

Xianran Li, Ph.D.

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Education

- 09/2003 – 07/2008 Ph.D. in Crop Genetics and Breeding
China Agricultural University, Beijing, China
- 09/1996 – 07/2000 B.Sc. in Beijing Institute of Technology, Beijing, China

Professional experience

- 05/2018 – present Adjunct Associate Professor, Graduate School Faculty, Iowa State University
- 10/2015 – present Scientist I, Iowa State University
- 10/2013 – 10/2015 Research Assistant Professor, Iowa State University
- 01/2013 – 10/2013 Postdoc Research Associate, Iowa State University
- 12/2008 – 12/2012 Postdoc Research Associate, Kansas State University
- 07/2000 – 04/2003 Group leader of Beijing Genomics Institute (BGI)

Grants

1. Advancing phenomics capacity to empower biological research. NSF-USDA: EAGER. Co-PI. (2016-2018, \$260,000)
2. Decipher natural variation underlying pseudo-overdominance heterosis. ISU CBC Seed Grant Initiative. Co-PI. (2019, \$15,000)
3. Screen the targeted region with CRISPR-Cas9 editing technology to rapidly identify the underlying gene contributing to heterosis. ISU CBC Seed Grant Initiative. Co-PI. (2017, \$10,000)

Invited oral presentations

1. Crop genome divergence along domestication captured by base composition from genome-wide SNPs. The 5th Conference on Plant Genome Evolution | September 29 – October 1, 2019 | Sitges, Spain
2. Evolution of African agroecosystem: condensed tannins. Shandong Agricultural University | July 9, 2019 | Tai'an, China
3. Allelochemicals targeted to balance competing selection forces in African agroecosystem. China Agricultural University | July 7, 2019 | Beijing, China
4. *In-season* and *on-target* prediction for traits of complex plasticity in diverse environments. Plant and Animal Genome XXVII Conference | January 12 – 16, 2019 | San Diego, CA
5. Chromosomal deletions within the *RPAD* locus drove parallel domestication of plant architecture in Asian and African rice. Plant and Animal Genome XXVII Conference | January 12 – 16, 2019 | San Diego, CA
6. Turbocharging gene banks from genetic and environmental perspectives. 2018 ASA and CSSA Meeting | November 4 – 7, 2018 | Baltimore, MD
7. Dissection of genetic and environmental determinants advances phenotype prediction. September 11, 2018 | USDA ARS, Lubbock, TX
8. From complex to simple: dissecting genetic and environmental determinants advances phenotype prediction. The 12th Congress of the International Plant Molecular Biology | August 5 – 10, 2018 | Montpellier, France
9. Knowledge discovery and data mining: dynamics of genome size and composition. Plant and Animal

Genome XXV Conference | January 14 – 18, 2017 | San Diego, CA

10. Connecting DNA repair genes with genome divergence through base composition at polymorphic site. Plant and Animal Genome XXIV Conference | January 9 – 13, 2016 | San Diego, CA
11. Gene *v.s.* non-gene: contribution to maize agricultural traits. July 17, 2013 | China Agricultural University, Beijing, China
12. Genome-wide association studies identify genic and non-genic contributions to quantitative trait variation in maize. The 8th International Purdue Symposium on Statistics. June 22 – 24, 2012 | Purdue University, West Lafayette, IN
13. A conserved bound on variation of chromosome size among eukaryotes. September 26, 2011 | USDA Hard Winter Wheat Genetics Research Unit, Manhattan, KS

Professional contributions

- Journal reviewer: *Plant Biotechnology Journal*, *Journal of Experimental Botany*, *Bioinformatics*, *BMC Genomics*, *Journal of Heredity*, *Molecular Genetics and Genomics*, *Genes*, *Crop Science*, *Theoretical and Applied Genetics*, *PLoS One*, *Scientific Reports*, and *Plants*.
- Workshop organizer of “Hybridization, heterosis and balancing selection” at Plant and Animal Genome Conference (2019 and 2018)

