

Reports of the MASC Subcommittees

Bioinformatics

Compiled by Nicholas Provart (nicholas.provart@utoronto.ca) with input from MASC Bioinformatics Subcommittee members and the wider *Arabidopsis* community.



Arabidopsis Informatics – TAIR, BAR and the National Center for Genome Resources (NCGR) in New Mexico collaborated to ensure that the data and tools formerly provided by Araport remain available to the community. Araport's JBrowse instance migrated to TAIR, Thalemine was redeployed with updated data at the BAR, and a new tool for exploring micro- and macrosynteny in *Arabidopsis thaliana* ecotypes was released by the NCGR.

TAIR also continues to provide quarterly public releases of year-old datasets (https://www.Arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases). The 18th public release from TAIR contains cumulative curated data sets up to March 31, 2018. Educators can continue to request access to the “full” version of TAIR for teaching purposes. We look forward to integrating JBrowse into TAIR in the coming year.

TAIR: With help from members of the Araport and GMOD projects, TAIR installed the latest version of JBrowse at TAIR (see an example region here: <https://bit.ly/2Qhb5xC>) starting with the tracks that were available at Araport, fixing ones that had become non-functional and adding to these with new community tracks, e.g. TRAP-seq data under hypoxia from Lee and Bailey-Serres (2019). TAIR staff also performed software updates and technical improvements, updating TAIR's BLAST service (<https://www.arabidopsis.org/Blast/index.jsp>) to the latest version of NCBI BLAST (2.9.0) and providing a graphical display of alignments.

TAIR curators continued to extract experimental gene function data from the current literature and codify the data in the form of annotations to Gene Ontology and Plant Ontology terms as well as curated gene summaries, alleles and phenotypes, and gene symbols. In 2019 TAIR started an initiative to add GO terms for sets of genes for which there were no GO annotations at all, by reviewing linked literature, and adding annotations where possible. TAIR continues to produce quarterly updates of current data for subscribers (https://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Subscriber_Data_Releases), and year old data for use by all (https://www.arabidopsis.org/download/index-auto.jsp?dir=/download_files/Public_Data_Releases).

Bio-Analytic Resource (BAR): BAR rolled out a revived and updated version of Araport's Thalemine at <https://bar.utoronto.ca/thalemine/> as part of the aforementioned multi-lab effort to resuscitate Araport.

The BAR also published its eFP-Seq Browser at https://bar.utoronto.ca/eFP-Seq_Browser/ for exploring RNA-seq data as both read map profiles and summarized gene expression levels across two large compendia, in order to be able to quickly identify samples with the highest level of expression or where alternative splicing might be occurring (Sullivan *et al.*, 2019).

NCGR: Andrew Farmer and Alan Cleary developed their Genome Context Viewer (GCV) to enable the dynamic comparison of multiple genomes on the basis of their shared functional elements such as genes (Cleary and Farmer, 2017). An instance of the GCV is now running at <https://gcv-arabidopsis.ncgr.org> as the third component of the revamped Araport. The reference *Arabidopsis thaliana* Col-0 genome (TAIR10/Araport11) and genomes from several other data sources, including two sets of newly assembled *A. thaliana* genomes of various ecotypes from Jiao and Schneeberger (2020) and from the 1001 Genomes project from the Weigel lab (Bemm, Kubica, and Weigel, unpublished), as well as a number of Brassicaceae genomes from Phytozome and the BMAP project are available. Check it out!

Large-scale Data Sets of Note

Edward Marcotte's group used co-fractionation mass spectrometry to identify protein complexes in 13 plant species, including *Arabidopsis*. An astonishing 3,076,999 pairwise interactions were elucidated in this amazing study, which permits the identification of conserved and rewired protein complexes in plants (McWhite *et al.*, 2020). The data set is searchable at <http://plants.proteincomplexes.org/search>.

The Gazzarrini and Lumba Labs (Carianopol *et al.* 2019, <https://doi.org/10.1038/s42003-020-0866-8>) identified 125 SnRK1 complex interacting proteins using a meso-scale Y2H screening approach against ABA-regulated gene products. The Desveaux Lab (Cao *et al.* 2019, <https://doi.org/10.1111/tpj.14425>) generated an ABA-T3SE interactome network (ATIN) between *P. syringae* Type 3 Secreted Effectors (T3SEs) and *Arabidopsis* proteins encoded by ABA-regulated genes in order to further understand how plant pathogens can manipulate endogenous hormone signaling pathways. ATIN consists of 476 PPIs between 97 *Arabidopsis* ABA-regulated gene products and 56 T3SEs from four pathovars of *P. syringae*, as determined using Y2H.

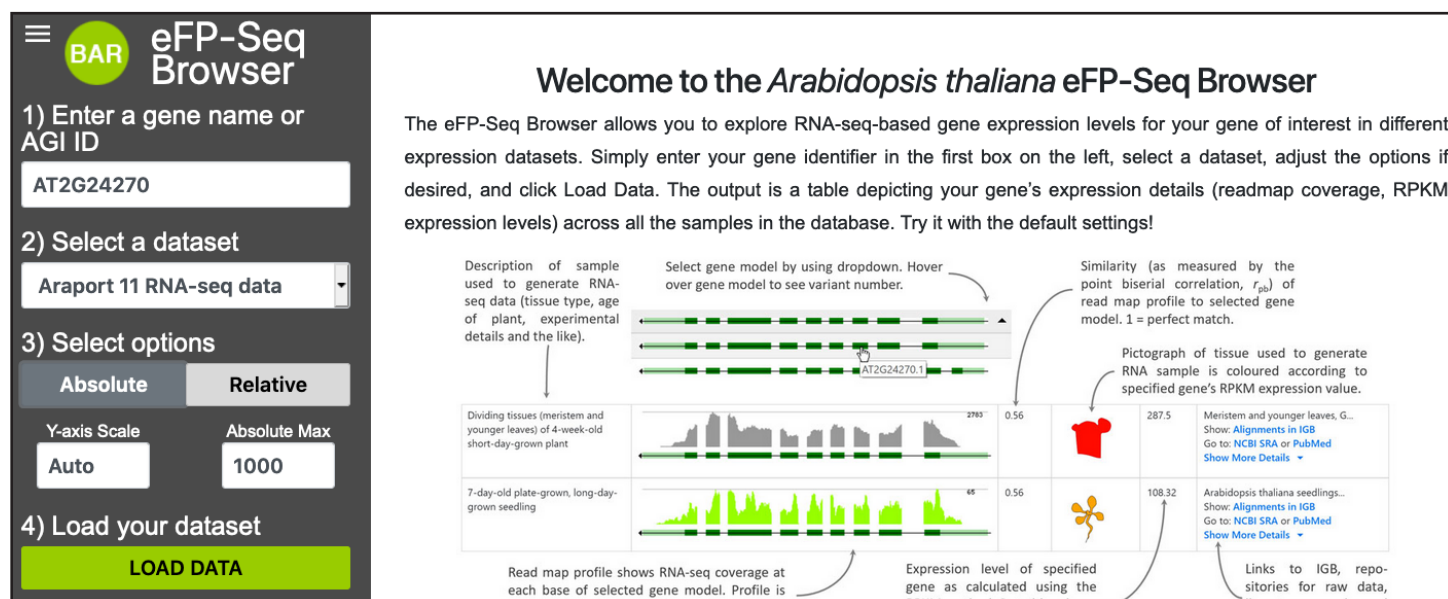


Figure 2. https://bar.utoronto.ca/eFP-Seq_Browser/

Also in terms of plant-pathogen interactions, The Guttman and Desveaux Labs (Laflamme *et al.*, 2020) published an analysis of the plant pan-genome immunity landscape using their PsyTEC compendium, which consisted of 529 representative *P. syringae* T3SEs screened against *Arabidopsis* to identify those which trigger an immune response. The results showed that relatively few genes (including two novel ones) in *Arabidopsis* recognize the majority of *P. syringae* effectors.

An interesting large-scale data set for *Arabidopsis* and 12 other species was generated by a “meltome” analysis, using a mass-spec-based proteomics approach for 48,000 proteins across 13 species covering melting temperatures of 30–90 °C (Jarzab *et al.*, 2020).

scRNA-Seq Search Tools. While several scRNA-seq data sets were published in the past year, two useful tools are now available to query some of these data sets. The Wang Lab developed its Root Cell Atlas search tool at <http://wanglab.sippe.ac.cn/rootatlas/> based on scRNA-seq data they generated (Zhang *et al.*, 2019) and the BAR's eFP Browser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi?dataSource=Single_Cell) provides the ability to query scRNA-seq data from Ryu *et al.* (2019).

A Plant Cell Atlas project kicked-off in 2019 (Rhee *et al.*, 2019), which will provide unprecedented cell-level resolution of many different ‘omes in plants, along with models to describe cell growth and behaviour. Keep an eye on <http://www.plantcellatlas.org/> for updates!

Pedagogy, Policy and Outreach: Nicholas Provart released a Plant Bioinformatic Methods Specialization encompassing 4 courses on Coursera.org: Bioinformatic Methods I, Bioinformatic Methods II, Plant Bioinformatics, and a Plant Bioinformatics Capstone. See <https://www.coursera.org/specializations/plant-bioinformatic-methods>. You can audit the courses for free, or obtain certificates for a small fee.

