

Sanzhen Liu

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Education

Iowa State University

Ames, US

PH.D. IN GENETICS, ADVISOR: PATRICK SCHNABLE

August 2004 - April 2010

- minor in Statistics

Xiamen University

Xiamen, China

M.S. AND B.S. IN MICROBIOLOGY, M.S. ADVISOR: WENJIN SU

September 1993 - July 2000

- minor in Computer Science

Experience

Kansas State University

Manhattan, US

ASSOCIATE PROFESSOR

April 2019 - present

- 90% research (plant genetics, genomics, plant diseases)
- 10% teaching (bioinformatics)

ASSISTANT PROFESSOR

July 2013 - April 2019

- 90% research (plant genetics, genomics, plant diseases)
- 10% teaching (bioinformatics)

Iowa State University

Ames, US

POST-DOCTORAL RESEARCH ASSOCIATE

May 2010 - July 2013

- maize plant genetics and genomics, mentor: Patrick Schnable

BioStar Genechip, Inc

Shanghai, China

R&D Scientist

November 2000 - July 2004

- Development of genotyping platforms through SNP microarray

Research Interests

- Biology of dispensable supernumerary chromosomes in fungi
- Genetic bases of plant resistance to pathogens and other agronomic traits
- Genetic bases of plant regeneration
- Phenotypic consequence of genomic structural variation
- Deep learning in genomics

Teaching

- Bioinformatics Applications (PLPTH813, Spring 2017; Spring 2019, Spring 2021)
- Bioinformatics Applications (PLPTH613, Spring 2015; 2016)
- Workshop: Gene expression profiling (Summer 2014; 2015; 2017; 2018; 2022, co-instructor)
- Workshop: R programming (Summer 2014, co-instructor)

Awards & Honors

AWARDS

- 2022-2025 Phenotypic and molecular characterization of genes associated with begetative nitrogen use efficiency in sorghum, **DOE**, award#: 25-6222-1165-002 (co-PI)
- 2021-2025 Dynamic mini-chromosomes: mechanisms of exchange, stability, and causation of fungal pathogen adaptation, **NSF-NIFA/Plant-Biotic Interactions (PBI)**, **Co-funded by NSF and USDA**, NSF award#: 2011500 and USDA NIFA award#: 2021-09630 (PI)
- 2019-2023 Assessing Genome Alterations and Phenotypic Variations in CRISPR/Cas9-mediated Transgenic Tomato and Chemical-Mutagenized Tomato, **AFRI-Biotechnology Risk Assessment Research Grants Program, USDA NIFA**, award#: 2019-33522-299986 (co-PI)
- 2018-2023 Under the Hood: The Genetic Components of Maize Transformation, **NSF Plant Genome Research Program (PGRP)**, award#: 1741090 (PI)
- 2018-2022 Analyses of Bacterial Avirulence and Virulence Loci and Host Resistance of Maize Goss's Wilt, **NSF-NIFA/Plant-Biotic Interactions (PBI)**, award#: 2018-67013-28511 (PI)
- 2018-2023 Phase II IUCRC at Kansas State University: Center for Wheat Genetic Resources (WGRC), **NSF/IUCRC**, award#: 1822162 (Co-PI)
- 2018-2021 New Technology for Rapid Molecular Mapping and Deployment of Yellow Rust Resistance in Kansas Wheat, **Kansas Wheat Commission**, award#: BG5855 (PI)
- 2018-2021 RII Track-1: Microbiomes of Aquatic, **Plant and Soil Systems Across Kansas, NSF**, award#: 1656006, (Participant)
- 2016-2018 Improvement of Hard Winter Wheat for FHB Resistance, **USDA**, SCA (Co-PI)
- 2016-2017 Identification of Morphological Traits Correlated with Performance of Hybrid Corn under Drought Stress Through Time-lapse Imaging, Kansas Corn Commission, (PI)
- 2014-2015 Identification of trait-associated genetic markers with an efficient bulked strategy, **Kansas Wheat Commission**, award#: PP29738 (PI)
- 2014-2017 Transformative strategy for controlling rice disease in developing countries, **Bill and Melinda Gates Foundation**, award#: 6-10570-01 (Co-PI)

