

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

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

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

Honors & Awards

2013	Sui Tong Chan Fung Fund for the Promotion of Study and Research in Genetics Iowa State University
2012	W. Young and W.E. Loomis travel award Iowa State University
2011	W. Young and W.E. Loomis travel award Iowa State University

Invited Presentations

Sept. 2017	The Cost of Domestication: Biological Knowledge Informed Genomic Selection HZAU and UNL Joint Symposium	Lincoln, NE, US
Mar. 2017	ZeaBigData: a community curated data sharing platform The 59th Annual Maize Genetics Conference	St. Louis, MO, US
Feb. 2016	Evolutionary constraint improves genomic-enabled prediction for heterosis Bay Area Population Genomics (BAPG) meeting XIII	UC Berkeley, CA, US
Oct. 2014	Using next-generation sequencing for genome-wide association and prediction in plants Plant Sciences Departmental Seminar	UC Davis, CA, US
Mar. 2014	Big data meets genomics: GWAS and genomic selection of yield related traits in maize Plant Sciences Departmental Seminar	Wuhan, China
Mar. 2014	Insights into heterosis The 56th Annual Maize Genetics Conference	Beijing, China
Feb. 2013	GBS-enabled GWAS: identification and validation of KRN-associated SNPs in maize Gordon Research Conference on Quantitative Genetics and Genomics	Galveston, TX, US
Feb. 2012	Identification and validation of maize loci controlling a yield component trait via 2nd generation Bayesian-based GWAS AB&G Seminar Series	Ames, IA, US

Current Funding

2017-2018	Recount RNA-seq reads on AGPv4 genome to facilitate genetic studies for maize community XSEDE-allocated computational resources, \$1,400	XSEDE by the NSF
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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.**
- Bilinski, Paul, Patrice Albert, James A Birchler, Jeremy J Berg, Mark Grote, Anne Lorant, Juvenal Quezada, Jinliang Yang, Jeffrey Ross-Ibarra. **Adaptive and parallel clinal reductions in genome size within *Zea mays* taxa.**
- Yang, Jinliang, Yeh CT, Fernando RL, Dekkers JCM, Garrick DJ, Nettleton D, Schnable PS. **Identification and genetic validation of nucleotide variants associated with the kernel row number trait of maize: an empirical comparison of GWAS approaches.**
- Yang, Jinliang, Li Li, Haiying Jiang, Cheng-Ting Yeh, Dan Nettleton, and Patrick Schnable. **Dominant gene action accounts for much of the genetic variance and provides insight into heterosis in maize.**
- 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*.**

2017

- 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.

2016

- 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.** bioRxiv (2016): 086132. Submitted to PLOS Genetics, in revision.

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, Wacław 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.