29	10	330	0.8	2.35	0.125
PENISP	57	PENIECHI	44	POS	2	27	15	325	1.3	0.02	0.888
PENISP	57	PENIEXPA	45	POS	7	22	62	278	5.4	0.29	0.590
PENISP	57	PENIGLAN	46	NEG	0	29	13	327	1.0	2.55	0.110
PENISP	57	PENIGRIS	47	POS	4	25	19	321	1.8	1.83	0.176
PENISP	57	PENIIMPL	48	POS	2	27	17	323	1.5	0.00	1.000
PENISP	57	PENIISLA	49	NEG	0	29	11	329	0.9	2.41	0.121
PENISP	57	PENIITAL	50	NEG	0	29	11	329	0.9	2.41	0.121
PENISP	57	PENIMICZ	51	NEG	0	29	14	326	1.1	2.63	0.105
PENISP	57	PENIOXAL	52	POS	2	27	19	321	1.7	0.02	0.888
PENISP	57	PENIPURP	53	POS	4	25	5	335	0.7	12.27	0.000
PENISP	57	PENIRAIS	54	POS	4	25	22	318	2.0	1.21	0.271
PENISP	57	PENIREST	55	POS	1	28	8	332	0.7	0.07	0.791
PENISP	57	PENISIMP	56	POS	3	26	17	323	1.6	0.63	0.427
PENISP01	58	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENISP01	58	ALTEALTE	2	NEG	7	2	320	40	8.0	2.46	0.117
PENISP01	58	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
PENISP01	58	ASPECAND	4	POS	2	7	17	343	0.5	2.51	0.113
PENISP01	58	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENISP01	58	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENISP01	58	ASPENIGE	7	POS	6	3	120	240	3.1	2.98	0.084
PENISP01	58	ASPEOCHR	8	NEG	1	8	71	289	1.8	1.14	0.286
PENISP01	58	ASPEORYZ	9	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	ASPESP	10	NEG	1	8	66	294	1.6	0.99	0.320
PENISP01	58	ASPESYDO	11	POS	2	7	44	316	1.1	0.15	0.699
PENISP01	58	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENISP01	58	ASPEVERS	13	POS	7	2	189	171	4.8	1.35	0.245
PENISP01	58	AUREPULL	14	NEG	5	4	288	72	7.2	4.88	0.027
PENISP01	58	CHAEGLOB	15	POS	3	6	21	339	0.6	6.87	0.009
PENISP01	58	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISP01	58	CLADCLAD	17	NEG	3	6	182	178	4.5	1.84	0.175
PENISP01	58	CLADHERB	18	NEG	1	8	86	274	2.1	1.66	0.198
PENISP01	58	CLADSP	19	POS	3	6	61	299	1.6	0.70	0.403
PENISP01	58	CLADSPHA	20	POS	4	5	137	223	3.4	0.00	1.000
PENISP01	58	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	EPICNIGR	23	POS	6	3	194	166	4.9	0.18	0.671
PENISP01	58	EUROHERB	24	POS	8	1	237	123	6.0	1.19	0.275
PENISP01	58	FUSAOXYS	25	NEG	0	9	20	340	0.5	2.17	0.141
PENISP01	58	FUSASP	26	NEG	1	8	58	302	1.4	0.75	0.386
PENISP01	58	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENISP01	58	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENISP01	58	MUCORACE	29	POS	6	3	85	275	2.2	6.60	0.010
PENISP01	58	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENISP01	58	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480
PENISP01	58	PENIATRA	32	POS	1	8	8	352	0.2	0.38	0.538
PENISP01	58	PENIAURA	33	POS	4	5	40	320	1.1	6.39	0.011
PENISP01	58	PENIBREV	34	NEG	1	8	85	275	2.1	1.63	0.202
PENISP01	58	PENICHRY	35	POS	6	3	185	175	4.7	0.32	0.572
PENISP01	58	PENICOMM	36	POS	3	6	91	269	2.3	0.03	0.862
PENISP01	58	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	PENICORY	38	POS	6	3	102	258	2.6	4.52	0.034
PENISP01	58	PENICRUS	39	POS	2	7	12	348	0.3	4.19	0.041
PENISP01	58	PENICTNG	40	NEG	0	9	34	326	0.8	2.41	0.121
PENISP01	58	PENICTRM	41	POS	3	6	49	311	1.3	1.43	0.232
PENISP01	58	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENISP01	58	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENISP01	58	PENIECHI	44	POS	2	7	15	345	0.4	3.05	0.081
PENISP01	58	PENIEXPA	45	POS	7	2	62	298	1.7	17.38	0.000
PENISP01	58	PENIGLAN	46	POS	1	8	12	348	0.3	0.11	0.740
PENISP01	58	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENISP01	58	PENIIMPL	48	NEG	0	9	19	341	0.5	2.16	0.142
PENISP01	58	PENIISLA	49	NEG	0	9	11	349	0.3	2.32	0.128
PENISP01	58	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENISP01	58	PENIMICZ	51	POS	1	8	13	347	0.3	0.08	0.777
PENISP01	58	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENISP01	58	PENIPURP	53	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	PENIRAIS	54	POS	1	8	25	335	0.6	0.03	0.862
PENISP01	58	PENIREST	55	NEG	0	9	9	351	0.2	2.48	0.115
PENISP01	58	PENISIMP	56	POS	1	8	19	341	0.5	0.00	1.000
PENISP01	58	PENISP	57	NEG	0	9	29	331	0.7	2.29	0.130
PENISP26	59	ACRESP	1	POS	6	47	19	297	3.6	1.27	0.260
PENISP26	59	ALTEALTE	2	NEG	43	10	284	32	47.0	4.36	0.037
PENISP26	59	ALTESP	3	NEG	1	52	15	301	2.3	1.72	0.190
PENISP26	59	ASPECAND	4	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	ASPEFUMI	5	POS	4	49	21	295	3.6	0.00	1.000
PENISP26	59	ASPEGLAU	6	POS	7	46	18	298	3.6	2.95	0.086
PENISP26	59	ASPENIGE	7	POS	25	28	101	215	18.1	4.02	0.045
PENISP26	59	ASPEOCHR	8	NEG	10	43	62	254	10.3	0.10	0.752
PENISP26	59	ASPEORYZ	9	NEG	1	52	8	308	1.3	0.58	0.446
PENISP26	59	ASPESP	10	POS	14	39	53	263	9.6	2.23	0.135
PENISP26	59	ASPESYDO	11	POS	7	46	39	277	6.6	0.00	1.000
PENISP26	59	ASPEUSTU	12	POS	4	49	20	296	3.5	0.00	1.000
PENISP26	59	ASPEVERS	13	NEG	27	26	169	147	28.2	0.24	0.624
PENISP26	59	AUREPULL	14	POS	43	10	250	66	42.1	0.02	0.888
PENISP26	59	CHAEGLOB	15	POS	5	48	19	297	3.5	0.40	0.527
PENISP26	59	CHRSPMSP	16	POS	3	50	11	305	2.0	0.14	0.708
PENISP26	59	CLADCLAD	17	POS	28	25	157	159	26.6	0.08	0.777
PENISP26	59	CLADHERB	18	NEG	2	51	85	231	12.5	14.78	0.000
PENISP26	59	CLADSP	19	POS	13	40	51	265	9.2	1.68	0.195
PENISP26	59	CLADSPHA	20	NEG	16	37	125	191	20.3	2.11	0.146
PENISP26	59	CONISP	21	NEG	1	52	9	307	1.4	0.73	0.393

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISP26	59	EMERNIDU	22	POS	3	50	7	309	1.4	0.95	0.330
PENISP26	59	EPICNIGR	23	NEG	23	30	177	139	28.7	3.44	0.064
PENISP26	59	EUROHERB	24	POS	38	15	207	109	35.2	0.53	0.467
PENISP26	59	FUSAOXYS	25	POS	4	49	16	300	2.9	0.17	0.680
PENISP26	59	FUSASP	26	NEG	6	47	53	263	8.5	1.45	0.229
PENISP26	59	GEOMPANN	27	NEG	0	53	12	304	1.7	3.46	0.063
PENISP26	59	MUCOPLUM	28	POS	16	37	57	259	10.5	3.49	0.062
PENISP26	59	MUCORACE	29	POS	16	37	75	241	13.1	0.70	0.403
PENISP26	59	PAECSP	30	NEG	1	52	7	309	1.2	0.44	0.507
PENISP26	59	PAECVARI	31	NEG	5	48	45	271	7.2	1.35	0.245
PENISP26	59	PENIATRA	32	POS	6	47	3	313	1.3	16.39	0.000
PENISP26	59	PENIAURA	33	POS	7	46	37	279	6.3	0.01	0.920
PENISP26	59	PENIBREV	34	POS	17	36	69	247	12.4	2.12	0.145
PENISP26	59	PENICHRYS	35	POS	29	24	162	154	27.4	0.10	0.752
PENISP26	59	PENICOMM	36	POS	15	38	79	237	13.5	0.12	0.729
PENISP26	59	PENICOPR	37	POS	4	49	6	310	1.4	3.56	0.059
PENISP26	59	PENICORY	38	POS	20	33	88	228	15.5	1.69	0.194
PENISP26	59	PENICRUS	39	NEG	2	51	12	304	2.0	0.16	0.689
PENISP26	59	PENICTNG	40	POS	6	47	28	288	4.9	0.10	0.752
PENISP26	59	PENICTRM	41	POS	10	43	42	274	7.5	0.75	0.386
PENISP26	59	PENIDECU	42	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	PENIDIGI	43	NEG	0	53	10	306	1.4	3.13	0.077
PENISP26	59	PENIECHI	44	POS	5	48	12	304	2.4	2.12	0.145
PENISP26	59	PENIEXPA	45	POS	13	40	56	260	9.9	0.97	0.325
PENISP26	59	PENIGLAN	46	POS	2	51	11	305	1.9	0.09	0.764
PENISP26	59	PENIGRIS	47	POS	5	48	18	298	3.3	0.54	0.462
PENISP26	59	PENIIMPL	48	POS	4	49	15	301	2.7	0.27	0.603
PENISP26	59	PENIISLA	49	NEG	1	52	10	306	1.6	0.89	0.345
PENISP26	59	PENIITAL	50	POS	2	51	9	307	1.6	0.00	1.000
PENISP26	59	PENIMICZ	51	POS	4	49	10	306	2.0	1.34	0.247
PENISP26	59	PENIOXAL	52	POS	4	49	17	299	3.0	0.10	0.752
PENISP26	59	PENIPURP	53	POS	3	50	6	310	1.3	1.35	0.245
PENISP26	59	PENIRAIS	54	POS	4	49	22	294	3.7	0.02	0.888
PENISP26	59	PENIREST	55	POS	3	50	6	310	1.3	1.35	0.245
PENISP26	59	PENISIMP	56	POS	6	47	14	302	2.9	2.97	0.085
PENISP26	59	PENISP	57	POS	8	45	21	295	4.2	3.38	0.066
PENISP26	59	PENISP01	58	POS	2	51	7	309	1.3	0.04	0.841
PENISP64	60	ACRESP	1	NEG	0	10	25	334	0.7	2.26	0.133
PENISP64	60	ALTEALTE	2	NEG	7	3	320	39	8.9	5.68	0.017
PENISP64	60	ALTESP	3	NEG	0	10	16	343	0.4	2.16	0.142
PENISP64	60	ASPECAND	4	POS	1	9	18	341	0.5	0.00	1.000
PENISP64	60	ASPEFUMI	5	POS	1	9	24	335	0.7	0.05	0.823
PENISP64	60	ASPEGLAU	6	NEG	0	10	25	334	0.7	2.26	0.133
PENISP64	60	ASPENIGE	7	POS	6	4	120	239	3.4	1.99	0.158
PENISP64	60	ASPEOCHR	8	POS	3	7	69	290	2.0	0.20	0.655
PENISP64	60	ASPEORYZ	9	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	ASPESP	10	POS	3	7	64	295	1.8	0.32	0.572
PENISP64	60	ASPESYDO	11	NEG	1	9	45	314	1.3	0.53	0.467
PENISP64	60	ASPEUSTU	12	POS	1	9	23	336	0.7	0.04	0.841
PENISP64	60	ASPEVERS	13	NEG	3	7	193	166	5.3	3.26	0.071
PENISP64	60	AUREPULL	14	NEG	7	3	286	73	7.9	1.30	0.254
PENISP64	60	CHAEGLOB	15	POS	2	8	22	337	0.7	1.22	0.269
PENISP64	60	CHRSPMSP	16	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	CLADCLAD	17	NEG	2	8	183	176	5.0	5.08	0.024
PENISP64	60	CLADHERB	18	NEG	1	9	86	273	2.4	1.97	0.160
PENISP64	60	CLADSP	19	POS	4	6	60	299	1.7	2.24	0.134
PENISP64	60	CLADSPHA	20	NEG	3	7	138	221	3.8	0.76	0.383
PENISP64	60	CONISP	21	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	EMERNIDU	22	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	EPICNIGR	23	NEG	4	6	196	163	5.4	1.53	0.216
PENISP64	60	EUROHERB	24	NEG	5	5	240	119	6.6	2.11	0.146
PENISP64	60	FUSAOXYS	25	POS	3	7	17	342	0.5	7.69	0.006

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISP64	60	FUSASP	26	NEG	0	10	59	300	1.6	3.37	0.066
PENISP64	60	GEOMPANN	27	POS	2	8	10	349	0.3	4.51	0.034
PENISP64	60	MUCOPLUM	28	POS	2	8	71	288	2.0	0.15	0.699
PENISP64	60	MUCORACE	29	NEG	2	8	89	270	2.5	0.52	0.471
PENISP64	60	PAECSP	30	NEG	0	10	8	351	0.2	2.49	0.115
PENISP64	60	PAECVARI	31	POS	2	8	48	311	1.4	0.02	0.888
PENISP64	60	PENIATRA	32	POS	1	9	8	351	0.2	0.28	0.597
PENISP64	60	PENIAURA	33	POS	2	8	42	317	1.2	0.09	0.764
PENISP64	60	PENIBREV	34	NEG	1	9	85	274	2.3	1.93	0.165
PENISP64	60	PENICHR	35	NEG	4	6	187	172	5.2	1.16	0.281
PENISP64	60	PENICOMM	36	POS	4	6	90	269	2.6	0.49	0.484
PENISP64	60	PENICOPR	37	POS	1	9	9	350	0.3	0.20	0.655
PENISP64	60	PENICORY	38	POS	3	7	105	254	2.9	0.09	0.764
PENISP64	60	PENICRUS	39	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	PENICTNG	40	POS	2	8	32	327	0.9	0.41	0.522
PENISP64	60	PENICTRM	41	POS	3	7	49	310	1.4	1.01	0.315
PENISP64	60	PENIDECU	42	NEG	0	10	19	340	0.5	2.17	0.141
PENISP64	60	PENIDIGI	43	NEG	0	10	10	349	0.3	2.32	0.128
PENISP64	60	PENIECHI	44	POS	1	9	16	343	0.5	0.00	1.000
PENISP64	60	PENIEXPA	45	NEG	0	10	69	290	1.9	3.80	0.051
PENISP64	60	PENIGLAN	46	NEG	0	10	13	346	0.4	2.20	0.138
PENISP64	60	PENIGRIS	47	NEG	0	10	23	336	0.6	2.22	0.136
PENISP64	60	PENIIMPL	48	NEG	0	10	19	340	0.5	2.17	0.141
PENISP64	60	PENIISLA	49	NEG	0	10	11	348	0.3	2.26	0.133
PENISP64	60	PENIITAL	50	NEG	0	10	11	348	0.3	2.26	0.133
PENISP64	60	PENIMICZ	51	POS	1	9	13	346	0.4	0.04	0.841
PENISP64	60	PENIOXAL	52	POS	1	9	20	339	0.6	0.01	0.920
PENISP64	60	PENIPURP	53	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENIRAIS	54	POS	2	8	24	335	0.7	0.99	0.320
PENISP64	60	PENIREST	55	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENISIMP	56	POS	1	9	19	340	0.5	0.00	1.000
PENISP64	60	PENISP	57	POS	1	9	28	331	0.8	0.12	0.729
PENISP64	60	PENISP01	58	NEG	0	10	9	350	0.2	2.39	0.122
PENISP64	60	PENISP26	59	POS	3	7	50	309	1.4	0.95	0.330
PENISPIN	61	ACRESP	1	NEG	7	135	18	209	9.6	1.76	0.185
PENISPIN	61	ALTEALTE	2	NEG	125	17	202	25	127.8	0.20	0.655
PENISPIN	61	ALTESP	3	NEG	6	136	10	217	6.2	0.12	0.729
PENISPIN	61	ASPECAND	4	POS	9	133	10	217	7.3	0.33	0.566
PENISPIN	61	ASPEFUMI	5	POS	11	131	14	213	9.6	0.14	0.708
PENISPIN	61	ASPEGLAU	6	POS	13	129	12	215	9.6	1.50	0.221
PENISPIN	61	ASPENIGE	7	POS	63	79	63	164	48.5	10.00	0.002
PENISPIN	61	ASPEOCHR	8	POS	35	107	37	190	27.7	3.36	0.067
PENISPIN	61	ASPEORYZ	9	POS	6	136	3	224	3.5	2.00	0.157
PENISPIN	61	ASPESP	10	POS	26	116	41	186	25.8	0.01	0.920
PENISPIN	61	ASPESYDO	11	POS	25	117	21	206	17.7	4.85	0.028
PENISPIN	61	ASPEUSTU	12	POS	12	130	12	215	9.2	0.97	0.325
PENISPIN	61	ASPEVERS	13	NEG	73	69	123	104	75.4	0.39	0.532
PENISPIN	61	AUREPULL	14	POS	117	25	176	51	112.8	0.98	0.322
PENISPIN	61	CHAEGLOB	15	POS	10	132	14	213	9.2	0.01	0.920
PENISPIN	61	CHRSPMSP	16	POS	8	134	6	221	5.4	1.40	0.237
PENISPIN	61	CLADCLAD	17	POS	85	57	100	127	71.2	8.11	0.004
PENISPIN	61	CLADHERB	18	NEG	23	119	64	163	33.5	7.66	0.006
PENISPIN	61	CLADSP	19	POS	29	113	35	192	24.6	1.20	0.273
PENISPIN	61	CLADSPHA	20	POS	57	85	84	143	54.3	0.24	0.624
PENISPIN	61	CONISP	21	NEG	1	141	9	218	3.9	4.87	0.027
PENISPIN	61	EMERNIDU	22	POS	6	136	4	223	3.9	1.18	0.277
PENISPIN	61	EPICNIGR	23	NEG	72	70	128	99	77.0	1.38	0.240
PENISPIN	61	EUROHERB	24	POS	95	47	150	77	94.3	0.00	1.000
PENISPIN	61	FUSAOXYS	25	POS	11	131	9	218	7.7	1.76	0.185
PENISPIN	61	FUSASP	26	NEG	17	125	42	185	22.7	3.28	0.070
PENISPIN	61	GEOMPANN	27	POS	5	137	7	220	4.6	0.01	0.920
PENISPIN	61	MUCOPLUM	28	POS	30	112	43	184	28.1	0.14	0.708

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENISPIN	61	MUCORACE	29	POS	37	105	54	173	35.0	0.14	0.708
PENISPIN	61	PAECSP	30	NEG	2	140	6	221	3.1	1.34	0.247
PENISPIN	61	PAECVARI	31	NEG	18	124	32	195	19.3	0.30	0.584
PENISPIN	61	PENIATRA	32	POS	6	136	3	224	3.5	2.00	0.157
PENISPIN	61	PENIAURA	33	POS	22	120	22	205	16.9	2.27	0.132
PENISPIN	61	PENIBREV	34	POS	42	100	44	183	33.1	4.52	0.034
PENISPIN	61	PENICHRY	35	POS	78	64	113	114	73.5	0.73	0.393
PENISPIN	61	PENICOMM	36	POS	37	105	57	170	36.2	0.01	0.920
PENISPIN	61	PENICOPR	37	POS	7	135	3	224	3.9	3.05	0.081
PENISPIN	61	PENICORY	38	NEG	38	104	70	157	41.6	0.91	0.340
PENISPIN	61	PENICRUS	39	NEG	5	137	9	218	5.4	0.25	0.617
PENISPIN	61	PENICTNG	40	POS	16	126	18	209	13.1	0.80	0.371
PENISPIN	61	PENICTRM	41	NEG	19	123	33	194	20.0	0.22	0.639
PENISPIN	61	PENIDECU	42	NEG	6	136	13	214	7.3	0.77	0.380
PENISPIN	61	PENIDIGI	43	NEG	3	139	7	220	3.9	0.79	0.374
PENISPIN	61	PENIECHI	44	NEG	6	136	11	216	6.5	0.28	0.597
PENISPIN	61	PENIEXPA	45	POS	28	114	41	186	26.6	0.07	0.791
PENISPIN	61	PENIGLAN	46	NEG	1	141	12	215	5.0	6.83	0.009
PENISPIN	61	PENIGRIS	47	POS	10	132	13	214	8.9	0.08	0.777
PENISPIN	61	PENIIMPL	48	POS	8	134	11	216	7.3	0.01	0.920
PENISPIN	61	PENIISLA	49	NEG	4	138	7	220	4.2	0.21	0.647
PENISPIN	61	PENIITAL	50	NEG	2	140	9	218	4.2	2.96	0.085
PENISPIN	61	PENIMICZ	51	POS	7	135	7	220	5.4	0.39	0.532
PENISPIN	61	PENIOXAL	52	NEG	6	136	15	212	8.1	1.42	0.233
PENISPIN	61	PENIPURP	53	POS	4	138	5	222	3.5	0.00	1.000
PENISPIN	61	PENIRAIS	54	POS	11	131	15	212	10.0	0.04	0.841
PENISPIN	61	PENIREST	55	POS	4	138	5	222	3.5	0.00	1.000
PENISPIN	61	PENISIMP	56	POS	13	129	7	220	7.7	5.15	0.023
PENISPIN	61	PENISP	57	POS	16	126	13	214	11.2	2.98	0.084
PENISPIN	61	PENISP01	58	POS	5	137	4	223	3.5	0.52	0.471
PENISPIN	61	PENISP26	59	POS	32	110	21	206	20.4	11.48	0.001
PENISPIN	61	PENISP64	60	POS	7	135	3	224	3.9	3.05	0.081
PENIVARI	62	ACRESP	1	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ALTEALTE	2	NEG	10	2	317	40	10.6	1.10	0.294
PENIVARI	62	ALTESP	3	NEG	0	12	16	341	0.5	2.16	0.142
PENIVARI	62	ASPECAND	4	NEG	0	12	19	338	0.6	2.20	0.138
PENIVARI	62	ASPEFUMI	5	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ASPEGLAU	6	POS	1	11	24	333	0.8	0.13	0.718
PENIVARI	62	ASPENIGE	7	POS	7	5	119	238	4.1	2.21	0.137
PENIVARI	62	ASPEOCHR	8	POS	7	5	65	292	2.3	9.48	0.002
PENIVARI	62	ASPEORYZ	9	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	ASPESP	10	POS	4	8	63	294	2.2	1.01	0.315
PENIVARI	62	ASPESYDO	11	NEG	1	11	45	312	1.5	0.78	0.377
PENIVARI	62	ASPEUSTU	12	NEG	0	12	24	333	0.8	2.32	0.128
PENIVARI	62	ASPEVERS	13	POS	9	3	187	170	6.4	1.56	0.212
PENIVARI	62	AUREPULL	14	POS	10	2	283	74	9.5	0.00	1.000
PENIVARI	62	CHAEGLOB	15	POS	3	9	21	336	0.8	4.19	0.041
PENIVARI	62	CHRSPMSP	16	POS	1	11	13	344	0.5	0.00	1.000
PENIVARI	62	CLADCLAD	17	POS	9	3	176	181	6.0	2.13	0.144
PENIVARI	62	CLADHERB	18	NEG	2	10	85	272	2.8	0.84	0.359
PENIVARI	62	CLADSP	19	POS	6	6	58	299	2.1	7.02	0.008
PENIVARI	62	CLADSPHA	20	POS	9	3	132	225	4.6	5.59	0.018
PENIVARI	62	CONISP	21	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	EMERNIDU	22	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	EPICNIGR	23	POS	8	4	192	165	6.5	0.34	0.560
PENIVARI	62	EUROHERB	24	POS	11	1	234	123	8.0	2.48	0.115
PENIVARI	62	FUSAOXYS	25	POS	1	11	19	338	0.7	0.04	0.841
PENIVARI	62	FUSASP	26	NEG	1	11	58	299	1.9	1.29	0.256
PENIVARI	62	GEOMPANN	27	POS	1	11	11	346	0.4	0.03	0.862
PENIVARI	62	MUCOPLUM	28	NEG	1	11	72	285	2.4	1.91	0.167
PENIVARI	62	MUCORACE	29	NEG	2	10	89	268	3.0	0.99	0.320
PENIVARI	62	PAECSP	30	POS	1	11	7	350	0.3	0.23	0.632

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIVARI	62	PAECVARI	31	NEG	1	11	49	308	1.6	0.93	0.335
PENIVARI	62	PENIATRA	32	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	PENIAURA	33	POS	2	10	42	315	1.4	0.00	1.000
PENIVARI	62	PENIBREV	34	POS	4	8	82	275	2.8	0.24	0.624
PENIVARI	62	PENICHRV	35	NEG	4	8	187	170	6.2	2.54	0.111
PENIVARI	62	PENICOMM	36	POS	4	8	90	267	3.1	0.09	0.764
PENIVARI	62	PENICOPR	37	POS	1	11	9	348	0.3	0.10	0.752
PENIVARI	62	PENICORY	38	POS	4	8	104	253	3.5	0.00	1.000
PENIVARI	62	PENICRUS	39	POS	1	11	13	344	0.5	0.00	1.000
PENIVARI	62	PENICTNG	40	POS	2	10	32	325	1.1	0.16	0.689
PENIVARI	62	PENICTRM	41	POS	2	10	50	307	1.7	0.03	0.862
PENIVARI	62	PENIDECU	42	POS	1	11	18	339	0.6	0.02	0.888
PENIVARI	62	PENIDIGI	43	NEG	0	12	10	347	0.3	2.22	0.136
PENIVARI	62	PENIECHI	44	POS	2	10	15	342	0.6	1.76	0.185
PENIVARI	62	PENIEXPA	45	POS	4	8	65	292	2.2	0.89	0.345
PENIVARI	62	PENIGLAN	46	NEG	0	12	13	344	0.4	2.16	0.142
PENIVARI	62	PENIGRIS	47	NEG	0	12	23	334	0.8	2.30	0.129
PENIVARI	62	PENIIMPL	48	POS	1	11	18	339	0.6	0.02	0.888
PENIVARI	62	PENIISLA	49	NEG	0	12	11	346	0.4	2.19	0.139
PENIVARI	62	PENIITAL	50	NEG	0	12	11	346	0.4	2.19	0.139
PENIVARI	62	PENIMICZ	51	NEG	0	12	14	343	0.5	2.15	0.143
PENIVARI	62	PENIOXAL	52	POS	1	11	20	337	0.7	0.05	0.823
PENIVARI	62	PENIPURP	53	NEG	0	12	9	348	0.3	2.27	0.132
PENIVARI	62	PENIRAIS	54	POS	1	11	25	332	0.9	0.16	0.689
PENIVARI	62	PENIREST	55	POS	1	11	8	349	0.3	0.16	0.689
PENIVARI	62	PENISIMP	56	POS	3	9	17	340	0.7	5.75	0.016
PENIVARI	62	PENISP	57	POS	2	10	27	330	0.9	0.37	0.543
PENIVARI	62	PENISP01	58	POS	1	11	8	349	0.3	0.16	0.689
PENIVARI	62	PENISP26	59	NEG	1	11	52	305	1.7	1.05	0.306
PENIVARI	62	PENISP64	60	NEG	0	12	10	347	0.3	2.22	0.136
PENIVARI	62	PENISPIN	61	POS	6	6	136	221	4.6	0.28	0.597
PENIVERR	63	ACRESP	1	NEG	0	9	25	335	0.6	2.22	0.136
PENIVERR	63	ALTEALTE	2	POS	9	0	318	42	8.0	0.31	0.578
PENIVERR	63	ALTESP	3	POS	1	8	15	345	0.4	0.03	0.862
PENIVERR	63	ASPECAND	4	NEG	0	9	19	341	0.5	2.16	0.142
PENIVERR	63	ASPEFUMI	5	POS	1	8	24	336	0.6	0.02	0.888
PENIVERR	63	ASPEGLAU	6	POS	1	8	24	336	0.6	0.02	0.888
PENIVERR	63	ASPENIGE	7	NEG	3	6	123	237	3.1	0.17	0.680
PENIVERR	63	ASPEOCHR	8	POS	2	7	70	290	1.8	0.05	0.823
PENIVERR	63	ASPEORYZ	9	POS	2	7	7	353	0.2	7.85	0.005
PENIVERR	63	ASPESP	10	POS	2	7	65	295	1.6	0.01	0.920
PENIVERR	63	ASPESYDO	11	NEG	1	8	45	315	1.1	0.40	0.527
PENIVERR	63	ASPEUSTU	12	POS	1	8	23	337	0.6	0.01	0.920
PENIVERR	63	ASPEVERS	13	NEG	4	5	192	168	4.8	0.75	0.386
PENIVERR	63	AUREPULL	14	NEG	7	2	286	74	7.2	0.29	0.590
PENIVERR	63	CHAEGLOB	15	POS	1	8	23	337	0.6	0.01	0.920
PENIVERR	63	CHRSPMSP	16	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	CLADCLAD	17	POS	6	3	179	181	4.5	0.44	0.507
PENIVERR	63	CLADHERB	18	NEG	0	9	87	273	2.1	4.35	0.037
PENIVERR	63	CLADSP	19	POS	3	6	61	299	1.6	0.70	0.403
PENIVERR	63	CLADSPHA	20	NEG	2	7	139	221	3.4	1.81	0.179
PENIVERR	63	CONISP	21	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	EMERNIDU	22	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	EPICNIGR	23	POS	5	4	195	165	4.9	0.07	0.791
PENIVERR	63	EUROHERB	24	NEG	5	4	240	120	6.0	1.11	0.292
PENIVERR	63	FUSAOXYS	25	POS	2	7	18	342	0.5	2.28	0.131
PENIVERR	63	FUSASP	26	NEG	1	8	58	302	1.4	0.75	0.386
PENIVERR	63	GEOMPANN	27	NEG	0	9	12	348	0.3	2.27	0.132
PENIVERR	63	MUCOPLUM	28	POS	2	7	71	289	1.8	0.06	0.806
PENIVERR	63	MUCORACE	29	NEG	1	8	90	270	2.2	1.81	0.179
PENIVERR	63	PAECSP	30	NEG	0	9	8	352	0.2	2.59	0.108
PENIVERR	63	PAECVARI	31	NEG	1	8	49	311	1.2	0.50	0.480



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIVERR	63	PENIATRA	32	POS	2	7	7	353	0.2	7.85	0.005
PENIVERR	63	PENIAURA	33	NEG	1	8	43	317	1.1	0.36	0.549
PENIVERR	63	PENIBREV	34	POS	3	6	83	277	2.1	0.10	0.752
PENIVERR	63	PENICHR	35	NEG	2	7	189	171	4.7	4.55	0.033
PENIVERR	63	PENICOMM	36	POS	5	4	89	271	2.3	2.92	0.087
PENIVERR	63	PENICOPR	37	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENICORY	38	POS	3	6	105	255	2.6	0.01	0.920
PENIVERR	63	PENICRUS	39	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	PENICTNG	40	POS	1	8	33	327	0.8	0.15	0.699
PENIVERR	63	PENICTRM	41	POS	3	6	49	311	1.3	1.43	0.232
PENIVERR	63	PENIDECU	42	NEG	0	9	19	341	0.5	2.16	0.142
PENIVERR	63	PENIDIGI	43	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENIECHI	44	NEG	0	9	17	343	0.4	2.17	0.141
PENIVERR	63	PENIEXPA	45	POS	3	6	66	294	1.7	0.50	0.480
PENIVERR	63	PENIGLAN	46	NEG	0	9	13	347	0.3	2.24	0.134
PENIVERR	63	PENIGRIS	47	NEG	0	9	23	337	0.6	2.19	0.139
PENIVERR	63	PENIIMPL	48	POS	1	8	18	342	0.5	0.00	1.000
PENIVERR	63	PENIISLA	49	POS	1	8	10	350	0.3	0.21	0.647
PENIVERR	63	PENIITAL	50	NEG	0	9	11	349	0.3	2.32	0.128
PENIVERR	63	PENIMICZ	51	NEG	0	9	14	346	0.3	2.21	0.137
PENIVERR	63	PENIOXAL	52	NEG	0	9	21	339	0.5	2.17	0.141
PENIVERR	63	PENIPURP	53	POS	1	8	8	352	0.2	0.38	0.538
PENIVERR	63	PENIRAIS	54	NEG	0	9	26	334	0.6	2.24	0.134
PENIVERR	63	PENIREST	55	NEG	0	9	9	351	0.2	2.48	0.115
PENIVERR	63	PENISIMP	56	NEG	0	9	20	340	0.5	2.17	0.141
PENIVERR	63	PENISP	57	POS	3	6	26	334	0.7	5.05	0.025
PENIVERR	63	PENISP01	58	NEG	0	9	9	351	0.2	2.48	0.115
PENIVERR	63	PENISP26	59	POS	4	5	49	311	1.3	4.51	0.034
PENIVERR	63	PENISP64	60	NEG	0	9	10	350	0.2	2.39	0.122
PENIVERR	63	PENISPIN	61	NEG	3	6	139	221	3.5	0.45	0.502
PENIVERR	63	PENIVARI	62	NEG	0	9	12	348	0.3	2.27	0.132
PENIVIRI	64	ACRESP	1	POS	5	63	20	281	4.6	0.00	1.000
PENIVIRI	64	ALTEALTE	2	NEG	59	9	268	33	60.3	0.55	0.458
PENIVIRI	64	ALTESP	3	POS	3	65	13	288	3.0	0.09	0.764
PENIVIRI	64	ASPECAND	4	POS	5	63	14	287	3.5	0.37	0.543
PENIVIRI	64	ASPEFUMI	5	POS	8	60	17	284	4.6	2.39	0.122
PENIVIRI	64	ASPEGLAU	6	NEG	3	65	22	279	4.6	1.27	0.260
PENIVIRI	64	ASPENIGE	7	NEG	21	47	105	196	23.2	0.59	0.442
PENIVIRI	64	ASPEOCHR	8	POS	15	53	57	244	13.3	0.17	0.680
PENIVIRI	64	ASPEORYZ	9	NEG	0	68	9	292	1.7	3.53	0.060
PENIVIRI	64	ASPESP	10	NEG	10	58	57	244	12.4	0.98	0.322
PENIVIRI	64	ASPESYDO	11	POS	9	59	37	264	8.5	0.00	1.000
PENIVIRI	64	ASPEUSTU	12	NEG	2	66	22	279	4.4	2.53	0.112
PENIVIRI	64	ASPEVERS	13	NEG	28	40	168	133	36.1	5.38	0.020
PENIVIRI	64	AUREPULL	14	POS	54	14	239	62	54.0	0.03	0.862
PENIVIRI	64	CHAEGLOB	15	POS	8	60	16	285	4.4	2.81	0.094
PENIVIRI	64	CHRSPMSP	16	POS	4	64	10	291	2.6	0.42	0.517
PENIVIRI	64	CLADCLAD	17	POS	36	32	149	152	34.1	0.14	0.708
PENIVIRI	64	CLADHERB	18	NEG	7	61	80	221	16.0	9.09	0.003
PENIVIRI	64	CLADSP	19	POS	15	53	49	252	11.8	0.92	0.337
PENIVIRI	64	CLADSPHA	20	POS	28	40	113	188	26.0	0.18	0.671
PENIVIRI	64	CONISP	21	POS	3	65	7	294	1.8	0.30	0.584
PENIVIRI	64	EMERNIDU	22	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	EPICNIGR	23	POS	40	28	160	141	36.9	0.51	0.475
PENIVIRI	64	EUROHERB	24	POS	46	22	199	102	45.2	0.01	0.920
PENIVIRI	64	FUSAOXYS	25	NEG	3	65	17	284	3.7	0.49	0.484
PENIVIRI	64	FUSASP	26	NEG	9	59	50	251	10.9	0.76	0.383
PENIVIRI	64	GEOMPANN	27	NEG	1	67	11	290	2.2	1.68	0.195
PENIVIRI	64	MUCOPLUM	28	POS	14	54	59	242	13.5	0.00	1.000
PENIVIRI	64	MUCORACE	29	POS	25	43	66	235	16.8	5.80	0.016
PENIVIRI	64	PAECSP	30	NEG	0	68	8	293	1.5	3.31	0.069
PENIVIRI	64	PAECVARI	31	POS	11	57	39	262	9.2	0.25	0.617

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIVIRI	64	PENIATRA	32	NEG	1	67	8	293	1.7	1.02	0.313
PENIVIRI	64	PENIAURA	33	POS	9	59	35	266	8.1	0.03	0.862
PENIVIRI	64	PENIBREV	34	POS	18	50	68	233	15.9	0.28	0.597
PENIVIRI	64	PENICHR	35	NEG	30	38	161	140	35.2	2.34	0.126
PENIVIRI	64	PENICOMM	36	POS	21	47	73	228	17.3	0.96	0.327
PENIVIRI	64	PENICOPR	37	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENICORY	38	POS	23	45	85	216	19.9	0.59	0.442
PENIVIRI	64	PENICRUS	39	POS	5	63	9	292	2.6	1.82	0.177
PENIVIRI	64	PENICTNG	40	NEG	6	62	28	273	6.3	0.13	0.718
PENIVIRI	64	PENICTRM	41	NEG	7	61	45	256	9.6	1.42	0.233
PENIVIRI	64	PENIDECU	42	NEG	2	66	17	284	3.5	1.48	0.224
PENIVIRI	64	PENIDIGI	43	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENIECHI	44	NEG	3	65	14	287	3.1	0.16	0.689
PENIVIRI	64	PENIEXPA	45	POS	19	49	50	251	12.7	3.97	0.046
PENIVIRI	64	PENIGLAN	46	POS	3	65	10	291	2.4	0.01	0.920
PENIVIRI	64	PENIGRIS	47	POS	5	63	18	283	4.2	0.02	0.888
PENIVIRI	64	PENIIMPL	48	POS	4	64	15	286	3.5	0.00	1.000
PENIVIRI	64	PENIISLA	49	NEG	1	67	10	291	2.0	1.45	0.229
PENIVIRI	64	PENIITAL	50	NEG	1	67	10	291	2.0	1.45	0.229
PENIVIRI	64	PENIMICZ	51	POS	4	64	10	291	2.6	0.42	0.517
PENIVIRI	64	PENIOXAL	52	POS	5	63	16	285	3.9	0.13	0.718
PENIVIRI	64	PENIPURP	53	POS	3	65	6	295	1.7	0.54	0.462
PENIVIRI	64	PENIRAIS	54	NEG	4	64	22	279	4.8	0.46	0.498
PENIVIRI	64	PENIREST	55	POS	3	65	6	295	1.7	0.54	0.462
PENIVIRI	64	PENISIMP	56	NEG	1	67	19	282	3.7	3.57	0.059
PENIVIRI	64	PENISP	57	POS	9	59	20	281	5.3	2.48	0.115
PENIVIRI	64	PENISP01	58	POS	2	66	7	294	1.7	0.02	0.888
PENIVIRI	64	PENISP26	59	POS	13	55	40	261	9.8	1.09	0.296
PENIVIRI	64	PENISP64	60	POS	2	66	8	293	1.8	0.08	0.777
PENIVIRI	64	PENISPIN	61	NEG	26	42	116	185	26.2	0.03	0.862
PENIVIRI	64	PENIVARI	62	POS	5	63	7	294	2.2	3.00	0.083
PENIVIRI	64	PENIVERR	63	NEG	1	67	8	293	1.7	1.02	0.313
PENIVULP	65	ACRESP	1	NEG	1	21	24	323	1.5	0.75	0.386
PENIVULP	65	ALTEALTE	2	POS	20	2	307	40	19.5	0.00	1.000
PENIVULP	65	ALTESP	3	POS	1	21	15	332	1.0	0.24	0.624
PENIVULP	65	ASPECAND	4	NEG	1	21	18	329	1.1	0.40	0.527
PENIVULP	65	ASPEFUMI	5	NEG	1	21	24	323	1.5	0.75	0.386
PENIVULP	65	ASPEGLAU	6	NEG	0	22	25	322	1.5	3.03	0.082
PENIVULP	65	ASPENIGE	7	POS	8	14	118	229	7.5	0.00	1.000
PENIVULP	65	ASPEOCHR	8	NEG	4	18	68	279	4.3	0.19	0.663
PENIVULP	65	ASPEORYZ	9	NEG	0	22	9	338	0.5	2.18	0.140
PENIVULP	65	ASPESP	10	POS	8	14	59	288	4.0	4.00	0.046
PENIVULP	65	ASPESYDO	11	NEG	2	20	44	303	2.7	0.68	0.410
PENIVULP	65	ASPEUSTU	12	NEG	0	22	24	323	1.4	2.96	0.085
PENIVULP	65	ASPEVERS	13	NEG	7	15	189	158	11.7	5.22	0.022
PENIVULP	65	AUREPULL	14	POS	20	2	273	74	17.5	1.22	0.269
PENIVULP	65	CHAEGLOB	15	POS	3	19	21	326	1.4	0.91	0.340
PENIVULP	65	CHRSPMSP	16	POS	2	20	12	335	0.8	0.59	0.442
PENIVULP	65	CLADCLAD	17	POS	13	9	172	175	11.0	0.42	0.517
PENIVULP	65	CLADHERB	18	NEG	0	22	87	260	5.2	8.68	0.003
PENIVULP	65	CLADSP	19	POS	6	16	58	289	3.8	0.96	0.327
PENIVULP	65	CLADSPHA	20	POS	10	12	131	216	8.4	0.24	0.624
PENIVULP	65	CONISP	21	POS	3	19	7	340	0.6	6.64	0.010
PENIVULP	65	EMERNIDU	22	NEG	0	22	10	337	0.6	2.20	0.138
PENIVULP	65	EPICNIGR	23	POS	13	9	187	160	11.9	0.06	0.806
PENIVULP	65	EUROHERB	24	POS	16	6	229	118	14.6	0.17	0.680
PENIVULP	65	FUSAOXYS	25	POS	3	19	17	330	1.2	1.61	0.204
PENIVULP	65	FUSASP	26	NEG	3	19	56	291	3.5	0.37	0.543
PENIVULP	65	GEOMPANN	27	POS	1	21	11	336	0.7	0.07	0.791
PENIVULP	65	MUCOPLUM	28	NEG	2	20	71	276	4.4	2.48	0.115
PENIVULP	65	MUCORACE	29	POS	8	14	83	264	5.4	1.12	0.290
PENIVULP	65	PAECSP	30	NEG	0	22	8	339	0.5	2.18	0.140