HONORS

- | | | |
|------|---|-----------------|
| 2010 | Research Excellence Award, Iowa State University | Ames, US |
| 2004 | Outstanding Young Professionals in Yangpu, Shanghai | Shanghai, China |

Publication

Google Scholar: <https://scholar.google.com/citations?user=GCzXdxYAAAAJ&hl=en>

* co-first author; & co-corresponding author

Preprints

1. **S Liu**^{*}, G Lin, SR Ramachandran, G Cruppe, D Cook, KF Pedley, B Valent[&]. 2022 Rapid mini-chromosome divergence among fungal isolates causing wheat blast outbreaks in Bangladesh and Zambia, *bioRxiv*, 2022.06.18.496690
2. H Cheng, JD Washburn, Y Hao, Z Zhang, J Yang, **S Liu**^{*}. 2021 Trait association and prediction through integrative k-mer analysis, *bioRxiv*, 2021.11.17.468725
3. M Zhao, Z Peng, Y Qin, L Zhang, B Tian, Y Chen, Y Liu, G Lin, H Zheng, C He, K Lv, HN Trick, Y Liu, MJ Cho, S Park, H Wei, J Zheng, FF White[&], **S Liu**^{*}. Bacterium-Enabled Transient Gene Activation by Artificial Transcription Factor for Resolving Gene Regulation in Maize, *bioRxiv*, 2021.02.05.429970 (*Plant Cell*, in revision)

