Jinliang Yang POSTDOCTORAL SCHOLAR · UNL

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Education

Educat	ion	
	e University NTERDEPARTMENTAL GENETICS	Ames, IA, USA Sep. 2008 - Sep. 2014
China Agricultural University M.S. IN BIOCHEMISTRY AND MOLECULAR BIOLOGY		Beijing, China Sep. 2005 - Aug. 2008
_	Ccultural University D-ENGINEERING	Beijing, China Sep. 2001 - Aug. 2005
Profess	sional Experience	
Schnable Lab, University of Nebraska, Lincoln POSTDOCTORAL RESEARCHER		Lincoln, NE, USA Jan. 2017 - Present
Ross-Ibarra Lab, University of California, Davis POSTDOCTORAL RESEARCHER		Davis, CA, USA Oct. 2014 - Dec. 2016
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
Teachi	ng	
2015	Guest lecture on RNA-seq analysis Ecological Genomics (graduate level)	UC Davis
Honors	s & Awards	
2013	Sui Tong Chan Fung Fund for the Promotion of Study and Research in Genetics Iowa State University	
2012 2011	W. Young and W.E. Loomis travel award Iowa State University W. Young and W.E. Loomis travel award Iowa State University	
Invited	Presentations	
Mar. 2017	ZeaBigData: a community curated data sharing platform The 59th Annua Maize Genetics Conference	St. Louis, MO, US
Feb. 2016	heterosis Bay Area Population Genomics (BAPG) meeting XIII	UC Berkeley, CA, US
Oct. 2014	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 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 Identification and validation of maize loci controlling a yield component trait via 2nd generation Bayesian-based GWAS AB&G Seminar Series

Galveston, TX, US

Ames, IA, US

Current Funding

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

Soogle 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, accepted.

2016

• Yang, Jinliang, Sofiane Mezmouk, 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. 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).
- 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, Waclaw 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

- 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.