Plantae Presents How to read a scientific paper Featuring Mary Williams and Michelle Facette



Tuesday, January 17, 2023 8:00 AM PST | 11:00 AM EST | 4:00 PM GMT | 12:00 AM Beijing **Recording available at:** https://plantae.org/plantaepresents-how-to-read-a-scientific-paper/

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American Society of Plant Biologists

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Webinar Logistics

Technical issues?

Email Jayson Padilla at jpadilla@aspb.org or let us know in the chat/questions box

If you are currently unable to hear any audio, check your internet speed or try dialing in.





Tuesday, January 17, 2023 8:00 AM PST | 11:00 AM EST | 4:00 PM GMT | 12:00 AM Beijing

Speakers:

- Dr. Mary Williams, Features Editor @ The Plant Cell and Plant Physiology
- Dr. Michelle Facette, Assistant Professor @ U Mass Amherst

Moderator:

Xiaohui Li, PhD Candidate @ Purdue University West Lafayette





Outline for the webinar:

- Speaker introduction, by Xiaohui Li
- How to read a scientific paper, by Dr. Mary Williams
- Case study of the selected paper, by Dr. Michelle Facette
- ♣ Q & A
- Concluding remarks and useful links for further study

Attendees:

Please type your questions in the Q&A box 🔍 (问答 / Preguntas y respuestas) anytime during the webinar.



Speaker: Mary Williams, PhD

Features Editor for *The Plant Cell* and *Plant Physiology*

Principal Investigator of the NSF-funded LEAPS: RCN: ROOT & SHOOT (Rooting Out Oppression Together and SHaring Our Outcomes

Transparently)

Mary Williams spent the first half of her professional career as a professor at a small liberal arts college (Harvey Mudd College) during which time she was chair of the ASPB Education Committee. In 2009 she joined the staff at ASPB.

She's active on <u>Twitter</u> and <u>Mastodon</u> as @PlantTeaching, and her greatest joy comes from seeing the spark of recognition when she helps someone understand a difficult concept, whether about photosynthesis or the effects of systemic racism.





How to read a scientific paper

Why are you reading this paper?



Curiosity

As a class assignment

To advance your research

Mary Williams, PhD



Features Editor, *Plant Physiology* and *The Plant Cell*

https://genomic.social/@PlantTeaching/

As a peer-reviewer



Some of the questions you'll seek to answer when you read a paper



What is the **question**? What new insights and applications come from the work?

What **methods** are used and are they appropriate?



What **results** are presented and how do the authors interpret their data?

> Do the **conclusions** fit our current framework of understanding?







Anatomy of a scientific paper



TITLE

AUTHOR INFORMATION

ABSTRACT: A summary of the study and findings, written by the author.

INTRODUCTION: A statement of what is currently known about the study subject that articulates the questions being investigated. It cites other scholarly works, lays the foundations for the study, and sometimes states a hypothesis to be tested.

RESULTS: A description of the research conducted and the results obtained.

Results are presented as tables, large datasets, and figures, which can include graphs, videos, diagrams, and photographs.

Some papers include additional supporting data as a supplement.

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-				_

Figure legend

DISCUSSION: An analysis and interpretation of the data presented that integrates the new information with prior findings, states the implications of the work, and sometimes generates new hypotheses tobe tested.

METHODS: A description of how the studies were conducted, with sufficient detail so that others can repeat them exactly.

REFERENCES: The list of the articles cited in the paper that provide information on the research topic and the methods used.



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METHODS: A description of how the studies were conducted, with sufficient detail so that others can repeat them exactly.

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How I read most papers

- 1. Title
- 2. Abstract
- 3. Intro (skim)
- 4.
- 5. Results – focus on figures
- 6.
- methods
- - the results or methods

Summary figure (if available) Discussion – referring back to figures

7. Only occasionally do I read the

8. I don't "read" the list of references, but use it as a source for additional background information

9. Sometimes I look at supplemental data to get more information about



Some of the questions you'll seek to answer when you read a paper



Qualitative data: Usually photographs (formerly drawings). Plants, tissues, cells, colonies





Nehemiah Grew's Anatomy of Plants (1680)













Often qualitative data can be quantified



Quantitative data: Measurements, counts, dose-response curves, transcript abundance, etc.