Selected referred publications (*, co-corresponding author; #, co-1st author)

1. Yuyue Wu, Tingting Guo, Qi Mu, Jinyu Wang, Xin Li, Yun Wu, Bin Tian, Ming Li Wang, Guihua Bai, Ramasamy Perumal, Harold Trick, Scott Bean, Ismail Dweikat, Mitchell Tuinstra, Geoffrey Morris, Tesfaye Tesso, Jianming Yu*, and **Xianran Li***. Allelochemicals targeted to balance competing selections in African agroecosystems. *Nature Plants*. 2019, doi: 10.1038/s41477-019-0563-0.
2. Zhihai Zhang, Xuan Zhang, Zhelong Lin, Jian Wang, Hangqiu Liu, Leina Zhou, Shuyang Zhong Yan Li Can Zhu, Jinsheng Lai, **Xianran Li**, Jianming Yu, and Zhongwei Lin. A large transposon insertion in the *Stiff1* promoter controls stalk strength in maize. *Plant Cell*. 2019, doi:10.1105/tpc.19.00486.
3. Steffen Knauer, Marie Javelle, Lin Li, **Xianran Li**, Xiaoli Ma, Kokulapalan Wimalanathan, Sunita Kumari, Robyn Johnston, Samuel Leiboff, Robert Meeley, Patrick Schnable, Doreen Ware, Carolyn Lawrence-Dill, Jianming Yu, Gary Meuhlbauer, Michael Scanlon, and Marja Timmermans. A high-resolution gene expression atlas links dedicated meristem genes to key architectural traits. *Genome Research*. 2019, 1962-1973.
4. Jinyu Wang, **Xianran Li***, Kyung Do Kim, Michael Scanlon, Scott Jackson, Nathan Springer, and Jianming Yu*. Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. *Genome Biology*. 2019, 20:74.
5. Si Nian Char, Jialu Wei, Qi Mu, **Xianran Li**, Zhuanyuan Zhang, Keith Edwards, Jianming Yu, and Bing Yang. An *Agrobacterium*-delivered CRISPR/Cas9 system for targeted mutagenesis in sorghum. *Plant Biotechnology Journal*. 2019, doi: 10.1111/pbi.13229.
6. Tingting Guo, Xiaoqin Yu, **Xianran Li**, Haozhe Zhang, Chengsong Zhu, Sherry Flint-Garcia, Michael McMullen, James Holland, Randall Wissler, and Jianming Yu. Optimal designs for genomic prediction in hybrid crops. *Molecular Plant*. 2019, 3:390-401.
7. Xin Li[#], Tingting Guo[#], Qi Mu, **Xianran Li***, and Jianming Yu*. Genomic and environmental determinants and their interplay underlying phenotypic plasticity. *PNAS*. 2018, 115: 6679-6684.
8. Yongzhen Wu[#], Shuangshuang Zhao[#], **Xianran Li[#]**, Bosen Zhang, Liyun Jiang, Yanyan Tang, Jie Zhao, Xin Ma, Hongwei Cai, Chuanqing Sun, and Lubin Tan. Deletions linked to *PROG1* gene