References

- Cao, F.Y., Khan, M., Taniguchi, M., Mirmiran, A., Moeder, W., Lumba, S., Yoshioka, K., and Desveaux, D. (2019). A host–pathogen interactome uncovers phytopathogenic strategies to manipulate plant ABA responses. *Plant J.* 100: 187–198.
- Carianopol, C.S., Chan, A.L., Dong, S., Provart, N.J., Lumba, S., and Gazzarrini, S. (2020). An abscisic acid-responsive protein interaction network for sucrose non-fermenting related kinase1 in abiotic stress response. *Commun. Biol.* 3: 145.
- Cleary, A. and Farmer, A. (2017). Genome Context Viewer: visual exploration of multiple annotated genomes using microsynteny. *Bioinformatics* 34: 1562–1564.
- Jarzab, A. *et al.* (2020). Meltome atlas—thermal proteome stability across the tree of life. *Nat. Methods* 17: 495–503.
- Jiao, W.-B. and Schneeberger, K. (2020). Chromosome-level assemblies of multiple *Arabidopsis* genomes reveal hotspots of rearrangements with altered evolutionary dynamics. *Nat. Commun.* 11: 989.
- Laflamme, B., Dillon, M.M., Martel, A., Almeida, R.N.D., Desveaux, D., and Guttman, D.S. (2020). The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. *Science* 367: 763.
- Lee, T.A. and Bailey-Serres, J. (2019). Integrative Analysis from the Epigenome to Translatome Uncovers Patterns of Dominant Nuclear Regulation during Transient Stress. *Plant Cell* 31: 2573–2595.
- McWhite, C.D. *et al.* (2020). A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. *Cell* 181: 460-474.e14.

Rhee, S.Y., Birnbaum, K.D., and Ehrhardt, D.W. (2019). Towards Building a Plant Cell Atlas. *Trends Plant Sci.* 24: 303–310.

Ryu, K.H., Huang, L., Kang, H.M., and Schiefelbein, J. (2019). Single-Cell RNA Sequencing Resolves Molecular Relationships Among Individual Plant Cells. *Plant Physiol.* 179: 1444.

Sullivan, A. *et al.* (2019). An 'eFP-Seq Browser' for visualizing and exploring RNA sequencing data. *Plant J.* 100: 641–654.

Zhang, T.-Q., Xu, Z.-G., Shang, G.-D., and Wang, J.-W. (2019). A Single-Cell RNA Sequencing Profiles the Developmental Landscape of Arabidopsis Root. *Mol. Plant* 12: 648–660.

Clone-Based Functional Genomics Resources (ORFeomics)

Motoaki Seki (Chair)
motoaki.seki@riken.jp
RIKEN CSRS

Joe Ecker (Co-Chair)
ecker@salk.edu
Salk Institute



ORFeomics subcommittee has tracked the progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes. Our recent search showed that now about 23,000 Arabidopsis protein-coding genes have been isolated as Full-length cDNA (ORF) clones. One of the last unexplored continents of Arabidopsis are the remaining 6,000 protein-coding genes. After that, only the non-coding genes remain to be isolated.

With the completion of isolating all 29,000 Arabidopsis protein-coding genes, comprehensive analysis of plant gene function will become possible by various functional analyses using transgenic and protein expression approaches.

Recently developed Open Tools and Resources for Arabidopsis Researchers

We prepared the updated list of Full-length cDNA and ORF clones that are available from Resource Centers (Please see the attachment table).

Recent or Future activities of Subcommittee members..

Subcommittee goals:

Keeping tracking progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes.

ORFeomics subcommittee would like to propose a new project to collect all ORF (full-length cDNA) clones from every Arabidopsis protein-coding gene so as to test protein-protein, protein-DNA and protein-RNA interactions.

The human whole ORFeome project is already ongoing. Arabidopsis is a model plant, thus this will represent the first big plant ORFeome project. On completion it might be possible to start synthetic biology using the whole gene set of Arabidopsis to allow functional studies of corresponding proteomes

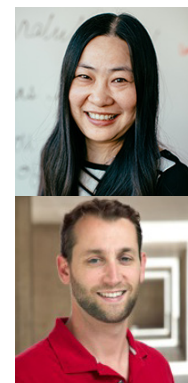
Selected Publication

Ali, M.R.M., Uemura, T., Ramadan, A., Adachi, K., Nemoto, K., Nozawa, A., Hoshino, R., Abe, H., Sawasaki, T. and Arimura, G.I. (2019) The Ring-Type E3 Ubiquitin Ligase JUL1 Targets the VQ-Motif Protein JAV1 to Coordinate Jasmonate Signaling. *Plant Physiol.* 179:1273-1284.

Epigenetics and Epigenomics

Xuehua Zhong (Co-Chair)
xuehua.zhong@wisc.edu
University of Wisconsin-Madison, USA

Robert Schmitz (Co-Chair)
schmitz@uga.edu
University of Georgia, USA



Arabidopsis thaliana has proven to be the workhorse for elucidating mechanistic underpinnings of numerous epigenetic phenomena. Recent emphasis by the research community has been on studying the interaction between parental epigenomes throughout sexual reproduction and epigenetic regulation of environmental adaptation.

These studies are revealing the importance of small RNAs, histone modifications, and DNA methylation in epigenome reinforcement, in detection of self from non-self, and in responding to versatile environmental challenges. While genetic and genomic studies continue to provide important insights, recent biochemical efforts have reconstructed the core and regulatory components of

Creator	Format	Focus	Validation	Scale	URL	Stock center
ORF clones						
SSP/RIKEN/Salk Institute	Univector pUNI51		Full sequence	14,398	signal.salk.edu/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
Salk/Invitrogen	Gateway entry		Full sequence	12,114	signal.salk.edu/cdnastatus.html http://methylo.me.salk.edu/cgi-bin/clones.cgi	ABRC
CCSB/Salk	Y2H clones	Plant Interactome Network Map	Full sequence	18,258	http://interactome.dfc.harvard.edu/A_thaliana/host.php	ABRC
TIGR	Gateway entry	Hypothetical genes	Full sequence	3,041	www.tigr.org/tdb/hypos/	ABRC
Peking-Yale Joint Center	Gateway entry	Transcription factors	5' and 3' end seq.	1,282		ABRC
Dinesh-Kumar et al.	Gateway expression	TAP-tagged transcription factor	5' and 3' end seq.	15,543		ABRC
REGIA	Gateway entry	Transcription factors	5' and 3' end seq.	982	gabi.rzpd.de/materials/	GABI/RZPD
Dinesh-Kumar et al.	Gateway entry, no stop pLIC-CTAP	Plant protein chips	5' and 3' end seq.	7,300	plants.gersteinlab.org/	ABRC
ATOME collection	Gateway entry		5' and 3' end seq.	6,448	http://urgv.evry.inra.fr/ATOMEdb	ABRC, CNRGV
Doonan et al.	Gateway Expression	GFP fusion for subcellular location		155		ABRC
Callis et al.	Gateway entry	Protein ubiquitination	Full sequence	111	plantsubq.genomics.purdue.edu	ABRC
Sheen et al.	Expression	Epitope tagged MAPK	Full sequence	100	genetics.mgh.harvard.edu/sheenweb/category_genes.html	ABRC
Steve Clouse	Gateway expression	N-terminal Flag/His tagged kinases		855 (73 new in 2015)	http://www4.ncsu.edu/~sclouse/Clouse2010.htm	ABRC
Frommer et al.	Gateway entry, no stop	Membrane and signaling proteins	5' and 3' end seq.	2,712	http://associomics.org	ABRC
Frommer et al.	Gateway Expression (mbSUS clones)	Membrane and signaling proteins	5' and 3' end seq.	5,414	http://associomics.org	ABRC
AIST/RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	1,998	https://plant.rtc.riken.jp/resource/tfclone/tfclone_list.html	BRC
RIKEN	Gateway entry, no stop	Transcription factor	Full sequence	399	https://plant.rtc.riken.jp/resource/tfclone/tfclone_list.html	BRC
Allie Gaudinier and Siobhan Brady	Y1H, AD vector	Transcription factor	Full sequence	635		ABRC
SALK/Promega	pIX-HALO vector			12,069		ABRC
O'Malley et al.	pIX-HALO vector	Transcription factor	Full sequence	1,315		ABRC
Guillaume Pilot	pDONRZEO vector	Membrane protein	5' and 3' end seq	192		ABRC
Pruneda-Paz et al.	Gateway Entry, no stop	Transcription factor	Full sequence	1,956		ABRC
Pruneda-Paz et al.	Gateway Destination, no stop, pDEST22	Transcription factor	Full sequence	1,956		ABRC
Lao et al.	Gateway DONR, no stop, pDONR223	glycosyltransferases	Full sequence	429	http://gt.jbei.org/	ABRC
Amita Kaundal et al.	Gateway DONR, no stop, pDONR201			26		ABRC
cDNA clones						
RIKEN/SSP/Salk Institute	λ ZAP or λ PS		Full sequence/ 5' and 3' end seq.	22,671	https://plant.rtc.riken.jp/resource/rafi/rafi_list.html	BRC
MPI-MG	Gateway expression		5' end seq.	4,500	gabi.rzpd.de/materials/	GABI/RZPD
Génoscope/LTI	Gateway entry		Full single pass seq.	28,866	www.genoscope.cns.fr/Arabidopsis	CNRGV

Table 1. List of available ORF Resources.

key epigenetic complexes and has linked them to various signaling pathways. Several epigenome editing approaches have also been developed to target specific DNA methylation pathways to selected regions of the genome to initiate silencing.

