YIN LIANGWEI

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EDUCATION

M. Sc. Bioinformatics	Miami University, USA	2021.12
B. Sc. Biotechnology	Hubei University of Chinese Medicine, China	2018.06

RESEARCH EXPERIENCE

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

Project: Analysis of maize subgenomes reveals no pronounced bias in pericentromeric regions

  a. Evolutionary features of whole genome duplicated genes in different genomic locations

- Identify subgenome blocks and compare number of duplicates, transposons (TEs), and recombination rates of duplicates..
- Calculate and compare evolutionary rates (nucleotide substitution rates: Ka, Ks, w).
- Transcriptome profiling of dominant expressed homoeologs.
- Protein abundance profiling of dominant expressed homoeologs.

  b. Epigenetic features of duplicated genes in different genomic locations

- Examine genome-wide TE variation: the distance of duplicates to its nearest TEs and the proportion of TE contents over the flanking regions of duplicates.
- Dissect RNA-directed DNA methylation pathway: whole genome bisulfite sequencing (WGBS) analysis and small RNA analysis.
- Perform ChIP-seq analysis to explore the enrichment of covalent histone marks (H2A.Z, H3K4me1, H3Kme3, H3Kac) over duplicates.

  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 rates 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

- Tracked, collected, filtered, and analyzed clinical data
- Worked directly with the marketing from big pharmacy companies such as Johnson

Clinical coordinator	Mingma Shanghai (Genetic Consulting)	2018

- Sorting out clinical information of rare-disease patients

- 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

2021	Teaching Assistant
	BIO256 (Intro. Bioinformatics), Miami University
2020/2019	Teaching Assistant
	BIO115/116 (Intro. Biology Lab), Miami University

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 schorlarship (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. Gene dominance in maize is largely absent in pericentromeric regions. Submitted to *Plant Cell*.

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. Submitted to *Plant Physiology*.

REFERENCE

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