Peer-reviewed publications

4. G Lin, S Liu. 2022. The Canu genome assembly pipeline using Nanopore long reads. *Bio-101*, e4501.

5. SA Sprague, TM Tamang, T Steiner, Q Wu, Y Hu, T Kakeshpour, J Park, J Yang, Z Peng, B Bergkamp, I Somayanda, M Peterson, EO Garcia, Y Hao, PS Amand, G Bai, PA Nakata, I Rieu, DP Jackson, N Cheng, B Valent, KD Hirschi, SVK Jagadish, **S Liu**, FF White, S Park. 2022 Redox-engineering enhances maize thermotolerance and grain yield in the field, *Plant Biotechnol J*, 10.1111/pbi.13866
6. G Lin, H Chen, B Tian, SK Sehgal, L Singh, J Xie, P Juliana, N Singh, N Rawat, S Shrestha, D Wilson, H Shult, H Lee, VK Tiwari, RP Singh, MJ Guttieri, HN Trick, J Poland, RL Bowden, G Bai, B Gill, **S Liu**[&]. 2022 Cloning of the Broadly Effective Wheat Leaf Rust Resistance Gene *Lr42* Transferred from *Aegilops tauschii*, *Nat Commun*, 13:3044.
7. Y Wang, J Zhang, M Sun, C He, K Yu, B Zhao, R Li, J Li, Z Yang, X Wang, H Duan, J Fu, S Liu, X Zhang, J Zheng. 2021 Multi-omics analyses reveal systemic insights into maize vivipary, *Plants* (Basel), 10:2437.
8. G Shi, G Kariyawasam, **S Liu**, Y Leng, S Zhong, S Ali, P Moolhuijzen, CS Moffat, JB Rasmussen, TL Friesen, JD Faris, Z Liu. 2022 A conserved hypothetical gene is required but not sufficient for Ptr ToxC production in *Pyrenophora tritici-repentis*, *Mol Plant Microbe Interact*, MPMI12210299R.
9. G Lin, C He, J Zheng, DH Koo, H Le, H Zheng, TM Tamang, J Lin, Y Liu, M Zhao, Y Hao, F McFarland, B Wang, Y Qin, H Tang, DR McCarty, H Wei, MJ Cho, S Park, H Kaeppler, S Kaeppler, Y Liu, NM Springer, PS Schnable, G Wang, FF White, **S Liu**[&]. 2021 Chromosome-level Genome Assembly of a Regenerable Maize Inbred Line A188, *Genome biology*, 22:175
10. J Hong, C Gunasekara, C He, **S Liu**, J Huang, H Wei. 2021 Identification of biological pathway and process regulators using sparse partial least squares and triple-gene mutual interaction, *Scientific Reports*, 11:13174
11. GK Kariyawasam, N Wyatt, G Shi, **S Liu**, C Yan, Y Ma, S Zhong, JB Rasmussen, P Moolhuijzen, CS Moffat, TL Friesen, Z Liu. 2021 A genome-wide genetic linkage map and reference quality genome sequence for a new race in the wheat pathogen *Pyrenophora tritici-repentis*, *Fungal Genetics and Biology*, 152:103571.
