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PROFESSIONAL EXPERIENCE

September 2014 until now, Postdoc Research Associate,
Jianming Yu's group <Quantitative genetics and maize breeding>,
Department of Agronomy, Iowa State University, Ames, Iowa, 50011, USA.

September 2008 to July 2014, Master and Ph.D.,
Jiansheng Li's group <Maize genetics and breeding>,
Chinese Agricultural University, Beijing, 100193, China.

Jiankang Wang's group <Quantitative genetics and molecular design breeding>,
Institute of Crop Science, Chinese Academy of Agriculture Sciences, Beijing, 100081,
China.

September 2009 to November 2009, Visiting fellow,
Rex Bernardo's group <Crop genetics and breeding>,
Department of Agronomy and Plant Genetics, University of Minnesota, Minneapolis,
Minnesota, 55455, USA.

May 2012 to November 2012, Visiting fellow,
Jianbing Yan's group <Maize genetics and molecular breeding>,
Department of Life Science, Huazhong Agricultural University, Wuhan, Hubei, 430070,
China.

September 2004 to June 2008, Bachelor,
College of Bioengineering, Chengdu University of Technology, Chengdu, Sichuan,
610059, China.

PUBLICATIONS

Tingting Guo, Xiaoqing Yu, Xianran Li, Haozhe Zhang, Chengsong Zhu, Sherry Flint-Garcia, Michael D. McMullen, James B. Holland, Randall J. Wisser, and Jianming Yu. Design thinking and data mining to streamline genomic selection. 2018. Prepared

Xin Li*, **Tingting Guo***, Qi Mu, and Xianran Li, Jianming Yu. Genetic and environmental determinants and their interplay underlying phenotypic plasticity. 2018. Reviewed under Proc Nat Acad Sci.

Danilo Hottis Lyra, Ítalo Stefanine Correia Granato, Pedro Patric Pinho Morais, Filipe Couto Alves, Anna Rita Marcondes Santos, Xiaoqing Yu, **Tingting Guo**, Jianming Yu, Roberto

Fritsche-Neto. Controlling population structure in the genomic prediction of tropical maize hybrids. 2018. Prepared.

Xiaoqing Yu, Samuel Leiboff, Xianran Li, **Tingting Guo**, Natalie Todt, Gary J. Muehlbauer, Marja C. P. Timmermans, Xiaoyu Zhang, Patrick S. Schnable, Michael J. Scanlon & Jianming Yu. Turbocharging gene banks via genomic prediction in micro-world: a case study of maize shoot apical meristem. 2018. Prepared.

Xiaoqing Yu, Xianran Li, **Tingting Guo**, Chengsong Zhu, Yuye Wu, Sharon E. Mitchell, Kraig L. Roozeboom, Donghai Wang, Ming Li Wang, Gary A. Pederson, Tesfaye T. Tesso, Patrick S. Schnable, Rex Bernardo & Jianming Yu. Genomic prediction contributing to a promising global strategy to turbocharge gene banks. 2016. Nat Plants 2:16150–16150.

Tingting Guo, Ning Yang, Qingchun Pan, Hao Tong, Xiaohong Yang, Jihua Tang, Jiankang Wang, Jiansheng Li, Jianbing Yan. Dissection of genetic basis of grain yield heterosis through high density SNP map with an “immortalized F₂” population of maize. 2014. Theor Appl Genet 127:2149–2158

Hui Li, Zhiyu Peng, Xiaohong Yang, Weidong Wang, Junjie Fu, Jianhua Wang, Yingjia Han, Yuchao Chai, **Tingting Guo**, Ning Yang, Jie Liu, Marilyn L Warburton, Yanbing Cheng, Xiaomin Hao, Pan Zhang, Jinyang Zhao, Yunjun Liu, Guoying Wang, Jiansheng Li & Jianbing Yan. Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. 2013. Nat Genet 45: 43–50.

Tingting Guo, Huihui Li, Jihua Tang, jiansheng Li, Rex bernardo, Jianbing Yan, Zhiwu Zhang, Jiankang Wang. Prediction of F₁ hybrid performance between recombinant inbred lines derived from two inbred lines in maize. 2013. Theor Appl Genet 126(1):189–201

Weiwei Wen*, **Tingting Guo***, Victor. H. Chavez Tovar, Jiangkang Wang, Jianbing Yan, Suketoshi Taba. The strategy and potential utilization of temperate germplasm for tropical germplasm improvement—a case study of maize (*Zea Mays* L.). 2012. Molecular Breeding. 29: 951–962.

*Authors contributed equally.

RESEARCH EXPERIENCE

- Study applied quantitative genetics, including QTL linkage mapping and association mapping, genomic prediction, and plant breeding simulation.
- Develop advanced models to predict hybrid performance in an immortalized F₂ population of maize. The applied prediction models include BLUP (best linear unbiased prediction), Ridge regression model, Bayesian lasso regression etc.
- Extend BLUP model to predict vigor of progenies derived from different heterotic populations.
- Dissect genetic basis of grain yield heterosis through high density bin map in maize.
- Investigate gene diversity on metabolite pathway among heterotic groups.
- Streamline genomic prediction using data mining and data thinking.

- Dissect environmental and genetic determinants underlying Genomic by environmental interaction.

BASIC SKILLS

- Proficient in Microsoft Office, SAS, R.
 - Programing Macro in SAS, and programing function and package in R.
 - Have a basic familiarity of Linux operation system.
- Proficient in simulation breeding software and gene mapping software.
 - QuLine, IciMapping, Cartographer/WinQTLCart, Mapmaker, JoinMap, NTSYS, Tassel,
 - Association mapping tools: Structure, GAPIT, TASSEL, Impute2, Beagle.
 - Experienced in breeding tool IBP and Prism.
- Knowledge in Breeding and Genetics.
 - Molecular genetics, quantitative genetics, and plant breeding.
- Knowledge in data mining.
 - Data processing, data curing, data learning and prediction.
- Teaching and presenting.
 - Instructor in class: Advanced plant breeding.
 - Speaker in PAG and Maize genetic meeting.
- Language: Chinese/English.