

# YIN LIANGWEI

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## EDUCATION

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

## RESEARCH EXPERIENCE

08/2019-present      Master Graduate Assistant  
Cellular, Molecular, Structural Biology/Advisor: Dr. Meixia Zhao

**Project:** Chromatin and epigenetic features shape maize two subgenomes

- a. Evolutionary features of whole genome homologs in different genomic locations
  - Identify subgenome blocks and compare the distribution of genes, transposons (TEs), and recombination rates of genes.
  - Calculate and compare evolutionary rates (nucleotides substitution rates: Ka, Ks, w) of homologs.
  - Transcriptome profiling of dominant expressed homologs.
  - Protein abundance profiling of dominant expressed homologs.
- b. Epigenetic features of duplicated genes in different genomic locations
  - Examine genome-wide TE variation: the distance of homologs to its nearest TEs and the proportion of TE contents over the flanking regions of homologs.
  - Dissect RNA-directed DNA methylation pathway: whole genome bisulfite sequencing (WGBS) analysis of DNA methylation and small RNA analysis of 24 nucleotide small interference RNA.
  - Perform ChIP-seq analysis to explore the enrichment of covalent histone marks (H2A.Z, H3K4me1, H3Kme3, H3Kac) over homologs.
- c. Distribution and evolution of chromatin accessible regions (ACRs) of two subgenomes
  - Compare the distribution of ACRs flanking duplicates and peak values of ACRs.
  - Compare chromatin loops of distal ACRs to duplicates from HIC-seq data.
  - Identify syntenic ACRs in maize subgenomes and compare their evolutionary rates (K).
  - Examine effects of the retention and deletion of conserved ACRs on its targeted homologous genes.

**Project:** *Mop1* mutation affects recombination rates in maize

- a. Sample preparation for DNA resequencing experiments.
- b. Examine recombination rate of *mop1* mutant and wildtype by genotyping with indel markers.
- c. SNPs (single nucleotide polymorphism) calling analysis.

**Skills:** Maize fieldwork; Genotyping; Python (numpy, pandas, matplotlib), MySQL; cloud computing (ohio supercomputer center), Linux; 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/Bowtie2, Bedtools

## PROFESSIONAL EXPERIENCE

Data analyst	Shanghai Transmedia (Clinical data)	2019
<ul style="list-style-type: none"><li>• Tracked, collected, filtered, and analyzed clinical data</li><li>• Worked directly with the marketing from big pharmacy companies such as Johnson</li></ul>		
Clinical coordinator	Mingma Shanghai (Genetic Consulting)	2018
<ul style="list-style-type: none"><li>• Sorting out clinical information of rare-disease patients</li></ul>		

- Manage product tracking forms and ensure product quality
- Serve as the coordinator between researchers and the managers
- Learn the workflow of genetic counseling in ACMG

## **TEACHING EXPERIENCE**

Teaching Assistant	BIO256 Intro. Bioinformatics	2021
Teaching Assistant	BIO115/116 Intro. Biology Laboratory	2020/2019

## **CORE COURSES**

Bioinformatics Computing Skill, Molecular Biology, Advanced Cell Biology  
Genetics, Pharmacology, Introduction of clinical medicine, Health statistics

## **CERTIFICATE**

MiniMBA	Miami University	2021
The third-prize scholarship (5 times)	Hubei University of Chinese Medicine	2014-2018

## **POSTER**

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

## **PUBLICATION**

**Yin, Liangwei;** Zhao, Meixia. Analysis of maize subgenomes reveals no pronounced bias in pericentromeric regions. In preparation for the manuscript.

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. (revision)