- participate in plant architecture domestication in Asian and African rice. *Nature Communications*. 2018, 9:4157.
9. James McNellie, Junping Chen, **Xianran Li**, and Jianming Yu. Genetic mapping of foliar and tassel heat stress tolerance in field grown maize. *Crop Science*. 2018, 58: 2484-2493.
 10. Matthew Dziermit, Xianran Li, and Jianming Yu. Dissection of leaf angle variation in maize through genetic mapping and meta-analysis. *Plant Genome*. 2018, doi: 10.3835/plantgenome2018.05.0024.
 11. Adam Vanous, Candice Gardner, Michael Blanco, Adam Martin-Schwarze, Jinyu Wang, **Xianran Li**, Alexander Lipka, Sherry Flint-Garcia, Martin Bohn, Jode Edwards, and Thomas Lübberstedt. Stability analysis of kernel quality traits in exotic derived maize doubled haploid lines. *Plant Genome*. 2018, doi:10.3835/plantgenome2017.12.0114.
 12. Xiaoqin Yu, **Xianran Li**, Tingting Guo, Chengsong Zhu, Yuye Wu, Sharon Mitchell, Kraig Roozeboom, Donghai Wang, Ming Li Wang, Gary Pederson, Tesfaye Tesso, Patrick Schnable, Rex Bernardo, and Jianming Yu. Genomics Prediction contributing to a promising global strategy to turbocharge gene banks. *Nature Plants*. 2016, 2: 16150.
 13. Sivakumar Sukumaran, Xin Li, **Xianran Li**, Chensong Zhu, Guihua Bai, Ramasamy Perumal, Mitchell Tuinstra, Sharon Mitchell, Tesfaye Tesso, and Jianming Yu. QTL mapping for grain yield, flowering time, and stay-green traits in sorghum with genotyping-by-sequencing markers. *Crop Science*. 2016, 56: 1429-1142.
 14. **Xianran Li**, Michael Scanlon, and Jianming Yu. Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. *Nucleic Acids Research*. 2015, 43: 3614-3625.
 15. Xin Li, **Xianran Li**, Eyal Fridman, Tesfaye Tesso, and Jianming Yu. Dissecting repulsion linkage in the *Dw3* region for sorghum plant height provides insights into heterosis. *PNAS*. 2015, 112: 11823-11828.
 16. Samuel Leiboff, **Xianran Li**, Alvis Hu, Natalie Todt, Jinliang Yang, Xiao Li, Xiaoqing Yu, Gary Muehlbauer, Marja Timmermans, Jianming Yu, Patrick Schnable, and Michael Scanlon. Genetic control of morphometric diversity in the maize shoot apical meristem. *Nature Communications*. 2015, 6:8974.
 17. **Xianran Li**, Chengsong Zhu, Cheng-Ting Yeh, Wei Wu, Elizabeth Takacs, Katherine Petsch, Feng Tian, Guihua Bai, Edward Buckler, Gary Muehlbauer, Marja Timmermans, Michael Scanlon, Patrick Schnable, and Jianming Yu. Genic and non-genic contributions to natural variation of quantitative traits in maize. *Genome Research*. 2012, 22: 2436-2444.
 18. Yuye Wu, **Xianran Li**, Wenwen Xiang, Chengsong Zhu, Zhongwei Lin, Yun Wu, Jiarui Li, Guihua Bai, Ming Li Wang, Harold Trick, Scott Bean, Mitchell Tuinstra, Tesfaye Tesso, and Jianming Yu. Presence of tannins in sorghum grains is conditioned by different natural alleles of *Tan1*. *PNAS*. 2012, 109: 10281-10286.
 19. Zhongwei Lin, **Xianran Li**, Laura Shannon, Cheng-Ting Yeh, Ming Li Wang, Guihua Bai, Zhao Peng, Jiarui Li, Harold Trick, Thomas Clemente, John Doebley, Patrick Schnable, Mitchell Tuinstra, Tesfaye Tesso, Frank White, and Jianming Yu. Parallel domestication of genes encoding *Shattering1* in cereals. *Nature Genetics*. 2012, 44: 720-4.
 20. Vitara Pungpapong, William Muir, **Xianran Li**, Dabao Zhang, and Min Zhang. A fast and efficient approach for genomic selection with high density markers. *G3: Genes / Genomes / Genetics*. 2012, 2: 1179-1184.
 21. **Xianran Li**[#], Chengsong Zhu[#], Zhongwei Lin[#], Yun Wu, Dabao Zhang, Guihua Bai, Weixing Song, Jianxin Ma, Gary Muehlbauer, Michael Scanlon, Min Zhang*, and Jianming Yu*. Chromosome size in diploid eukaryotic species centers on the average length with a conserved boundary. *Molecular*

