

Peng Zhou

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RESEARCH EXPERIENCES

Post Doctoral Associate, University of Minnesota

- ✚ Constructing gene regulatory networks across different tissues for multiple maize accessions to understand the genetic basis of heterosis;

Graduate Research Assistant, Dept. of Plant Pathology, University of Minnesota

- ✚ Developed a computational pipeline to thoroughly scan and accurately annotate small defense-related peptides in plant genomes;
- ✚ Constructed *de novo* genome assemblies of several *Medicago* accessions with Illumina HiSeq platform, identified population-specific sequences and built a *Medicago* Pan-genome;
- ✚ Systematically analyzed genome-wide architecture and segregating polymorphisms (SNPs, Insertion/Deletions, Copy Number Variation, complex structural variation) of defense-related gene families (NBS-LRRs, CRPs) in natural *Medicago* populations;

EDUCATION

- ✚ 2015 | University of Minnesota, Ph.D. in Plant Pathology & Bioinformatics
- ✚ 2009 | Xi'an Jiaotong University, M.S. in Forensic Genetics
- ✚ 2007 | Xi'an Jiaotong University, B.E., in Biological Engineering & Computer Science and Technology

SKILLS & KNOWLEDGE

- ✚ **Bioinformatics:** Very familiar with Unix environment; Strong programming background with Perl, R, C++ and Python; 5+ years' experience of high performance computing;
- ✚ **NGS analysis:** Extensive experience with next generation sequencing data including quality control, read alignment, variant calling and population genetics analysis;
- ✚ **Population Genomics:** Experience analyzing genome-wide variation patterns and focus on specific gene families to discover interesting biological findings;
- ✚ **Communication and Project Management:** Good presentation skills; Experience in team collaboration, project management and writing scientific reports.

PUBLICATIONS

- ✚ Zhou, P., Silverstein, K. A. T., et al. (2017) Exploring structural variation and gene family architecture with De Novo assemblies of 15 *Medicago* genomes. *BMC Genomics*.

- ✚ Moll, K. M., Zhou, P., *et al.* (2017) Strategies for utilizing BioNano and Dovetail explored through a second reference quality assembly for the legume model, *Medicago truncatula*. *BMC Genomics*.
- ✚ Miller, J. R., Zhou, P., *et al.* (2017) Hybrid assembly with long and short reads improves discovery of gene family expansions. *BMC Genomics*.
- ✚ Young, N.D., Zhou, P. and Silverstein, K.A. (2016) Exploring structural variants in environmentally sensitive gene families. *Curr. Opin. Plant Biol.*, 30, 19–24.
- ✚ Yoder, J., Stanton-Geddes, J., Zhou, P., Briskine, R., Young, N. and Tiffin, P. (2014) Genomic signature of adaptation to climate in *Medicago truncatula*. *Genetics*.
- ✚ Nallu, S., Silverstein, K.A., Zhou, P., Young, N.D. and Vandenbosch, K.A. (2014) Patterns of divergence of a large family of nodule cysteine-rich peptides in accessions of *Medicago truncatula*. *The Plant Journal*.
- ✚ Zhou, P., Silverstein, K. A. T., Gao L., *et al.* (2013) Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). *BMC Bioinformatics*.
- ✚ Paape, T., Bataillon, T., Zhou, P., *et al.* (2013) Selection, genome-wide fitness effects and evolutionary rates in the model legume *Medicago truncatula*. *Molecular Ecology*.
- ✚ Paape, T., Zhou, P., Branca, A., Briskine, R., Young, N., & Tiffin, P. (2012). Fine scale population recombination rates, hotspots and correlates of recombination in the *Medicago truncatula* genome. *Genome Biology and Evolution*.
- ✚ Young, N. D., Debellé, F., Oldroyd, G. E. D., Geurts, R., Cannon, S. B., Udvardi, M. K., Benedito, V. A., *et al.* (2011). The *Medicago* genome provides insight into the evolution of rhizobial symbioses. *Nature*.
- ✚ Branca, A., Paape, T. D., Zhou, P., Briskine, R., Farmer, A. D., Mudge, J., Bharti, A. K., *et al.* (2011). Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume *Medicago truncatula*. *Proceedings of the National Academy of Sciences*.

PRESENTATIONS

- ✚ Peng Zhou. Toward a *Medicago* pan-genome: Assembling and comparing multiple genomes. Powerpoint presentation at Medicago truncatula Workshop in Ardmore, September 18-21, 2016
- ✚ Peng Zhou, Kevin A. T. Silverstein, *et al.* Detecting secreted peptides in plants using SPADA (Secreted Peptide Alignment Discovery Algorithm). Poster presentation at Plant and Animal Genome XXI Conference in San Diego, January 12-16, 2013
- ✚ Peng Zhou, Kevin A. T. Silverstein, *et al.* Population-Scale Deep Sequencing Reveals Extensive Structural Variation in *Medicago* species. Poster presentation at MSI Reserach Exhibition, April 25, 2011

AWARDS

- ✚ **2013.** Doctoral Dissertation Fellowship, University of Minnesota
- ✚ **2013, 2011, 2010.** MPI Travel Award, University of Minnesota
- ✚ **2012.** Elwin Stewart Graduate Student Travel Award, Department of Plant Pathology, University of Minnesota