Jiawen Wen

1453 Fifield Hall
Gainesville, FL 32611-0680
wen.jiawen@ufl.edu
863-3174-384
Google Scholar: https://scholar.google.com/citations?user=ET_5xuIAAAAJ&hl=en
Personal website: https://sarrajww.github.io/Jiawen_Wen.github.io/

SUMMARY

Six years of bioinformatic analysis experience in plant genomics and microbiomes, specializing in multi-omics analysis of plant metabolite biosynthetic pathways and pathogen-host interaction mechanisms.

EDUCATION

University of Florida, USA August 2022 - Present

Ph.D. student of Plant Pathology
Research: The haplotype-resolved genome of *Swinglea glutinosa* and pangenome analysis provide insight into resistance against *Candidatus* Liberibacter asiaticus

University of Chinese Academy of Sciences, China August 2019 - June 2022

Master of Science, Genomics
Thesis: Multi-omics Analysis Shed Light on the Gene Regulation Network of Flavonoid Synthesis in *Citrus reticulata* cv. Chachiensis

Shandong Agricultural University, China September 2015 - June 2019

Bachelor's Degree in Agronomy, Horticulture
Thesis: RNA *de novo* Assembly and Flavonoid Metabolism Analysis of Citrus Peel from Different Places in Guangdong Province
Honors/Awards: Level Two Scholarship (Oct. 2017)
Outstanding Graduate Award (Nov. 2018)

PEER-REVIEWED PUBLICATIONS

1. **Jiawen Wen**#, Yayu Wang#, Xu Lu#, Huimin Pan#, Dian Jin, Jialing Wen, Canzhi Jin, Sunil Kumar Sahu, Jianmu Su, Xinyue Luo, Xiaohuan Jin, Jiao Zhao, Hong Wu, E-Hu Liu & Huan Liu (2024). An integrated multi-omics approach reveals polymethoxylated flavonoid biosynthesis in *Citrus reticulata* cv. Chachiensis. ***Nature Communications***, 15(1), 3991. https://doi.org/10.1038/s41467-024-48235-y
2. Xiaoen Huang#, Hongge Jia#, Jin Xu, Yuanchun Wang, **Jiawen Wen**, Nian Wang (2023). Transgene-free genome editing of vegetatively propagated and perennial plant species in the T0 generation via a co-editing strategy. ***Nature Plants***, 9(10), 1591–1597. https://doi.org/10.1038/s41477-023-01520-y
3. Jin Xu#, Yayu Wang#, Yunzeng Zhang, Nadia Riera, Jinyun Li, Kelley J Clark, Tao Jin, Hongyun Chen, **Jiawen Wen**, Wenbo Ma, Huan Liu, Nian Wang (2023). Host genetic traits underlying the composition/assembly of the citrus microbiome. 2023. ***Phytobiomes Journal*** 2023 7:3, 401-411
4. Haixia Chen#, Tsan-Yu Chiu#, Sunil Kumar Sahu, Haixi Sun, **Jiawen Wen**, Jianbo Sun, Qiyuan Li, Yangfan Tang, Hong Jin, Huan Liu (2022). Transcriptomic analyses provide new insights into green and purple color pigmentation in *Rheum tanguticum* medicinal plants. ***PeerJ*** 10:e14265 https://doi.org/10.7717/peerj.14265

5. Yayu Wang$^{\#}$, Xiaolin Wang$^{\#}$, Shuai Sun, Canzhi Jin, Jianmu Su, Jinpu Wei, Xinyue Luo, **Jiawen Wen**, Tong Wei, Sunil Kumar Sahu, Hongfeng Zou, Hongyun Chen, Zhixin Mu, Gengyun Zhang, Xin Liu, Xun Xu, Lone Gram, Huanming Yang, Ertao Wang & Huan Liu (2022). GWAS, MWAS and mGWAS provide insights into precision agriculture based on genotype-dependent microbial effects in foxtail millet. ***Nature Communications*** 13, 5913. https://doi.org/10.1038/s41467-022-33238-4

PROFESSIONAL SOCIETY MEMBERSHIP

- American Phytopathological Society (2023-Present)

RESEARCH EXPERIENCE

Pangenome analysis and multi-omics analysis on *Swinglea glutinosa* (Sg)

August 2022 – present

- Assembled Sg genome into haplotype-resolved and chromosome-level
- Performed gene annotation of Sg genome
- Pangenome analysis of 25 citrus and citrus relative species
- Proteomic and metabolomic analysis of Sg phloem extracts
- Applied machine learning methods in gene identification

Multi-omics analysis on *Citrus reticulata* cv. Chachiensis (CRC)

September 2020 - June 2022 (major results published in ***Nature Communications***)

- Assembled CRC genome into chromosome-level scale level
- Performed gene annotation with an integrated strategy (RNA-seq, ab initio and homology-based)
- Investigated CRC specific metabolites through metabolomics analysis
- Investigated metabolites-specific gene expression patterns along the different fruit-developing stage from 200 RNA-seq samples
- Identified a key enzyme involved in the biosynthetic pathway of polymethoxylated flavonoid

Investigating the diversity of soil microbiome in Australian main agricultural regions April 2020 - June 2022

- Developed a workflow mining 16S rRNA genes from Shotgun Metagenomic Sequencing data
- Performed assemble on soil samples
- Profiled the functional capacity of the 337M soil gene catalogue
- Investigated antibiotic-resistance genes from the soil metagenome dataset
- Constructed nearly 700 metagenome-assembled genomes (MAGs) from the metagenomic dataset

SKILLS

Programming: Python, R, Linux, Perl, Shell, Nextflow, Slurm

NVIDIA Certificates of Fundamentals of Deep Learning, and Fundamentals of Accelerated Data Science

WORK EXPERIENCE

Horticulture Research (https://academic.oup.com/hr) Impact Factor 7.6

March 2020 - November 2020
Editor Intern, Horticulture Research Editorial Board

- Wrote brief introduction of articles published in the journal *Horticulture Research* at social media

REVIEWER EXPERIENCE

Journal Peer Review

- Volunteer reviewer for *Gene Reports* and *Plant Physiology and Biochemistry*
- Reviewed manuscripts in the field of genome-editing and plant stress response

REFERENCES

Dr. Nian Wang
Professor of Department of Microbiology and Cell Science
Citrus Research and Education Center, IFAS, University of Florida
Address: 700 experiment station road, Lake Alfred, FL 33850
Email: nianwang@ufl.edu
Phone: 863-956-8828