- Biology and Evolution*. 2011, 28: 1901-1911.
22. Chengson Zhu, **Xianran Li**, and Jianming Yu. Integrating Rare-variant testing, function prediction, and gene network in composite resequencing-based genome-wide association studies (CR-GWAS). *G3: Genes / Genomes / Genetics*. 2011, 1: 233-243.
 23. James Nelson, Shichen Wang, Yuye Wu, **Xianran Li**, Ginny Antony, Frank White, and Jianming Yu. Single-nucleotide polymorphism discovery by high-throughput sequencing in sorghum. *BMC Genomics*. 2011, 12:352.
 24. **Xianran Li**, ..., and Chuanqing Sun. Isolation and characterization of conserved non-coding sequences among rice (*Oryza Sativa* L.) paralogous regions. *Molecular Genetics and Genomics*. 2009, 281: 11-18.
 25. **Xianran Li**, ..., and Chuanqing Sun. Patterns of nucleotide diversity in wild and cultivated rice. *Plant Systematics and Evolution*. 2009, 281: 97-106.
 26. Ligu Wang, Lili Hao, **Xianran Li**, ..., and Jun Yu. SNP deserts of Asian cultivated rice: genomic regions under domestication. *Journal of Evolutionary Biology*. 2009, 22: 751-761.
 27. Lubin Tan, **Xianran Li**, Fengxia Liu, ..., and Chuanqing Sun. Control of a key transition from prostrate to erect growth in rice domestication. *Nature Genetics*. 2008, 40: 1360-1364.
 28. **Xianran Li**, ..., and Chuanqing Sun. Construction of the physical map of *gpa7* locus reveals a large segment is deleted during the rice domestication. *Plant Cell Reports*. 2008, 27: 1087-1092.
 29. **Xianran Li**, ..., and Chuanqing Sun. Construction of a bacterial artificial chromosome (BAC) library of common wild rice (*Oryza rufipogon* Griff.) for map-based cloning of genes selected during the domestication of rice. *Biotechnology Letters*. 2008, 30: 555-561.
 30. Zhongwei Lin, Megan E. Griffith, **Xianran Li**, Zuofen Zhug, ..., Daoxin Xie, and Chuanqing Sun. Origin of seed shattering in rice (*Oryza sativa* L.). *Planta*. 2007, 226: 11-20.
 31. Jun Yu, Jun Wang, Wei Lin, ..., **Xianran Li**, ..., Jian Wang, Gane Ka-Shu Wong, and Huanming Yang. The Genomes of *Oryza sativa*: A history of duplications. *PLoS Biology*. 2005, 3: 266-281.
 32. Jun Yu, Songnian Hu, Jun Wang, ..., **Xianran Li**, ..., Jian Wang, Gane Ka-Shu Wong, and Huanming Yang. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science*. 2002, 296: 79-92.
 33. Jun Yu, Songnian Hu, Jun Wang, ..., **Xianran Li**, ..., and Huanming Yang. A draft sequence of the rice (*Oryza sativa* L. subsp. *indica*) genome. *Chinese Science Bulletin*. 2001, 46: 1937-1942.
- (Under review)
34. Tingting Guo, Qi Mu, Jinyu Wang, Adam Vanous, **Xianran Li***, and Jianming Yu*. Dynamic effects of flowering-time genes underlying phenotypic plasticity in rice.
 35. **Xianran Li**, Tingting Guo, Jinyu Wang, ..., and Jianming Yu. Phenotypic plasticity analyses reveal gene-environment interplay and enable genome-wide across-environment prediction.
 36. Xiaoqing Yu, Samuel Leibo, **Xianran Li**, Tingting Guo, Natalie Ronning, Xiaoyu Zhang, Gary Muehlbauer, Marja Timmermans, Patrick Schnable, Michael Scanlon, and Jianming Yu. Genomic prediction of maize micro-phenotypes provides insights for optimizing selection and mining diversity.