While the field continues to work on the basic epigenetic mechanisms in genome function and development, a new focus on linking signaling pathways to chromatin dynamics has emerged. Another major focus of the field is exploring how epigenetic mechanisms are conserved and/or vary in plant species, particularly crop plants. Even though many chromatin/DNA methylation pathways are conserved, there is a surprising amount

of variation in certain enzymatic components and how they are utilized by host genomes for gene regulation, transposon silencing, and genome stability.

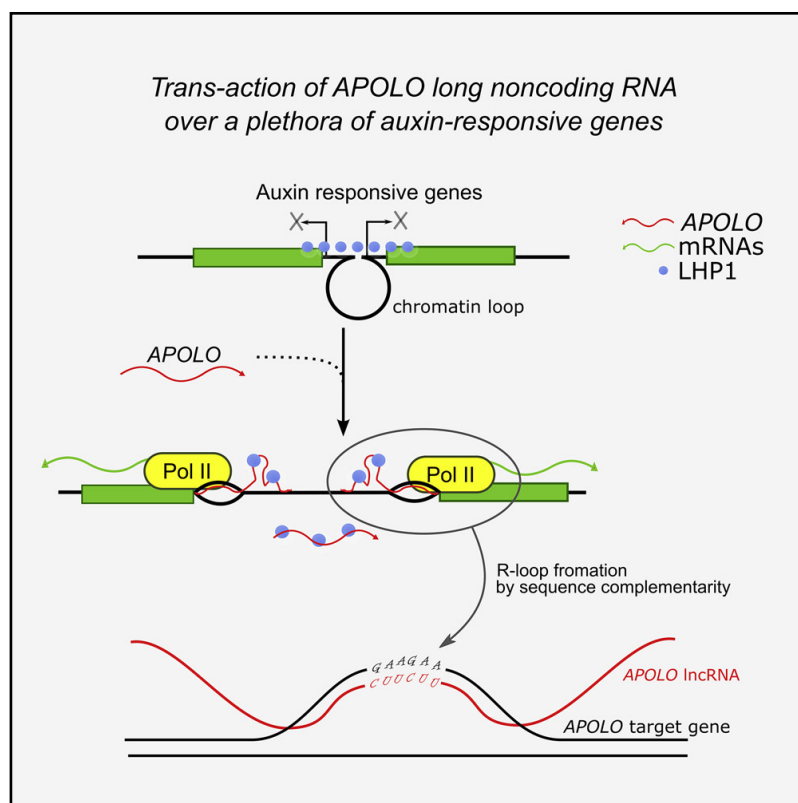


Figure 3: R-Loop Mediated trans Action of the APOLO Long Noncoding RNA

Recently developed Open Tools and Resources for Arabidopsis Researchers

Developed a website for a collection of ~20,000 Arabidopsis RNA-seq datasets <http://ipf.sustc.edu.cn/pub/athrna/> This is an important community resource containing ~20,000 Arabidopsis RNA-seq datasets of various genetics mutants, developmental stages, biotic and abiotic stress treatments, etc. More importantly, it contains many wild-type Col-0 samples from different labs worldwide as a further reference for any Col-0 samples from individual lab. This resource is particularly useful to search for potential new regulators (both genetic and environmental factors) of given genes and pathways.

A similar website containing large collection of whole genome bisulfite sequencing datasets is currently under construction and will be available to the global community upon completion

Recent or Future activities of Subcommittee members

The Epigenetics and Epigenomics Subcommittee members organized and participated several epigenetic sections associated with various international conferences in 2019. These were held at Plant Genomes Conference and Gordon Research Conference in USA, Japanese Society of Plant Physiologists 60th Annual Meeting, 30th ICAR and plant epigenetics symposium in China, European workshop on plant chromatin in Germany, Mini-symposium on Epigenetic stress memory in Michigan State

University and Wisconsin, and Symposium on Impact of Nuclear Domains on Plant Phenotypes in Spain. The Subcommittee members have also organized laboratory workshop on cell type-specific nuclei purification by INTACT at Frontiers and Techniques in Plant Science at CSHL.

The combined activities of Subcommittee members have enhanced the appreciation of the importance of epigenetic regulation in plant biology, boosted the interests, and strengthened international collaborations and coordination to understand the roles and regulation of plant epigenetics/epigenomics. This research topic has also attracted a large amount of interest from the media and the general public.

Conferences and Workshops

2019

- Plant & Animal Genomes Conference, San Diego, CA, January 2019 (Session on Plant Epigenetics & Epigenomics)
- Japanese Society of Plant Physiologists 60th Annual Meeting, Nagoya, Japan, March 2019 (Session on inheritance and rewriting of cellular memory in plants)
- 30th International Conference on Arabidopsis Research, Wuhan, China, June 2019 (Plenary and concurrent sessions on Epigenetics)

- Epigenetic workshop, Nanjing Agricultural University, Nanjing, China, June 2019
European workshop on plant chromatin, MPI Cologne, June 2019

- CSHL Frontiers and Techniques in Plant Science, CSHL, NY, June 2019

- SEB-INDEPTH Symposium on Impact of Nuclear Domains on Plant Phenotypes, Madrid, Spain, December 2019. <https://www.brookes.ac.uk/indepth/>

2020

- Cold Spring Harbor-Asia Conference: Integrative Epigenetics in Plants, Awaji, Japan December, 2020

Selected Publications

Ariel F, Lucero L, Christ A, et al. R-Loop Mediated trans Action of the APOLO Long Noncoding RNA. *Mol Cell*. 2020;77(5):1055–1065.e4. doi:10.1016/j.molcel.2019.12.015

Fang, X., Wang, L., Ishikawa, R., Li, Y., Fiedler, M., Liu, F., Calder, G., Rowan, B., Weigel, D., Li, P., & Dean, C. (2019). Arabidopsis FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. *Nature*, 569(7755), 265–269. doi:10.1038/s41586-019-1165-8

Gallego-Bartolomé J, Liu W, Kuo PH, *et al.* Co-targeting RNA Polymerases IV and V Promotes Efficient De Novo DNA Methylation in Arabidopsis. *Cell*. 2019;176(5):1068-1082.e19. doi:10.1016/j.cell.2019.01.029

He S, Vickers M, Zhang J, Feng X. Natural depletion of histone H1 in sex cells causes DNA demethylation, heterochromatin decondensation and transposon activation. *Elife*. 2019;8:e42530. doi:10.7554/eLife.42530

Kirkbride RC, Lu J, Zhang C, Mosher RA, Baulcombe DC, Chen ZJ. Maternal small RNAs mediate spatial-temporal regulation of gene expression, imprinting, and seed development in Arabidopsis *Proc Natl Acad Sci U S A*. 2019;116(7):2761-2766. doi:10.1073/pnas.1807621116

Metabolomics

Wolfram Weckwerth (Co-chair)
wolfram.weckwerth@univie.ac.at
University of Vienna

Takayuki Tohge (Co-Chair)
tohge@bs.naist.jp
Nara Institute of Science and Technology,
Nara, Japan



The Arabidopsis metabolomics platform mostly represented by the activities of the members of the Multinational Arabidopsis Steering Committee is a strong pillar for functional analysis not only in this model plant. Many tools have been developed in this model system that are trend-setting for the application in crop plant research. What is a clear future trajectory of research is the systematic metabolomic analysis of germplasm collections of *Arabidopsis thaliana* and the linkage to genome wide association studies and genomic prediction.

Arabidopsis also serves as a model system for translational research for crop plants as more and more large germplasm collections with whole genome sequences are available (Weckwerth *et al.* 2020).

At the moment there is no better curated database available for any plant system than the 1001 genome collection of natural Arabidopsis accessions (Alonso-Blanco *et al.* 2016). Another research area is ecological metabolomics with natural Arabidopsis populations (Nagler *et al.* 2018). The combination of metabolomics and whole-genome data of large collections of accessions in their native habitats as well as in common garden experiments enables the analysis of evolutionary adaptation processes from genome to metabolic plasticity.

Alonso-Blanco *et al.* (2016) 1,135 genomes reveal the global pattern of polymorphism in *Arabidopsis thaliana*. *Cell* 166: 481-491

Nagler *et al.* (2018) Eco-Metabolomics and Metabolic Modeling: Making the Leap From Model Systems in the Lab to Native Populations in the Field. *Front Plant Sci* 9: 1556

Weckwerth *et al.* (2020) PANOMICS meets Germplasm. *Plant Biotechnol J*. doi: 10.1111/pbi.13372.

Recently developed Open Tools and Resources for Arabidopsis Researchers

Databases

<http://plasma.riken.jp/>

A cheminformatics approach to characterize metabolomes in stable-isotope-labeled organisms.

