Curriculum Vitae

Zhikai Liang

Plant and microbial biology department
University of Minnesota-Twin Cities

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Education

PhD Agronomy, Department of Agronomy and Horticulture (with James C. Schnable), University of Nebraska-Lincoln, Lincoln, USA, 2015-present

Major in Agronomy and Minor in Statistics

BA Agronomy, Nanjing Agricultural University, Nanjing, China, 2007-2011

Major in Plant Genetics and Breeding

Professional Experience

Postdoctoral Associate, Department of Plant and Microbial Biology, University of Minnesota-Twin Cities (with Nathan M. Springer), St. Paul, USA, 2019.11-present

Postdoctoral Associate, Department of Agronomy and Horticulture, University of Nebraska-Lincoln (with James C. Schnable), Lincoln, USA, 2019.8-2019.11

Research Assistant, Department of Agronomy and Horticulture, University of Nebraska-Lincoln, Lincoln, USA, 2015-2019

Research Assistant, Department of Biochemistry, Molecular Biology, Entomology and Plant Pathology, Mississippi State University, Starkville, USA, 2012-2015

Research Assistant, State Key Laboratory of Crop Genetics & Germplasm Enhancement, Nanjing Agriculture University, Nanjing, China, 2010-2012

Publications

Google Scholar

9. **Liang Z**, Gupta SK, Yeh CT,...,Yang J,Varshney RK, Schnable PS, Schnable JC (2018) Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. G3: Genes|Genomes|Genetics doi: 10.1534/g3.118.200242

   Selected as the outstanding scientific article in the Research Program-Asia at ICRISAT

8. **Liang Z**, Schnable JC (2018) Functional Divergence Between Subgenomes and Gene Pairs After Whole Genome Duplications. Molecular Plant doi: 10.1016/j.molp.2017.12.010

7. **Liang Z**, Pandey P, Stoerger V, Xu Y, Qiu Y, Ge Y, Schnable JC (2017) Conventional and hyperspectral time-series imaging of maize lines widely used in field trials. GigaScience doi: 10.1093/gigascience/gix117

   Selected as an oral presentation by 2017 American Geophysical Union Fall Meeting, December 2017

6. Zhang Y, Ngu DW, Carvalho D, **Liang Z**, Qiu Y, Roston RL, Schnable JC (2017) Differentially Regulated Orthologs in Sorghum and the Subgenomes of Maize. The Plant Cell doi: 10.1105/tpc.17.00354

   Selected as an Editor's Choice by MaizeGDB Editorial Board, August 2017

5. Lai X*, Behera B*, **Liang Z**, Lu Y, Deogun JS, Schnable JC (2017) STAG-CNS: An Order-Aware Conserved Non-coding Sequences Discovery Tool For Arbitrary Numbers of Species. Molecular Plant doi: 10.1016/j.molp.2017.05.010.

4. Choudhury SD, Samal A, Stoerger V, Schnable JC, **Liang Z**, Yu J (2016) Automated Vegetative Stage Phenotyping Analysis of Maize Plants using Visible Light Images. 22nd ACM SIGKDD Conference on Knowledge Discovery and Data Mining. San Francisco, California, USA

3. **Liang Z**, Schnable JC (2016) RNA-seq based analysis of population structure within the maize inbred B73. PLoS ONE doi: 10.1371/journal.pone.0157942

   Selected as an oral presentation by 58th Maize Genetics Conference, March 2016

2. Lv Y, **Liang Z**, Ge M, Qi W, Zhang T, Lin F, Peng Z, Zhao H (2016) Genome-wide identification and functional prediction of nitrogen-responsive intergenic and intronic long non-coding RNAs in maize (Zea mays L.). BMC Genomics doi: 10.1186/s12864-016-2650-1

1. Zhang Y, Zheng J, **Liang Z**, Liang Y, Peng Z, Wang C. (2015) Verification and evaluation of grain QTLs using RILs from TD70 x Kasalath in rice. Genet Mol Res doi: 10.4238/2015.November.18.53

Manuscripts under Review/Preprints

4. Jarquin D, Howard R, **Liang Z**, Gupta SK, Schnable JC, Crossa J (2019) Enhancing hybrid prediction in pearl millet using genomic and/or multi-environment phenotypic information of inbreds.