+ drug

- drug

Students T-Test x-axis: 2 categories (- or + drug) y-axis: continuous (tumor size)



Regression Analysis

x-axis: continuous (drug dose) y-axis: continuous (tumor size)



Chi-Square Test x-axis: >2 categories (drug A, B, etc.) y-axis: >2 categories (dead or alive)



ANOVA x-axis: >2 categories (drug A, B, etc.) y-axis: continuous (tumor size)





Relative expression level (log₂FC)

Data are presented so that you can examine the experimental results and see if you agree with how they are interpreted.

Check the statistical tests too.





Summary figures and data, summary models:









Supplemental figures and data:

Supplemental data

The following materials are available in the online version of this article.

Supplemental Figure S1. Toxicity of secreted proteins and other compounds from Botrytis rely on protein activity.

Supplemental Figure S2. Transient expression control of candidates from Botrytis.

Supplemental Figure S3. Expression control of truncated Hip1 derivatives and cysteine mutants.

Supplemental Figure S4. Protein expression and structure prediction of Hip1.

Supplemental Figure S5. Hip1 toxicity is unaltered when fused to GFP but dependence on the presence of a SP.

Supplemental Figure S6. Virus-induced gene silencing of BAK1 and SOBIR1 in *N*. benthamiana.

Supplemental Figure S7. Analysis of Botrytis hip1 overexpression strains.

Supplemental Figure S8. Secondary lesion formation by Botrytis.

Supplemental Table S1. List of tested candidate genes.

Supplemental Table S2. Alignment of Hip1 homologs.

Supplemental Table S3. Primers used in this study.



Supplemental Figure S6. Virus induced gene silencing of BAK1 and SOBIR1 in N. benthamiana. (A) Control plants in comparison to BAK1 silencing (B) 20 days' post TRV1/TRV2 infiltration. RT-qPCR of BAK1 (C) and SOBIR1 (D) silenced plants. The control (TRV2:GUS) was set to hundred percent and the experiment carried out three times (n=3). Bar graph shows the mean of three biological replicates with the standard error. The images were digitally extracted for better comparison. Scale bars = 2 cm.

Supplemental table S1. List of tested candidate genes.

Candidate	Gene Accession	Function [PFAM output/assigned]	Fold change [in vitro vs infection]	Size [kDa]
C1	Bcin01g06010	Glycosyl hydrolases family 16	-2.1	40
C2	Bcin02g07100	GDSL-like Lipase / Acylhydrolase family	12.8	28
C3	Bcin03g05720	unknown	30.5	17
C4	Bcin06g06410	Fungal cellulose binding domain	165	40
C5	Bcin07g02650	Cellulase (glycosyl hydrolase family 5)	215	45
C6	Bcin14g00850	Glycosyl hydrolases family 28 / BcPG1	3.1	40
C7	Bcin15g03150	Pro-kumamolisin, activation domain / Sedolisin	3.5	60
C8	Bcin01g11160	Glycosyl hydrolases family 28 / Exopolygalacturonase	17.1	45
C9	Bcin08g00280	Serine carboxypeptidase	12	50
C10	Bcin08g02970	Pectinesterase / BcPME1	2.4	38
C11	Bcin09g04790	Glycosyl hydrolases family 39	47	52
C12	Bcin11g06400	unknown	-2	15

figures ∞

tables



The peer review process (classic and new)





If available, look at the peer reviews or editorial decision letter

Qualified reviewers each evaluate the paper independently





Then, in the **post-review** *consultation*, the reviewers discuss their reviews, and work with the editor to write a response with recommendations to the author

REPORT:(The report shows the major requests for revision and author responses. Minor comments for revision and miscellaneous correspondence are not included. The original format may not be reflected in this compilation, but the reviewer comments and author responses are not edited, except to correct minor typographical or spelling errors that could be a source of ambiguity.)

