

# Wenbin (Bean) Zhou

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## Work Experience

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

## Education

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

## Teaching Experience

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**2023 May**                UNC Pembroke Guest Lecturer in Evolutionary Biology  
**2022 Jun**                UNC Summer Institute on College Teaching  
**2022 May**                UNC Basic assembly and annotation of Genomes workshop  
**2020 & 2021**            NCSU Plant Systematics PB403/503 Lab TA  
**2019**                      NCSU Plant Biology PB200 Lab TA (non major students)  
**2018 & 2019**            NCSU Plant Biology PB250 Lab TA

## Grants

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**2019 Jul**                Arnold Arboretum at Harvard University, Shiu-Ying Hu Student/Post-Doctoral Exchange Award (\$5000)  
**2019 May**                North Carolina State University, Charles W. Stuber Graduate Student Award (\$1000 for travel)  
**2019 Apr**                ASPT, Travel Grant for Botany 2019 in Tucson (\$200 for travel)  
**2018 Jul**                North Carolina State Graduate, Plant & Microbial Biology department travel award (\$200 for travel)

## Current Research Projects

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Genome-environment interactions in Grasses (Poaceae) and Rushes (Juncaceae) using whole genome sequencing methods (Advisors: Dr. Corbin Jones and Dr. Alan Jones)

## Papers

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### in Review:

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*. (Minor Revision)

### Papers in Preparation:

**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.

**Zhou, W.**, Poindexter, D., Skelly, T.J., Winshell, J., Copenhaver, G., Jones, C.D., Randall, J.,  
Range-wide ex situ seed conservation and population genetic architecture analysis in Venus 'flytrap (*Dionaea muscipula*).

**Zhou, W.**, Sakaguchi, S., A New *Torreya* Species Discovered in Japan Sheds Light on the Biogeography of *Torreya* Between China and Japan.

**Zhou, W.**, Poindexter, D., Wang, J., Whole genome comparison between *Selaginella apoda* and *Selaginella ludoviciana* from shade vs. open habitats.

### Peer Reviewed Publications: (\* Corresponding author)

2024. Lou, F., **Zhou, W.**, Tunc-Ozdemir, M., Yang, J., Velazhahan, V., Tate, C.G. and Jones, A.M., VPS26 Moonlights as a  $\beta$ -Arrestin-like Adapter for a 7-Transmembrane RGS Protein in *Arabidopsis thaliana*. *Biochemistry*, 63(22), 2990-2999.
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.
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.
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.
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.
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.
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.
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.
2022. **Zhou, W.**, Soghigian, J., Xiang, Q.Y., A new pipeline for removing paralogs in target enrichment data. *Systematic Biology*, 71(2): 410-425.

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.
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.
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.
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., Natural selection and repeated patterns of molecular evolution following allopatric divergence. ***Elife***, 8, p.e45199.
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.
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.
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.
2016. Guan, R., Zhao, Y., Zhang, H., Fan, G., Liu, X., **Zhou, W.**, Shi, C., Wang, J., Liu, W., Liang, X., Fu, Y., Draft genome of the living fossil *Ginkgo biloba*. ***Gigascience***, 5(1), 49.
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.
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.
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.

## Talks

### Abstracts of Talks and Posters at Conferences:

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 Fluidigm 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:

<b>2023 Aug</b>	Duke University, Pryor & Windham Lab
<b>2021 Nov</b>	University of North Carolina at Chapel Hill, Alan Weakley Lab
<b>2021 Oct</b>	Hainan University, Huafeng Wang Lab
<b>2018 Apr</b>	North Carolina State University, Genomic Sciences & Biomathematics Symposium
<b>2018 Feb</b>	North Carolina State University, Plant Biology Recruitment Seminar

#### **Honors**

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<b>2010 &amp; 2012</b>	Third-class scholarship for Outstanding Students (twice)
<b>2010</b>	University-Level Merit Student
<b>2010</b>	Second-class scholarship for Outstanding Students

#### **Professional Societies**

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Botanical Society of America (BSA)

Society of Systematic Biologists (SSB)

#### **Scientific Software (<https://github.com/Bean061/>)**

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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