Tsugawa *et al* (2019) *Nat Methods*. 16: 295-298.

doi: 10.1038/s41592-019-0358-2

Sample preparation for metabolomics

Metabolomics in the Context of Plant Natural Products Research: From Sample Preparation to Metabolite Analysis.

Salem *et al* (2020) *Metabolites*. 10: E37

doi: 10.3390/metabo10010037

Pathway analysis for model organisms

PathBank: a comprehensive pathway database for model organisms.

Wishart *et al* (2020) *Nucleic Acids Res*. 48: D470-D478

doi: 10.1093/nar/gkz861

Method of GCMS for volatile apocarotenoid in Arabidopsis
Volatile apocarotenoid discovery and quantification in Arabidopsis thaliana: optimized sensitive analysis via HS-SPME-GC/MS.

Rivers *et al* (2019) *Metabolomics* 15: 79

doi: 10.1007/s11306-019-1529-y

Rapid protocol for subcellular plant metabolism analysis
Resolving subcellular plant metabolism.

Fürtauer *et al* (2019) *Plant J* 100: 438-455

doi: 10.1111/tpj.14472

Recent or Future activities of Subcommittee members.

Since metabolomics is an important component of Arabidopsis 'omics, a continuous goal of this subcommittee will be to promote metabolomics research of Arabidopsis leading to functional genomics and systems biology. Full integration of Arabidopsis-based metabolomics research with the activity of the Metabolomics Society (<http://www.metabolomicssociety.org/>) is also an important goal of this subcommittee.

Several members of the subcommittee are involved in drawing up the plant biology specific documentation for the Metabolomics Society.

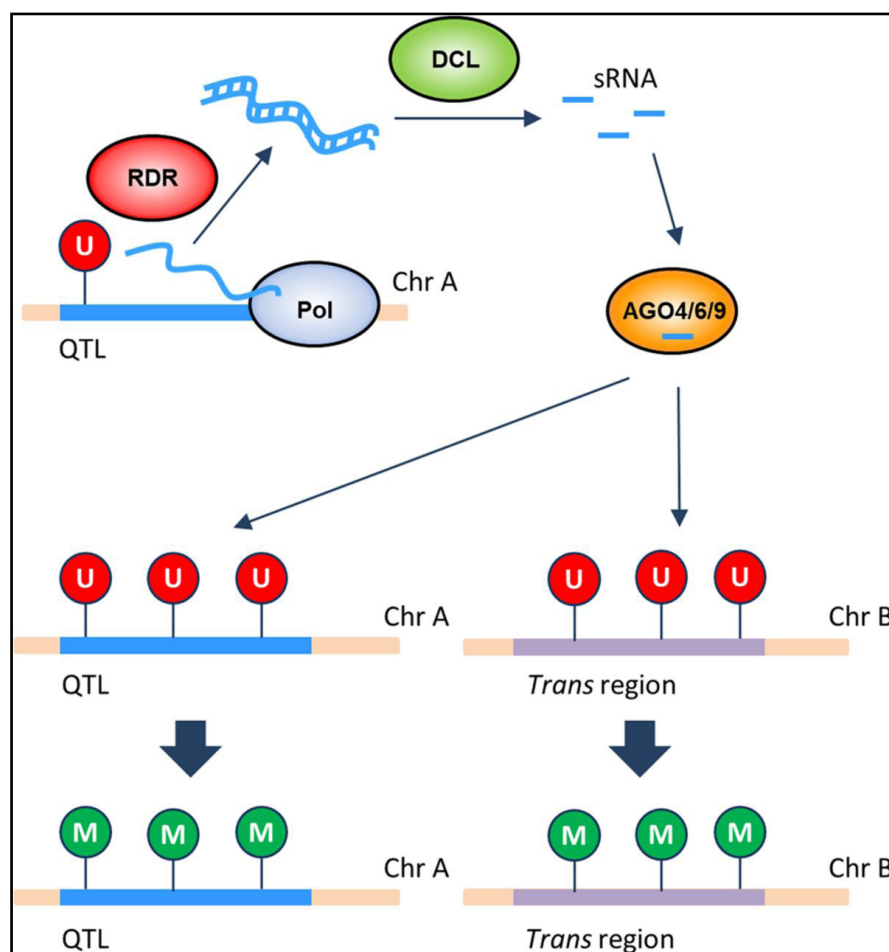


Figure 4: Theoretical model for the regulation of DNA methylation by differential targeting of sRNA to loci in trans. Changes in DNA methylation can be induced directly by differential recruitment of components of the RdDM pathway, or indirectly by post-transcriptional silencing of genes. (DCL) Dicer, (M) methylated, (Pol) RNA polymerase, (RDR) RNA-dependent RNA polymerase, (U) unmethylated.

In addition this committee will aim to establish a mechanism that allows the dissemination of metabolomics datasets to the wider Arabidopsis community and encourage and facilitate initiatives for the integration of metabolomic datasets with other omic datasets. This will involve depositing metabolomic data in a usable format for data integration. A specific webpage for these MASC metabolomics subcommittee activities will be discussed.

Future Activities of the Subcommittee.

The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where the subcommittee members can join. The web interface will provide user with a user-friendly tool to search for *Arabidopsis thaliana* metabolomics data in available databases. In addition, the people in plant metabolomics community actively provide open tools and resources useful for Arabidopsis researchers as indicated above

Conferences, Workshops and Training events

2020/6/21-24 Phytochemical Society of North America, Kelowna, Canada. Now in 2021.

<https://psna2020.ca/>

2020/7/6-10 Metabolomics 2020, Shanghai, China

<http://metabolomics2020.org/>

Selected Publications

Kooke R, Morgado L, Becker F, van Eekelen H, Hazarika R, Zheng Q, de Vos RCH, Johannes F and Keurentjes JJB (2019) Epigenetic mapping of the Arabidopsis metabolome reveals mediators of the epigenotype-phenotype map. *Genome Res* 29: 96-106

Kozuka T, Sawada Y, Imai H, Kana, M, Hirai MY, Mano S, Uemura M, Nishimura M, Kusaba M and Nagatani A. (2020) Regulation of Sugar and Storage Oil Metabolism by Phytochrome during De-etiolation. *Plant Physiol* 182: 1114-1129

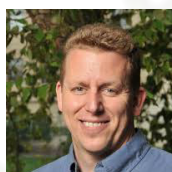
Perez de Souza L, Garbowicz K, Brotman Y, Tohge T and Fernie AR. (2020) The Acetate Pathway Supports Flavonoid and Lipid Biosynthesis in Arabidopsis. *Plant Physiol* 182: 857-869

Mangel N, Fudge JB, Li KT, Wu TY, Tohge T, Fernie AR, Szurek B, Fitzpatrick TB, Grissem W, Vanderschuren H (2019) Enhancement of vitamin B6 levels in rice expressing Arabidopsis vitamin B6 biosynthesis de novo genes. *Plant J* 99: 1047-1065

Shimizu Y, Rai A, Okawa Y, Tomatsu H, Sato M, Kera K, Suzuki H, Saito K, Yamazaki M (2019) Metabolic diversification of nitrogen-containing metabolites by the expression of a heterologous lysine decarboxylase gene in Arabidopsis. *Plant J* 100: 505-521

Natural Variation and Comparative Genomics

J. Chris Pires (Chair)
piresjc@missouri.edu
University of Missouri



Ya-Long Guo (Co-Chair)
yalong.guo@ibcas.ac.cn
State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences



Recently developed Open Tools and Resources for Arabidopsis Researchers

- AraPheno: AraPheno is a public database collection of Arabidopsis thaliana phenotypes. This Database allows to search and filter for public phenotypes and to obtain additional meta-information.
<https://arapheno.1001genomes.org/>

- JBrowse at TAIR: The current NV/GV tracks of interest are the 1001 Genomes track.

We have additional Phytozome13 tracks for orthologous genes in 61 other plant species that are in testing on our dev server that should go live within the next month.

<https://www.arabidopsis.org/servlets/jbrowse/arabidopsis?default=true>

- Thalemine/Araport now includes several complete A. thaliana genomes now from the Schneeberger lab and the 1001 Genomes Project (Zmienko et al, 2020)
<https://bar.utoronto.ca/thalemine/begin.do>

- Andrew Farmer's Genome Context Viewer (GCV) loaded 14 Arabidopsis thaliana assembled genomes. This links to new Araport: GCV, TAIR's resuscitation of the Araport JBrowse tracks, and the Provart lab's reinstating of Thalemine at the BAR. An instance of this viewer has been set up and is now running from NCGR (<https://gcv-arabidopsis.ncgr.org>) as the third component of the "second generation" Araport. The viewer provides convenient links to related resources for genes and genomic regions, thereby facilitating traversal into the other components of the reconfigured Araport project as well as other relevant tools. The gene family classifications utilized by the current instance are based on PANTHER 14.1 (Mi et al., 2013, doi: 10.1093/nar/gks1118) and links are provided to the trees developed for these families by the PhyloGenes project (phylogenes.org).

Recent or Future activities of Subcommittee members.

