

# 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

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

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|-----------|---|---------------------|
| Mar. 2017 | <b>ZeaBigData: a community curated data sharing platform</b> The 59th Annual Maize Genetics Conference                            | St. Louis, MO, US   |
| Feb. 2016 | <b>Evolutionary constraint improves genomic-enabled prediction for heterosis</b> Bay Area Population Genomics (BAPG) meeting XIII | UC Berkeley, CA, US |
| Oct. 2014 | <b>Using next-generation sequencing for genome-wide association and prediction in plants</b> Plant Sciences Departmental Seminar  | UC Davis, CA, US    |
| Mar. 2014 | <b>Big data meets genomics: GWAS and genomic selection of yield related traits in maize</b> Plant Sciences Departmental Seminar   | Wuhan, China        |
| Mar. 2014 | <b>Insights into heterosis</b> 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

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- 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

## Publications

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### 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

- 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. Jeddloh, 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

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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.

## Peer Reviews

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### THE PLANT JOURNAL (1)

- Liu *et al.*, 2017, Genetic architecture of domestication syndrome in sorghum.

### THE PLANT CELL (1)

- Xiao and Yan. *et al.*, 2015, Low-freq variants play critical roles in the maize ear genetic architecture.

### BMC GENOMICS (4)

- Xu *et al.*, 2016, Exploring IBD segments and putative function to dissect the patterns of foundation parents formation in maize. **twice**
- Pan and Yan *et al.*, 2015, recombination landscape.
- Weng *et al.*, 2015, Genetic dissection of maize plant architecture with an ultra-high density bin map based on recombinant inbred lines.

### MOLECULAR PLANT (4)

- Kwong *et al.*, 2016, development and validation of a high density SNP genotyping array for African oil palm. **reviewed twice**
- Clevenger *et al.*, 2016, Genome-wide SNP genotyping resolves signatures of selection and tetrasomic recombination in peanut. **reviewed twice**

### BIOINFORMATICS (1)

- Fournier-level *et al.*, 2016, GWAlpha.