

Justin W. Walley, Ph.D.

Iowa State University – Plant Pathology & Microbiology

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Education

Doctor of Philosophy, Plant Biology, 2009

University of California, Davis, CA

Master of Science, Botany, 2005

Miami University, Oxford, OH

Bachelor of Science, Biology, 2001

Mount Union College, Alliance, OH

Professional Experience

- 2020-Present Associate Professor, Department of Plant Pathology & Microbiology, Iowa State University
- 2015-2020 Assistant Professor, Department of Plant Pathology & Microbiology, Iowa State University
- 2009-2014 Postdoctoral Scholar, Division of Biological Sciences, University of California - San Diego (UCSD)
- 2004-2009 Graduate Student, Department of Plant Biology, University of California - Davis (UCD)
- 2001-2004 Graduate Student, Department of Botany, Miami University (Miami U)

Grants

- 2020-2023 Roles of Auxin Pathways Driving Maize Root Growth. USDA-NIFA. \$450,000
(Awarded to PI Kelley and CoPI Walley)
- 2018-2022 Elucidation of roles that protein acetylation plays in mediating plant-pathogen interactions. NSF-PBI. \$750,000
(Awarded to Walley)
- 2018-2021 Network-Based Discovery of Brassinosteroid Regulation of Plant Growth and Stress Responses. NSF-MCB. \$900,000
(Awarded to PI Yin and CoPI Walley)
- 2018-2021 Development of novel phenomics tools and approaches to study Northern Corn Leaf Blight. ISU Plant Sciences Institute. \$225,000
(Awarded to Walley)
- 2017-2020 Crosstalk between Brassinosteroid and autophagy pathways in the regulation of plant growth and stress response. NIH-NIGMS. \$1,220,914
(Awarded to PI Yin and CoPIs Walley & Bassham)
-Walley received an additional \$88,326 supplemental equipment award in 2018.
- 2020-2021 Tools and resources to explore maize multi-omics data. USDA-ARS. \$54,170
(Awarded to Walley)

2021-2024 Regulatory Networks that Control Autophagy to Enable Environmental Stress Resilience in Plants. NSF-MCB. \$796,021
(Awarded to PI Bassham and CoPI Walley)

Fellowships and Honors

2018- Faculty Scholar, ISU Plant Sciences Institute
2013-14 San Diego Center for Systems Biology Seed Grant
2010-13 NIH Ruth L. Kirschstein NRSA Postdoctoral Fellowship
2009 ASPB-Pioneer Hi-Bred International Graduate Student Prize
2008 Russell Fellowship - most outstanding Plant Biology graduate student (UCD)
2008 Graduate Student Travel Award (UCD) – ASPB meeting invited presentation
2007-08 Trainee, NIH Training Grant in Molecular and Cellular Biology (UCD)
2007 Elsie Taylor Stocking Memorial Fellowship (UCD)
2005 Phi Sigma Biological Honor Society (UCD)
2005 Dupont Travel Award (UCD Section of Plant Biology)
2004 Sigma Xi, The Scientific Honor Society (Miami U)
2003 Phi Kappa Phi Honorary Society (Miami U)
2002 Center for Bioinformatics and Functional Genomics Fellowship (Miami U)
2002 National Garden Clubs Inc. Scholarship
2002 Garden Club of Ohio Scholarship
2001 The Shumaker Physiology Prize (MUC)
2000 Tomsich Awards for Excellence (MUC)

Editorial Board

2016-Present Scientific Reports
2018-Present Frontiers in Plant Science

Manuscript Peer Reviewer

Nature Communications, Nature Plants, PLoS Pathogens, Molecular Plant, Molecular and Cellular Proteomics, Plant Physiology, Molecular Plant Microbe Interactions, Journal of Integrative Plant Biology, Journal of Proteome Research, Proteomics, Journal of Experimental Botany, PLoS One, Plant Molecular Biology Reporter, Phytopathology, Scientific Reports, PeerJ, Data in Brief

