

**Yinping Jiao, Ph.D.**  
Department of Plant and Soil Science  
Texas Tech University Lubbock, TX 79409-2122  
Phone: 806-834-6696  
yijiao@ttu.edu

### Profession Experience

---

01/2020 - Present     Assistant Professor, Texas Tech University  
08/2015 - 06/2017     Research Associate, USDA-ARS  
09/2012 - 12/2019     Computational Postdoctoral Fellow, Cold Spring Harbor Laboratory

### Education

---

2012    Ph.D.    China Agricultural University, Plant Genetics and Breeding  
2007    B.S.     Shandong Agricultural University, Biotechnology

### Awards and Honors

---

2021    The Plant Journal Fellow  
2012    Doctoral Graduate with Most Distinction, China Agricultural University

### Publications

---

1. Gladman, N., Olson, A., Wei, S., Chougule, K., Lu, Z., Tello-Ruiz, M., Meijs, I., Van Buren, P., **Jiao, Y.**, Wang, B., Kumar, V., Kumari, S., Zhang, L., Burke, J., Chen, J., Burow, G., Hayes, C., Emendack, Y., Xin, Z. & Ware, D. 2022. SorghumBase: a web-based portal for sorghum genetic information and community advancement. *Planta*, 255, 35.
2. Tello-Ruiz, M. K., Naithani, S., Gupta, P., Olson, A., Wei, S., Preece, J., **Jiao, Y.**, Wang, B., Chougule, K., Garg, P., Elser, J., Kumari, S., Kumar, V., Contreras-Moreira, B., Naamati, G., George, N., Cook, J., Bolser, D., D'eustachio, P., Stein, L. D., Gupta, A. Xu, W., Regala, J., Papatheodorou, I., Kersey, P. J., Flicek, P., Taylor, C., Jaiswal, P. & Ware, D. 2021. Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. *Nucleic Acids Res*, 49, D1452-D1463.
3. Wang, L., Lu, Z., Regulski, M., **Jiao, Y.**, Chen, J., Ware, D. & Xin, Z. BSaseq: an interactive and integrated web-based workflow for identification of causal mutations in bulked F2 populations. *Bioinformatics*. 2020
4. Wang, B., Tseng, E., Baybayan, P., Eng, K., Regulski, M., **Jiao, Y.**, Wang, L., Olson, A., Chougule, K., Buren, P. V. & Ware, D. Variant phasing and haplotypic expression from long-read sequencing in maize. *Communication Biol*, 2020, 3, 78.
5. Gladman N, **Jiao, Y** Lee Y.K, Zhang L, Chopra R, Regulski M, Burow G, Hayes C, Christensen S.A, Dampanaboina L, Chen J, Burke J, Ware D, and Xin Z. Fertility of Pedicellate

Spikelets in Sorghum Is Controlled by a Jasmonic Acid Regulatory Module. *International journal of molecular sciences*. 2019, 20