We have received reviews of your manuscript entitled "S-acylated and Nuclear-Localized SOS3/CBL4 Stabilizes GIGANTEA to Regulate Arabidopsis Flowering Time under Saline Stress." Thank you for submitting your best work to The Plant Cell. The editorial board agrees that the work you describe is substantive, falls within the scope of the journal, and may become acceptable for publication, pending revision and potential re-review.

TPC2021-RA-00153 1st Editorial decision – revision requested Mar. 31, 2022



The peer review process (classic and new)







https://elifesciences.org/articles/83889











Why you should read scientific papers



Reading papers gives you the opportunity to understand the world. Be open minded, expand your horizons. Read beyond your comfort zone!



Reading papers gives you ideas to enhance your own research. What new methods are available that could help you ask your own questions?



Reading papers as a reviewer lets you help others improve their studies, and ensures that the information that is shared with the public is sound.

Reading papers helps develop your ability to understand and analyze data. Be a detective – are the experiments solid and the data interpreted reasonably, or are important clues overlooked?





Anatomy of a scientific paper



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METHODS: A description of how the studies were conducted, with sufficient detail so that others can repeat them exactly.

REFERENCES: The list of the articles cited in the paper that provide information on the research topic and the methods used.

Case study: Reading a Primary Research Article from Plant Physiology

This case study examines a recent article published in the journal Plant Physiology. The full article is appended to this PDF. Because of space constraints, only the major points from the paper are covered in the case study, and the biochemical pathway is presented in simplified form.





Centre, Norwich NR4 7UH, United Kingdom, and Institute of Biological, Environmental, and Rural Science berystwyth University, Gogerddan Campus, Aberystwyth, Ceredigion SY23 3EB, United Kingdom (T.H.N.E.

returnidio, the major pigments present in the progenition purple-flowered wild-type pos. These usuals, combined with the finding that the F375H gene conspectates with 1 in a genetic mapping population, strongly support our hypothesis that the 8 gene of pos-consequents to a F375H gene. The molecular characterization of genes involved in pigmentation in pos-provides

In-text citation: Full citation: is found at the end of the article

13.21) and fla-113 885. These n precurse pferol, generat in-3-plucoside be seen in a 20065 al pigmer

tation has a long history, beginning with crosses made between white- and purple-flowered varieties of gar den pea (Pisau satuwu: Knight, 1799; Mendel, 1866). Later crosses made between white-flowered P. saturation and rese-pink-flowered Pirum arresse defined two factors conferring flower color as A and B, respectively Techermak, 1911). The white flowers of pea authorganio ubibition (a) mutants lack anthocyanins and flavones (Statham et al., 1972), in accordance with the role of A as a fundamental factor for pigmentation (Tschermak 1911: De Haan, 19303. Another locus in pea, a2, similarly confers a white-flowered phenotype lacking anthocya nins and other flavonoid compounds (Marx et al., 1989) It was shown that A and A2 regulate the expression of genes encoding flavonoid biosynthetic enzymes (Harker et al., 1990; Ulman and Strommer, 1998), and recently they were identified as a basic helix-loog-helix (bHLH) cription factor and a WD40 sapeat protein, respec tively (Hellens et al., 2000). They are likely to be components of the Myb-bHLH-WD40 transcription factor emplex that regulates flavoroid biosynthesis in all plant species studied so far (Kors et al., 2005; Reman and





Speaker: Michelle Facette, PhD

Assistant Professor Department of Biology University of Massachusetts, Amherst

The Facette lab studies the cellular mechanisms of asymmetric cell division and stomatal function, primarily using maize as a model, and using a combination of microscopy, protein biochemistry and genetics approaches. Before joining the faculty of U Mass in 2018, she was an assistant professor at University of New Mexico for two years. Previously, she did her PhD work at Stanford University studying plant cell walls, and her postdoc work at UCSD focused on asymmetric cell division. She is active on Twitter as <u>@facette_lab</u>.