Teaching

2019-Present GDCB544 - Introduction to Bioinformatics
2016-Present PLP692 – Molecular Biology of Plant-Pathogen Interactions
2016-Present BCBio 402 - Fundamentals of Systems Biology and Network Science
2004 Co-instructor: workshop on the use of the LI-6400 Portable Photosynthesis System Universidad Autonoma de Tamaulipas, Mexico
2001-03 Teaching Assistant (Miami University): Plant Physiology, Advanced Plant Physiology and General Biology
2000-01 Laboratory assistant, Fundamentals of Biology lab (MUC)

Leadership/Service

2019-2021	Bioinformatics & Computational Biology Graduate Program Associate Chair (Will begin a two-year appointment as program chair (DOGE) in 2021)
2019	USDA-ARS hiring Committee for a computational biologist within MaizeGDB
2019-Present	Multinational Arabidopsis Steering Committee (MASC) - Natural Variation and Comparative Genomics subcommittee
2019	Faculty search committee for a systems biologist in the GDCB department
2019-Present	Department Seminar Committee – PLPM
2018-Present	Bioinformatics & Computational Biology Graduate Program Supervisory Committee
2017	Co-Chair for the Loomis Symposium
2016-Present	Predictive Plant Phenomics (P3) Curriculum Committee
2016-Present	Department Social Committee Chair – PLPM
2008-09	Seminar Representative, Plant Biology GSA (UCD)
2007-08	Student Representative, Plant Biology Faculty Search Committee (UCD)
2007-08	Recruitment/Colloquium Chair, Plant Biology GSA (UCD)
2006-07	Annual Recruitment Organizer, Plant Biology Graduate Group (UCD)
2005-06	President, Plant Biology Graduate Student Association (UCD)
2003	Botany Student Representative, Graduate Student Association (Miami U)

Publications

* Walley Corresponding Author

- Montes C, Liao CY, Nolan TM, Song G, Clark NM, Guo H, Bassham DC, Yin Y, **Walley JW***. Interplay between brassinosteroids and TORC signaling in Arabidopsis revealed by integrated multi-dimensional analysis. *bioRxiv*. DOI: 10.1101/2021.02.12.431003
- Dash L, McEwan RE, Montes C, Mejia L, **Walley JW**, Dilkes BP, Kelley DR. *slim shady* is a novel allele of PHYTOCHROME B present in the T-DNA line SALK_015201. *bioRxiv*. DOI: 10.1101/2021.02.12.430994.
- Song G, Olatunji D, Montes C, Clark NM, Pu Y, Kelley DR, **Walley JW***. Quantitative proteomics reveals extensive lysine ubiquitination in the Arabidopsis root proteome and uncovers novel transcription factor stability states. *bioRxiv*. DOI: 10.1101/2021.01.07.425780.
- Clark NM, Nolan TM, Wang P, Song G, Montes C, Guo H, Sozzani R, Yin Y, **Walley JW***. (2020). Integrated omics networks reveal the temporal signaling events of brassinosteroid response in Arabidopsis. *bioRxiv*. DOI: 10.1101/2020.09.04.283788.
- Xiang L, Nolan TM, Bao Y, Elmore M, Tuel T, Gai J, Shah D, Huser NM, Hurd AM, McLaughlin SA, Howell SH, **Walley JW**, Yin Y, Tang L. (2020). Robotic Assay for Drought (RoAD): An Automated Phenotyping System for Brassinosteroid and Drought Response. *bioRxiv*. DOI: 10.1101/2020.06.01.128199.