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PENIVULP	65	PAECVARI	31	NEG	1	21	49	298	3.0	2.54	0.111
PENIVULP	65	PENIATRA	32	POS	2	20	7	340	0.5	1.89	0.169
PENIVULP	65	PENIAURA	33	POS	4	18	40	307	2.6	0.35	0.554
PENIVULP	65	PENIBREV	34	POS	7	15	79	268	5.1	0.51	0.475
PENIVULP	65	PENICHRY	35	NEG	10	12	181	166	11.4	0.69	0.406
PENIVULP	65	PENICOMM	36	POS	9	13	85	262	5.6	2.13	0.144
PENIVULP	65	PENICOPR	37	POS	2	20	8	339	0.6	1.50	0.221
PENIVULP	65	PENICORY	38	POS	7	15	101	246	6.4	0.00	1.000
PENIVULP	65	PENICRUS	39	POS	3	19	11	336	0.8	3.67	0.055
PENIVULP	65	PENICTNG	40	POS	4	18	30	317	2.0	1.25	0.264
PENIVULP	65	PENICTRM	41	NEG	3	19	49	298	3.1	0.14	0.708
PENIVULP	65	PENIDECU	42	NEG	1	21	18	329	1.1	0.40	0.527
PENIVULP	65	PENIDIGI	43	POS	1	21	9	338	0.6	0.02	0.888
PENIVULP	65	PENIECHI	44	POS	3	19	14	333	1.0	2.43	0.119
PENIVULP	65	PENIEXPA	45	POS	5	17	64	283	4.1	0.05	0.823
PENIVULP	65	PENIGLAN	46	POS	1	21	12	335	0.8	0.11	0.740
PENIVULP	65	PENIGRIS	47	NEG	0	22	23	324	1.4	2.90	0.089
PENIVULP	65	PENIIMPL	48	NEG	0	22	19	328	1.1	2.64	0.104
PENIVULP	65	PENIISLA	49	NEG	0	22	11	336	0.7	2.23	0.135
PENIVULP	65	PENIITAL	50	NEG	0	22	11	336	0.7	2.23	0.135
PENIVULP	65	PENIMICZ	51	POS	1	21	13	334	0.8	0.15	0.699
PENIVULP	65	PENIOXAL	52	POS	3	19	18	329	1.3	1.40	0.237
PENIVULP	65	PENIPURP	53	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENIRAIS	54	POS	3	19	23	324	1.6	0.67	0.413
PENIVULP	65	PENIREST	55	NEG	0	22	9	338	0.5	2.18	0.140
PENIVULP	65	PENISIMP	56	NEG	1	21	19	328	1.2	0.45	0.502
PENIVULP	65	PENISP	57	POS	4	18	25	322	1.7	2.09	0.148
PENIVULP	65	PENISP01	58	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENISP26	59	NEG	3	19	50	297	3.2	0.17	0.680
PENIVULP	65	PENISP64	60	POS	1	21	9	338	0.6	0.02	0.888
PENIVULP	65	PENISPIN	61	NEG	8	14	134	213	8.5	0.19	0.663
PENIVULP	65	PENIVARI	62	POS	1	21	11	336	0.7	0.07	0.791
PENIVULP	65	PENIVERR	63	POS	1	21	8	339	0.5	0.00	1.000
PENIVULP	65	PENIVIRI	64	POS	7	15	61	286	4.1	1.92	0.166
PHOMHERB	66	ACRESP	1	POS	10	98	15	246	7.3	0.99	0.320
PHOMHERB	66	ALTEALTE	2	POS	99	9	228	33	95.7	1.01	0.315
PHOMHERB	66	ALTESP	3	POS	6	102	10	251	4.7	0.21	0.647
PHOMHERB	66	ASPECAND	4	POS	6	102	13	248	5.6	0.00	1.000
PHOMHERB	66	ASPEFUMI	5	NEG	7	101	18	243	7.3	0.14	0.708
PHOMHERB	66	ASPEGLAU	6	POS	10	98	15	246	7.3	0.99	0.320
PHOMHERB	66	ASPENIGE	7	NEG	36	72	90	171	36.9	0.11	0.740
PHOMHERB	66	ASPEOCHR	8	POS	26	82	46	215	21.1	1.63	0.202
PHOMHERB	66	ASPEORYZ	9	NEG	2	106	7	254	2.6	0.71	0.399
PHOMHERB	66	ASPESP	10	NEG	11	97	56	205	19.6	7.31	0.007
PHOMHERB	66	ASPESYDO	11	NEG	10	98	36	225	13.5	1.88	0.170
PHOMHERB	66	ASPEUSTU	12	NEG	4	104	20	241	7.0	2.67	0.102
PHOMHERB	66	ASPEVERS	13	NEG	55	53	141	120	57.4	0.43	0.512
PHOMHERB	66	AUREPULL	14	POS	96	12	197	64	85.8	7.60	0.006
PHOMHERB	66	CHAEGLOB	15	POS	8	100	16	245	7.0	0.05	0.823
PHOMHERB	66	CHRSPMSP	16	NEG	4	104	10	251	4.1	0.13	0.718
PHOMHERB	66	CLADCLAD	17	POS	68	40	117	144	54.2	9.34	0.002
PHOMHERB	66	CLADHERB	18	POS	35	73	52	209	25.5	5.93	0.015
PHOMHERB	66	CLADSP	19	NEG	17	91	47	214	18.8	0.45	0.502
PHOMHERB	66	CLADSPHA	20	POS	60	48	81	180	41.3	18.43	0.000
PHOMHERB	66	CONISP	21	POS	3	105	7	254	2.9	0.09	0.764
PHOMHERB	66	EMERNIDU	22	NEG	2	106	8	253	2.9	1.01	0.315
PHOMHERB	66	EPICNIGR	23	POS	70	38	130	131	58.5	6.34	0.012
PHOMHERB	66	EUROHERB	24	POS	78	30	167	94	71.7	1.97	0.160
PHOMHERB	66	FUSAOXYS	25	NEG	4	104	16	245	5.9	1.41	0.235
PHOMHERB	66	FUSASP	26	POS	20	88	39	222	17.3	0.49	0.484
PHOMHERB	66	GEOMPANN	27	POS	6	102	6	255	3.5	1.64	0.200
PHOMHERB	66	MUCOPLUM	28	NEG	18	90	55	206	21.4	1.23	0.267

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PHOMHERB	66	MUCORACE	29	POS	35	73	56	205	26.6	4.36	0.037
PHOMHERB	66	PAECSP	30	NEG	0	108	8	253	2.3	4.98	0.026
PHOMHERB	66	PAECVARI	31	POS	21	87	29	232	14.6	3.85	0.050
PHOMHERB	66	PENIATRA	32	POS	5	103	4	257	2.6	1.92	0.166
PHOMHERB	66	PENIAURA	33	NEG	12	96	32	229	12.9	0.24	0.624
PHOMHERB	66	PENIBREV	34	POS	28	80	58	203	25.2	0.40	0.527
PHOMHERB	66	PENICHR	35	NEG	54	54	137	124	55.9	0.30	0.584
PHOMHERB	66	PENICOMM	36	NEG	26	82	68	193	27.5	0.28	0.597
PHOMHERB	66	PENICOPR	37	POS	4	104	6	255	2.9	0.16	0.689
PHOMHERB	66	PENICORY	38	POS	38	70	70	191	31.6	2.19	0.139
PHOMHERB	66	PENICRUS	39	NEG	2	106	12	249	4.1	2.42	0.120
PHOMHERB	66	PENICTNG	40	POS	10	98	24	237	10.0	0.03	0.862
PHOMHERB	66	PENICTRM	41	POS	20	88	32	229	15.2	1.98	0.159
PHOMHERB	66	PENIDECU	42	POS	8	100	11	250	5.6	1.01	0.315
PHOMHERB	66	PENIDIGI	43	POS	6	102	4	257	2.9	3.29	0.070
PHOMHERB	66	PENIECHI	44	POS	5	103	12	249	5.0	0.07	0.791
PHOMHERB	66	PENIEXPA	45	POS	25	83	44	217	20.2	1.60	0.206
PHOMHERB	66	PENIGLAN	46	POS	4	104	9	252	3.8	0.04	0.841
PHOMHERB	66	PENIGRIS	47	NEG	6	102	17	244	6.7	0.34	0.560
PHOMHERB	66	PENIIMPL	48	NEG	2	106	17	244	5.6	4.42	0.036
PHOMHERB	66	PENIISLA	49	POS	5	103	6	255	3.2	0.74	0.390
PHOMHERB	66	PENIITAL	50	POS	5	103	6	255	3.2	0.74	0.390
PHOMHERB	66	PENIMICZ	51	POS	5	103	9	252	4.1	0.06	0.806
PHOMHERB	66	PENIOXAL	52	POS	8	100	13	248	6.2	0.45	0.502
PHOMHERB	66	PENIPURP	53	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENIRAIS	54	NEG	7	101	19	242	7.6	0.25	0.617
PHOMHERB	66	PENIREST	55	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENISIMP	56	NEG	2	106	18	243	5.9	4.84	0.028
PHOMHERB	66	PENISP	57	NEG	5	103	24	237	8.5	2.87	0.090
PHOMHERB	66	PENISP01	58	POS	4	104	5	256	2.6	0.41	0.522
PHOMHERB	66	PENISP26	59	NEG	13	95	40	221	15.5	0.97	0.325
PHOMHERB	66	PENISP64	60	NEG	1	107	9	252	2.9	2.92	0.087
PHOMHERB	66	PENISPIN	61	NEG	39	69	103	158	41.6	0.52	0.471
PHOMHERB	66	PENIVARI	62	POS	7	101	5	256	3.5	3.71	0.054
PHOMHERB	66	PENIVERR	63	NEG	2	106	7	254	2.6	0.71	0.399
PHOMHERB	66	PENIVIRI	64	POS	24	84	44	217	19.9	1.13	0.288
PHOMHERB	66	PENIVULP	65	NEG	5	103	17	244	6.4	0.88	0.348
PHOMSP	67	ACRESP	1	POS	6	56	19	288	4.2	0.52	0.471
PHOMSP	67	ALTEALTE	2	POS	59	3	268	39	54.9	2.43	0.119
PHOMSP	67	ALTESP	3	POS	5	57	11	296	2.7	1.53	0.216
PHOMSP	67	ASPECAND	4	POS	4	58	15	292	3.2	0.04	0.841
PHOMSP	67	ASPEFUMI	5	NEG	2	60	23	284	4.2	2.24	0.134
PHOMSP	67	ASPEGLAU	6	POS	6	56	19	288	4.2	0.52	0.471
PHOMSP	67	ASPENIGE	7	NEG	21	41	105	202	21.2	0.04	0.841
PHOMSP	67	ASPEOCHR	8	NEG	10	52	62	245	12.1	0.83	0.362
PHOMSP	67	ASPEORYZ	9	POS	2	60	7	300	1.5	0.00	1.000
PHOMSP	67	ASPESP	10	NEG	9	53	58	249	11.3	0.99	0.320
PHOMSP	67	ASPESYDO	11	POS	11	51	35	272	7.7	1.36	0.244
PHOMSP	67	ASPEUSTU	12	NEG	3	59	21	286	4.0	0.75	0.386
PHOMSP	67	ASPEVERS	13	POS	37	25	159	148	32.9	0.99	0.320
PHOMSP	67	AUREPULL	14	POS	53	9	240	67	49.2	1.27	0.260
PHOMSP	67	CHAEGLOB	15	NEG	0	62	24	283	4.0	6.55	0.010
PHOMSP	67	CHRSPMSP	16	NEG	1	61	13	294	2.4	1.82	0.177
PHOMSP	67	CLADCLAD	17	POS	43	19	142	165	31.1	10.11	0.001
PHOMSP	67	CLADHERB	18	POS	21	41	66	241	14.6	3.72	0.054
PHOMSP	67	CLADSP	19	NEG	9	53	55	252	10.8	0.69	0.406
PHOMSP	67	CLADSPHA	20	POS	30	32	111	196	23.7	2.77	0.096
PHOMSP	67	CONISP	21	POS	2	60	8	299	1.7	0.02	0.888
PHOMSP	67	EMERNIDU	22	NEG	1	61	9	298	1.7	1.02	0.313
PHOMSP	67	EPICNIGR	23	POS	40	22	160	147	33.6	2.71	0.100
PHOMSP	67	EUROHERB	24	NEG	35	27	210	97	41.2	3.86	0.049
PHOMSP	67	FUSAOXYS	25	POS	4	58	16	291	3.4	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PHOMSP	67	FUSASP	26	POS	14	48	45	262	9.9	1.86	0.173
PHOMSP	67	GEOMPANN	27	NEG	1	61	11	296	2.0	1.42	0.233
PHOMSP	67	MUCOPLUM	28	NEG	7	55	66	241	12.3	4.06	0.044
PHOMSP	67	MUCORACE	29	NEG	12	50	79	228	15.3	1.50	0.221
PHOMSP	67	PAECSP	30	NEG	0	62	8	299	1.3	3.11	0.078
PHOMSP	67	PAECVARI	31	POS	9	53	41	266	8.4	0.00	1.000
PHOMSP	67	PENIATRA	32	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENIAURA	33	NEG	6	56	38	269	7.4	0.66	0.417
PHOMSP	67	PENIBREV	34	NEG	14	48	72	235	14.5	0.10	0.752
PHOMSP	67	PENICHRYS	35	NEG	31	31	160	147	32.1	0.20	0.655
PHOMSP	67	PENICOMM	36	NEG	12	50	82	225	15.8	1.88	0.170
PHOMSP	67	PENICOPR	37	POS	2	60	8	299	1.7	0.02	0.888
PHOMSP	67	PENICORY	38	NEG	15	47	93	214	18.2	1.25	0.264
PHOMSP	67	PENICRUS	39	NEG	1	61	13	294	2.4	1.82	0.177
PHOMSP	67	PENICTNG	40	NEG	3	59	31	276	5.7	2.39	0.122
PHOMSP	67	PENICTRM	41	NEG	4	58	48	259	8.7	4.39	0.036
PHOMSP	67	PENIDECU	42	NEG	2	60	17	290	3.2	1.14	0.286
PHOMSP	67	PENIDIGI	43	POS	3	59	7	300	1.7	0.49	0.484
PHOMSP	67	PENIECHI	44	NEG	1	61	16	291	2.9	2.45	0.118
PHOMSP	67	PENIEXPA	45	NEG	9	53	60	247	11.6	1.22	0.269
PHOMSP	67	PENIGLAN	46	NEG	2	60	11	296	2.2	0.27	0.603
PHOMSP	67	PENIGRIS	47	NEG	1	61	22	285	3.9	3.75	0.053
PHOMSP	67	PENIIMPL	48	NEG	2	60	17	290	3.2	1.14	0.286
PHOMSP	67	PENIISLA	49	POS	2	60	9	298	1.9	0.08	0.777
PHOMSP	67	PENIITAL	50	NEG	1	61	10	297	1.9	1.22	0.269
PHOMSP	67	PENIMICZ	51	POS	3	59	11	296	2.4	0.01	0.920
PHOMSP	67	PENIOXAL	52	NEG	2	60	19	288	3.5	1.49	0.222
PHOMSP	67	PENIPURP	53	POS	2	60	7	300	1.5	0.00	1.000
PHOMSP	67	PENIRAIS	54	NEG	3	59	23	284	4.4	1.03	0.310
PHOMSP	67	PENIREST	55	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENISIMP	56	POS	4	58	16	291	3.4	0.01	0.920
PHOMSP	67	PENISP	57	NEG	4	58	25	282	4.9	0.50	0.480
PHOMSP	67	PENISP01	58	NEG	0	62	9	298	1.5	3.30	0.069
PHOMSP	67	PENISP26	59	NEG	4	58	49	258	8.9	4.60	0.032
PHOMSP	67	PENISP64	60	NEG	0	62	10	297	1.7	3.50	0.061
PHOMSP	67	PENISPIN	61	POS	26	36	116	191	23.9	0.22	0.639
PHOMSP	67	PENIVARI	62	NEG	0	62	12	295	2.0	3.90	0.048
PHOMSP	67	PENIVERR	63	NEG	1	61	8	299	1.5	0.83	0.362
PHOMSP	67	PENIVIRI	64	NEG	7	55	61	246	11.4	3.13	0.077
PHOMSP	67	PENIVULP	65	NEG	2	60	20	287	3.7	1.67	0.196
PHOMSP	67	PHOMHERB	66	NEG	17	45	91	216	18.2	0.25	0.617
PITHCHAR	68	ACRESP	1	NEG	1	25	24	319	1.8	1.04	0.308
PITHCHAR	68	ALTEALTE	2	POS	24	2	303	40	23.0	0.09	0.764
PITHCHAR	68	ALTESP	3	POS	3	23	13	330	1.1	1.88	0.170
PITHCHAR	68	ASPECAND	4	POS	2	24	17	326	1.3	0.02	0.888
PITHCHAR	68	ASPEFUMI	5	POS	4	22	21	322	1.8	1.98	0.159
PITHCHAR	68	ASPEGLAU	6	POS	3	23	22	321	1.8	0.36	0.549
PITHCHAR	68	ASPENIGE	7	POS	13	13	113	230	8.9	2.41	0.121
PITHCHAR	68	ASPEOCHR	8	POS	6	20	66	277	5.1	0.05	0.823
PITHCHAR	68	ASPEORYZ	9	POS	1	25	8	335	0.6	0.03	0.862
PITHCHAR	68	ASPEP	10	NEG	3	23	64	279	4.7	1.37	0.242
PITHCHAR	68	ASPESYDO	11	POS	4	22	42	301	3.3	0.03	0.862
PITHCHAR	68	ASPEUSTU	12	POS	2	24	22	321	1.7	0.02	0.888
PITHCHAR	68	ASPEVERS	13	NEG	12	14	184	159	13.8	0.89	0.345
PITHCHAR	68	AUREPULL	14	NEG	17	9	276	67	20.6	4.35	0.037
PITHCHAR	68	CHAEGLOB	15	POS	3	23	21	322	1.7	0.45	0.502
PITHCHAR	68	CHRSPMSP	16	POS	4	22	10	333	1.0	7.16	0.007
PITHCHAR	68	CLADCLAD	17	NEG	11	15	174	169	13.0	1.06	0.303
PITHCHAR	68	CLADHERB	18	NEG	3	23	84	259	6.1	3.03	0.082
PITHCHAR	68	CLADSP	19	POS	9	17	55	288	4.5	4.60	0.032
PITHCHAR	68	CLADSPHA	20	POS	12	14	129	214	9.9	0.43	0.512
PITHCHAR	68	CONISP	21	POS	1	25	9	334	0.7	0.07	0.791

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
PITHCHAR	68	EMERNIDU	22	POS	1	25	9	334	0.7	0.07	0.791
PITHCHAR	68	EPICNIGR	23	POS	16	10	184	159	14.1	0.33	0.566
PITHCHAR	68	EUROHERB	24	NEG	12	14	233	110	17.3	6.16	0.013
PITHCHAR	68	FUSAOXYS	25	POS	4	22	16	327	1.4	3.53	0.060
PITHCHAR	68	FUSASP	26	NEG	2	24	57	286	4.2	2.17	0.141
PITHCHAR	68	GEOMPANN	27	NEG	0	26	12	331	0.9	2.38	0.123
PITHCHAR	68	MUCOPLUM	28	NEG	3	23	70	273	5.1	1.82	0.177
PITHCHAR	68	MUCORACE	29	NEG	6	20	85	258	6.4	0.19	0.663
PITHCHAR	68	PAECSP	30	POS	1	25	7	336	0.6	0.01	0.920
PITHCHAR	68	PAECVARI	31	NEG	3	23	47	296	3.5	0.37	0.543
PITHCHAR	68	PENIATRA	32	POS	2	24	7	336	0.6	1.30	0.254
PITHCHAR	68	PENIAURA	33	POS	4	22	40	303	3.1	0.06	0.806
PITHCHAR	68	PENIBREV	34	NEG	6	20	80	263	6.1	0.07	0.791
PITHCHAR	68	PENICHRYS	35	NEG	12	14	179	164	13.5	0.64	0.424
PITHCHAR	68	PENICOMM	36	POS	9	17	85	258	6.6	0.77	0.380
PITHCHAR	68	PENICOPR	37	POS	1	25	9	334	0.7	0.07	0.791
PITHCHAR	68	PENICORY	38	POS	14	12	94	249	7.6	6.93	0.008
PITHCHAR	68	PENICRUS	39	POS	3	23	11	332	1.0	2.60	0.107
PITHCHAR	68	PENICTNG	40	POS	4	22	30	313	2.4	0.60	0.439
PITHCHAR	68	PENICTRM	41	NEG	2	24	50	293	3.7	1.60	0.206
PITHCHAR	68	PENIDECU	42	NEG	1	25	18	325	1.3	0.60	0.439
PITHCHAR	68	PENIDIGI	43	NEG	0	26	10	333	0.7	2.28	0.131
PITHCHAR	68	PENIECHI	44	POS	2	24	15	328	1.2	0.09	0.764
PITHCHAR	68	PENIEXPA	45	POS	5	21	64	279	4.9	0.04	0.841
PITHCHAR	68	PENIGLAN	46	POS	2	24	11	332	0.9	0.42	0.517
PITHCHAR	68	PENIGRIS	47	NEG	0	26	23	320	1.6	3.18	0.075
PITHCHAR	68	PENIIMPL	48	NEG	1	25	18	325	1.3	0.60	0.439
PITHCHAR	68	PENIISLA	49	POS	1	25	10	333	0.8	0.11	0.740
PITHCHAR	68	PENIITAL	50	NEG	0	26	11	332	0.8	2.33	0.127
PITHCHAR	68	PENIMICZ	51	POS	1	25	13	330	1.0	0.27	0.603
PITHCHAR	68	PENIOXAL	52	POS	2	24	19	324	1.5	0.00	1.000
PITHCHAR	68	PENIPURP	53	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENIRAIS	54	NEG	1	25	25	318	1.8	1.12	0.290
PITHCHAR	68	PENIREST	55	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENISIMP	56	POS	2	24	18	325	1.4	0.01	0.920
PITHCHAR	68	PENISP	57	NEG	1	25	28	315	2.0	1.36	0.244
PITHCHAR	68	PENISP01	58	POS	1	25	8	335	0.6	0.03	0.862
PITHCHAR	68	PENISP26	59	POS	5	21	48	295	3.7	0.20	0.655
PITHCHAR	68	PENISP64	60	POS	2	24	8	335	0.7	0.99	0.320
PITHCHAR	68	PENISPIN	61	NEG	10	16	132	211	10.0	0.04	0.841
PITHCHAR	68	PENIVARI	62	NEG	0	26	12	331	0.9	2.38	0.123
PITHCHAR	68	PENIVERR	63	NEG	0	26	9	334	0.6	2.24	0.134
PITHCHAR	68	PENIVIRI	64	POS	5	21	63	280	4.8	0.02	0.888
PITHCHAR	68	PENIVULP	65	NEG	1	25	21	322	1.6	0.81	0.368
PITHCHAR	68	PHOMHERB	66	NEG	7	19	101	242	7.6	0.25	0.617
PITHCHAR	68	PHOMSP	67	NEG	4	22	58	285	4.4	0.22	0.639
RHIZORYZ	69	ACRESP	1	NEG	3	50	22	294	3.6	0.42	0.517
RHIZORYZ	69	ALTEALTE	2	POS	48	5	279	37	47.0	0.06	0.806
RHIZORYZ	69	ALTESP	3	POS	3	50	13	303	2.3	0.02	0.888
RHIZORYZ	69	ASPECAND	4	POS	5	48	14	302	2.7	1.41	0.235
RHIZORYZ	69	ASPEFUMI	5	POS	4	49	21	295	3.6	0.00	1.000
RHIZORYZ	69	ASPEGLAU	6	POS	5	48	20	296	3.6	0.29	0.590
RHIZORYZ	69	ASPENIGE	7	POS	22	31	104	212	18.1	1.13	0.288
RHIZORYZ	69	ASPEOCHR	8	NEG	10	43	62	254	10.3	0.10	0.752
RHIZORYZ	69	ASPEORYZ	9	NEG	0	53	9	307	1.3	2.98	0.084
RHIZORYZ	69	ASPESP	10	POS	13	40	54	262	9.6	1.23	0.267
RHIZORYZ	69	ASPESYDO	11	POS	7	46	39	277	6.6	0.00	1.000
RHIZORYZ	69	ASPEUSTU	12	POS	5	48	19	297	3.5	0.40	0.527
RHIZORYZ	69	ASPEVERS	13	POS	32	21	164	152	28.2	0.99	0.320
RHIZORYZ	69	AUREPULL	14	NEG	39	14	254	62	42.1	1.73	0.188
RHIZORYZ	69	CHAEGLOB	15	NEG	2	51	22	294	3.5	1.37	0.242
RHIZORYZ	69	CHRSPMSP	16	POS	3	50	11	305	2.0	0.14	0.708

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
RHIZORYZ	69	CLADCLAD	17	NEG	26	27	159	157	26.6	0.10	0.752
RHIZORYZ	69	CLADHERB	18	NEG	12	41	75	241	12.5	0.12	0.729
RHIZORYZ	69	CLADSP	19	NEG	9	44	55	261	9.2	0.07	0.791
RHIZORYZ	69	CLADSPHA	20	NEG	19	34	122	194	20.3	0.29	0.590
RHIZORYZ	69	CONISP	21	POS	3	50	7	309	1.4	0.95	0.330
RHIZORYZ	69	EMERNIDU	22	POS	2	51	8	308	1.4	0.00	1.000
RHIZORYZ	69	EPICNIGR	23	POS	29	24	171	145	28.7	0.00	1.000
RHIZORYZ	69	EUROHERB	24	NEG	35	18	210	106	35.2	0.05	0.823
RHIZORYZ	69	FUSAOXYS	25	POS	3	50	17	299	2.9	0.06	0.806
RHIZORYZ	69	FUSASP	26	NEG	8	45	51	265	8.5	0.16	0.689
RHIZORYZ	69	GEOMPANN	27	POS	2	51	10	306	1.7	0.04	0.841
RHIZORYZ	69	MUCOPLUM	28	POS	19	34	54	262	10.5	8.92	0.003
RHIZORYZ	69	MUCORACE	29	POS	17	36	74	242	13.1	1.39	0.238
RHIZORYZ	69	PAECSP	30	NEG	1	52	7	309	1.2	0.44	0.507
RHIZORYZ	69	PAECVARI	31	POS	10	43	40	276	7.2	1.01	0.315
RHIZORYZ	69	PENIATRA	32	NEG	1	52	8	308	1.3	0.58	0.446
RHIZORYZ	69	PENIAURA	33	NEG	6	47	38	278	6.3	0.14	0.708
RHIZORYZ	69	PENIBREV	34	POS	13	40	73	243	12.4	0.00	1.000
RHIZORYZ	69	PENICHRY	35	POS	28	25	163	153	27.4	0.00	1.000
RHIZORYZ	69	PENICOMM	36	POS	15	38	79	237	13.5	0.12	0.729
RHIZORYZ	69	PENICOPR	37	NEG	0	53	10	306	1.4	3.13	0.077
RHIZORYZ	69	PENICORY	38	POS	22	31	86	230	15.5	3.82	0.051
RHIZORYZ	69	PENICRUS	39	POS	3	50	11	305	2.0	0.14	0.708
RHIZORYZ	69	PENICTNG	40	NEG	3	50	31	285	4.9	1.50	0.221
RHIZORYZ	69	PENICTRM	41	NEG	7	46	45	271	7.5	0.17	0.680
RHIZORYZ	69	PENIDECU	42	POS	3	50	16	300	2.7	0.02	0.888
RHIZORYZ	69	PENIDIGI	43	POS	2	51	8	308	1.4	0.00	1.000
RHIZORYZ	69	PENIECHI	44	POS	4	49	13	303	2.4	0.56	0.454
RHIZORYZ	69	PENIEXPA	45	POS	15	38	54	262	9.9	3.05	0.081
RHIZORYZ	69	PENIGLAN	46	POS	2	51	11	305	1.9	0.09	0.764
RHIZORYZ	69	PENIGRIS	47	POS	6	47	17	299	3.3	1.82	0.177
RHIZORYZ	69	PENIIMPL	48	POS	5	48	14	302	2.7	1.41	0.235
RHIZORYZ	69	PENIISLA	49	NEG	0	53	11	305	1.6	3.30	0.069
RHIZORYZ	69	PENIITAL	50	NEG	1	52	10	306	1.6	0.89	0.345
RHIZORYZ	69	PENIMICZ	51	NEG	2	51	12	304	2.0	0.16	0.689
RHIZORYZ	69	PENIOXAL	52	NEG	1	52	20	296	3.0	2.60	0.107
RHIZORYZ	69	PENIPURP	53	NEG	0	53	9	307	1.3	2.98	0.084
RHIZORYZ	69	PENIRAIS	54	POS	6	47	20	296	3.7	1.05	0.306
RHIZORYZ	69	PENIREST	55	POS	2	51	7	309	1.3	0.04	0.841
RHIZORYZ	69	PENISIMP	56	POS	3	50	17	299	2.9	0.06	0.806
RHIZORYZ	69	PENISP	57	POS	10	43	19	297	4.2	8.66	0.003
RHIZORYZ	69	PENISP01	58	POS	2	51	7	309	1.3	0.04	0.841
RHIZORYZ	69	PENISP26	59	POS	8	45	45	271	7.6	0.00	1.000
RHIZORYZ	69	PENISP64	60	NEG	0	53	10	306	1.4	3.13	0.077
RHIZORYZ	69	PENISPIN	61	NEG	17	36	125	191	20.4	1.41	0.235
RHIZORYZ	69	PENIVARI	62	NEG	1	52	11	305	1.7	1.05	0.306
RHIZORYZ	69	PENIVERR	63	NEG	1	52	8	308	1.3	0.58	0.446
RHIZORYZ	69	PENIVIRI	64	POS	12	41	56	260	9.8	0.44	0.507
RHIZORYZ	69	PENIVULP	65	NEG	3	50	19	297	3.2	0.17	0.680
RHIZORYZ	69	PHOMHERB	66	NEG	12	41	96	220	15.5	1.71	0.191
RHIZORYZ	69	PHOMSP	67	POS	9	44	53	263	8.9	0.03	0.862
RHIZORYZ	69	PITHCHAR	68	POS	4	49	22	294	3.7	0.02	0.888
SCOPBREV	70	ACRESP	1	NEG	1	32	24	312	2.2	1.59	0.207
SCOPBREV	70	ALTEALTE	2	NEG	27	6	300	36	29.2	2.48	0.115
SCOPBREV	70	ALTESP	3	POS	2	31	14	322	1.4	0.00	1.000
SCOPBREV	70	ASPECAND	4	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	ASPEFUMI	5	POS	3	30	22	314	2.2	0.04	0.841
SCOPBREV	70	ASPEGLAU	6	NEG	2	31	23	313	2.2	0.29	0.590
SCOPBREV	70	ASPENIGE	7	NEG	11	22	115	221	11.3	0.09	0.764
SCOPBREV	70	ASPEOCHR	8	POS	12	21	60	276	6.4	5.43	0.020
SCOPBREV	70	ASPEORYZ	9	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	ASPESP	10	NEG	5	28	62	274	6.0	0.50	0.480

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
SCOPBREV	70	ASPESYDO	11	POS	5	28	41	295	4.1	0.05	0.823
SCOPBREV	70	ASPEUSTU	12	NEG	1	32	23	313	2.2	1.48	0.224
SCOPBREV	70	ASPEVERS	13	NEG	15	18	181	155	17.5	1.23	0.267
SCOPBREV	70	AUREPULL	14	NEG	23	10	270	66	26.2	2.79	0.095
SCOPBREV	70	CHAEGLOB	15	POS	5	28	19	317	2.2	3.03	0.082
SCOPBREV	70	CHRSPMSP	16	POS	2	31	12	324	1.3	0.06	0.806
SCOPBREV	70	CLADCLAD	17	NEG	15	18	170	166	16.5	0.56	0.454
SCOPBREV	70	CLADHERB	18	NEG	7	26	80	256	7.8	0.30	0.584
SCOPBREV	70	CLADSP	19	POS	7	26	57	279	5.7	0.14	0.708
SCOPBREV	70	CLADSPHA	20	NEG	11	22	130	206	12.6	0.63	0.427
SCOPBREV	70	CONISP	21	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	EMERNIDU	22	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	EPICNIGR	23	POS	18	15	182	154	17.9	0.02	0.888
SCOPBREV	70	EUROHERB	24	POS	28	5	217	119	21.9	4.66	0.031
SCOPBREV	70	FUSAOXYS	25	POS	4	29	16	320	1.8	1.90	0.168
SCOPBREV	70	FUSASP	26	NEG	4	29	55	281	5.3	0.78	0.377
SCOPBREV	70	GEOMPANN	27	NEG	1	32	11	325	1.1	0.35	0.554
SCOPBREV	70	MUCOPLUM	28	NEG	6	27	67	269	6.5	0.22	0.639
SCOPBREV	70	MUCORACE	29	NEG	7	26	84	252	8.1	0.48	0.488
SCOPBREV	70	PAECSP	30	POS	1	32	7	329	0.7	0.07	0.791
SCOPBREV	70	PAECVARI	31	POS	5	28	45	291	4.5	0.00	1.000
SCOPBREV	70	PENIATRA	32	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	PENIAURA	33	POS	4	29	40	296	3.9	0.06	0.806
SCOPBREV	70	PENIBREV	34	POS	8	25	78	258	7.7	0.01	0.920
SCOPBREV	70	PENICHRY	35	NEG	9	24	182	154	17.1	9.81	0.002
SCOPBREV	70	PENICOMM	36	POS	14	19	80	256	8.4	4.55	0.033
SCOPBREV	70	PENICOPR	37	POS	1	32	9	327	0.9	0.20	0.655
SCOPBREV	70	PENICORY	38	POS	10	23	98	238	9.7	0.00	1.000
SCOPBREV	70	PENICRUS	39	POS	3	30	11	325	1.3	1.42	0.233
SCOPBREV	70	PENICTNG	40	NEG	2	31	32	304	3.0	0.94	0.332
SCOPBREV	70	PENICTRM	41	POS	6	27	46	290	4.7	0.20	0.655
SCOPBREV	70	PENIDECU	42	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	PENIDIGI	43	POS	2	31	8	328	0.9	0.46	0.498
SCOPBREV	70	PENIECHI	44	NEG	0	33	17	319	1.5	3.09	0.079
SCOPBREV	70	PENIEXPA	45	POS	12	21	57	279	6.2	6.22	0.013
SCOPBREV	70	PENIGLAN	46	NEG	0	33	13	323	1.2	2.71	0.100
SCOPBREV	70	PENIGRIS	47	NEG	1	32	22	314	2.1	1.38	0.240
SCOPBREV	70	PENIIMPL	48	NEG	1	32	18	318	1.7	0.98	0.322
SCOPBREV	70	PENIISLA	49	POS	1	32	10	326	1.0	0.27	0.603
SCOPBREV	70	PENIITAL	50	NEG	0	33	11	325	1.0	2.53	0.112
SCOPBREV	70	PENIMICZ	51	NEG	1	32	13	323	1.3	0.52	0.471
SCOPBREV	70	PENIOXAL	52	NEG	1	32	20	316	1.9	1.18	0.277
SCOPBREV	70	PENIPURP	53	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENIRAIS	54	POS	5	28	21	315	2.3	2.40	0.121
SCOPBREV	70	PENIREST	55	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENISIMP	56	POS	3	30	17	319	1.8	0.33	0.566
SCOPBREV	70	PENISP	57	POS	3	30	26	310	2.6	0.00	1.000
SCOPBREV	70	PENISP01	58	POS	1	32	8	328	0.8	0.13	0.718
SCOPBREV	70	PENISP26	59	POS	6	27	47	289	4.7	0.16	0.689
SCOPBREV	70	PENISP64	60	NEG	0	33	10	326	0.9	2.45	0.118
SCOPBREV	70	PENISPIN	61	POS	15	18	127	209	12.7	0.46	0.498
SCOPBREV	70	PENIVARI	62	POS	4	29	8	328	1.1	6.23	0.013
SCOPBREV	70	PENIVERR	63	POS	3	30	6	330	0.8	4.02	0.045
SCOPBREV	70	PENIVIRI	64	NEG	5	28	63	273	6.1	0.55	0.458
SCOPBREV	70	PENIVULP	65	POS	3	30	19	317	2.0	0.17	0.680
SCOPBREV	70	PHOMHERB	66	NEG	8	25	100	236	9.7	0.75	0.386
SCOPBREV	70	PHOMSP	67	NEG	3	30	59	277	5.6	2.21	0.137
SCOPBREV	70	PITHCHAR	68	NEG	2	31	24	312	2.3	0.35	0.554
SCOPBREV	70	RHIZORYZ	69	NEG	4	29	49	287	4.7	0.42	0.517
SCOPCAND	71	ACRESP	1	POS	4	23	21	321	1.8	1.77	0.183
SCOPCAND	71	ALTEALTE	2	POS	24	3	303	39	23.9	0.07	0.791
SCOPCAND	71	ALTESP	3	POS	2	25	14	328	1.2	0.10	0.752



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
SCOPCAND	71	ASPECAND	4	NEG	1	26	18	324	1.4	0.65	0.420
SCOPCAND	71	ASPEFUMI	5	POS	3	24	22	320	1.8	0.28	0.597
SCOPCAND	71	ASPEGLAU	6	NEG	1	26	24	318	1.8	1.12	0.290
SCOPCAND	71	ASPENIGE	7	POS	10	17	116	226	9.2	0.01	0.920
SCOPCAND	71	ASPEOCHR	8	POS	7	20	65	277	5.3	0.39	0.532
SCOPCAND	71	ASPEORYZ	9	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	ASPESP	10	POS	8	19	59	283	4.9	1.81	0.179
SCOPCAND	71	ASPESYDO	11	POS	4	23	42	300	3.4	0.01	0.920
SCOPCAND	71	ASPEUSTU	12	POS	2	25	22	320	1.8	0.04	0.841
SCOPCAND	71	ASPEVERS	13	POS	17	10	179	163	14.3	0.75	0.386
SCOPCAND	71	AUREPULL	14	NEG	20	7	273	69	21.4	0.92	0.337
SCOPCAND	71	CHAEGLOB	15	POS	4	23	20	322	1.8	2.00	0.157
SCOPCAND	71	CHRSPMSP	16	NEG	0	27	14	328	1.0	2.54	0.111
SCOPCAND	71	CLADCLAD	17	NEG	13	14	172	170	13.5	0.17	0.680
SCOPCAND	71	CLADHERB	18	NEG	4	23	83	259	6.4	1.82	0.177
SCOPCAND	71	CLADSP	19	NEG	4	23	60	282	4.7	0.39	0.532
SCOPCAND	71	CLADSPHA	20	POS	13	14	128	214	10.3	0.81	0.368
SCOPCAND	71	CONISP	21	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	EMERNIDU	22	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	EPICNIGR	23	POS	16	11	184	158	14.6	0.12	0.729
SCOPCAND	71	EUROHERB	24	POS	19	8	226	116	17.9	0.06	0.806
SCOPCAND	71	FUSAOXYS	25	POS	2	25	18	324	1.5	0.00	1.000
SCOPCAND	71	FUSASP	26	NEG	3	24	56	286	4.3	0.98	0.322
SCOPCAND	71	GEOMPANN	27	POS	3	24	9	333	0.9	3.34	0.068
SCOPCAND	71	MUCOPLUM	28	POS	7	20	66	276	5.3	0.34	0.560
SCOPCAND	71	MUCORACE	29	POS	8	19	83	259	6.7	0.15	0.699
SCOPCAND	71	PAECSP	30	POS	1	26	7	335	0.6	0.01	0.920
SCOPCAND	71	PAECVARI	31	POS	9	18	41	301	3.7	8.00	0.005
SCOPCAND	71	PENIATRA	32	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIAURA	33	POS	5	22	39	303	3.2	0.62	0.431
SCOPCAND	71	PENIBREV	34	POS	9	18	77	265	6.3	1.09	0.296
SCOPCAND	71	PENICHR	35	POS	15	12	176	166	14.0	0.04	0.841
SCOPCAND	71	PENICOMM	36	NEG	4	23	90	252	6.9	2.40	0.121
SCOPCAND	71	PENICOPR	37	POS	1	26	9	333	0.7	0.08	0.777
SCOPCAND	71	PENICORY	38	POS	14	13	94	248	7.9	6.05	0.014
SCOPCAND	71	PENICRUS	39	POS	2	25	12	330	1.0	0.25	0.617
SCOPCAND	71	PENICTNG	40	POS	3	24	31	311	2.5	0.00	1.000
SCOPCAND	71	PENICTRM	41	POS	5	22	47	295	3.8	0.16	0.689
SCOPCAND	71	PENIDECU	42	NEG	0	27	19	323	1.4	2.92	0.087
SCOPCAND	71	PENIDIGI	43	POS	1	26	9	333	0.7	0.08	0.777
SCOPCAND	71	PENIECHI	44	POS	2	25	15	327	1.2	0.06	0.806
SCOPCAND	71	PENIEXPA	45	NEG	5	22	64	278	5.1	0.08	0.777
SCOPCAND	71	PENIGLAN	46	POS	1	26	12	330	1.0	0.24	0.624
SCOPCAND	71	PENIGRIS	47	NEG	0	27	23	319	1.7	3.26	0.071
SCOPCAND	71	PENIIMPL	48	NEG	0	27	19	323	1.4	2.92	0.087
SCOPCAND	71	PENIISLA	49	POS	1	26	10	332	0.8	0.13	0.718
SCOPCAND	71	PENIITAL	50	POS	1	26	10	332	0.8	0.13	0.718
SCOPCAND	71	PENIMICZ	51	NEG	0	27	14	328	1.0	2.54	0.111
SCOPCAND	71	PENIOXAL	52	POS	2	25	19	323	1.5	0.00	1.000
SCOPCAND	71	PENIPURP	53	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIRAIS	54	NEG	1	26	25	317	1.9	1.20	0.273
SCOPCAND	71	PENIREST	55	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENISIMP	56	POS	2	25	18	324	1.5	0.00	1.000
SCOPCAND	71	PENISP	57	NEG	2	25	27	315	2.1	0.21	0.647
SCOPCAND	71	PENISP01	58	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENISP26	59	NEG	2	25	51	291	3.9	1.84	0.175
SCOPCAND	71	PENISP64	60	NEG	0	27	10	332	0.7	2.30	0.129
SCOPCAND	71	PENISPIN	61	POS	12	15	130	212	10.4	0.21	0.647
SCOPCAND	71	PENIVARI	62	POS	1	26	11	331	0.9	0.18	0.671
SCOPCAND	71	PENIVERR	63	POS	1	26	8	334	0.7	0.04	0.841
SCOPCAND	71	PENIVIRI	64	NEG	4	23	64	278	5.0	0.58	0.446
SCOPCAND	71	PENIVULP	65	POS	2	25	20	322	1.6	0.01	0.920

