

# Jinliang Yang

ASSISTANT PROFESSOR · UNL

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## Education

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<b>Iowa State University</b> <b>PH.D.</b> IN INTERDEPARTMENTAL GENETICS	Ames, IA, USA Sep. 2008 - Sep. 2014
<b>China Agricultural University</b> <b>M.S.</b> IN BIOCHEMISTRY AND MOLECULAR BIOLOGY	Beijing, China Sep. 2005 - Aug. 2008
<b>China Agricultural University</b> <b>B.S.</b> IN BIO-ENGINEERING	Beijing, China Sep. 2001 - Aug. 2005

## Professional Experience

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<b>University of Nebraska-Lincoln</b> ASSISTANT PROFESSOR	Lincoln, NE, USA Jul. 2017 - present
<b>Ross-Ibarra Lab, University of California, Davis</b> POSTDOCTORAL RESEARCHER	Davis, CA, USA Oct. 2014 - Jun. 2017
<b>Schnable Lab, Iowa State University</b> RESEARCH ASSISTANT	Ames, IA, USA Sep. 2008 - Sep. 2014
<b>Lai Lab, China Agricultural University</b> RESEARCH ASSISTANT	Beijing, China Sep. 2005 - Aug. 2008

## Teaching

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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

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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

#### 2018

- C. Miao, **J. Yang**, J. C. Schnable, **Optimizing the identification of causal variants across varying genetic architectures in crops**, Plant Biotechnology Journal (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.

## Invited Presentations (past three years)

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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>

## Professional Service

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<b>NFHC technical project manager search committee member</b> NEBRASKA FOOD FOR HEALTH CENTER	<i>UNL</i> <i>Feb, 2019</i>
<b>Poster Judge</b> 2018 UNL PLANT BREEDING SYMPOSIUM POSTER COMPETITION	<i>Lincoln, NE, USA</i> <i>March 2018</i>
<b>Organizing Committee Member</b> THE 3RD INTERNATIONAL SYMPOSIUM ON BROOMCORN MILLET	<i>Fort Collins, CO, USA</i> <i>August 8-12, 2018</i>
<b>Associate Editor</b> G3: GENES, GENOMES, GENETICS	<i>June, 2018-</i>

