

Jinliang Yang

ASSISTANT PROFESSOR · UNL

363 Keim Hall, Department of Agronomy and Horticulture, University of Nebraska-Lincoln, NE 68583

☎ (+1) 402-472-1408 | ✉ jinliang.yang@unl.edu | 🏠 jyanglab.com | 📱 jyanglab | 🐦 JinliangYang

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

Schnable Lab, University of Nebraska-Lincoln

Lincoln, NE, USA

POSTDOCTORAL RESEARCHER

Jan. 2017 - Jun. 2017

Ross-Ibarra Lab, University of California, Davis

Davis, CA, USA

POSTDOCTORAL RESEARCHER

Oct. 2014 - Dec. 2016

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

2018	Guest lecture on Genomic Prediction ASCI944/STAT844 Quantitative Methods for Genomics of Complex Traits (graduate level)	UNL
2017	Guest lecture on Maize Genomics and Genetics Crop Genomics (graduate level)	UNL
2015	Guest lecture on RNA-seq analysis Ecological Genomics (graduate level)	UC Davis

Current Funding

2018	Epigenetic regulation during seed development in maize Co-PI, \$52,373	Mississippi INBRE through NIH
2018-2022	Leveraging genomic prediction and exploiting exotic alleles for maize nutritional quality Co-PI, \$490,000 (returned by PI due to his personal reasons)	USDA NIFA
2017-2018	Recount RNA-seq reads on AGPv4 genome to facilitate genetic studies for maize community PI, XSEDE-allocated computational resources, \$1,400	XSEDE through NSF

Publications

Google Scholar Citation Metrics

MANUSCRIPTS IN PREPARATION

- **Yang, Jinliang**, Qing Li, John Doebley, Nathan Springer, and Jeffrey Ross-Ibarra. **Population Genetic Modeling of methylation variation in a natural teosinte population.**
- Kent, V. Tyler, Arun Durvasula, Siddharth Bhadra-Lobo, **Jinliang Yang**, Eric J. Fuchs, Griselda Arrieta-Espinoza, Jeffrey Ross-Ibarra **Population genomic assessment of crop-wild gene flow in the endangered wild rice *Oryza glumaepatula*.**

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* (2017).
- 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), in press.

2017

- **Yang, Jinliang**, Sofiane Mezouk, Andy Baumgarten, Edward S. Buckler, Katherine E. Guill, Michael D. McMullen, Rita H. Mumm, and Jeffrey Ross-Ibarra. **Incomplete dominance of deleterious alleles contributes substantially to trait variation and heterosis in maize.** *PLOS Genetics* (2017), in press.
- Hung-Ying Lin, Qiang Liu, Xiao Li, **Jinliang Yang**, Sanzhen Liu, Yinlian Huang, Michael J. Scanlon, Dan Nettleton, Patrick Schnable. **eRD_GWAS reveals substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation** *Genome Biology* (2017), in press.
- Zhaobin Dong, Wei Li, Erica Unger-Wallace, **Jinliang Yang**, Erik Vollbrecht, George 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), in press.
- Hao, Jingjie, **Jinliang Yang**, Jiangli Dong, Shui-zhang Fei. **Characterization of *BdCBF* genes and Genome-wide Transcriptome Profiling of *BdCBF3*-dependent and -independent Cold Stress Responses in *Brachypodium Distachyon*.** *Plant Science* (2017), 262: 52-61.

2015

- **Yang, Jinliang**, Haiying Jiang, Cheng-Ting Yeh, Jianming Yu, Jeffrey A. Jeddelloh, Dan Nettleton, and Patrick 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* 84, no. 3 (2015): 587-596.
- Sosso, Davide, Dangping Luo, Qin-Bao Li, Joelle Sasse, **Jinliang Yang**, Ghislaine Gendrot et al. **Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport.** *Nature genetics* (2015).
- Leiboff, Samuel, Xianran Li, Heng-Cheng Hu, Natalie Todt, **Jinliang Yang**, Xiao Li et al. **Genetic control of morphometric diversity in the maize shoot apical meristem.** *Nature Communications* 6 (2015).

2014 AND BEFORE

- **Yang, Jinliang.** **Genome-wide association studies to dissect the genetic architecture of yield-related traits in maize and the genetic basis of heterosis.** (2014).
- Liu, Sanzhen, Kai Ying, Cheng-Ting Yeh, **Jinliang Yang**, Ruth Swanson-Wagner, Wei Wu et al. **Changes in genome content generated via segregation of non-allelic homologs.** *The Plant Journal* 72, no. 3 (2012): 390-399.
- Koesterke, Lars, Dan Stanzione, Matt Vaughn, Stephen M. Welch, Waclaw Kusnierczyk, **Jinliang Yang**, et al. **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*, pp. 523-530. IEEE, 2011.

Patent Applications

- 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

Feb. 2018	The Genetic Cost of Maize Domestication University of Missouri: Plant Science Seminar Series	<i>Columbia, MO, US</i>
Jan. 2018	Phenotypic effects of deleterious alleles and their contributions to heterosis in maize PAG XXVI	<i>San Diego, CA, US</i>
Jan. 2018	Mining Big Data in Maize: from genetics of deleterious alleles to epigenetics of methylation variatio PAG XXVI	<i>San Diego, CA, US</i>
Nov. 2017	The Cost of Maize Domestication: Deleterious Alleles and Beyond Northeast Normal University	<i>Changchun, China</i>
Nov. 2017	Agricultural Big Data and Insights for Maize Breeding The 10th CAU Maize Breeding School	<i>Beijing, China</i>
Octo. 2017	Big Data in Maize: From Genetics of Bad Alleles to Epigenetics of Methylation Variation Complex Biosystem Seminar	<i>Lincoln, NE, US</i>
Octo. 2017	The Cost of Domestication: Deleterious alleles and Beyond Animal Breeding and Genetics Group Seminar	<i>Lincoln, NE, US</i>
Sept. 2017	The Cost of Domestication: Biological Knowledge Informed Genomic Selection HZAU and UNL Joint Symposium	<i>Lincoln, NE, US</i>
Mar. 2017	ZeaBigData: a community curated data sharing platform The 59th Annual Maize Genetics Conference	<i>St. Louis, MO, US</i>
Feb. 2016	Evolutionary constraint improves genomic-enabled prediction for heterosis Bay Area Population Genomics (BAPG) meeting XIII	<i>UC Berkeley, CA, US</i>
Oct. 2014	Using next-generation sequencing for genome-wide association and prediction in plants Plant Sciences Departmental Seminar	<i>UC Davis, CA, US</i>
Mar. 2014	Big data meets genomics: GWAS and genomic selection of yield related traits in maize Plant Sciences Departmental Seminar	<i>Wuhan, China</i>
Mar. 2014	Insights into heterosis The 56th Annual Maize Genetics Conference	<i>Beijing, China</i>
Feb. 2013	GBS-enabled GWAS: identification and validation of KRN-associated SNPs in maize Gordon Research Conference on Quantitative Genetics and Genomics	<i>Galveston, TX, US</i>
Feb. 2012	Identification and validation of maize loci controlling a yield component trait via 2nd generation Bayesian-based GWAS AB&G Seminar Series	<i>Ames, IA, US</i>