

Wen-Hsi Kuo

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PROFESSIONAL SUMMARY

My research interests focus on investigating the genetic mechanisms of adaptive traits in plants. I have a solid understanding and hands-on experience in NGS, including experimental design, customized library preparation, sequencing data analyses and interpretations. I am skilled in linking genetics to desired phenotypes (image analyses, qPCR) via GWAS and QTL mapping. I have extensive computational experience working on HPC and using R for data visualizations and statistical analyses. Finally, I enjoy working with people, including extensive mentoring experiences and collaborations with scientists.

EDUCATION

- Ph.D, Ecology & Evolution (DBBS)**, Washington University in St. Louis, MO. May 2024
Thesis: Understanding mechanisms of local adaptation in white clover (*Trifolium repens* L.): insights from a phenotypic cline and population genomics
- M.S., Ecology & Evolution**, National Taiwan University, Taiwan December 2014
Thesis: Ectopic expression of *SsCYC* in *Nicotiana benthamiana* and optimizing regeneration system of *Sinningia speciosa*
- B.S., Life Science**, National Taiwan University, Taiwan (GPA: 3.76/4.00). July 2012

PROFESSIONAL EXPERIENCE

- Missouri Botanical Garden, MO** May 2024 – present
Postdoctoral Fellow in Center for Conservation and Sustainable Development, supervised by Dr. Christine Edwards
- Investigate the genetic and phenotypic diversity of Midwest endangered species.
- Washington University in St. Louis, MO** August 2018 – April 2024
Graduate Researcher in Evolutionary Genomics Lab, supervised by Dr. Kenneth M. Olsen
- Investigated the regulation of HCN detoxification and tolerance genes in white clover.
 - Studied the genomics of copy number variation and their contributions to rapid climatic adaptation in white clover.
 - Investigated the genetics underlying climatic adaptation in the context of population structure in white clover.
 - Conducted QTL-mapping and RNA-seq to locate drought tolerance-related genes in white clover.
- Biodiversity Research Center, Academia Sinica, Taiwan** May 2016 – June 2018
Research Assistant in Plant Systematic & Biogeography Lab, supervised by Dr. Kuo-Fang Chung
- Investigated the immigration history of multiple paper making species in genus *Broussonetia* by chloroplast genome sequencing and microsatellite markers.
 - Re-circumscribed the taxonomic status of genus *Broussonetia* with molecular evidence.
 - Collaborated with international botanists to conduct plant field collections in Taiwan, Vietnam, and the Philippines.
- National Taiwan University, Taiwan**
Graduate Researcher in EvoDevo Lab, supervised by Dr. Chun-Neng Wang July 2012 – April 2015
- Studied the molecular mechanism of floral symmetry development in African violet and *Gloxinia*.
 - Established and optimized the Agrobacterium-mediated genetic transformation system in *Gloxinia*.
- National Institute of Genetics, Mishima, Shizuoka, Japan** July 2011 – September 2011

Summer Intern Student in Division of Agricultural Genetics, supervised by Dr. Tetsuji Kakutani

- Investigated the DNA methylation of a *de novo* introduced retrotransposon (LTR-RT) in *Arabidopsis*.

SKILLS

- Illumina customized library preparation, data analyses, result interpretations, including SNP calling, population structure analysis, GWAS, environmental association, QTL mapping and RNA-seq.
- PacBio HiFi data processing, including *de novo* genome assembly with Omni-C and linkage map assisted scaffolding, and structural variant discovery.
- qPCR with single or multiplex exp. design, statistical analyses, result interpretation.
- Designing and constructing QTL mapping populations in the greenhouse, including the application of quantitative drought stress.
- Phenotyping, including python-based image analysis, biomass measurement, water potential and osmotic potential measurements.
- *Agrobacterium*-mediated genetic transformation of *Arabidopsis* (floral dipping) and tobacco (tissue culture).
- Paraffin sectioning, including sample preparation, microtome and microscope operation, RNA *in situ* hybridization.
- Molecular biology techniques, including DNA/RNA extraction, PCR, electrophoresis, gene cloning, vector construction, Northern/Southern blotting.
- Extensive experiences in working on HPC, including using Docker and R programming language.
- Proficient in English and native in Mandarin.

PUBLICATIONS

Kuo, W. H., Cunningham, E., Guo, E., Olsen, K. M. (2024). Genetics and plasticity of white leaf mark variegation in white clover (*Trifolium repens* L.). *Annals of Botany*. (in press)

Kuo, W. H., Zhong, L., Wright, S. J., Goad, D., Olsen, K. M. (2024). Beyond cyanogenesis: Temperature gradients drive environmental adaptation in North American white clover (*Trifolium repens* L.). *Molecular Ecology*. doi: [10.1111/mec.17484](https://doi.org/10.1111/mec.17484)

Kuo, W. H., Wright, S. J., Small, L., Olsen, K. M. (2024). *De novo* genome assembly of white clover (*Trifolium repens* L.) reveals that copy number variation contributes to rapid climatic adaptation. *BMC Biology*. (in press)