12. TM Tamang, SA Sprague, T Kakeshpour, **S Liu**, FF White, S Park. 2021 Ectopic expression of a heterologous Glutaredoxin enhances drought tolerance and grain yield in field grown maize, *International Journal of Molecular Sciences*, 22:5331
13. W Deng, K Zhang, C He, **S Liu**, H Wei. 2021 HB-PLS: A statistical method for identifying biological process or pathway regulators by integrating Huber loss and Berhu penalty with partial least squares regression, *Forestry Research*, 1:6
14. C He, G Lin, H Wei, H Tang, FF White, B Valent, **S Liu**[&]. 2020 Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences, *NAR Genomics and Bioinformatics*, 2:lqaa075
15. C He, Y Du, J Fu, E Zeng, S Park, FF White, J Zheng[&], **S Liu**[&]. 2020 Early drought-responsive genes are variable and relevant to drought tolerance, *G3: Genes, Genomes, Genetics*, 10:1657-1670
16. C Miao, Y Xu, **S Liu**, PS Schnable, JC Schnable. 2020 Increased power and accuracy of causal locus identification in time series genome-wide association in sorghum, *Plant Physiology*, 183:1898-1909
17. J Xie, G Guo, Y Wang, T Hu, L Wang, J Li, D Qiu, Y Li, Q Wu, P Lu, Y Chen, L Dong, M Li, H Zhang, P Zhang, K Zhu, B Li, K Deal, Y Zhang, M Luo, **S Liu**, Y Gu, H Li, Z Liu. 2020 A rare single nucleotide variant in Pm5e confers powdery mildew resistance in common wheat, *New Phytologist*, 228: 1011-1026
18. C Ji, Z Ji, B Liu, C He, H Liu, **S Liu**, B Yang, G Chen. 2020 Xa1 allelic R genes activate rice blight resistance suppressed by interfering TAL effectors, *Plant communications*, 1:100087
19. A Gupta, L Hua, G Lin, I Molnar, J Dolezel, **S Liu**, W Li. 2020 Multiple origins of Indian dwarf wheat by mutations targeting the TREE domain of a GSK3-like kinase for drought tolerance, phosphate uptake, and grain quality, *Theor Appl Genet*, 134:633-645
20. BA Pandian, A Varanasi, AR Vennapusa, R Sathishraj, G Lin, M Zhao, M Tunnell, T Tesso, **S Liu**, PV Prasad, J Mithila. 2020 Characterization, Genetic Analyses, and Identification of QTLs Conferring Metabolic Resistance to a 4-Hydroxyphenylpyruvate Dioxygenase Inhibitor in Sorghum (*Sorghum bicolor*), *Frontiers in plant science*, 11:1890
21. AL Perez-Quintero, M Ortiz-Castro, JM Lang, A Rieux, G Wu, **S Liu**, TA Chapman, C Chang, J Ziegler, Z Peng, FF White, MC Plazas, JE Leach, K Broders. 2020 Genomic Acquisitions in Emerging Populations of

