

Wei Zhang

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EDUCATION

September 2009-June 2016 Ph.D., Botany, Sichuan University, Chengdu, China
September 2013-September 2015 Visiting Ph.D., University of California, Davis, CA U.S.A.
September 2001-June 2005 B.S., Horticulture, China Agricultural University, Beijing, China

APPOINTMENTS

2020-Present Assistant Feature Editor, Plant Physiology
2017-Present Postdoc Fellow, Department of Plant Pathology, Kansas State University, Manhattan, KS USA
2005-2008 Agriculture Extension Agent, Beijing Multi-grass Formulation Co., Ltd., Beijing, China

AWARDS & FELLOWSHIPS

2013-2015 Chinese Government Scholarship, Sichuan University

INVITED TALKS

2020 Plant Biology Conference 2020, American Society of Plant Biologists, Washington DC, USA
2017 Department of Plant Pathology, Kansas State University, Manhattan, KS, USA.
2016 Earlham Institute, Norwich, UK

SKILL SET

Wet lab: Experience with short reads Illumina RNA-seq, ChIP-seq, HiC-seq, ATAC-seq library preparation and sequencing. Experience with high molecular weight DNA extraction for long reads Nanopore and PacBio sequencing. Experience with genomic DNA and total RNA extraction. Experience with PCR and quantitative RT-PCR. Experience with high-throughput secondary metabolites extraction and quantification by HPLC and GC-MS. Experience with gene cloning, *Agrobacterium* transformation of Arabidopsis or Nicotiana, and Nicotiana tissue culture.

Dry lab: Good at R and Command line. Familiar with Python and Jupyter notebook. Bioinformatical analysis of genomic, transcriptomic and epigenomic data and modeling multi-omics data by statistical analysis and machine learning methods.

PUBLICATIONS

- 2021 Huang J., Rowe R., Zhang W., Suelter T., Valent B., Cook D.E. (2021). CRISPR-Cas12a induced DNA double-strand breaks are repaired by locus-dependent and error-prone pathways in a fungal pathogen. **bioRxiv**. Doi: <https://doi.org/10.1101/2021.09.08.459484>
- 2021 Zhang W. (2021). One to rule both: shared histone deacetylases regulate Medicago root and nodule development. **Plant Physiology** 183 (3). doi: <https://doi.org/10.1093/plphys/kiab213>
- 2021 Zhang W. (2021). Piecing together the puzzles of allopolyploid evolution in six Brassica crops. **Plant Physiology** 185 (5). doi: <https://doi.org/10.1093/plphys/kiab079>
- 2021 Zhang W.*, Huang J.*, Cook D.E. (2021). Histone modification dynamics at H3K27 are associated with altered transcription of *in planta* induced genes in *Magnaporthe oryzae*. **PLoS Genetics** 17 (2). Doi: <https://doi.org/10.1371/journal.pgen.1009376>
- 2021 Sharma V.K., Marla S., Zheng W.G., Mishra D., Huang J., Zhang W., Morris G.P., Cook D.E. (2021). RNA silencing by CRISPR in plants does not require Cas13. **bioRxiv**. Doi: <https://doi.org/10.1101/2021.05.20.445036>
- 2020 Soltis N.E., Caseys C., Zhang W., Corwin J.A., Atwell S., and Kliebenstein D.J. (2020). Pathogen Genetic Control of Transcriptome Variation in the Arabidopsis thaliana-Botrytis cinerea Pathosystem. **Genetics** 215 (1). doi: <https://doi.org/10.1534/genetics.120.303070>
- 2020 Zhang W. (2020). Dynamic N¹-Methyladenosine in Plant Messenger RNA. **Plant Physiology** 183 (4). doi: <https://doi.org/10.1104/pp.20.00747>