3. Dai X, Xu Z, **Liang Z**, Tu X, Zhong S, Schnable JC, Li P (2019) Using Machine Learning and Gene Nonhomology Features to Predict Gene Ontology. bioRixv. doi: 10.1101/730473v1

2. Hurst P, **Liang Z**, Smith C, Yerka M, Sigmon B, Rodriguez O, Schnable JC (2019) Genome Wide Analysis of Ga1-s Modifiers in Maize. bioRxiv. doi: 10.1101/543264

1. **Liang Z**, Qiu Y, Schnable JC (2019) Distinct Characteristics of Genes Associated with Phenome-Wide Variation in Maize (*Zea mays*). bioRxiv. doi: 10.1101/534503

   Selected as an oral presentation by 61st Maize Genetics Conference, March 2019

Presentations

Oral Presentations

11. **Liang Z** (2019) Invited talk in Chinese Genomics Meetup online (CGM) see Recorded Video.

10. **Liang Z** (2019) Coupling precise genomic and phenomic data on functional gene mining in maize. Invited talk in University of Georgia. Athens. Georgia.

9. **Liang Z** (2019) Coupling precise genomic and phenomic data on functional gene mining in maize. Invited talk in North Carolina State University. Raleigh. North Carolina.

8. **Liang Z**, Dai X and Schnable JC (2019) Zeavolution Online Meet-up (Hosted by Prof. Jeffrey Ross-Ibarra).

7. **Liang Z**, Qiu Y, Schnable JC (2019) Genome-Phenome Wide Association Study (GPWAS): Using high dimensional phenotype data to identify the the genes that specify the traits of maize. 61st Maize Genetics Conference. St. Louis. Missouri.

6. **Liang Z** (2019) Coupling precise genomic and phenomic data on functional gene mining in maize. Invited talk in Donald Danforth Plant Science Center. St. Louis. Missouri.

5. **Liang Z**, Bai G, Stoerger V, Qiu Y, Ge Y, Schnable JC. (2018) Advances in phenomic studies of expired patent maize hybrids and related public inbreds. Invited talk in Food and Crop Research Institute in Jiangsu Academy of Agricultural Sciences (JAAS). Nanjing, Jiangsu, China.

4. **Liang Z**, Bai G, Hurst P, Stoerger V, Shi Y, Qiu Y, Ge Y, Schnable JC. (2018) Fields and controlled environment phenotyping of North American maize lines from modern breeding programs. 2nd Asian-Pacific Plant Phenotyping Conference. Nanjing, Jiangsu, China.

3. **Liang Z**, Bai G, Stoerger V, Qiu Y, Ge Y, Schnable JC. (2018) Plant Phenomics-Phenotypes in dynamics, precision, diversity and high-throughput. Invited talk in China National Rice Research Institute in China Academy of Agricultural Sciences (CAAS), Hangzhou, Zhejiang, China.

2. **Liang Z**, Pandey P, Stoerger V, Xu Y, Qiu Y, Ge Y, Schnable JC. (2017) Changeable heritability of maize phenotypes across development quantified by HTP. Plant Science Innovation 2017 Annual Report. Lincoln, Nebraska.

1. **Liang Z**, Schnable JC. (2016) B73 maize population structure analysis by RNA-seq data. 58th Maize Genetics Conference. Jacksonville, Florida.

Poster Presentations

20. Meng X, Prust H, **Liang Z**, Dai X, Brandi S, Schnable JC (2019) Specialization of the separate male and female inflorescences of maize. 61st Maize Genetics Conference. St. Louis. Missouri.

19. Sigmon BA, **Liang Z**, Pester NS, Meier MA, Eskridge KM, Ramamurthy RK, Alfano JR, Yang J, Schnable JC (2019) Effects of Nitrogen Deficiency on Flowering Time and Inflorescence Morphology in a Maize Diversity Panel. Phenome 2019. Tuscon, Arizona.