This is an exciting time for the Comparative Genomics community as there is movement to establish the plant order Brassicales as a model clade and a large

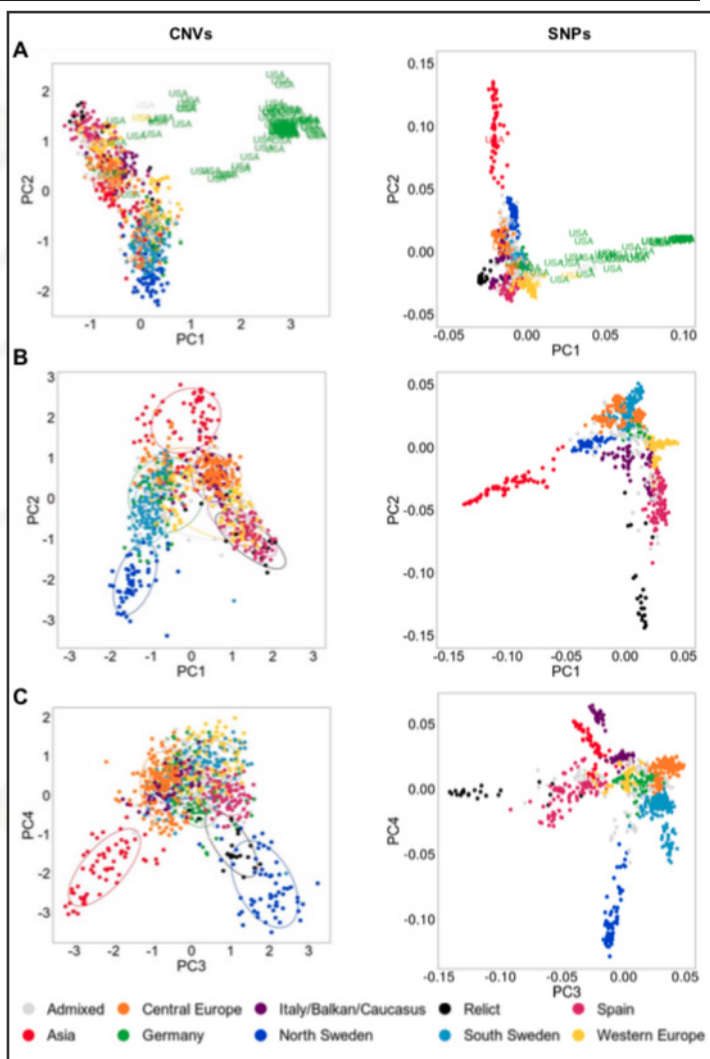


Figure 5: A. *thaliana* population structure based on the analysis of CNV genotypes. Principal component analysis (PCA) was performed on 1,060 accessions and on genotyping data from 1,050 CNV-PCGs (left). For comparison, another PCA was performed on the same set of accessions and 117,232 SNPs from the 1001 Genomes Project (right). A, PC1 and PC2 components; all accessions were included. USA accessions assigned to the Germany subgroup were distinguished from the other samples. B, PC1 and PC2 components; USA accessions from the Germany subgroup were excluded from the analysis. C, PC3 and PC4 components; all accessions were included. The accessions in PCA plots are colored based on their 1001 Genomes Project grouping.

proposal is being assembled for that research. This is enhanced by the discovery of a new family of Brassicales that will feed into this new classification (Swanepoel et al, 2020).

Selected Publications

de Jong M, Tavares H, Pasam RK, Butler R, Ward S, George G, Melnyk C, Challis R, Kover PX, Leyser O (2019) Natural variation in Arabidopsis shoot branching plasticity in response to nitrate supply affects fitness. PLOS Genetics 15(9): e1008366. doi:10.1371/journal.pgen.1008366

Niu XM, Xu YC, Li ZW, Bian YT, Hou XH, Chen JF, Zou YP, Jiang J, Wu Q, Ge S, Balasubramanian S, Guo YL (2019) Transposable elements drive rapid phenotypic variation in *Capsella rubella*. *Proc Natl Acad Sci U S A* 116: 6908-6913.

Seung D, Echevarría-Poza A, Steuernagel B, Smith AM. (2020) Natural Polymorphisms in *Arabidopsis* Result in Wide Variation or Loss of the Amylose Component of Starch. *Plant Physiol.* 182: 870-881. doi: 10.1104/pp.19.01062

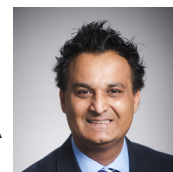
Swanepoel W, Chase MW, Christenhusz MJM, Maurin O, Forest F, van Wyk AE. (2020). From the frying pan: an unusual dwarf shrub from Namibia turns out to be a new brassicalean family. *Phytotaxa*. 439 (3): 171–185. doi:10.11646/phytotaxa.439.3.1

Togninalli M, Seren Ü, Freudenthal J, Monroe JG, Meng D, Nordborg M, Weigel D, Borgwardt K, Korte A, Grimm DG (2020) AraPheno and the AraGWAS Catalog 2020: a major database update including RNA-Seq and knockout mutation data for *Arabidopsis thaliana*. *Nucleic Acids Research* 48 Issue D1, <https://doi.org/10.1093/nar/gkz925>

Zmienko A, Marszałek-Zenczak M, Wojciechowski P, Samelak-Czajka A, Luczak M, Kozłowski P, Karłowski WM, Figlerowicz M (2020) AthCNV: A map of DNA copy number variations in the *Arabidopsis thaliana* genome. *The Plant Cell* Apr 2020, tpc.00640.2019; DOI: 10.1105/tpc.19.00640

Plant Immunity

Shahid Mukhtar
smukhtar@uab.edu
University of Alabama at Birmingham, USA



The concept of growth to defense tradeoffs in plants has been known for over three decades (Coley *et al.*, 1985). Upon activation of antimicrobial or anti-herbivore defenses, plants redirect their limited resources to invest in the immune response at the cost of growth, development, reproduction, and overall yield. However, the molecular mechanisms governing this balancing act have only recently begun to be elucidated.

Upon infection with the bacterial pathogen *Pseudomonas syringae*, a massive reprogramming of transcriptional and translational activities occurs to boost the immune response while hampering growth and development. It is now well established that a small subset of mRNAs that possess upstream Open Reading Frames (uORFs) in their 5' UTRs are selectively translated in response to immune stimulation, while general translational activities are attenuated. This process is dependent on a phosphorylation of eukaryotic Initiation Factor 2B (eIF2B) by GCN2 (General Control Nonderepressible 2), a sensor kinase conserved in all eukaryotes. While the molecular mechanisms underlying growth to defense tradeoffs are complex and multifaceted, hormone crosstalk has emerged as a major player in regulating tradeoffs needed to achieve a balance.

Recently, it was shown that *Arabidopsis* GCN2 differentially contributes to pre- and post-invasive immunity against *P. syringae* through abscisic acid biosynthesis and signaling (Liu *et al.*, 2019, doi:10.1038/s42003-019-0544-x). Moreover, the construction of large scale protein-protein interaction networks not only illuminated the first layer of plant immunity but also highlighted the molecular circuitry of how plant extracellular receptors perceive growth signals vs. immune signals. These interaction patterns help to mechanistically understand how an immune signal in PTI (Pattern-Triggered Immunity) can override basic developmental and growth programs, and relay downstream messages to promote defense responses (Ahmed *et al.*, 2018, doi:10.1038/s41467-018-04632-8 ; Smakowska-Luzan *et al.*, 2018, doi:10.1038/nature25184).

Another topic that is currently gaining a lot of momentum is how the plant hosts differentiate friends from foes – specifically, how the roots and leaves discriminate between signals of beneficial vs. pathogenic microbes. This process is in a large part accomplished by the identification of receptors for microbe/pathogens-associated molecular patterns (PAMPs/MAMPs) and damage-associated molecular patterns (DAMPs) (Zhou *et al.*, 2020, doi:10.1016/j.cell.2020.01.013).

The recent advances in sequencing technology allow us to gain deeper insights into the community of leaf and root microbiota and their influence on plant growth. In parallel, *Arabidopsis* genetics provides means to identify

the important components for the host interaction with beneficial/commensal microbes (Teixeira *et al.*, 2019, doi: 10.1016/j.mib.2019.08.003). The ultimate goal of this research is to apply the resulting knowledge for agriculture to contribute food security worldwide.

In the second layer of defense, pathogen molecules or effectors are recognized by R (resistance) proteins, where NLRs (NOD-like receptors) play prominent roles. NLR biology is another fast growing field of molecular plant-microbe interactions. Both plant as well as animal NLR research was substantially boosted within the past year, and major steps were taken that will enable the community to discover new mechanisms, develop new cutting-edge technologies and to dive deeper into the fascinating world of plant immunity and plant-microbe interactions.

The solving of the first plant NLR full length protein structure by cryo-electron microscopy and the discovery of an enzymatic (NADase) activity of plant-, animal- and bacterial TIR domains are only two major discoveries of the recent year (Burdett *et al.*, 2019, doi:10.1016/j.chom.2019.07.020; Wan *et al.*, 2019, doi: 10.1126/science.aax1771; Wang *et al.*, 2019, doi: 10.1126/science.aav5870; Wang *et al.*, 2019, doi: 10.1126/science.aav5868). The primary goal of a virulent pathogen is not to interfere or suppress immune response, but to acquire nutrients, which will allow its survival, growth and multiplication, and in the long term – its evolutionary success. During effector-triggered susceptibility (ETS), pathogens utilize a suite of effectors to evade receptor-mediated recognition, suppress immune responses and acquire nutrients.