- Xanthomonas vasicola pv. vasculorum Infecting Corn in the United States and Argentina, *Phytopathology*, 110:1161–1173
22. V Yadav, F Yang, MH Reza, **S Liu**, B Valent, K Sanyal, NI Naqvi. 2019 Cellular Dynamics and Genomic Identity of Centromeres in Cereal Blast Fungus, *mBio*, 10:e01581-19
 23. Z Peng, Y Hu, J Zhang, JC Huguet-Tapia, AK Block, S Park, S Sapkota, Z Liu, **S Liu**, FF White. 2019 Xanthomonas translucens commandeers the host rate-limiting step in ABA biosynthesis for disease susceptibility. *Proceedings of the National Academy of Sciences*, 116:20938–20946
 24. Z Peng, E Oliveira-Garcia, G Lin, Y Hu, M Dalby, P Migeon, H Tang, M Farman, D Cook, FF White, B Valent[&], **S Liu**[&]. 2019 Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus, *Plos Genetics*, 15: e1008272
 25. L Li, Y Du, C He, CR Dietrich, J Li, X Ma, R Wang, Q Liu, **S Liu**, G Wang, PS Schnable, J Zheng, 2019 Maize glossy6 is involved in cuticular wax deposition and drought tolerance, *J Exp Bot*, 70:3089-3099
 26. J Zheng, E Zeng, Y Du, C He, Y Hu, Z Jiao, K Wang, W Li, M Ludens, J Fu, H Wang, FF White, G Wang, **S Liu**[&]. 2019 Temporal small RNA expression profiling under drought reveals a potential regulatory role of small nucleolar RNAs in the drought responses of Maize, *Plant Genome*, 12:180058
 27. J Zheng, C He, Y Qin, G Lin, W Park, M Sun, J Li, X Lu, C Zhang, CT Yeh, C Gunasekara, E Zeng, H Wei, PS Schnable, G Wang, **S Liu**[&], 2019 Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize, *Plant J*, 97:530-542
 28. H Guo, TM Nolan, G Song, **S Liu**, Z Xie, J Chen, PS Schnable, JW Walley, Y Yin, 2018 FERONIA receptor kinase contributes to plant immunity by suppressing jasmonic acid signaling in Arabidopsis thaliana, *Curr Biol*, 28:3316-3324
 29. N Rawat, A Schoen, L Singh, A Mahlandt, DL Wilson, **S Liu**, G Lin, BS Gill, VK Tiwari. 2018 TILL-D: An Aegilops tauschii TILLING resource for wheat improvement, *Front Plant Sci*, 9:1665
 30. **S Liu**^{*}, JC Schnable^{*}, A Ott, CT Yeh, NM Springer, J Yu, G Muehlbauer, MCP Timmermans, MJ Scanlon, PS Schnable, 2018 Intragenic meiotic crossovers generate novel alleles with transgressive expression levels, *Mol Bio Evol*, 35:2762–2772
 31. W Deng, K Zhang, **S Liu**, P Zhao, S Xu, H Wei. 2018 JRmGRN: Joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions, *Bioinformatics*, 34:3470-3478
 32. YMAY Bandara, DK Weerasooriya, **S Liu**, CR Little. 2018 The necrotrophic fungus *Macrophomina phaseolina* promotes charcoal rot susceptibility in grain sorghum through induced host cell wall-degrading enzymes. *Phytopathology*, 108:948-956
 33. Y Hu, J Ren, Z Peng, AA Umana, H Le, T Danilova, J Fu, H Wang, A Robertson, SH Hulbert, FF White, **S Liu**[&]. 2018 Analysis of extreme phenotype bulk copy number variation (XP-CNV) identified the association of rp1 with resistance to Goss's wilt of maize. *Front Plant Sci*, 9:110
 34. A Ott^{*}, **S Liu**[&], JC Schnable, CT Yeh, C Wang, PS Schnable. 2017 Tunable Genotyping-By-Sequencing enables reliable genotyping of heterozygous loci. *Nucleic Acids Res*, gkx853
 35. A Wen A, M Jayawardana, J Fiedler, S Sapkota, G Shi, Z Peng, **S Liu**, FF White, Z Liu. 2017 Genetic mapping of a major gene in triticale conferring resistance to bacterial leaf streak. *Theor Appl Genet*, 131, 649–658
 36. Marla, SM, S Shiva, R Welti, **S Liu**, J Burke, GP Morris, 2017 Comparative transcriptome and lipidome analyses reveal molecular chilling responses in chilling-tolerant sorghums. *Plant Genome*, 10:1-16
 37. NF Charkhabi, NJ Booher, Z Peng, L Wang, H Rahimian, M Shams-Bakhsh, Z Liu, **S Liu**, FF White, AJ Bogdanove, 2017 Complete genome sequencing and targeted mutagenesis reveal virulence contributions of Tal2 and Tal4b of Xanthomonas translucens pv. undulosa ICMP11055 in bacterial leaf streak of wheat. *Front Microbiol*, 8:1488
 38. W Mei, **S Liu**, JC Schnable, CT Yeh, NM Springer, PS Schnable, WB Barbazuk, 2017 A Comprehensive analysis of alternative splicing in paleopolyploid maize. *Front Plant Sci*, 8:694
 39. H Ye, **S Liu**, B Tang, J Chen, Z Xie, TM Nolan, H Jiang, H Guo, HY Lin, L Li, Y Wang, H Tong, M Zhang, C Chu, Z Li, M Aluru, S Aluru, PS Schnable, Y Yin, 2017 RD26 mediates crosstalk between drought and brassinosteroid signalling pathways. *Nat Commun*, 8:14573

