

**YIN LIANGWEI**  
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## Education

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

## Research Experiences

### **Project I :** Chromatin and epigenetic features shape subgenome in maize

- Evolutionary feature 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 siRNA pattern.
- Dominant expression pattern under classified chromosome region
  1. Transcriptome profiling of subgenome across multiple tissues
  2. Protein abundance profiling of subgenome across multiple tissues
  3. Perform ChIPseq analysis to examine histone marks enrichment of high- and low-expressed genes
- Histone marks feature of subgenome genes
  1. Perform ChIPseq analysis to examine histone modifications on differentially evolutionary genes
  2. Histone features of classified chromosome region
  3. Chromosome segments identification by ChroHMM
  4. Examine enrichment of TE and histone marks surrounding classified genes

### **Project I I :** *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, Cuflinks, HTSeq, MACS2, ChromHMM, Bismark, Bowtie, Bedtools

## Work Experiences

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

## Poster presentations

**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).