Zhikai Yang

PHD · QUANTITATIVE GENETICS

University of Nebraska-Lincoln

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Education

University of Nebraska-Lincoln *Lincoln, NE, USA*

PHD, QUANTITATIVE GENETICS *08/2018 - 05/2024*

- Minor in statistics
- Advisor: Dr. Jinliang Yang
- Grade: 3.90/4.00

Purdue University *West Lafayette, IN, USA*

MS, CROP PHYSIOLOGY *08/2016 - 05/2018*

- Advisor: Dr. Cankui Zhang
- Grade: 4.00/4.00

Northwest A & F University *Yangling, Shaanxi, China*

BS, SEED SCIENCE & ENGINEERING *09/2012 - 07/2016*

- Grade: 92/100 (1st place in my college with around 240 students)

Teaching Experience

Teaching AGRO 215 Genetics *Lincoln, NE, USA*

UNIVERSITY OF NEBRASKA-LINCOLN *08/2021 - 12/2021*

- Lab experiment demonstration, answering questions, grading
- I received great reviews from both students and instructor and got Milton Mohr Fellowship, which needs candidate to show great communication and mentoring skills

Research Experience

Leveraging Gene Regulatory Network to Detect Epistasis for Heterosis in Maize *Lincoln, NE, USA*

UNIVERSITY OF NEBRASKA-LINCOLN *05/2023 - present*

- Using random forest based method to construct GRN for maize
- TWAS considering epistasis inferred from GRN
- Genomic prediction of heterosis considering epistasis inferred from GRN

Integration of multi-omics data to predict agronomic phenotypes in maize *Lincoln, NE, USA*

UNIVERSITY OF NEBRASKA-LINCOLN *04/2022 - 11/2023*

- Using rr-BLUP based method to predict UAV collected agronomic traits with both genome and microbiome
- We found microbiome-enabled GS model significantly outperformed the conventional model for image-extracted time-series traits, with up to 4.1% improvement (an average of 3.7%). The improvement was more prominent in low N than high N conditions (8.4% — 40.2% of relative improvement), consistent with the idea that certain beneficial microbes can promote plant nutrient uptake, especially under low N conditions. Additionally, we identified some mediator microbes, such as *Massilia putida*, are known to promote plant growth under LN. These large-effect ASVs or microbial agents could be leveraged as seed or soil additives to improve crop performance for sustainable agriculture.

Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize

Lincoln, NE, USA

UNIVERSITY OF NEBRASKA-LINCOLN

08/2018 - 04/2022

- GWAS of 106 agronomy and metabolites traits in maize
- High-dimensional mediation analysis for 106 agronomy and metabolite traits in maize
- Evaluation of performance of high-dimensional mediation analysis via simulation
- We detected N=736 unique mediating genes, explaining an average of 12.7% phenotypic variance due to mediation. Noticeably, 83/736 (11%) genes were identified in mediating more than one trait, suggesting the prevalence of pleiotropic mediating effects. Among those pleiotropic mediators, benzoxazinone synthesis 13 (*Bx13*), a well-characterized gene encoding a 2-oxoglutarate-dependent dioxygenase, was identified as a mediator regulating 40 agronomic and metabolic traits in different tissues. Further genetic and genomic analyses of the *Bx13* and adjacent mediating genes suggested a 3D co-regulation modulation likely affects their expression levels and eventually leads to phenotypic consequences

Physical contacts-enabled genetic epistasis detection in domestication from Teosinte to Modern Maize

Lincoln, NE, USA

UNIVERSITY OF NEBRASKA-LINCOLN

06/2021 - 12/2021

- GBLUP-based estimation of genetic epistasis of 3D genome interaction via HiChIP

Carbohydrate phloem loading mechanism in tobacco

West Lafayette, IN, USA

PURDUE UNIVERSITY

01/2017 - 05/2017

- Made RNAi construct of gene SUC2
- Did tobacco tissue culture and transformation
- qRT-PCR of tobacco leaves to measure the expression level of SUC2
- Measured photosynthesis, carbohydrate and starch content of tobacco leaves

C and N transport and assimilation in rice and potato

West Lafayette, IN, USA

PURDUE UNIVERSITY

08/2016 - 05/2018

- Made constructs pCOYMV :: GUS , pPP2:: AtSUC2 for rice
- Did potato tissue culture and transformation
- Extracted DNA and RNA to identify transgenic rice and quantify the gene expression
- Tetrazolium test to determine the viability of rice seeds and potato tubers
- Measured photosynthesis, fluorescence, chlorophyll, protein, sugar, starch concentration, stem height and width of potato