Be kind to yourself!



Prepare yourself:

- Get the materials
- Give yourself sufficient time
- Orient yourself (check the figures)
- Take notes
- Its okay to not understand everything the first time through!
- Get help: Google & colleagues



The Plant Cell, Vol. 32: 3408–3424, November 2020, www.plantcell.org © 2020 ASPB.

BREAKTHROUGH REPORT

Evolutionary Variation in MADS Box Dimerization Affects Floral Development and Protein Abundance in Maize

María Jazmín Abraham-Juárez,^{a,b,1} Amanda Schrager-Lavelle,^{a,c,1} Jarrett Man,^a Clinton Whipple,^d Pubudu Handakumbura,^{a,e} Courtney Babbitt,^a and Madelaine Bartlett^{a,2}

https://academic.oup.com/plcell/article/32/11/3408/609939





Part 1: The introduction.

Do I know the background that I need to know to understand this paper?



What is the ABC(DE) model?

This paper is about B family genes.

Pay attention to petals and stamens!

Wait – what do maize flowers look like?!



Vignati, E., Lipska, M., Dunwell, J. M., Caccamo, M., & Simkin, A. J. (2022). Fruit Development in Sweet Cherry. *Plants*, *11*(12), 1531.









family." Frontiers in Plant Science 12 (2021): 635500.

How do different flowers have different morphologies?

- How do genes that are conserved across different species lead to different morphologies?
 - How do related transcription factor gene families lead to different floral morphologies?
 - How do interactions of proteins important for floral development lead to variation in morphology?
- How do variants of the floral B class gene, STERILE TASSEL SILKY EAR (STS1), and its binding partners, affect maize floral development?





Part 2: The results (aka Figures and Supplemental Data, with methods)





Figure 1. B-Class Dimerization Has Subtle Effects on Floral Development in Maize.

Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408–3424, https://doi.org/10.1105/tpc.20.00300

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heterodimerizes rescues

homodimerizes also rescues!

What did they do?

>sts1 mutants do not have stamens or lodicules (petals)

Made transgenic plants that express different versions of STS1-YFP.

Do these STS1 versions both "rescue" the mutant phenotype? **Do they look the same?**





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Figure 1 conclusions:

The B class gene STS1 is important for anther development.

STS1 can partner with and function with SI1, another B class gene, or itself, and make relatively normal flowers

BUT those flowers show some variation in morphology (anther size). and the expression domains are slightly different.





How do different flowers have different morphologies?

- How do genes that are conserved across different species lacksquarelead to different morphologies?
 - How do related transcription factor gene families lead to •
 - different floral morphologies?
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- How do variants of the floral B class gene, STERILE TASSEL SILKY EAR (STS1), and its binding partners, affect maize floral development?



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Figure 1 conclusions:

The B class gene STS1 is important for anther development.

STS1 can partner with and function with SI1, another B class gene, or itself, and make relatively normal flowers

BUT those flowers show some variation in morphology (anther size). and the expression domains are slightly different. What is the next question?

STS1 is a transcription factor. Do the genes expressed in flowers change when STS1 homo- or hetero-dimerizes?





Figure 2. B-Class Dimerization Remodels Transcription in Developing Tassel Flowers.

Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408–3424, https://doi.org/10.1105/tpc.20.00300

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What do you do when there is an unfamiliar graph?





Figure 2. B-Class Dimerization Remodels Transcription in Developing Tassel Flowers.

Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408–3424, https://doi.org/10.1105/tpc.20.00300

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Check the text and the legend. **These are RNA-seq data!**

What was the question? Do the genes expressed in flowers change when STS1 homo- or hetero-dimerizes?







Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408-3424, https://doi.org/10.1105/tpc.20.00300

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What do you do when there is an unfamiliar graph?

What is the question being asked? How does it tie into the "big picture" question?

