

Wenbin “Bean” Zhou, Ph.D.

Postdoctoral Research Associate

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EDUCATION

2021	Ph.D.	Plant Biology	North Carolina State University	Raleigh, NC
2016	MSc	Plant Biology	Zhejiang University	Zhejiang, China
2013	BSc	Bio-technology	Zhejiang A & F University	Zhejiang, China

RESEARCH EXPERIENCE

Postdoctoral Research Associate - University of North Carolina at Chapel Hill 2021 Sep - Present

- Microbial Evolution on UTI disease (Advisor: Dr. Corbin Jones)
- Genome-environment interactions in grasses (Poaceae) and rushes (Juncaceae) using whole genome sequencing methods. (Advisors: Dr. Corbin Jones and Dr. Alan Jones)

TEACHING EXPERIENCE

May 2023	Evolutionary Biology, Guest Lecturer, UNC Pembroke
May 2022	Basic assembly and annotation of Genomes workshop, Lecturer, UNC
2020, 2021	Systematic Botany PB403/503 Lab TA, NCSU
2019	Plant Biology PB200 Lab TA (non-major students), NCSU
2018, 2019	Plant Biology PB250 Lab TA, NCSU
June 2022	UNC Summer Institute on College Teaching, certificate

PUBLICATIONS

Papers in Preparation

- Zhou, W.**, Sakaguchi, S., Bypassing the Batch Effects to Improve the Reusability of RAD-seq Data: A Case Study of Recurrent Hybridization in the Japanese *Torreya* Species Complex. (under review Molecular Ecology Resources)
- Zhou, W.**, Poindexter, D., Skelly, T.J., Winshell, J., Copenhaver, G., Jones, C.D., Randall, J., Sea-level and climate changes drive lineage diversification in the imperiled Venus flytrap (*Dionaea muscipula* J. Ellis, Droseraceae). (submitted to Molecular Ecology)
- Zhou, W.**, Poindexter, D., Armijos, C.E., Urquia, D., An, H., Jones, A.M., Jones, C.D. Looking for adaptation to shade: Whole genome comparison between two rush species from shade vs. open habitat. (targeted for New Phytologist)
- Zhou, W.**, Poindexter, D., Wang, J., Whole genome comparison between *Selaginella apoda* and *Selaginella ludoviciana* from shade vs. open habitats. (targeted for New Phytologist)

Peer Reviewed Publications: (* Corresponding author)