Another emerging frontier in plant immunity, namely the nutrient war between the host and pathogen has been in the limelight. Specifically, the research programs aiming to understand how pathogens can hijack the host transcriptional machinery by directly or indirectly altering the host signaling and/or biosynthetic pathways to siphon sugars and amino acids. Other very exciting developments were achieved in the field of small RNAs and their role in plant-microbe (pathogenic as well as symbiotic) interactions and their potential cross-kingdom trafficking via so called exosomes or exosomal membranes/vesicles (Vincent *et al.*, 2019, doi:10.3389/fpls.2019.01626).

Finally, new biochemical (Bio-ID labelling) and genetic/genome-editing (optimized CRSIPR/CAS) tools have been developed and optimized for plant research (Khan *et al.*, 2018, doi:10.1038/s41598-018-27500-3; Cui *et al.*, 2019, doi:10.1186/s13007-019-0500-2; Ahmad *et al.*, 2020, doi:10.1002/jcp.29052).

Recently developed Open Tools and Resources for Arabidopsis Researchers

- ProteomicsDB and ATHENA databases (Mass-spectrometry-based draft of the Arabidopsis proteome – Mergner *et al.*, 2020 Nature, 579: 409-414)
- EffectorK (www.effectork.org) – (EffectorK, a comprehensive resource to mine for pathogen effector targets in the Arabidopsis proteome – Gonzalez-Fuente *et al.*, 2020 bioRxiv)
- *P. syringae* Type III Effector Compendium (PsyTEC) – (The pan-genome effector-triggered immunity landscape of a host-pathogen interaction – Laflamme *et al.*, 2020 Science)
- Prime genome editing in rice and wheat – Lin *et al.*, 2020 Nature Biotechnology
- Super-Agrobacterium ver. 4: Improving the Transformation Frequencies and Genetic Engineering Possibilities for Crop Plants doi:10.3389/fpls.2019.01204
- New biosensor for detection of ethylene gas in fruits and leaves doi:10.1038/s41467-019-13758-2

Recent or Future activities of Subcommittee members.

The members of plant immunity subcommittee organized workshop/conference sessions, and presented talks and posters at various international conferences in 2019. These include 2019 IS-MPMI XVIII Congress, in Glasgow, Scotland, International workshop of plants and nematodes interaction” at the RIKEN Yokohama, Japan institute, Systems Biology and machine learning workshop at PAG, San Diego, “Plant Signaling in Abiotic and Biotic Stress”, Columbia, MO (May 2019), Southern Section of American Society of Plant Biologists (SS-ASPB) in March 2019 (Clemson University, SC, USA), and NSF-sponsored workshop “Reintegrating Biology Jumpstart” (Atlanta, December 2019).

A subcommittee member in collaboration with other scientists from the community developed valuable tools. This includes (1) a new biosensor for ethylene gas and successfully detected ethylene production in fruits and also in Arabidopsis leaves during PAMP-triggered immunity and effector-triggered immunity (Nat Commun. doi: 10:5746, 2019); and (2) Super-Agrobacterium that gives higher transformation efficiency in plants by introducing both the ACC deaminase (acdS) and GABA transaminase (gabT) genes, whose resultant enzymes degrade ACC, the ethylene precursor, and GABA, respectively (Front Plant Sci. doi: 10:1204, 2019). The subcommittee members have also organized laboratory workshops on training of high school teachers in plant biology and plant blindness as well as hands on training to minority students in plant pathology.

In summary, the combined efforts of subcommittee members have contributed tremendously in the field of plant immunity, enhanced national and international

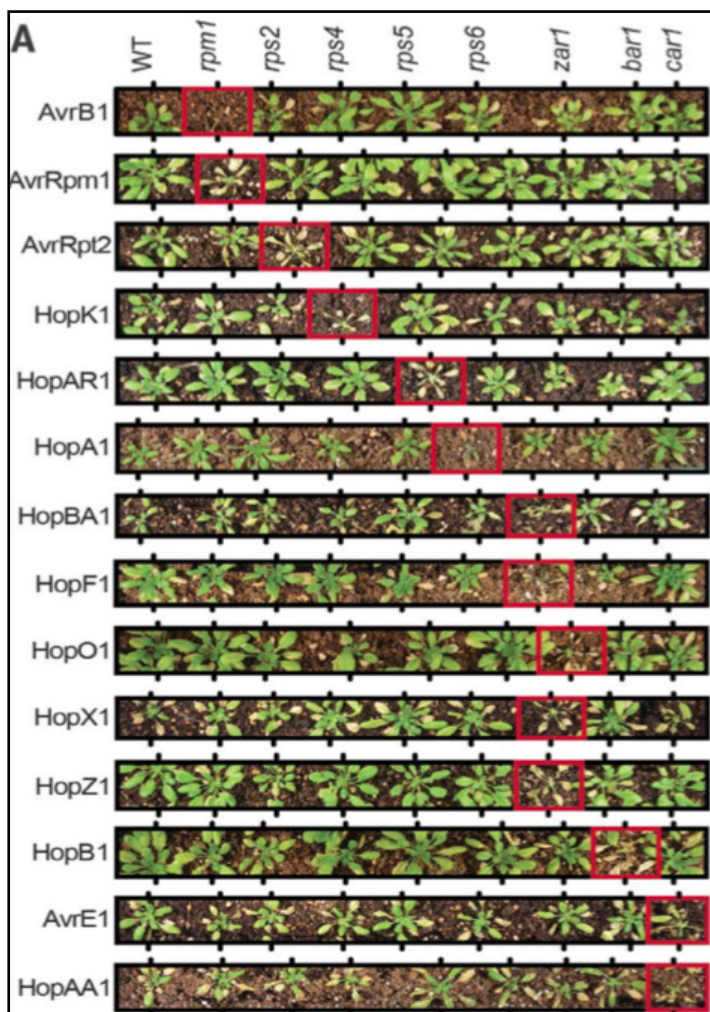


Figure 6. NLR specificity for each ETI-eliciting effector family. (A) Representative plant images after bacteria expressing each ETI-eliciting effector (left) were spray-inoculated onto wild-type (WT) or mutant *A. thaliana* Col-0 plants lacking a single NLR (top). Red boxes indicate loss-of-ETI interactions (HopF1r was formerly HopF2a).

collaborations, contributed in the development of novel and innovative tools, and participated in outreach activities.

Conferences, Workshops and Training events

- 4th International Conference “Plant Biotic Stresses & Resistance Mechanisms IV” at the Technische Universität of Vienna (19-20 February 2020)
- International Congress of Nematology (ICN) in 2020
- International workshop of the interaction of *Arabidopsis* and root-knot nematodes at RIKEN (2020)
- PCBI - Plant Cell Biology International Meeting, June 1 - 5, 2020, at OAC, Chania, Crete, Greece (postponed to 2021 due to COVID-19 pandemic)
- PAG 2021, organize systems biology and machine learning workshop.

Selected Publications

Laflamme, B., Dillon, M.M., Martel, A., Almeida, R.N.D., Desveaux, D. and Guttman, D.S. (2020) The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. *Science*, 367, 763-768

Vong, K., Eda, S., Kadota, Y., Nasibullin, I., Wakatake, T., Yokoshima, S., Shirasu, K. and Tanaka, K. (2019) An artificial metalloenzyme biosensor can detect ethylene gas in fruits and *Arabidopsis* leaves. *Nat Commun*, 10, 5746.

Wan, L., Essuman, K., Anderson, R.G., Sasaki, Y., Monteiro, F., Chung, E.H., Osborne Nishimura, E., DiAntonio, A., Milbrandt, J., Dangl, J.L. and Nishimura, M.T. (2019) TIR domains of plant immune receptors are NAD(+)-cleaving enzymes that promote cell death. *Science*, 365, 799-803.

Wang, J., Wang, J., Hu, M., Wu, S., Qi, J., Wang, G., Han, Z., Qi, Y., Gao, N., Wang, H.W., Zhou, J.M. and Chai, J. (2019) Ligand-triggered allosteric ADP release primes a plant NLR complex. *Science*, 364.

Zhou, F., Emonet, A., Denervaud Tendon, V., Marhavy, P., Wu, D., Lahaye, T. and Geldner, N. (2020) Co-incidence of Damage and Microbial Patterns Controls Localized Immune Responses in Roots. *Cell*, 180, 440-453 e418

Proteomics

Joshua Heazlewood (Chair)
jheazlewood@unimelb.edu.au
University of Melbourne



<http://www.masc-proteomics.org/>

The proteomics subcommittee of MASC has tasked itself with the dissemination and visualization of protein-associated data from studies that have employed *Arabidopsis*. These started with data generated by proteomic surveys, but has extended to protein-protein interactions, subcellular localizations and post-translational modifications. The initial development of *Arabidopsis* community portals mostly focused on genomics, genetics and genes. This was not surprising given the community efforts to sequence the genome and develop molecular genetic resources. A very similar process occurred in other reference organisms such as yeast and *Drosophila*.

