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 | 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 | 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 | 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 | 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 | 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 2020-06-30.

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 = 9.618

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 = 1923
· H-index = 13
· I10-index = 14

data from Google Scholar
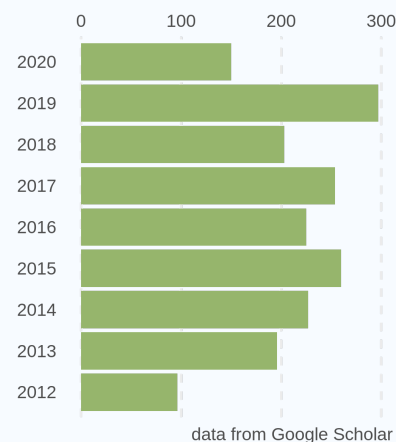
Transposable elements contribute to dynamic genome content in maize

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 = 12.084

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 **Exploring structural variants in environmentally sensitive gene families**

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

2020 — **Meta gene regulatory networks in maize refine functionally relevant regulatory interactions**

Plant and Animal Genome XXVIII Conference 📍San Diego, CA

2019 — **Exploring Functional Transcriptomics using Gene Regulatory Networks in Maize.**

61st Annual Maize Genetics Conference 📍St. Louis, MO

2018 — **Documenting the Manifestations of Heterosis in Co-expression Networks for Maize**

Plant and Animal Genome XXVI Conference 📍San Diego, CA

2014 — **The Medicago Pan-Genome Reveals Large-scale Variation**

Plant and Animal Genome XXII Conference 📍San Diego, CA

2013 — **Detecting secreted peptides in plants using SPADA (Secreted Peptide Alignment Discovery Algorithm)**

Plant and Animal Genome XXI Conference 📍San Diego, CA

2011 — **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