18. **Liang Z**, Qiu Y, Schnable JC (2019) Genome-Phenome Wide Association Study (GPWAS): A model coupling high dimensional phenotypes to identify genes controlling pleiotropic phenotypic variation in maize (*Zea mays*). PAG XXVII, San Diego, California.

17. Dai X, **Liang Z**, Carvalho D, Li P, Schnable JC (2018) Identification of new genes involved in C4 photosynthesis using comparative genomes and big data. 2018 Nebraska Plant Science Retreat, Nebraska City, Nebraska.

16. Carvalho DS, **Liang Z**, Butera C, Stoerger V, Schnable JC (2018) High-throughput imaging and phenotyping of panicoid grain crops. 3rd International Symposium on Broomcorn Millet, Fort Collins, Colorado.

15. **Liang Z**, Pandey P, Stoerger V, Xu Y, Qiu Y, Ge Y, Schnable JC (2018) High-throughput imaging of maize lines from public and private sectors employed in field trials. Supercomputing and Life Sciences Symposium. Lincoln, Nebraska.

14. Miao C, Pandey P, **Liang Z**, Carvalho D, Ye X, Stoerger V, Xu Y, Ge Y, Schnable JC. (2018) Analysis of sorghum time-series phenotype data using functional ANOVA and machine learning. Phenome 2018. Tuscon, Arizona.

13. **Liang Z**, Bai G, Ge Y, Rodriguez O, Schnable JC. (2018) Field phenotype prediction on maize using novel phenomic tools and environmental information. 2018 NIFA FACT G2F Workshop. Ames, Iowa.

12. Schnable JC, Pandey P, Ge Y, Xu Y, Qiu Y, **Liang Z**. (2017) Lessons From Paired Data From ex-PVP Maize Lines in Agronomic Field Trials and RGB And Hyperspectral Time-Series Imaging In Controlled Environments. AGU 2017 Fall Meeting. New Orleans, Louisiana.

11. Sivakumar A, Shi Y, Li J, Ge Y, Schnable JC, Rodriguez O, **Liang Z**. (2017) Breeding for Increased Water Use Efficiency in Corn (Maize) Using a Low-Altitude Unmanned Aircraft System. AGU 2017 Fall Meeting. New Orleans, Louisiana.

10. **Liang Z**, Pandey P, Stoerger V, Xu Y, Qiu Y, Ge Y, Schnable JC. (2017) Conventional and hyperspectral time-series image data sets of maize inbred lines widely used in North American field trials. Nebraska EPSCoR RII Track 1 Grant External Review Panel Visit. Lincoln, Nebraska.

9. **Liang Z**, Bai G, Ge Y, Rodriguez O, Schnable JC. (2017) Field phenotype prediction on maize using novel phenomic tools and environmental ininformation. Plant Sicence Symposium "Predictive Crop Design: Genome to Phenome". Lincoln, Nebraska.

8. Sallam A, Jarquin D, **Liang Z**, Schnable JC, Lorenz A, Rodriguez O. (2017) Investigation of genetic structure and diversity of a subset of commercial popcorn inbred lines. 2017 UNL Plant Breeding and Genetics Symposium. Lincoln, Nebraska.

7. Zhang Y, Ngu DW, **Liang Z**, Carvalho D, Qiu Y, Roston RL, Schnable JC. (2017) Early transcriptional responses of conserved genes to cold diverge more slowly than downstream changes in panicoid grasses. 59th Maize Genetics Conference. St. Louis, Missouri.

6. **Liang Z**, Bai G, Ge Y, Rodriguez O, Schnable JC. (2017) Field phenotype prediction on maize using novel phenomic tools and environmental information. 59th Maize Genetics Conference. St. Louis, Missouri.

5. **Liang Z**, Bashyam S, Agarwal B, Samal A, Bai G, Chaudhury SD, Rodriguez O, Qiu Y, Ge Y, Schnable JC. (2016) Maize Phenomap1 and Phenomap2 datasets: Integration with genomes to fields. 4th International Plant Phenotyping Symposium. Texcoco, Mexico.

