

14/03/2024

Part A. PERSONAL INFORMATION

CV date	28/08/2024
----------------	------------

First name	Wenjie		
Family name	Mu		
Gender (*)	Male	Birth date (dd/mm/yyyy)	27/06/1996
Social Security, Passport, ID number	221020218249, ED7176132, Z1764105X		
e-mail	Axolotl233@gmail.com	URL Web	
Open Researcher and Contributor ID (ORCID) ()	0009-0001-3606-2735		

(*) Mandatory

(**) If you have

A.1. Current position*

University/Institution	Unversidad of Zaragoza
Department/Center	Departamento de Ciencias Agrarias y del Medio Natural
Advisor	Pilar Catalán

(*) If you have any

A.2. Education

Degree/Master	University	Year
Bachelor Degree in Biology	University of Lanzhou, China	2015-2019
Master Degree in Ecology	University of Lanzhou, China	2019-2022

Part B.

CV SUMMARY (max. 3500 characters, including spaces). Describe the information that you consider more relevant, for example, research interests, studies, research experience, fellowships, awards, honors, scientific dissemination activities, etc. Indicate the skills or techniques that you have acquired that may be useful for the execution of a doctoral thesis.

I got my Master's degree in Ecology from Lanzhou University in 2022. Over the past few years, I have been dedicated to decoding the scenario of plant speciation and adaptive evolution using comparative genomics and bioinformatics methods. Recently, I have studied the evolutionary trajectories of two related species of the genus *Brachypodium*. I am interested in the co-evolution of endophytes with their host plants. The interactions between plants and endophytes range from beneficial (mutualistic) to potentially harmful (pathogenic). Genomic insights into these interactions offer new perspectives for comprehending the contributions of endophytes to plant hosts and the broader ecosystem.

After several years of research career (Jianquan Liu's lab in Lanzhou University, Lanzhou Veterinary Research Institute), I have been enriched with various research experiences and skills in bioinformatics, including research paper reading and writing, statistical, programming for genomic and critical thinking abilities.

I am a highly motivated and adaptable individual with a fervent passion for evolutionary biology. I am seeking a position in an environment that is both challenging and progressive.

B.1. Brief summary of the Undergraduate Thesis (or equivalent) and score obtained (maximum 1000 characters, including blank spaces).

My bachelor thesis was a transcriptomic study involving comparative transcriptomic analysis of four *Populus alba* var. *pyramidalis* tissues (root, stem, leaf, xylem) treated with three different salt concentrations (0, 150mm and 300mm). This study created a pipeline for transcriptomic studies in non-model species and discovered a large number of *Populus alba* var. *pyramidalis* genes that may play a role in salt stress.



B.2. Brief summary of the Master's Thesis and score obtained (*maximum 1000 characters, including blank spaces*).

During my master's degree, I assembled and annotated multiple plant genomes at the chromosome level including *Tetracentron sinense* Oliv., *Sinoswertia tetraptera*, *Ricotia lunaria*, *Brachypodium stacei* and *Brachypodium hybridum*. My master thesis focused on the primary sympatric speciation event of *Brachypodium stacei* in Evolution Canyon I (EC-I), Israel. Our results suggested that environmental heterogeneity between the two slopes on EC-I, especially differences in water conditions, play an important role in shaping genetic divergence in the two adjacent *B. stacei* populations. This study provides an empirical example of a model of plant sympatric speciation driven by ecological selection.

Part C. RELEVANT SCIENTIFIC RESULTS (if you have any)

C.1. Publications.

