

# Jinliang Yang

ASSISTANT PROFESSOR · UNL

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## Education

**Iowa State University**

Ames, IA, USA

**PH.D. IN INTERDEPARTMENTAL GENETICS**

Sep. 2008 - Sep. 2014

**China Agricultural University**

Beijing, China

**M.S. IN BIOCHEMISTRY AND MOLECULAR BIOLOGY**

Sep. 2005 - Aug. 2008

**China Agricultural University**

Beijing, China

**B.S. IN BIO-ENGINEERING**

Sep. 2001 - Aug. 2005

## Professional Experience

**University of Nebraska-Lincoln**

Lincoln, NE, USA

ASSISTANT PROFESSOR

Jul. 2017 - present

**Ross-Ibarra Lab, University of California, Davis**

Davis, CA, USA

POSTDOCTORAL RESEARCHER

Oct. 2014 - Jun. 2017

**Schnable Lab, Iowa State University**

Ames, IA, USA

RESEARCH ASSISTANT

Sep. 2008 - Sep. 2014

**Lai Lab, China Agricultural University**

Beijing, China

RESEARCH ASSISTANT

Sep. 2005 - Aug. 2008

## Teaching

|              |  |          |
|--------------|--|----------|
| Fall, 2019   | <b>Lecturer</b> AGRO/ASCI-931 Population Genetics (graduate level)   | UNL      |
| Fall, 2019   | <b>Lecturer</b> LEFE-891-003 Complex Biosystems Seminar  | UNL      |
| Fall, 2018   | <b>Lecturer</b> AGRO/ASCI-931 Population Genetics (graduate level)   | UNL      |
| Fall, 2018   | <b>Guest Lecturer</b> Life 891 Complex Biosystems (graduate level)   | UNL      |
| Spring, 2018 | <b>Guest lecturer on Genomic Prediction</b> ASCI944/STAT844 Quantitative Methods for Genomics of Complex Traits (graduate level) | UNL      |
| Fall, 2017   | <b>Guest lecturer on Maize Genomics and Genetics</b> Crop Genomics (graduate level)  | UNL      |
| 2015         | <b>Guest lecture on RNA-seq analysis</b> Ecological Genomics (graduate level)  | UC Davis |

## Current Funding

|           |   |                               |
|-----------|---|-------------------------------|
| 2019-2022 | <b>Rescuing the Fixed Deleterious Alleles for Genome-Enabled Micronutrients Improvement in Maize</b> PI, \$500,000  | USDA NIFA                     |
| 2018-2019 | <b>Leveraging genomics, phenomics and irrigation management (GPI) to improve water use efficiency of maize</b> PI, \$20,000                                     | NU System Science             |
| 2018-2019 | <b>Integrating Big Data in Agriculture to Facilitate Plant Breeding</b> PI, \$9,925   | UNL Layman Grant              |
| 2018-2019 | <b>Identification of metabolic traits related to drought resistance in maize which has been lost during domestication and breeding processes</b> Co-PI, \$9,955 | UNL Layman Grant              |
| 2018-2019 | <b>Epigenetic regulation during seed development in maize</b> Co-PI, \$52,373 (\$10,000 to UNL)   | Mississippi INBRE through NIH |

## Publications

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### Google Scholar Citation Metrics

#### PREPRINT

- C. Miao, T. P. Hoban, A. Pages, Z. Xu, E. Rodene, J. Ubbens, I. Stavness, **J. Yang**, and J. C. Schnable, **Simulated plant images improve maize leaf counting accuracy**, bioRxiv (2019).

#### 2019

- Y. Ge, A. Atefi, H. Zhang, C. Miao, R. K. Ramamurthy, B. Sigmon, **J. Yang**, J. C. Schnable, **High-throughput analysis of leaf physiological and chemical traits with VIS-NIR-SWIR spectroscopy: A case study with a maize diversity panel**, Plant Methods (2019).
- H. Liu, Q. Wang, M. Chen, Y. Ding, X. Yang, J. Liu, X. Li, C. Zhou, Q. Tian, Y. Lu, D. Fan, J. Shi, L. Zhang, C. Kang, M. Sun, F. Li, Y. Wu, Y. Zhang, B. Liu, X.Y. Zhao, Q. Feng, **J. Yang**, B. Han, J. Lai, X.S. Zhang, X. Huang, **Genome-wide identification and analysis of heterotic loci in three maize hybrids**, Plant Biotechnology Journal (2019).
- C. Miao, **J. Yang**, J. C. Schnable, **Optimizing the identification of causal variants across varying genetic architectures in crops**, Plant Biotechnology Journal (2019).