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
SCOPCAND	71	PHOMHERB	66	NEG	7	20	101	241	7.9	0.38	0.538
SCOPCAND	71	PHOMSP	67	NEG	3	24	59	283	4.5	1.19	0.275
SCOPCAND	71	PITHCHAR	68	POS	3	24	23	319	1.9	0.22	0.639
SCOPCAND	71	RHIZORYZ	69	NEG	2	25	51	291	3.9	1.84	0.175
SCOPCAND	71	SCOPBREV	70	NEG	2	25	31	311	2.4	0.41	0.522
SPHASP	72	ACRESP	1	POS	2	11	23	333	0.9	0.48	0.488
SPHASP	72	ALTEALTE	2	POS	13	0	314	42	11.5	0.76	0.383
SPHASP	72	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
SPHASP	72	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
SPHASP	72	ASPEFUMI	5	POS	1	12	24	332	0.9	0.18	0.671
SPHASP	72	ASPEGLAU	6	POS	1	12	24	332	0.9	0.18	0.671
SPHASP	72	ASPENIGE	7	NEG	3	10	123	233	4.4	1.33	0.249
SPHASP	72	ASPEOCHR	8	NEG	2	11	70	286	2.5	0.55	0.458
SPHASP	72	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	ASPESP	10	POS	3	10	64	292	2.4	0.01	0.920
SPHASP	72	ASPESYDO	11	NEG	1	12	45	311	1.6	0.92	0.337
SPHASP	72	ASPEUSTU	12	NEG	0	13	24	332	0.9	2.37	0.124
SPHASP	72	ASPEVERS	13	NEG	5	8	191	165	6.9	1.85	0.174
SPHASP	72	AUREPULL	14	POS	13	0	280	76	10.3	2.31	0.129
SPHASP	72	CHAEGLOB	15	NEG	0	13	24	332	0.9	2.37	0.124
SPHASP	72	CHRSPMSP	16	POS	1	12	13	343	0.5	0.00	1.000
SPHASP	72	CLADCLAD	17	POS	9	4	176	180	6.5	1.25	0.264
SPHASP	72	CLADHERB	18	POS	6	7	81	275	3.1	2.62	0.106
SPHASP	72	CLADSP	19	NEG	1	12	63	293	2.3	1.71	0.191
SPHASP	72	CLADSPHA	20	NEG	4	9	137	219	5.0	0.73	0.393
SPHASP	72	CONISP	21	POS	2	11	8	348	0.4	3.98	0.046
SPHASP	72	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	EMICNIGR	23	POS	12	1	188	168	7.1	6.37	0.012
SPHASP	72	EUROHERB	24	NEG	8	5	237	119	8.6	0.46	0.498
SPHASP	72	FUSAOXYS	25	POS	1	12	19	337	0.7	0.07	0.791
SPHASP	72	FUSASP	26	NEG	1	12	58	298	2.1	1.48	0.224
SPHASP	72	GEOMPANN	27	NEG	0	13	12	344	0.4	2.16	0.142
SPHASP	72	MUCOPLUM	28	NEG	2	11	71	285	2.6	0.58	0.446
SPHASP	72	MUCORACE	29	POS	4	9	87	269	3.2	0.04	0.841
SPHASP	72	PAECSP	30	NEG	0	13	8	348	0.3	2.30	0.129
SPHASP	72	PAECVARI	31	NEG	1	12	49	307	1.8	1.08	0.299
SPHASP	72	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
SPHASP	72	PENIBREV	34	NEG	3	10	83	273	3.0	0.13	0.718
SPHASP	72	PENICHRY	35	NEG	5	8	186	170	6.7	1.59	0.207
SPHASP	72	PENICOMM	36	NEG	1	12	93	263	3.3	3.32	0.068
SPHASP	72	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENICORY	38	POS	4	9	104	252	3.8	0.04	0.841
SPHASP	72	PENICRUS	39	POS	1	12	13	343	0.5	0.00	1.000
SPHASP	72	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
SPHASP	72	PENICTRM	41	NEG	0	13	52	304	1.8	3.58	0.058
SPHASP	72	PENIDECU	42	NEG	0	13	19	337	0.7	2.23	0.135
SPHASP	72	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENIECHI	44	NEG	0	13	17	339	0.6	2.19	0.139
SPHASP	72	PENIEXPA	45	NEG	2	11	67	289	2.4	0.45	0.502
SPHASP	72	PENIGLAN	46	POS	1	12	12	344	0.5	0.00	1.000
SPHASP	72	PENIGRIS	47	POS	3	10	20	336	0.8	3.89	0.049
SPHASP	72	PENIIMPL	48	POS	1	12	18	338	0.7	0.05	0.823
SPHASP	72	PENIISLA	49	POS	1	12	10	346	0.4	0.03	0.862
SPHASP	72	PENIITAL	50	POS	1	12	10	346	0.4	0.03	0.862
SPHASP	72	PENIMICZ	51	POS	2	11	12	344	0.5	2.21	0.137
SPHASP	72	PENIOXAL	52	POS	3	10	18	338	0.7	4.60	0.032
SPHASP	72	PENIPURP	53	POS	1	12	8	348	0.3	0.11	0.740
SPHASP	72	PENIRAIS	54	POS	1	12	25	331	0.9	0.21	0.647
SPHASP	72	PENIREST	55	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENISIMP	56	NEG	0	13	20	336	0.7	2.26	0.133
SPHASP	72	PENISP	57	POS	2	11	27	329	1.0	0.25	0.617

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
SPHASP	72	PENISP01	58	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENISP26	59	POS	4	9	49	307	1.9	1.73	0.188
SPHASP	72	PENISP64	60	NEG	0	13	10	346	0.4	2.20	0.138
SPHASP	72	PENISPIN	61	NEG	3	10	139	217	5.0	2.11	0.146
SPHASP	72	PENIVARI	62	NEG	0	13	12	344	0.4	2.16	0.142
SPHASP	72	PENIVERR	63	NEG	0	13	9	347	0.3	2.24	0.134
SPHASP	72	PENIVIRI	64	POS	5	8	63	293	2.4	2.35	0.125
SPHASP	72	PENIVULP	65	POS	2	11	20	336	0.8	0.75	0.386
SPHASP	72	PHOMHERB	66	POS	7	6	101	255	3.8	2.80	0.094
SPHASP	72	PHOMSP	67	NEG	2	11	60	296	2.2	0.27	0.603
SPHASP	72	PITHCHAR	68	POS	3	10	23	333	0.9	3.05	0.081
SPHASP	72	RHIZORYZ	69	POS	2	11	51	305	1.9	0.09	0.764
SPHASP	72	SCOPBREV	70	NEG	1	12	32	324	1.2	0.43	0.512
SPHASP	72	SCOPCAND	71	POS	1	12	26	330	1.0	0.24	0.624
STACCHAR	73	ACRESP	1	POS	1	12	24	332	0.9	0.18	0.671
STACCHAR	73	ALTEALTE	2	POS	12	1	315	41	11.5	0.00	1.000
STACCHAR	73	ALTESP	3	NEG	0	13	16	340	0.6	2.17	0.141
STACCHAR	73	ASPECAND	4	POS	1	12	18	338	0.7	0.05	0.823
STACCHAR	73	ASPEFUMI	5	NEG	0	13	25	331	0.9	2.41	0.121
STACCHAR	73	ASPEGLAU	6	POS	1	12	24	332	0.9	0.18	0.671
STACCHAR	73	ASPENIGE	7	NEG	4	9	122	234	4.4	0.31	0.578
STACCHAR	73	ASPEOCHR	8	POS	3	10	69	287	2.5	0.00	1.000
STACCHAR	73	ASPEORYZ	9	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	ASPESP	10	POS	4	9	63	293	2.4	0.70	0.403
STACCHAR	73	ASPESYDO	11	POS	3	10	43	313	1.6	0.57	0.450
STACCHAR	73	ASPEUSTU	12	POS	1	12	23	333	0.9	0.16	0.689
STACCHAR	73	ASPEVERS	13	POS	8	5	188	168	6.9	0.11	0.740
STACCHAR	73	AUREPULL	14	NEG	10	3	283	73	10.3	0.33	0.566
STACCHAR	73	CHAEGLOB	15	POS	1	12	23	333	0.9	0.16	0.689
STACCHAR	73	CHRSPMSP	16	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	CLADCLAD	17	POS	9	4	176	180	6.5	1.25	0.264
STACCHAR	73	CLADHERB	18	POS	7	6	80	276	3.1	5.22	0.022
STACCHAR	73	CLADSP	19	NEG	1	12	63	293	2.3	1.71	0.191
STACCHAR	73	CLADSPHA	20	POS	7	6	134	222	5.0	0.79	0.374
STACCHAR	73	CONISP	21	POS	1	12	9	347	0.4	0.07	0.791
STACCHAR	73	EMERNIDU	22	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	EPICNIGR	23	POS	9	4	191	165	7.1	0.68	0.410
STACCHAR	73	EUROHERB	24	POS	9	4	236	120	8.6	0.01	0.920
STACCHAR	73	FUSAOXYS	25	POS	1	12	19	337	0.7	0.07	0.791
STACCHAR	73	FUSASP	26	NEG	0	13	59	297	2.1	3.95	0.047
STACCHAR	73	GEOMPANN	27	POS	1	12	11	345	0.4	0.02	0.888
STACCHAR	73	MUCOPLUM	28	NEG	1	12	72	284	2.6	2.16	0.142
STACCHAR	73	MUCORACE	29	NEG	3	10	88	268	3.2	0.21	0.647
STACCHAR	73	PAECSP	30	NEG	0	13	8	348	0.3	2.30	0.129
STACCHAR	73	PAECVARI	31	NEG	0	13	50	306	1.8	3.48	0.062
STACCHAR	73	PENIATRA	32	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENIAURA	33	POS	2	11	42	314	1.6	0.00	1.000
STACCHAR	73	PENIBREV	34	NEG	1	12	85	271	3.0	2.85	0.091
STACCHAR	73	PENICHRY	35	NEG	6	7	185	171	6.7	0.48	0.488
STACCHAR	73	PENICOMM	36	NEG	3	10	91	265	3.3	0.28	0.597
STACCHAR	73	PENICOPR	37	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENICORY	38	POS	7	6	101	255	3.8	2.80	0.094
STACCHAR	73	PENICRUS	39	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	PENICTNG	40	NEG	0	13	34	322	1.2	2.75	0.097
STACCHAR	73	PENICTRM	41	POS	2	11	50	306	1.8	0.07	0.791
STACCHAR	73	PENIDECU	42	POS	1	12	18	338	0.7	0.05	0.823
STACCHAR	73	PENIDIGI	43	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENIECHI	44	NEG	0	13	17	339	0.6	2.19	0.139
STACCHAR	73	PENIEXPA	45	POS	3	10	66	290	2.4	0.00	1.000
STACCHAR	73	PENIGLAN	46	NEG	0	13	13	343	0.5	2.15	0.143
STACCHAR	73	PENIGRIS	47	POS	1	12	22	334	0.8	0.13	0.718
STACCHAR	73	PENIIMPL	48	NEG	0	13	19	337	0.7	2.23	0.135

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
STACCHAR	73	PENIISLA	49	NEG	0	13	11	345	0.4	2.17	0.141
STACCHAR	73	PENIITAL	50	NEG	0	13	11	345	0.4	2.17	0.141
STACCHAR	73	PENIMICZ	51	NEG	0	13	14	342	0.5	2.15	0.143
STACCHAR	73	PENIOXAL	52	POS	1	12	20	336	0.7	0.09	0.764
STACCHAR	73	PENIPURP	53	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENIRAIS	54	POS	1	12	25	331	0.9	0.21	0.647
STACCHAR	73	PENIREST	55	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENISIMP	56	NEG	0	13	20	336	0.7	2.26	0.133
STACCHAR	73	PENISP	57	NEG	0	13	29	327	1.0	2.55	0.110
STACCHAR	73	PENISP01	58	NEG	0	13	9	347	0.3	2.24	0.134
STACCHAR	73	PENISP26	59	NEG	0	13	53	303	1.9	3.63	0.057
STACCHAR	73	PENISP64	60	NEG	0	13	10	346	0.4	2.20	0.138
STACCHAR	73	PENISPIN	61	NEG	3	10	139	217	5.0	2.11	0.146
STACCHAR	73	PENIVARI	62	POS	1	12	11	345	0.4	0.02	0.888
STACCHAR	73	PENIVERR	63	POS	1	12	8	348	0.3	0.11	0.740
STACCHAR	73	PENIVIRI	64	NEG	2	11	66	290	2.4	0.43	0.512
STACCHAR	73	PENIVULP	65	NEG	0	13	22	334	0.8	2.31	0.129
STACCHAR	73	PHOMHERB	66	POS	5	8	103	253	3.8	0.19	0.663
STACCHAR	73	PHOMSP	67	POS	4	9	58	298	2.2	0.99	0.320
STACCHAR	73	PITHCHAR	68	POS	1	12	25	331	0.9	0.21	0.647
STACCHAR	73	RHIZORYZ	69	NEG	1	12	52	304	1.9	1.21	0.271
STACCHAR	73	SCOPBREV	70	POS	3	10	30	326	1.2	1.75	0.186
STACCHAR	73	SCOPCAND	71	POS	2	11	25	331	1.0	0.35	0.554
STACCHAR	73	SPHASP	72	POS	2	11	11	345	0.5	2.55	0.110
TRICSP	74	ACRESP	1	POS	2	5	23	339	0.5	2.43	0.119
TRICSP	74	ALTEALTE	2	POS	7	0	320	42	6.2	0.13	0.718
TRICSP	74	ALTESP	3	POS	1	6	15	347	0.3	0.14	0.708
TRICSP	74	ASPECAND	4	POS	1	6	18	344	0.4	0.06	0.806
TRICSP	74	ASPEFUMI	5	NEG	0	7	25	337	0.5	2.19	0.139
TRICSP	74	ASPEGLAU	6	POS	1	6	24	338	0.5	0.00	1.000
TRICSP	74	ASPENIGE	7	POS	3	4	123	239	2.4	0.01	0.920
TRICSP	74	ASPEOCHR	8	NEG	0	7	72	290	1.4	3.23	0.072
TRICSP	74	ASPEORYZ	9	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	ASPESP	10	NEG	0	7	67	295	1.3	3.07	0.080
TRICSP	74	ASPESYDO	11	POS	1	6	45	317	0.9	0.19	0.663
TRICSP	74	ASPEUSTU	12	POS	1	6	23	339	0.5	0.00	1.000
TRICSP	74	ASPEVERS	13	NEG	2	5	194	168	3.7	2.88	0.090
TRICSP	74	AUREPULL	14	POS	6	1	287	75	5.6	0.00	1.000
TRICSP	74	CHAEGLOB	15	POS	1	6	23	339	0.5	0.00	1.000
TRICSP	74	CHRSPMSP	16	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	CLADCLAD	17	POS	6	1	179	183	3.5	2.31	0.129
TRICSP	74	CLADHERB	18	NEG	1	6	86	276	1.7	1.07	0.301
TRICSP	74	CLADSP	19	NEG	1	6	63	299	1.2	0.52	0.471
TRICSP	74	CLADSPHA	20	POS	4	3	137	225	2.7	0.42	0.517
TRICSP	74	CONISP	21	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	EMERNIDU	22	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	EPICNIGR	23	POS	5	2	195	167	3.8	0.29	0.590
TRICSP	74	EUROHERB	24	POS	5	2	240	122	4.7	0.01	0.920
TRICSP	74	FUSAOXYS	25	POS	1	6	19	343	0.4	0.04	0.841
TRICSP	74	FUSASP	26	POS	2	5	57	305	1.1	0.16	0.689
TRICSP	74	GEOMANN	27	NEG	0	7	12	350	0.2	2.45	0.118
TRICSP	74	MUCOPLUM	28	NEG	1	6	72	290	1.4	0.72	0.396
TRICSP	74	MUCORACE	29	POS	3	4	88	274	1.7	0.47	0.493
TRICSP	74	PAECSP	30	NEG	0	7	8	354	0.2	2.92	0.087
TRICSP	74	PAECVARI	31	POS	2	5	48	314	1.0	0.38	0.538
TRICSP	74	PENIATRA	32	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENIAURA	33	POS	1	6	43	319	0.8	0.16	0.689
TRICSP	74	PENIBREV	34	POS	2	5	84	278	1.6	0.01	0.920
TRICSP	74	PENICHRY	35	NEG	3	4	188	174	3.6	0.74	0.390
TRICSP	74	PENICOMM	36	NEG	0	7	94	268	1.8	4.00	0.046
TRICSP	74	PENICOPR	37	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENICORY	38	POS	6	1	102	260	2.1	8.38	0.004

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
TRICSP	74	PENICRUS	39	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	PENICTNG	40	POS	1	6	33	329	0.6	0.04	0.841
TRICSP	74	PENICTRM	41	POS	1	6	51	311	1.0	0.28	0.597
TRICSP	74	PENIDECU	42	NEG	0	7	19	343	0.4	2.21	0.137
TRICSP	74	PENIDIGI	43	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENIECHI	44	NEG	0	7	17	345	0.3	2.24	0.134
TRICSP	74	PENIEXPA	45	NEG	1	6	68	294	1.3	0.63	0.427
TRICSP	74	PENIGLAN	46	POS	1	6	12	350	0.3	0.28	0.597
TRICSP	74	PENIGRIS	47	POS	1	6	22	340	0.4	0.01	0.920
TRICSP	74	PENIIMPL	48	POS	1	6	18	344	0.4	0.06	0.806
TRICSP	74	PENIISLA	49	NEG	0	7	11	351	0.2	2.53	0.112
TRICSP	74	PENIITAL	50	NEG	0	7	11	351	0.2	2.53	0.112
TRICSP	74	PENIMICZ	51	NEG	0	7	14	348	0.3	2.34	0.126
TRICSP	74	PENIOXAL	52	POS	1	6	20	342	0.4	0.03	0.862
TRICSP	74	PENIPURP	53	NEG	0	7	9	353	0.2	2.75	0.097
TRICSP	74	PENIRAIS	54	NEG	0	7	26	336	0.5	2.19	0.139
TRICSP	74	PENIREST	55	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENISIMP	56	NEG	0	7	20	342	0.4	2.20	0.138
TRICSP	74	PENISP	57	NEG	0	7	29	333	0.6	2.22	0.136
TRICSP	74	PENISP01	58	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENISP26	59	POS	2	5	51	311	1.0	0.29	0.590
TRICSP	74	PENISP64	60	NEG	0	7	10	352	0.2	2.63	0.105
TRICSP	74	PENISPIN	61	NEG	2	5	140	222	2.7	0.88	0.348
TRICSP	74	PENIVARI	62	NEG	0	7	12	350	0.2	2.45	0.118
TRICSP	74	PENIVERR	63	POS	1	6	8	354	0.2	0.66	0.417
TRICSP	74	PENIVIRI	64	NEG	1	6	67	295	1.3	0.60	0.439
TRICSP	74	PENIVULP	65	POS	1	6	21	341	0.4	0.02	0.888
TRICSP	74	PHOMHERB	66	POS	5	2	103	259	2.1	4.23	0.040
TRICSP	74	PHOMSP	67	NEG	0	7	62	300	1.2	2.93	0.087
TRICSP	74	PITHCHAR	68	POS	1	6	25	337	0.5	0.00	1.000
TRICSP	74	RHIZORYZ	69	NEG	0	7	53	309	1.0	2.68	0.102
TRICSP	74	SCOPBREV	70	NEG	0	7	33	329	0.6	2.27	0.132
TRICSP	74	SCOPCAND	71	POS	1	6	26	336	0.5	0.00	1.000
TRICSP	74	SPHASP	72	POS	1	6	12	350	0.3	0.28	0.597
TRICSP	74	STACCHAR	73	POS	1	6	12	350	0.3	0.28	0.597
TRICVIRI	75	ACRESP	1	POS	9	102	16	242	7.5	0.20	0.655
TRICVIRI	75	ALTEALTE	2	NEG	96	15	231	27	98.4	1.05	0.306
TRICVIRI	75	ALTESP	3	NEG	2	109	14	244	4.8	3.41	0.065
TRICVIRI	75	ASPECAND	4	POS	8	103	11	247	5.7	0.84	0.359
TRICVIRI	75	ASPEFUMI	5	POS	12	99	13	245	7.5	3.23	0.072
TRICVIRI	75	ASPEGLAU	6	POS	8	103	17	241	7.5	0.00	1.000
TRICVIRI	75	ASPENIGE	7	NEG	37	74	89	169	37.9	0.11	0.740
TRICVIRI	75	ASPEOCHR	8	POS	27	84	45	213	21.7	1.92	0.166
TRICVIRI	75	ASPEORYZ	9	POS	3	108	6	252	2.7	0.02	0.888
TRICVIRI	75	ASPESP	10	NEG	20	91	47	211	20.2	0.04	0.841
TRICVIRI	75	ASPESYDO	11	NEG	11	100	35	223	13.8	1.32	0.251
TRICVIRI	75	ASPEUSTU	12	NEG	7	104	17	241	7.2	0.11	0.740
TRICVIRI	75	ASPEVERS	13	NEG	54	57	142	116	59.0	1.54	0.215
TRICVIRI	75	AUREPULL	14	POS	91	20	202	56	88.1	0.44	0.507
TRICVIRI	75	CHAEGLOB	15	NEG	6	105	18	240	7.2	0.63	0.427
TRICVIRI	75	CHRSPMSP	16	POS	10	101	4	254	4.2	9.87	0.002
TRICVIRI	75	CLADCLAD	17	POS	56	55	129	129	55.7	0.00	1.000
TRICVIRI	75	CLADHERB	18	NEG	26	85	61	197	26.2	0.03	0.862
TRICVIRI	75	CLADSP	19	POS	26	85	38	220	19.3	3.51	0.061
TRICVIRI	75	CLADSPHA	20	POS	46	65	95	163	42.4	0.52	0.471
TRICVIRI	75	CONISP	21	POS	5	106	5	253	3.0	1.09	0.296
TRICVIRI	75	EMERNIDU	22	POS	4	107	6	252	3.0	0.12	0.729
TRICVIRI	75	EPICNIGR	23	NEG	52	59	148	110	60.2	3.90	0.048
TRICVIRI	75	EUROHERB	24	NEG	72	39	173	85	73.7	0.28	0.597
TRICVIRI	75	FUSAOXYS	25	POS	8	103	12	246	6.0	0.55	0.458
TRICVIRI	75	FUSASP	26	NEG	17	94	42	216	17.8	0.15	0.699
TRICVIRI	75	GEOMPANN	27	POS	4	107	8	250	3.6	0.00	1.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
TRICVIRI	75	MUCOPLUM	28	POS	26	85	47	211	22.0	1.02	0.313
TRICVIRI	75	MUCORACE	29	POS	28	83	63	195	27.4	0.00	1.000
TRICVIRI	75	PAECSP	30	NEG	2	109	6	252	2.4	0.50	0.480
TRICVIRI	75	PAECVARI	31	NEG	10	101	40	218	15.0	3.38	0.066
TRICVIRI	75	PENIATRA	32	POS	5	106	4	254	2.7	1.74	0.187
TRICVIRI	75	PENIAURA	33	POS	15	96	29	229	13.2	0.20	0.655
TRICVIRI	75	PENIBREV	34	POS	33	78	53	205	25.9	3.17	0.075
TRICVIRI	75	PENICHRYS	35	NEG	50	61	141	117	57.5	3.27	0.071
TRICVIRI	75	PENICOMM	36	POS	33	78	61	197	28.3	1.21	0.271
TRICVIRI	75	PENICOPR	37	POS	4	107	6	252	3.0	0.12	0.729
TRICVIRI	75	PENICORY	38	POS	38	73	70	188	32.5	1.56	0.212
TRICVIRI	75	PENICRUS	39	NEG	3	108	11	247	4.2	1.03	0.310
TRICVIRI	75	PENICTNG	40	POS	17	94	17	241	10.2	6.06	0.014
TRICVIRI	75	PENICTRM	41	POS	21	90	31	227	15.6	2.51	0.113
TRICVIRI	75	PENIDECU	42	POS	8	103	11	247	5.7	0.84	0.359
TRICVIRI	75	PENIDIGI	43	NEG	3	108	7	251	3.0	0.13	0.718
TRICVIRI	75	PENIECHI	44	POS	8	103	9	249	5.1	1.67	0.196
TRICVIRI	75	PENIEXPA	45	NEG	20	91	49	209	20.8	0.13	0.718
TRICVIRI	75	PENIGLAN	46	POS	4	107	9	249	3.9	0.06	0.806
TRICVIRI	75	PENIGRIS	47	POS	7	104	16	242	6.9	0.04	0.841
TRICVIRI	75	PENIIMPL	48	POS	9	102	10	248	5.7	2.05	0.152
TRICVIRI	75	PENIISLA	49	POS	4	107	7	251	3.3	0.02	0.888
TRICVIRI	75	PENIITAL	50	NEG	3	108	8	250	3.3	0.29	0.590
TRICVIRI	75	PENIMICZ	51	POS	6	105	8	250	4.2	0.59	0.442
TRICVIRI	75	PENIOXAL	52	NEG	6	105	15	243	6.3	0.16	0.689
TRICVIRI	75	PENIPURP	53	POS	3	108	6	252	2.7	0.02	0.888
TRICVIRI	75	PENIRAIS	54	NEG	4	107	22	236	7.8	3.67	0.055
TRICVIRI	75	PENIREST	55	POS	6	105	3	255	2.7	4.22	0.040
TRICVIRI	75	PENISIMP	56	NEG	5	106	15	243	6.0	0.58	0.446
TRICVIRI	75	PENISP	57	POS	13	98	16	242	8.7	2.54	0.111
TRICVIRI	75	PENISP01	58	NEG	1	110	8	250	2.7	2.64	0.104
TRICVIRI	75	PENISP26	59	POS	16	95	37	221	15.9	0.02	0.888
TRICVIRI	75	PENISP64	60	NEG	3	108	7	251	3.0	0.13	0.718
TRICVIRI	75	PENISPIN	61	POS	46	65	96	162	42.7	0.42	0.517
TRICVIRI	75	PENIVARI	62	POS	7	104	5	253	3.6	3.42	0.064
TRICVIRI	75	PENIVERR	63	POS	5	106	4	254	2.7	1.74	0.187
TRICVIRI	75	PENIVIRI	64	NEG	18	93	50	208	20.5	0.75	0.386
TRICVIRI	75	PENIVULP	65	POS	9	102	13	245	6.6	0.81	0.368
TRICVIRI	75	PHOMHERB	66	POS	33	78	75	183	32.5	0.00	1.000
TRICVIRI	75	PHOMSP	67	NEG	13	98	49	209	18.7	3.49	0.062
TRICVIRI	75	PITHCHAR	68	POS	9	102	17	241	7.8	0.09	0.764
TRICVIRI	75	RHIZORYZ	69	POS	21	90	32	226	15.9	2.18	0.140
TRICVIRI	75	SCOPBREV	70	POS	13	98	20	238	9.9	1.05	0.306
TRICVIRI	75	SCOPCAND	71	NEG	6	105	21	237	8.1	1.31	0.252
TRICVIRI	75	SPHASP	72	POS	6	105	7	251	3.9	0.96	0.327
TRICVIRI	75	STACCHAR	73	POS	4	107	9	249	3.9	0.06	0.806
TRICVIRI	75	TRICSP	74	POS	4	107	3	255	2.1	1.35	0.245
ULOCCHAR	76	ACRESP	1	POS	4	51	21	293	3.7	0.02	0.888
ULOCCHAR	76	ALTEALTE	2	POS	52	3	275	39	48.7	1.61	0.204
ULOCCHAR	76	ALTESP	3	POS	5	50	11	303	2.4	2.30	0.129
ULOCCHAR	76	ASPECAND	4	NEG	2	53	17	297	2.8	0.78	0.377
ULOCCHAR	76	ASPEFUMI	5	POS	5	50	20	294	3.7	0.20	0.655
ULOCCHAR	76	ASPEGLAU	6	NEG	3	52	22	292	3.7	0.51	0.475
ULOCCHAR	76	ASPENIGE	7	NEG	15	40	111	203	18.8	1.74	0.187
ULOCCHAR	76	ASPEOCHR	8	POS	15	40	57	257	10.7	1.93	0.165
ULOCCHAR	76	ASPEORYZ	9	NEG	1	54	8	306	1.3	0.64	0.424
ULOCCHAR	76	ASPESP	10	NEG	9	46	58	256	10.0	0.32	0.572
ULOCCHAR	76	ASPESYDO	11	NEG	6	49	40	274	6.9	0.36	0.549
ULOCCHAR	76	ASPEUSTU	12	NEG	0	55	24	290	3.6	5.84	0.016
ULOCCHAR	76	ASPEVERS	13	NEG	28	27	168	146	29.2	0.25	0.617
ULOCCHAR	76	AUREPULL	14	POS	50	5	243	71	43.7	4.44	0.035
ULOCCHAR	76	CHAEGLOB	15	POS	4	51	20	294	3.6	0.00	1.000

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
ULOCCHAR	76	CHRSPMSP	16	POS	3	52	11	303	2.1	0.10	0.752
ULOCCHAR	76	CLADCLAD	17	POS	36	19	149	165	27.6	5.37	0.020
ULOCCHAR	76	CLADHERB	18	NEG	9	46	78	236	13.0	2.37	0.124
ULOCCHAR	76	CLADSP	19	POS	11	44	53	261	9.5	0.14	0.708
ULOCCHAR	76	CLADSPHA	20	POS	27	28	114	200	21.0	2.72	0.099
ULOCCHAR	76	CONISP	21	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	EMERNIDU	22	POS	3	52	7	307	1.5	0.83	0.362
ULOCCHAR	76	EPICNIGR	23	POS	37	18	163	151	29.8	3.85	0.050
ULOCCHAR	76	EUROHERB	24	POS	39	16	206	108	36.5	0.38	0.538
ULOCCHAR	76	FUSAOXYS	25	POS	4	51	16	298	3.0	0.11	0.740
ULOCCHAR	76	FUSASP	26	POS	11	44	48	266	8.8	0.46	0.498
ULOCCHAR	76	GEOMPANN	27	NEG	0	55	12	302	1.8	3.56	0.059
ULOCCHAR	76	MUCOPLUM	28	NEG	9	46	64	250	10.9	0.76	0.383
ULOCCHAR	76	MUCORACE	29	POS	16	39	75	239	13.6	0.43	0.512
ULOCCHAR	76	PAECSP	30	NEG	0	55	8	306	1.2	2.89	0.089
ULOCCHAR	76	PAECVARI	31	POS	9	46	41	273	7.5	0.20	0.655
ULOCCHAR	76	PENIATRA	32	POS	3	52	6	308	1.3	1.21	0.271
ULOCCHAR	76	PENIAURA	33	NEG	3	52	41	273	6.6	3.35	0.067
ULOCCHAR	76	PENIBREV	34	NEG	11	44	75	239	12.8	0.64	0.424
ULOCCHAR	76	PENICHRY	35	NEG	28	27	163	151	28.5	0.08	0.777
ULOCCHAR	76	PENICOMM	36	POS	18	37	76	238	14.0	1.37	0.242
ULOCCHAR	76	PENICOPR	37	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	PENICORY	38	POS	20	35	88	226	16.1	1.19	0.275
ULOCCHAR	76	PENICRUS	39	POS	4	51	10	304	2.1	1.17	0.279
ULOCCHAR	76	PENICTNG	40	POS	7	48	27	287	5.1	0.52	0.471
ULOCCHAR	76	PENICTRM	41	POS	10	45	42	272	7.8	0.54	0.462
ULOCCHAR	76	PENIDECU	42	POS	4	51	15	299	2.8	0.20	0.655
ULOCCHAR	76	PENIDIGI	43	POS	2	53	8	306	1.5	0.00	1.000
ULOCCHAR	76	PENIECHI	44	POS	3	52	14	300	2.5	0.00	1.000
ULOCCHAR	76	PENIEXPA	45	POS	16	39	53	261	10.3	3.82	0.051
ULOCCHAR	76	PENIGLAN	46	POS	2	53	11	303	1.9	0.12	0.729
ULOCCHAR	76	PENIGRIS	47	POS	5	50	18	296	3.4	0.42	0.517
ULOCCHAR	76	PENIIMPL	48	NEG	1	54	18	296	2.8	2.38	0.123
ULOCCHAR	76	PENIISLA	49	POS	3	52	8	306	1.6	0.55	0.458
ULOCCHAR	76	PENIITAL	50	NEG	1	54	10	304	1.6	0.96	0.327
ULOCCHAR	76	PENIMICZ	51	NEG	2	53	12	302	2.1	0.20	0.655
ULOCCHAR	76	PENIOXAL	52	POS	4	51	17	297	3.1	0.05	0.823
ULOCCHAR	76	PENIPURP	53	NEG	0	55	9	305	1.3	3.04	0.081
ULOCCHAR	76	PENIRAIS	54	POS	5	50	21	293	3.9	0.13	0.718
ULOCCHAR	76	PENIREST	55	NEG	1	54	8	306	1.3	0.64	0.424
ULOCCHAR	76	PENISIMP	56	NEG	1	54	19	295	3.0	2.57	0.109
ULOCCHAR	76	PENISP	57	NEG	3	52	26	288	4.3	0.98	0.322
ULOCCHAR	76	PENISP01	58	POS	3	52	6	308	1.3	1.21	0.271
ULOCCHAR	76	PENISP26	59	POS	10	45	43	271	7.9	0.44	0.507
ULOCCHAR	76	PENISP64	60	NEG	0	55	10	304	1.5	3.21	0.073
ULOCCHAR	76	PENISPIN	61	NEG	21	34	121	193	21.2	0.04	0.841
ULOCCHAR	76	PENIVARI	62	POS	2	53	10	304	1.8	0.06	0.806
ULOCCHAR	76	PENIVERR	63	POS	4	51	5	309	1.3	4.18	0.041
ULOCCHAR	76	PENIVIRI	64	POS	12	43	56	258	10.1	0.26	0.610
ULOCCHAR	76	PENIVULP	65	POS	4	51	18	296	3.3	0.02	0.888
ULOCCHAR	76	PHOMHERB	66	POS	24	31	84	230	16.1	5.66	0.017
ULOCCHAR	76	PHOMSP	67	POS	14	41	48	266	9.2	2.77	0.096
ULOCCHAR	76	PITHCHAR	68	POS	4	51	22	292	3.9	0.05	0.823
ULOCCHAR	76	RHIZORYZ	69	NEG	6	49	47	267	7.9	1.00	0.317
ULOCCHAR	76	SCOPBREV	70	POS	8	47	25	289	4.9	1.75	0.186
ULOCCHAR	76	SCOPCAND	71	POS	7	48	20	294	4.0	1.93	0.165
ULOCCHAR	76	SPHASP	72	POS	5	50	8	306	1.9	4.13	0.042
ULOCCHAR	76	STACCHAR	73	POS	3	52	10	304	1.9	0.20	0.655
ULOCCHAR	76	TRICSP	74	POS	3	52	4	310	1.0	2.44	0.118
ULOCCHAR	76	TRICVIRI	75	NEG	14	41	97	217	16.5	0.94	0.332
WALLSEBI	77	ACRESP	1	POS	7	83	18	261	6.1	0.04	0.841
WALLSEBI	77	ALTEALTE	2	NEG	78	12	249	30	79.8	0.74	0.390

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
WALLSEBI	77	ALTESP	3	NEG	3	87	13	266	3.9	0.70	0.403
WALLSEBI	77	ASPECAND	4	NEG	4	86	15	264	4.6	0.39	0.532
WALLSEBI	77	ASPEFUMI	5	NEG	5	85	20	259	6.1	0.59	0.442
WALLSEBI	77	ASPEGLAU	6	POS	7	83	18	261	6.1	0.04	0.841
WALLSEBI	77	ASPENIGE	7	NEG	30	60	96	183	30.7	0.10	0.752
WALLSEBI	77	ASPEOCHR	8	POS	20	70	52	227	17.6	0.35	0.554
WALLSEBI	77	ASPEORYZ	9	POS	3	87	6	273	2.2	0.06	0.806
WALLSEBI	77	ASPESP	10	POS	23	67	44	235	16.3	3.75	0.053
WALLSEBI	77	ASPESYDO	11	NEG	10	80	36	243	11.2	0.40	0.527
WALLSEBI	77	ASPEUSTU	12	NEG	5	85	19	260	5.9	0.44	0.507
WALLSEBI	77	ASPEVERS	13	POS	59	31	137	142	47.8	6.75	0.009
WALLSEBI	77	AUREPULL	14	POS	72	18	221	58	71.5	0.00	1.000
WALLSEBI	77	CHAEGLOB	15	POS	9	81	15	264	5.9	1.69	0.194
WALLSEBI	77	CHRSPMSP	16	NEG	2	88	12	267	3.4	1.48	0.224
WALLSEBI	77	CLADCLAD	17	POS	48	42	137	142	45.1	0.33	0.566
WALLSEBI	77	CLADHERB	18	NEG	16	74	71	208	21.2	2.67	0.102
WALLSEBI	77	CLADSP	19	NEG	13	77	51	228	15.6	0.99	0.320
WALLSEBI	77	CLADSPHA	20	POS	43	47	98	181	34.4	4.09	0.043
WALLSEBI	77	CONISP	21	POS	3	87	7	272	2.4	0.00	1.000
WALLSEBI	77	EMERNIDU	22	POS	5	85	5	274	2.4	2.37	0.124
WALLSEBI	77	EPICNIGR	23	NEG	48	42	152	127	48.8	0.10	0.752
WALLSEBI	77	EUROHERB	24	POS	70	20	175	104	59.8	6.25	0.012
WALLSEBI	77	FUSAOXYS	25	POS	6	84	14	265	4.9	0.11	0.740
WALLSEBI	77	FUSASP	26	POS	17	73	42	237	14.4	0.49	0.484
WALLSEBI	77	GEOMPANN	27	POS	3	87	9	270	2.9	0.09	0.764
WALLSEBI	77	MUCOPLUM	28	NEG	16	74	57	222	17.8	0.49	0.484
WALLSEBI	77	MUCORACE	29	POS	23	67	68	211	22.2	0.01	0.920
WALLSEBI	77	PAECOSP	30	POS	2	88	6	273	2.0	0.14	0.708
WALLSEBI	77	PAECVARI	31	NEG	9	81	41	238	12.2	1.71	0.191
WALLSEBI	77	PENIATRA	32	NEG	2	88	7	272	2.2	0.30	0.584
WALLSEBI	77	PENIAURA	33	NEG	10	80	34	245	10.7	0.21	0.647
WALLSEBI	77	PENIBREV	34	POS	23	67	63	216	21.0	0.19	0.663
WALLSEBI	77	PENICHRY	35	NEG	43	47	148	131	46.6	0.98	0.322
WALLSEBI	77	PENICOMM	36	POS	28	62	66	213	22.9	1.62	0.203
WALLSEBI	77	PENICOPR	37	NEG	2	88	8	271	2.4	0.49	0.484
WALLSEBI	77	PENICORY	38	POS	32	58	76	203	26.3	1.89	0.169
WALLSEBI	77	PENICRUS	39	POS	4	86	10	269	3.4	0.00	1.000
WALLSEBI	77	PENICTNG	40	NEG	7	83	27	252	8.3	0.56	0.454
WALLSEBI	77	PENICTRM	41	POS	15	75	37	242	12.7	0.40	0.527
WALLSEBI	77	PENIDECU	42	NEG	4	86	15	264	4.6	0.39	0.532
WALLSEBI	77	PENIDIGI	43	NEG	1	89	9	270	2.4	2.10	0.147
WALLSEBI	77	PENIECHI	44	POS	9	81	8	271	4.2	6.34	0.012
WALLSEBI	77	PENIEXPA	45	POS	23	67	46	233	16.8	3.11	0.078
WALLSEBI	77	PENIGLAN	46	NEG	3	87	10	269	3.2	0.19	0.663
WALLSEBI	77	PENIGRIS	47	POS	10	80	13	266	5.6	3.81	0.051
WALLSEBI	77	PENIIMPL	48	NEG	3	87	16	263	4.6	1.37	0.242
WALLSEBI	77	PENIISLA	49	NEG	2	88	9	270	2.7	0.71	0.399
WALLSEBI	77	PENIITAL	50	POS	3	87	8	271	2.7	0.02	0.888
WALLSEBI	77	PENIMICZ	51	NEG	3	87	11	268	3.4	0.34	0.560
WALLSEBI	77	PENIOXAL	52	POS	6	84	15	264	5.1	0.04	0.841
WALLSEBI	77	PENIPURP	53	NEG	1	89	8	271	2.2	1.77	0.183
WALLSEBI	77	PENIRAIS	54	POS	8	82	18	261	6.3	0.30	0.584
WALLSEBI	77	PENIREST	55	NEG	2	88	7	272	2.2	0.30	0.584
WALLSEBI	77	PENISIMP	56	POS	7	83	13	266	4.9	0.75	0.386
WALLSEBI	77	PENISP	57	NEG	6	84	23	256	7.1	0.50	0.480
WALLSEBI	77	PENISP01	58	POS	3	87	6	273	2.2	0.06	0.806
WALLSEBI	77	PENISP26	59	POS	15	75	38	241	12.9	0.30	0.584
WALLSEBI	77	PENISP64	60	NEG	1	89	9	270	2.4	2.10	0.147
WALLSEBI	77	PENISPIN	61	NEG	32	58	110	169	34.6	0.61	0.435
WALLSEBI	77	PENIVARI	62	POS	5	85	7	272	2.9	1.16	0.281
WALLSEBI	77	PENIVERR	63	NEG	1	89	8	271	2.2	1.77	0.183
WALLSEBI	77	PENIVIRI	64	NEG	11	79	57	222	16.6	3.62	0.057



Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
WALLSEBI	77	PENIVULP	65	NEG	5	85	17	262	5.4	0.20	0.655
WALLSEBI	77	PHOMHERB	66	NEG	23	67	85	194	26.3	1.05	0.306
WALLSEBI	77	PHOMSP	67	NEG	13	77	49	230	15.1	0.72	0.396
WALLSEBI	77	PITHCHAR	68	NEG	2	88	24	255	6.3	5.26	0.022
WALLSEBI	77	RHIZORYZ	69	NEG	12	78	41	238	12.9	0.24	0.624
WALLSEBI	77	SCOPBREV	70	POS	11	79	22	257	8.1	1.08	0.299
WALLSEBI	77	SCOPCAND	71	POS	8	82	19	260	6.6	0.18	0.671
WALLSEBI	77	SPHASP	72	POS	4	86	9	270	3.2	0.05	0.823
WALLSEBI	77	STACCHAR	73	POS	6	84	7	272	3.2	2.35	0.125
WALLSEBI	77	TRICSP	74	POS	2	88	5	274	1.7	0.03	0.862
WALLSEBI	77	TRICVIRI	75	POS	35	55	76	203	27.1	3.85	0.050
WALLSEBI	77	ULOCCHAR	76	POS	16	74	39	240	13.4	0.50	0.480
YEAST	78	ACRESP	1	POS	22	290	3	54	21.1	0.04	0.841
YEAST	78	ALTEALTE	2	POS	279	33	48	9	276.5	0.83	0.362
YEAST	78	ALTESP	3	POS	15	297	1	56	13.5	0.47	0.493
YEAST	78	ASPECAND	4	NEG	16	296	3	54	16.1	0.14	0.708
YEAST	78	ASPEFUMI	5	POS	25	287	0	57	21.1	3.71	0.054
YEAST	78	ASPEGLAU	6	NEG	20	292	5	52	21.1	0.88	0.348
YEAST	78	ASPENIGE	7	POS	108	204	18	39	106.5	0.09	0.764
YEAST	78	ASPEOCHR	8	POS	61	251	11	46	60.9	0.02	0.888
YEAST	78	ASPEORYZ	9	NEG	7	305	2	55	7.6	1.07	0.301
YEAST	78	ASPESP	10	POS	58	254	9	48	56.7	0.10	0.752
YEAST	78	ASPESYDO	11	POS	42	270	4	53	38.9	1.29	0.256
YEAST	78	ASPEUSTU	12	NEG	18	294	6	51	20.3	2.66	0.103
YEAST	78	ASPEVERS	13	NEG	164	148	32	25	165.7	0.41	0.522
YEAST	78	AUREPULL	14	NEG	243	69	50	7	247.7	3.48	0.062
YEAST	78	CHAEGLOB	15	POS	24	288	0	57	20.3	3.51	0.061
YEAST	78	CHRSPMSP	16	POS	14	298	0	57	11.8	1.57	0.210
YEAST	78	CLADCLAD	17	NEG	148	164	37	20	156.4	6.61	0.010
YEAST	78	CLADHERB	18	NEG	64	248	23	34	73.6	11.66	0.001
YEAST	78	CLADSP	19	POS	58	254	6	51	54.1	1.66	0.198
YEAST	78	CLADSPHA	20	NEG	110	202	31	26	119.2	8.30	0.004
YEAST	78	CONISP	21	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	EMERNIDU	22	POS	9	303	1	56	8.5	0.00	1.000
YEAST	78	EPICNIGR	23	NEG	168	144	32	25	169.1	0.22	0.639
YEAST	78	EUROHERB	24	POS	210	102	35	22	207.2	0.51	0.475
YEAST	78	FUSAOXYS	25	POS	19	293	1	56	16.9	1.02	0.313
YEAST	78	FUSASP	26	POS	50	262	9	48	49.9	0.02	0.888
YEAST	78	GEOMANN	27	NEG	10	302	2	55	10.2	0.28	0.597
YEAST	78	MUCOPLUM	28	POS	64	248	9	48	61.7	0.41	0.522
YEAST	78	MUCORACE	29	NEG	75	237	16	41	76.9	0.67	0.413
YEAST	78	PAECSP	30	POS	7	305	1	56	6.8	0.07	0.791
YEAST	78	PAECVARI	31	NEG	40	272	10	47	42.3	1.37	0.242
YEAST	78	PENIATRA	32	POS	9	303	0	57	7.6	0.69	0.406
YEAST	78	PENIAURA	33	POS	39	273	5	52	37.2	0.33	0.566
YEAST	78	PENIBREV	34	NEG	72	240	14	43	72.7	0.17	0.680
YEAST	78	PENICHRY	35	NEG	159	153	32	25	161.5	0.75	0.386
YEAST	78	PENICOMM	36	POS	80	232	14	43	79.5	0.00	1.000
YEAST	78	PENICOPR	37	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	PENICORY	38	POS	98	214	10	47	91.3	3.83	0.050
YEAST	78	PENICRUS	39	POS	12	300	2	55	11.8	0.06	0.806
YEAST	78	PENICTNG	40	NEG	28	284	6	51	28.8	0.39	0.532
YEAST	78	PENICTRM	41	POS	46	266	6	51	44.0	0.40	0.527
YEAST	78	PENIDECU	42	NEG	14	298	5	52	16.1	2.80	0.094
YEAST	78	PENIDIGI	43	NEG	7	305	3	54	8.5	3.01	0.083
YEAST	78	PENIECHI	44	NEG	14	298	3	54	14.4	0.36	0.549
YEAST	78	PENIEXPA	45	POS	61	251	8	49	58.3	0.64	0.424
YEAST	78	PENIGLAN	46	NEG	10	302	3	54	11.0	1.36	0.244
YEAST	78	PENIGRIS	47	NEG	17	295	6	51	19.5	3.08	0.079
YEAST	78	PENIIMPL	48	POS	18	294	1	56	16.1	0.87	0.351
YEAST	78	PENIISLA	49	POS	10	302	1	56	9.3	0.03	0.862
YEAST	78	PENIITAL	50	NEG	9	303	2	55	9.3	0.46	0.498

Taxon A	#	Taxon B	#	CORR	A+B+	A+B-	A-B+	A-B-	$\Sigma(A+B+)$	$X^2$	p
YEAST	78	PENIMICZ	51	POS	13	299	1	56	11.8	0.25	0.617
YEAST	78	PENIOXAL	52	NEG	17	295	4	53	17.8	0.61	0.435
YEAST	78	PENIPURP	53	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENIRAIS	54	POS	22	290	4	53	22.0	0.07	0.791
YEAST	78	PENIREST	55	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENISIMP	56	POS	19	293	1	56	16.9	1.02	0.313
YEAST	78	PENISP	57	POS	27	285	2	55	24.5	1.12	0.290
YEAST	78	PENISP01	58	POS	8	304	1	56	7.6	0.01	0.920
YEAST	78	PENISP26	59	POS	45	267	8	49	44.8	0.02	0.888
YEAST	78	PENISP64	60	POS	9	303	1	56	8.5	0.00	1.000
YEAST	78	PENISPIN	61	POS	123	189	19	38	120.1	0.52	0.471
YEAST	78	PENIVARI	62	POS	12	300	0	57	10.2	1.21	0.271
YEAST	78	PENIVERR	63	POS	9	303	0	57	7.6	0.69	0.406
YEAST	78	PENIVIRI	64	POS	61	251	7	50	57.5	1.25	0.264
YEAST	78	PENIVULP	65	POS	19	293	3	54	18.6	0.00	1.000
YEAST	78	PHOMHERB	66	NEG	88	224	20	37	91.3	1.46	0.227
YEAST	78	PHOMSP	67	NEG	47	265	15	42	52.4	5.21	0.022
YEAST	78	PITHCHAR	68	POS	26	286	0	57	22.0	3.92	0.048
YEAST	78	RHIZORYZ	69	POS	45	267	8	49	44.8	0.02	0.888
YEAST	78	SCOPBREV	70	POS	30	282	3	54	27.9	0.65	0.420
YEAST	78	SCOPCAND	71	NEG	22	290	5	52	22.8	0.54	0.462
YEAST	78	SPHASP	72	POS	11	301	2	55	11.0	0.15	0.699
YEAST	78	STACCHAR	73	POS	11	301	2	55	11.0	0.15	0.699
YEAST	78	TRICSP	74	POS	6	306	1	56	5.9	0.20	0.655
YEAST	78	TRICVIRI	75	POS	97	215	14	43	93.9	0.69	0.406
YEAST	78	ULOCCHAR	76	POS	47	265	8	49	46.5	0.00	1.000
YEAST	78	WALLSEBI	77	POS	79	233	11	46	76.1	0.65	0.420

## **APPENDIX C**

Calculations of sampling efficiency

Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
1	67	15	5	92.5	76	32	15	10	68.8
2	85	12	2	97.6	77	35	10	4	88.6
3	90	21	7	92.2	78	94	19	8	91.5
4	95	22	12	87.4	79	146	24	4	97.3
5	115	24	9	92.2	80	272	17	4	98.5
6	31	14	7	77.4	81	928	15	4	99.6
7	61	13	5	91.8	82	175	11	1	99.4
8	75	14	8	89.3	83	93	19	5	94.6
9	115	29	10	91.3	84	502	14	3	99.4
10	144	18	4	97.2	85	228	13	2	99.1
11	73	16	5	93.2	86	34	12	3	91.2
12	37	13	5	86.5	87	79	19	9	88.6
13	134	25	6	95.5	88	104	15	3	97.1
14	287	18	8	97.2	89	178	14	1	99.4
15	59	15	6	89.8	90	133	12	7	94.7
16	98	13	5	94.9	91	263	12	4	98.5
17	72	9	2	97.2	92	25	11	4	84.0
18	131	14	6	95.4	93	131	12	5	96.2
19	293	18	3	99.0	94	109	14	3	97.2
20	102	20	8	92.2	95	88	13	6	93.2
21	264	18	9	96.6	96	118	12	3	97.5
22	179	17	6	96.6	97	245	14	9	96.3
23	57	18	12	78.9	98	40	12	8	80.0
24	84	14	7	91.7	99	39	15	7	82.1
25	51	12	5	90.2	100	43	12	5	88.4
26	81	23	10	87.7	101	185	12	2	98.9
27	44	15	9	79.5	102	70	28	13	81.4
28	58	9	4	93.1	103	218	12	3	98.6
29	123	20	9	92.7	104	62	18	8	87.1
30	268	16	5	98.1	105	40	22	13	67.5
31	367	21	9	97.5	106	28	15	9	67.9
32	72	19	9	87.5	107	94	23	8	91.5
33	214	17	6	97.2	108	27	7	4	85.2
34	115	11	4	96.5	109	151	14	7	95.4
35	67	21	10	85.1	110	48	23	15	68.8
36	46	19	9	80.4	111	51	12	5	90.2
37	97	22	8	91.8	112	137	16	4	97.1
38	82	16	7	91.5	113	152	12	3	98.0
39	50	18	12	76.0	114	924	10	4	99.6
40	33	11	4	87.9	115	49	8	2	95.9
41	167	21	10	94.0	116	40	14	10	75.0
42	241	16	3	98.8	117	36	8	5	86.1
43	57	15	7	87.7	118	98	16	5	94.9
44	81	19	7	91.4	119	106	12	4	96.2
45	65	13	5	92.3	120	58	9	4	93.1
46	1647	17	3	99.8	121	231	10	2	99.1
47	70	22	8	88.6	122	81	6	2	97.5
48	80	16	7	91.3	123	54	17	5	90.7
49	23	7	6	73.9	124	144	12	3	97.9
50	51	9	4	92.2	125	68	18	10	85.3
51	16	8	5	68.8	126	37	10	3	91.9
52	860	11	2	99.8	127	132	20	8	93.9
53	101	19	7	93.1	128	44	12	4	90.9
54	77	18	7	90.9	129	22	12	10	54.5
55	87	13	2	97.7	130	99	13	5	94.9
56	93	16	6	93.5	131	31	15	7	77.4
57	186	16	6	96.8	132	73	11	3	95.9
58	71	17	7	90.1	133	24	9	3	87.5
59	52	13	4	92.3	134	74	10	4	94.6
60	108	12	4	96.3	135	65	10	4	93.8
61	230	20	4	98.3	136	13	7	4	69.2
62	113	18	8	92.9	137	8	6	4	50.0
63	52	17	8	84.6	138	27	12	6	77.8
64	65	15	8	87.7	139	109	10	2	98.2
65	156	12	1	99.4	140	65	23	12	81.5
66	147	12	4	97.3	141	97	12	3	96.9
67	59	11	3	94.9	142	32	7	2	93.8
68	124	14	5	96.0	143	60	14	7	88.3
69	105	13	3	97.1	144	155	12	4	97.4
70	76	15	6	92.1	145	263	14	4	98.5
71	72	20	8	88.9	146	60	9	2	96.7
72	196	23	7	96.4	147	187	15	5	97.3
73	51	15	7	86.3	148	732	14	3	99.6
74	80	20	7	91.3	149	53	12	7	86.8
75	161	8	3	98.1	150	35	11	5	85.7

Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
151	88	12	5	94.3	226	542	14	2	99.6
152	40	8	1	97.5	227	149	16	4	97.3
153	145	18	9	93.8	228	207	17	6	97.1
154	141	7	3	97.9	229	26	10	4	84.6
155	189	9	3	98.4	230	221	11	4	98.2
156	18	8	3	83.3	231	120	11	2	98.3
157	199	11	3	98.5	232	137	6	0	100.0
158	22	11	6	72.7	233	80	15	4	95.0
159	106	15	4	96.2	234	295	15	6	98.0
160	112	11	2	98.2	235	112	15	3	97.3
161	109	14	5	95.4	236	154	24	6	96.1
162	44	8	0	100.0	237	55	11	3	94.5
163	106	15	7	93.4	238	58	7	2	96.6
164	93	12	5	94.6	239	140	12	5	96.4
165	160	14	6	96.3	240	152	10	4	97.4
166	652	14	2	99.7	241	247	18	6	97.6
167	134	14	2	98.5	242	35	13	5	85.7
168	125	8	2	98.4	243	22	6	2	90.9
169	194	20	4	97.9	244	136	13	2	98.5
170	276	16	2	99.3	245	272	15	4	98.5
171	88	8	1	98.9	246	43	6	3	93.0
172	137	13	4	97.1	247	70	9	5	92.9
173	159	23	6	96.2	248	52	6	2	96.2
174	201	19	7	96.5	249	17	8	5	70.6
175	202	15	1	99.5	250	25	11	5	80.0
176	83	7	4	95.2	251	48	14	3	93.8
177	282	16	5	98.2	252	24	10	5	79.2
178	98	10	2	98.0	253	210	15	5	97.6
179	190	10	1	99.5	254	129	18	6	95.3
180	71	14	5	93.0	255	23	7	3	87.0
181	177	22	8	95.5	256	368	21	5	98.6
182	147	19	4	97.3	257	45	9	3	93.3
183	53	8	2	96.2	258	25	13	4	84.0
184	44	12	6	86.4	259	234	10	4	98.3
185	129	25	11	91.5	260	366	19	4	98.9
186	108	15	5	95.4	261	59	8	2	96.6
187	45	12	5	88.9	262	98	14	6	93.9
188	166	17	3	98.2	263	27	8	2	92.6
189	300	11	1	99.7	264	66	15	5	92.4
190	82	21	6	92.7	265	33	7	1	97.0
191	33	8	4	87.9	266	30	11	5	83.3
192	24	7	4	83.3	267	125	15	5	96.0
193	1103	18	5	99.5	268	61	13	3	95.1
194	186	12	3	98.4	269	56	16	4	92.9
195	87	18	6	93.1	270	43	9	3	93.0
196	733	7	2	99.7	271	144	15	5	96.5
197	65	11	3	95.4	272	849	8	2	99.8
198	93	13	5	94.6	273	331	12	4	98.8
199	257	12	3	98.8	274	79	17	8	89.9
200	134	12	3	97.8	275	309	18	4	98.7
201	173	15	5	97.1	276	166	6	2	98.8
202	137	11	3	97.8	277	233	11	3	98.7
203	103	20	4	96.1	278	45	8	2	95.6
204	473	15	2	99.6	279	237	12	1	99.6
205	91	13	3	96.7	280	71	7	2	97.2
206	147	14	4	97.3	281	76	13	4	94.7
207	161	13	6	96.3	282	67	14	5	92.5
208	46	14	6	87.0	283	100	20	5	95.0
209	56	10	5	91.1	284	331	18	7	97.9
210	168	10	4	97.6	285	30	12	8	73.3
211	157	10	2	98.7	286	231	13	2	99.1
212	302	7	2	99.3	287	88	8	2	97.7
213	48	11	5	89.6	288	6	5	4	33.3
214	46	9	5	89.1	289	200	8	2	99.0
215	63	20	8	87.3	290	55	12	3	94.5
216	258	14	5	98.1	291	10	7	5	50.0
217	62	12	6	90.3	292	54	12	2	96.3
218	44	9	2	95.5	293	112	13	4	96.4
219	90	16	7	92.2	294	84	13	6	92.9
220	223	10	6	97.3	295	761	16	5	99.3
221	52	6	2	96.2	296	150	14	2	98.7
222	66	11	5	92.4	297	190	13	4	97.9
223	96	12	4	95.8	298	48	10	2	95.8
224	276	14	4	98.6	299	99	14	3	97.0
225	140	13	5	96.4	300	181	13	3	98.3

Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage	Sample No.	No. of isolates	Total No. Species	No. of spp. seen once	Percent Coverage
301	93	5	2	97.8	336	133	13	3	97.7
302	34	11	4	88.2	337	138	6	3	97.8
303	313	16	8	97.4	338	78	12	6	92.3
304	520	12	5	99.0	339	50	10	6	88.0
305	178	16	5	97.2	340	34	11	5	85.3
306	131	10	1	99.2	341	37	10	4	89.2
307	207	10	2	99.0	342	63	9	5	92.1
308	55	6	1	98.2	343	38	12	5	86.8
309	197	14	3	98.5	344	27	12	5	81.5
310	22	8	4	81.8	345	13	7	3	76.9
311	38	12	7	81.6	346	3	2	1	66.7
312	261	16	4	98.5	347	25	12	4	84.0
313	70	19	9	87.1	348	7	4	2	71.4
314	150	10	5	96.7	349	47	6	2	95.7
315	137	10	3	97.8	350	8	5	3	62.5
316	15	7	3	80.0	351	21	7	3	85.7
317	173	17	5	97.1	352	20	9	3	85.0
318	95	15	4	95.8	353	62	14	6	90.3
319	142	15	6	95.8	354	46	13	7	84.8
320	94	11	4	95.7	355	42	8	1	97.6
321	652	13	3	99.5	356	27	10	3	88.9
322	147	2	1	99.3	357	23	9	4	82.6
323	61	8	2	96.7	358	69	10	3	95.7
324	121	9	3	97.5	359	86	14	3	96.5
325	249	18	5	98.0	360	27	10	3	88.9
326	27	13	7	74.1	361	19	8	4	78.9
327	52	11	2	96.2	362	31	10	3	90.3
328	153	10	1	99.3	363	9	6	4	55.6
329	82	14	5	93.9	364	48	11	3	93.8
330	120	10	3	97.5	365	18	5	3	83.3
331	586	12	2	99.7	366	24	9	3	87.5
332	93	13	5	94.6	367	51	8	0	100.0
333	106	17	4	96.2	368	25	10	4	84.0
334	43	11	4	90.7	369	21	10	4	81.0
335	76	6	1	98.7					

## APPENDIX D

Alignment of sequences of nuclear ribosomal DNA, ITS1-5.SS-ITS2  
and partial 28S region from *Penicillium* subgen. *Penicillium*

---

Invariant bases are indicated by an asterisk

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	1	10	20	30	40	50
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. camemberti</i> NRRL875	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. echinulatum</i> NRRL1151	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. crustosum</i> NRRL968	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. viridicatum</i> NRRL961	AAGGATCATTACCGAGTGAGGGCCC	-TTT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. aurantiogriseum</i> NRRL971	AAGGATCATTACCGAGTGAGGGCCC	-TTT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. polonicum</i> NRRL995	AAGGATCATTACCGAGTGAGGGCCC	-TTT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. viridicatum</i> NRRL958	AAGGATCATTACCGAGTGAGGGCCC	-TTT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. chrysogenum</i> NRRL821	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. chrysogenum</i> NRRL807	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. griseoroseum</i> NRRL820	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. chrysogenum</i> NRRL824	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. griseoroseum</i> NRRL832	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. griseofulvum</i> NRRL734	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. griseofulvum</i> NRRL2300	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. coprophilum</i> NRRL13627	AAGGATCATTACCGAGTGAGGGCCC	-TTT	-GGGTCCAACCTCCCACCCAT	48		
<i>P. digitatum</i> NRRL786	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. sclerotigenum</i> NRRL3461	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>Eu. egyptiacum</i> NRRL2090	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>Eu. crustaceum</i> NRRL3332	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. expansum</i> NRRL974	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. turbatum</i> NRRL757	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>H. paradoxus</i> NRRL2162	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. atramentosum</i> NRRL795	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. swiecickii</i> NRRL918	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. kojigenum</i> NRRL3442	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. raistrickii</i> NRRL2039	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. soppii</i> NRRL2023	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. canescens</i> NRRL910	AAGGATCATTACCGAGCGAGAATTC	-TCT	-GAATTCACCTCCCACCCGT	48		
<i>P. atrovenetum</i> NRRL2571	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	49		
<i>P. canescens</i> NRRL2147	AAGGATCATTACCGAGTGAGGGCCCCTCG	-GGGTCCAACCTCCCACCCGT	49			
<i>P. waksmanii</i> NRRL777	AAGGATCATTACCGAGTGAGGGCCCCTCG	-GGGTCCAACCTCCCACCCGT	49			
<i>P. miczynskii</i> NRRL1077	AAGGATCATTACCGAGTGAGGGCCCCTCG	-GGGTCCAACCTCCCACCCGT	49			
<i>Eu. shearii</i> NRRL715	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. roseopurpureum</i> NRRL733	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. roseopurpureum</i> NRRL2064	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. sumatrense</i> NRRL779	AAGGATCATTACCGAGTGAGGGCCCCTCG	-GGGTCCAACCTCCCACCCGT	49			
<i>P. paxilli</i> NRRL2008	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. citrinum</i> NRRL1841	AAGGATCATTACCGAGTGCGGGCCCCTCG	-GGGCCAACCTCCCACCCGT	49			
<i>P. sartoryi</i> NRRL783	AAGGATCATTACCGAGTGCGGGCCCCTCG	-GGGCCAACCTCCCACCCGT	49			
<i>P. westlingii</i> NRRL800	AAGGATCATTACCGAGTGCGGGCCCCTCG	-GGGCCAACCTCCCACCCGT	49			
<i>P. charlesii</i> NRRL778	AAGGATCATTACCGAGTGCGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. fellutanum</i> NRRL746	AAGGATCATTACCGAGTGCGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. spinulosum</i> NRRL728	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. spinulosum</i> NRRL1750	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. thomii</i> NRRL2077	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>Eu. lapidosum</i> NRRL718	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. thomii</i> NRRL760	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. purpurescens</i> NRRL720	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. glabrum</i> NRRL766	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. asperosporum</i> NRRL3411	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. lividum</i> NRRL754	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. adametzii</i> NRRL736	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. adametzii</i> NRRL737	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. bilaii</i> NRRL3391	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. adametzioides</i> NRRL3405	AAGGATCATTACCGAGTGAGGGCCT	-TC	-GGGTCCAACCTCCCACCCGT	47		
<i>P. herquei</i> NRRL1040	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. sclerotiorum</i> NRRL2074	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. decumbens</i> NRRL742	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		
<i>P. decumbens</i> NRRL741	AAGGATCATTACCGAGTGAGGGCCC	-TCT	-GGGTCCAACCTCCCACCCGT	48		



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1      10      20      30      40      50
                                +-----+-----+-----+-----+
P.turbatum NRRL759             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.corylophilum NRRL803        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.corylophilum NRRL802        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.corylophilum NRRL793        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCAT 48
P.melinii NRRL2041            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.velutinum NRRL2069          AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.raciborskii NRRL2150        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.restrictum NRRL25744        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.restrictum NRRL1748         AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.citreonigrum NRRL761        AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.cinerascens NRRL748         AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.vinaceum NRRL739           AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.oxalicum NRRL790           AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.oxalicum NRRL787           AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.donkii NRRL5562            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.fuscum NRRL721             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.janthinellum NRRL2016      AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.raperi NRRL2674            AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.daleae NRRL922             AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.ochrochloron NRRL926       AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.simplicissimum NRRL1075     AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.rolfsii NRRL1078           AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
Eu.cinnamopurpureum NRRL3326 AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.thermophilum NRRL735       AAGGATCATTACCGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
P.clavariiformis NRRL2482     AAGGATCATTACTGAGTGAGGGCCC-TCT-GGGTCCAACCTCCCACCCGT 48
                                ***** * * * * * * * * * *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	51	60	70	80	90	100
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.camemberti</i> NRRL875	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.echinulatum</i> NRRL1151	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.crustosum</i> NRRL968	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.viridicatum</i> NRRL961	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.aurantiogriseum</i> NRRL971	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.polonicum</i> NRRL995	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.viridicatum</i> NRRL958	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.chrysogenum</i> NRRL821	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.chrysogenum</i> NRRL807	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.griseoroseum</i> NRRL820	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.chrysogenum</i> NRRL824	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.griseoroseum</i> NRRL832	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.griseofulvum</i> NRRL734	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.griseofulvum</i> NRRL2300	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.coprophilum</i> NRRL13627	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.digitatum</i> NRRL786	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.sclerotigenum</i> NRRL3461	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>Eu.egyptiacum</i> NRRL2090	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>Eu.crustaceum</i> NRRL3332	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.expansum</i> NRRL974	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.turbatum</i> NRRL757	GTTTA-TTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>H.paradoxus</i> NRRL2162	GTTTA-TTGTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.atramentosum</i> NRRL795	GTTTA-TTGTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.swiecickii</i> NRRL918	GTTTA-TTATACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.kojigenum</i> NRRL3442	GTTTA-TTATACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.raistrickii</i> NRRL2039	GTTTA-TTATACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.soppii</i> NRRL2023	GTTTA-TTATACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.canescens</i> NRRL910	GTTTA-TTGTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.atrovenetum</i> NRRL2571	GTTTA-TTGTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT	GTTTACCTT
<i>P.canescens</i> NRRL2147	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>P.waksmanii</i> NRRL777	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>P.miczynskii</i> NRRL1077	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>Eu.shearaii</i> NRRL1515	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.roseopurpureum</i> NRRL733	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.roseopurpureum</i> NRRL2064	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.sumatrense</i> NRRL779	GTTTAACGAACCCTT	GTTTACCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	96
<i>P.paxilli</i> NRRL2008	GTTTAACGAACC	-TTGTTGCTT	CGGCGGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>P.citrinum</i> NRRL1841	GTTGCCCGAACCTAT	GTTTACCTT	CGGCGGCCCC	-----	-----	81
<i>P.sartoryi</i> NRRL783	GTTGCCCGAACCTAT	GTTTACCTT	CGGCGGCCCC	-----	-----	81
<i>P.westlingii</i> NRRL800	GTTGCCCGAACCTAT	GTTTACCTT	CGGCGGCCCC	-----	-----	81
<i>P.charlesii</i> NRRL778	GTATACTTACCG	-TGTTGCTT	CGGCGGCCCCGCC	-TGCCA	-GGCCGCCG	94
<i>P.fellutanum</i> NRRL746	GTATACTTACCG	-TGTTGCTT	CGGCGGCCCCGCC	-TGCCA	-GGCCGCCG	94
<i>P.spinulosum</i> NRRL728	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.spinulosum</i> NRRL1750	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.thomii</i> NRRL2077	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>Eu.lapidosum</i> NRRL718	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.thomii</i> NRRL760	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.purpurescens</i> NRRL720	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.glabrum</i> NRRL766	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.asperosporum</i> NRRL3411	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGAGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.lividum</i> NRRL754	GTTTA-TTGTACCTT	GTTTACCTT	CGGTGCGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.adametzii</i> NRRL736	GTTTATTGTACCTT	GTTTACCTT	CGGCAGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>P.adametzii</i> NRRL737	GTTTATTGTACCTT	GTTTACCTT	CGGCAGCCCCGCC	-TCAC	-GGCCGCCG	95
<i>P.bilaii</i> NRRL3391	GTCTC	-TTGTACCATGTTGCTT	CGGCAGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.adametziioides</i> NRRL3405	GTCTA	-TTGTACCATGTTGCTT	CGGCAGCCCCGCC	-TTAT	-GGCCGCCG	93
<i>P.herquei</i> NRRL1040	GTTTA-TTGTACCTT	GTTTACCTT	CGGCAGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.sclerotiorum</i> NRRL2074	GTTTA-TTGTACCTT	GTTTACCTT	CGGCAGCCCCGCC	-TCAC	-GGCCGCCG	94
<i>P.decumbens</i> NRRL742	GTCTA	-TTGTACCTT	CGGCGGCCCCGCC	-GCAA	-GGCCGCCG	94
<i>P.decumbens</i> NRRL741	GTCTA	-TTGTACCTT	CGGCGGCCCCGCC	-GCAA	-GGCCGCCG	94

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    51         60         70         80         90         100
                    +-----+-----+-----+-----+-----+
P.turbatum NRRL759      GTCTA-TTGTACCTTGGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.corylophilum NRRL803  GTTTA-TTGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.corylophilum NRRL802  GTTTA-TTGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.corylophilum NRRL793  GTTTA-TTGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.melinii NRRL2041      GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.velutinum NRRL2069    GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.raciborskii NRRL2150  GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.restrictum NRRL25744  GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.restrictum NRRL1748   GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.citreonigrum NRRL761  GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.cinerascens NRRL748   GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.vinaceum NRRL739      GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-GCAA--GGCCGCCG 94
P.oxalicum NRRL790      GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.oxalicum NRRL787      GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.donkii NRRL5562       GTCTA-TTGTACCTTGGTTGCTTCGGCGGGCCCGCCATCATGTGGCCGCCG 97
P.fusum NRRL721         GTCTA-TTGTACCTTGGTTGCTTCGGTGGGCCCGCCCTTTAT--GGCCGCCG 95
P.janthinellum NRRL2016 GTTTA-TCATACCTAGTTGCTTCGGCGGGCCCGCCGTCA--GGCCGCCG 94
P.raperi NRRL2674       GTTTA-TCATACCTAGTTGCTTCGGCGGGCCCGCCGTCA--GGCCGCCG 95
P.daleae NRRL922        GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 94
P.ochrochloron NRRL926  GTTTA-TT-TACCTTGGTTGCTTCGGCGGGCCCGCC-TCAC--GGCCGCCG 93
P.simplicissimum NRRL1075 GTTTA-TT-TACCTTGGTTGCTTCGGCGAGCCCGCC-TCAC--GGCCGCCG 93
P.rolfsii NRRL1078      GTTTA-TCGTACCTTGGTTGCTTCGGCGAGCCCGCC-TCAC--GGCCGCCG 94
Eu.cinnamopurpureum NRRL3326 GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCCGTCA--GGCCGCCG 94
P.thermophilum NRRL735  GTTTA-TCGTACCTTGGTTGCTTCGGCGGGCCCGCCGCA--GGCCGCCG 94
P.clavariiformis NRRL2482 GTTTA-TTGTACCATGTTGCTTCGGCGGGCCCGCCATTGC--GGCCGCCG 95
**                      ***** * **          ****
```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	101	110	120	130	140	150
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.camemberti</i> NRRL875	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.echinulatum</i> NRRL1151	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.crustosum</i> NRRL968	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.viridicatum</i> NRRL961	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.aurantiogriseum</i> NRRL971	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	143		
<i>P.polonicum</i> NRRL995	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--CCGAA	142		
<i>P.viridicatum</i> NRRL958	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.chrysogenum</i> NRRL821	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.chrysogenum</i> NRRL807	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.griseoroseum</i> NRRL820	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.chrysogenum</i> NRRL824	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.griseoroseum</i> NRRL832	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.griseofulvum</i> NRRL734	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	141		
<i>P.griseofulvum</i> NRRL2300	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	141		
<i>P.coprophilum</i> NRRL13627	GGGGGCT	--TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.digitatum</i> NRRL786	GGGGGCT	--CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC	--CCGAA	142		
<i>P.sclerotigenum</i> NRRL3461	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	141		
<i>Eu.egyptiacum</i> NRRL2090	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>Eu.crustaceum</i> NRRL3332	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.expansum</i> NRRL974	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	142		
<i>P.turbatum</i> NRRL757	GGGGGCT	--CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	140		
<i>H.paradoxus</i> NRRL2162	GGGGGCT	--TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC	--ACGAA	141		
<i>P.atramentosum</i> NRRL795	GGGGGCT	--TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCC	--TCGAA	141		
<i>P.swiecickii</i> NRRL918	GGGGGCT	--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT	--C-GAA	139		
<i>P.kojigenum</i> NRRL3442	GGGGGCT	--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT	--C-GAA	139		
<i>P.raistrickii</i> NRRL2039	GGGGGCT	--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT	--C-GAA	139		
<i>P.soppii</i> NRRL2023	GGGGGCT	--TCTGCCCCCGGGCCCGTGCCTGCCGAAGACACT	--TAGAA	140		
<i>P.canescens</i> NRRL910	GGGGGCA	--TCTGCCCCCGGGCCCGCGCCCGCCGAAGACACT	--T-GAA	139		
<i>P.atrovenetum</i> NRRL2571	GGGGGCA	--TCTGCTCCCGGGCCCGCGCCCGCCGAAGACACT	--T-GAA	140		
<i>P.canescens</i> NRRL2147	GGGGGCAT	--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCACC	--TGTGAA	141		
<i>P.waksmanii</i> NRRL777	GGGGGCAT	--CCGCCCCCGGGCCCGCGCCCGCCGAAGCCACC	--TGTGAA	141		
<i>P.miczynskii</i> NRRL1077	GGGGGCAT	--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCACC	--TGTGAA	141		
<i>Eu.shearpii</i> NRRL15	GGGGGCAT	--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACT	--TGTGAA	140		
<i>P.roseopurpureum</i> NRRL733	GGGGGCAT	--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACT	--TGTGAA	140		
<i>P.roseopurpureum</i> NRRL2064	GGGGGCAT	--CCGCCCCCGGGCCCGCGCCCGCCGAAGACACT	--TGTGAA	140		
<i>P.sumatrense</i> NRRL779	GGGGGCTC	--CTGCCCCCGGGCCCGCGCCCGCCGAAGCCCC	--CCTGAA	142		
<i>P.paxilli</i> NRRL2008	GGGGGCTCT	CTCTGCCCCCGGGCCCGCGCCCGCCGAAGACACT	--TGTGAA	143		
<i>P.citrinum</i> NRRL1841	-----	-----C-GCGCCCGCCGACGGCCCC	--CCTGAA	106		
<i>P.sartoryi</i> NRRL783	-----	-----C-GCGCCCGCCGACGGCCCC	--CCTAAA	106		
<i>P.westlingii</i> NRRL800	-----	-----C-GCGCCCGCCGACGGCCCC	--CCTGAA	106		
<i>P.charlesii</i> NRRL778	GGGGGCAA	--CCGCCCCCGGGCCCGCGCCCGCCGAAGACCCC	--AACGAA	140		
<i>P.fellutanum</i> NRRL746	GGGGGCAA	--CCGCCCCCGGGCCCGCGCCCGCCGAAGACCCC	--CACGAA	140		
<i>P.spinulosum</i> NRRL728	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.spinulosum</i> NRRL1750	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.thomii</i> NRRL2077	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>Eu.lapidosum</i> NRRL718	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.thomii</i> NRRL760	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.purpurescens</i> NRRL720	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.glabrum</i> NRRL766	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACT	--ATTGAA	140		
<i>P.asperosporum</i> NRRL3411	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAGACACC	--ATTGAA	140		
<i>P.lividum</i> NRRL754	GGGGGCTTCT	--GCCCCCGGGTCCCGCGCGCACCCGAAGACACC	--ATTGAA	140		
<i>P.adametzii</i> NRRL736	GGGGGCCTCT	--GCCCCCGGGCCCGCGCCTGCCGAAGACACC	--CTTGAA	141		
<i>P.adametzii</i> NRRL737	GGGGGCCTCT	--GCCCCCGGGCCCGCGCCTGCCGAAGACACC	--CTTGAA	141		
<i>P.bilalii</i> NRRL3391	GGGGGCATCT	--GCCCCCGGGCCCGCGCCCGCCGAAGCCCC	--TCTGAA	140		
<i>P.adametziioides</i> NRRL3405	GGGGCTAACC	--GCCC-CGGGCCCGCGCCTGCCGAAGACCCC	--TCTGAA	138		
<i>P.herquei</i> NRRL1040	GGGGGCTTCT	--GCCCCCGGGCCCGCGCCTGCCGAGACACC	--TTTGAA	141		
<i>P.sclerotiorum</i> NRRL2074	GGGGGCTTCT	--GCCCCCGGGCCCGCGCCTGCCGAGACAAT	--CTTGAA	140		
<i>P.decumbens</i> NRRL742	GGGGGCTTCT	--GCCCCCGGGCCCGCGCCCGCCGAAGACACC	--ATTGAA	140		
<i>P.decumbens</i> NRRL741	GGGGGCTTCT	--GCCCCCGGGCCCGCGCCCGCCGAAGACACC	--ATTGAA	140		

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                101      110      120      130      140      150
                +-----+-----+-----+-----+-----+
P.turbatum NRRL759      GGGGGCTTCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL803  GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL802  GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.corylophilum NRRL793  GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.melinii NRRL2041      GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.velutinum NRRL2069    GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.raciborskii NRRL2150  GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.restrictum NRRL25744  GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.restrictum NRRL1748   GGGGGCTTCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.citreonigrum NRRL761  GGGGGCATCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.cinerascens NRRL748   GGGGGCATCT--GCCCTCTGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.vinaceum NRRL739      GGGGGCTTCC--GTCCCCGGGCCCGCGCCCGCCGAAGACACC--TGTGAA 140
P.oxalicum NRRL790      GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACACAAACGAA 142
P.oxalicum NRRL787      GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACACAAACGAA 142
P.donkii NRRL5562       GGGGGCATCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 143
P.fuscum NRRL721        GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 141
P.janthinellum NRRL2016 GGGGGCATCC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 140
P.raperi NRRL2674       GGGGGCACC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 141
P.daleae NRRL922        GGGGGCACC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 140
P.ochrochloron NRRL926  GGGGGCATCT--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 139
P.simplicissimum NRRL1075 GGGGGCACC--GCCCCCGGGCCCGCGCCCGCCGAAGACACC--ATTGAA 139
P.rolfsii NRRL1078      GGGGGCATCC--GCCCCCGGGCCCGCGCTCGCCGAAGACACC--ATTGAA 140
Eu.cinnamopurpureum NRRL3326 GGGG-CTTCG-TGCC-CGGGCCCGTGCCCGCCGAAGACACC--ATTGAA 139
P.chermesinum NRRL735   GGGG-CATCC--GCC-CGGGCCCGCGCCCGCCGAAGACACC--CCTGAA 138
P.clavariiformis NRRL2482 GGGGGCCTTT-TGTCCCCGGGCCTGTGCCCGCCGAAGACACT---TGAA 140
                * * * * * * * * * * * * * *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	151	160	170	180	190	200
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.camemberti</i> NRRL875	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.echinulatum</i> NRRL1151	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.crustosum</i> NRRL968	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.viridicatum</i> NRRL961	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.aurantiogriseum</i> NRRL971	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	189		
<i>P.polonicum</i> NRRL995	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.viridicatum</i> NRRL958	CTCT-GTCTGAAGATTGAAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.chrysogenum</i> NRRL821	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.chrysogenum</i> NRRL807	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.griseoroseum</i> NRRL820	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.chrysogenum</i> NRRL824	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.griseoroseum</i> NRRL832	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.griseofulvum</i> NRRL734	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	187		
<i>P.griseofulvum</i> NRRL2300	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	187		
<i>P.coprophilum</i> NRRL13627	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.digitatum</i> NRRL786	CTCT-GTCTGAAGATTGCAGTCTGAGTGA	---	AAAC-GAAATTATTTAAA	187		
<i>P.sclerotigenum</i> NRRL3461	CTCT-GTCTGAAGATTGCAGTCTGAGTGA	---	AAATAGAAATTATTTAAA	187		
<i>Eu.egyptiacum</i> NRRL2090	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>Eu.crustaceum</i> NRRL3332	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.expansum</i> NRRL974	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	188		
<i>P.turbatum</i> NRRL757	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	186		
<i>H.paradoxus</i> NRRL2162	CTCT-GTATGAAGATTGCAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	187		
<i>P.atramentosum</i> NRRL795	CTCT-GTCTGAAGATTGTAGTCTGAGTGA	---	AAATATAAAATTATTTAAA	187		
<i>P.swiecickii</i> NRRL918	CTCT-GTCTGAAGATTGTAGTCTGAGTAA	---	AAATATAAAATTATTTAAA	185		
<i>P.kojigenum</i> NRRL3442	CTCT-GTCTGAAGATTGTAGTCTGAGTAA	---	AAATATAAAATTATTTAAA	185		
<i>P.raistrickii</i> NRRL2039	CTCT-GTCTGAAGATTGTAGTCTGAGTAT	---	AAATATAAAATTATTTAAA	185		
<i>P.soppii</i> NRRL2023	CTCT-GTCTGAAGATTGTAGTCTGAGTAA	---	AAATATAAAATTATTTAAA	186		
<i>P.canescens</i> NRRL910	CTCT-GTATGAAAATTGCAGTCTGAGTCT	---	AAATATAAAATTATTTAAA	185		
<i>P.atrovenetum</i> NRRL2571	CTCT-GTCTGAAGATTGCAGTCTGAGTCT	---	AAATATAAAATTATTTAAA	186		
<i>P.canescens</i> NRRL2147	CGCT-GTCTGAAGTATGCAGTCTGAGACA	---	ATTATTTAAATTAATTAAA	187		
<i>P.waksmanii</i> NRRL777	CGCT-GTCTGAAGTATGCAGTCTGAGACA	---	ATTATTTAAATTAATTAAA	187		
<i>P.miczynskii</i> NRRL1077	CTCT-GTCTGAAGTATGCAGTCTGAGACA	---	ATTATTTAAATTAATTAAA	187		
<i>Eu.shearpii</i> NRRL715	CTCT-GTCTGAAGATTGCAGTCTGAGAAA	---	CTATTTAAATTAATTAAA	185		
<i>P.roseopurpureum</i> NRRL733	CACT-GTCTGAAGT-TGCAGTCTGAGAAA	---	CTAGCTAAATTAAGTTAAA	185		
<i>P.roseopurpureum</i> NRRL2064	CACT-GTCTGAAGT-TGCAGTCTGAGAAA	---	CTAGCTAAATTAAGTTAAA	185		
<i>P.sumatrense</i> NRRL779	CGCT-GTCTGAAGT-TGCAGTCTGAGAAA	---	CTAGCTAAATTAAGTTAAA	187		
<i>P.paxilli</i> NRRL2008	CGCT-GTATGAAGATTGCAGTCTGAGAAA	---	CTAGCTAAATTAAGTTAAA	190		
<i>P.citrinum</i> NRRL1841	CGCT-GTCTGAAGT-TGCAGTCTGAGACCT	---	ATAACGAAATTAAGTTAAA	152		
<i>P.sartoryi</i> NRRL783	CGCT-GTCTGAAGT-TGCAGTCTGAGACCT	---	ATAACGAAATTAAGTTAAA	152		
<i>P.westlingii</i> NRRL800	CGCT-GTCTGAAGT-TGCAGTCTGAGACCT	---	ATAACGAAATTAAGTTAAA	152		
<i>P.charlesii</i> NRRL778	CTCT-TG-T-ACCTTGCAGTCTGAGCGAT	---	AAGCATAAATTA-TTAAA	183		
<i>P.fellutanum</i> NRRL746	CTCT-TTCT--ACCTTGCAGTCTGAGCGAT	---	AAGCATAAATTA-TTAAA	184		
<i>P.spinulosum</i> NRRL728	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.spinulosum</i> NRRL1750	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.thomii</i> NRRL2077	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>Eu.lapidosum</i> NRRL718	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.thomii</i> NRRL760	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.purpurescens</i> NRRL720	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.glabrum</i> NRRL766	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.asperosporum</i> NRRL3411	CTCT-GTCTGAAGATTGCAGTCTGAGCATA	---	AA--CTAAATAAGTTAAA	185		
<i>P.lividum</i> NRRL754	CTCT-GTATGAAGATTGCAGTCTGAGCGAA	---	AA--CTAAATGAGTTAAA	185		
<i>P.adametzii</i> NRRL736	CGCT-GTCTGAAGTTTGCAGTCTGAGCGAA	---	AAGCAAATTTA-TTAAA	187		
<i>P.adametzii</i> NRRL737	CGCT-GTCTGAAGTTTGCAGTCTGAGCGAA	---	AAGCAAATTTA-TTAAA	187		
<i>P.bilalii</i> NRRL3391	CGCT-GTCTGAAGATTGCAGTCTGAGCGAT	---	AAGCAAATTTATTTAAA	187		
<i>P.adametziioides</i> NRRL3405	CGCT-GTCTGAAGATTGCCGCTGAGCGAA	---	ACATATAAATTTATTTAAA	185		
<i>P.herquei</i> NRRL1040	CGCT-GTCTGAAGTTTGCAGTCTGAGCGA	---	TTAGCTAAATTAAGTTAAA	187		
<i>P.sclerotiorum</i> NRRL2074	CGCT-GTCTGAAGAATGCAGTCTGAGCGAT	---	TAAGCAAATTAAGTTAAA	187		
<i>P.decumbens</i> NRRL742	CGCT-GTCTGAAGATTGCAGTCTGAGCAA	---	TTAGCTAAATTAAGTTAAA	186		
<i>P.decumbens</i> NRRL741	CGCT-GTCTGAAGATTGCAGTCTGAGCAA	---	TTAGCTAAATTAAGTTAAA	186		

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	151	160	170	180	190	200	
	+-----+-----+-----+-----+-----+						
<i>P.turbatum</i> NRRL759	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.corylophilum</i> NRRL803	CACT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.corylophilum</i> NRRL802	CACT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.corylophilum</i> NRRL793	CACT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.melinii</i> NRRL2041	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.velutinum</i> NRRL2069	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.raciborskii</i> NRRL2150	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.restrictum</i> NRRL25744	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.restrictum</i> NRRL1748	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGCTAAATAAGTTAAA	186	
<i>P.citreonigrum</i> NRRL761	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGTTAAATAACTTAAA	186	
<i>P.cinerascens</i> NRRL748	CGCT-GTCTGAAGATTGCAGTCTGAGCAA				---TTAGTTAAATAACTTAAA	186	
<i>P.vinaceum</i> NRRL739	CGCT-GTATGAAGATTGCAGTCTGAGCGA				---AAAGCTAAATTTGTTAAA	186	
<i>P.oxalicum</i> NRRL790	CTCTTGCTGAAGATTGCAGTCTGAG-TAC				--TTGACTAAATCAGTTAAA	189	
<i>P.oxalicum</i> NRRL787	CTCTTGCTGAAGATTGCAGTCTGAG-TAC				--TTGACTAAATCAGTTAAA	189	
<i>P.donkii</i> NRRL5562	CGCT-GTCTGAAGATTGCAGTCTGAGCAGA				--TTAGCTAAATCAGTTAAA	190	
<i>P.fuscum</i> NRRL721	CGCT-GTCTGAAGATTGCAGTCTGAGCAGA				--TTAGCTAAATCAGTTAAA	188	
<i>P.janthinellum</i> NRRL2016	CGCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTAGCTAAATCAGTTAAA	186	
<i>P.raperi</i> NRRL2674	CGCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTAGCTAAATCAGTTAAA	187	
<i>P.daleae</i> NRRL922	CGCT-GTCTGAAGATTGCAGTCTGAGCATC				--TTAGCTAAATCAGTTAAA	187	
<i>P.ochrochloron</i> NRRL926	CTCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTAACTAAATCAGTTAAA	185	
<i>P.simplicissimum</i> NRRL1075	CTCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTAGCTAAATCAGTTAAA	185	
<i>P.rolfsii</i> NRRL1078	CTCT-GTCTGAAGATTGCAGTCTGAGTGA				---TTAACTAAATCAGTTAAA	186	
<i>Eu.cinnamopurpureum</i> NRRL3326	CGCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTAGCTAAATTAGTTAAA	185	
<i>P.chermesinum</i> NRRL735	CGCT-GTCTGAAGATTGCAGTCTGAGCGA				---TTA-TTAAATTATTTAAA	183	
<i>P.clavariiformis</i> NRRL2482	CTCTTGCTGATGGTTGCAGTCTGAGTTGTGATTATTATAATCAATTAAA					190	
	* * *	*	**	*****		* * *	*****

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	201	210	220	230	240	250
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. camemberti</i> NRRL875	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. echinulatum</i> NRRL1151	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. crustosum</i> NRRL968	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. viridicatum</i> NRRL961	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. aurantiogriseum</i> NRRL971	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					239
<i>P. polonicum</i> NRRL995	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. viridicatum</i> NRRL958	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. chrysogenum</i> NRRL821	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. chrysogenum</i> NRRL807	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. griseoroseum</i> NRRL820	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. chrysogenum</i> NRRL824	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. griseoroseum</i> NRRL832	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. griseofulvum</i> NRRL734	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. griseofulvum</i> NRRL2300	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. coprophilum</i> NRRL13627	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. digitatum</i> NRRL786	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. sclerotigenum</i> NRRL3461	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>Eu. egyptiacum</i> NRRL2090	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>Eu. crustaceum</i> NRRL3332	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. expansum</i> NRRL974	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					238
<i>P. turbatum</i> NRRL757	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					236
<i>H. paradoxus</i> NRRL2162	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. atramentosum</i> NRRL795	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. swiecickii</i> NRRL918	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. kojigenum</i> NRRL3442	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. raistrickii</i> NRRL2039	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. soppii</i> NRRL2023	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					236
<i>P. canescens</i> NRRL910	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. atrovenetum</i> NRRL2571	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					236
<i>P. canescens</i> NRRL2147	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. waksmanii</i> NRRL777	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. miczynskii</i> NRRL1077	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>Eu. shearii</i> NRRL1515	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. roseopurpureum</i> NRRL733	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. roseopurpureum</i> NRRL2064	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. sumatrense</i> NRRL779	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. paxilli</i> NRRL2008	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					240
<i>P. citrinum</i> NRRL1841	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					202
<i>P. sartoryi</i> NRRL783	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					202
<i>P. westlingii</i> NRRL800	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					202
<i>P. charlesii</i> NRRL778	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					233
<i>P. fellutanum</i> NRRL746	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					234
<i>P. spinulosum</i> NRRL728	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. spinulosum</i> NRRL1750	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. thomii</i> NRRL2077	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>Eu. lapidosum</i> NRRL718	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. thomii</i> NRRL760	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. purpurescens</i> NRRL720	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. glabrum</i> NRRL766	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. asperosporum</i> NRRL3411	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. lividum</i> NRRL754	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. adametzii</i> NRRL736	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. adametzii</i> NRRL737	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. bilaii</i> NRRL3391	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. adametzioides</i> NRRL3405	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					235
<i>P. herquei</i> NRRL1040	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. sclerotiorum</i> NRRL2074	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					237
<i>P. decumbens</i> NRRL742	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					236
<i>P. decumbens</i> NRRL741	ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGA					236



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                201      210      220      230      240      250
                +-----+-----+-----+-----+
P.turbatum NRRL759      ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL803  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL802  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.corylophilum NRRL793  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.melinii NRRL2041      ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.velutinum NRRL2069    ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.raciborskii NRRL2150  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.restrictum NRRL25744  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.restrictum NRRL1748   ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.citreonigrum NRRL761  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.cinerascens NRRL748   ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.vinaceum NRRL739     ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.oxalicum NRRL790     ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 239
P.oxalicum NRRL787     ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 239
P.donkii NRRL5562      ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 240
P.fuscum NRRL721       ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 238
P.janthinellum NRRL2016 ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
P.raperi NRRL2674      ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 237
P.daleae NRRL922       ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 237
P.ochrochloron NRRL926 ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 235
P.simplicissimum NRRL1075 ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 235
P.rolfsii NRRL1078     ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 236
Eu.cinnamopurpureum NRRL3326 ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 235
P.thermophilum NRRL735  ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 233
P.clavariiformis NRRL2482 ACTTTCAACAACGGATCTCTTGGTTCGGCATCGATGAAGAACGCAGCGA 240
*****
```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	251	260	270	280	290	300
	+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.camemberti</i> NRRL875	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.echinulatum</i> NRRL1151	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.crustosum</i> NRRL968	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.viridicatum</i> NRRL961	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.aurantiogriseum</i> NRRL971	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				288
<i>P.polonicum</i> NRRL995	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.viridicatum</i> NRRL958	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.chrysogenum</i> NRRL821	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.chrysogenum</i> NRRL807	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.griseoroseum</i> NRRL820	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.chrysogenum</i> NRRL824	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.griseoroseum</i> NRRL832	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.griseofulvum</i> NRRL734	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.griseofulvum</i> NRRL2300	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.coprophilum</i> NRRL13627	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.digitatum</i> NRRL786	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.sclerotigenum</i> NRRL3461	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>Eu.egyptiacum</i> NRRL2090	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>Eu.crustaceum</i> NRRL3332	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.expansum</i> NRRL974	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.turbatum</i> NRRL757	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>H.paradoxus</i> NRRL2162	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.atramentosum</i> NRRL795	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.swiecickii</i> NRRL918	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.kojigenum</i> NRRL3442	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.raistrickii</i> NRRL2039	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.soppii</i> NRRL2023	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.canescens</i> NRRL910	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.atrovenetum</i> NRRL2571	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.canescens</i> NRRL2147	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.waksmanii</i> NRRL777	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.miczynskii</i> NRRL1077	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>Eu.shearrii</i> NRRL1515	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.roseopurpureum</i> NRRL733	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.roseopurpureum</i> NRRL2064	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.sumatrense</i> NRRL779	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.paxilli</i> NRRL2008	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				290
<i>P.citrinum</i> NRRL1841	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				252
<i>P.sartoryi</i> NRRL783	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				252
<i>P.westlingii</i> NRRL800	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				252
<i>P.charlesii</i> NRRL778	AATGCGATAAGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				283
<i>P.fellutanum</i> NRRL746	AATGCGATAAGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				284
<i>P.spinulosum</i> NRRL728	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.spinulosum</i> NRRL1750	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.thomii</i> NRRL2077	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>Eu.lapidosum</i> NRRL718	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.thomii</i> NRRL760	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.purpurescens</i> NRRL720	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.glabrum</i> NRRL766	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.asperosporum</i> NRRL3411	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.lividum</i> NRRL754	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.adametzii</i> NRRL736	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.adametzii</i> NRRL737	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.bilalii</i> NRRL3391	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.adametziioides</i> NRRL3405	AATGCGATAACTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				285
<i>P.herquei</i> NRRL1040	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.sclerotiorum</i> NRRL2074	AATGCGATAAATAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				287
<i>P.decumbens</i> NRRL742	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286
<i>P.decumbens</i> NRRL741	AATGCGATACGTAATGTGAATTGCA	-AATTCAGTGAATCATCGAGTCTTT				286

