Jinliang Yang

Department of Plant Sciences
University of California
One Shields Ave.
Davis, CA 95616

Phone: (515) 509-4552
Email: jolyang@ucdavis.edu
Homepage: http://yangjl.com
GitHub: https://github.com/yangjl

Professional Experience

2014-present	Postdoctoral Researcher with Jeffrey Ross-Ibarra, UC Davis
2008-2014	Research Assistant with Patrick Schnable, Iowa State University
2006-2008	Research Assistant with Jinsheng Lai, China Agricultural University

Education

2008-2014	PhD, Interdepartmental Genetics, Iowa State University
2005-2008	MS, Biochemistry and Molecular Biology, China Agricultural University
2001-2005	BS, Bio-engineering, China Agricultural University

Teaching Experience

2015	Guest lecture on RNA-seq analysis, (ECS243, graduate ecological genomics), UC Davis

Selected Awards

PhD Scholarship from Chinese Scholarship Council (2008-2012)

Sui Tong Chan Fung Fund for the Promotion of Study and Research in Genetics (Nov. 2013)

W. Young and W.E. Loomis travel award (Oct. 2012)

Scholarship for outstanding learning, China Agricultural University (2002)

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.

Presentations

Evolutionary constraint improves genomic-enabled prediction for heterosis, Bay Area Population Genomics (BAPG) meeting XIII at UC Berkeley. Feb. 2016.

Using next-generation sequencing for genome-wide association and prediction in plants, Plant Sciences Departmental Seminar, UC Davis. Oct. 2014.

Big data meets genomics: GWAS and genomic selection of yield related traits in maize, Huazhong Agricultural University, Wuhan, China. Mar. 2014.

Insights into heterosis, 56th Annual Maize Genetics Conference, Beijing, China. Mar. 2014.

GBS-enabled GWAS: identification and validation of KRN-associated SNPs in maize, Gordon Research Conference on Quantitative Genetics and Genomics, Galveston, TX. Feb. 2013.

Identification and validation of maize loci controlling a yield component trait via 2nd generation Bayesian-based GWAS AB&G Seminar Series, Ames, IA. Feb. 2012.

Publications

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**. (In Review)

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).

Yang, Jinliang, Haiying Jiang, Cheng-Ting Yeh, Jianming Yu, Jeffrey A. Jeddeloh, 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).

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**. *In* 2011 IEEE International Symposium on Parallel and Distributed Processing Workshops and Phd Forum, pp. 523-530. IEEE, 2011.

Manuscripts in Preparation

Yang, Jinliang, Sofiane Mezmouk, Andy Baumgarten, Edward S. Buckler, Katherine E. Guill, Michael D. McMullen, Rita H. Mumm, Jeffrey Ross-Ibarra. **Incorporation of evolutionary constraint improves genomic prediction of hybrid phenotypes**

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**.

Yang, Jinliang, Aaron Kusmec, Takeshi Yoshihara, Wei Zhang, Dan Nettleton, Edgar Spalding, Patrick Schnable. **Moon phase correlates with maize root growth in a genotype-specific manner**.

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***

Wang, Li, Timothy M Beissinger, Anne Lorant, **Jinliang Yang**, Jeffrey Ross-Ibrarra, Matthew B. Hufford. **Demography and evolution of maize diffusion across the Americas**