2026. Fitzpatrick, C.R., Smith, R.A., Hige, J., Law, T.F., Russ, D. et al., **Zhou, W.** Grant, S.R. Mougous, J.D., Jones, C.D., Dangel, Jeffery L. Streptomyces enrichment in roots during drought is uncoupled from plant benefit and is driven by host suppression of iron uptake and immunity. *Cell*.
2026. Shouse, E.M., Aragón-Raygoza, A., Tallerday, E.J., Healy, T., **Zhou, W.**, Boeshore, S.L., Burr, C., Jones, C., Schaller, G.E., Strable, J. and Kieber, J.J. Cytokinin histidine kinase receptors regulate multiple aspects of rice growth and development. *Plant Physiology*, p.kiag215.
2025. Sun, Y.X., **Zhou, W.**, Xiang, Q.Y., Genomic data uncover complex hybridization and evolutionary history of the bunchberry species complex (*Cornus* L., Cornaceae), *Horticulture Research*. uhaf026. <https://doi.org/10.1093/hr/uhaf026>.
2024. Lou, F., **Zhou, W.**, Tunc-Ozdemir, M., Yang, J., Velazhahan, V., Tate, C.G. and Jones, A.M., VPS26 Moonlights as a β -Arrestin-like Adapter for a 7-Transmembrane RGS Protein in *Arabidopsis thaliana*. *Biochemistry*, 63(22), 2990-2999. <https://doi.org/10.1021/acs.biochem.4c00361>
2024. Xie, P., Guo, Y., Teng, Y., **Zhou, W.** and Yu, Y., GeneMiner: A tool for extracting phylogenetic markers from next-generation sequencing data. *Molecular Ecology Resources*, 24(3), p.e13924. <https://doi.org/10.1111/1755-0998.13924>
2023. Du, Z.Y., Xiang, Q.Y., Cheng, J., **Zhou, W.**, Wang, Q.F., Soltis, D.E., Soltis, P.S., An updated phylogeny, biogeography, and PhyloCode-based classification of Cornaceae based on three sets of genomic data. *American Journal of Botany*, 110(2), p.e16116. <https://doi.org/10.1002/ajb2.16116>
2023. **Zhou, W.***, Armijos, E.C., Lee, C., Lu, R.S., Wang, J., Ruhlman, A.T., Jansen, K.R., Jones, A.M., Jones, C.D., Plastid Genome Assembly Using Long-Read Data. *Molecular Ecology Resources*, 23(6), 1442-1457. <https://doi.org/10.1111/1755-0998.13787>
2023. **Zhou, W.***, Shi, W., Soltis, P.S., Soltis, D.E. and Xiang, Q.Y., Foliar Endophyte Diversity in Eastern Asian-Eastern North American disjunct tree species—influences of host identity, environment, phylogeny, and geographic isolation. *Frontiers in Plant Science*, 14, p.1274746. <https://doi.org/10.3389/fpls.2023.1274746>
2022. Zhang, Z., Xie, P., Guo, Y., **Zhou, W.**, Liu, E. and Yu, Y., Easy353: A tool to get Angiosperms353 genes for phylogenomic research. *Molecular Biology and Evolution*, 39(12), p.msac261. <https://doi.org/10.1093/molbev/msac261>
2022. **Zhou, W.***, Xiang, Q.Y., Phylogenomics and Biogeography of *Castanea* and *Hamamelis* - a comparison between RAD-seq and Hyb-Seq data. *Molecular Phylogenetics and Evolution*, 176, 107529. <https://doi.org/10.1016/j.ympev.2022.107529>
2022. **Zhou, W.***, Harris, A.J., Xiang, Q.Y., Phylogenomics and biogeography of *Torreya* (Taxaceae) – Integrating data from three organelle genomes, morphology, and fossils and a practical method for reducing missing data from RAD-seq. *Journal of Systematics and Evolution*, 60(6), 1241-1262. <https://doi.org/10.1111/jse.12838>
2022. **Zhou, W.**, Soghigian, J., Xiang, Q.Y., A new pipeline for removing paralogs in target enrichment data. *Systematic Biology*, 71(2): 410-425. <https://doi.org/10.1093/sysbio/syab044>
2021. Wahlsteen, E., **Zhou, W.**, Xiang, Q.Y., Rushforth, K., Rediscovery of the lost little dogwood *Cornus wardiana* (Cornaceae)—its phylogenetic and morphological distinction and implication in the origin of the Arctic-Sino-Himalayan disjunction. *Journal of Systematics and Evolution*, 59(2), 405-416. <https://doi.org/10.1111/jse.12576>
2020. **Zhou, W.***, Xiang, Q.Y., Wen, J., Phylogenomics, biogeography, and evolution of morphology and ecological niche of the eastern Asian-eastern North American *Nyssa* (Nyssaceae). *Journal of Systematics and Evolution*, 58(5), 571-603. <https://doi.org/10.1111/jse.12599>
2020. Lindelof, K., Lindo, J.A., **Zhou, W.**, Ji, X., Xiang, Q.Y., Phylogenomics, biogeography, and evolution of the blue- or white-fruited dogwoods (*Cornus*)—insights into morphological and ecological niche divergence following intercontinental geographic isolation. *Journal of Systematics and Evolution*, 58(5), 604-645. <https://doi.org/10.1111/jse.12676>
2019. Dong, Y., Chen, S., Cheng, S., **Zhou, W.**, Ma, Q., Chen, Z., Fu, C.X., Liu, X., Zhao, Y.P., Soltis, P.S., Wong, G.K.S., Soltis, D.E., Xiang, Q.Y., Natural selection and repeated patterns of molecular evolution following allopatric divergence. *Elife*, 8, p.e45199. <https://doi.org/10.7554/eLife.45199>