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                251      260      270      280      290      300
                +-----+-----+-----+-----+-----+
P.turbatum NRRL759      AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL803  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL802  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.corylophilum NRRL793  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.melinii NRRL2041      AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.velutinum NRRL2069    AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.raciborskii NRRL2150  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.restrictum NRRL25744  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.restrictum NRRL1748   AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.citreonigrum NRRL761  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.cinerascens NRRL748   AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.vinaceum NRRL739      AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.oxalicum NRRL790      AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 289
P.oxalicum NRRL787      AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 289
P.donkii NRRL5562       AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 290
P.fuscum NRRL721        AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 288
P.janthinellum NRRL2016 AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
P.raperi NRRL2674       AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.daleae NRRL922        AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 287
P.ochrochloron NRRL926  AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.simplicissimum NRRL1075 AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.rolfsii NRRL1078      AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 286
Eu.cinnamopurpureum NRRL3326 AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 285
P.chermesinum NRRL735   AATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 283
P.clavariiformis NRRL2482 AATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTT 290
                *****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	301	310	320	330	340	350
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	GAACGCACATTGC	CCCCCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>P.camemberti</i> NRRL875	GAACGCACATTGC	CCCCCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>P.echinulatum</i> NRRL1151	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.crustosum</i> NRRL968	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.viridicatum</i> NRRL961	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.aurantiogriseum</i> NRRL971	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		338
<i>P.polonicum</i> NRRL995	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.viridicatum</i> NRRL958	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.chrysogenum</i> NRRL821	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.chrysogenum</i> NRRL807	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.griseoroseum</i> NRRL820	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.chrysogenum</i> NRRL824	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.griseoroseum</i> NRRL832	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.griseofulvum</i> NRRL734	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>P.griseofulvum</i> NRRL2300	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>P.coprophilum</i> NRRL13627	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.digitatum</i> NRRL786	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>P.sclerotigenum</i> NRRL3461	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>Eu.egyptiacum</i> NRRL2090	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>Eu.crustaceum</i> NRRL3332	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.expansum</i> NRRL974	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.turbatum</i> NRRL757	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>H.paradoxus</i> NRRL2162	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.atramentosum</i> NRRL795	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.swiecickii</i> NRRL918	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.kojigenum</i> NRRL3442	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.raistrickii</i> NRRL2039	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.soppii</i> NRRL2023	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		336
<i>P.canescens</i> NRRL910	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.atrovenetum</i> NRRL2571	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>P.canescens</i> NRRL2147	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>P.waksmanii</i> NRRL777	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>P.miczynskii</i> NRRL1077	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>Eu.shearaii</i> NRRL715	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.roseopurpureum</i> NRRL733	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.roseopurpureum</i> NRRL2064	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.sumatrense</i> NRRL779	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		337
<i>P.paxilli</i> NRRL2008	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		340
<i>P.citrinum</i> NRRL1841	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		302
<i>P.sartoryi</i> NRRL783	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		302
<i>P.westlingii</i> NRRL800	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		302
<i>P.charlesii</i> NRRL778	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		333
<i>P.fellutanum</i> NRRL746	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		334
<i>P.spinulosum</i> NRRL728	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.spinulosum</i> NRRL1750	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.thomii</i> NRRL2077	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>Eu.lapidosum</i> NRRL718	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.thomii</i> NRRL760	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.purpurescens</i> NRRL720	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.glabrum</i> NRRL766	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.asperosporum</i> NRRL3411	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.lividum</i> NRRL754	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		335
<i>P.adametzii</i> NRRL736	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.adametzii</i> NRRL737	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.bilaii</i> NRRL3391	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.adametziioides</i> NRRL3405	GAACGCACATTGC	GCCCTCTGGTATT	CCGGAGGGCATG	CCTGTCCGAGCG		335
<i>P.herquei</i> NRRL1040	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.sclerotiorum</i> NRRL2074	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		337
<i>P.decumbens</i> NRRL742	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336
<i>P.decumbens</i> NRRL741	GAACGCACATTGC	CCCCCTGGTATT	CCGGGGGGCATG	CCTGTCCGAGCG		336

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                301      310      320      330      340      350
                                +-----+-----+-----+-----+
P.turbatum NRRL759             GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL803        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL802        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.corylophilum NRRL793        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.melinii NRRL2041            GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.velutinum NRRL2069          GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.raciborskii NRRL2150        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.restrictum NRRL25744        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.restrictum NRRL1748         GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.citreonigrum NRRL761        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.cinerascens NRRL748         GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.vinaceum NRRL739            GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.oxalicum NRRL790            GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 339
P.oxalicum NRRL787            GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 339
P.donkii NRRL5562             GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 340
P.fuscum NRRL721              GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 338
P.janthinellum NRRL2016       GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
P.raperi NRRL2674             GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 337
P.daleae NRRL922              GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 337
P.ochrochloron NRRL926        GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 335
P.simplicissimum NRRL1075     GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 335
P.rolfsii NRRL1078            GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 336
Eu.cinnamopurpureum NRRL3326  GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 335
P.chermesinum NRRL735         GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 333
P.clavariiformis NRRL2482     GAACGCACATTGCGCCCCCTGGTATTCGGGGGGGCATGCCTGTCCGAGCG 340
*****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	351	360	370	380	390	400
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. camemberti</i> NRRL875	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. echinulatum</i> NRRL1151	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. crustosum</i> NRRL968	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCCCCGA	385			
<i>P. viridicatum</i> NRRL961	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. aurantiogriseum</i> NRRL971	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	386			
<i>P. polonicum</i> NRRL995	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. viridicatum</i> NRRL958	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. chrysogenum</i> NRRL821	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. chrysogenum</i> NRRL807	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. griseoroseum</i> NRRL820	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. chrysogenum</i> NRRL824	TCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. griseoroseum</i> NRRL832	TCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. griseofulvum</i> NRRL734	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	384			
<i>P. griseofulvum</i> NRRL2300	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	384			
<i>P. coprophilum</i> NRRL13627	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. digitatum</i> NRRL786	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCCCCGA	384			
<i>P. sclerotigenum</i> NRRL3461	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGT	384			
<i>Eu. egyptiacum</i> NRRL2090	TCATTACTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>Eu. crustaceum</i> NRRL3332	TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. expansum</i> NRRL974	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. turbatum</i> NRRL757	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	384			
<i>H. paradoxus</i> NRRL2162	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCCCCGA	385			
<i>P. atramentosum</i> NRRL795	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	385			
<i>P. swiecickii</i> NRRL918	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGT-CCCCCGA	383			
<i>P. kojigenum</i> NRRL3442	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	383			
<i>P. raistrickii</i> NRRL2039	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	383			
<i>P. soppii</i> NRRL2023	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCGA	384			
<i>P. canescens</i> NRRL910	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC	-GT-CCCCCTT	383			
<i>P. atrovenetum</i> NRRL2571	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC	-GT-CCCCCTC	384			
<i>P. canescens</i> NRRL2147	TCATTGCTGCCCTCCAGCCCGGCTGTTGTGTTGGGCCCC	-G-CCCCCTT	385			
<i>P. waksmanii</i> NRRL777	TCATTGCTGCCCTCCAGCCCGGCTGTTGTGTTGGGCCCC	-G-CCCCCTT	385			
<i>P. miczynskii</i> NRRL1077	TCATTGCTGCCCTCCAGCCCGGCTGTTGTGTTGGGCCCC	-G-CCCCCTT	385			
<i>Eu. shearii</i> NRRL1515	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCC	-GT-CCTCCCGA	384			
<i>P. roseopurpureum</i> NRRL733	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGT	-CCCCCGA	384			
<i>P. roseopurpureum</i> NRRL2064	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGT	-CCCCCGA	384			
<i>P. sumatrense</i> NRRL779	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCCGT	-CCCCCGA	387			
<i>P. paxilli</i> NRRL2008	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCTCGT	-CCCCCGA	388			
<i>P. citrinum</i> NRRL1841	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GTCCCCCGA	350			
<i>P. sartoryi</i> NRRL783	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GTCCCCCGA	350			
<i>P. westlingii</i> NRRL800	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCC	-GTCCCCCGA	350			
<i>P. charlesii</i> NRRL778	TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGC	-CCG-CCCCCGA	379			
<i>P. fellutanum</i> NRRL746	TCATTACTGCCCTCAAGCCCGGCTTGTGTGTTGGGC	-CCG-CCCCCGA	380			
<i>P. spinulosum</i> NRRL728	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. spinulosum</i> NRRL1750	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. thomii</i> NRRL2077	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>Eu. lapidosum</i> NRRL718	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. thomii</i> NRRL760	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. purpurescens</i> NRRL720	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. glabrum</i> NRRL766	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. aspersporum</i> NRRL3411	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGC	-TCCGTCCCCCGA	382			
<i>P. lividum</i> NRRL754	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCCT	-GTCCCCCTC	383			
<i>P. adametzii</i> NRRL736	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT	-CCCCCGA	385			
<i>P. adametzii</i> NRRL737	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT	-CCCCCGA	385			
<i>P. bilaii</i> NRRL3391	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGT	-CCTCCCGA	385			
<i>P. adametzioides</i> NRRL3405	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGTCTC	-GT-CCCCCGA	380			
<i>P. herquei</i> NRRL1040	TCATTGCTGCCCTCAAGCCCGGCTTGTGTGTTGGGCCTC	-GTCCCCCGA	385			
<i>P. sclerotiorum</i> NRRL2074	TCATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGTCTT	-GTCCCCCGA	384			
<i>P. decumbens</i> NRRL742	TCATTGCTGCCCTTAAGCACGGCTTATGTGTTGGGCCTCCGT	-CCTCCCGA	384			
<i>P. decumbens</i> NRRL741	TCATTGCTGCCCTTAAGCACGGCTTATGTGTTGGGCCTCCGT	-CCTCCCGA	384			



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	401	410	420	430	440	450
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	TC	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	434			
<i>P.camemberti</i> NRRL875	TC	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	434			
<i>P.echinulatum</i> NRRL1151	TT	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	434			
<i>P.crustosum</i> NRRL968	TC	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	434			
<i>P.viridicatum</i> NRRL961	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.aurantiogriseum</i> NRRL971	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	434			
<i>P.polonicum</i> NRRL995	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.viridicatum</i> NRRL958	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.chrysogenum</i> NRRL821	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.chrysogenum</i> NRRL807	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.griseoroseum</i> NRRL820	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.chrysogenum</i> NRRL824	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.griseoroseum</i> NRRL832	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.griseofulvum</i> NRRL734	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.griseofulvum</i> NRRL2300	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.coprophilum</i> NRRL13627	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.digitatum</i> NRRL786	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.sclerotigenum</i> NRRL3461	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>Eu.egyptiacum</i> NRRL2090	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>Eu.crustaceum</i> NRRL3332	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.expansum</i> NRRL974	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.turbatum</i> NRRL757	T--	-TCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>H.paradoxus</i> NRRL2162	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.atramentosum</i> NRRL795	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.swiecickii</i> NRRL918	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.kojigenum</i> NRRL3442	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.raistrickii</i> NRRL2039	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.soppii</i> NRRL2023	T--	-CCCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	432			
<i>P.canescens</i> NRRL910	C--	-CCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.atrovenetum</i> NRRL2571	C--	-CCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.canescens</i> NRRL2147	C--	-CCGGGGGGGCGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.waksmanii</i> NRRL777	C--	-CCGGGGGGGCGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.miczynskii</i> NRRL1077	C--	-CCGGGGGGGCGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>Eu.shearpii</i> NRRL715	T	-CCGGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	433			
<i>P.roseopurpureum</i> NRRL733	A--	-CCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.roseopurpureum</i> NRRL2064	A--	-CCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	432			
<i>P.sumatrense</i> NRRL779	CTG	-CCGGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	437			
<i>P.paxilli</i> NRRL2008	---	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.citrinum</i> NRRL1841	--	-GCGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	398			
<i>P.sartoryi</i> NRRL783	--	-GCGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	398			
<i>P.westlingii</i> NRRL800	--	-GCGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	398			
<i>P.charlesii</i> NRRL778	---	-CGGGGCGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	423			
<i>P.fellutanum</i> NRRL746	---	-C---GGGGCGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	424			
<i>P.spinulosum</i> NRRL728	-----	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.spinulosum</i> NRRL1750	-----	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.thomii</i> NRRL2077	-----	-GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>Eu.lapidosum</i> NRRL718	-----	-GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.thomii</i> NRRL760	-----	-GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.purpurescens</i> NRRL720	-----	-GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.glabrum</i> NRRL766	-----	-GGGGACGGGTCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.asperosporum</i> NRRL3411	-----	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	425			
<i>P.lividum</i> NRRL754	--	-TCC-GGGGACAGGCCCCGAAAGGCAGCGGCGGCACCGAGTCCGGTCCT	430			
<i>P.adametzii</i> NRRL736	--	-CCC-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT	432			
<i>P.adametzii</i> NRRL737	--	-CCC-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT	432			
<i>P.bilalii</i> NRRL3391	--	-CCCGGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT	433			
<i>P.adametziioides</i> NRRL3405	--	-CCC-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT	427			
<i>P.herquei</i> NRRL1040	--	-CCGCGGGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGTGTCCGGTCCT	433			
<i>P.sclerotiorum</i> NRRL2074	-----	-GGGAACAGGCCCCGAAAGGCAGTGGCGGCACCG--TCCGATCT	425			
<i>P.decumbens</i> NRRL742	T-TGG	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			
<i>P.decumbens</i> NRRL741	T-TGG	-GGGGACGGGCCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCT	431			



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	401	410	420	430	440	450	
	+-----+-----+-----+-----+-----+						
<i>P.turbatum</i> NRRL759	T-TGG--	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.corylophilum</i> NRRL803	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.corylophilum</i> NRRL802	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.corylophilum</i> NRRL793	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.melinii</i> NRRL2041	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.velutinum</i> NRRL2069	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.raciborskii</i> NRRL2150	T-CCC-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.restrictum</i> NRRL25744	C-CCG--	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.restrictum</i> NRRL1748	T-CCG-	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 432
<i>P.citreonigrum</i> NRRL761	C-CCG--	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 430
<i>P.cinerascens</i> NRRL748	C-CCG--	GAGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 430
<i>P.vinaceum</i> NRRL739	-----	GGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 425
<i>P.oxalicum</i> NRRL790	T-TCC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 436
<i>P.oxalicum</i> NRRL787	T-TCC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 436
<i>P.donkii</i> NRRL5562	T-CTC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 437
<i>P.fusum</i> NRRL721	T-CTC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 435
<i>P.janthinellum</i> NRRL2016	C-TCCCGGGGG	CGGGCCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 434	
<i>P.raperi</i> NRRL2674	C-TCC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 433
<i>P.daleae</i> NRRL922	C-TCCCGGGGG	CGGGCCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 435	
<i>P.ochrochloron</i> NRRL926	T-CCC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.simplicissimum</i> NRRL1075	T-CCC-	GGGGGGCGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 431
<i>P.rolfsii</i> NRRL1078	T-TTC-	GGGGGGCGG	ACCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 432
<i>Eu.cinnamopurpureum</i> NRRL3326	-----	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCATCG	CGTCCGGT	CCT 425
<i>P.thermesinum</i> NRRL735	-----	GGGGACGGG	CCCCGAAAGG	CAGCGG	CGGCACCG	CGTCCGGT	CCT 423
<i>P.clavariiformis</i> NRRL2482	CTGTGGGGGG	ACGGGCCCGAAAGG	CAGCGG	CGGCACCTGT	GCCTGGT	CCT 440	
	* * * * *						

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	451	460	470	480	490	500
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.camemberti</i> NRRL875	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.echinulatum</i> NRRL1151	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.crustosum</i> NRRL968	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.viridicatum</i> NRRL961	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.aurantiogriseum</i> NRRL971	CGAGCGTATGGG	GCTTTGT	CACCCGCTCC	GTAGGCCCGGCCGGCGCTT		482
<i>P.polonicum</i> NRRL995	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.viridicatum</i> NRRL958	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.chrysogenum</i> NRRL821	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.chrysogenum</i> NRRL807	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.griseoroseum</i> NRRL820	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.chrysogenum</i> NRRL824	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.griseoroseum</i> NRRL832	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.griseofulvum</i> NRRL734	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.griseofulvum</i> NRRL2300	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.coprophilum</i> NRRL13627	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.digitatum</i> NRRL786	CGAGCGTATGGG	GCTTTGT	CACCCGCTCC	GTAGGCCCGGCCGGCGCTT		480
<i>P.sclerotigenum</i> NRRL3461	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>Eu.egyptiacum</i> NRRL2090	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>Eu.crustaceum</i> NRRL3332	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.expansum</i> NRRL974	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.turbatum</i> NRRL757	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>H.paradoxus</i> NRRL2162	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.atramentosum</i> NRRL795	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.swiecickii</i> NRRL918	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.kojigenum</i> NRRL3442	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.raistrickii</i> NRRL2039	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.soppii</i> NRRL2023	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.canescens</i> NRRL910	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.atrovenetum</i> NRRL2571	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.canescens</i> NRRL2147	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.waksmanii</i> NRRL777	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.miczynskii</i> NRRL1077	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>Eu.shearaii</i> NRRL715	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		482
<i>P.roseopurpureum</i> NRRL733	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.roseopurpureum</i> NRRL2064	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.sumatrense</i> NRRL779	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		486
<i>P.paxilli</i> NRRL2008	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.citrinum</i> NRRL1841	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		447
<i>P.sartoryi</i> NRRL783	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		447
<i>P.westlingii</i> NRRL800	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		447
<i>P.charlesii</i> NRRL778	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		470
<i>P.fellutanum</i> NRRL746	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		471
<i>P.spinulosum</i> NRRL728	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.spinulosum</i> NRRL1750	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.thomii</i> NRRL2077	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>Eu.lapidosum</i> NRRL718	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.thomii</i> NRRL760	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.purpurescens</i> NRRL720	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.glabrum</i> NRRL766	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.asperosporum</i> NRRL3411	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.lividum</i> NRRL754	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		478
<i>P.adametzii</i> NRRL736	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.adametzii</i> NRRL737	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		480
<i>P.bilalii</i> NRRL3391	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.adametziioides</i> NRRL3405	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		475
<i>P.herquei</i> NRRL1040	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		481
<i>P.sclerotiorum</i> NRRL2074	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		473
<i>P.decumbens</i> NRRL742	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479
<i>P.decumbens</i> NRRL741	CGAGCGTATGGG	GCTTTGT	CACCCGCTCT	GTAGGCCCGGCCGGCGCTT		479