#### 2018

- R. Shao, H. Zheng, **J. Yang**, S. Jia, T. Liu, Y. Wang, J. Guo, Q. Yang, G. Kang, **Proteomics Analysis Reveals That Nitric Oxide Regulates Photosynthesis of Maize Seedlings under Water Deficiency**, Nitric Oxide (2018).
- **J. Yang**, C. E. Yeh, R. K. Ramamurthy, X. Qi, R. L. Fernando, J. C.M. Dekkers, D. J. Garrick, D. Nettleton and P. S. Schnable. **Empirical Comparisons of Different Statistical Models to Identify and Validate Kernel Row Number-Associated Variants from Structured Multiparent Mapping Populations of Maize**, G3: Genes Genomes Genetics (2018).
- Z. Liang, S. K. Gupta, C. T. Yeh, Y. Zhang, D. W. Ngu, R. Kumar, H. T. Patil, K. D. Mungra, D. V. Yadav, A. Rathore, R. K. Srivastava, R. Gupkta, **J. Yang**, R. K. Varshney, P. S. Schnable, J. C. Schnable. **Phenotypic data from inbred parents can improve genomic prediction in pearl millet hybrids**, G3: Genes Genomes Genetics (2018).
- C. Miao, J. Fang, P. Liang, D. Li, X. Zhang, **J. Yang**, J. C. Schnable, H. Tang. **Genotype-Corrector: improved genotype calls for genetic mapping**, Scientific Reports (2018).
- M. Bezruczyk, T. Hartwig, M. Horschman, S. N. Char, **J. Yang**, B. Yang, D. Sosso, W. Frommer. **Impaired phloem loading in genome-edited triple knock-out mutants of SWEET13 sucrose transporters**, New Phytologist (2018).
- P. Bilinski, P. S. Albert, J. J. Berg, J. Birchler, M. Grote, A. Lorant, J. Quezada, K. Swarts, **J. Yang**, J. Ross-Ibarra. **Parallel altitudinal clines reveal adaptive evolution of genome size in Zea mays**, PLOS Genetics (2018).

#### 2017

- **J. Yang**, S. Mezmouk, A. Baumgarten, E. S. Buckler, K. E. Guill, M. D. McMullen, R. H. Mumm, and J. Ross-Ibarra. **Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize**, PLOS Genetics (2017).
- H.-Y. Lin, Q. Liu, X. Li, **J. Yang**, S. Liu, Y. Huang, M. J. Scanlon, D. Nettleton, P. S. Schnable. **eRD\_GWAS reveals substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation**, Genome Biology (2017).
- Z. Dong, W. Li, E. Unger-Wallace, **J. Yang**, E. Vollbrecht, G. S. Chuck. **Ideal crop plant architecture is mediated by tassels replace upper ears1, a BTB/POZ ankyrin repeat gene 5 targeted by TEOSINTE BRANCHED1**, PNAS (2017).
- J. Hao, **J. Yang**, J. Dong, S.-z. Fei. **Characterization of BdCBF genes and Genome-wide Transcriptome Profiling of BdCBF3-dependent and -independent Cold Stress Responses in Brachypodium Distachyon**, Plant Science (2017).

## 2016 AND BEFORE

- **J. Yang**, H. Jiang, C.-T. Yeh, J. Yu, J. A. Jeddelloh, D. Nettleton, and P. S. Schnable. **Extreme-phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel**, The Plant Journal (2015).
- D. Sosso, D. Luo, Q.-B. Li, J. Sasse, **J. Yang**, G. Gendrot, M. Suzuki, K. E. Koch, D. R. McCarty, P. S. Chourey, P. M. Rogowsky, J. Ross-Ibarra, B. Yang, and W. B. Frommer. **Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport**, Nature genetics (2015).
- S. Leiboff, X. Li, H.-C. Hu, N. Todt, **J. Yang**, X. Li, X. Yu, G. J. Muehlbauer, M. C. P. Timmermans, J. Yu, P. S. Schnable, and M. J. Scanlon. **Genetic control of morphometric diversity in the maize shoot apical meristem**, Nature Communications (2015).
- **J. Yang**. **Genome-wide association studies to dissect the genetic architecture of yield-related traits in maize and the genetic basis of heterosis**, Iowa State University (2014).
- S. Liu, K. Ying, C.-T. Yeh, **J. Yang**, R. Swanson-Wagner, W. Wu, Todd Richmond, D. J. Gerhardt, J. Lai, N. Springer, D. Nettleton, J. A. Jeddelloh, P. S. Schnable. **Changes in genome content generated via segregation of non-allelic homologs**, The Plant Journal (2012).
- L. Koesterke, D. Stanzione, M. Vaughn, S. M. Welch, W. Kusnierczyk, **J. Yang**, C.-T. Yeh, D. Nettleton, P. S. Schnable. **An efficient and scalable implementation of SNP-pair interaction testing for genetic association studies**, IEEE International Symposium on Parallel and Distributed Processing Workshops and Phd Forum (2011).