- Reem NT, Chambers L, Zhang N, Abdullah SF, Chen Y, Feng G, Gao S, Soto-Burgos J, Pogorelko G, Bassham DC, Anderson CT, **Walley JW**, Zabolina OA. (2020) Post-Synthetic Reduction of Pectin Methylesterification Causes Morphological Abnormalities and Alterations to Stress Response in *Arabidopsis thaliana*. *Plants*, 9, 1558. DOI: 10.3390/plants9111558.
- Parry G et al. (2020). Current status of the multinational Arabidopsis community. *Plant Direct*. DOI: 10.1002/pld3.248.
- Song G, Montes C, Walley JW*. (2020). Quantitative profiling of protein abundance and phosphorylation state in plant tissues using Tandem Mass Tags. *Plant Proteomics: Methods and Protocols, Third Edition*. 147-156. DOI: 10.1007/978-1-0716-0528-8_11.
- Zander M, Lewsey M, Clark N, Yin L, Bartlett A, Saldierna Guzmán JP, Hann E, Langford AE, Jow B, Wise A, Nery JR, Chen H, Bar-Joseph Z, **Walley JW**, Solano R, Ecker JR. (2020). Integrated multi-omic framework of the plant response to jasmonic acid. *Nature Plants*, 6, 290-302. DOI: 10.1038/s41477-020-0605-7.
- Jia H, Song G, Werth EG, **Walley JW**, Hicks LM, Jones AM. (2019). Receptor-like kinase phosphorylation of Arabidopsis heterotrimeric G-Protein G α - subunit AtGPA1. *Proteomics*. Vol 19, 1900265. DOI: 10.1002/pmic.201900265.
- Clark N, Shen Z, Briggs SP, **Walley JW**, Kelley DR. (2019). Auxin induces widespread proteome remodeling in Arabidopsis seedlings. *Proteomics*. Vol 19, 1900199 DOI: 10.1002/pmic.201900199.
- Jiang H, Tang B, Xie Z, Nolan T, Ye H, Song G, **Walley JW**, Yin Y. (2019). GSK3-like kinase BIN2 phosphorylates RD26 to potentiate drought signaling in Arabidopsis. *The Plant Journal*. DOI: 10.1111/tpj.14484.
- Wu HL, Song G, **Walley JW**, Hsu PY (2019). The tomato translational landscape revealed by transcriptome assembly and ribosome profiling. *Plant Physiology*. Vol 181(1) 367-380. DOI: 10.1104/pp.19.00541.
- Zhang Y, Song G, Lal N, Nagalakshmi U, Li Y, Zheng W, Huang P, Branon T, Ting A, **Walley JW***, Dinesh-Kumar S (2019). TurboID-based proximity labeling reveals that UBR7 is a regulator of N NLR immune receptor-mediated immunity. *Nature Communications*. 10, Article number 3252. DOI: 10.1038/s41467-019-11202-z.
- Zhang J, Wu S, Boehlein SK, McCarty DR, Song G, **Walley JW**, Myers A, Settles AM (2019). Maize defective kernel5 is a bacterial TamB homologue required for chloroplast envelope biogenesis. *Journal of Cell Biology*. 218 (8): 2638–2658. DOI: 10.1083/jcb.201807166.
- Pu Y, **Walley JW**, Shen Z, Lang M, Briggs SP, Estelle M, Kelley D (2019). Quantitative early auxin root proteomics identifies GAUT10, a galacturonosyltransferase, as a novel regulator of root meristem maintenance. *Molecular & Cellular Proteomics*. 18 (6): 1157-1170. doi.org/10.1074/mcp.RA119.001378.
- Abdulghani M, Song G, Kaur H, **Walley JW**, Tuteja G (2019). Comparative Analysis of the Transcriptome and Proteome during Mouse Placental Development. *Journal of Proteome Research*. 18:2088–2099