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                451      460      470      480      490      500
                                +-----+-----+-----+-----+
P.turbatum NRRL759              CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCGGCCGGCGCCT 479
P.corylophilum NRRL803          CGAGCGTATGGG-GCTTTGTACCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.corylophilum NRRL802          CGAGCGTATGGG-GCTTTGTACCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.corylophilum NRRL793          CGAGCGTATGGG-GCTTTGTACCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.melinii NRRL2041              CGAGCGTATGGG-GCTTCGCTTCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.velutinum NRRL2069            CGAGCGTATGGG-GCTTCGCTTCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.raciborskii NRRL2150          CGAGCGTATGGG-GCTTCGCTTCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.restrictum NRRL25744          CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGCCGGCGCCT 480
P.restrictum NRRL1748           CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGCCGGCGCCT 481
P.citreonigrum NRRL761          CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 478
P.cinerascens NRRL748           CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGTCGGCCGGCGCCT 478
P.vinaceum NRRL739              CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 473
P.oxalicum NRRL790              CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 484
P.oxalicum NRRL787              CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 484
P.donkii NRRL5562               CGAGCGTATGGG-GCTTTGTACCCGCTCT-GTAGGCCCGCCGGCGCCT 485
P.fuscum NRRL721                CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 483
P.janthinellum NRRL2016         CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 482
P.raperi NRRL2674               CGAGCGTATGGG-GCTTCGTCACCCGCTCC-GTAGGCCCGCCGGCGCCT 481
P.daleae NRRL922                CGAGCGTATGGG-GCTTTGTACCCGCTCT-GTAGGCCCGCCGGCGCCT 483
P.ochrochloron NRRL926          CGAGCGTATGGG-GCTTTGTACCCGCTCC-GTAGGCCCGCCGGCGCCT 479
P.simplicissimum NRRL1075       CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 479
P.rolfsii NRRL1078              CGAGCGTATGGG-GCTTCGTCACCCGCTCT-GTAGGCCCGCCGGCGCCT 480
Eu.cinnamopurpureum NRRL3326    CGAGCGTATGGG-GCTTCGTCACCCGCTCTTGTAGGCCCGCCGGCGCCA 474
P.chermesinum NRRL735           CGAGCGTATGGG-GCTTTGTACCCGCTCTTGCAGGCCCGCCGGCGCCA 472
P.clavariiformis NRRL2482       CGAGCGTATGGGAGCTTTGTCACCCGCTCT-GTAGGCCAGGCCGGCGCCT 489
***** ** * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    501      510      520      530      540      550
                    +-----+-----+-----+-----+-----+
P.camemberti NRRL874      --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.camemberti NRRL875      --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.echinulatum NRRL1151    --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.crustosum NRRL968      --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.viridicatum NRRL961    --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.aurantiogriseum NRRL971 --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 524
P.polonicum NRRL995      --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.viridicatum NRRL958    --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL821    --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL807    --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseoroseum NRRL820   --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.chrysogenum NRRL824   --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseoroseum NRRL832   --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.griseofulvum NRRL734   --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
P.griseofulvum NRRL2300  --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
P.coprophilum NRRL13627 --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.digitatum NRRL786      --GCCGATCAAC---CCCAAATT-TTTAATCCAGGTTGACCTCGGATCAG 524
P.sclerotigenum NRRL3461 --GCCGATCAAC---CCCAA--TT-TTTTATCCAGGTTGACCTCGGATCAG 523
Eu.egyptiacum NRRL2090   --GCCGATCAAC---CCAAA--C-TTCTAT--AGGTTGACCTCGGATCAG 521
Eu.crustaceum NRRL3332   --GCCGATCAAC---CCCAA--T-TTTTAT--AGGTTGACCTCGGATCAG 521
P.expansum NRRL974       --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 523
P.turbatum NRRL757       --GCCGATCAAC---CCAAA--T-TTTTATCCAGGTTGACCTCGGATCAG 522
H.paradoxus NRRL2162     --GCCGATCAAC---CAAAT---TTTTATCCAGGTTGACCTCGGATCAG 522
P.atramentosum NRRL795   --GCCGATCAAC---CAAAA---TTTTTCCAGGTTGACCTCGGATCAG 522
P.swiecickii NRRL918     --GCCGATCAAC---CAAAT---TTTTATCCAGGTTGACCTCGGATCAG 520
P.kojigenum NRRL3442     --GCCGATCAAC---CAAAT---TTTTATCCAGGTTGACCTCGGATCAG 520
P.raistrickii NRRL2039   --GCCGATCAAC---CAAAT---TTTTATCCAGGTTGACCTCGGATCAG 520
P.soppii NRRL2023        --GCCGATCAAC---CAAAT---TTTT-TCCAGGTTGACCTCGGATCAG 520
P.canescens NRRL910      --GCCGATCAAC---CAAAA--C-TTTTTTCCAGGTTGACCTCGGATCAG 521
P.atrovenetum NRRL2571   --GCCGATCAAC---CACAA--A-TTTTTTCCAGGTTGACCTCGGATCAG 522
P.canescens NRRL2147     --GCCGACCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.waksmanii NRRL777      --GCCGACCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.miczynskii NRRL1077   --GCCGACCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
Eu.shearpii NRRL15       --GCCGACCCCC---TCAATCTATTTTTT--CAGGTTGACCTCGGATCAG 524
P.roseopurpureum NRRL733 --GCCGACCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.roseopurpureum NRRL2064 --GCCGACCCCC---TCAATCTATTTTTT-CAGGTTGACCTCGGATCAG 525
P.sumatrense NRRL779     --GCCGACCCCAA---CCCTAAATTTTTT-CAGGTTGACCTCGGATCAG 530
P.paxilli NRRL2008       --GCCGACCCCC---CCTCAATCTTAAAC-CAGGTTGACCTCGGATCAG 522
P.citrinum NRRL1841      --GCCGACCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.sartoryi NRRL783       --GCCGACCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.westlingii NRRL800     --GCCGACCCCA---ACCTTTAATTATCT-CAGGTTGACCTCGGATCAG 491
P.charlesii NRRL778      --GCCGACCCCC---CAACCTTTTTTTTT--CAGGTTGACCTCGGATCAG 513
P.fellutanum NRRL746     --GCCGACCCCTCCAACCTTTTTTTTTTTTTCAGGTTGACCTCGGATCAG 519
P.spinulosum NRRL728     --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.spinulosum NRRL1750    --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.thomii NRRL2077        --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
Eu.lapidosum NRRL718     --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.thomii NRRL760         --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.purpurescens NRRL720   --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.glabrum NRRL766        --GCCGACA--AC---CAATCATCCTTTTTTCAGGTTGACCTCGGATCAG 516
P.asperosporum NRRL3411  --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 514
P.lividum NRRL754        --GCCGACA--AC---CCATCATCCTTT--TCAGGTTGACCTCGGATCAG 519
P.adametzii NRRL736      --GCCGACC--CT---C-ATCATCCTTTTTTCAGGTTGACCTCGGATCAG 522
P.adametzii NRRL737      --GCCGACC--CT---C-ATCATCCTTTTTTCAGGTTGACCTCGGATCAG 522
P.bilalii NRRL3391       --GCCGACC--CT---CCAACCCATTTTTTTCAGGTTGACCTCGGATCAG 524
P.adametziioides NRRL3405 --GTCGACC--CC---C-AATCTATTTTTTTCAGGTTGACCTCGGATCAG 517
P.herquei NRRL1040       TAGCCGACG--AC---ACAATCT-TTTTTTTCAGGTTGACCTCGGATCAG 525
P.sclerotiorum NRRL2074  --GCCGAC---C---CCAATCAATCTTTTTTCAGGTTGACCTCGGATCAG 514
P.decumbens NRRL742      --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521
P.decumbens NRRL741      --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521

```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    501      510      520      530      540      550
                    +-----+-----+-----+-----+-----+
P.turbatum NRRL759      --GCCGAACA-CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 521
P.corylophilum NRRL803 --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.corylophilum NRRL802 --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.corylophilum NRRL793 --GCCGACAACCA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.melinii NRRL2041      --GCCGACAACAA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.velutinum NRRL2069    --GCCGACAACAA---TCAATCTTTTTT---CAGGTTGACCTCGGATCAG 522
P.raciborskii NRRL2150 --GCCGACAACAA---TCAATCTTTTTT-T-CAGGTTGACCTCGGATCAG 523
P.restrictum NRRL25744 --GCCGACA--CA---TCAATCTTTTTTTC-CAGGTTGACCTCGGATCAG 522
P.restrictum NRRL1748  --GCCGACA--CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 522
P.citreonigrum NRRL761 --GCCGACA--CA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 519
P.cinerascens NRRL748  --GCCGACA--CA---TCAATCTTTTTT-T-CAGGTTGACCTCGGATCAG 519
P.vinaceum NRRL739     --GCCGACA-CCA---TCAATCTTTTTT-C-CAGGTTGACCTCGGATCAG 515
P.oxalicum NRRL790     --GCCGGCGAACA---C-CATCAATCTTAACCAGGTTGACCTCGGATCAG 528
P.oxalicum NRRL787     --GCCGGCGAACA---C-CATCAATCTTAACCAGGTTGACCTCGGATCAG 528
P.donkii NRRL5562      --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 528
P.fuscum NRRL721       --GCCGGCAACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 526
P.janthinellum NRRL2016 --GCCGGCGACCC---C-CCTCAATCTTCTCAGGTTGACCTCGGATCAG 526
P.raperi NRRL2674      --GCCGGCGACCC---C-CCTCAATCTTCTCAGGTTGACCTCGGATCAG 525
P.daleae NRRL922       --GCCGGCGACCC---C-CCTCAATCTTTC-CAGGTTGACCTCGGATCAG 526
P.ochrochloron NRRL926 --GCCGGCGACCC---CCAATCAATCTATC-CAGGTTGACCTCGGATCAG 523
P.simplicissimum NRRL1075 --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 522
P.rolfsii NRRL1078     --GCCGGCGACCC---C-AATCAATCTATC-CAGGTTGACCTCGGATCAG 523
Eu.cinnamopurpureum NRRL3326 --GCCGAC----C---CCAACCATT-TTCTCAGGTTGACCTCGGATCAG 514
P.thermophilum NRRL735 --GCCGAC----C---CCAACCATTCTTCTCAGGTTGACCTCGGATCAG 513
P.clavariiformis NRRL2482 --GCCACAA-----CCA-T--TTTTTATCCAGGTTGACCTCGGATCAG 527
                    * *                               *****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	551	560	570	580	590	600
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.camemberti</i> NRRL875	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.echinulatum</i> NRRL1151	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.crustosum</i> NRRL968	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.viridicatum</i> NRRL961	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.aurantiogriseum</i> NRRL971	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.polonicum</i> NRRL995	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.viridicatum</i> NRRL958	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.chrysogenum</i> NRRL821	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.chrysogenum</i> NRRL807	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.griseoroseum</i> NRRL820	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.chrysogenum</i> NRRL824	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.griseoroseum</i> NRRL832	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.griseofulvum</i> NRRL734	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.griseofulvum</i> NRRL2300	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.coprophilum</i> NRRL13627	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.digitatum</i> NRRL786	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.sclerotigenum</i> NRRL3461	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>Eu.egyptiacum</i> NRRL2090	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					571
<i>Eu.crustaceum</i> NRRL3332	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					571
<i>P.expansum</i> NRRL974	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					573
<i>P.turbatum</i> NRRL757	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>H.paradoxus</i> NRRL2162	GTAGGGATACCCGCTCAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA					572
<i>P.atramentosum</i> NRRL795	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.swiecickii</i> NRRL918	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					570
<i>P.kojigenum</i> NRRL3442	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					570
<i>P.raistrickii</i> NRRL2039	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					570
<i>P.soppii</i> NRRL2023	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					570
<i>P.canescens</i> NRRL910	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					571
<i>P.atrovenetum</i> NRRL2571	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.canescens</i> NRRL2147	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>P.waksmanii</i> NRRL777	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>P.miczynskii</i> NRRL1077	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>Eu.shearpii</i> NRRL715	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.roseopurpureum</i> NRRL733	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>P.roseopurpureum</i> NRRL2064	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>P.sumatrense</i> NRRL779	GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA					580
<i>P.paxilli</i> NRRL2008	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.citrinum</i> NRRL1841	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					541
<i>P.sartoryi</i> NRRL783	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					541
<i>P.westlingii</i> NRRL800	GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA					541
<i>P.charlesii</i> NRRL778	GTAGGGATACCCGCTGAACTTAAGCATATCAATCAGCGGAGGAAAAGAAA					563
<i>P.fellutanum</i> NRRL746	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					569
<i>P.spinulosum</i> NRRL728	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					564
<i>P.spinulosum</i> NRRL1750	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					564
<i>P.thomii</i> NRRL2077	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					566
<i>Eu.lapidosum</i> NRRL718	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					566
<i>P.thomii</i> NRRL760	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					566
<i>P.purpurescens</i> NRRL720	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					566
<i>P.glabrum</i> NRRL766	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					566
<i>P.asperosporum</i> NRRL3411	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					564
<i>P.lividum</i> NRRL754	GTAGGGATACCCGCTGAACTTAAGCATATCAATGAGCGGAGGAAAAGAAA					569
<i>P.adametzii</i> NRRL736	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.adametzii</i> NRRL737	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					572
<i>P.bilalii</i> NRRL3391	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					574
<i>P.adametziioides</i> NRRL3405	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					567
<i>P.herquei</i> NRRL1040	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					575
<i>P.sclerotiorum</i> NRRL2074	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					564
<i>P.decumbens</i> NRRL742	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					571
<i>P.decumbens</i> NRRL741	GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA					571

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    551      560      570      580      590      600
                    +-----+-----+-----+-----+-----+
P.turbatum NRRL759      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 571
P.corylophilum NRRL803  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.corylophilum NRRL802  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.corylophilum NRRL793  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.melinii NRRL2041      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.velutinum NRRL2069    GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.raciborskii NRRL2150  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.restrictum NRRL25744  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.restrictum NRRL1748   GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.citreonigrum NRRL761  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 569
P.cinerascens NRRL748   GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 569
P.vinaceum NRRL739      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 565
P.oxalicum NRRL790      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.oxalicum NRRL787      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.donkii NRRL5562       GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 578
P.fuscum NRRL721        GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.janthinellum NRRL2016 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.raperi NRRL2674       GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 575
P.daleae NRRL922        GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 576
P.ochrochloron NRRL926  GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
P.simplicissimum NRRL1075 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 572
P.rolfsii NRRL1078      GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 573
Eu.cinnamopurpureum NRRL3326 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 564
P.chermesinum NRRL735   GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 563
P.clavariiformis NRRL2482 GTAGGGATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAA 577
*****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	601	610	620	630	640	650
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. camemberti</i> NRRL875	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. echinulatum</i> NRRL1151	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. crustosum</i> NRRL968	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. viridicatum</i> NRRL961	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. aurantiogriseum</i> NRRL971	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. polonicum</i> NRRL995	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. viridicatum</i> NRRL958	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. chrysogenum</i> NRRL821	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. chrysogenum</i> NRRL807	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. griseoroseum</i> NRRL820	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. chrysogenum</i> NRRL824	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. griseoroseum</i> NRRL832	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. griseofulvum</i> NRRL734	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. griseofulvum</i> NRRL2300	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. coprophilum</i> NRRL13627	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. digitatum</i> NRRL786	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. sclerotigenum</i> NRRL3461	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>Eu. egyptiacum</i> NRRL2090	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					621
<i>Eu. crustaceum</i> NRRL3332	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					621
<i>P. expansum</i> NRRL974	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					623
<i>P. turbatum</i> NRRL757	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>H. paradoxus</i> NRRL2162	CCAACAGGGATTGCCCCACTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. atramentosum</i> NRRL795	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. swiecickii</i> NRRL918	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					620
<i>P. kojigenum</i> NRRL3442	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					620
<i>P. raistrickii</i> NRRL2039	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					620
<i>P. soppii</i> NRRL2023	CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					620
<i>P. canescens</i> NRRL910	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					621
<i>P. atrovenetum</i> NRRL2571	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. canescens</i> NRRL2147	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>P. waksmanii</i> NRRL777	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>P. miczynskii</i> NRRL1077	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>Eu. shearii</i> NRRL1515	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. roseopurpureum</i> NRRL733	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>P. roseopurpureum</i> NRRL2064	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>P. sumatrense</i> NRRL779	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					630
<i>P. paxilli</i> NRRL2008	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. citrinum</i> NRRL1841	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					591
<i>P. sartoryi</i> NRRL783	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					591
<i>P. westlingii</i> NRRL800	CCAACCGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					591
<i>P. charlesii</i> NRRL778	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					613
<i>P. fellutanum</i> NRRL746	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					619
<i>P. spinulosum</i> NRRL728	CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT					614
<i>P. spinulosum</i> NRRL1750	CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT					614
<i>P. thomii</i> NRRL2077	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					616
<i>Eu. lapidosum</i> NRRL718	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					616
<i>P. thomii</i> NRRL760	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					616
<i>P. purpurescens</i> NRRL720	CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT					616
<i>P. glabrum</i> NRRL766	CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT					616
<i>P. asperosporum</i> NRRL3411	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					614
<i>P. lividum</i> NRRL754	CCAACAGGGATTACCTCAGTAACGGCGAGTGAAGCGGTAAGAGCTCAAAT					619
<i>P. adametzii</i> NRRL736	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. adametzii</i> NRRL737	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					622
<i>P. bilaii</i> NRRL3391	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					624
<i>P. adametzioides</i> NRRL3405	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					617
<i>P. herquei</i> NRRL1040	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					625
<i>P. sclerotiorum</i> NRRL2074	CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					614
<i>P. decumbens</i> NRRL742	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					621
<i>P. decumbens</i> NRRL741	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT					621



Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                     601       610       620       630       640       650
                                     +-----+-----+-----+-----+
P.turbatum NRRL759                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 621
P.corylophilum NRRL803              CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.corylophilum NRRL802              CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.corylophilum NRRL793              CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.melinii NRRL2041                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.velutinum NRRL2069                CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.raciborskii NRRL2150              CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.restrictum NRRL25744              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.restrictum NRRL1748               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.citreonigrum NRRL761              CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 619
P.cinerascens NRRL748               CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 619
P.vinaceum NRRL739                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 615
P.oxalicum NRRL790                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.oxalicum NRRL787                  CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.donkii NRRL5562                   CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 628
P.fuscum NRRL721                    CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.janthinellum NRRL2016             CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.raperi NRRL2674                   CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 625
P.daleae NRRL922                    CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 626
P.ochrochloron NRRL926              CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
P.simplicissimum NRRL1075           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 622
P.rolfsii NRRL1078                 CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 623
Eu.cinnamopurpureum NRRL3326        CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 614
P.chermesinum NRRL735               CCAACAGGGATTGCCCCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 613
P.clavariiformis NRRL2482           CCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGGCAAGAGCTCAAAT 627
***** ** * *****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	651	660	670	680	690	700
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. camemberti</i> NRRL875	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. echinulatum</i> NRRL1151	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. crustosum</i> NRRL968	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. viridicatum</i> NRRL961	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					673
<i>P. aurantiogriseum</i> NRRL971	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. polonicum</i> NRRL995	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					673
<i>P. viridicatum</i> NRRL958	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					673
<i>P. chrysogenum</i> NRRL821	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. chrysogenum</i> NRRL807	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. griseoroseum</i> NRRL820	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. chrysogenum</i> NRRL824	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. griseoroseum</i> NRRL832	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. griseofulvum</i> NRRL734	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					672
<i>P. griseofulvum</i> NRRL2300	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					672
<i>P. coprophilum</i> NRRL13627	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					673
<i>P. digitatum</i> NRRL786	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. sclerotigenum</i> NRRL3461	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					673
<i>Eu. egyptiacum</i> NRRL2090	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					671
<i>Eu. crustaceum</i> NRRL3332	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					671
<i>P. expansum</i> NRRL974	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					673
<i>P. turbatum</i> NRRL757	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					672
<i>H. paradoxus</i> NRRL2162	TTGAAAGCTGACTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					672
<i>P. atramentosum</i> NRRL795	TTGAAAGCTGACTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					672
<i>P. swiecickii</i> NRRL918	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					670
<i>P. kojigenum</i> NRRL3442	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					670
<i>P. raistrickii</i> NRRL2039	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					670
<i>P. soppii</i> NRRL2023	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					670
<i>P. canescens</i> NRRL910	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					671
<i>P. atrovenetum</i> NRRL2571	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					672
<i>P. canescens</i> NRRL2147	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					675
<i>P. waksmanii</i> NRRL777	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					675
<i>P. miczynskii</i> NRRL1077	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGTAGAGGATGCCTT					675
<i>Eu. shearii</i> NRRL715	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					674
<i>P. roseopurpureum</i> NRRL733	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					675
<i>P. roseopurpureum</i> NRRL2064	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					675
<i>P. sumatrense</i> NRRL779	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					680
<i>P. paxilli</i> NRRL2008	TTGAAAGCTGGCCCCCTCGGGGTCGCATTGTAATTTGCAGAGGATGCCTT					672
<i>P. citrinum</i> NRRL1841	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					641
<i>P. sartoryi</i> NRRL783	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					641
<i>P. westlingii</i> NRRL800	TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCCTT					641
<i>P. charlesii</i> NRRL778	TTGAAAGCTGGCCCCCTCGGGGTCGCATTGTAATTTGCAGAGGATGCCTT					663
<i>P. fellutanum</i> NRRL746	TTGAAAGCTGGCCCCCTCGGGGTCGCATTGTAATTTGCAGAGGATGCCTT					669
<i>P. spinulosum</i> NRRL728	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					664
<i>P. spinulosum</i> NRRL1750	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					664
<i>P. thomii</i> NRRL2077	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					666
<i>Eu. lapidosum</i> NRRL718	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					666
<i>P. thomii</i> NRRL760	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					666
<i>P. purpurescens</i> NRRL720	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					666
<i>P. glabrum</i> NRRL766	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					666
<i>P. asperosporum</i> NRRL3411	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					664
<i>P. lividum</i> NRRL754	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					669
<i>P. adametzii</i> NRRL736	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					672
<i>P. adametzii</i> NRRL737	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					672
<i>P. bilaii</i> NRRL3391	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					674
<i>P. adametzioides</i> NRRL3405	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					667
<i>P. herquei</i> NRRL1040	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					675
<i>P. sclerotiorum</i> NRRL2074	TTGAAAGCTGGCTCCTTCGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					664
<i>P. decumbens</i> NRRL742	TTGAAAGCTGGCCCCCTTGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					671
<i>P. decumbens</i> NRRL741	TTGAAAGCTGGCCCCCTTGGGGTCCGCATTGTAATTTGCAGAGGATGTTT					671

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                     651       660       670       680       690       700
                                     +-----+-----+-----+-----+
P.turbatum NRRL759                 TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 671
P.corylophilum NRRL803             TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.corylophilum NRRL802             TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.corylophilum NRRL793             TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.melinii NRRL2041                 TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.velutinum NRRL2069              TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.raciborskii NRRL2150            TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.restrictum NRRL25744            TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.restrictum NRRL1748             TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.citreonigrum NRRL761            TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 669
P.cinerascens NRRL748             TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 669
P.vinaceum NRRL739                TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 665
P.oxalicum NRRL790                TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.oxalicum NRRL787                TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.donkii NRRL5562                 TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 678
P.fuscum NRRL721                  TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.janthinellum NRRL2016           TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.raperi NRRL2674                 TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 675
P.daleae NRRL922                  TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 676
P.ochrochloron NRRL926            TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
P.simplicissimum NRRL1075         TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 672
P.rolfsii NRRL1078               TTGAAAGCTGGCTCCTTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 673
Eu.cinnamopurpureum NRRL3326      TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 664
P.chermesinum NRRL735            TTGAAAGCTGGCCCCCTCGGGTCCGCATTGTAATTTGCAGAGGATGCTT 663
P.clavariiformis NRRL2482         TTGAAATCTGGCGTCTTTGGCGTCCGAGTTGTAATTTGCAGAGGATGCTT 677
***** ** * * * ** * ** * ***** ***** **
```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	701	710	720	730	740	750
	+-----+-----+-----+-----+					
P.camemberti NRRL874	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.camemberti NRRL875	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.echinulatum NRRL1151	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.crustosum NRRL968	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.viridicatum NRRL961	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.aurantiogriseum NRRL971	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.polonicum NRRL995	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.viridicatum NRRL958	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.chrysogenum NRRL821	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.chrysogenum NRRL807	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.griseoroseum NRRL820	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.chrysogenum NRRL824	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.griseoroseum NRRL832	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.griseofulvum NRRL734	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
P.griseofulvum NRRL2300	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
P.coprophilum NRRL13627	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.digitatum NRRL786	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 724
P.sclerotigenum NRRL3461	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
Eu.egyptiacum NRRL2090	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 721
Eu.crustaceum NRRL3332	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 721
P.expansum NRRL974	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 723
P.turbatum NRRL757	CGGGAGCGGT	CCCCATCTA	AGTTCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
H.paradoxus NRRL2162	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
P.atramentosum NRRL795	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
P.swiecickii NRRL918	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 720
P.kojigenum NRRL3442	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 720
P.raistrickii NRRL2039	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 720
P.soppii NRRL2023	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	ACGTCATAG	AGGGTG 720
P.canescens NRRL910	CGGGAGCGGT	CCCCATCTA	AGTTCCCT	GGAACGGG	ACGTCATAG	AGGGTG 721
P.atrovenetum NRRL2571	CGGGAGCGGT	CCCCATCTA	AGTTCCCT	GGAACGGG	ACGTCATAG	AGGGTG 722
P.canescens NRRL2147	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
P.waksmanii NRRL777	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
P.miczynskii NRRL1077	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
Eu.shearirii NRRL715	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 724
P.roseopurpureum NRRL733	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
P.roseopurpureum NRRL2064	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
P.sumatrense NRRL779	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 730
P.paxilli NRRL2008	CGGGAGCGGT	CCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 722
P.citrinum NRRL1841	CGGGAACGG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 691
P.sartoryi NRRL783	CGGGAACGG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 691
P.westlingii NRRL800	CGGGAACGG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 691
P.charlesii NRRL778	CGGGCGTGG	CCCCCTGTCTA	AGTGCCCT	GGAACGGG	CCGTCAGAG	AGGGTG 713
P.fellutanum NRRL746	CGGGCGTGG	CCCCCTGTCTA	AGTGCCCT	GGAACGGG	CCGTCAGAG	AGGGTG 719
P.spinulosum NRRL728	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 714
P.spinulosum NRRL1750	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 714
P.thomii NRRL2077	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 716
Eu.lapidosum NRRL718	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 716
P.thomii NRRL760	CGGAAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 716
P.purpurescens NRRL720	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 716
P.glabrum NRRL766	CGGGAGCAG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 716
P.asperosporum NRRL3411	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 714
P.lividum NRRL754	CGGAAGCAG	CCCCCATCTA	AGTACCCT	GGAACGGG	TCGTCATAG	AGGGTG 719
P.adametzii NRRL736	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CTGTCATAG	AGGGTG 722
P.adametzii NRRL737	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CTGTCATAG	AGGGTG 722
P.bilalii NRRL3391	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CTGTCATAG	AGGGTG 724
P.adametziioides NRRL3405	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CTGTCATAG	AGGGTG 717
P.herquei NRRL1040	CGGGAGCAG	CCCCCATCTA	AGTGCCCT	GGAACGGG	CCGTCATAG	AGGGTG 725
P.sclerotiorum NRRL2074	CGGGAGTGG	CCCCCATCTA	AGTGTCCT	GGAACGGG	ACCGTCATAG	AGGGTG 714
P.decumbens NRRL742	CGGGAGTGG	CCCCCATCTA	AGTGCTCT	GGAACGGG	CCGTCATAG	AGGGTG 721
P.decumbens NRRL741	CGGGAGTGG	CCCCCATCTA	AGTGCTCT	GGAACGGG	CCGTCATAG	AGGGTG 721

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

              701      710      720      730      740      750
              +-----+-----+-----+-----+
P.turbatum NRRL759      CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 721
P.corylophilum NRRL803  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.corylophilum NRRL802  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.corylophilum NRRL793  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.melinii NRRL2041      CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.velutinum NRRL2069    CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.raciborskii NRRL2150  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 723
P.restrictum NRRL25744  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.restrictum NRRL1748   CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 722
P.citreonigrum NRRL761  CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 719
P.cinerascens NRRL748   CGGGAGTGGCCCCCATCTAAGTGCTCTGGAACGGGCCGTCATAGAGGGTG 719
P.vinaceum NRRL739      CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 715
P.oxalicum NRRL790      CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.oxalicum NRRL787      CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.donkii NRRL5562       CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 728
P.fuscum NRRL721        CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.janthinellum NRRL2016 CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.raperi NRRL2674       CGGGAGCGGTCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 725
P.daleae NRRL922        CGGGAGCGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 726
P.ochrochloron NRRL926 CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 723
P.simplicissimum NRRL1075 CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 722
P.rolfsii NRRL1078     CGGGAGTGGCCCCCATCTAAGTGCCCTGGAACGGGCCGTCATAGAGGGTG 723
Eu.cinnamopurpureum NRRL3326 CGGGAGCGGTCCCCATCTAAGTACCCTGGAACGGGTCGTCATAGAGGGTG 714
P.thermesinum NRRL735   CGGAGGCAGCCCCCGTCTAAGTACCCTGGAACGGGTCGTCATAGAGGGTG 713
P.clavariiformis NRRL2482 CGGATACAGCCCCCTGTCTAAGTGCCCTGGAACGGGCCGTCGGAGAGGGTG 727
***          *  ***  *****  *****  ***  *****
```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	751	760	770	780	790	800
	+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. camemberti</i> NRRL875	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. echinulatum</i> NRRL1151	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. crustosum</i> NRRL968	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. viridicatum</i> NRRL961	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. aurantiogriseum</i> NRRL971	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. polonicum</i> NRRL995	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. viridicatum</i> NRRL958	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. chrysogenum</i> NRRL821	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. chrysogenum</i> NRRL807	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. griseoroseum</i> NRRL820	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. chrysogenum</i> NRRL824	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. griseoroseum</i> NRRL832	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. griseofulvum</i> NRRL734	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. griseofulvum</i> NRRL2300	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. coprophilum</i> NRRL13627	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. digitatum</i> NRRL786	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. sclerotigenum</i> NRRL3461	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>Eu. egyptiacum</i> NRRL2090	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					771
<i>Eu. crustaceum</i> NRRL3332	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					771
<i>P. expansum</i> NRRL974	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					773
<i>P. turbatum</i> NRRL757	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>H. paradoxus</i> NRRL2162	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. atramentosum</i> NRRL795	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. swiecickii</i> NRRL918	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					770
<i>P. kojigenum</i> NRRL3442	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					770
<i>P. raistrickii</i> NRRL2039	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					770
<i>P. soppii</i> NRRL2023	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					770
<i>P. canescens</i> NRRL910	AAAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					771
<i>P. atrovenetum</i> NRRL2571	AAAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. canescens</i> NRRL2147	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>P. waksmanii</i> NRRL777	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>P. miczynskii</i> NRRL1077	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>Eu. shearii</i> NRRL15	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. roseopurpureum</i> NRRL733	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>P. roseopurpureum</i> NRRL2064	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>P. sumatrense</i> NRRL779	AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					780
<i>P. paxilli</i> NRRL2008	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. citrinum</i> NRRL1841	AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					741
<i>P. sartoryi</i> NRRL783	AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					741
<i>P. westlingii</i> NRRL800	AGAATCCCGTCTGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					741
<i>P. charlesii</i> NRRL778	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					763
<i>P. fellutanum</i> NRRL746	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					769
<i>P. spinulosum</i> NRRL728	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					764
<i>P. spinulosum</i> NRRL1750	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					764
<i>P. thomii</i> NRRL2077	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					766
<i>Eu. lapidosum</i> NRRL718	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					766
<i>P. thomii</i> NRRL760	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					766
<i>P. purpurescens</i> NRRL720	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					766
<i>P. glabrum</i> NRRL766	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					766
<i>P. asperosporum</i> NRRL3411	AAAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					764
<i>P. lividum</i> NRRL754	AGAATCCCGTATGGGATGGGGTGTCTGCGCCCATGTGAAACTCCTTCGAC					769
<i>P. adametzii</i> NRRL736	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. adametzii</i> NRRL737	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					772
<i>P. bilaii</i> NRRL3391	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					774
<i>P. adametzioides</i> NRRL3405	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					767
<i>P. herquei</i> NRRL1040	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					775
<i>P. sclerotiorum</i> NRRL2074	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCGTGTGAAGCTCCTTCGAC					764
<i>P. decumbens</i> NRRL742	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCATGTGAAACTCCTTCGAC					771
<i>P. decumbens</i> NRRL741	AGAATCCCGTATGGGATGGGGTGTCCGCGCCCATGTGAAACTCCTTCGAC					771



Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	801	810	820	830	840	850
	+-----+-----+-----+-----+-----+					
P.camemberti NRRL874	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.camemberti NRRL875	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.echinulatum NRRL1151	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.crustosum NRRL968	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.viridicatum NRRL961	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.aurantiogriseum NRRL971	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.polonicum NRRL995	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.viridicatum NRRL958	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.chrysogenum NRRL821	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.chrysogenum NRRL807	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.griseoroseum NRRL820	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.chrysogenum NRRL824	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.griseoroseum NRRL832	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.griseofulvum NRRL734	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.griseofulvum NRRL2300	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.coprophilum NRRL13627	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.digitatum NRRL786	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.sclerotigenum NRRL3461	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
Eu.egyptiacum NRRL2090	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					821
Eu.crustaceum NRRL3332	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					821
P.expansum NRRL974	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					823
P.turbatum NRRL757	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
H.paradoxus NRRL2162	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.atramentosum NRRL795	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.swiecickii NRRL918	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					820
P.kojigenum NRRL3442	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					820
P.raistrickii NRRL2039	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					820
P.soppii NRRL2023	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					820
P.canescens NRRL910	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					821
P.atrovenetum NRRL2571	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.canescens NRRL2147	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
P.waksmanii NRRL777	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
P.miczynskii NRRL1077	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
Eu.shearrii NRRL15	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.roseopurpureum NRRL733	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
P.roseopurpureum NRRL2064	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
P.sumatrense NRRL779	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					830
P.paxilli NRRL2008	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.citrinum NRRL1841	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					791
P.sartoryi NRRL783	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					791
P.westlingii NRRL800	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					791
P.charlesii NRRL778	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					813
P.fellutanum NRRL746	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					819
P.spinulosum NRRL728	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					814
P.spinulosum NRRL1750	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					814
P.thomii NRRL2077	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					816
Eu.lapidosum NRRL718	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					816
P.thomii NRRL760	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					816
P.purpurescens NRRL720	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					816
P.glabrum NRRL766	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					816
P.asperosporum NRRL3411	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					814
P.lividum NRRL754	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					819
P.adametzii NRRL736	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.adametzii NRRL737	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					822
P.bilalii NRRL3391	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					824
P.adametziioides NRRL3405	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					817
P.herquei NRRL1040	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					825
P.sclerotiorum NRRL2074	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					814
P.decumbens NRRL742	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					821
P.decumbens NRRL741	GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT					821



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

      801      810      820      830      840      850
      +-----+-----+-----+-----+-----+
P.turbatum NRRL759      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 821
P.corylophilum NRRL803  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.corylophilum NRRL802  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.corylophilum NRRL793  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.melinii NRRL2041      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.velutinum NRRL2069    GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.raciborskii NRRL2150  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 823
P.restrictum NRRL25744  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.restrictum NRRL1748   GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.citreonigrum NRRL761  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 819
P.cinerascens NRRL748   GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 819
P.vinaceum NRRL739      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 815
P.oxalicum NRRL790      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 828
P.oxalicum NRRL787      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 828
P.donkii NRRL5562       GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 828
P.fusum NRRL721         GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 826
P.janthinellum NRRL2016 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 826
P.raperi NRRL2674       GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 825
P.daleae NRRL922        GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 826
P.ochrochloron NRRL926  GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 823
P.simplicissimum NRRL1075 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 822
P.rolfsii NRRL1078      GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 823
Eu.cinnamopurpureum NRRL3326 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 814
P.chermesinum NRRL735   GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 813
P.clavariiformis NRRL2482 GAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGTGGTAAATTTTCATCT 827
*****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	851	860	870	880	890	900
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.camemberti</i> NRRL875	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.echinulatum</i> NRRL1151	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.crustosum</i> NRRL968	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.viridicatum</i> NRRL961	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.aurantiogriseum</i> NRRL971	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.polonicum</i> NRRL995	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.viridicatum</i> NRRL958	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.chrysogenum</i> NRRL821	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.chrysogenum</i> NRRL807	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.griseoroseum</i> NRRL820	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.chrysogenum</i> NRRL824	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.griseoroseum</i> NRRL832	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.griseofulvum</i> NRRL734	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.griseofulvum</i> NRRL2300	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.coprophilum</i> NRRL13627	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.digitatum</i> NRRL786	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.sclerotigenum</i> NRRL3461	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>Eu.egyptiacum</i> NRRL2090	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	871			
<i>Eu.crustaceum</i> NRRL3332	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	871			
<i>P.expansum</i> NRRL974	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	873			
<i>P.turbatum</i> NRRL757	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>H.paradoxus</i> NRRL2162	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.atramentosum</i> NRRL795	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.swiecickii</i> NRRL918	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	870			
<i>P.kojigenum</i> NRRL3442	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	870			
<i>P.raistrickii</i> NRRL2039	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	870			
<i>P.soppii</i> NRRL2023	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	870			
<i>P.canescens</i> NRRL910	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	871			
<i>P.atrovenetum</i> NRRL2571	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.canescens</i> NRRL2147	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>P.waksmanii</i> NRRL777	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>P.miczynskii</i> NRRL1077	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>Eu.shearaii</i> NRRL715	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.roseopurpureum</i> NRRL733	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>P.roseopurpureum</i> NRRL2064	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>P.sumatrense</i> NRRL779	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	880			
<i>P.paxilli</i> NRRL2008	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.citrinum</i> NRRL1841	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	841			
<i>P.sartoryi</i> NRRL783	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	841			
<i>P.westlingii</i> NRRL800	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	841			
<i>P.charlesii</i> NRRL778	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	863			
<i>P.fellutanum</i> NRRL746	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	869			
<i>P.spinulosum</i> NRRL728	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	864			
<i>P.spinulosum</i> NRRL1750	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	864			
<i>P.thomii</i> NRRL2077	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	866			
<i>Eu.lapidosum</i> NRRL718	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	866			
<i>P.thomii</i> NRRL760	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	866			
<i>P.purpurescens</i> NRRL720	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	866			
<i>P.glabrum</i> NRRL766	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	866			
<i>P.asperosporum</i> NRRL3411	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	864			
<i>P.lividum</i> NRRL754	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	869			
<i>P.adametzii</i> NRRL736	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.adametzii</i> NRRL737	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	872			
<i>P.bilaii</i> NRRL3391	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	874			
<i>P.adametziioides</i> NRRL3405	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	867			
<i>P.herquei</i> NRRL1040	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	875			
<i>P.sclerotiorum</i> NRRL2074	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	864			
<i>P.decumbens</i> NRRL742	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	871			
<i>P.decumbens</i> NRRL741	AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGT	GATCGAA	871			

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

      851      860      870      880      890      900
      +-----+-----+-----+-----+-----+
P.turbatum NRRL759      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 871
P.corylophilum NRRL803  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.corylophilum NRRL802  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.corylophilum NRRL793  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.melinii NRRL2041      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.velutinum NRRL2069    AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.raciborskii NRRL2150  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.restrictum NRRL25744  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.restrictum NRRL1748   AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.citreonigrum NRRL761  AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.cinerascens NRRL748   AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 869
P.vinaceum NRRL739      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 865
P.oxalicum NRRL790      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.oxalicum NRRL787      AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.donkii NRRL5562       AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 878
P.fuscum NRRL721        AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 876
P.janthinellum NRRL2016 AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 876
P.raperi NRRL2674       AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 875
P.daleae NRRL922        AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 876
P.ochrochloron NRRL926  AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
P.simplicissimum NRRL1075 AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 872
P.rolfsii NRRL1078      AAAGCTAAATACTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 873
Eu.cinnamopurpureum NRRL3326 AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 864
P.chermesinum NRRL735   AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 863
P.clavariiformis NRRL2482 AAAGCTAAATATTGGCCGGAGACCGATAGCGCACAAGTAGAGTGATCGAA 877
*****

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	901	910	920	930	940	950
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. camemberti</i> NRRL875	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. echinulatum</i> NRRL1151	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. crustosum</i> NRRL968	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. viridicatum</i> NRRL961	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. aurantiogriseum</i> NRRL971	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. polonicum</i> NRRL995	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. viridicatum</i> NRRL958	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. chrysogenum</i> NRRL821	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. chrysogenum</i> NRRL807	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. griseoroseum</i> NRRL820	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. chrysogenum</i> NRRL824	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. griseoroseum</i> NRRL832	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. griseofulvum</i> NRRL734	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. griseofulvum</i> NRRL2300	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. coprophilum</i> NRRL13627	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. digitatum</i> NRRL786	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. sclerotigenum</i> NRRL3461	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>Eu. egyptiacum</i> NRRL2090	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	921
<i>Eu. crustaceum</i> NRRL3332	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	921
<i>P. expansum</i> NRRL974	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	923
<i>P. turbatum</i> NRRL757	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>H. paradoxus</i> NRRL2162	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. atramentosum</i> NRRL795	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. swiecickii</i> NRRL918	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	920
<i>P. kojigenum</i> NRRL3442	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	920
<i>P. raistrickii</i> NRRL2039	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	920
<i>P. soppii</i> NRRL2023	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	920
<i>P. canescens</i> NRRL910	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	921
<i>P. atrovenetum</i> NRRL2571	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. canescens</i> NRRL2147	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	925
<i>P. waksmanii</i> NRRL777	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	925
<i>P. miczynskii</i> NRRL1077	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	925
<i>Eu. shearii</i> NRRL715	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. roseopurpureum</i> NRRL733	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	925
<i>P. roseopurpureum</i> NRRL2064	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	925
<i>P. sumatrense</i> NRRL779	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	930
<i>P. paxilli</i> NRRL2008	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	922
<i>P. citrinum</i> NRRL1841	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	891
<i>P. sartoryi</i> NRRL783	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAC	AGCACGTGAA	ATTGTTGA	891
<i>P. westlingii</i> NRRL800	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	891
<i>P. charlesii</i> NRRL778	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	913
<i>P. fellutanum</i> NRRL746	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	919
<i>P. spinulosum</i> NRRL728	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	914
<i>P. spinulosum</i> NRRL1750	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	914
<i>P. thomii</i> NRRL2077	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	916
<i>Eu. lapidosum</i> NRRL718	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	916
<i>P. thomii</i> NRRL760	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	916
<i>P. purpurescens</i> NRRL720	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	916
<i>P. glabrum</i> NRRL766	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	916
<i>P. asperosporum</i> NRRL3411	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	914
<i>P. lividum</i> NRRL754	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	919
<i>P. adametzii</i> NRRL736	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. adametzii</i> NRRL737	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	922
<i>P. bilaii</i> NRRL3391	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	924
<i>P. adametzioides</i> NRRL3405	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	917
<i>P. herquei</i> NRRL1040	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	925
<i>P. sclerotiorum</i> NRRL2074	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	914
<i>P. decumbens</i> NRRL742	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	921
<i>P. decumbens</i> NRRL741	AGATGAAAAGC	ACTTTGAAAAG	GAGAGTTAAAA	AGCACGTGAA	ATTGTTGA	921

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

          901      910      920      930      940      950
          +-----+-----+-----+-----+-----+
P.turbatum NRRL759      AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 921
P.corylophilum NRRL803  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.corylophilum NRRL802  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.corylophilum NRRL793  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.melinii NRRL2041      AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.velutinum NRRL2069    AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.raciborskii NRRL2150  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 923
P.restrictum NRRL25744  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.restrictum NRRL1748   AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 922
P.citreonigrum NRRL761  AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 919
P.cinerascens NRRL748   AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 919
P.vinaceum NRRL739      AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 915
P.oxalicum NRRL790      AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 928
P.oxalicum NRRL787      AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 928
P.donkii NRRL5562       AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 928
P.fuscum NRRL721        AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 926
P.janthinellum NRRL2016 AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 926
P.raperi NRRL2674       AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 925
P.daleae NRRL922        AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 926
P.ochrochloron NRRL926  AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 923
P.simplicissimum NRRL1075 AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 922
P.rolfsii NRRL1078      AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 923
Eu.cinnamopurpureum NRRL3326 AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 914
P.chermesinum NRRL735   AGATGAAAAGCACTTTGAAAAGAGAGTTAAAAAGCACGTGAAATTGTTGA 913
P.clavariiformis NRRL2482 AGATGAAAAGCACTTTGAAAAGAGAGTTAAACAGCACGTGAAATTGTTGA 927
*****

```

Penicillium spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	951	960	970	980	990	1000
	+-----+-----+-----+-----+-----+					
P.camemberti NRRL874	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.camemberti NRRL875	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.echinulatum NRRL1151	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.crustosum NRRL968	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.viridicatum NRRL961	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.aurantiogriseum NRRL971	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.polonicum NRRL995	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.viridicatum NRRL958	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.chrysogenum NRRL821	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.chrysogenum NRRL807	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.griseoroseum NRRL820	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.chrysogenum NRRL824	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.griseoroseum NRRL832	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.griseofulvum NRRL734	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
P.griseofulvum NRRL2300	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
P.coprophilum NRRL13627	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.digitatum NRRL786	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.sclerotigenum NRRL3461	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
Eu.egyptiacum NRRL2090	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	970
Eu.crustaceum NRRL3332	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	970
P.expansum NRRL974	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	972
P.turbatum NRRL757	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
H.paradoxus NRRL2162	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
P.atramentosum NRRL795	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
P.swiecickii NRRL918	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	969
P.kojigenum NRRL3442	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	969
P.raistrickii NRRL2039	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	969
P.soppii NRRL2023	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGTGGGGTT	-CAGCCGGCATT	C	969
P.canescens NRRL910	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	970
P.atrovenetum NRRL2571	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	971
P.canescens NRRL2147	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	974
P.waksmanii NRRL777	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	974
P.miczynskii NRRL1077	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	974
Eu.shearpii NRRL715	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	973
P.roseopurpureum NRRL733	AAGGGAAGCGCTT	TGCGATCAGACT	CGCCACGGGGTT	-CAGCCGGCATT	C	974
P.roseopurpureum NRRL2064	AAGGGAAGCGCTT	TGCGATCAGACT	CGCCACGGGGTT	-CAGCCGGCATT	C	974
P.sumatrense NRRL779	AAGGGAAGCGCTT	TGCGATCAGACT	CGCCCGGGGGTT	-CAGCCGGCATT	C	979
P.paxilli NRRL2008	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTCCGGGGTT	-CAGCCGGCATT	C	971
P.citrinum NRRL1841	AAGGGAAGCGCTT	TGCGACCAGACT	CGCCCGGGGGTT	-CAGCCGGCATT	C	940
P.sartoryi NRRL783	AAGGGAAGCGCTT	TGCGACCAGACT	CGCCCGGGGGTT	-CAGCCGGCATT	C	940
P.westlingii NRRL800	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	940
P.charlesii NRRL778	AAGGGAAGCGCTT	TGCGACCAGACT	CGCCACGGGGTT	-CAACCGCTTTC	C	962
P.fellutanum NRRL746	AAGGGAAGCGCTT	TGCGACCAGACT	CGCCACGGGGTT	-CAACCGCTTTC	C	968
P.spinulosum NRRL728	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	963
P.spinulosum NRRL1750	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	963
P.thomii NRRL2077	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	965
Eu.lapidosum NRRL718	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	965
P.thomii NRRL760	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	965
P.purpurescens NRRL720	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	965
P.glabrum NRRL766	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	965
P.asperosporum NRRL3411	AAGGGAAGCGCTT	TGCGATCAGACT	CGCTTGGGGTT	-CAGCCGGCATT	C	963
P.lividum NRRL754	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGGGGGTT	-CAACCGCATT	C	968
P.adametzii NRRL736	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTACGGGGTT	-CAGCTACCTTC	C	971
P.adametzii NRRL737	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTACGGGGTT	-CAGCTACCTTC	C	971
P.bilalii NRRL3391	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTACGGGGTT	-CAGCTACCTTC	C	973
P.adametziioides NRRL3405	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTACGGGGTT	-CAGCTACCTTC	C	966
P.herquei NRRL1040	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTACGGGGTT	-CAGCCGGCTTTC	C	974
P.sclerotiorum NRRL2074	AAGGGAAGCGCTT	TGCGATCAGACT	CGCCGACGGGGTT	-CAGCTGCCTTC	C	963
P.decumbens NRRL742	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGCATT	C	970
P.decumbens NRRL741	AAGGGAAGCGCTT	TGCGACCAGACT	CGCTCGCGGGGTT	-CAGCCGGTATT	C	970

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

          951          960          970          980          990          1000
          +-----+-----+-----+-----+-----+
P.turbatum NRRL759      AAGGGAAGCGCTTGCACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 970
P.corylophilum NRRL803  AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.corylophilum NRRL802  AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.corylophilum NRRL793  AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.melinii NRRL2041     AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.velutinum NRRL2069   AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 971
P.raciborskii NRRL2150 AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 972
P.restrictum NRRL25744 AAGGGAAGCGCTTGCACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 971
P.restrictum NRRL1748  AAGGGAAGCGCTTGCACCAGACTCGCCTGCGGGGTT-CAGCCGGTATTC 971
P.citreonigrum NRRL761 AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 968
P.cinerascens NRRL748  AAGGGAAGCGCTTGCACCAGACTCGCCTACGGGGTT-CAGCCGGTATTC 968
P.vinaceum NRRL739     AAGGGAAGCGCTTGCAGACTAGACTCGCCACGGGGTAACAGCCGCTATTC 965
P.oxalicum NRRL790     AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 977
P.oxalicum NRRL787     AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 977
P.donkii NRRL5562      AAGGGAAGCGCTTGCACCAGACTCGCTCGGGGGTT-CAGCCGGCATTC 977
P.fuscum NRRL721       AAGGGAAGCGCTTGCACCAGACTCGCTCGGGGGTT-CAGCCGGCATTC 975
P.janthinellum NRRL2016 AAGGGAAGCGCTTGCACCAGACTCGCTCGGGGGTT-CAGCCGGCCTTC 975
P.raperi NRRL2674      AAGGGAAGCGCTTGCACCAGACTCGCTCGGGGGTT-CAGCCGGCCTTC 974
P.daleae NRRL922       AAGGGAAGCGCTTGCACCAGACTCGCCCGGGGGTT-CAGCCGGCATTC 975
P.ochrochloron NRRL926 AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 972
P.simplicissimum NRRL1075 AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 971
P.rolfsii NRRL1078     AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 972
Eu.cinnamopurpureum NRRL3326 AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 963
P.thermophilum NRRL735 AAGGGAAGCGCTTGCACCAGACTCGCCACGGGGTT-CAGCCGGCATTC 962
P.clavariiformis NRRL2482 AAGGGAAGCGCTTGCACCAGACTCGCTTGCAGGGTT-CAGCCGGGATTC 976
          *****          *****          *****          *****          ** *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	1001	1010	1020	1030	1040	1050
	+-----+-----+-----+-----+-----+					
<i>P.camemberti</i> NRRL874	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.camemberti</i> NRRL875	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.echinulatum</i> NRRL1151	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.crustosum</i> NRRL968	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.viridicatum</i> NRRL961	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.aurantiogriseum</i> NRRL971	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.polonicum</i> NRRL995	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.viridicatum</i> NRRL958	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.chrysogenum</i> NRRL821	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.chrysogenum</i> NRRL807	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.griseoroseum</i> NRRL820	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.chrysogenum</i> NRRL824	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.griseoroseum</i> NRRL832	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.griseofulvum</i> NRRL734	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>P.griseofulvum</i> NRRL2300	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>P.coprophilum</i> NRRL13627	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.digitatum</i> NRRL786	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1023
<i>P.sclerotigenum</i> NRRL3461	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>Eu.egyptiacum</i> NRRL2090	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1020
<i>Eu.crustaceum</i> NRRL3332	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1020
<i>P.expansum</i> NRRL974	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1022
<i>P.turbatum</i> NRRL757	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>H.paradoxus</i> NRRL2162	GTGCCGGTGTATTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>P.atramentosum</i> NRRL795	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>P.swiecickii</i> NRRL918	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1019
<i>P.kojigenum</i> NRRL3442	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1019
<i>P.raistrickii</i> NRRL2039	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1019
<i>P.soppii</i> NRRL2023	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1019
<i>P.canescens</i> NRRL910	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1020
<i>P.atrovenetum</i> NRRL2571	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1021
<i>P.canescens</i> NRRL2147	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1024
<i>P.waksmanii</i> NRRL777	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1024
<i>P.miczynskii</i> NRRL1077	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1024
<i>Eu.shearrii</i> NRRL715	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1023
<i>P.roseopurpureum</i> NRRL733	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1024
<i>P.roseopurpureum</i> NRRL2064	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1024
<i>P.sumatrense</i> NRRL779	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1029
<i>P.paxilli</i> NRRL2008	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1021
<i>P.citrinum</i> NRRL1841	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					990
<i>P.sartoryi</i> NRRL783	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					990
<i>P.westlingii</i> NRRL800	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					990
<i>P.charlesii</i> NRRL778	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1012
<i>P.fellutanum</i> NRRL746	GGGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1018
<i>P.spinulosum</i> NRRL728	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCTGG					1013
<i>P.spinulosum</i> NRRL1750	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCTGG					1013
<i>P.thomii</i> NRRL2077	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCTGG					1015
<i>Eu.lapidosum</i> NRRL718	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCTGG					1015
<i>P.thomii</i> NRRL760	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCTGG					1015
<i>P.purpurescens</i> NRRL720	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1015
<i>P.glabrum</i> NRRL766	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1015
<i>P.asperosporum</i> NRRL3411	GTGCCGGTGTACTTCCCCAGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1013
<i>P.lividum</i> NRRL754	GTGCCGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGTCGG					1018
<i>P.adametzii</i> NRRL736	GGGTAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1021
<i>P.adametzii</i> NRRL737	GGGTAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1021
<i>P.bilalii</i> NRRL3391	GGGTGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1023
<i>P.adametziioides</i> NRRL3405	GGGCAGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1016
<i>P.herquei</i> NRRL1040	GGGCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1024
<i>P.sclerotiorum</i> NRRL2074	GGGCAGGTGTACTTCCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1013
<i>P.decumbens</i> NRRL742	GTACCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1020
<i>P.decumbens</i> NRRL741	GTACCCGGTGTACTTCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG					1020



