YiFan Xiong

Education

Fujian Agriculture and Forestry University | Fuzhou, Fujian Province, CN

Sep. 2019 - Jun. 2022

M.S. in Bioengineering. GPA: 3.33/4.0

Wuhan Institute of Bioengineering | Wuhan, Hubei Province, CN

Sep. 2015 - Jun. 2019

• B.S. in Bioengineering. GPA: 3.56/4.0

Work experience

TsingHua University

Jul. 2024 - Present

XGlab, Research Assistant, Supervisor: Prof. Xuegong Zhang

- Evaluate the biological meaning in different Large Language Models' gene embedding.
- Identify core TFs combinations in T cells reprogramming and cell development using the algorithm scDirect.

Suzhou Dynamic Biosystems Ltd.

Jun. 2023 - Jun. 2024

Department of Bioinformatic, Bioinformatics Engineer

- Coding for Single-cell RNA-seq data analysis and virsulize. Independently developed R package cellPCT.
- Well-Paired-Seq platform single-cell data testing and troubleshooting.

Fuzhou Institue of Data Technology

Jul. 2022 - Jun. 2023

Department of Digital Medicine, Bioinformatics Engineer

- Data collection, normalization and cell type annotation for hECA2.0 Sigle-cell database.
- Multi-Omics pipeline construction and NGS data analysis.

Research Experience

Undergraduate Research Assistant

Supervisor: Prof. Junlin Zhang & Prof. Zhongming Fang

Sep. 2016 - Jun. 2019

Extraction and identification of anti-cancer bioactive peptides from traditional Chinese medicine

• Experiments including DNA extraction, PCR, vector construction, protein extraction, SDS-PAGE and cell culture, et al.

Functional verification of QinFeng tea by constructing Hyperuricemia animal models

- Construct mouse Hyperuricemia models using two protocols: a high-purine diet and the injection of uric acid metabolism enzymes inhibitors.
- Evaluate the models using quantitative analysis of uric acid and data processing.

Leaf transcriptome analysis of rice transgenic materials(Published)

- *OsAAP3* transgenic rice leaf tissue RNA-seq data analysis, from rawdata to DEG identification and gene functional enrichment analysis.
- Writting part of the paper and visualizing data.

Graduate Student Researcher

Plant Functional genomics lab | Supervisor: Prof. Shoukai Lin

Jun. 2019 - Jul. 2022

Identify Calcium-dependent protein kinase gene family in *Fragaria vesca* and their functions under biotic stresses(Published)

Explore the evolutionary history and sequence pattern of FvCDPKs.

• Conduct transcriptome analysis of wild strawberry under different pathogen infections.

Reveal the role of *EjCDPK* members in response to freezing stress in *Eriobotrya japonica* fruitlets(Preprint)

- Identification of CDPK genes in loguat. Analysis gene sequence and protein motif patterns.
- Use weighted gene co-expression network analysis associated with physiological and biochemical traits to identify freezing stress response gene.
- Over-express the target gene in *Arabidopsis*, revealing that it can increase resistance to freezing stress.

Physiological and transcriptome analysis of *Eriobotrya japonica* fruitlets under freezing stress(Under review)

- Genome-wide identification of Loquat protein kinase using plant kinase HMM models.
- Determining expression patterns of freezing-stress-related protein kinases.

Publications

- **Yifan Xiong**, Shunquan Lin, Jincheng Wu, Shoukai Lin (2024). Identification and Expression Analysis of CDPK Family in *Eriobotrya japonica*, reveals *EjCDPK25* in Response to Freezing Stress in Fruitlets. *bioRxiv*. https://doi.org/10.1101/2024.05.01.591999
- Yifan Xiong, Dahe Lin, Shiwei Ma, Chunhua Wang, Shoukai Lin (2022). Genome-wide identification of the calcium-dependent protein kinase gene family in fragaria vesca and expression analysis under different biotic stresses.
 European Journal of Plant Pathology. 164(2):283-98. https://doi.org/10.1007/s10658-022-02560-4
- Wei Qilang, Zhenwei Yan, Yifan Xiong, and Zhongming Fang (2021). Altered Expression of OsAAP3 Influences Rice
 Lesion Mimic and Leaf Senescence by Regulating Arginine Transport and Nitric Oxide Pathway. *International Journal of Molecular Sciences*, 22, no.4: 2181. https://doi.org/10.3390/ijms22042181
- Jia Li, Xiaocheng Jia, Liyun Liu, Xianmei Cao, **Yifan Xiong**, Yaodong Yang, *et al.* (2020). Comparative biochemical and transcriptome analysis provides insights into the regulatory mechanism of striped leaf albinism in arecanut (*Areca catechu L.*). *Industrial Crops and Products*, 154:112734. https://doi.org/10.1016/j.indcrop.2020.112734

Bioinformatic Skills

- Programming languages: R, Python and shell
- NGS data analysis: scRNA-seq, bulk RNA-seq(miRNA, lncRNA, circRNA),WGS, WGBS, ATAC-seq
- Workflow Management: WDL, Snakemake
- · Code Management and Version Control: Github and Gitlab
- Servers and Environment Manager: Conda, Docker, Slurm

Acdemic activates

Poster presentation

The 10th National Symposium on Loquat Lanxi, Zhejiang province	May. 2021
 Submit an abstract on the topic of Identification calcium sensors in loqut 	
Academic poster competition for Graduate Student Fujian Agriculture and Forestry University	May. 2022
 Oral and poster presentation on the topic of my gradute thesis 	
Digital Medicine Algorithm Innovation Competition Fuzhou, Fujian province	Aug. 2022
Organization assistant	
The 2nd Symposium of Fujian Bioinformation Society Fuzhou, Fujian province	Feb. 2023

Honors & Awards

Scholarship for Undergraduates 3rd Place Wuhan Institute of Bioengineering	Dec. 2015
Annual Outstanding Undergraduates Wuhan Institute of Bioengineering	Dec. 2016
National English Competition for Undergraduates 3rd Place Wuhan Institute of Bioengineering	May. 2017
Scholarship for Undergraduates 2nd Place Wuhan Institute of Bioengineering	Dec. 2017
Scholarship for Undergraduates 1st Place Wuhan Institute of Bioengineering	Dec. 2018
Outstanding Graduates Wuhan Institute of Bioengineering	Jun. 2019
Scholarship for Graduates Fujian Agriculture and Forestry University	Jun. 2020
Academic Achievements Prize for Graduates Fujian Agriculture and Forestry University	Jun. 2022