Mu W, Li K, Yang Y, Breiman A, Yang J, Wu Y, Wu S, Zhu M, Liu J, Nevo E, Catalán P. (2023). Scattered differentiation of unlinked loci across the genome underlines ecological divergence of the selfing grass *Brachypodium stacei*. *PNAS* 120: e2304848120. **JCRQ1 IF=11.0, MULTIDISCIPLINARY SCIENCES.**

Mu W, Li K, Yang Y, Breiman A, Yang J, Wu J, Zhu M, Wang S, Catalán P, Nevo E, Liu J. (2023). Subgenomic stability of progenitor genomes during repeated allotetraploid origins of the same grass *Brachypodium hybridum*. *Molecular Biology and Evolution* 40(12): msad259. doi: 10.1093/molbev/msad259. PMID: 38000891; PMCID: PMC10708906. **JCRQ1 IF=10.7, EVOLUTIONARY BIOLOGY.**

Qu, K., Liu, A., Yin, M., **Mu, W.**, Wu, S., Hu, H., ... & Ren, G. (2023). A genome assembly for *Orinus kokonorica* provides insights into the origin, adaptive evolution and further diversification of two closely related grass genera. *Communications Biology*, 6(1), 1223.

Wang, Y., Guo, A., Zou, Y., **Mu, W.**, Zhang, S., Shi, Z., ... & Wang, S. (2023). Interaction between tissue-dwelling helminth and the gut microbiota drives mucosal immunoregulation. *npj Biofilms and Microbiomes*, 9(1), 43.

Zhu, M., Wang, Z., Yang, Y., Wang, Z., **Mu, W.**, & Liu, J. (2023). Multi-omics reveal differentiation and maintenance of dimorphic flowers in an alpine plant on the Qinghai-Tibet Plateau. *Molecular Ecology*, 32(6), 1411-1424.

Zhang, H., Du, X., Dong, C., Zheng, Z., **Mu, W.**, Zhu, M., ... & Yang, Y. (2022). Genomes and demographic histories of the endangered *Bretschneidera sinensis* (Akaniaceae). *GigaScience*, 11, giac050.

Ren, G., Jiang, Y., Li, A., Yin, M., Li, M., **Mu, W.**, ... & Liu, J. (2022). The genome sequence provides insights into salt tolerance of *Achnatherum splendens* (Gramineae), a constructive species of alkaline grassland. *Plant Biotechnology Journal*, 20(1), 116-128.

Ma J, Sun P, Wang D, ..., **Mu, W.**, ... & Yongzhi Yang (2021). The *Chloranthus sessilifolius* genome provides insight into early diversification of angiosperms. *Nature Communications*, 21(12), 1-13

Li, M., Yang, Y., Xu, R., **Mu, W.**, Li, Y., Mao, X., ... & Liu, J. (2021). A chromosome-level genome assembly for the Tertiary relict plant *Tetracentron sinense* Oliv. (Trochodendraceae). *Molecular Ecology Resources*, 21(4), 1186-1199.



C.2. Conferences and meetings, indicating your type of participation (invited speaker, oral presentation, poster, etc.)

2022/5 The 2022 National Systematic and Evolutionary Botany Symposium and the 15th Youth Academic Forum. Guangzhou, China

2023/8 The national congress of plant biology. Lanzhou, China

C.3. Research projects and research lines, indicating your personal contribution

2019/9 - 2020/10: Comparative and population genomic analysis of *Tetracentron sinense*

Contribution: Genome assembly and annotation, population structure and demography inference.

2019/9 - 2020/6: Genomic and transcriptomic analysis of *Achnatherum splendens*

Contribution: Comparative genomic analysis, statistical analysis, and data visualization.

2020/3 - 2021/12: Genomic and transcriptomic analysis of *Orinus kokonorica*

Contribution: Genome assembly improvement and genome annotation.

2021/2 - 2023/9: Ecological divergence and adaptive evolution of *Brachypodium stacei*

Contribution: Genome assembly and annotation, population genetic analysis, physiological parameter measurement, transcriptomic analysis, and manuscript writing.

2021/2 - 2023/9: Comparative genomic and phylogenetic analysis of *Brachypodium hybridum*

Contribution: Genome assembly and annotation, population genetic analysis, phylogenetic inference, comparative genomic analysis based on pan-genome framework, transcriptomic analysis, and manuscript writing.

C.4. Contracts, patents and other technological results, indicating your personal contribution

C.5. Other merits

- **Research assistant position**. Lanzhou Veterinary Research Institute. Chinese Academy of Agricultural Sciences. Lanzhou, China. 01/07/2022-30/06/2024. Genomics, microbiome, grasses, evolutionary interactions.