4. **Liang Z**, Bashyam S, Samal A, Choudhury SD, Geng B, Ge Y, Rodriguez O, Schnable JC. (2016) Computer vision based phenotyping of panicoid crops. 2016 Nebraska Plant Science Retreat. Nebraska City, Nebraska.

3. **Liang Z**, Bashyam S, Samal A, Choudhury SD, Geng B, Ge Y, Rodriguez O, Schnable JC. (2016) Computer vision based phenotyping of panicoid crops. 2016 Purdue Plant Science Symposium. West Lafaytte, Indiana.

2. **Liang Z**, Schnable JC. (2016) B73 maize population structure analysis by RNA-seq data. 2016 UNL Plant Breeding and Genetics Symposium. Lincoln, Nebraska.

1. **Liang Z**, Schnable JC. (2015) B73 maize population structure analysis by RNA-seq data. Plant Science Symposium "Plant Phenomics: from pixels to traits". Lincoln, Nebraska.

Patent/Copyright

Ren W, Jing X, Wen Z, **Liang Z**. (2018) NTsets: Normality Test sets integrated function and figure methods for continuous variables.

Computer Based Analysis Background

Python, R, Linux Bash Shell, Image Processing, Machine Learning, Deep Learning, Matlab (Basic)

Wetlab Background

RNA-seq library preparation, Various types of PCR, Western Blotting, Molecular Cloning, SDS-PAGE, Immunoprecipitation, Plant Suspension cell cultivation, Conventional plant transformation

Awards

3. 2019 Larrick and Whitmore Graduate Student Travel Grant.

2. 2017 2nd Midwest Big Data Summer School - Iowa State University, Travel Scholarship.

1. 2016 DuPont Plant Sciences Symposia Series - Purdue Plant Science Symposium, Travel Scholarship.

Professional Membership

Genetics Society of America (GSA)

American Society of Plant Biologist (ASPB)

Consortium for Integrated Translational Biology (CITB) at UNL

North American Plant Phenotyping Network (NAPPN)

Teaching Experience

Guest Lecturer, BCH8654 Intermediary Metabolism, Graduate Level, Mississippi State University (2014)

Enrolled Representative Courses

5. Multiple Regression (STAT 870)

4. Applied Multivariate Statistics (STAT 873)

3. Statistical Genomics (ASCI 896)

2. Statistic methods in Research (STAT 801)

1. Design and analysis standard (STAT 802)

Mentoring and Outreach

10. Mentor. Xiangdong (Brian) Liu in Department of Plant Pathology, on performing GWAS on ear traits of maize 282 panel in N plus and N deficiency field.

9. Evaluator. Undergraduate Creative Activities & Research Experiences (UCARE) 2019-2020 program at UNL.

8. Plantae Fellow. 2019 Plantae Fellows program.

7. Mentor. Mentored Complex Life Sciences first-year PhD rotation student Nate Korth, on performing GWAS on multiple grass species (Jan, 2018 - March, 2018)

6. Fascination of Plants Day 2017. Demonstrated the CoGe Comparative Genomic Tool to High School Student (May 18, 2017)

5. Committee. 2017 Dupont Pioneer - UNL Plant Breeding Symposium (2016 - 2017).

4. Mentor. Menotored Lab Undergraduate Student, Thomas Hoban, on screening sorghum root hairless mutant. (Oct.2016 - Oct.2017)

3. Mentor. Menotored Lab Undergraduate Student, Logan Olson, on maize diversity panel maintenance and propagation (Oct.2016 - Oct.2017)

2. Mentor. NSF REU (Research Experiences for Undergraduates) Sites Program Student, Kyle Johnsen. (June to August, 2016)

1. "Sunday with a scientist" Educated children on measuring plant seed phenotypes from computer vision. (May 15, 2016)

External Reviewer

BMC Genomics, Horticulture Research, The Plant Genome, Plant Methods, Crop Science, Scientific Reports, Plant Direct, International Journal of Molecular Sciences, Agronomy, Genes, Plants, PLoS ONE, PeerJ, Plant Molecular Biology Reporter, Biomolecules