2019. Chen, C., Zheng, L., Ma, Q., **Zhou, W.**, Zhao, Y., Fu, C., Impacts of Domestication on Population Genetics of a Traditional Chinese Medicine, *Atractylodes macrocephala* (Asteraceae), ***Journal of Systematics and Evolution***, 57(3), 222-233. <https://doi.org/10.1111/jse.12446>
2018. **Zhou, W.**, Ji, X., Obata, S., Pais, A., Dong, Y., Peet, R., Xiang, Q.Y., Resolving relationships and phylogeographic history of the *Nyssa sylvatica* complex using data from RAD-seq and species distribution modeling, ***Molecular Phylogenetics and Evolution***, 126, pp.1-16. <https://doi.org/10.1016/j.ympev.2018.04.001>
2018. Koch, M., Hohmann, N., Wolf, E., Rigault, P., **Zhou, W.**, Kiefer, M., Zhao, Y., Fu, C., *Ginkgo biloba*'s footprint of dynamic Pleistocene history dates back only 400,000 years ago and indicates multiple range expansions and retractions, ***BMC Genomics***, 19(1), 299. <https://doi.org/10.1186/s12864-018-4673-2>
2016. Guan, R., Zhao, Y., Zhang, H., Fan, G., Liu, X., **Zhou, W.**, Shi, C., Wang, J., Liu, W., Liang, X., Fu, Y., Ma, K., Zhao, L., Zhang, F., Lu, Z., Lee, S., Xu, X., Wang, J., Yang, H., Fu, C., Ge, S., Chen, W., Draft genome of the living fossil *Ginkgo biloba*. ***Gigascience***, 5(1), 49. <https://doi.org/10.1186/s13742-016-0154-1>
2016. **Zhou, W.**, Cheng, Z., Zhao, Y.P., Fu, C.X., Contribution of environmental and genetic variation to chemical similarity of Maca (*Lepidium meyenii* Walp.). ***Journal of Zhejiang University***, 42(6), 731-738. <https://doi.org/10.3785/j.issn.1008-9209.2015.12.131>
2016. Sun, Z.S., **Zhou, W.**, Jin, X., Ohi-Toma, T., Li, P., Fu, C.X., A tale of two islands: parallel evolution of dwarfism in *Smilax biflora* (Smilacaceae). ***Phytotaxa***, 245(2), 89-106. <http://dx.doi.org/10.11646/phytotaxa.245.2.1>
2013. Shao, R., Shen, Y., **Zhou, W.**, Fang, J., Zheng, B., Recent advances for plant ATP-binding cassette transporters. ***Journal of Zhejiang AF University***, 30, 761-768. <https://doi.org/10.11833/j.issn.2095-0756.2013.05.020>

PRESENTATIONS

Abstracts of Talks and Posters at Conferences

2026. **Zhou, W.**, Randall, J. Genome-wide Molecular Data Reveal Complex Phylogeography of the Imperiled Venus Flytrap (*Dionaea muscipula* J. Ellis, Droseraceae) 5th Carolina Biodiversity Collaborative Symposium, May 21, NCBG, Chapel Hill, NC, US. (Invited talk and received a **Venus Flytrap Champion award**)
2026. Randall, J, **Zhou, W.**. Genome-wide Molecular Data Reveal Complex Phylogeography of the Imperiled Venus Flytrap (*Dionaea muscipula* J. Ellis, Droseraceae) Carnivorous & Exotic Plant Symposium & Expo, May 17, Kernersville, NC, US. (Invited talk)
2026. **Zhou, W.**, Randall, J. Genome-wide Molecular Data Reveal Complex Phylogeography of the Imperiled Venus Flytrap (*Dionaea muscipula* J. Ellis, Droseraceae) North Carolina Rare Plant Meeting, April 1, NCBG, Chapel Hill, NC, US. (Invited talk)
2026. **Zhou, W.**, Randall, J. Genome-wide Molecular Data Reveal Complex Phylogeography of the Imperiled Venus Flytrap (*Dionaea muscipula* J. Ellis, Droseraceae) Venus Flytrap Working Group Meeting, January 20, NCBG, Chapel Hill, NC, US.
2025. **Zhou, W.**, Sakaguchi, S., A New *Torreya* species and its cryptical hybrid Discovered in Japan Sheds Light on the reoccurring hybridization events in late Oligocene. Botany 2025, July 25, Palm Springs, CA, US.
2025. **Zhou, W.**, Poindexter, D., Jones, A.M., Jones, C.D., Looking for adaptation to shade: Genome comparison between two rush species from shade vs. open and wetland vs. dryland habitats. Botany 2025, July 25, Palm Springs, CA, US.
2022. **Zhou, W.**, Jones, A.M., Jones, C.D., Hybrid genome sequencing to reveal genomic evolution associated with different environmental niches in Grasses. Botany 2022, July 24, Anchorage, AK, US. (poster)
2021. **Zhou, W.**, Harris, AJ, Xiang, Q.Y. An integrative approach to test biographical hypotheses in nutmeg yew (*Torreya*) and a practical method for reducing missing data from RAD-seq. Botany 2021,