*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1001      1010      1020      1030      1040      1050
                                +-----+-----+-----+-----+
P.turbatum NRRL759             GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1020
P.corylophilum NRRL803        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.corylophilum NRRL802        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.corylophilum NRRL793        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.melinii NRRL2041            GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.velutinum NRRL2069          GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.raciborskii NRRL2150        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
P.restrictum NRRL25744        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.restrictum NRRL1748         GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.citreonigrum NRRL761        GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1018
P.cinerascens NRRL748         GTACCGGTGTA...TCCCCGTGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1018
P.vinaceum NRRL739            GTAGCCGTGCA...TCCCCGTGGTCGGGCCAGCGTCGGTTTGGGCGGCCGG 1015
P.oxalicum NRRL790            GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.oxalicum NRRL787            GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.donkii NRRL5562             GTGCCGGTGTACT...CCCCCGAGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1027
P.fuscum NRRL721              GTGCCGGTGTACT...CCCCCGAGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.janthinellum NRRL2016       GGGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.raperi NRRL2674             GGGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1024
P.daleae NRRL922              GTGCCGGTGTACT...CCCCACGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1025
P.ochrochloron NRRL926        GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
P.simplicissimum NRRL1075     GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1021
P.rolfsii NRRL1078           GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1022
Eu.cinnamopurpureum NRRL3326  GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1013
P.thermophilum NRRL735        GTGCCGGTGTACT...CCCCCGGGCGGGCCAGCGTCGGTTTGGGCGGCCGG 1012
P.clavariiformis NRRL2482     GTGCCGGTGTACT...CCCCGTGGTCGGGCCAGCGTCGGTTTGGGCGGCCGG 1026
                                *      *** * *****      ***** * * * * * * * * * *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	1051	1060	1070	1080	1090	1100
	+-----+-----+-----+-----+-----+					
<i>P. camemberti</i> NRRL874	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1071			
<i>P. camemberti</i> NRRL875	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1071			
<i>P. echinulatum</i> NRRL1151	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1071			
<i>P. crustosum</i> NRRL968	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1071			
<i>P. viridicatum</i> NRRL961	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. aurantiogriseum</i> NRRL971	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1071			
<i>P. polonicum</i> NRRL995	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. viridicatum</i> NRRL958	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. chrysogenum</i> NRRL821	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. chrysogenum</i> NRRL807	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. griseoroseum</i> NRRL820	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. chrysogenum</i> NRRL824	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. griseoroseum</i> NRRL832	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. griseofulvum</i> NRRL734	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>P. griseofulvum</i> NRRL2300	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>P. coprophilum</i> NRRL13627	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. digitatum</i> NRRL786	TCAAAGGCCCTCGGAAGGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1071			
<i>P. sclerotigenum</i> NRRL3461	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>Eu. egyptiacum</i> NRRL2090	TCAAAGGCCCTCGGAAGGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1068			
<i>Eu. crustaceum</i> NRRL3332	TCAAAGGCCCTCGGAAGGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1068			
<i>P. expansum</i> NRRL974	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1070			
<i>P. turbatum</i> NRRL757	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>H. paradoxus</i> NRRL2162	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>P. atramentosum</i> NRRL795	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>P. swiecickii</i> NRRL918	TCAAAGGCCCTCGGAAGGTAACGCCCTCGGGGCGTCTTATAGCCGAG	1069				
<i>P. kojigenum</i> NRRL3442	TCAAAGGCCCTCGGAAGGTAACGCCCTCGGGGCGTCTTATAGCCGAG	1069				
<i>P. raistrickii</i> NRRL2039	TCAAAGGCCCTCGGAAGGTAACGCCCTCGGGGCGTCTTATAGCCGAG	1069				
<i>P. soppii</i> NRRL2023	TCAAAGGCCCTCGGAAGGTAACGCCCTCGGGGCGTCTTATAGCCGAG	1069				
<i>P. canescens</i> NRRL910	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1068			
<i>P. atrovenetum</i> NRRL2571	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1069			
<i>P. canescens</i> NRRL2147	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1072			
<i>P. waksmanii</i> NRRL777	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1072			
<i>P. miczynskii</i> NRRL1077	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1072			
<i>Eu. shearii</i> NRRL1515	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1071			
<i>P. roseopurpureum</i> NRRL733	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1072			
<i>P. roseopurpureum</i> NRRL2064	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1072			
<i>P. sumatrense</i> NRRL779	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1077			
<i>P. paxilli</i> NRRL2008	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1069			
<i>P. citrinum</i> NRRL1841	TCAAAGGCCCTCGGAAGGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1038			
<i>P. sartoryi</i> NRRL783	TCAAAGGCCCTCGGAAGGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1038			
<i>P. westlingii</i> NRRL800	TCAAAGGCCCTCGGAAGGTAACGCCCT	--AGGGCGTCTTATAGCCGAG	1038			
<i>P. charlesii</i> NRRL778	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1060			
<i>P. fellutanum</i> NRRL746	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAGG	1066			
<i>P. spinulosum</i> NRRL728	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1061			
<i>P. spinulosum</i> NRRL1750	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1061			
<i>P. thomii</i> NRRL2077	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1063			
<i>Eu. lapidosum</i> NRRL718	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1063			
<i>P. thomii</i> NRRL760	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1063			
<i>P. purpurescens</i> NRRL720	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1063			
<i>P. glabrum</i> NRRL766	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1063			
<i>P. asperosporum</i> NRRL3411	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCAAG	1061			
<i>P. lividum</i> NRRL754	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1066			
<i>P. adametzii</i> NRRL736	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1069			
<i>P. adametzii</i> NRRL737	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1069			
<i>P. bilaii</i> NRRL3391	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1071			
<i>P. adametzioides</i> NRRL3405	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1064			
<i>P. herquei</i> NRRL1040	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1072			
<i>P. sclerotiorum</i> NRRL2074	TCAAAGGCCCTAGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCTAG	1061			
<i>P. decumbens</i> NRRL742	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1068			
<i>P. decumbens</i> NRRL741	TCAAAGGCCCTCGGAATGTAACGCCCT	--CGGGCGTCTTATAGCCGAG	1068			

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1051      1060      1070      1080      1090      1100
                                +-----+-----+-----+-----+-----+
P.turbatum NRRL759             TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1068
P.corylophilum NRRL803        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.corylophilum NRRL802        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.corylophilum NRRL793        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.melinii NRRL2041            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.velutinum NRRL2069          TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.raciborskii NRRL2150        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGGG 1070
P.restrictum NRRL25744        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.restrictum NRRL1748         TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1069
P.citreonigrum NRRL761        TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1066
P.cinerascens NRRL748         TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGAG 1066
P.vinaceum NRRL739            TCAAAGGCCCTCGGAATGTAACGCCTCT--CGGGGCGTCTTATAGCCGGG 1063
P.oxalicum NRRL790            TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.oxalicum NRRL787            TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.donkii NRRL5562             TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1075
P.fuscum NRRL721              TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.janthinellum NRRL2016       TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.raperi NRRL2674             TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1072
P.daleae NRRL922              TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1073
P.ochrochloron NRRL926        TCAAAGGCCCTTGGGAATGTACCGCCCC--CGGGGCGGCTTATAGCCAAG 1070
P.simplicissimum NRRL1075     TCAAAGGCCCTTGGGAATGTACCGCCCC--CGGGGCGGCTTATAGCCAAG 1069
P.rolfsii NRRL1078           TCAAAGGCCCTTGGGAATGTACCGCCCC--CGGGGCGTCTTATAGCCAAG 1070
Eu.cinnamopurpureum NRRL3326  TCAAAGGCCCTCGGAATGTAACGCCCT--CGGGGCGTCTTATAGCCGAG 1061
P.thermophilum NRRL735        TCAAAGGCCCTCGGAATGTAACGCCCCC--CGGGGCGTCTTATAGCCGAG 1060
P.clavariiformis NRRL2482     TCAAAGGCCCTCGGAATGTAGCACCTC---GGGTGTCTTATAGCCAGG 1072
* * * * *      * * * * * * * * * *      * * * * * * * * * * *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

	1101	1110	1120	1130	1140	1150																		
	+-----+-----+-----+-----+-----+																							
<i>P. camemberti</i> NRRL874	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. camemberti</i> NRRL875	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. echinulatum</i> NRRL1151	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. crustosum</i> NRRL968	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. viridicatum</i> NRRL961	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. aurantiogriseum</i> NRRL971	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. polonicum</i> NRRL995	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. viridicatum</i> NRRL958	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. chrysogenum</i> NRRL821	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. chrysogenum</i> NRRL807	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. griseoroseum</i> NRRL820	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. chrysogenum</i> NRRL824	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. griseoroseum</i> NRRL832	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. griseofulvum</i> NRRL734	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. griseofulvum</i> NRRL2300	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. coprophilum</i> NRRL13627	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. digitatum</i> NRRL786	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. sclerotigenum</i> NRRL3461	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>Eu. egyptiacum</i> NRRL2090	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1118
<i>Eu. crustaceum</i> NRRL3332	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1118
<i>P. expansum</i> NRRL974	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1120
<i>P. turbatum</i> NRRL757	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>H. paradoxus</i> NRRL2162	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. atramentosum</i> NRRL795	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. swiecickii</i> NRRL918	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. kojigenum</i> NRRL3442	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. raistrickii</i> NRRL2039	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. soppii</i> NRRL2023	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. canescens</i> NRRL910	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1118
<i>P. atrovenetum</i> NRRL2571	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. canescens</i> NRRL2147	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>P. waksmanii</i> NRRL777	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>P. miczynskii</i> NRRL1077	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>Eu. shearii</i> NRRL715	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. roseopurpureum</i> NRRL733	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>P. roseopurpureum</i> NRRL2064	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>P. sumatrense</i> NRRL779	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1127
<i>P. paxilli</i> NRRL2008	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. citrinum</i> NRRL1841	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1088
<i>P. sartoryi</i> NRRL783	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1088
<i>P. westlingii</i> NRRL800	GGT	GCA	ATG	CG	AC	TGC	CTAG	AC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1088
<i>P. charlesii</i> NRRL778	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1110
<i>P. fellutanum</i> NRRL746	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1116
<i>P. spinulosum</i> NRRL728	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1111
<i>P. spinulosum</i> NRRL1750	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1111
<i>P. thomii</i> NRRL2077	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1113
<i>Eu. lapidosum</i> NRRL718	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1113
<i>P. thomii</i> NRRL760	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1113
<i>P. purpurescens</i> NRRL720	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1113
<i>P. glabrum</i> NRRL766	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1113
<i>P. asperosporum</i> NRRL3411	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1111
<i>P. lividum</i> NRRL754	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1116
<i>P. adametzii</i> NRRL736	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. adametzii</i> NRRL737	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1119
<i>P. bilaii</i> NRRL3391	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1121
<i>P. adametzioides</i> NRRL3405	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1114
<i>P. herquei</i> NRRL1040	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1122
<i>P. sclerotiorum</i> NRRL2074	GGT	GTC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1111
<i>P. decumbens</i> NRRL742	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1118
<i>P. decumbens</i> NRRL741	GGT	GCC	ATG	CG	GC	CTG	CCCG	GAC	CG	AG	GA	AC	GC	GC	TT	CG	GC	TC	GC	G	AC	GC	T	1118

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1101      1110      1120      1130      1140      1150
                                +-----+-----+-----+-----+
P.turbatum NRRL759             GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1118
P.corylophilum NRRL803        GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.corylophilum NRRL802        GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.corylophilum NRRL793        GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.melinii NRRL2041            GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.velutinum NRRL2069          GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.raciborskii NRRL2150        GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1120
P.restrictum NRRL25744        GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.restrictum NRRL1748         GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1119
P.citreonigrum NRRL761        GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCACGGACGCT 1116
P.cinerascens NRRL748         GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCACGGACGCT 1116
P.vinaceum NRRL739            GGTGCCATGCGGCCAGCCAGACCGAGGATCGCGCTTCGGCACGGACGCT 1113
P.oxalicum NRRL790            GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.oxalicum NRRL787            GGTGCCATGCGGCCAGCCAGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.donkii NRRL5562             GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1125
P.fusum NRRL721               GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.janthinellum NRRL2016       GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.raperi NRRL2674             GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1122
P.daleae NRRL922              GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1123
P.ochrochloron NRRL926        GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
P.simplicissimum NRRL1075     GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1119
P.rolfsii NRRL1078            GGTGCCATGCGGCCAGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1120
Eu.cinnamopurpureum NRRL3326  GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1111
P.chermesinum NRRL735         GGTGCCATGCGGCCTGCCCGGACCGAGGAACGCGCTTCGGCTCGGACGCT 1110
P.clavariiformis NRRL2482     GGTGCAATGCGGCCTGCCTGGACCGAGGAACGCGCTTCGGCACGGACGCT 1122
                                ****  ****  *   *   ****  *****  *****  *****  *

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1151      1160      1170
                                +-----+-----+---
P.camemberti NRRL874          GGCATAATGGTCGTAAGCGACC 1143
P.camemberti NRRL875          GGCATAATGGTCGTAAGCGACC 1143
P.echinulatum NRRL1151       GGCATAATGATCGTAAGCGACC 1143
P.crustosum NRRL968          GGCATAATGATCGTAAGCGACC 1143
P.viridicatum NRRL961        GGCATAATGGTCGTAAGCGACC 1142
P.aurantiogriseum NRRL971    GGCATAATGGTCGTAAGCGACC 1143
P.polonicum NRRL995           GGCATAATGGTCGTAAGCGACC 1142
P.viridicatum NRRL958        GGCATAATGGTCGTAAGCGACC 1142
P.chrysogenum NRRL821        GGCATAATGGTCGTAAGCGACC 1142
P.chrysogenum NRRL807        GGCATAATGGTCGTAAGCGACC 1142
P.griseoroseum NRRL820       GGCATAATGGTCGTAAGCGACC 1142
P.chrysogenum NRRL824        GGCATAATGGTCGTAAGCGACC 1142
P.griseoroseum NRRL832       GGCATAATGGTCGTAAGCGACC 1142
P.griseofulvum NRRL734       GGCATAATGGTCGTAAGCGACC 1141
P.griseofulvum NRRL2300      GGCATAATGGTCGTAAGCGACC 1141
P.coprophilum NRRL13627      GGCATAATGATCGTAAGCGACC 1142
P.digitatum NRRL786          GGCATAATGATCGTAAGCGACC 1143
P.sclerotigenum NRRL3461     GGCATAATGGTCGTAAGCGACC 1142
Eu.egyptiacum NRRL2090       GGCATAATGGTCGTAAGCGACC 1140
Eu.crustaceum NRRL3332       GGCATAATGGTCGTAAGCGACC 1140
P.expansum NRRL974           GGCATAATGGTCGTAAGCGACC 1142
P.turbatum NRRL757           GGCATAATGGTCGTAAGCGACC 1141
H.paradoxus NRRL2162         GGCATAATGGTCGTAAGCGACC 1141
P.atramentosum NRRL795       GGCATAATGGTCGTAAGCGACC 1141
P.swiecickii NRRL918         GGCATAATGGTCGTAAGCGACC 1141
P.kojigenum NRRL3442         GGCATAATGGTCGTAAGCGACC 1141
P.raistrickii NRRL2039       GGCATAATGGTCGTAAGCGACC 1141
P.soppii NRRL2023            GGCATAATGGTCGTAAGCGACC 1141
P.canescens NRRL910          GGCATAATGGTCGTAAGCGACC 1140
P.atrovenetum NRRL2571       GGCATAATGGTCGTAAGCGACC 1141
P.canescens NRRL2147         GGCATAATGGTCGTAAGCGACC 1144
P.waksmanii NRRL777          GGCATAATGGTCGTAAGCGACC 1144
P.miczynskii NRRL1077        GGCATAATGGTCGTAAGCGACC 1144
Eu.shearrii NRRL715          GGCATAATGGTCGTAAGCGACC 1143
P.roseopurpureum NRRL733     GGCATAATGGTCGTAAGCGACC 1144
P.roseopurpureum NRRL2064    GGCATAATGGTCGTAAGCGACC 1144
P.sumatrense NRRL779         GGCATAATGGTCGTAAGCGACC 1149
P.paxilli NRRL2008           GGCATAATGGTCGTAAGCGACC 1141
P.citrinum NRRL1841          GGCATAATGGTCGTAAGCGACC 1110
P.sartoryi NRRL783           GGCATAATGGTCGTAAGCGACC 1110
P.westlingii NRRL800         GGCATAATGGTCGTAAGCGACC 1110
P.charlesii NRRL778          GGCATAATGGTCGTAAGCGACC 1132
P.fellutanum NRRL746         GGCATAATGGTCGTAAGCGACC 1138
P.spinulosum NRRL728         GGCATAATGGTCGTAAGCGACC 1133
P.spinulosum NRRL1750        GGCATAATGGTCGTAAGCGACC 1133
P.thomii NRRL2077            GGCATAATGGTCGTAAGCGACC 1135
Eu.lapidusum NRRL718         GGCATAATGGTCGTAAGCGACC 1135
P.thomii NRRL760             GGCATAATGGTCGTAAGCGACC 1135
P.purpurescens NRRL720       GGCATAATGGTCGTAAGCGACC 1134
P.glabrum NRRL766            GGCATAATGGTCGTAAGCGACC 1135
P.asperosporum NRRL3411      GGCATAATGGTCGTAAGCGACC 1133
P.lividum NRRL754            GGCATAATGGTCGTAAGCGACC 1138
P.adametzii NRRL736          GGCATAATGGTCGTAAGCGACC 1141
P.adametzii NRRL737          GGCATAATGGTCGTAAGCGACC 1141
P.bilaii NRRL3391            GGCTTAATGGTCGTAAGCGACC 1143
P.adametziioides NRRL3405    GGCTTAATGGTCGTAAGCGACC 1136
P.herquei NRRL1040           GGCATAATGGTCGTAAGCGACC 1144
P.sclerotiorum NRRL2074     GGCATAATGGTCGTAAGCGACC 1133
P.decumbens NRRL742          GGCATAATGGTCGTAAGCGACC 1140
P.decumbens NRRL741          GGCATAATGGTCGTAAGCGACC 1140

```

*Penicillium* spp., nuclear rDNA, ITS1-5.8S-ITS2 and partial 28S sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                1151      1160      1170
                                +-----+-----+---
P.turbatum NRRL759             GGCATAATGGTCGTAAGCGACC 1140
P.corylophilum NRRL803         GGCATAATGGTCGTAAGCGACC 1141
P.corylophilum NRRL802         GGCATAATGGTCGTAAGCGACC 1141
P.corylophilum NRRL793         GGCATAATGGTCGTAAGCGACC 1141
P.melinii NRRL2041             GGCATAATGGTCGTAAGCGACC 1141
P.velutinum NRRL2069           GGCATAATGGTCGTAAGCGACC 1141
P.raciborskii NRRL2150         GGCATAATGGTCGTAAGCGACC 1142
P.restrictum NRRL25744         GGCATAATGGTCGTAAGCGACC 1141
P.restrictum NRRL1748          GGCATAATGGTCGTAAGCGACC 1141
P.citreonigrum NRRL761         GGCATAATGGTCGTAAGCGACC 1138
P.cinerascens NRRL748          GGCATAATGGTCGTAAGCGACC- 1137
P.vinaceum NRRL739             GGCATAATGGTCGTAAGCGACC 1135
P.oxalicum NRRL790             GGCATAATGGTCGTAAGCGACC 1147
P.oxalicum NRRL787             GGCATAATGGTCGTAAGCGACC 1147
P.donkii NRRL5562              GGCATAATGGTCGTAAGCGACC 1147
P.fuscum NRRL721               GGCATAATGGTCGTAAGCGACC 1145
P.janthinellum NRRL2016        GGCATAATGGTCGTAAGCGACC 1145
P.raperi NRRL2674              GGCATAATGGTCGTAAGCGACC 1144
P.daleae NRRL922               GGCATAATGGTCGTAAGCGACC 1145
P.ochrochloron NRRL926         GGCATAATGGTCGTAAGCGACC 1142
P.simplicissimum NRRL1075      GGCATAATGGTCGTAAGCGACC 1141
P.rolfsii NRRL1078             GGCATAATGGTCGTAAGCGACC 1142
Eu.cinnamopurpureum NRRL3326   GGCATAATGGTCGTAAGCGACC 1133
P.thermophilum NRRL735         GGCATAATGGTCGTAAGCGACC 1132
P.clavariiformis NRRL2482      GGCATAATGGTCGTAAGCGACC 1144
                                * * * * * * * * * * * * * * *

```

## APPENDIX E

Alignment of sequences of nuclear ribosomal DNA, ITS1-5.8S-ITS2 region  
from 46 taxa from *Penicillium* subgen. *Pencillium*

---

Invariant bases indicated by an asterisk



*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

1         10         20         30         40         50
+-----+-----+-----+-----+-----+
P.canescens NRRL910[T] AAGGATCATTACCGAGCGAGAATTCTCT-GAATTCAAACCTCCCACCCGTG
P.atrovenetum NRRL2571[T] AAGGATCATTACCGAGCGAGGATTCTCTCGAATCCAACCTCCCACCCGTG
P.chrysogenum NRRL807[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum C8.24 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.notatum NRRL821[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.griseoroseum NRRL820[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum C8.12 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.nalgiovense NRRL911[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrysogenum NRRL824 Fleming strn AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.notatum NRRL832 Biourge strn AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.egyptiacum NRRL2090[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.crustaceum NRRL3332[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL5880 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.aethiopicum CBS484.84[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.gris.v.dipodomyicola NRRL13487[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.camemberti NRRL874[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.caseicolum NRRL875[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.crustosum NRRL968 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL961 AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.aurantiogriseum NRRL971[T] AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.polonicum NRRL995[T] AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.polonicum C74.1 AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.viridicatum NRRL958[T] AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCGTG
P.echinulatum NRRL1151[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.sclerotigenum NRRL786[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.sclerotigenum NRRL3461[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.olsonii CBS232.32[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.coprophilum NRRL13627[T] AAGGATCATTACCGAGTGAGGGCCCTTT-GGGTCCAACCTCCCACCCATG
P.griseofulvum NRRL734[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.griseofulvum NRRL2300[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.chrys.v.dipodomys NRRL13485[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.expansum NRRL974 Biourge strn AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.turbatum NRRL757[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
?H.paradoxus NRRL2162[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.atramentosum NRRL795[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.swiecickii NRRL918[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.kojigenum NRRL3442[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.raistrickii NRRL2039[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.soppii NRRL2023[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompectum B65.4 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompectum DAOM193712[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.stoloniferum ATCC10111[T] AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCTTG
P.brevicompectum B251 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.brevicompectum B132.1 AAGGATCATTACCGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
Eu.lapidusum NRRL718[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
P.bilaii NRRL3391[T] AAGGATCATTACTGAGTGAGGGCCCTCT-GGGTCCAACCTCCCACCCGTG
***** ** * * * * *

```

*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    51         60         70         80         90         100
                    +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]      TTTATTGTACCTTGTGCTTCGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.atrovenetum NRRL2571[T]  TTTATTGTACCTTGTGCTTCGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.chrysogenum NRRL807[T]   TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.chrysogenum C8.24        TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.notatum NRRL821[T]       TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.griseoroseum NRRL820[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.chrysogenum C8.12        TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.nalgiovense NRRL911[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.chrysogenum NRRL824 Fleming strn  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.notatum NRRL832 Biourge strn      TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
Eu.egyptiacum NRRL2090[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
Eu.crustaceum NRRL3332[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.viridicatum NRRL5880     TTTATTTTCCCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.aethiopicum CBS484.84[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.gris.v.dipodomyicola NRRL13487[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.camemberti NRRL874[T]    TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.caseicolum NRRL875[T]    TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.crustosum NRRL968        TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.viridicatum NRRL961      TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.aurantiogriseum NRRL971[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.polonicum NRRL995[T]     TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.polonicum C74.1          TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.viridicatum NRRL958[T]   TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.echinulatum NRRL1151[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.sclerotigenum NRRL786[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.sclerotigenum NRRL3461[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.olsonii CBS232.32[T]     TTTATTTT-ACCTTATTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.coprophilum NRRL13627[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.griseofulvum NRRL734[T]  TTTATTTT-ACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.griseofulvum NRRL2300[T]  TTTATTTT-ACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.chrys.v.dipodomys NRRL13485[T]  TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTAACCTGGCCGCCGGGG
P.expansum NRRL974 Biourge strn      TTTATTTTACCTTGTGCTTCGGCGGGCCCGCCTTTACTGGCCGCCGGGG
P.turbatum NRRL757[T]      TTTATTGTACCTTGTGCTTCGGCGGGCCCGCCTTTA-TGGCCGCCGGGG
?H.paradoxus NRRL2162[T]    TTTATTGTACCTTGTGCTTCGGCGGGCCCGCCTTG-TGGCCGCCGGGG
P.atramentosum NRRL795[T]   TTTATTGTACCTTGTGCTTCGGCGGGCCCGCCTTTA-TGGCCGCCGGGG
P.swiecickii NRRL918[T]     TTTATTATACCTTGTGCTTCGGCGGGCCCGCGTAT--GGCCGCCGGGG
P.kojigenum NRRL3442[T]     TTTATTATACCTTGTGCTTCGGCGGGCCCGCGTAT--GGCCGCCGGGG
P.raistrickii NRRL2039[T]   TTTATTATACCTTGTGCTTCGGCGGGCCCGCGTCA--GGCCGCCGGGG
P.soppii NRRL2023[T]        TTTATTATACCTTGTGCTTTGGCGGGCCCGCCTCAC--GGCCGCCGGGG
P.brevicompectum B65.4      TTTATTTTACCTTGTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompectum DAOM193712[T]  TTTATTTTACCTTGTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.stoloniferum ATCC10111[T]  TTTATTTTACCTTGTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompectum B251       TTTATTTTACCTTGTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
P.brevicompectum B132.1     TTTATTTT-ACCTTGTGCTTCGGCGAGCCTGCCTTTT--GGCTGCCGGGG
Eu.lapidosum NRRL718[T]     TTTATTGTACCTTGTGCTTCGGTGCCCGCCTCAC--GGCCGCCGGGG
P.bilaii NRRL3391[T]       TCTCTTGTACCATGTTGCTTCGGCGAGCCCGCCTCAC--GGCCGCCGGGG
* * * * *          * * * * *          * * * * *          * * * * *          * * * * *

```

*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                     101       110       120       130       140       150
                                     +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]              GGCA-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACACCT-TGAACTCTGT
P.atrovenetum NRRL2571[T]           GGCA-TCTGCTCCCGGGCCCGCGCCCGCCGAAGACACCT-TGAACTCTGT
P.chrysogenum NRRL807[T]            GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.chrysogenum C8.24                 GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.notatum NRRL821[T]               GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.griseoroseum NRRL820[T]          GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.chrysogenum C8.12                GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.nalgiovense NRRL911[T]           GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.chrysogenum NRRL824 Fleming strn  GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.notatum NRRL832 Biourge strn     GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
Eu.egyptiacum NRRL2090[T]          GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
Eu.crustaceum NRRL3332[T]          GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.viridicatum NRRL5880             GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.aethiopicum CBS484.84[T]         GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.gris.v.dipodomyicola NRRL13487[T] GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.camemberti NRRL874[T]            GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.caseicolum NRRL875[T]            GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.crustosum NRRL968                GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.viridicatum NRRL961              GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.aurantiogriseum NRRL971[T]       GGCTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.polonicum NRRL995[T]             GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCGAACTCTGT
P.polonicum C74.1                  GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCGAACTCTGT
P.viridicatum NRRL958[T]           GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.echinulatum NRRL1151[T]          GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.sclerotigenum NRRL786[T]         GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCGAACTCTGT
P.sclerotigenum NRRL3461[T]        GGCT-CACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.olsonii CBS232.32[T]             GGTT-CACACCCCGGGCCCGCGCCCGCCGAAGACTC-CGAACTCTGT
P.coprophilum NRRL13627[T]         GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.griseofulvum NRRL734[T]          GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.griseofulvum NRRL2300[T]         GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.chrys.v.dipodomys NRRL13485[T]   GGCT-TACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.expansum NRRL974 Biourge strn    GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.turbatum NRRL757[T]              GGCT-CACGCCCCCGGGCCCGCGCCCGCCGAAGACACCT-CGAACTCTGT
?H.paradoxus NRRL2162[T]           GGCT-TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCACGAACTCTGT
P.atramentosum NRRL795[T]          GGCT-TACGCTCCCGGGCCCGCGCCCGCCGAAGACACCCCTCGAACTCTGT
P.swiecickii NRRL918[T]            GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.kojigenum NRRL3442[T]            GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.raistrickii NRRL2039[T]          GGCT-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACATCT-CGAACTCTGT
P.soppii NRRL2023[T]               GAGT-TCTGCCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompectum B65.4             GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompectum DAOM193712[T]     GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.stoloniferum ATCC10111[T]        GACG-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompectum B251              GACA-TCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGT
P.brevicompectum B132.1            GACG-TCAGTCCCCGGGTCCGTGCTCGCCGAGACACCTTAGAACTCTGT
Eu.lapidosum NRRL718[T]            GGCT-TCTGCCCCCGGGTCCGCGCGCACCCGAGACACCATTAGAACTCTGT
P.bilaii NRRL3391[T]              GGCA-TCTGCCCCCGGGCCCGCGCCCGCCGAAGACCCCTCGAACTCTGT
*                               ***** ** ** * * * * * * * * * * * * * * * * * * * * * *

```

*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                151      160      170      180      190      200
                                +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]          ATGAAAATTGCAGTCTGAGT-CTAAATATAAATTATTTAAAACTTTCAAC
P.atrovenetum NRRL2571[T]       ATGAAAATTGCAGTCTGAGT-CTAAATATAAATTATTTAAAACTTTCAAC
P.chrysogenum NRRL807[T]       CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.chrysogenum C8.24            CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.notatum NRRL821[T]          CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.griseoroseum NRRL820[T]      CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.chrysogenum C8.12           CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.nalgiovense NRRL911[T]      CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.chrysogenum NRRL824 Fleming strn CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.rotatum NRRL832 Biourge strn CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
Eu.egyptiacum NRRL2090[T]     CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
Eu.crustaceum NRRL3332[T]     CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL5880        CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.aethiopicum CBS484.84[T]    CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.gris.v.dipodomyicola NRRL13487[T] CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.camemberti NRRL874[T]       CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.caseicolum NRRL875[T]       CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.crustosum NRRL968           CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL961        CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.aurantiogriseum NRRL971[T]  CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.polonicum NRRL995[T]        CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.polonicum C74.1            CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.viridicatum NRRL958[T]     CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.echinulatum NRRL1151[T]    CTGAAGATTGAAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.sclerotigenum NRRL786[T]   CTGAAGATTGCAGTCTGAGT-GAAAAC-GAAATTATTTAAAACTTTCAAC
P.sclerotigenum NRRL3461[T]  CTGAAGATTGCAGTCTGAGT-GAAAATAGAAATTATTTAAAACTTTCAAC
P.olsonii CBS232.32[T]      CTGAAGAATGCAGTCTGAGA-ACAAATATAAATTATTTAAAACTTTCAAC
P.coprophilum NRRL13627[T]   CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.griseofulvum NRRL734[T]    CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.griseofulvum NRRL2300[T]   CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.chrys.v.dipodomyis NRRL13485[T] CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.expansum NRRL974 Biourge strn CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.turbatum NRRL757[T]       CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
?H.paradoxus NRRL2162[T]    ATGAAGATTGCAGTCTGAGT-GAAAATATAAATTATTTAAAACTTTCAAC
P.atramentosum NRRL795[T]   CTGAAGATTGTAGTCTGAGT-GAAAAATAAATTATTTAAAACTTTCAAC
P.swiecickii NRRL918[T]     CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.kojigenum NRRL3442[T]     CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.raistrickii NRRL2039[T]   CTGAAGATTGTAGTCTGAGT-ATAAATATAAATTATTTAAAACTTTCAAC
P.soppii NRRL2023[T]       CTGAAGATTGTAGTCTGAGT-AAAAATATAAATTATTTAAAACTTTCAAC
P.brevicompectum B65.4     CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompectum DAOM193712[T] CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.stoloniferum ATCC10111[T] CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompectum B251     CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
P.brevicompectum B132.1    CTGAAGATTGTAGTCTGAGA-TTAAATATAAATTATTTAAAACTTTCAAC
Eu.lapidosum NRRL718[T]    CTGAAGATTGCAGTCTGAGC-ATAAACTAAA-TAAGTTAAAACTTTCAAC
P.bilaii NRRL3391[T]      CTGAAGATTGCAGTCTGAGCGATAAGCAAAAATTATTTAAAACTTTCAAC
**** * ** ***** ** * * *****

```

Penicillium subgenus Penicillium, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                201      210      220      230      240      250
                +-----+-----+-----+-----+-----+
P.canescens NRRL910[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.atrovenetum NRRL2571[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum NRRL807[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum C8.24 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.notatum NRRL821[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseoroseum NRRL820[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum C8.12 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.nalgiovense NRRL911[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrysogenum NRRL824 Fleming strn AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.notatum NRRL832 Biourge strn AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.egyptiacum NRRL2090[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.crustaceum NRRL3332[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL5880 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.aethiopicum CBS484.84[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.gris.v.dipodomyicola NRRL13487[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.camemberti NRRL874[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.caseicolum NRRL875[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.crustosum NRRL968 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL961 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.aurantiogriseum NRRL971[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.polonicum NRRL995[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.polonicum C74.1 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.viridicatum NRRL958[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.echinulatum NRRL1151[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.sclerotigenum NRRL786[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.sclerotigenum NRRL3461[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.olsonii CBS232.32[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.coprophilum NRRL13627[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseofulvum NRRL734[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.griseofulvum NRRL2300[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.chrys.v.dipodomys NRRL13485[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.expansum NRRL974 Biourge strn AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.turbatum NRRL757[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
?H.paradoxus NRRL2162[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.atramentosum NRRL795[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.swiecickii NRRL918[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.kojigenum NRRL3442[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.raistrickii NRRL2039[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.soppii NRRL2023[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompectum B65.4 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompectum DAOM193712[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.stoloniferum ATCC10111[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompectum B251 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.brevicompectum B132.1 AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
Eu.lapidusum NRRL718[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
P.bilaii NRRL3391[T] AACGGATCTCTTGGTTCGGGCATCGATGAAGAACGCAGCGAAATGCGATA
*****
```

Penicillium subgenus Penicillium, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                251      260      270      280      290      300
                +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]      CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.atrovenetum NRRL2571[T]   CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum NRRL807[T]   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum C8.24        CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.notatum NRRL821[T]       CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseoroseum NRRL820[T]  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum C8.12        CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.nalgiovense NRRL911[T]   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrysogenum NRRL824 Fleming strn CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.notatum NRRL832 Biourge strn  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.egyptiacum NRRL2090[T]   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.crustaceum NRRL3332[T]   CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL5880     CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.aethiopicum CBS484.84[T]  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.gris.v.dipodomyicola NRRL13487[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.camemberti NRRL874[T]    CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.caseicolum NRRL875[T]    CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.crustosum NRRL968        CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL961     CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.aurantiogriseum NRRL971[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.polonicum NRRL995[T]    CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.polonicum C74.1         CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.viridicatum NRRL958[T]  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.echinulatum NRRL1151[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.sclerotigenum NRRL786[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.sclerotigenum NRRL3461[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.olsonii CBS232.32[T]    CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.coprophilum NRRL13627[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseofulvum NRRL734[T]  CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.griseofulvum NRRL2300[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.chrys.v.dipodomys NRRL13485[T] CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.expansum NRRL974 Biourge strn CGTAATGTGAATTGCA-AATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.turbatum NRRL757[T]     CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
?H.paradoxus NRRL2162[T]  CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.atramentosum NRRL795[T] CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.swiecickii NRRL918[T]   CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.kojigenum NRRL3442[T]   CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.raistrickii NRRL2039[T] CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.soppii NRRL2023[T]     CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompectum B65.4    CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompectum DAOM193712[T] CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.stoloniferum ATCC10111[T] CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompectum B251     CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.brevicompectum B132.1   CGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
Eu.lapidusum NRRL718[T]   ACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
P.bilaii NRRL3391[T]     ACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
*****
```

*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                301      310      320      330      340      350
                                +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]          TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.atrovenetum NRRL2571[T]      TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum NRRL807[T]      TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum C8.24           TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.notatum NRRL821[T]          TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseoroseum NRRL820[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum C8.12           TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.nalgiovense NRRL911[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrysogenum NRRL824 Fleming strn TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.notatum NRRL832 Biourge strn TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
Eu.egyptiacum NRRL2090[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
Eu.crustaceum NRRL3332[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.viridicatum NRRL5880       TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.aethiopicum CBS484.84[T]   TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.gris.v.dipodomyicola NRRL13487[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.camemberti NRRL874[T]     TTGCGCCCCCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.caseicolum NRRL875[T]     TTGCGCCCCCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.crustosum NRRL968         TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.viridicatum NRRL961       TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.aurantiogriseum NRRL971[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.polonicum NRRL995[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.polonicum C74.1          TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.viridicatum NRRL958[T]   TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.echinulatum NRRL1151[T]  TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.sclerotigenum NRRL786[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.sclerotigenum NRRL3461[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.olsonii CBS232.32[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.coprophilum NRRL13627[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseofulvum NRRL734[T]   TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.griseofulvum NRRL2300[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.chrys.v.dipodomys NRRL13485[T] TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.expansum NRRL974 Biourge strn TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.turbatum NRRL757[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
?H.paradoxus NRRL2162[T]   TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.atramentosum NRRL795[T]  TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.swiecickii NRRL918[T]   TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.kojigenum NRRL3442[T]   TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.raistrickii NRRL2039[T] TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.soppii NRRL2023[T]     TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompectum B65.4    TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompectum DAOM193712[T] TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.stoloniferum ATCC10111[T] TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompectum B251    TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.brevicompectum B132.1  TTGCGCCTCTGGTATTCCGGAGGGGCATGCCTGTCCGAGCGTCATTGCTG
Eu.lapidosum NRRL718[T]  TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
P.bilaii NRRL3391[T]     TTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTG
*****

```

*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                351      360      370      380      390      400
                                +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]          CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCCCC-TTCCCGGGGG
P.atrovenetum NRRL2571[T]       CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCCCC-TCCCGGGGGG
P.chrysogenum NRRL807[T]        CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.chrysogenum C8.24             CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.notatum NRRL821[T]            CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.griseoroseum NRRL820[T]       CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.chrysogenum C8.12             CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.nalgiovense NRRL911[T]        CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.chrysogenum NRRL824 Fleming strn CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.notatum NRRL832 Biourge strn  CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
Eu.egyptiacum NRRL2090[T]       CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
Eu.crustaceum NRRL3332[T]       CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.viridicatum NRRL5880         CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.aethiopicum CBS484.84[T]      CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.gris.v.dipodomyicola NRRL13487[T] CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.camemberti NRRL874[T]        CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.caseicolum NRRL875[T]        CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.crustosum NRRL968            CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.viridicatum NRRL961          CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.aurantiogriseum NRRL971[T]    CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.polonicum NRRL995[T]         CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.polonicum C74.1              CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.viridicatum NRRL958[T]       CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.echinulatum NRRL1151[T]      CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.sclerotigenum NRRL786[T]     CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.sclerotigenum NRRL3461[T]    CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.olsonii CBS232.32[T]        CCCTCAAGCCCGGCTTGTGTGTTGGGT-CTCGTCCCTCCGATC-CTGGAGG
P.coprophilum NRRL13627[T]     CCCTCAAGCCCGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.griseofulvum NRRL734[T]      CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.griseofulvum NRRL2300[T]     CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.chrys.v.dipodomys NRRL13485[T] CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.expansum NRRL974 Biourge strn CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.turbatum NRRL757[T]         CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
?H.paradoxus NRRL2162[T]       CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.atramentosum NRRL795[T]      CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.swiecickii NRRL918[T]        CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCGATC-CCGGGGG
P.kojigenum NRRL3442[T]        CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.raistrickii NRRL2039[T]      CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.soppii NRRL2023[T]          CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCCGATC-CCGGGGG
P.brevicompectum B65.4        CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCTCC--TT-CCGGGGG
P.brevicompectum DAOM193712[T] CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCTCC--TT-CCGGGGG
P.stoloniferum ATCC10111[T]    CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCTCC--TT-CCGGGGG
P.brevicompectum B251         CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCTCC--TT-CCGGGGG
P.brevicompectum B132.1       CCCTCAAGCACGGCTTGTGTGTTGGGC-CCCCTCCTCC--TT-CCGGGGG
Eu.lapidusum NRRL718[T]       CCCTCAAGCACGGCTTGTGTGTTGGGC-TCCGTCCCCC--C----GGGG
P.bilaii NRRL3391[T]          CCCTCAAGCACGGCTTGTGTGTTGGGCCTCCGTCCCTCC--CCCGGGGG
*****

```



Penicillium subgenus Penicillium, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                                     401         410         420         430         440         450
                                     +-----+-----+-----+-----+-----+
P.canescens NRRL910[T]              ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.atrovenetum NRRL2571[T]           ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum NRRL807[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum C8.24                 ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.notatum NRRL821[T]                ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseoroseum NRRL820[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum C8.12                 ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.nalgiovense NRRL911[T]           ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrysogenum NRRL824 Fleming strn  ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.notatum NRRL832 Biourge strn     ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
Eu.egyptiacum NRRL2090[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
Eu.crustaceum NRRL3332[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL5880              ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.aethiopicum CBS484.84[T]         ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.gris.v.dipodomyicola NRRL13487[T] ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.camemberti NRRL874[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.caseicolum NRRL875[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.crustosum NRRL968                ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL961              ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.aurantiogriseum NRRL971[T]       ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.polonicum NRRL995[T]             ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.polonicum C74.1                  ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.viridicatum NRRL958[T]           ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.echinulatum NRRL1151[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.sclerotigenum NRRL786[T]         ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.sclerotigenum NRRL3461[T]        ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.olsonii CBS232.32[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.coprophilum NRRL13627[T]         ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseofulvum NRRL734[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.griseofulvum NRRL2300[T]         ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.chrys.v.dipodomys NRRL13485[T]   ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.expansum NRRL974 Biourge strn    ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.turbatum NRRL757[T]              ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
?H.paradoxus NRRL2162[T]           ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.atramentosum NRRL795[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.swiecickii NRRL918[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.kojigenum NRRL3442[T]            ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.raistrickii NRRL2039[T]          ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCGAGCGTATG
P.soppii NRRL2023[T]              ACGGGCCCGAAAGGCAGCGGGCGGCACCGAGTCCGGT-CCTCGAGCGTATG
P.brevicompectum B65.4             ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompectum DAOM193712[T]     ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.stoloniferum ATCC10111[T]        ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompectum B251              ACGGGCCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
P.brevicompectum B132.1            ACGGGTCCGAAAGGCAGCGGGCGGCACCGCGTCCGGT-CCTCAAGCGTATG
Eu.lapidusum NRRL718[T]            ACGGGTCCGAAAGGCAGCGGGCGGCACCGAGTCCGGT-CCTCGAGCGTATG
P.bilaii NRRL3391[T]              ACGGGCCCGAAAGGCAGCGGGCGGCACCGTGTCCGGT-CCTCGAGCGTATG
*****

```



*Penicillium* subgenus *Penicillium*, nuclear rDNA ITS1-5.8S-ITS2 sequences

CLUSTAL X (1.8) multiple sequence alignment