## Patent Applications

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- Schnable PS, OTT A, **Yang J**. **Intercrossed ex-PVP lines**. 2014. (PENDING)
- Schnable PS, **Yang J**. **Identification of QTLs and trait-associated SNPs controlling six yield component traits in maize**. 2013. (PENDING)
- Schnable PS, **Yang J**, Swanson-Wagner RA, Nettleton D. **QTL regulating ear productivity traits in maize**. U.S. Patent No. 8779233. Filed July 12, 2011.

## Professional Service

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### NAPB Local Host Committee Member

NAPB ANNUAL MEETING

UNL

2019 - now

### Plant Growth Facilities Faculty Advisory Committee Member

UNL PLANT GROWTH FACILITIES

UNL

2019 - now

### NFHC Technical Project Manager Search Committee Member

NEBRASKA FOOD FOR HEALTH CENTER

UNL

Feb, 2019

### Poster Judge

2018 UNL PLANT BREEDING SYMPOSIUM POSTER COMPETITION

Lincoln, NE, USA

March 2018

### Organizing Committee Member

THE 3RD INTERNATIONAL SYMPOSIUM ON BROOMCORN MILLET

Fort Collins, CO, USA

August 8-12, 2018

### Distance Ed Specialist search committee member

DEPARTMENT OF AGRONOMY AND HORTICULTURE

UNL

June, 2018

## Invited Presentations (past three years)

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|            |  |                          |
|------------|--|--------------------------|
| Oct. 2019  | <b>DNA Methylome Selection Reshapes Gene Regulation and Affects Maize Adaptation</b> The 2nd annual Symposium on the Evolutionary Genomics of Adaptation | <i>Lincoln</i>           |
| April 2019 | <b>Maize phenomics and quantitative genetics</b> Center for Root & Rhizobiome Innovation (CRR) retreat   | <i>Lincoln</i>           |
| March 2019 | <b>Dissecting the Genetic Basis of Biological Nitrogen Fixation (BNF) in a Landrace of Maize</b> Nebraska Corn Board                                     | <i>Lincoln</i>           |
| Feb. 2019  | <b>Landscape and variation of DNA methylation during maize domestication and improvement</b> Zeavolution Online Meeting                                  |                          |
| May 2018   | <b>Understand the Genetic Architectures of Complex Traits</b> Panzea Online Meeting  |                          |
| Feb. 2018  | <b>The Genetic Cost of Maize Domestication</b> University of Missouri: Plant Science Seminar Series  | <i>Columbia, MO, US</i>  |
| Jan. 2018  | <b>Phenotypic effects of deleterious alleles and their contributions to heterosis in maize</b> PAG XXVI  | <i>San Diego, CA, US</i> |
| Jan. 2018  | <b>Mining Big Data in Maize: from genetics of deleterious alleles to epigenetics of methylation variation</b> PAG XXVI                                   | <i>San Diego, CA, US</i> |
| Nov. 2017  | <b>The Cost of Maize Domestication: Deleterious Alleles and Beyond</b> Northeast Normal University   | <i>Changchun, China</i>  |
| Nov. 2017  | <b>Agricultural Big Data and Insights for Maize Breeding</b> The 10th CAU Maize Breeding School  | <i>Beijing, China</i>    |
| Octo. 2017 | <b>Big Data in Maize: From Genetics of Bad Alleles to Epigenetics of Methylation Variation</b> Complex Biosystem Seminar                                 | <i>Lincoln, NE, US</i>   |
| Octo. 2017 | <b>The Cost of Domestication: Deleterious alleles and Beyond</b> Animal Breeding and Genetics Group Seminar  | <i>Lincoln, NE, US</i>   |
| Sept. 2017 | <b>The Cost of Domestication: Biological Knowledge Informed Genomic Selection</b> HZAU and UNL Joint Symposium   | <i>Lincoln, NE, US</i>   |
| Mar. 2017  | <b>ZeaBigData: a community curated data sharing platform</b> The 59th Annual Maize Genetics Conference   | <i>St. Louis, MO, US</i> |