

PENG ZHOU

Post Doctoral Associate at [University of Minnesota](#) working on maize genomics, gene regulation, heterosis and stress response.

I am broadly interested in genomics, computational biology, data integration and visualization.



RESEARCH EXPERIENCE

present
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2016

Post Doctoral Associate

Department of Plant and Microbial Biology

📍 University of Minnesota, Twin Cities

- Elucidate hybrid vigor using multi-omics approach; data mining on functional gene regulations; elucidation of transcriptional regulatory differences underlying stress response; integrating multi-omics dataset for transcriptional network construction.
- Nathan M. Springer Lab

2016
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2015

AgroInformatics Analyst

Department of Applied Economics

📍 University of Minnesota, Twin Cities

- Design and implement a generic database and user interface for storing genotyping, breeding and phenotyping information for soybean breeding programs.

2015
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2009

Research Assistant

Department of Plant Pathology

📍 University of Minnesota, Twin Cities

- *Medicago truncatula* reference genome assembly, characterization of structural variation in the population, pan-genome construction



EDUCATION

2015
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2009

Ph.D. Plant Pathology & Bioinformatics

University of Minnesota, Twin Cities

📍 St. Paul US

- Thesis: Defense-related gene families in the model legume, *Medicago truncatula*: computational analysis, pan-genome characterization, and structural variation
- Advisor: Prof. Neivn D. Young

2009
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2007

M.S. Forensic Medicine

Xi'an Jiaotong University

📍 Xi'an CN

- Thesis: Dissection of Common Mitochondrial Haplogroups using Coding Region SNPs
- Advisor: Prof. Shengbin Li



CONTACT

🌐 github.com/orionzhou

🔗 orionzhou.github.io

✉ zhoupenggeni@gmail.com

📞 (+1) 6125323168

LANGUAGE SKILLS

R	
Python	
Perl	
C++	
Bash	
Javascript	

Last updated on 2020-06-27.

2007
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2003

- **B.E. Biological Engineering & Computer Science and Technology**
Xi'an Jiaotong University 📍 Xi'an CN



TEACHING EXPERIENCE

2012
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2011

- **PLPA5001: Introductory Plant Pathology**
Department of Plant Pathology 📍 University of Minnesota, Twin Cities
 - Teach laboratory sessions, lead discussion sections, answer questions and grade examinations.

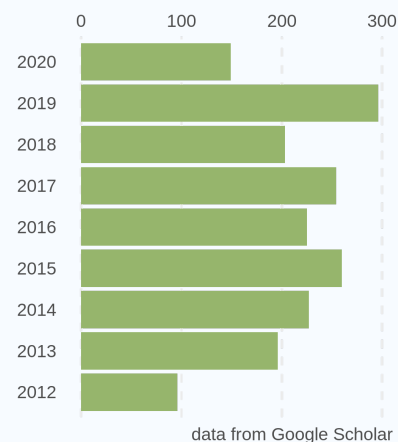


PUBLICATIONS

2020

- **Cis-regulatory elements within TEs can influence expression of nearby maize genes**
bioRxiv. 2020. p. 2020.05.20.107169.
 - Noshay JM, Marand AP, Anderson SN, **Zhou P**, Guerra MKM, Lu Z, et al
 - **Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes**
bioRxiv. 2020. p. 2020.05.21.109744
 - Crisp PA, Marand AA, Noshay JM, **Zhou P**, Lu Z, Schmitz RJ, et al
 - **Widespread imprinting of transposable elements and young genes in the maize endosperm**
bioRxiv. 2020. p. 2020.04.08.032573.
 - Anderson SN, **Zhou P**, Higgins K, Brandvain Y, Springer NM
 - **Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions**
Plant Cell. 2020, 32: 1377-1396.
 - **Zhou P**, Li Z, Magnusson E, Cano FAG, Crisp PA, Noshay J, Grotewold E, HirschC, Briggs SP, Springer NM
 - Impact Factor = 8.631
 - **Variation and Inheritance of Small RNAs in Maize Inbreds and F1 Hybrids**
Plant Physiol. 2020, 182: 318-331.
 - Crisp PA, Hammond R, **Zhou P**, Vaillancourt B, Lipzen A, Daum C, et al
- 2019
- **Monitoring the interplay between transposable element families and DNA methylation in maize**
PLoS Genet. 2019, 15: e1008291.
 - Noshay JM, Anderson SN, **Zhou P**, Ji L, Ricci W, Lu Z, et al

