

# Curriculum Vitae

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## Work experience:

➤ **2021.9 – Present** Postdoc at University of North Carolina at Chapel Hill

## Education:

➤ **2016.8 – 2021.8** Ph.D. in Plant Biology, North Carolina State University, USA

➤ **2013.8 – 2016.6** MSc in Plant Biology, Zhejiang University, China

➤ **2009.8 – 2013.6** BSc in Bio-technology, Zhejiang A & F University, China

## Researches:

- **Genome-environment interactions in grasses (Poaceae) using both illumina sequencing and Nanopore sequencing methods (Advisors: Dr. Dr. Corbin Jones and Dr. Alan Jones)**
- **Phylogenomic and biogeographic studies of *Nyssa* (Nyssaceae), *Hamamelis* (Hamamelidaceae), *Castanea* (Fagaceae), and *Torreya* (Taxaceae) using RAD-seq, Fluidigm sequencing, and Hyb-Seq methods (Advisor: Dr. Jenny Xiang)**
- **Comparative analyses of endophyte diversity in eastern Asian-Eastern North American disjunct plant species pairs (Advisor: Dr. Jenny Xiang)**
- **Phylogeography of *Ginkgo biloba* using plastid genomic and comparative transcriptomic approaches. (Advisor: Dr. Yunpeng Zhao)**
- **Contribution of environmental and genetic variation to chemical similarity of maca (*Lepidium meyenii* Walp.) (Advisor: Dr. Yunpeng Zhao)**

## Honors:

- **2019.3 – 2020.3** Shiu-Ying Hu Student/Post-Doctoral Exchange Award (Arnold Arboretum at Harvard University)
- **2019.5** Charles W. Stuber Graduate Student Award at NC State

- **2019.4** ASPT Travel Grant for Botany 2019 in Tucson
- **2018.7** Graduate Travel award from Plant & Microbial Biology at NC State
- **2010 – 2012** Third-class scholarship for Outstanding Students (twice)
- **2009 – 2010** University-Level Merit Student
- **2009 – 2010** Second-class scholarship for Outstanding Students

## Publications:

- Zhou, W.**, Harris, A.J., Xiang, Q.Y. 2022. 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*. (IF: 4.098, JCR: Q1)
- Zhou, W.**, Soghigian, J., Xiang, Q.Y., 2021. A new pipeline for removing paralogs in target enrichment data. *Systematic Biology*. (IF: 15.683, JCR: Q1)
- Zhou, W.\***, Xiang, Q.Y.\*, Wen, J., 2020. 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), pp.571-603. (IF: 4.098, JCR: Q1)
- Lindelof, K., Lindo, J.A., **Zhou, W.**, Ji, X., Xiang, Q.Y., 2020. 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*. (IF: 4.098, JCR: Q1)
- Wahlsteen, E., **Zhou, W.**, Xiang, Q.Y., Rushforth, K., 2020. 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. (IF: 4.098, JCR: Q1)
- 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., 2019. Natural selection and repeated patterns of molecular evolution following allopatric divergence. *Elife*, 8, p.e45199. (IF: 8.1, JCR: Q1)
- Chen, C., Zheng, L., Ma, Q., **Zhou, W.**, Zhao, Y., Fu, C., 2019, Impacts of Domestication on Population Genetics of a Traditional Chinese Medicine, *Atractylodes macrocephala* (Asteraceae), *Journal of Systematics and Evolution*, 57(3), pp.222-233. (IF: 4.098, JCR: Q1)
- Zhou, W.**, Ji, X., Obata, S., Pais, A., Dong, Y., Peet, R., Xiang, Q.Y., 2018, 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. (IF: 4.286, JCR: Q2)

- Koch, M., Hohmann, N., Wolf, E., Rigault, P., **Zhou, W.**, Kiefer, M., Zhao, Y., Fu, C., 2018, 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), p.299. (IF: 3.729, JCR: Q2)
- Guan, R., Zhao, Y., Zhang, H., Fan, G., Liu, X., Zhou, W., Shi, C., Wang, J., Liu, W., Liang, X., Fu, Y., 2016. Draft genome of the living fossil *Ginkgo biloba*. *Gigascience*, 5(1), p.49. (IF: 6.871, JCR: Q2)
- Zhou, W.**, Cheng, Z., Zhao, Y.P., Fu, C.X., 2016. Contribution of environmental and genetic variation to chemical similarity of Maca (*Lepidium meyenii* Walp.). *Journal of Zhejiang University*, 42(6): 731-738.
- Sun, Z.S., Zhou, W., Jin, X., Ohi-Toma, T., Li, P., Fu, C.X., 2016. A tale of two islands: parallel evolution of dwarfism in *Smilax biflora* (Smilacaceae). *Phytotaxa*, 245(2), pp.89-106. (IF: 1.240, JCR: Q4)
- Shao, R., Shen, Y., **Zhou, W.**, Fang, J., Zheng, B., 2013. Recent advances for plant ATP-binding cassette transporters. *Journal of Zhejiang AF University*, 30, pp.761-768.

### **Papers in review or revision**

- Zhou, W.**, Xiang, Q.Y. Major Revision. Phylogenomics and Biogeography of *Castanea* and *Hamamelis* - a comparison between RAD-seq and Hyb-Seq data. *Molecular Phylogenetics and Evolution*. (IF: 4.286, JCR: Q2)

### **Talks:**

#### **Abstracts of Talks and Posters at Important Conferences:**

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:**

- 2021.11      UNC Alan Weakley Lab  
2021.10      Hainan University Huafeng Wang Lab  
2018.4        NCSU Genomic Sciences & Biomathematics Symposium  
2018.2        NCSU Plant Biology Recruitment Seminar

### **Teaching Experience:**

- 2022.6            UNC Summer Institute on College Teaching  
2022.5            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

### **Professional Societies:**

Botanical Society of America (BSA)  
Society of Systematic Biologists (SSB)

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

PPD — Putative Paralogs Detection for Enrichment Data  
RADADOR — RAD-seq Allele Dropout Remedy