40. H Lin, Q Liu, X Li, J Yang, **S Liu**, Y Huang, MJ Scanlon, D Nettleton, PS Schnable. 2017 Substantial contribution of genetic variation in the expression of transcription factors to phenotypic variation revealed by eRD-GWAS. **Genome Biology**, 18:192
41. K Obasa, FF White, J Fellers, M Kennelly, **S Liu**, B Katz, J Tomich, D Moore, H Shinogle, K Kel-ley, 2017 A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in *Rhizoctonia solani*. **Phytobiomes**, 1:14-23
42. **S Liu**^{*}, J Zheng, P Migeon, J Ren, Y Hu, C He, H Liu, J Fu, FF White, C Toomajian, G Wang[&], 2017 Unbiased k-mer analysis reveals changes in copy number of highly repetitive sequences during maize domestication and improvement. **Sci Rep**, 7:42444
43. T Nolan, **S Liu**, H Guo, L Li, P Schnable, Y Yin, 2017 Identification of brassinosteroid target genes by chromatin immunoprecipitation followed by high-throughput sequencing (ChIP-seq) and RNA-sequencing. **Methods Mol Biol**, 1564:63-79
44. L Li, S Hey, **S Liu**, Q Liu, C McNinch, HC Hu, TJ Wen, C Marcon, A Paschold, W Bruce, PS Schnable, F Hochholdinger, 2016 Characterization of maize roothairless6 which encodes a D-type cellulose synthase and controls the switch from bulge formation to tip growth. **Sci Rep**, 6:34395
45. MS Chen, **S Liu**, H Wang, X Cheng, M El Bouhssini, RJ Whitworth, 2016 Genes expressed differentially in hessian fly larvae feeding in resistant and susceptible plants. **Int J Mol Sci**, 17:E1324
46. J Zhang, J Huguet, Y Hu, J Jones, N Wang, **S Liu**, FF White, 2016 Homologs of CsLOB1 in citrus function as disease susceptibility genes in citrus canker. **Mol Plant Pathol**, 18:798-810
47. MS Chen, **S Liu**, H Wang, X Cheng, M El Bouhssini, RJ Whitworth, 2016 Massive shift in gene expression during transitions between developmental stages of the gall midge, *Mayetiola Destructor*. **PLoS One**, 11:e0155616
48. M Arif, GY Busot, R Mann, B Rodoni, **S Liu**, JP Stack, 2016 Emergence of a new population of *Rathayibacter toxicus*: An ecologically complex, geographically isolated bacterium. **PLoS One**, 11:e0156182
49. Z Peng, Ying H, J Xie, N Potnis, A Akhunova, J Jones, Z Liu, FF White[&], **S Liu**[&], 2016 Long read and single molecule DNA sequencing simplifies genome assembly and TAL effector gene analysis of *Xanthomonas translucens*. **BMC Genomics**, 17:21
50. J Zhou, Z Peng, J Long, D Sosso, B Liu, J Eom, S Huang, **S Liu**, CV Cruz, WB Frommer, FF White, B Yang, 2015 Gene targeting by the TAL effector PthXo2 reveals cryptic resistance gene for bacterial blight of rice. **Plant J**, 82: 632-43
51. L Li, S Hill-Skinner, **S Liu**, D Beuchle, HM Tang, CT Yeh, D Nettleton, PS Schnable, 2015 The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase (FPGS). **Plant J**, 81:493-504
52. J Nestler^{*}, **S Liu**^{*}, TJ Wen, A Paschold, C Marcon, HM Tang, D Li, L Li, RB Meeley, H Sakai, W Bruce, PS Schnable, F Hochholdinger, 2014 Roothairless5, which functions in maize (*Zea mays* L.) root hair initiation and elongation encodes a monocot-specific NADPH oxidase. **Plant J**, 79: 729-740
53. Y Zhang, A Paschold, C Marcon, **S Liu**, H Tai, J Nestler, CT Yeh, N Opitz, C Lanz, PS Schnable, F Hochholdinger, 2014 The Aux/IAA gene rum1 involved in seminal and lateral root formation controls vascular patterning in maize (*Zea mays* L.) primary roots. **J Exp Bot**, 65: 4919-30
54. X Wang, J Chen, Z Xie, **S Liu**, T Nolan, H Ye, M Zhang, H Guo, PS Schnable, Z Li, Y Yin, 2014 Histone lysine methyltransferase SDG8 is involved in brassinosteroid regulated gene expression in *Arabidopsis thaliana*. **Mol Plant**, 7:1303-1315
55. W Cai, C Wang, Y Li, C Yao, L Shen, **S Liu**, X Bao, PS Schnable, J Girton, J Johansen, KM Johansen, 2014 Genome-wide analysis of regulation of gene expression and H3K9me2 distribution by JIL-1 kinase mediated histone H3S10 phosphorylation in *Drosophila*. **Nucleic Acids Res**, 42: 5456-5467
56. HM Tang^{*}, **S Liu**^{*}, S Hill-Skinner, W Wu, D Reed, CT Yeh, DS Nettleton, PS Schnable[&], 2014 The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. **Plant J**, 77: 380-392
57. L Li, D Li, **S Liu**, X Ma, CR Dietrich, HC Hu, G Zhang, Z Liu, J Zheng, G Wang, PS Schnable, 2013 The maize glossy13 gene, cloned via BSR-Seq and Seq-Walking encodes a putative ABC transporter required for the normal accumulation of epicuticular waxes. **PLoS One**, 8: e82333

