

## **JINLIANG YANG**

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### **EDUCATION AND RESEARCH EXPERIENCE:**

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| 2014-present | Postdoctoral Scholar in Dept. of Plant Sciences, University of California, Davis, CA, US<br>Supervised by Dr. Jeffrey Ross-Ibarra |
| 2008-2014    | Ph.D. in Interdepartmental Genetics, Iowa State University, Ames, IA, US<br>Supervised by Dr. Patrick Schnable                    |
| 2005-2008    | M.S. in Biochemistry and Molecular Biology, China Agricultural University, Beijing, CHN   |
| 2001-2005    | B.S. in Bioengineering, China Agricultural University, Beijing, CHN   |

### **AWARDS:**

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| Nov. 2013 | Sui Tong Chan Fung Fund for the Promotion of Study and Research in Genetics |
| Feb. 2012 | Spring 2012 W. Young and W.E. Loomis travel award                           |
| Oct. 2010 | Fall 2010 W. Young and W.E. Loomis travel award                             |
| 2008-2012 | PhD Scholarship from CSC (Chinese Scholarship Council)                      |
| 2002      | Scholarship for outstanding learning, China Agricultural University         |

### **PUBLICATIONS:**

1. **J Yang**, CT Yeh, RL Fernando, JCM Dekkers, DJ Garrick, D Nettleton, and PS Schnable. Identification and cross-validation of maize loci controlling Kernel Row Number (KRN) variation via GWAS. PLOS ONE. In press
2. **J Yang**, H Jiang, CT Yeh, JA Jeddelloh, D Nettleton, and PS Schnable. Identification of SNPs controlling maize Kernel Row Number (KRN) via an

Extreme Phenotype Genome-Wide Association Study (XP-GWAS). The Plant Journal. In press

3. S Liu, K Ying, CT Yeh, **J Yang**, R Swanson-Wagner, W Wu, T Richmond, et al. (2012). Changes in genome content generated via segregation of non-allelic homologs. The Plant Journal : for cell and molecular biology, 72(3), 390–9. doi:10.1111/j.1365-3113X.2012.05087.x

4. L Koesterke, D Stanzione, M Vaughn, SM Welch, W Kusnierczyk, **J Yang**, CT Yeh, D Nettleton, and PS Schnable. (2011). An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies. 2011 IEEE International Symposium on Parallel and Distributed Processing Workshops and Phd Forum, 523–530. doi:10.1109/IPDPS.2011.190

## **PAPERS IN PREPARATION:**

1. **J Yang**, L Li, H Jiang, CT Yeh, RL Fernando, JCM Dekkers, DJ Garrick, D Nettleton, and PS Schnable. A GWAS for trait-associated SNPs that exhibit dominance effects provides insight into the origin of heterotic groups.

2. **J Yang**, A Kusmec, T Yoshihara, W Zhang, D Nettleton, E Spalding, and PS Schnable. Moon phase correlates with maize root growth in a genotype-specific manner.

3. **J Yang**, S Mezmouk, A Baumgarten, ES Buckler, KE Guill, MD McMullen, RH Mumm, and J Ross-Ibarra. Incorporation of evolutionary constraint improves genomic prediction of hybrid phenotype.

## **PATENT APPLICATIONS:**

PS Schnable, **J Yang**, RA Swanson-Wagner, D Nettleton. 2011. QTL regulating ear productivity traits in maize. U.S. Patent No. 8779233. Filed July 12, 2011.

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

PS Schnable, A OTT, **J Yang**. 2014, Intercrossed ex-PVP lines.

## **TEACHING:**

Guest lecture, Feb 23<sup>rd</sup>, 2015, RNA-seq: Experimental design and differential expression analysis.

## **PEER REVIEWS:**

Peer reviewed papers for The Plant Cell and BMC genomics.

## **SELECTED PRESENTATIONS:**

Plant Sciences Departmental Seminar, UC Davis, October 22<sup>nd</sup>, 2014, Using next-generation sequencing for genome-wide association and prediction in plants.

Huazhong Agricultural University, March. 24<sup>th</sup>, 2014, Big Data meets Genetics: GWAS and Genomic Selection of Yield Related Traits in Maize.

56<sup>th</sup> Annual Maize Genetics Conference, March. 14<sup>th</sup>, 2014, Insights into Heterosis.

Gordon Research Conference on Quantitative Genetics and Genomics, Feb. 18<sup>th</sup>, 2013, GBS-enabled GWAS: Identification and Validation of Kernel Row Number-associated SNPs in Maize.

Spring Semester 2012 AB&G Seminar Series, Iowa State University, Feb. 7<sup>th</sup>, 2012 Identification and validation of maize loci controlling a yield component trait via 2<sup>nd</sup> generation Bayesian-based GWAS.

## **SELECTED POSTERS & ABSTRACTS:**

54<sup>th</sup> Annual Maize Genetics Conference, March 15<sup>th</sup>-18<sup>th</sup>, 2012.

**J Yang**, W Wu, CT Yeh, DJ Garrick, J Yu, D Nettleton, PS Schnable, Identification and validation of maize loci controlling a yield component trait via 2<sup>nd</sup> generation Bayesian-based GWAS.

53<sup>rd</sup> Annual Maize Genetics Conference, March 18<sup>th</sup>-21<sup>st</sup>, 2011.

**J Yang**, DJ Garrick, JCM Dekkers, CT Yeh, J Yu, D Nettleton, PS Schnable, Bayesian-based GWAS: identification of loci controlling variation in yield component traits in the Nested Association Mapping (NAM) population.

The Plant & Animal Genome XVIII Conference, Jan. 9<sup>th</sup>-13<sup>th</sup>, 2010.

**J Yang**, RA Swanson-Wagner, D Nettleton, PS Schnable, Fine mapping a QTL regulating variation in kernel row number in maize.

The Plant & Animal Genome XVII Conference, Jan. 10<sup>th</sup>-14<sup>th</sup>, 2009.

**J Yang**, RA Swanson-Wagner, D Nettleton, PS Schnable, Identification of QTLs controlling heterosis for seedling dry weight and cob weight in maize.

## **STATISTICAL SHORT COURSES:**

Animal Breeding & Genetics Short Courses, Summer 2010 at Iowa State University.

Summer Institute in Statistical Genetics, Module 15: Mixed Models in Quantitative Genetics and Module 20: Advanced R Programming for Bioinformatics, 2011 at University of Washington.