Identification of the salinity stress responsive miRNA in Triticum Dicoccoides

Yangling, Shaanxi, China

NORTHWEST A & F UNIVERSITY

09/2014 - 07/2016

- Learned Linux, Perl, Shell to facilitate the bioinformatics analysis of RNA-seq data
- Analyzed high-throughput sequencing data of miRNA using miRDeep2

Publications

Zhikai Yang, Tianjing Zhao, Cheng Hao, Jinliang Yang. 2023. Microbiome-enabled genomic selection improves prediction accuracy for nitrogen-related traits in maize. G3 Genes|Genomes|Genetics, doi: https://academic.oup.com/g3journal/advance-article/doi/10.1093/g3journal/jkad286/7479790

Zhikai Yang, Gen Xu, Qi Zhang, Toshihiro Obata, Jinliang Yang. 2022. Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize. Genetics, DOI: 10.1093/genetics/iyac057.

Xiaoming He, ..., **Zhikai Yang**, Peng Yu. 2024. Heritable microbiome variation is correlated with source environment in locally adapted maize varieties. Nature Plants, doi: https://doi.org/10.1038/s41477-024-01654-7.

Qi Zhang, **Zhikai Yang**, Jinliang Yang. 2024. Dissecting the colocalized GWAS and eQTLs with mediation analysis for high dimensional exposures and confounders. Biometrics, doi: https://doi.org/10.1101/2022.09.08.507169.

Jinlong Li, ..., **Zhikai Yang**, Shaojiang Chen. 2020. Genomic selection to optimize doubled haploid-based hybrid breeding in maize. bioRxiv, doi:https://doi.org/10.1101/2020.09.08.287672.

Presentations

Zhikai Yang. "Bridging the gap between genotype and phenotype via gene expression using genome-wide mediation analysis in maize". 2021 Cold Spring Harbor Laboratory Plant Genomes and Systems Biology Meeting, online.

Zhikai Yang. "Genome-wide mediation analysis: an empirical study to connect phenotype with genotype via intermediate transcriptomic data in maize". 2022 Maize Genetics Meeting, Saint Louis, MO.

Zhikai Yang. "Microbiome-enabled genomic selection model improves prediction accuracy for image-extracted traits in maize". 2023 Plant & Animal Genome Conference, San Diego, CA.

Zhikai Yang. "Microbiome-enabled genomic selection (MEGS): a method to enrich breeder's toolbox". 2023 Maize Genetics Meeting, Saint Louis, MO.

Leadership

2017 Graduate Student Plant Science Symposium   *West Lafayette, IN*
PURDUE UNIVERISTY   *Aug 2017*
- As a member of the committee, I participated in the preparation for the symposium and honored to be the judge for the travel scholarship

Professional Development

Deep Learning Specialization   *13 weeks*
COURSERA   *Jun 2023*
- Neural Networks and Deep Learning (4 weeks)
- Improving Deep Neural Networks: Hyperparameter Tuning, Regularization and Optimization (3 weeks)
- Structuring Machine Learning Projects (2 weeks)
- Convolutional Neural Networks (4 weeks)

High Throughput Computing on Open Science Grid   *1 week*
UNIVERSITY OF WISCONSIN-MADISON   *Aug 2021*
- Introduction to HTC and HTCondor
- Introduction to OSG and the OSPool
- Troubleshooting jobs

MCMC for Genetics   *3 days*
UNIVERSITY OF WASHINGTON-SEATTLE   *Jul 2020*
- Derive the (analytic) posterior distribution for a Binomial proportion given a conjugate (Beta) prior
- Implement a Metropolis-Hastings algorithm to sample from this posterior distribution and check that it matches the analytic form
- Derive the posterior distribution for cluster memberships given a prior on clusters and a likelihood for each cluster
- Implement a Gibbs sampler to sample from cluster memberships given data from a mixture of product-Bernoulli distributions
- Apply the structure software to a real dataset and interpret the output

Modern Programming in Genomic Prediction   *1 week*
UNIVERSITY OF CALIFORNIA-DAVIS   *Jun 2019*
- Mixed effects models with polygenic, maternal and permanent environment effects
- Use of pedigree information
- Iterative methods for solving linear systems, e.g, Jocobi
- GBLUP and Bayesian alphabet
- Variance component estimation

Honors & awards

Dec 2022   **Milton Mohr Fellowship**, University of Nebraska-Lincoln

Dec 2021   **Scholarship of Plant Genomes and Systems Biology**, Cold Spring Harbor Laboratory

Jun 2020   **Scholarship of Summer Institute in Statistical Genetics (SISG)**, University of Washington