58. **S Liu**, AP Hsia, PS Schnable, 2013 Digestion-ligation-amplification (DLA): a simple genome walking method to amplify unknown sequences flanking mutator (Mu) transposons and thereby facilitate gene cloning. *Methods Mol Biol*, 1057: 167-176
59. L Lin, K Petsch, R Shimizu, **S Liu**, WW Xu, K Ying, J Yu, MJ Scanlon, PS Schnable, MCP Timmermans, NM Springer, GJ Muehlbauer, 2012 Mendelian and non-Mendelian regulation of gene expression in maize. *PLoS Genet*, 9: e1003202
60. **S Liu**, K Ying, CT Yeh, J Yang, RA Swanson-Wagner, W Wu, T Richmond, DJ Gerhardt, J Lai, NM Springer, DS Nettleton, JA Jeddelloh, PS Schnable, 2012 Changes in genome content generated via segregation of non-allelic homologs. *Plant J*, 72: 390-399
61. **S Liu**, CT Yeh, HM Tang, DS Nettleton, PS Schnable, 2012 Gene mapping via bulked segregant RNA-Seq (BSR-Seq), *PLoS One*, 7: e36406
62. SR Eichten, JM Foerster, N de Leon, K Ying, CT Yeh, **S Liu**, JA Jeddelloh, PS Schnable, SM Kaeppler, NM Springer, 2011 B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. *Plant Physiol*, 156: 1679-1690
63. SR Eichten, RA Swanson-Wagner, J Schnable, AJ Waters, PJ Hermanson, **S Liu**, CT Yeh, Y Jia, K Gendler, M Freeling, PS Schnable, MW Vaughn, NM Springer, 2011 Heritable epigenetic variation among Maize inbreds, *PLoS Genet*, 7: e1002372
64. **S Liu**, HD Chen, I Makarevitch, R Shirmer, SJ Emrich, CR Dietrich, WB Barbazuk, NM Springer, PS Schnable, 2010 High-throughput genetic mapping of mutants via quantitative single nucleotide polymorphism typing. *Genetics*, 184: 19-26
65. PS Schnable, *et al.*, 2009 The B73 maize genome: complexity, diversity, and dynamics. *Science*, 326: 1112-1115
66. **S Liu**, CR Dietrich, PS Schnable, 2009 DLA-based strategies for cloning insertion mutants: cloning the gl4 locus of maize using Mu transposon tagged alleles. *Genetics*, 183: 1215-1225
67. **S Liu**, CT Yeh, T Ji, K Ying, H Wu, HM Tang, Y Fu, DS Nettleton, PS Schnable, 2009 Mu transposon insertion sites and meiotic recombination events co-localize with epigenetic markers for open chromatin across the maize genome. *PLoS Genet*, 5: e1000733
68. **S Liu**, Y Li, X Fu, M Qiu, B Jiang, H Wu, R Li, Y Mao, Y Xie, 2005 Analysis of the factors affecting the accuracy of detection for single base alterations by oligonucleotide microarray. *Exp Mol Med*, 37: 71-77
69. **S Liu**, Y Li, R Li, M Qiu, W Shen, J Gu, Y Wang, M Sun, Y Mao, Y Xie, 2004 [Detecting genetic polymorphisms of CYP1 A1 and GSTM1 simultaneously with oligonucleotide microarray]. *Yi Chuan Xue Bao*, 31: 1045-1052
70. Q Wei*, **S Liu***, J Huang, X Mao, X Chu, Y Wang, M Qiu, Y Mao, Y Xie, Y Li, 2004 Comparison of hybridization behavior between double and single strands of targets and the application of asymmetric PCR targets in cDNA microarray. *J Biochem Mol Biol*, 37: 439-444
71. Y Li, T Li, **S Liu**, M Qiu, Z Han, Z Jiang, R Li, K Ying, Y Xie, Y Mao, 2004 Systematic comparison of the fidelity of aRNA, mRNA and T-RNA on gene expression profiling using cDNA microarray. *J Biotechnol*, 107: 19-28.
72. Y Luo, H Xu, Y Li, Z Han, M Qiu, Q Chen, **S Liu**, S Ni, Y Xie, Y Mao, 2003 Validation of cDNA microarray technology. *Yi Chuan Xue Bao*, 30: 611-618