With the development of mass spectrometry at the start of the 21st century and the availability of high-quality genome sequence data, a great deal of information about *Arabidopsis* proteins was being generated. As indicated, the *Arabidopsis* community portals (The *Arabidopsis* Information Resource and Munich Information Center for Protein Sequences) were mainly compiling gene-centric information. As a result, a number of groups working in the area of proteomics started to create data repositories

that sought to capture protein-based information generated in-house and also data generated by colleagues. Much of these initial large-scale proteomic datasets resided in supplemental material that was impenetrable to the community. Thus the rise of proteomic-based portals started to occur by the mid 2000s. The researchers developing these databases became the nucleus of the proteomics subcommittee of MASC.

Recently developed Open Tools and Resources for Arabidopsis Researchers

The subcommittee has been committed to the task of proteomics data centralization and visualization. Over the past year, updates have been made to various proteomic data repositories, see list at <http://www.masc-proteomics.org/>. Subcommittee member Klaas Van Wijk was successful in obtaining an NSF-funded Plant Peptide Atlas project that will see plant proteomic data made available through the Institute for Systems Biology, Peptide Atlas portal (<http://www.peptideatlas.org/>). The objective of the Peptide Atlas is to enable the annotation of eukaryotic genomes through a thorough validation of expressed proteins.

Recent or Future activities of Subcommittee members

The members of the proteomics subcommittee (MASCP) maintain a range of online resources with a focus on collating data associated with Arabidopsis proteins. Many of these resources house extensive proteomic data from experiments conducted on Arabidopsis and other species. As the volume of data increases, some discussions about the value of these repositories has occurred. The subcommittee is examining how best to port proteomic data into ePlant e.g. abundance, protein evidence and post-translational modifications. A number of significant updates and surveys of the Arabidopsis proteome has occurred in 2019 / 2020 (see selected publications). The subcommittee intends to look at how these data can be incorporated into current community portals.

Selected Publications

McWhite CD, Papoulas O, Drew K, Cox RM, June V, Dong OX, Kwon T, Wan C, Salmi ML, Roux SJ, Browning KS, Chen ZJ, Ronald PC, Marcotte EM (2020) A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. *Cell*. 16;181(2):460-474

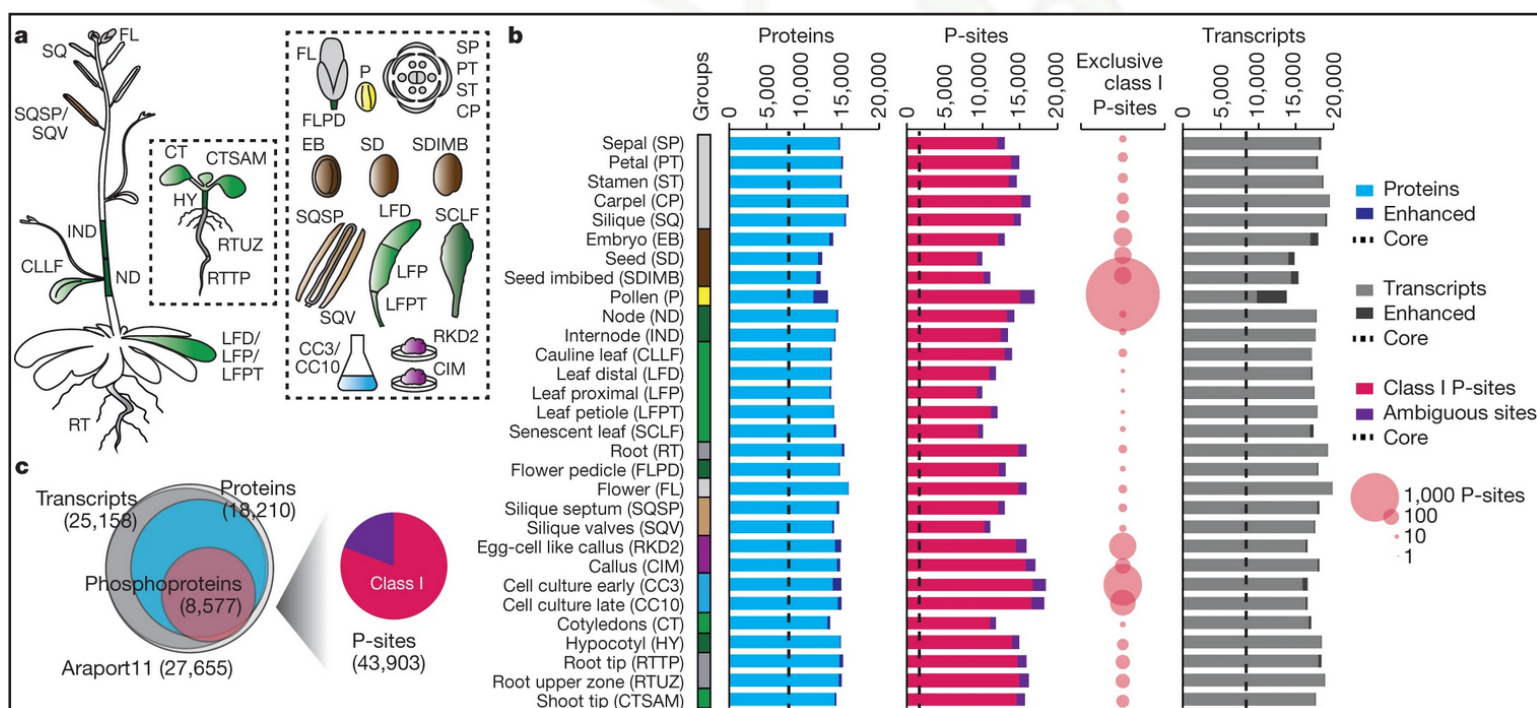


Figure 7. Schematic of tissue samples analysed, coloured according to morphology group (abbreviations defined in b): flower (light grey); seed (dark brown); pollen (yellow); stem (dark green); leaf (light green); root (dark grey); fruit (light brown); callus (magenta); cell culture (blue). b, Number of identifications at the protein, P-site and transcript levels for all tissues (n = 1 measurement per tissue). Dashed lines indicate the number of core proteins, P-sites or transcripts detected in all tissues. Tissue-enhanced proteins or transcripts are marked by a darker colour. P-sites with high-confidence amino acid localization (class I sites; more than 0.75 localization probability) are shown in pink; ambiguous site localizations are in purple. The number of P-sites exclusively detected in one tissue is shown by circles. c, Total number and overlap of identified gene loci in the transcriptome, proteome and phosphoproteome datasets compared with Araport11 (left), and the total number of identified P-sites and the proportion of class I sites (right).

Mergner J, Frejno M, List M, Papacek M, Chen X, Chaudhary A, Samaras P *et al* (2020) Mass-spectrometry-based draft of the Arabidopsis proteome. *Nature* 579: 409-414

Millar AH, Heazlewood JL, Giglione C, Holdsworth MJ, Bachmair A, Schulze WX (2019) The Scope, Functions, and Dynamics of Posttranslational Protein Modifications. *Annual Review of Plant Biology* 70: 119-151

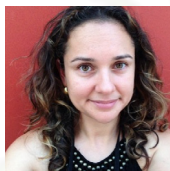
Niehaus M, Straube H, Kunzler P, Rugen N, Hegermann J, Gialvalisco P, Eubel H, Witte CP, Herde M (2020) Rapid Affinity Purification of Tagged Plant Mitochondria (Mito-AP) for Metabolome and Proteome Analyses. *Plant Physiol* 182: 1194-1210

Romero-Barrios N, Monachello D, Dolde U, Wong A, San Clemente H, Cayrel A, Johnson A, Lurin C, Vert G (2020) Advanced Cataloging of Lysine-63 Polyubiquitin Networks by Genomic, Interactome, and Sensor-Based Proteomic Analyses. *Plant Cell* 32: 123-138

Zhang H, Liu P, Guo T, Zhao H, Bensaddek D, Aebersold R, Xiong L (2019) Arabidopsis proteome and the mass spectral assay library. *Sci Data* 6: 278

Systems and Synthetic Biology

Siobhan Brady (Chair)
sbrady@ucdavis.edu
UC Davis, USA



Research related to our subcommittee has been highly active over the last year, with many more exciting findings on the way. Proteome, protein-protein and molecular interactions are now easily identifiable and searchable through the Arabidopsis Interactions Viewer; <http://bar.utoronto.ca/interactions2/> (Dong *et al.*, 2020); the Loop system of plasmids are open-source and scalable and will enable rapid, modular and multiplexed vector construction for synthetic biology (Pollak *et al.*, 2019), and the TuxNet tool enables the general Arabidopsis community to process RNAseq data and infer gene regulatory interactions and networks (Spurney *et al.*, 2020).

