



Cairo University
Faculty of Veterinary Medicine
Microbiology Department

Phenotypic and genotypic characterization of *Pseudomonas aeruginosa* from different sources

Presented By

Amal Ibrahim Attia Mansour

(B.V.Sc. - 2005)

For the degree of M.V.Sc.

(Bacteriology, Immunology and Mycology)

Under the supervision of

Prof. Dr. NASHWA A.EZZ ELDIN

Professor of Microbiology

Faculty of Veterinary Medicine

Cairo University

Dr. EL-MOUSTAFA E.MOHAMED

Lecturer of Microbiology

Faculty of Veterinary Medicine

Cairo University

Dr. MAHMOUD D.E-LHARIRI

Professor of Microbiology

Faculty of Veterinary Medicine

Cairo University

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Cairo University

Faculty of Veterinary Medicine

Department of Bacteriology, Mycology and Immunology

Name: *Amal Ibrahem Attia Mansour*

Title of thesis: Phenotypic and genotypic characterization of *Pseudomonas aeruginosa* from different sources.

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Supervisors:

Prof. Dr. Nashwa Abd Elsalam Ezzeldeen

Professor of Microbiology

Faculty of Veterinary Medicine, Cairo University

Dr. Elmoustafa Mohamed

Lecturer of Microbiology

Faculty of Veterinary Medicine, Cairo University

Dr. Mahmoud Elhariri

Assistant Professor of Microbiology

Faculty of Veterinary Medicine, Cairo University

Abstract

In the present study the total number of *P.aeruginosa* isolated from 568 samples of animal and human origins represented as follows 450 bovine samples, 65 dog samples, and 53 samples of human origins, Positive isolates were 63 with an incidence of 11%. The *P. aeruginosa* recovery rate from milk samples of cows (8.4%), from nasopharyngeal swabs of calves (9.5%) while, dog clinical samples (9.4%) and For human the recovery rate (18.8%) .The serogrouping reveled the most prevalent serogroupes O8 (50 %) , O6 (25%) On the other hand, serogroupes O3, O4, O5, O9 and O11 could not be recorded among bovine isolates. In dogs the serogroupe O4 was the most prevalent one (53.8%), & serogroupe O5 (46.2%). The human isolates revealed the most frequent serogroupes O8 (60%) & O6 (40%). The *P. aeruginosa* antimicrobial sensitivity were applied for all isolates which were variable in resistance patterns and most of isolates were MDR. The heat-shock gene detection by The PCR assay was applied and. all examined isolates are positive for groE gene confirming conventional biochemical characterization of isolates. Flagellin gene amplified product length 1020 bp separated in all but tested *P. aeruginosa* isolates. The molecular weight of tested 6 isolates revealed that protein molecular weight was varied in between 45 kDa lane 1.2.5 & 6. The other isolates (Lane 3 & 4) were produced molecular weight 50 kDa.

Keywords: *Pseudomonas aeruginosa*- Flagellin- Genetic – RFLP

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