Invited talks

1. Revealing Gene Regulation of Cuticular Wax Biosynthesis Using Artificial Transcription Factors, Apr 2022, Maize Genetics Meeting, St. Louis, MO, US
2. Genetic and Genomic Exploration of Maize, Wheat, and Pathogens, Jan 2022, University of Missouri, Columbia, MO, US
3. Bacterium-Enabled Gene Activation by Artificial Transcription Factor for Resolving Gene Regulation in Maize, Mar 2021, EPSCoR annual online meeting
4. Long-read A188 maize genome assembly and short-mer guided error estimation, Jan 2020, Plants & Animals Genomics, San Diego, CA, US

5. Genetic Dissection of Disease Resistance to Goss's Wilt in Maize, Jan 2019, Plants & Animals Genomics, San Diego, CA, US
6. Cloning of wheat leaf rust resistance gene Lr42, Jan 2019, Plants & Animals Genomics, San Diego, CA, US
7. Genomic Exploration of Plant Pathogens and Host Resistance, Oct 2018, UNL, NE, US
8. Genome Technologies for Enhancing Plant Disease Resistance, Nov 2018, BAE KSU, KS, US
9. Genome Assembly of the Wheat Blast Fungus, Jan 2018, Plants & Animals Genomics, San Diego, CA, US
10. Efficient Mapping Approaches to Identify Trait-associated Genomic Variation, June 2017, Northeast Forestry University, Harbin, China
11. Efficient Bulk Approaches to Map Trait-associated Genomic Variation, May 2017, Fujian Agriculture and Forestry University, Fujian, China
12. Map Trait-associated Genomic Variation Through Next-Generation Sequencing, April 2017, Colorado State University, CO, US
13. Genetic Dissection of Disease Resistance via Analysis of Extreme Phenotype Copy Number Variation, March 2017, 2017 Corn Breeding Research Meeting, St. Louis, US
14. Identification of Trait-associated Genomic Variation in Plants Through Next-Generation Sequencing, March 2016, University of Florida, FL, US
15. Discovery of Structural Variation and Identification of Trait-associated Variation in Maize, Dec 2014, University of South Dakota, SD, US
16. Great Needs for Statistical Approaches in Genomics, Sept 2014, Department of Statistics, Kansas State University, KS, US
17. Applications of NGS-based Genotyping Tools to Facilitate Research in Genomics and Genetics, July 2014, Xiamen University, Xiamen, China
18. Tunable Genotyping-By-Sequencing, Jan 2014, Plants & Animals Genomics, San Diego, CA, US
19. Discovery of Structural Variation and Trait-associated Variation in Maize, Mar 2013, Virginia Tech University, Blacksburg, VA, US
20. Discovery of Structural Variation and Trait-associated Variation in Maize, Feb 2013, Kansas State University, Manhattan, KS, US
21. SeqWalking, a Fast and Efficient Genome Walking Approach to Facilitate Gene Cloning, Jan 2013, Plants & Animals Genomics, San Diego, CA, US
22. Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq), Mar 2012, The 54th Maize Genetics Conference, Portland, OR, US
23. Application of Next-gen Sequencing in Finding Trait-associated Genomic Variation, Sept 2011, The 19th Beijing Seed Congress, Beijing, China
24. Applying NGS in Plant Genetics and Genomics, May 2011, Chinese Academy of Agricultural Sciences, Beijing, China
25. Application Examples of Next-gen Sequencing in Plant Genetic Research, Jan 2011, China Agriculture University, Beijing, China
26. Recurrent de novo Copy Number Variation Generated via Segregation of Non-allelic Homologs, Mar 2011, The 53th Maize Genetics Conference, St. Charles, IL, US

Services

2022	Committee for the K-State Sarachek Award
2020-2022	Departmental Award Committee
2022-present	Admission Committee of the Genetics Program at KSU
2021-present	Scientific Advisor for the NSF project "Genomics of the perennial/annual dichotomy in the grass tribe <i>Triticeae</i> "
2020-present	Departmental Committee on Planning
2020-2021	Departmental Graduate student scholarship committee
2018-2021	University Graduate Council at KSU

2018-2022 Editorial Board member for Crop Journal
2017-2021 Editorial Board member for Scientific Reports

Affiliations

- Interdepartmental Genetics Program, Faculty
- Member of AAAS
- Member of GSA
- Member or Sigma Xi

Training workshops

2008	Analysis of Genetic Data on Related Individual, Summer Institute of Biostatistics	<i>UW</i>
2008	QTL mapping, Summer Institute of Biostatistics	<i>UW</i>
2011	Gene Expression Profiling, Summer Institute of Biostatistics	<i>UW</i>
2012	Statistical Methods for Genome-enabled Selection	<i>ISU</i>
2012	R Programming, Iowa State University	<i>ISU</i>

Outreach

2009	Judge in State Science + Technology Fair	<i>ISU</i>
2010	Plant Germplasm&Genomics Outreach to American Indian	<i>ISU</i>
2016	Kids-day-on-the-farm event	<i>KSU</i>