Kuo, W. H., Small, L., Olsen, K. M. (2023). Variable expression of cyanide detoxification and tolerance genes in cyanogenic and acyanogenic white clover (*Trifolium repens* L.). *American Journal of Botany*. doi: [10.1002/ajb2.16233](https://doi.org/10.1002/ajb2.16233)

Santangelo, J. S., Battlay, P., Hendrickson, B. T., **Kuo, W. H.**, Olsen, K. M., Kooyers, N. J., Johnson, M. T. J., Hodgins, K. A., Ness, R. W. (2023). Haplotype-Resolved, Chromosome-Level Assembly of White Clover (*Trifolium repens* L., Fabaceae). *Genome Biology and Evolution*, 15(8). doi: [10.1093/gbe/evad146](https://doi.org/10.1093/gbe/evad146)

Kuo, W. H., Liu, S. H., Chang, C. C., Hsieh, C. L., Li, Y. H., Ito, T., Won, H., Kokubugata, G., Chung, K. F. (2022). Plastome phylogenomics of *Allaeanthus*, *Broussonetia* and *Malaisia* (Dorstenieae, Moraceae) and the origin of *B. × kazinoki*. *Journal of plant research*, 135: 203–220. doi: [10.1007/s10265-022-01369-w](https://doi.org/10.1007/s10265-022-01369-w)

Pan, Z. J., Nien, Y. C., Shih, Y. A., Chen, T. Y., Lin, W. D., **Kuo, W. H.**, Hsu, H. C., Tu, S. L., Chen, J. C., Wang, C.N. Transcriptomic Analysis Suggests Auxin Regulation in Dorsal-Ventral Petal Asymmetry of Wild Progenitor *Sinningia*

speciosa. International Journal of Molecular Sciences, 23(4): 2073. doi: 10.3390/ijms23042073

Kokubugata, G., Nakamura, K., **Kuo, W.H.**, Qi, Z.C., Chung, K.F., Fu, C.X., Suzuki, Y., Yokota, M. (2019). Reappraisal of *Tashiroea* as a genus independent of *Bredia* (Melastomataceae) based on molecular data. *Phytotaxa*, 392(1): 75-83. doi: 10.11646/phytotaxa.392.1.8

Kuo, W. H., Hung, Y. L., Wu, H. W., Hong, C. Y., Wang, C. N. (2018). Shoot regeneration process and optimization of *Agrobacterium*-mediated transformation in *Sinningia speciosa*. *Plant Cell, Tissue and Organ Culture*, 134: 301-316. doi:10.1007/s11240-018-1424-7

Hsu, H.J., He, C.W., **Kuo W.H.**, Hsin K.T., Lu, J.Y., Pan, Z.J., Wang, C.N. (2018). Genetic Analysis of Floral Symmetry Transition in African Violet Suggests the Involvement of *Trans*-acting Factor for *CYCLOIDEA* Expression Shifts. *Frontiers in Plant Science*, 9: 1008. doi: 10.3389/fpls.2018.01008

Chung, K. F., **Kuo, W. H.**, Hsu, Y. H., Li, Y. H., Rubite, R. R., & Xu, W. B. (2017). Molecular recircumscription of *Broussonetia* (Moraceae) and the identity and taxonomic status of *B. kaempferi* var. *australis*. *Botanical Studies*, 58: 11. doi:10.1186/s40529-017-0165-y

Penailillo, J., **Kuo, W. H.**, Olivares, G., Silva-Poblete, G., Pena-Ahumada, B., Munoz, S., Moncada X., Chung, K. F., Seelenfreund, D., Seelenfreund, A. (2017). Characterization of microsatellites for *Broussonetia papyrifera* (Moraceae). *Applications in Plant Sciences*, 5(8): 1700044. doi: 10.3732/apps.1700044

HONORS AND AWARDS

- William H. Danforth Plant Sciences Fellowship (stipend and research funding, 2019 – 2023, USD 130K)
- Ministry of Education Studying Abroad Scholarship (2021 – 2022, USD 32K)
- Honorable Mention in 2014 NTU & NTNU Joint Symposium on Ecology and Evolutionary Biology.
- 2014 Best Plant Science Master Thesis Award, Taiwan Society of Plant Biologists.

TEACHING EXPERIENCE

Washington University in St. Louis, MO, USA

August 2019 – April 2024

Teaching Assistant for Evolution course (Bio3501), lectured by Dr. Kenneth Olsen (2019 FALL & 2023 FALL)

- Leading discussion session, grading essay & exam.

Undergraduate student research mentor

- **Grace Li**. Niche evolution of *Trifolium* spp. in North America. (2020 SUMMER)
- **Nicholas Ho**. Comparison of drought tolerance of white clover and its two progenitor species. (2021 SUMMER & FALL)
- **Eimear Cunningham**. Leaf mark polymorphism in white clover – underlying genetics and physiological impacts. (2021 SUMMER)
- **Emily Guo**. Underlying genetics of leaf thickness variation in white clover in a QTL mapping population. (2023 SPRING)

Biodiversity Research Center, Academia Sinica, Taiwan

May 2016 – June 2018

- Mentoring three summer interns for their summer projects.

National Taiwan University, Taiwan

Teaching Assistant of General Botany Lab

September 2012 – June 2014

- Lecturing, mentoring, and supporting students during experiments. Roughly 30 students per class.