- Check the legend/text headings.
- Check the axes!
- Refer to the methods.
- Google is your friend...
- Its okay to ask for help! (Be kind to yourself)

Sometimes you might not "get it" all. Try at least to figure out what the question is the experiment addresses, and how it relates to the big picture.



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Figure 2 conclusions:

STS1-HOM and STS1-HET result in different genes being expressed. STS1-HOM seems to have *more* differentially expressed genes.

WAIT!! What did figure 1 say about STS1-HOM and **STS1-HET** again?



Figure 1 conclusions:

STS1 can partner with and function with SI1, another B class gene, or itself, and make relatively normal flowers.

BUT those flowers show some variation in morphology





Figure 2 conclusions:

STS1-HOM and STS1-HET result in different genes being expressed. STS1-HOM seems to have *more* differentially expressed genes.

How are they different??

"Big data" like transcriptomics and proteomics are not always easy to understand from a simple figure. The text can really help here.

In the text:

"These GOterms, specific to STS1-HOM, were almost all related to chromatin assembly and protein modification."

Nitty gritty details for experts: Check the supplemental data.



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What did we learn so far?

- STS1 can function as a homodimer (engineered) or a heterodimer (wildtype)
- Different dimerization leads to subtly different floral morphologies. •
- Different dimerization leads to different gene expression. •

What about the protein-protein interactions? How are they different? Figure 3!





Figure 3. B-Class Dimerization Affects Protein Abundance and Protein Complex Assembly in Developing Tassels.

Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408–3424, <u>https://doi.org/10.1105/tpc.20.00300</u>

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Conclusions from Figure 3:

- STS1-HET and STS1-HOM have overlapping, but also distinct, binding partners.
- STS1-HOM protein is more abundant, but STS-HET RNA is more abundant
 - implies regulation on the protein level
- Both STS1-HET and STS1-HOM are ubiquitinated.



Part 3: The discussion

Integration of the results -from within the paper -from across the field Is there a model? (Its okay to draw your own!)





Figure 4. An Activation-Degradation Model for the Consequences of Differential B-Class Dimerization.

Plant Cell, Volume 32, Issue 11, November 2020, Pages 3408–3424, <u>https://doi.org/10.1105/tpc.20.00300</u>

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Did the authors answer the questions? What is outstanding? What do YOU want to know next? Are there any techniques you are still confused by?

Are there any holes? Are all the assumptions correct? Could the data be interpreted another way? (Check those methods!)

Check:

In a nutshell (in the Plant Cell): good for next steps! Are there reviews available? What is in supplemental data you may have missed? Check Google Scholar – what have the authors done next? Who has cited this?

Do you want to re-read the earlier figures, now you "know" the story? Talk about it with colleagues!



Be kind to yourself!



Moderator: Xiaohui Li

PhD Candidate

Department of Botany and Plant Pathology Center for Plant Biology Purdue University, West Lafayette

Xiaohui Li is a cell biologist who occasionally do some coding. He is currently studying the mechanism and regulation of the exocytosis process in plant cells, using a combination of quantitative cell biology, chemical genetics and computational biology approaches. Beyond that, he has broad interests in plant biology, including cell dynamics, evolution and hostmicrobe interactions. Xiaohui is now serving as a Plantae Fellow and can be reached on Twitter as @Xiao_hui_Li.





Attendees:

Please type your questions in the Q&A box **户** (问答 /

Preguntas y respuestas).





Useful links

How to Read a Scientific Paper? By Mary Williams

https://blog.aspb.org/how-to-read-a-scientific-paper-and-case-study-reading-a-plant-physiology-article/ https://blog.aspb.org/wp-content/uploads/2016/08/HowtoReadScientificPaper.pdf

Navigating a Scientific Paper, By ASPB Plantae Fellows Rose McNelly and Shiqi Zhang https://plantae.org/navigating-a-scientific-paper/

Plantae Blogs https://plantae.org/plantae-blog/

Plantae Presents

https://plantae.org/education/plantae_presents/