6. Dampanaboina L, **Jiao Y**, Chen J, Gladman N, Chopra R, Burow G, Hayes C, Christensen S.A, Burk J, Ware D, and Xin Z. Sorghum MSD3 Encodes an omega-3 Fatty Acid Desaturase that Increases Grain Number by Reducing Jasmonic Acid Levels. *International journal of molecular sciences*. 2019.20.
7. Chen J, **Jiao Y**, Laza H, Payton P, Ware D, and Xin Z. Identification of the First Nuclear Male Sterility Gene (Male-sterile 9) in Sorghum. *The Plant Genome*. 2019,12.
8. Wittmeyer K, Cui J, Chatterjee D, Lee T, Tan Q, Xue W, Jiao Y, Wang P, Gaffoor I, Ware D, Blake Meyers C. B, Chopra S. The dominant and poor penetrant phenotypes of the maize mutation Unstable factor for orange1 are caused by DNA methylation changes at a linked transposon. *The Plant Cell*. 2018. 30 (12):3006-3023.
9. **Jiao Y**, Lee Y, Gladman N, Chopra R, Christensen S, Regulski M, Burow G, Hayes C, Burke J, Ware D, Xin Z. *MSDI* regulates pedicellate spikelet fertility through the jasmonic acid pathway in sorghum. *Nature Communications*. 2018, 9: 822.
10. **Jiao Y**, Burow G, Gladman N, Acosta-Martinez V, Chen J, Burke J, Ware D, Xin Z. Efficient identification of causal mutations through sequencing of bulked F2 from two allelic bloomless mutants of sorghum bicolor. *Frontiers in plant science*, 2018, 8 (2267).
11. Sun S, Zhou Y, Chen J, Shi J, Zhao H, Zhao H, Song W, Zhang M, Cui Y, Dong X, Liu H, Ma X, **Jiao Y**, Wang B, Wei X, Stein JC, Glaubitz JC, Lu F, Yu G, Liang C, Fengler K, Li B, Rafalski A, Schnable PS, Ware DH, Buckler ES, Lai J. Extensive intraspecific gene order and gene structural variations between Mo17 and other maize genomes. *Nature Genetics*. 2018
12. Springer N, [24 authors], **Jiao Y**, [25 authors], Brutnell T. The W22 genome: a foundation for maize functional genomics and transposon biology. *Nature Genetics*. 2018
13. Xin Z, Chen J, **Jiao Y**, Gladman N, Hayes C, Burow G, Emendack Y, Burke JJ. Registration of BTx623ms8, a New and Easily Identifiable Nuclear Male Sterile Mutant in Sorghum. *Journal of Plant Registrations*. 2018
14. **Jiao Y**, Peluso P, Shi J, Liang T, Stitzer MC, Wang B, Campbell MS, Stein JC, Wei X, Chin CS, Guill K, Regulski M, Kumari S, Olson A, Gent J, Schneider KL, Wolfgruber TK, May MR, Springer NM, Antoniou E, McCombie WR, Presting GG, McMullen M, Ross-Ibarra J, Dawe RK, Hastie A, Rank DR, Ware D. Improved maize reference genome with single-molecule technologies. *Nature*. 2017;546(7659):524-7.
15. Bukowski R, Guo X, Lu Y, Zou C, He B, Rong Z, Wang B, Xu D, Yang B, Xie C, Fan L, Gao S, Xu X, Zhang G, Li Y, **Jiao Y**, Doebley JF, Ross-Ibarra J, Lorant A, Buffalo V, Romay MC, Buckler ES, Ware D, Lai J, Sun Q, Xu Y. Construction of the third generation Zea mays haplotype map. *GigaScience*. 2017, gix134-gix134

