Junli Zhang

Postdoctoral Scholar · UC Davis

Your address here, City, State xxxxxx

(+1) xxx-xxx-xxxx | zhjl86@gmail.com | pinbo | junli-zhang-2016 | aswillow

Education

Department of Plant Sciences, University of California, Davis — *Davis, California, USA*
Postdoctoral Scholar in Dubcovsky's lab — *Nov 2013 - Present*

Department of PSES, University of Idaho — *Moscow, Idaho, USA*
Ph.D. in Plant Science — *Aug 2008 - Dec 2013*

College of Agronomy, Northwest A&F University — *Yangling, Shaanxi, China*
B.S. in Agronomy — *Sep. 2004 - Jul. 2008*

Skills

Basic Programming	Python, Perl, Markdown, LaTeX, R, SAS, Shell Script
Quantitative Genetics	Linkage mapping, association mapping, fine mapping
Lab Skills	Common lab procedures used in molecular genetics
Statistics	Good at experiment design and statistical analysis
Bioinformatics	Shell Script, Slurm usage, blast, exome capture
Software	Microsoft Office, R, SAS, MapMaker 3.0b, QTL Cartographer, TASSEL, GAPIT, R/qtl
Languages	English, Chinese

Experience

Dubcovsky's lab, Department of Plant Sciences, University of California, Davis — *Davis, CA, USA*
Postdoctoral Scholar — *Nov. 2013 - Present*

- Fine Mapping and Cloning Genes Related to Drought Tolerance and Yield Components in Wheat
- Genome-wide Association Study on Water Use Efficiency and Yield Components of Wheat Using an Association Mapping Panel and Nested Association Mapping Panel
- Genome-wide Association Mapping of Stripe Rust Resistance in Spring Hexaploid Wheat from National Small Grains Collection (NSGC)

Chen's Lab, Department of PSES, University of Idaho — *Moscow, ID, USA*
Research Assistant — *Aug 2008 - Oct 2013*

- Association Mapping of Hagberg Falling Number in Hard White Spring Wheat
- Water and Nitrogen Use Efficiency Study of Triticeae CAP (TCAP) Wheat and Barley Collections (Canopy spectrum reflectance and genome-wide association mapping)
- Quantitative Trait Locus (QTL) Mapping of Grain Yield and Physiological Traits Using a Population of Recombinant Inbred Lines of Common Wheat
- Study on Barley Yellow Dwarf Virus (BYDV) Resistance of Bread Wheat by RNAi Technique Using Both Virus-Induced Gene Silencing (VIGS) and Transgenic Methods

Honors & Awards

2011-2012	Easton, Gene and Marlene PSES Scholarship	*University of Idaho*
2010-2011	Pure Line Scholarship & Toevs, John L. & Lois K. Scholarship	*University of Idaho*

Professional Affiliation

Since 2011	American Society of Agronomy (ASA)	*USA*
Since 2011	Crop Science Society of America (CSSA)	*USA*

Publications

Google Scholar Citation Metrics

ResearchGate Profile

2017

- Dong, Z., J.M. Hegarty, **J. Zhang**, W. Zhang, S. Chao, X. Chen, Y. Zhou, and J. Dubcovsky. 2017. Validation and characterization of a QTL for adult plant resistance to stripe rust on wheat chromosome arm 6BS (*Yr78*). Theor Appl Genet: Available at `https://link.springer.com/article/10.1007/s00122-017-2946-9`. (**First 3 authors contributed equally**)
- Liu, Y., **J. Zhang**, Y.-G. Hu, and J. Chen. 2017. Dwarfing genes *Rht4* and *Rht-B1b* affect plant height and key agronomic traits in common wheat under two water regimes. Field Crops Research 204: 242–248.
- Wang, R., J. Chen, J.A. Anderson, **J. Zhang**, W. Zhao, J. Wheeler, N. Klassen, D.R. See, and Y. Dong. 2017. Genome-wide association mapping of Fusarium head blight resistance in spring wheat lines developed in the Pacific Northwest and CIMMYT. Phytopathology: Available at `http://apsjournals.apsnet.org/doi/abs/10.1094/PHYTO-02-17-0073-R`.

2016

- Bulli, P., **J. Zhang**, S. Chao, X. Chen, and M. Pumphrey. 2016. Genetic architecture of resistance to stripe rust in a global winter wheat germplasm collection. G3 6(8): 2237–2253.
- Chen, J., M.J. Guttieri, **J. Zhang**, D. Hole, E. Souza, and B. Goates. 2016a. A novel QTL associated with dwarf bunt resistance in Idaho 444 winter wheat. Theor Appl Genet: 1–10.
- Chen, J., J. Wheeler, K. O'Brien, W. Zhao, N. Klassen, **J. Zhang**, B. Bowman, Y. Wang, C. Jackson, J.M. Marshall, and X.M. Chen. 2016b. Registration of "UI Platinum" Hard White Spring Wheat. Journal of Plant Registrations 10(1): 36–40.

2015

- Bonman, J.M., E.M. Babiker, A. Cuesta-Marcos, K. Esvelt-Klos, G. Brown-Guedira, S. Chao, D. See, J. Chen, E. Akhunov, **J. Zhang**, H.E. Bockelman, and T.C. Gordon. 2015. Genetic diversity among wheat accessions from the USDA National Small Grains Collection. Crop Science 55(3): 1243–1253.
- Bowman, B.C., J. Chen, **J. Zhang**, J. Wheeler, Y. Wang, W. Zhao, S. Nayak, N. Heslot, H. Bockelman, and J.M. Bonman. 2015. Evaluating grain yield in spring wheat with canopy spectral reflectance. Crop Science 55(5): 1881–1890.
- Maccaferri, M., **J. Zhang**, P. Bulli, Z. Abate, S. Chao, D. Cantu, E. Bossolini, X. Chen, M. Pumphrey, and J. Dubcovsky. 2015. A genome-wide association study of resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*) in a worldwide collection of hexaploid spring wheat (*Triticum aestivum* L.). G3 5(3): 449–465. (**First 3 authors contributed equally**)

2014

- **Zhang, J.**, J. Chen, B.C. Bowman, K. O'Brien, J.M. Marshall, and J.M. Bonman. 2014a. Association mapping of Hagberg falling number in hard white spring wheat. Crop Science 54(3): 1243–1252.
- **Zhang, J.**, J. Chen, C. Chu, W. Zhao, J. Wheeler, E.J. Souza, and R.S. Zemetra. 2014b. Genetic dissection of QTL associated with grain yield in diverse environments. Agronomy 4(4): 556–578.
- Chen, J., G. Hu, **J. Zhang**, C. Chu, and Y. Wu. 2014. Mapping of STS markers developed from drought tolerance candidate genes and preliminary analysis of their association with yield-related traits in common wheat (*Triticum aestivum*). Cereal Research Communications 42(2): 199–208.

2013

- Chen, J., J. Wheeler, J. Clayton, W. Zhao, K. O'Brien, **J. Zhang**, C. Jackson, J.M. Marshall, B.D. Brown, K. Campbell, X.M. Chen, R. Zemetra, and E.J. Souza. 2013. Registration of "UI Stone" soft white spring wheat. Journal of Plant Registrations 7(3): 321–326.

2011

- Li, P., J. Chen, P. Wu, **J. Zhang**, C. Chu, D. See, G. Brown-Guedira, R. Zemetra, and E. Souza. 2011. Quantitative trait loci analysis for the effect of *Rht-B1* dwarfing gene on coleoptile length and seedling root length and number of bread wheat. Crop Sci. 51(6): 2561–2568.