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

Teaching Experience

2015   Guest lecture, Ecological Genomics (ECS243, graduate class), UC Davis

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

Selected Awards

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

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

3. PhD Scholarship from Chinese Scholarship Council (2008-2012)

Invited Presentations

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

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

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

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

5. 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.

Publications

1. **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**. (SUBMITTED)

2. **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** (IN PREPARATION)

3. **Yang, Jinliang**, Li L, Jiang H, Yeh CT, Fernando RL, Dekkers JCM, Garrick DJ, Nettleton D, and Schnable PS. **Dominant gene action accounts for much of the missing heritability in a GWAS and provides insight into heterosis**. (IN PREPARATION)

4. Leiboff, Samuel, Xianran Li, Heng-Cheng Hu, Natalie Todt, **Jinliang Yang**, Xiao Li, Xiaoqing Yu et al. **Genetic control of morphometric diversity in the maize shoot apical meristem**. Nature Communications 6 (2015).

5. **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.

6. Sosso, Davide, Dangping Luo, Qin-Bao Li, Joelle Sasse, **Jinliang Yang**, Ghislaine Gendrot, Masaharu Suzuki et al. **Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport**. Nature genetics (2015).

7. Liu, Sanzhen, Kai Ying, Cheng-Ting Yeh, **Jinliang Yang**, Ruth Swanson-Wagner, Wei Wu, Todd Richmond et al. **Changes in genome content generated via segregation of non-allelic homologs**. The Plant Journal 72, no. 3 (2012): 390-399.

8. Koesterke, Lars, Dan Stanzione, Matt Vaughn, Stephen M. Welch, Waclaw Kusnierczyk, **Jinliang Yang**, Cheng-Ting Yeh, Dan Nettleton, and Patrick S. Schnable. **An efficient and scalable implementation of SNP-pair interaction testing for genetic association studies**. In Parallel and Distributed Processing Workshops and Phd Forum (IPDPSW), 2011 IEEE International Symposium on, pp. 523-530. IEEE, 2011.

Patent Applications

1. 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.

2. Schnable PS, **Yang J**. **Identification of QTLs and trait-associated SNPs controlling six yield component traits in maize**. 2013. (PENDING)

3. Schnable PS, OTT A, **Yang J**. **Intercrossed ex-PVP lines**. 2014. (PENDING)