Our sub-committee hosted our first spectacular conference (iPSB) in Roscoff, France in 2018, and culminated in a special issue of *Molecular Plant* (volume 12, issue 6). The 2nd edition of this conference will be held in 2021 in Venice, Italy, and the CSHL Network Biology conference will be held in 2021. Several workshops in this subject area were convened in the past year and have resulted in two perspective papers concerning systems and synthetic biology and its future (Argueso *et al.*, 2019; Wurtzel *et al.*, 2019). Finally, Arabidopsis research concerning systems and synthetic biology include the first systematic detection of chromatin-based regulatory elements in plants (Lu *et al.*, 2019), mapping temporal regulatory interactions in the early

N response (Brooks *et al.*, 2019), stem-cell specific gene networks (Clark *et al.*, 2019), the use of single cell sequencing, gene networks and mathematical modeling to elucidate a switch in xylem cell differentiation (Turco *et al.*, 2019) and an overview of how to use quantitative systems biology approaches to unravel the complex network of genetic, microbial and metabolic interactions occurring during microbe-host (plant) interactions.

Recently developed Open Tools and Resources for Arabidopsis Researchers

Dong S, Lau V, Song R, Ierullo M, Esteban E, Wu Y, Sivieng T, Nahal H, Gaudinier A, Pasha A, Oughtred R, Dolinski K, Tyers M, Brady SM, Grene R, Usadel B, Provart NJ. (2019) Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. *Plant Physiology*. 179(4): 1893-1907.

Pollak B, Cerda A, Delmans M, Álamos S, Moyano T, West A, Gutiérrez RA, Patron NJ, Federici F, Haseloff J. (2019) Loop assembly: a simple and open system for recursive fabrication of DNA circuits. *New Phytologist*. 222(1):628-640.

Spurney RJ, Van den Broeck L, Clark NM, Fisher AP, de Luis Balaguer MA, Sozzani R. (2020). Tuxnet: a simple interface to process RNA sequencing data and infer gene regulatory networks. *Plant Journal*. 101(3):716-730.

Recent or Future activities of Subcommittee members.

A special Issue of *Molecular Plant* – “Plant Systems Biology” Volume 12, Issue 6, p727-892; with editorial contribution from Pascal Falter-Braun, Siobhan Brady, Rodrigo A. Gutierrez, Gloria M. Coruzzi, Gabriel Krouk

* Falter-Braun P, Brady S, Gutiérrez RA, Coruzzi GM, Krouk G. (2019). iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. *Molecular Plant* 12(6): 727-730

*The 2nd International Conference on Plant Systems Biology; September 21-25 2020 – due to COVID-19 concerns, please refer to the website for up-to-date information: <https://meetings.embo.org/event/20-plant-systems>

Conferences, Workshops and Training events

- OpenPlant Forum 2019 – Cambridge, UK <https://www.openplant.org/forum>

- 3rd International Conference on Plant Synthetic Biology, Bioengineering and Biotechnology, October 2019, Cambridge, UK <https://www.aiche.org/sbe/conferences/international-conference-on-plant-synthetic-biology-and-bioengineering/2019>

- Plant Synthetic Biology August, 2019, San Jose, USA <https://plantsyntheticbiology.org>

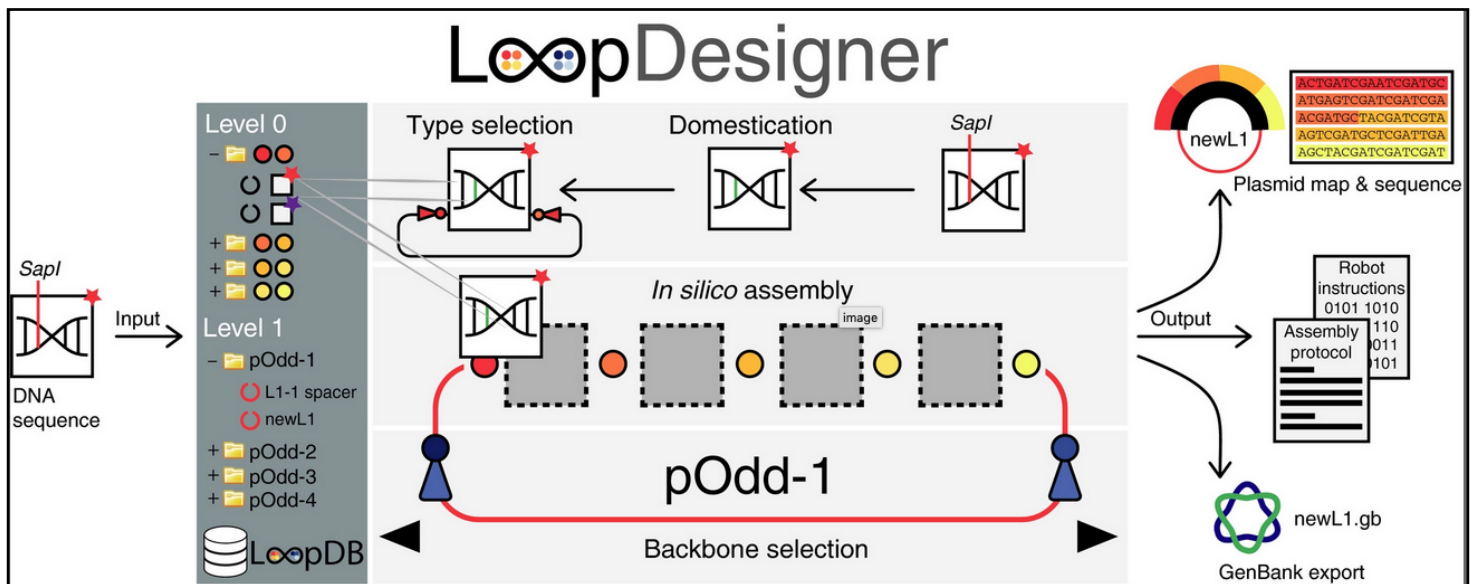


Figure 8. Design automation. A DNA sequence is submitted to LoopDesigner, which screens for BsaI and SapI sites and domesticates them to silent mutations where possible. A part type is specified for the assembly schema to save the part to the database library. To perform an in silico assembly, a receiver plasmid is selected which displays the compatible parts that can be placed in the current position of the assembly schema. As parts are included, the next compatible parts are displayed. When the assembly schema finds that all the parts required to complete the assembly are selected, the assembly simulation is performed. Then, LoopDesigner outputs the resulting plasmid map with its concurrent highlighted sequence and a protocol for Loop Type IIS reaction setup or export of GenBank sequence. Instructions to robots can be outputted if an API is provided with the required information (plasmid positions, ID mappings, robot functions) to produce the concurrent instruction file using Python scripting. The assembled part is then saved into the part library database for further assembly.

- NSR ERC Planning Workshop (2019); as a result of RiseEnAg: an Engineering Research Center for Rapid Innovations in Systems Engineering and Agricultural Sustainability (NSF EEC #1840440)

Planned for Coming Years:

- CSHL Systems Biology: Networks (2021). EMBO Conf. European Network Biology Conference, From Networks to Modelling: Hinxton, UK April 21-23 (2020). <https://www.ebi.ac.uk/training/events/2020/2nd-european-network-biology-conference-networks-modelling>
- 2nd International Plant Systems Biology Conference, Venice, September 21-25 (2020) <https://meetings.embo.org/event/20-plant-systems>

Products from Past Workshops:

Argueso CT, Assmann SM, Birnbaum KD, Chen S, Dinneny JR, Doherty CJ, Eveland AL, Friesner J, Greenlee VR, Law JA, Marshall-Colón A, Mason GA, O'Leary R, Peck SC, Schmitz RJ, Song L, Stern D, Varagona MJ, Walley JW, Williams CM. (2019) Directions for research and training in plant omics. *Plant Direct*. 3(4), e00133.

Wurtzel ET, Vickers CE, Hansn AD, Millar AH, Cooper M, Voss-Fels KP, Nikel PI, Erb TJ. (2019) Revolutionizing agriculture with synthetic biology. *Nature Plants*. 5(12):1207-1210

Selected Publications

Brooks MD, Cirrone J, Pasquino AV, Swift J, Alvarez JM, Mittal S, Juang C-L, Varala K, Gutiérrez RA, Krouk G, Shasha D, Coruzzi GM. (2019) Network Walking charts transcriptional dynamics of nitrogen signaling by integrating validated and predicted genome-wide interactions. *Nature Communications*. 10(1):1569.

Clark NM, Buckner E, Fisher AP, Nelson EC, Nguyen TT, Simmons AR, de Luis Balaguer MA, Butler-Smith T, Sheldon PJ, Bergmann DC, Williams CM, Sozzani R. (2019) Stem-cell-ubiquitous genes spatiotemporally coordinate division through regulation of stem-cell-specific gene networks. *Nature Communications*. 10:5574.

Lu Z, Marand AP, Ricci WA, Ethridge CL, Zhang X, Schmitz RJ. (2019) The prevalence, evolution and chromatin signatures of plant regulatory elements. *Nature Plants*. 5:1250-1259.

Rodriguez PA, Rothballer M, Chowdhury SP, Nussbaumer T, Gutjahr C, Falter-Braun P. (2019). *Systems Biology of Plant-Microbiome Interactions*. *Molecular Plant*. 12(6):804-821.

Turco GM, Rodriguez-Medina J, Siebert S, Han D, Valderamma-Gómez MÁ, Vahldick H, Shulse CN, Cole BJ, Juliano CE, Dickel DE, Savageau MA, Brady SM. (2019). Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. *Cell Reports*. 28(2):342-351.