- 2020 [Zhang W.](#) (2020). NLR-Annotator: A Tool for De Novo Annotation of Intracellular Immune Receptor Repertoire. **Plant Physiology** 183 (2). doi: <https://doi.org/10.1104/pp.20.00525>
- 2020 [Zhang W.](#) (2020). EPSIN1 Contributes to Plant Immunity by Modulating the Abundance of Pattern Recognition Receptors at the Plasma Membrane. **Plant Physiology** 183 (1). doi: <https://doi.org/10.1104/pp.20.00331>
- 2020 [Zhang W.](#) (2020). A GDSL Lipase Is Required for Anther and Pollen Development. **Plant Physiology** 182 (4). doi: <https://doi.org/10.1104/pp.20.00278>
- 2020 [Zhang W.](#), Wei L., Fan C., Dai T., Li S., Chen F., Xu Y. (2020). Tissue-specific accumulation profiles of phorbol esters in *Jatropha curcas* and gene induction in response to abiotic and biotic stresses. **bioRxiv**. doi: <https://doi.org/10.1101/2020.09.26.315010>
- 2019 [Zhang W.](#), Corwin J.A., Copeland D., Feusier J., Eshbaugh R., Cook D.E., Atwell S., and Kliebenstein D.J. (2019). Plant-Necrotroph Co-transcriptome Networks Illuminate a Metabolic Battlefield. **eLife** 8, e44279. doi: <https://doi.org/10.7554/eLife.44279.001>
- 2018 Atwell S., Corwin J.A., Soltis, N., [Zhang W.](#), Copeland D., Feusier J., Eshbaugh R., and Kliebenstein D.J. (2018). Resequencing and association mapping of the generalist pathogen *Botrytis cinerea*. **bioRxiv**. doi: <https://doi.org/10.1101/489799>.
- 2017 [Zhang W.](#), Corwin J.A., Eshbaugh R., Copeland D., Feusier J., Chen F., Atwell S., and Kliebenstein D.J. (2017). Plastic Transcriptomes Stabilize Immunity to Pathogen Diversity: The Jasmonic Acid and Salicylic Acid Networks Within the Arabidopsis/Botrytis Pathosystem. **The Plant Cell** 29 (11). doi: <https://doi.org/10.1105/tpc.17.00348>.
- 2016 [Zhang W.](#), Kwon S.T., Chen F., and Kliebenstein D.J. (2016). Isolate dependency of Brassica rapa resistance QTLs to *Botrytis cinerea*. **Frontiers in plant science** 7, 161. doi: <https://doi.org/10.3389/fpls.2016.00161>.
- 2015 Wei L., [Zhang W.](#), Yin L., Yan F., Xu Y., Chen F. (2015). Extraction and optimization of total triterpenoids from *Jatropha curcas* leaves using response surface methodology and evaluations of their antimicrobial and antioxidant capacities. **Electronic Journal of Biotechnology** 18 (2). Doi: <https://doi.org/10.1016/j.ejbt.2014.12.005>.
- 2014 Li S., [Zhang W.](#), Wei L., Huang X., Lin N., Xu Y., Chen F. (2014). Cloning and expression analysis of a C2H2 type zinc finger protein gene JcZFP1 from *Jatropha curcas* L. **Journal of Sichuan University** 51. doi: [10.3969/j.issn.0490-6756.2014.01.035](https://doi.org/10.3969/j.issn.0490-6756.2014.01.035).
- 2012 Chen F, Tang L, Wang Z, Yan F, Wei L, [Zhang W.](#) (2012) Method for extraction and separation purification of phorbol ester components of *Jatropha curcas* seeds. CN Patent 102,659,583
- 2011 [Zhang W.](#), Wang Z., Hu H., Yu D., Chen F. (2011). GC-MS analysis of volatile oil constituents from Shibawei Zhenbaoxiang. **Chin J of Pharm Anal** 31 (5).

In progress

- 2021 [Zhang W.*](#), Sia J.*, Jonckheere E., Cook D.E., Bogdan P. (2021). Inferring functional communities from partially observed biological networks exploiting geometric topology and side information. **In progress with Nature Communications**.
- 2021 [Zhang W.*](#), Sia J.*, Cheng MX., Bogdan P., Cook D.E. (2021). Predicting plant- microbe outcomes from dual species transcriptome by machine learning. **In progress**.

*These authors contributed equally.

SERVICES

Assistant Feature Editor for Plant Physiology from January 2020 to December 2021.

Peer reviewer for journals below:

Plant Direct, Theoretical and Applied Genetics, The Crop Journal, Functional & Integrative Genomics, Peer J, Journal of Plant Physiology, Journal of Agricultural and Food Chemistry, Genes, International Journal of Molecular Sciences, Molecules, Agriculture, Agronomy, Pathogens, Plants, Microorganisms