

Education

M. Sc. Bioinformatics, Miami University, USA	2019-present
B. Sc. Biotechnology, Hubei University of Chinese Medicine, China	2018

Research Experiences

Project I : Chromatin and epigenetic features shape subgenome in maize

- Evolutionary features of whole genome duplication
 1. Enrichment of genomic features of subgenome blocks
 2. Calculate and compare evolutionary rates of genes at different chromosome region
 3. Examine genome-wide DNA methylation.
 4. Examine genome-wide small interfering RNA pattern.
- Dominant expression pattern under classified chromosome regions
 1. Transcriptome profiling of subgenome across multiple tissues
 2. Protein abundance profiling of subgenome across multiple tissues
 3. Perform ChIP-seq analysis to examine histone marks enrichment over gene regions
- Evolution and transcription of accessible chromatin regions
 1. Analyze ATAC-seq data to examine its distribution and enrichment
 2. Comparisons of conserved accessible chromatin regions
 3. Examine enrichment of TEs near genes closest to accessible chromatin regions

Project II : *Mop1* mutation affects recombination rate in maize

1. Sample preparation for NGS experiment
2. Examine recombination rate of *mop1* mutant and wildtype
3. SNPs calling analysis for Big DNA resequencing data

Skills: Python (numpy, pandas, matplotlib), MySQL; cloud computing (ohio supercomputer center); DNA-seq, RNA-seq, Chip-seq, whole genome Bisulfite-seq and small RNA-seq analysis; BWA, GATK, Bcftools, Hisat2, Cufflinks, HTSeq, MACS2, ChromHMM, Bismark, Bowtie, Bedtools

Work Experiences

Graduate teaching assistant	Intro. Bioinformatics	2021
Graduate teaching assistant	Intro. Biology Laboratory	2020/2019
Data analyst	Shanghai Transmedia	2019
Clinical coordinator	Mingma Shanghai technologies	2018

Poster presentation

Yin et al., Chromatin types and epigenomic features shape the differentiation of the maize subgenomes. Maize Genetics Meeting, 2021.

Publications

Yin, Liangwei; Zhao, Meixia. Chromatin types and epigenomic features shape the differentiation of the maize subgenomes. In preparation for **Plant Journal**

Zhao, M., Ku, J. C., Liu, B., Yang, D., **Yin, L.**, Ferrell, T. J., ... & Lisch, D. (2021). The *mop1* mutation affects the recombination landscape in maize. **Proceedings of the National Academy of Sciences**, 118(7).

Li, Tong; **Yin, Liangwei**; Stoll, Claire; Lisch, Damon; Zhao, Meixia. Imprinted conserved non-coding sequences and novel imprinted genes introduced by Mutator transposons provide new insights into the mechanisms of genomic imprinting. (**Plant Cell**, Under Review).