- 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'Lexy R, Peck SC, Schmitz RJ, Song L, Stern D, Varagona MJ, **Walley JW**, Williams CM. (2019). Directions for research and training in plant omics: Big Questions and Big Data. *Plant Direct*. 1-16. doi: 10.1002/pld3.133.
- International Arabidopsis Informatics Consortium: Doherty C, Friesner J, Gregory B, Loraine A, Megraw M, Provart N, Slotkin RS, Town C, Assmann SA, Axtell M, Berardini T, Chen S, Gehan M, Huala E, Jaiswal P, Larson S, Li S, May S, Michael T, Pires C, Topp C, **Walley J**, Wurtele E (2019). Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. *Plant Direct*. 1–7. doi.org/10.1002/pld3.109.
- Song G, Brachova L, Nikolau BJ, Jones AM, **Walley JW*** (2018). Heterotrimeric G-protein-dependent proteome and phosphoproteome in unstimulated Arabidopsis root. *Proteomics*. 18, 1800323. doi.org/10.1002/pmic.201800323.
- Guo H, Nolan TM, Song G, Liu S, Xie Z, Chen J, Schnable P, **Walley JW**, Yin Y (2018). FERONIA Receptor Kinase Contributes to Plant Immunity by Suppressing Jasmonic Acid Signaling in Arabidopsis thaliana. *Current Biology*. 28(20): 3316-3324. doi.org/10.1016/j.cub.2018.07.078.
- Song G, Hsu PY, **Walley JW*** (2018). Assessment and refinement of sample preparation methods for deep and quantitative plant proteome profiling. *Proteomics*. 18(17), 1800220. doi.org/10.1002/pmic.201800220
- Lal NK, Nagalakshmi U, Hurlburt N, Flores R, Bak A, Sone P, Ma X, Song G, **Walley JW**, Shan L, He P, Casteel C, Fisher AJ, Dinesh-Kumar SP (2018). The receptor-like cytoplasmic kinase BIK1 localizes to the nucleus and regulates defense hormone expression during plant innate immunity. *Cell Host Microbe*. 23(4): 485-497. doi.org/10.1016/j.chom.2018.03.010.
- Walley JW***, Shen Z, McReynolds MR, Schmelz EA, Briggs SP (2018). Fungal Induced Protein Hyperacetylation Identified by Acetylome Profiling. *PNAS*. 115(1): 210-215. doi: 10.1073/pnas.1717519115
- Song G, McReynolds MR, **Walley JW*** (2017). Sample Preparation Protocols for Protein Abundance, Acetylome, and Phosphoproteome Profiling of Plant Tissues. *Plant Genomics. Methods in Molecular Biology*. pp 123–133. DOI:10.1007/978-1-4939-7003-2_9.
- Nolan TM, Brennan B, Yang M, Chen J, Zhang M, Li Z, Wang X, Bassham DC, **Walley JW**, Yin Y (2017). Selective Autophagy of BES1 Mediated by DSK2 Balances Plant Growth and Survival. *Developmental Cell*. 41: 33–46. DOI:10.1016/j.devcel.2017.03.013
- Walley JW**, Sartor RC, Shen Z, Schmitz RJ, Wu KJ, Urich MA, Nery JR, Smith LG, Schnable JC, Ecker JR, Briggs SP (2016). Integration of omic networks in a developmental atlas of maize. *Science*. 353(6301): 814–818. DOI:10.1126/science.aag1125
- Song G and **Walley JW*** (2016). Dynamic Protein Acetylation in Plant–Pathogen Interactions. *Frontiers in Plant Science*. DOI: 10.3389/fpls.2016.00421
- Walley JW**, Xiao Y, Wang J, Baidoo EE, Keasling JD, Shen Z, Briggs SP, Dehesh K (2015) Plastid-produced interorganelle stress signal MEcPP potentiates induction of the unfolded protein response in endoplasmic reticulum. *PNAS* 112(19): 6212-6217. doi.org/10.1073/pnas.1504828112.