- July 18-23, online. (Invited presentation for a Colloquium “Mechanisms underlying exceptional plant diversity across eastern Asia”).
2020. **Zhou, W.**, Soghigian, J., Xiang, Q.Y. A new approach for cleaning paralogs in Hybseq data from Angiosperm353 kit – application for the phylogenomic studies of *Castanea* and *Hamamelis* with comparison to RAD-seq data. Botany 2020, July 27-31, online. (Presentation)
2019. **Zhou, W.**, Xiang, Q.Y. Phylogenomics, Biogeography, and Post-Isolation Divergence of Eastern Asia-North American Disjunct Genera *Castanea*, *Hamamelis*, *Nyssa*, and *Torreya* – Insights into Morphostasis. Botany 2019, July 27-31, Tucson, AZ, US. (Presentation)
2018. **Zhou, W.**, Wen, J., Xiang, Q.Y. Phylogenomics of *Nyssa* from single-copy genes and Fluidgim sequencing – insights into biogeography and character evolution. Botany 2018. July 21-25, Rochester, MN, US. (Presentation)
2018. **Zhou, W.**, Xiang, Q.Y. Species delineation & phylogenomics in an eastern Asian-eastern North American disjunct genus – *Nyssa*. 2018 Genomic Sciences Biomathematics Symposium, April. Raleigh, NC, US. (Presentation)
2017. **Zhou, W.**, Li, S., Xiang, Q.Y. Understanding functional diversity and mechanisms of plant community assembly of eastern Asian and eastern North American disjunct forests through global secondary metabolite profiling: a test of HPLC-MS non-target method. XIX International Botanical Congress. July 23-29, Shenzhen, China. (Poster)
2016. **Zhou, W.**, Zhao, Y., Koch, M., Fu, C.X. Plastid genomes revealed three lineages of *Ginkgo biloba* diverged in the mid- to late-Pleistocene. 27th NC Plant Molecular Biology Retreat. International Biogeography Society (IBS) Special Meeting. May 4-8, Beijing, China. (Poster)

Invited Talks at Universities

2026 Mar	High Point University Biology Department, Spirit Seminar
2026 Jan	Venus Flytrap Working Group Meeting
2025 Sep	University of North Carolina at Chapel Hill, Biology Department, Lunch Bunch talk
2025 Apr	Beijing Forestry University
2025 Mar	Shanghai Chenshan Botanical Garden
2025 Mar	Wenzhou University, College of Life and Environmental Science
2023 Aug	Duke University, Pryer & Windham Lab
2021 Nov	University of North Carolina at Chapel Hill, Alan Weakley Lab
2021 Oct	Hainan University, Huafeng Wang Lab
2018 Apr	North Carolina State University, Genomic Sciences & Biomathematics Symposium
2018 Feb	North Carolina State University, Plant Biology Recruitment Seminar

GRANTS, TRAVEL AWARDS & HONORS

2026	Venus Flytrap barcoding project (\$15k)
2026	Venus Flytrap Champion award
2026	North Carolina Botanical Garden grant on Venus flytrap genomics (\$4k effective 2027)
2025	Botany 2025 Hardship Award (\$800)
2019	Arnold Arboretum at Harvard University, Shiu-Ying Hu Student/Post-Doctoral Exchange Award (\$5000)
2019	North Carolina State University, Charles W. Stuber Graduate Student Award (\$1k for travel)
2019	ASPT, Travel Grant for Botany 2019 in Tucson (\$200 for travel)
2018	North Carolina State Graduate, Plant & Microbial Biology Dept. Travel Award (\$200 for travel)
2010 & 2012	Third-class scholarship for Outstanding Students
2010	University-Level Merit Student
2010	Second-class scholarship for Outstanding Students

PROFESSIONAL SOCIETIES

Botanical Society of America (BSA)
Society of Systematic Biologists (SSB)
International Carnivorous Plant Society (ICPS)
North Carolina Rare Flora Member

SERVICE AND OUTREACH

Journal reviewer for: Molecular Ecology Resources, Molecular Phylogenetics and Evolution, New Phytologist, American Journal of Botany, Journal of Systematics and Evolution, Ecology and Evolution, Frontiers in Plant Science, BMC Plant Biology, Botanical Journal of the Linnean Society, International Journal of Plant Sciences, Journal of Biogeography, Scientific Reports, Conservation Genetics

Evolution Hamilton Award judge (2026)

UNC Chapel Hill – Biology Department Judge of Spring BIOL 295/395 Poster Sessions (2026)

BSA Grad Student Research Award Committee (2026)

Consulting service for Bioinformatics and Analytics Research Collaborative (BARC) at UNC Chapel Hill (2025)

Darwin Day exhibit in NC museum of Natural Science (2019).

Mentorship for undergraduates, visiting scholars, and graduates at Zhejiang University, NC State, UNC-Chapel Hill (2013 - present).

SCIENTIFIC SOFTWARE (<https://github.com/Bean061/>)

- ptGAUL Plastid Genome Assembly Using Long-read data
- PPD Putative Paralogs Detection for Enrichment Data
- RADADOR RAD-seq Allele Dropout Remedy
- GeneMiner Gene assembly for Next Generation Sequencing
- Easy353 An Efficient Tool Designed to Recover the Angiosperms353 Gene Set