```

                    501         510         520         530
                    +-----+-----+-----+-----+
P.canescens NRRL910[T] AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.atrovenetum NRRL2571[T] CAA--ATTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum NRRL807[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum C8.24 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.notatum NRRL821[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseoroseum NRRL820[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum C8.12 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.nalgiovense NRRL911[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrysogenum NRRL824 Fleming strn AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.notatum NRRL832 Biourge strn AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
Eu.egyptiacum NRRL2090[T] AAA--CTTCTAT--AGGTTGACCTCGGATCAGGTAG
Eu.crustaceum NRRL3332[T] CAA--TTTTTAT--AGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL5880 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.aethiopicum CBS484.84[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.gris.v.dipodomyicola NRRL13487[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.camemberti NRRL874[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.caseicolum NRRL875[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.crustosum NRRL968 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL961 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.aurantiogriseum NRRL971[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.polonicum NRRL995[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.polonicum C74.1 AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.viridicatum NRRL958[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.echinulatum NRRL1151[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.sclerotigenum NRRL786[T] CAAATTTTTAATCCAGGTTGACCTCGGATCAGGTAG
P.sclerotigenum NRRL3461[T] CAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.olsonii CBS232.32[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.coprophilum NRRL13627[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseofulvum NRRL734[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.griseofulvum NRRL2300[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.chrys.v.dipodomys NRRL13485[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.expansum NRRL974 Biourge strn AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.turbatum NRRL757[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
?H.paradoxus NRRL2162[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.atramentosum NRRL795[T] AAA--ATTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.swiecickii NRRL918[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.kojigenum NRRL3442[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.raistrickii NRRL2039[T] AAA--TTTTTATCCAGGTTGACCTCGGATCAGGTAG
P.soppii NRRL2023[T] AAA---TTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompectum B65.4 AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompectum DAOM193712[T] AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.stoloniferum ATCC10111[T] AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompectum B251 AAA--CTTTTTTCCAGGTTGACCTCGGATCAGGTAG
P.brevicompectum B132.1 AAA--CTTTTTATCAGGTTGACCTCGGATCAGGTAG
Eu.lapidusum NRRL718[T] ATCATCCTTTTTTCAGGTTGACCTCGGATCAGGTAG
P.bilaii NRRL3391[T] AACCCCATTTTTTCAGGTTGACCTCGGATCAGGTAG
                    *                ***** **

```

## APPENDIX F

Alignments of gene sequences from *P. brevicompactum*

---

Invariant bases indicated by an asterisk

*Penicillium brevicompactum*, benA locus

CLUSTAL X (1.8) multiple sequence alignment

```

      1          10          20          30          40          50          60
+-----+-----+-----+-----+-----+-----+
B132.1 TGGTATGTACCGCATCACGGTCTTTTTTTC-TCCCGCAATGGCTGGGCATCAATTGACAT 59
B65.4  TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 59
B251   TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 59
DAOM 193712 TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
ATCC 10111 TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B306.2 TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B117   TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B99    TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTAACAT 59
B244.1 TGGTATGTATCGCACCATGTTCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAT 60
B65.6  TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
B75.3  TGGTATGTATCGCACCATG-TCTTTTTCTTTTCCCGCTATGGCTGGGTATCAATTGACAA 59
DAOM 193710 TGGTAAGTCTCGGA---G---CTTTTTTTT---TCGC---GTTGGGTATCAATTGACAA 47
***** ** * * * * ***** * *** * **** * ***** **

      61          70          80          90          100         110         120
+-----+-----+-----+-----+-----+-----+
B132.1 CTTGCTAACTGACATCAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B65.4  TTTGCTAACTGGCTCTAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B251   TTTGCTAACTGGCTCTAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
DAOM 193712 TTTGCTAACTGGCTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
ATCC 10111 TTTGCTAACTGGCTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B306.2 TTTGCTAACTGGCTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B117   TTTGCTAACTGGCTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B99    TTTGCTAACTGATTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B244.1 TTTGCTAACTGGCTCAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 120
B65.6  TTTGCTAACTGGCTTAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
B75.3  TTTGCTAACTGGCTTAAAGGCAAACATATCTCCGGCGAGCACGGTCTCGATGGCGATGGAC 119
DAOM 193710 GTTGCTAACTGGATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGAC 107
*****          ***** ***** *****

     121         130         140         150         160         170         180
+-----+-----+-----+-----+-----+-----+
B132.1 AGTAAGTGG---AGCGTACTGGGATCCCATGTGGATTGG--TTCTGATATATTGTTAGGT 174
B65.4  AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B251   AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
DAOM 193712 AGTAAGTGGACGACTGTGTTTCAATTACGCGTGTATTGG--GTCTGAGATCTTGTTAGGT 177
ATCC 10111 AGTAAGTGGACGACTGTGTTTCAATTACGCGTGTATTGG--GTCTGAGATCTTGTTAGGT 177
B306.2 AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B117   AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B99    AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 177
B244.1 AGTAAGTGGACGACTGTGTTTCAATTACGCGTGGATTGG--GTCTGAGATCTTGTTAGGT 178
B65.6  AGTAAGTGGACGACTGTGTTTCAATTATGCGTGGATGGG--GTCTGAGATCTTGTTAGGT 177
B75.3  AGTAAGTGGACGACTGTGTTTCAATTATGCGTGGATGGG--GTCTGAGATCTTGTTAGGT 177
DAOM 193710 AGTAAGTTTA--ACAGTGATGGGGATTCTGGTGGATCACAGTCTGATATCTTGCTAGGT 165
*****      * * * * *      * * * *      * * * *      * * * * *

```

```

181      190      200      210      220      230      240
+-----+-----+-----+-----+-----+-----+
B132.1   ACAACGGTACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 234
B65.4    ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B251     ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
DAOM 193712 ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
ATCC 10111 ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B306.2   ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B117     ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B99      ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B244.1   ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 238
B65.6    ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
B75.3    ACAATGGCACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 237
DAOM 193710 ACAATGGTACCTCCGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTA 225
*****

241      250      260      270      280      290      300
+-----+-----+-----+-----+-----+-----+
B132.1   CAATGCCTTGATAAATTTTGTGTGTGTGTGTGCTACCCGG----ATTCTTTGACCTCCC 290
B65.4    CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B251     CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
DAOM 193712 CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
ATCC 10111 CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B306.2   CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B117     CAATGATGTGAAGAACTCTGGTTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B99      CAATGATGTGAAGAACTCTTGTGTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B244.1   CAATGATGTGAAGAACTCTTGTGTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 294
B65.6    CAATGATGTGAAGAACTCTTGTGTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
B75.3    CAATGATGTGAAGAACTCTTGTGTGTGCATTTTCTCACCTCA----TATTCTTGACCGCCC 293
DAOM 193710 CAATGACTGGG--AATCTTAATTTGTGCATCATCTGATCGGGCGTTTTTCTTTGACAATCT 283
***** * ** * ***** * * * * * * * * * * *

301      310      320      330      340      350      360
+-----+-----+-----+-----+-----+-----+
B132.1   AGGCTAGCGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 350
B65.4    AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B251     AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
DAOM 193712 AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
ATCC 10111 AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B306.2   AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B117     AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B99      AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B244.1   AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 354
B65.6    AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
B75.3    AGGCTAGTGGTGACAAGTACGTTCCCCGTGCCGTCCTCGTCGACTTGGAGCCCGGTACCA 353
DAOM 193710 AGGCCAGCGGTGACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCA 343
*****

361      370      380      390      400      410      420
+-----+-----+-----+-----+-----+-----+
B132.1   TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 410
B65.4    TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B251     TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
DAOM 193712 TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
ATCC 10111 TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B306.2   TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B117     TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B99      TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B244.1   TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 414
B65.6    TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
B75.3    TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 413
DAOM 193710 TGGACGCTGTCCGCTCCGGTCCCTTCGGCAAGCTTTTTCCGCCCGGACAACCTTCGTCTTCG 403
*****

```

	421	430	440	445	
	+-----+-----+-----+				
B132.1	GTCAGTCCGGTGCTGGTAACAAC				435
B65.4	GTCAATCCGGTGCTGGTAACAAC				438
B251	GTCAATCCGGTGCTGGTAACAAC				438
DAOM 193712	GTCAATCCGGTGCTGGTAACAAC				438
ATCC 10111	GTCAATCCGGTGCTGGTAACAAC				438
B306.2	GTCAATCCGGTGCTGGTAACAAC				438
B117	GTCAATCCGGTGCTGGTAACAAC				438
B99	GTCAGTCCGGTGCTGGTAACAAC				438
B244.1	GTCAGTCCGGTGCTGGTAACAAC				439
B65.6	GTCAGTCCGGTGCTGGTAACAAC				438
B75.3	GTCAGTCCGGTGCTGGTAACAAC				438
DAOM 193710	GTCAGTCCGGTGCTGGTAACAAC				428
	*****				

*Penicillium brevicompactum*, rDNA ITS1-5.8S-ITS2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

      1      10      20      30      40      50      60
+-----+-----+-----+-----+-----+-----+
B132.1 TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B65.4  TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B251   TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
DAOM 193712 TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
ATCC 10111 TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B306.2 TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B117   TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B99    TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B244.1 TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B65.6  TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
B75.3  TTCCGTAGGTGAAC-TGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 59
DAOM 193710 TTCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTC 60
*****

      61      70      80      90      100     110     120
+-----+-----+-----+-----+-----+-----+
B132.1 CCACCCGTGTTTATTT-ACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 116
B65.4  CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B251   CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
DAOM 193712 CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
ATCC 10111 CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B306.2 CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B117   CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B99    CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B244.1 CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B65.6  CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
B75.3  CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGAGCCTGCCTT--TTGGCTGCCGGGGG 117
DAOM 193710 CCACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCCGGGGG 120
*****

     121     130     140     150     160     170     180
+-----+-----+-----+-----+-----+-----+
B132.1 ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 176
B65.4  ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B251   ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
DAOM 193712 ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
ATCC 10111 ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B306.2 ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B117   ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B99    ACGTCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B244.1 ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B65.6  ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
B75.3  ACATCTGTCCCCGGGTCCGCGCTCGCCGAAGACACCTTAGAACTCTGTCTGAAGATTGTA 177
DAOM 193710 GCTTACGCCCCCGGGCCCGCGCCCGCCGAAGACACCTCGAACTCTGTCTGAAGATTGTA 180
* * *

*****

```



	181	190	200	210	220	230	240	
	+-----+-----+-----+-----+-----+-----+-----+							
B132.1	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							236
B65.4	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B251	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
DAOM 193712	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
ATCC 10111	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B306.2	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B117	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B99	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B244.1	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B65.6	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
B75.3	GTCTGAGATTAAATATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							237
DAOM 193710	GTCTGAGTAAAAATAAAATTATTTAAAACCTTTCAACAACGGATCTCTTGGTTCGGGCAT							240
	*****							
	241	250	260	270	280	290	300	
	+-----+-----+-----+-----+-----+-----+-----+							
B132.1	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							296
B65.4	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B251	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
DAOM 193712	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
ATCC 10111	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B306.2	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B117	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B99	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B244.1	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B65.6	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
B75.3	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCAGTGAATCATC							297
DAOM 193710	CGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCA-AATTCAGTGAATCATC							299
	*****							
	301	310	320	330	340	350	360	
	+-----+-----+-----+-----+-----+-----+-----+							
B132.1	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							356
B65.4	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B251	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
DAOM 193712	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
ATCC 10111	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B306.2	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B117	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B99	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B244.1	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B65.6	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
B75.3	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTC							357
DAOM 193710	GAGTCTTTGAACGCACATTGCGCCCTCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTC							359
	*****							
	361	370	380	390	400	410	420	
	+-----+-----+-----+-----+-----+-----+-----+							
B132.1	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCTCC--TTCCGGGGGACGGG							414
B65.4	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B251	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
DAOM 193712	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
ATCC 10111	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B306.2	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B117	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B99	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B244.1	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B65.6	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
B75.3	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCTCCGTCTCTCC--TTCCGGGGGACGGG							415
DAOM 193710	ATTGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCTCCGATCCGGGGGACGGG							419
	*****							

```

421      430      440      450      460      470      480
+-----+-----+-----+-----+-----+-----+
B132.1   TCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCACTCGC 474
B65.4    CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B251     CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
DAOM 193712 CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
ATCC 10111 CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B306.2   CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B117     CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B99      CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B244.1   CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B65.6    CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
B75.3    CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCAAGCGTATGGGGCTTTGTCAACCCGC 475
DAOM 193710 CCCGAAAGGCAGCGGGCGGCACCGCGTCCGGTCCCTCGAGCGTATGGGGCTTTGTCAACCCGC 479
*****

```

```

481      490      500      510      520      530      540
+-----+-----+-----+-----+-----+-----+
B132.1   TTTGTAGGCTGGCCGGCGCTTGCCGATCAACC-AAACTTTTTATCAGGTTGACCTCGGA 533
B65.4    TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B251     TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
DAOM 193712 TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
ATCC 10111 TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B306.2   TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B117     TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B99      TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B244.1   TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B65.6    TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
B75.3    TTTGTAGGACTGGCCGGCGCCTGCCGATCAACC-AAACTTTTTTCCAGGTTGACCTCGGA 534
DAOM 193710 TCTGTAGGCCCGCCGGCGCTTGCCGATCAACCCAAATTTTTATCCAGGTTGACCTCGGA 539
* ***** * ***** * ***** * ***** * ***** * *****

```

```

541      548
+-----+
B132.1   TCAGGTAG 541
B65.4    TCAGGTAG 542
B251     TCAGGTAG 542
DAOM 193712 TCAGGTAG 542
ATCC 10111 TCAGGTAG 542
B306.2   TCAGGTAG 542
B117     TCAGGTAG 542
B99      TCAGGTAG 542
B244.1   TCAGGTAG 542
B65.6    TCAGGTAG 542
B75.3    TCAGGTAG 542
DAOM 193710 TCAGGTAG 547
*****

```

## APPENDIX G

Alignments of gene sequences from *Penicillium chrysogenum*

---

Invariant bases indicated by an asterisk

*Penicillium chrysogenum*, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```

          1          10          20          30          40          50          60
+-----+-----+-----+-----+-----+-----+
NRRL_13485  GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACGCC-CGCAGC--CTGACTCA
NRRL_911    GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACGCC-CGCAGC--CTGACTCA
CBS_484.84  GACACTTACTTGAATGTGTACAAGGGTTACTACGTAAGACTCCTCGCAGCGCCTGGCTTA
C8.24      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_193710 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_155631 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_171025 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_178623 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_215337 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_216701 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
ATCC_10108  GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTCGCAAC--CTGACTTG
DAOM_215336 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGACTTG
DAOM_216700 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_212031 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_190864 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_175758 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_175176 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_175157 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_167036 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_155628 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_155627 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
DAOM_59494C GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
C200       GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
C317.1     GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
NASA       GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
NRRL_824   GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
C8.12     GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGCCTTG
C238      GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGACGCCTTCGCAGC--CTGACTTG
NRRL_13487 GACACTTACTTGAACGTGTACAAGGGTTACTACGTAAGCCGCCCGCAGT-CCGAATTTA
*****

```

*Penicillium chrysogenum*, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```

      61      70      80      90     100     110     120
      +-----+-----+-----+-----+-----+-----+
NRRL_13485 CAAGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
NRRL_911    CAAGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
CBS_484.84  CATGATTGGTAACTTACTTATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
C8.24      CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_193710 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_155631 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_171025 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_178623 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_215337 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_216701 CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
ATCC_10108  CAGGATCGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_215336 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_216700 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_212031 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_190864 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_175758 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_175176 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_175157 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_167036 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_155628 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_155627 CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
DAOM_59494C CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
C200       CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
C317.1     CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
NASA       CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
NRRL_824   CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
C8.12     CAGGGTTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
C238     CAGGATTGATA-CTAACTCATATATAGTTCACCGGAGATGGTGCTGGGCCGTGACCACGAC
NRRL_13487 TGAATTGATA-CTAACCCGTCTATAGTTCACCGGAGATGGTGCTGGGCCGTGATCAGCAC
          * * ** * * * * * *****

```

*Penicillium chrysogenum*, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```

                121      130      140      150      160      170      180
                +-----+-----+-----+-----+-----+-----+
NRRL_13485      GGTTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_911        GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
CBS_484.84      GGCTACTACTGGATCCGCGGTCGCGTCGACGATGTTGTCAATGTTTCTGGACACCGTCTG
C8.24          GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_193710     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155631     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_171025     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_178623     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_215337     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_216701     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
ATCC_10108      GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_215336     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_216700     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_212031     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_190864     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175758     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175176     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_175157     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_167036     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155628     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_155627     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
DAOM_59494C     GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C200            GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C317.1         GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NASA            GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_824        GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C8.12          GGCTATTACTGGATCCGCGGTCGTGTTGACGATGTCGTCAACGTTTCTGGACACCGTCTG
C238           GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
NRRL_13487     GGCTACTACTGGATCCGCGGTCGTGTCGACGATGTCGTCAACGTTTCTGGACACCGTCTG
** ** ***** ** ** ** ***** ***** *****

```

*Penicillium chrysogenum*, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```

                181      190      200      210      220      230      240
                +-----+-----+-----+-----+-----+-----+
NRRL_13485      TCCACCGCTGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
NRRL_911        TCCACCGCTGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
CBS_484.84      TCCACCGCCGAGATCGAGGCTGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACCTGT
C8.24          TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_193710     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_155631     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_171025     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_178623     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_215337     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_216701     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
ATCC_10108      TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_215336     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
DAOM_216700     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_212031     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_190864     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175758     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175176     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_175157     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_167036     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_155628     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_155627     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
DAOM_59494C    TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C200           TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C317.1         TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
NASA           TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
NRRL_824       TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C8.12         TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTATCTGC
C238          TCCACCGCCGAGATTGAGGCCGCTCTTCTCGAGCACCGTAAGTCCAACCACAGTACCTGC
NRRL_13487     TCCACCGCTGAGATCGAGGCCGCTCTTCTCGAGCACCGTAAGTGCAACCACAGTACATTC
*****  *****  *****  *****  *****  *****  *****  *

```

*Penicillium chrysogenum*, acuA locus

CLUSTAL X (1.8) multiple sequence alignment

```

                241      250      260      270      280      290
                +-----+-----+-----+-----+-----+-----+
NRRL_13485      CAAAAC TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCTGTTGCCGAGGCT
NRRL_911        CAAAAC TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCTGTTGCCGAGGCT
CBS_484.84     CAAAAA TCGCAAAATGAGCCCAAAC TAACTATGAACAGCTTCTGTTGCCGAGGCT
C8.24          CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_193710    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_155631    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_171025    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_178623    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_215337    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_216701    CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
ATCC_10108     CAAAAA TTGGAAC TGAGCCCAAAC TAACTACGAACAGCTTCCGTTGCCGAGGCT
DAOM_215336    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_216700    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_212031    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_190864    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175758    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175176    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_175157    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_167036    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_155628    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_155627    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
DAOM_59494C    CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
C200           CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
C317.1         CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
NASA           CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
NRRL_824       CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
C8.12         CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
C238          CAAAAA TTGCAACTGAGCCCAAAC TAACTATGAACAGCTTCCGTTGCCGAGGCT
NRRL_13487     AAAGAT TGCCAAC TGAGCCCAAAC TAACTATAAACAGCTTCTGTTGCCGAAGCT
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```



*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

          1          10          20          30          40          50          60
+-----+-----+-----+-----+-----+-----+
NRRL_911   TGGTAAGTCTCGGATCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTACTAACTG
NRRL_13485 TGGTAAGTGCCGGAGCTTTTTTTTTTCCGCGTTGGGTATCAATTGACAAGTTACTAACTG
C8.24     TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
ATCC_10108 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C238      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155631 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_171025 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_178623 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_193710 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_215337 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_216701 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C200      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C317.1    TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
NASA      TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
NRRL_824   TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_216700 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_215336 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_212031 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_189864 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175758 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175176 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_175157 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_167036 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155628 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_155627 TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
DAOM_59494C TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
C8.12     TGGTAAGTCTCGGAGCTTTTTTTTT--CGCGTTGGGTATCAATTGACAAGTTGCTAACTG
CBS_484.84 TGGTAAGTGTGTTGAGCTTTTTTT----CGCGTTGGGTATCAATTGACAAGTTACTAACCG
NRRL_13487 TGGTATGTGCC-GAGCTTTTTTCC--CGCGTTGGGTATCAATTGACAAGTTACTAACTG
***** **      ** ***** *****

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

          61          70          80          90          100          110          120
          +-----+-----+-----+-----+-----+-----+
NRRL_911   GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_13485 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C8.24     GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
ATCC_10108 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C238     GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155631 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_171025 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_178623 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_193710 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_215337 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_216701 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C200     GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C317.1   GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NASA     GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_824  GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_216700 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_215336 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_212031 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_189864 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175758 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175176 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_175157 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_167036 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155628 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_155627 GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
DAOM_59494C GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
C8.12    GATTACAGGCAAACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
CBS_484.84 AATTACAGGCAGACCATCTCTGGCGAGCACGGTCTCGATGGCGATGGACAGTAAGTTTAA
NRRL_13487 GATTACAGGCAAACCATTTCCGCGAGCACGGTCTCGATGGTGATGGACAGTAAGTT-AA
          ***** **

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

                121      130      140      150      160      170      180
                +-----+-----+-----+-----+-----+-----+
NRRL_911        CAGTGATGGGGATTCTGGTGGACTACACGTCTGATATATTGCTAGGTACAATGGTACCTC
NRRL_13485     CAGTGATGGGGATTCTGGTGGACCACACGTCTGATATATTGCTAGGTACAATGGTACCTC
C8.24          CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
ATCC_10108     CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C238           CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155631    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_171025    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_178623    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_193710    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_215337    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_216701    CAGTGATGGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C200           CAGTGATGGGGATTTTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C317.1         CAGTGATAGGGATTTTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NASA           CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NRRL_824       CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_216700    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_215336    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_212031    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_189864    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175758    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175176    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_175157    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_167036    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155628    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_155627    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
DAOM_59494C    CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
C8.12          CAGTGATAGGGATTCTGGTGGATCACACGTCTGATATCTTGCTAGGTACAATGGTACCTC
CBS_484.84     CAGTGATGGGG-TTTTGGTGGATAGCACGTCTGATATCTTGCTAGGTACAATGGTACCTC
NRRL_13487     TAGCGATGGCTTCTCCAGTAGATGACATGTCTGATATCTTGTTAGGTACAATGGTACCTC
                **  ***  *      *      **  **      **  *****  **  *****

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

                181      190      200      210      220      230      240
                +-----+-----+-----+-----+-----+-----+
NRRL_911        CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
NRRL_13485     CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C8.24          CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
ATCC_10108     CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C238          CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155631    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_171025    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_178623    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_193710    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_215337    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_216701    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C200          CGACCTCCAGCTCGAACGCATGAACGTCTACTTCAACCATGTGAGTACAAT-GGCTGGGA
C317.1        CGACCTCCAGCTCGAACGCATGAACGTCTACTTCAACCATGTGAGTACAAT-GGCTGGGA
NASA          CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
NRRL_824      CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_216700    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_215336    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_212031    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_189864    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175758    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175176    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_175157    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_167036    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155628    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_155627    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
DAOM_59494C    CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
C8.12         CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGA
CBS_484.84     CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTACAAT-GACTGGGG
NRRL_13487     CGACCTCCAGCTCGAGCGTATGAACGTCTACTTCAACCATGTGAGTATAGCCGATTGGGA
***** ** ***** * * ****
```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

                241      250      260      270      280      290      300
                +-----+-----+-----+-----+-----+-----+
NRRL_911        ATCGATCAATCGTGCATCATCTGATCGGATGTTTTCTTTGATAATCTAGGCCAGCGGTG
NRRL_13485     ATCGATCAATCGTGCATCATCTGATCGGATATTTTTCTTTGATAATCTAGGCCAGCGGTG
C8.24          ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
ATCC_10108     ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
C238          ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155631    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_171025    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_178623    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_193710    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_215337    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_216701    ATC--TTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
C200          ATCGATTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
C317.1        ATCGATTAATTGTGCATCATCTGATCGGGCGTTTTCTTTGACAATCTAGGCCAGCGGTG
NASA          ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
NRRL_824       ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_216700    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_215336    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_212031    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_189864    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175758    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175176    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_175157    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_167036    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155628    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_155627    ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
DAOM_59494C   ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
C8.12         ATCGATTGATTGTGCATCATCTGATCGGACGTTTTCTTTGACAATCTAGGCCAGCGGTG
CBS_484.84     ACCAATCAATCGTGCATCATCTGATCGGACGTTTCTTTGATAATCTAGGCCAGCGGTG
NRRL_13487     ACCGAT-AATCGTGCATCATCTGATCGGATCTTTTTCTTTGATAATCTAGGCCAGCGGTG
* * * * *

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

          301      310      320      330      340      350      360
          +-----+-----+-----+-----+-----+-----+
NRRL_911   ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NRRL_13485 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C8.24     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
ATCC_10108 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C238     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_155631 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_171025 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_178623 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_193710 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_215337 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
DAOM_216701 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C200     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
C317.1   ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NASA     ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
NRRL_824  ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_216700 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_215336 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_212031 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_189864 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175758 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175176 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_175157 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_167036 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_155628 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_155627 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
DAOM_59494C ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
C8.12    ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGATGCTGTCC
CBS_484.84 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
NRRL_13487 ACAAGTACGTTCCCCGTGCCGTTCTGGTCGATTTGGAGCCCGGTACCATGGACGCTGTCC
*****

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

          361          370          380          390          400          410          420
          +-----+-----+-----+-----+-----+-----+
NRRL_911   GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCATTCCGGGTG
NRRL_13485 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
C8.24     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
ATCC_10108 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
C238     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_155631 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_171025 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_178623 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_193710 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_215337 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_216701 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
C200     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
C317.1   GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
NASA     GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
NRRL_824  GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_216700 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_215336 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_212031 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_189864 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_175758 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_175176 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_175157 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_167036 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_155628 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_155627 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
DAOM_59494C GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
C8.12    GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
CBS_484.84 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGACAAC TTCGTCTTCGGTCAGTCCGGTG
NRRL_13487 GCTCCGGTCCCTTCGGCAAGCTTTTCCGCCCCGATAAC TTCGTCTTCGGTCAGTCCGGTG
*****

```

*Penicillium chrysogenum*, Bt2 locus

CLUSTAL X (1.8) multiple sequence alignment

```

                421      430
                +-----+-----
NRRL_911        CTGGTAACAACCTGG
NRRL_13485     CTGGTAACAACCTGG
C8.24          CTGGTAACAACCTGG
ATCC_10108     CTGGTAACAACCTGG
C238           CTGGTAACAACCTGG
DAOM_155631    CTGGTAACAACCTGG
DAOM_171025    CTGGTAACAACCTGG
DAOM_178623    CTGGTAACAACCTGG
DAOM_193710    CTGGTAACAACCTGG
DAOM_215337    CTGGTAACAACCTGG
DAOM_216701    CTGGTAACAACCTGG
C200           CTGGTAACAACCTGG
C317.1         CTGGTAACAACCTGG
NASA           CTGGTAACAACCTGG
NRRL_824       CTGGTAACAACCTGG
DAOM_216700    CTGGTAACAACCTGG
DAOM_215336    CTGGTAACAACCTGG
DAOM_212031    CTGGTAACAACCTGG
DAOM_189864    CTGGTAACAACCTGG
DAOM_175758    CTGGTAACAACCTGG
DAOM_175176    CTGGTAACAACCTGG
DAOM_175157    CTGGTAACAACCTGG
DAOM_167036    CTGGTAACAACCTGG
DAOM_155628    CTGGTAACAACCTGG
DAOM_155627    CTGGTAACAACCTGG
DAOM_59494C    CTGGTAACAACCTGG
C8.12          CTGGTAACAACCTGG
CBS_484.84     CTGGTAACAACCTGG
NRRL_13487     CTGGTAACAACCTGG
                *****

```



*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

      1      10      20      30      40      50      60
+-----+-----+-----+-----+-----+-----+
C8.24      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL13485  TCCGTAGGTGAACCTGCGGAAGGATCATTACTGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM193710 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C317.1     TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C238      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155631 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM171025 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM178623 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM215337 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM216701 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
ATCC_10108 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C200      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL911   TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175157 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM215336 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM216700 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM212031 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM190864 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175758 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM175176 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM167036 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155628 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM155627 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
DAOM59494C TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL824   TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NASA      TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
C8.12     TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
NRRL13487 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
CBS484.84 TCCGTAGGTGAACCTGCGGAAGGATCATTACCGAGTGAGGGCCCTCTGGGTCCAACCTCC
*****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

      61          70          80          90          100          110          120
      +-----+-----+-----+-----+-----+-----+
C8.24      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
NRRL13485  CACCCGTGTTTATTT-ACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM193710 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
C317.1     CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
C238      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM155631 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM171025 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM178623 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM215337 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM216701 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
ATCC_10108 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
C200      CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
NRRL911    CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM175157 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM215336 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM216700 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM212031 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM190864 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM175758 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM175176 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM167036 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM155628 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM155627 CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
DAOM59494C CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
NRRL824    CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
NASA       CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
C8.12     CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
NRRL13487  CACCCGTGTTTATTTTACCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
CBS484.84  CACCCGTGTTTATTTTTCCTTGTTGCTTCGGCGGGCCCGCCTTAAC TGCCGCGCCGGGGG
*****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                121      130      140      150      160      170      180
                +-----+-----+-----+-----+-----+-----+
C8.24           CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL13485      CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM193710     CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C317.1        CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C238          CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155631    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM171025    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM178623    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM215337    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM216701    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
ATCC_10108    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C200          CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL911       CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175157    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM215336    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM216700    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM212031    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM190864    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175758    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM175176    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM167036    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155628    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM155627    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
DAOM59494C    CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL824       CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NASA          CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
C8.12        CTTACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
NRRL13487     CTCACGCCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
CBS484.84     CTCACGCTCCCGGGCCCCGCGCCCGCCGAAGACACCCTCGAACTCTGTCTGAAGATTGTAG
** ** ** ** ** ** ** ** ** ** ** *

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                181      190      200      210      220      230      240
                +-----+-----+-----+-----+-----+-----+
C8.24           TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
NRRL13485      TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM193710     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
C317.1         TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
C238           TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM155631     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM171025     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM178623     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM215337     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM216701     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
ATCC_10108     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
C200           TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
NRRL911        TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM175157     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM215336     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM216700     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM212031     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM190864     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM175758     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM175176     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM167036     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM155628     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM155627     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
DAOM59494C     TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
NRRL824        TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
NASA           TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
C8.12          TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
NRRL13487      TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
CBS484.84      TCTGAGTGAAAATATAAATTATTTAAAAC TTTCAACAACGGATCTCTTGGTTCGGGCATC
*****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```
                241      250      260      270      280      290      300
                +-----+-----+-----+-----+-----+-----+
C8.24           GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL13485      GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM193710     GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C317.1        GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C238          GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155631    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM171025    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM178623    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM215337    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM216701    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
ATCC_10108    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C200          GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL911       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175157    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM215336    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM216700    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM212031    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM190864    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175758    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM175176    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM167036    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155628    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM155627    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
DAOM59494C    GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL824       GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NASA          GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
C8.12        GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
NRRL13487     GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
CBS484.84     GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGA
*****
```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

          301      310      320      330      340      350      360
          +-----+-----+-----+-----+-----+-----+
C8.24      GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL13485  GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM193710 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
C317.1     GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
C238      GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155631 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM171025 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM178623 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM215337 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM216701 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
ATCC_10108 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
C200      GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL911    GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175157 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM215336 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM216700 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM212031 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM190864 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175758 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM175176 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM167036 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155628 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM155627 GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
DAOM59494C GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL824    GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
NASA      GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
C8.12     GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
NRRL13487  GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
CBS484.84  GTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCAT
*****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                361      370      380      390      400      410      420
                +-----+-----+-----+-----+-----+-----+
C8.24           TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL13485      TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM193710     TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C317.1        TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C238          TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155631    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM171025    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM178623    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM215337    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM216701    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
ATCC_10108    TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C200          TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL911       TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175157    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM215336    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM216700    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM212031    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM190864    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175758    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM175176    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM167036    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155628    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM155627    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
DAOM59494C    TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL824       TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NASA          TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
C8.12        TTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
NRRL13487     TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
CBS484.84     TGCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCC
* *****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                421      430      440      450      460      470      480
                +-----+-----+-----+-----+-----+-----+
C8.24           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL13485      CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM193710     CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C317.1         CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C238           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155631    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM171025    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM178623    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM215337    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM216701    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
ATCC_10108    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C200           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL911        CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175157    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM215336    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM216700    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM212031    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM190864    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175758    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM175176    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM167036    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155628    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM155627    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
DAOM59494C    CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL824       CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NASA           CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
C8.12         CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
NRRL13487     CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
CBS484.84     CGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTC
*****

```



*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                481          490          500          510          520          530          540
                +-----+-----+-----+-----+-----+-----+
C8.24            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
NRRL13485       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM193710      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
C317.1          TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
C238            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM155631      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM171025      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM178623      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM215337      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM216701      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
ATCC_10108      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
C200            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
NRRL911         TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM175157      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM215336      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM216700      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM212031      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM190864      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM175758      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM175176      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM167036      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM155628      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM155627      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
DAOM59494C      TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
NRRL824         TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
NASA            TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
C8.12          TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
NRRL13487       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
CBS484.84       TGTAGGCCCGGCCGGCGCTTGCCGATCAACCCAAATTTTATCCAGGTTGACCTCGGATC
*****

```

*Penicillium chrysogenum*, ITS locus

CLUSTAL X (1.8) multiple sequence alignment

```

                    541
                    +-----
C8.24                AGGTAG
NRRL13485            AGGTAG
DAOM193710          AGGTAG
C317.1              AGGTAG
C238                AGGTAG
DAOM155631          AGGTAG
DAOM171025          AGGTAG
DAOM178623          AGGTAG
DAOM215337          AGGTAG
DAOM216701          AGGTAG
ATCC_10108          AGGTAG
C200                AGGTAG
NRRL911             AGGTAG
DAOM175157          AGGTAG
DAOM215336          AGGTAG
DAOM216700          AGGTAG
DAOM212031          AGGTAG
DAOM190864          AGGTAG
DAOM175758          AGGTAG
DAOM175176          AGGTAG
DAOM167036          AGGTAG
DAOM155628          AGGTAG
DAOM155627          AGGTAG
DAOM59494C          AGGTAG
NRRL824             AGGTAG
NASA                AGGTAG
C8.12              AGGTAG
NRRL13487           AGGTAG
CBS484.84           AGGTAG
                    *****
```

*Penicillium chrysogenum*, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```

          1          10          20          30          40          50          60
          +-----+-----+-----+-----+-----+-----+
C317.1    CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C200      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C8.24     CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
D193710   CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C238      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155631 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM171025 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM178623 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM215337 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM216701 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
ATCC10108 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL824   CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
C8.12     CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NASA      CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM59494C CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155627 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM155628 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM167036 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM215336 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM216700 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM212031 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM190864 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175758 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175176 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
DAOM175157 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
CBS_484.84 CTCTTCTACGCCGTTGGTCACGACCCCGCTAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL13485 CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTT
NRRL911   CTCTTCTACGCTGTTGGTCACGACCCCGCCAGTGGTCTCGTCAAGGGCCAGGTTGAGCTC
NRRL13487 CTCTTCTACGCTGTTGGTCACGACCCCGCCAATGCTCTCGTTAAGGGCCAGGTTGAGCTC
*****

```

*Penicillium chrysogenum*, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```

      61      70      80      90      100      110      120
      +-----+-----+-----+-----+-----+-----+
C317.1  GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTTGAGGGTGT
C200    GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTTGAGGGTGT
C8.24   GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
D193710 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
C238    GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM155631 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM171025 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM178623 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM215337 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM216701 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
ATCC10108 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
NRRL824  GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
C8.12   GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
NASA    GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM59494C GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM155627 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM155628 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM167036 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM215336 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM216700 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM212031 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM190864 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM175758 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM175176 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
DAOM175157 GACGACGAGGGATACATCATCACCAAGCCCGGTACTAGCTTCACTAACGTCGAGGGTGT
CBS_484.84 GACAGCGAGGGATATATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGT
NRRL13485 GATGACGAACAATACATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGT
NRRL911  GATGACGAACAATACATCATCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGT
NRRL13487 AATGATGAAGGATACATCGTCACCAAGCCCGGTACCAGCTTCACTAACGTCGAGGGTGT
      *      **      *** **

```

*Penicillium chrysogenum*, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```

                121      130      140      150      160      170      180
                +-----+-----+-----+-----+-----+-----+
C317.1          TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C200            TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C8.24          TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
D193710        TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
C238           TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM155631     TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM171025     TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM178623     TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM215337     TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
DAOM216701     TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
ATCC10108      TTCGCCTGCGGTGATGTTTCAGGACAAGCGGTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL824        TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
C8.12          TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
NASA           TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM59494C     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM155627     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM155628     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM167036     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM215336     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM216700     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM212031     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM190864     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175758     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175176     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
DAOM175157     TTCGCCTGCGGTGATGTTTCAGGATAAGCGCTACCGTCAGGCTATCACCAGTGCCGGTATG
CBS_484.84     TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATC
NRRL13485      TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL911        TTCGCCTGCGGTGATGTCCAGGATAAGCGCTACCGCCAGGCTATCACCAGTGCCGGTATG
NRRL13487      TTCGCCTGCGGTGATGTTTCAGGATAAGCGTTACCGCCAGGCTATCACCAGTGCCGGTATG
*****

```

*Penicillium chrysogenum*, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```

                181      190      200      210      220      230      240
                +-----+-----+-----+-----+-----+-----+
C317.1          TTCATACTTCAGCATCTCGTTCATAGTAATTGTAAGTTGGCTAACTCAATATTCTACCAG
C200            TTCATACTTCAGCATCTCGTTCATAGTAATTGTAAGTTGGCTAACTCAATATTCTACCAG
C8.24          TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
D193710        TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
C238           TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM155631     TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAATATTCTACCAG
DAOM171025     TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM178623     TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM215337     TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
DAOM216701     TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
ATCC10108      TTCATACTTCAGCATCTCGTTCATAGTAATTGCAAGTTGGCTAACTCAGTATTCTACCAG
NRRL824        TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
C8.12          TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
NASA           TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM59494C     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM155627     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM155628     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM167036     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM215336     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM216700     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM212031     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM190864     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175758     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175176     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
DAOM175157     TTCATACTTCAGCATCTCATTTCATAGTAATTGCAATTTGGCTAACTCAATATTCTACCAG
CBS_484.84     TTCATACTCCAGCG-----ACATTTTAATTATAGTT--GCTAACTCAAT-TTCTACTAG
NRRL13485      TTCATAACCCAGCATTTCCGTTGTCGTAATTGCGATTTAGCTAACTCAATATTCTACTAG
NRRL911        TTCATAACCCAGCATTTCCGTTGTCGTAATTGCGATTTAGCTAACTCAATATTCTACTAG
NRRL13487      TTCATACTCTATTGTTTCCTTTATATTAGCTGCATTTTC-GCTAACTCAACGTTCTACCAG
*****      *                * * * * * * * * * * * * * * * * * * * *

```

*Penicillium chrysogenum*, trxB locus

CLUSTAL X (1.8) multiple sequence alignment

```
                241      250      260      270      280      290      300
                +-----+-----+-----+-----+-----+-----+
C317.1          GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C200           GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C8.24          GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
D193710       GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
C238          GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155631    GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM171025    GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM178623    GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM215337    GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM216701    GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
ATCC10108     GATCTGGCTGTGTCGCTGCTCTCGAGGCCGAGAAGTTCATCGCCGAGACCGAGACTCACC
NRRL824       GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
C8.12         GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
NASA          GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM59494C   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155627   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM155628   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM167036   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM215336   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM216700   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM212031   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM190864   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175758   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175176   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
DAOM175157   GATCTGGCTGTGTCGCTGCTCTTGAGGCTGAGAAGTTCATCGCCGAGACCGAGACTCACC
CBS_484.84   GATCTGGCTGTGTTGCCGCCCTTGAGGCTGAGAAGTTCCTCGCCGACCTTGAGACTCACC
NRRL13485    GATCTGGCTGTGTCGCCGCCCTCGAGGCCGAGAAGTTCCTCGCCGAGACTGAGACTCACC
NRRL911      GATCTGGCTGTGTCGCCGCCCTCGAGGCCGAGAAGTTCCTCGCCGAGACTGAGACTCACC
NRRL13487    GATCTGGCTGTGTCGCCGCCCTCGAAGCCGAGAAGTTCCTCTCTGAGACCGAGACTCACC
***** ** ** ** ** ** ***** ** * ** *****
```

*Penicillium chrysogenum*, *trxB* locus

CLUSTAL X (1.8) multiple sequence alignment

```

          301
          +-----
C317.1    AGGAGG
C200      AGGAGG
C8.24     AGGAGG
D193710   AGGAGG
C238      AGGAGG
DAOM155631 AGGAGG
DAOM171025 AGGAGG
DAOM178623 AGGAGG
DAOM215337 AGGAGG
DAOM216701 AGGAGG
ATCC10108  AGGAGG
NRRL824    AGGAGG
C8.12     AGGAGG
NASA       AGGAGG
DAOM59494C AGGAGG
DAOM155627 AGGAGG
DAOM155628 AGGAGG
DAOM167036 AGGAGG
DAOM215336 AGGAGG
DAOM216700 AGGAGG
DAOM212031 AGGAGG
DAOM190864 AGGAGG
DAOM175758 AGGAGG
DAOM175176 AGGAGG
DAOM175157 AGGAGG
CBS_484.84 AGGAGG
NRRL13485  AGGAGG
NRRL911    AGGAGG
NRRL13487  AGGAGG
          *****
```