- Walley JW** and Briggs SP (2015) Dual use of peptide mass spectra: Protein atlas and genome annotation. *Current Plant Biology* 2: 21-24. doi.org/10.1016/j.cpb.2015.02.001
- Marcon C, Malik WA, **Walley JW**, Shen Z, Paschold A, Smith LG, Peipho H, Briggs SP, Hochholdinger F (2015) A high resolution tissue-specific proteome and phosphoproteome atlas of maize primary roots reveals functional gradients along the root axis. *Plant Physiology* 168(1): 233-246. DOI:10.1104/pp.15.00138
- Castellana NE, Shen Z, He Y, **Walley JW**, Cassidy CJ, Briggs SP, Bafna V (2014) An Automated Proteogenomic Method Utilizes Mass Spectrometry to Reveal Novel Genes in *Zea mays*. *Molecular & Cellular Proteomics* 13(1): 157-167. DOI:10.1074/mcp.M113.031260
- Walley JW**, Shen Z, Sartor RC, Wu KJ, Osborn J, Smith LG, Briggs SP (2013) Reconstruction of Protein Networks from an Atlas of Maize Seed Proteotypes. *PNAS* 110(49): E4808-4817. DOI:10.1073/pnas.1319113110.
- Walley JW**, Kliebenstein DJ, Bostock RM, and Dehesh K (2013) Fatty acids and early detection of pathogens. *Current Opinion in Plant Biology* 16(4):526-520. DOI: 10.1016/j.pbi.2013.06.011
- Savchenko T, **Walley JW**, Chehab EW, Xiao Y, Kaspi R, Pye MF, Mohammed ME, Lazarus C, Bostock RM and Dehesh K (2010) Arachidonic acid: an evolutionarily conserved signaling molecule modulates plant stress signaling networks. *Plant Cell* 22(10):3193-3205. DOI:10.1105/tpc.110.073858
- Walley JW** and Dehesh K (2010) Molecular mechanisms regulating general stress signaling networks in Arabidopsis. *Journal of Integrative Plant Biology* 52(4): 354-359. DOI:10.1111/j.1744-7909.2010.00940.x
- Walley JW**, Kelley DR, Savchenko T and Dehesh K (2010) Investigating the function of CAF1 deadenylases during plant stress responses. *Plant Signaling and Behavior* 5(7):802-805. doi.org/10.4161/psb.5.7.11578
- Rowe HC, **Walley JW**, Corwin J, Chan EKF, Dehesh K and Kliebenstein DJ (2010) Deficiencies in Jasmonate-Mediated Plant Defense Reveal Quantitative Variation in *Botrytis cinerea* Pathogenesis. *PLoS Pathogens* 6(4): e1000861. DOI: 10.1371/journal.ppat.1000861
- Walley JW*** and Huerta AJ (2010) Exposure to environmentally relevant levels of cadmium primarily impacts transpiration in field-grown soybean. *Journal of Plant Nutrition* 33(10):1519-1530. doi.org/10.1080/01904167.2010.489988
- Walley JW**, Kelley DR, Nestorova G, Hirschberg DL, Dehesh K (2010) *Arabidopsis* deadenylases AtCAF1a and AtCAF1b play overlapping and distinct roles in mediating environmental stress responses. *Plant Physiology* 152(2):866-875. DOI:10.1104/pp.109.149005
- Walley JW**, Rowe HC, Xiao Y, Chehab EW, Kliebenstein DJ, Wagner D and Dehesh K (2008) The Chromatin Remodeler SPLAYED Regulates Specific Stress Signaling Pathways. *PLoS Pathogens* 4(12): e1000237. doi.org/10.1371/journal.ppat.1000237
- Walley JW**, Coughlan S, Hudson ME, Covington MF, Kaspi R, Banu G, Harmer SL, and Dehesh K (2007) Mechanical Stress Induces Biotic and Abiotic Stress Responses via a Novel cis-Element. *PLoS Genetics* 3: e172. doi.org/10.1371/journal.pgen.0030172

Chehab EW, Raman G, **Walley JW**, Perea JV, Banu G, Theg S, and Dehesh K (2006)
Rice HYDROPEROXIDE LYASES with Unique Expression Patterns Generate
Distinct Aldehyde Signatures in Arabidopsis. *Plant Physiology* 141(1):121-134.
DOI:10.1104/pp.106.078592