16. Monaco MK, Naithani S, Stein J, Gupta P, Campbell M, Olson A, Wei S, Preece J, Geniza M, **Jiao Y**, Lee Y, Wang B, Mulvaney J, Chougule K, Elser J, Al-Bader N, Kumari S, Thomason J, Kumari V, Bolser D, Naamati G, Tapanari E, Fonseca N, Huerta L, Iqbal H, Keays M, Fuentes A, Tang A, Fabrega A, Weiser J, D'Eustachio P, Stein L, Petryszak R, Papatheodorou I, Kersey PJ, Taylor C, Jaiswal P, Ware D. Gramene 2018: Unifying Comparative Genomics and Pathway Resources for Plant Research. *Nucleic Acids Research*, 2017, gkx1111
17. Zhang K, Zheng G, Saul K, **Jiao Y**, Xin Z, Wang D. Evaluation of the multi-seeded (msd) mutant of sorghum for ethanol production. *Industrial Crops and Products*. 2017;97:345-53.
18. **Jiao Y**, Burke J, Chopra R, Burow G, Chen J, Wang B, Hayes C, Emendack Y, Ware D, Xin Z. A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. *The Plant Cell*. 2016;28(7):1551-62.
19. Wang B, Tseng E, Regulski M, Clark TA, Hon T, **Jiao Y**, Lu Z, Olson A, Stein JC, Ware D. Unveiling the complexity of the maize transcriptome by single-molecule long-read sequencing. *Nature Communications*. 2016;7:11708.
20. Xin Z, **Jiao Y**, Chopra R, Gladman N, Burow G, Hayes C, Chen J, Emendack Y, Ware D, Burke J. Pedigreed Mutant Library - A Unique Resource for Sorghum Improvement and Genomics. *Sorghum: State of the Art and Future Perspectives*. 2016 (book chapter).
21. Tello-Ruiz MK, Stein J, Wei S, Preece J, Olson A, Naithani S, Amarasinghe V, Dharmawardhana P, **Jiao Y**, Mulvaney J, Kumari S, Chougule K, Elser J, Wang B, Thomason J, Bolser DM, Kerhornou A, Walts B, Fonseca NA, Huerta L, Keays M, Tang YA, Parkinson H, Fabregat A, McKay S, Weiser J, D'Eustachio P, Stein L, Petryszak R, Kersey PJ, Jaiswal P, Ware D. Gramene 2016: comparative plant genomics and pathway resources. *Nucleic Acids Research*. 2016;44(D1):D1133-40.
22. Monaco MK, Stein J, Naithani S, Wei S, Dharmawardhana P, Kumari S, Amarasinghe V, Youens-Clark K, Thomason J, Preece J, Pasternak S, Olson A, **Jiao Y**, Lu Z, Bolser D, Kerhornou A, Staines D, Walts B, Wu G, D'Eustachio P, Haw R, Croft D, Kersey PJ, Stein L, Jaiswal P, Ware D. Gramene 2013: comparative plant genomics resources. *Nucleic Acids Research*. 2014;42(Database issue):D1193-9.
23. **Jiao Y**, Zhao H, Ren L, Song W, Zeng B, Guo J, Wang B, Liu Z, Chen J, Li W, Zhang M, Xie S, Lai J. Genome-wide genetic changes during modern breeding of maize. *Nature Genetics*. 2012;44(7):812-5.
24. Zhang M, Zhao H, Xie S, Chen J, Xu Y, Wang K, Zhao H, Guan H, Hu X, **Jiao Y**, Song W, Lai J. Extensive, clustered parental imprinting of protein-coding and noncoding RNAs in developing maize endosperm. *Proc Natl Acad Sci U S A*. 2011;108(50):20042-7.
25. **Jiao Y**, Song W, Zhang M, Lai J. Identification of novel maize miRNAs by measuring the precision of precursor processing. *BMC Plant Biology*. 2011;11:141.
26. Dong Y, Lu X, Song W, Shi L, Zhang M, Zhao H, **Jiao Y**, Lai J. Structural characterization of helitrons and their stepwise capturing of gene fragments in the maize genome. *BMC Genomics*.

2011;12:609.

27. Lai J, Li R, Xu X, Jin W, Xu M, Zhao H, Xiang Z, Song W, Ying K, Zhang M, **Jiao Y**, Ni P, Zhang J, Li D, Guo X, Ye K, Jian M, Wang B, Zheng H, Liang H, Zhang X, Wang S, Chen S, Li J, Fu Y, Springer NM, Yang H, Wang J, Dai J, Schnable PS, Wang J. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genetics*. 2010;42(11):1027-30.

### *Patents*

---

Xin, Z, Burow G. B, Hayes C. M, Ware D, Burke J. J and **Jiao Y**. Sorghum yield enhancement gene. US Patent App. 15/067,641, 2016

Xin Z, Burow G. B, Hayes C. M, Burke, J. J, Ware D and **Jiao Y**. Mutant Sorghum bicolor having enhanced seed yield. US Patent App. 15/086,992, 2016