- Citation = 1921
- H-index = 13
- I10-index = 14



- **Transposable elements contribute to dynamic genome content in maize**
Plant Journal. 2019, 100: 1052-1065.
 • Anderson SN, Stitzer MC, Brohammer AB, Zhou P, Noshay JM, O'Connor CH, et al
- **Highly Genotype- and Tissue-specific Single-Parent Expression Drives Dynamic Gene Expression Complementation in Maize Hybrids**
bioRxiv. 2019,. p. 668681.
 • Li Z, Zhou P, Della Coletta R, Zhang T, Brohammer AB, Vaillancourt B, et al
- **Dynamic Patterns of Gene Expression Additivity and Regulatory Variation throughout Maize Development**
Molecular Plant. 2019, 12: 410-425.
 • Zhou P, Hirsch CN, Briggs SP, Springer NM
 • Impact Factor = 10.812
- 2017 ● **Strategies for optimizing BioNano and Dovetail explored through a second reference quality assembly for the legume model**
BMC Genomics. 2017, 18: 578.
 • Moll KM*, Zhou P*, Ramaraj T, Fajardo D, Devitt NP, Sadowsky MJ, et al
- **Exploring structural variation and gene family architecture with De Novo assemblies of 15 Medicago genomes**
BMC Genomics. 2017, 18: 261.
 • Zhou P, Silverstein KAT, Ramaraj T, Guhlin J, Denny R, Liu J, et al
- 2016 ● **Putative cobalt- and nickel-binding proteins and motifs in *Streptococcus pneumonia***
Curr Opin Plant Biol. 2016, 30: 19–24.
 • Young ND, Zhou P, Silverstein KA
- 2013 ● **Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application)**
BMC Bioinformatics. 2013, 14: 335.
 • Zhou P, Silverstein KA, Gao L, Walton JD, Nallu S, Guhlin J, et al
- 2011 ● **Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume *Medicago truncatula***
Proc Natl Acad Sci U S A. 2011, 108: E864-70.
 • Branca A, Paape TD, Zhou P, Briskine R, Farmer AD, Mudge J, et al

- **The Medicago genome provides insight into the evolution of rhizobial symbioses**

Nature. 2011, 480: 520-524.

- Young ND, Debellé F, Oldroyd GED, ... , Zhou P, ..., et al
- 🏆 ESI Highly Cited Paper



PROFESSIONAL SERVICE

- **Reviewer for journals**

- Plant Biotechnology Journal
- Plant Science
- The Plant Genome
- Plant Direct
- Crop Science



CONFERENCE PRESENTATIONS

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| 2020 | <ul style="list-style-type: none"> ● Meta gene regulatory networks in maize refine functionally relevant regulatory interactions
Plant and Animal Genome XXVIII Conference 📍 San Diego, CA |
| 2019 | <ul style="list-style-type: none"> ● Exploring Functional Transcriptomics using Gene Regulatory Networks in Maize.
61st Annual Maize Genetics Conference 📍 St. Louis, MO |
| 2018 | <ul style="list-style-type: none"> ● Documenting the Manifestations of Heterosis in Co-expression Networks for Maize
Plant and Animal Genome XXVI Conference 📍 San Diego, CA |
| 2014 | <ul style="list-style-type: none"> ● The Medicago Pan-Genome Reveals Large-scale Variation
Plant and Animal Genome XXII Conference 📍 San Diego, CA |
| 2013 | <ul style="list-style-type: none"> ● Detecting secreted peptides in plants using SPADA (Secreted Peptide Alignment Discovery Algorithm)
Plant and Animal Genome XXI Conference 📍 San Diego, CA |
| 2011 | <ul style="list-style-type: none"> ● Population-Scale Deep Sequencing Reveals Extensive Structural Variation in Medicago species
Minnesota Supercomputing Institute Research Exhibition 📍 Minneapolis, MN ● Genome Distribution and Population Genetics of Nodule-Specific Cysteine-Rich (NCR) Peptides in Medicago
Plant and Animal Genome XIX Conference 📍 San Diego, CA |

- 2010 ● **A *Medicago truncatula* Hapmap as a Platform for Exploring the Genetics of Symbiosis**
Plant and Animal Genome XVIII Conference 📍 San Diego, CA

👥 INVITED PRESENTATIONS/SEMINARS

- 2019 ● **Co-expression based Gene Regulatory Networks Predict Functional Interactions in Maize**
📍 China Agriculture University, Beijing
- **Transcriptome Dynamics in Maize**
📍 Huazhong Agriculture University, Wuhan
- 2016 ● **Toward a *Medicago* Pan-genome: Assembling and Comparing Multiple Genomes**
Medicago truncatula Workshop 📍 Noble Research Institute, Ardmore
- **Assembling and Comparing Multiple High-Quality *Medicago* Genomes**
📍 Chinese Academy of Agricultural Sciences (CAAS), Beijing