

# Jinliang Yang

POSTDOCTORAL SCHOLAR · UC DAVIS

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## Education

**Iowa State University**

**PH.D.** IN INTERDEPARTMENTAL GENETICS

*Ames, IA, USA*

*Sep. 2008 - Sep. 2014*

**China Agricultural University**

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

*Beijing, China*

*Sep. 2005 - Aug. 2008*

**China Agricultural University**

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

*Beijing, China*

*Sep. 2001 - Aug. 2005*

## Professional Experience

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

POSTDOCTORAL RESEARCHER

*Davis, CA, USA*

*Oct. 2014 - Present*

**Schnable Lab, Iowa State University**

RESEARCH ASSISTANT

*Ames, IA, USA*

*Sep. 2008 - Sep. 2014*

**Lai Lab, China Agricultural University**

RESEARCH ASSISTANT

*Beijing, China*

*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

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** 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*

## Publications

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### Google Scholar Citation Metrics

#### MANUSCRIPTS IN PREPARATION

- 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*.**
- 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*.**

#### 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.

#### 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.