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: DR. 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 AND GRADUATE RESEARCH ASSISTANT *May 2010 - July 2013*

- maize plant genetics and genomics, mentor: Patrick Schnable

BioStar Genechip, Inc *Shanghai, China*

R&D Researcher *November 2000 - July 2004*

- managing human genotyping projects through microarray SNP chips

Research Interests

- Genetic bases of plant resistance to maize and wheat pathogens
- Mini-chromosome biology
- The genetic basis of plant regeneration
- Phenotypic consequence of genomic structural variation
- Deep learning in genomics

Teaching

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

Honors & Awards

FUNDING

2019-2022 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 (coPI)

2018-2022 Under the Hood: The Genetic Components of Maize Transformation, NSF Plant Genome Research Program (PGRP), award#: 1741090 (PI)

2018-2021 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 (Collaborator)

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	Medal for the Outstanding Young Professionals in Yangpu, BioStar Genechip	*Shanghai, China*

Publication

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

* co-first author; & co-corresponding author

1. 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***, lqaa075
2. 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
3. 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
4. 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
5. 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
6. 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***, doi: 10.1007/s00122-020-03719-5
7. 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

8. AL Perez-Quintero, M Ortiz-Castro, JM Lang, A Rieux, G Wu, S Liu, TA Chapman, C Chang, J Ziegle, 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
9. 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
10. 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(9): e1008272.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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
16. **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, msy174.
17. 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***, 1-9.
18. 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.
19. 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.
20. 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.
21. 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.
22. 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.
23. W Mei, **S Liu**, JC Schnable, CT Yeh, NM Springer, PS Schnable, WB Barbazuk, 2017 A Compre-hensive analysis of alternative splicing in paleopolyploid maize. ***Front Plant Sci***, 8:694.
24. 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.
25. 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.

26. **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.
27. 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.
28. 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.
29. 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(8):E1324.
30. 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***, doi: 10.1111/mpp.12441.
31. 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.
32. 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.
33. 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
34. 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
35. 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.
36. 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.
37. 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.
38. 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.
39. 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.
40. 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.
41. 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.
42. **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.
43. 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.

44. **S Liu**, K Ying, CT Yeh, J Yang, RA Swanson-Wagner, W Wu, T Richmond, DJ Gerhardt, J Lai, NM Springer, DS Nettleton, JA Jeddeloh, PS Schnable, 2012 Changes in genome content generated via segregation of non-allelic homologs. ***Plant J***, 72: 390-399.
45. **S Liu**, CT Yeh, HM Tang, DS Nettleton, PS Schnable, 2012 Gene mapping via bulked segregant RNA-Seq (BSR-Seq), ***PLoS One***, 7: e36406.
46. SR Eichten, JM Foerster, N de Leon, K Ying, CT Yeh, **S Liu**, JA Jeddeloh, PS Schnable, SM Kaeppler, NM Springer, 2011 B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. ***Plant Physiol***, 156: 1679-1690.
47. 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.
48. **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.
49. PS Schnable, et al., 2009 The B73 maize genome: complexity, diversity, and dynamics. **Science**, 326: 1112-1115.
50. **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.
51. **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.
52. **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.
53. **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.
54. 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.
55. 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.
56. 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. Genetic Dissection of Disease Resistance to Goss's Wilt in Maize, Jan 2019, Plants & Animals Genomics, San Diego, CA, US
2. Cloning of wheat leaf rust resistance gene Lr42, Jan 2019, Plants & Animals Genomics, San Diego, CA, US
3. Genomic Exploration of Plant Pathogens and Host Resistance, Oct 2018, UNL, NE, US
4. Genome Technologies for Enhancing Plant Disease Resistance, Nov 2018, BAE KSU, KS, US
5. Genome Assembly of the Wheat Blast Fungus, Jan 2018, Plants & Animals Genomics, San Diego, CA, US
6. Efficient Mapping Approaches to Identify Trait-associated Genomic Variation, June 2017, Northeast Forestry University, Harbin, China
7. Efficient Bulked Approaches to Map Trait-associated Genomic Variation, May 2017, Fujian Agriculture and Forestry University, Fujian, China
8. Map Trait-associated Genomic Variation Through Next-Generation Sequencing, April 2017, Colorado State University, CO, US
9. Genetic Dissection of Disease Resistance via Analysis of Extreme Phenotype Copy Number Variation, March 2017, 2017 Corn Breeding Research Meeting, St. Louis, US

10. Identification of Trait-associated Genomic Variation in Plants Through Next-Generation Sequencing, March 2016, University of Florida, FL
11. Discovery of Structural Variation and Identification of Trait-associated Variation in Maize, Dec 2014, University of South Dakota, SD, US
12. Great Needs for Statistical Approaches in Genomics, Sept 2014, Department of Statistics, Kansas State University, KS, US
13. Applications of NGS-based Genotyping Tools to Facilitate Research in Genomics and Genetics, July 2014, Xiamen University, Xiamen, China
14. Tunable Genotyping-By-Sequencing, Jan 2014, Plants & Animals Genomics, San Diego, CA, US
15. SeqWalking, a Fast and Efficient Genome Walking Approach to Facilitate Gene Cloning, Jan 2013, Plants & Animals Genomics, San Diego, CA, US
16. Gene Mapping via Bulked Segregant RNA-Seq (BSR-Seq), Mar 2012, The 54th Maize Genetics Conference, Portland, Oregon, US
17. Application of Next-gen Sequencing in Finding Trait-associated Genomic Variation, Sept 2011, The 19th Beijing Seed Congress, Beijing, China
18. Applying NGS in Plant Genetics and Genomics, May 2011, Chinese Academy of Agricultural Sciences, Beijing, China
19. Application Examples of Next-gen Sequencing in Plant Genetic Research, Jan 2011, China Agriculture University, Beijing, China
20. 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

2017-present	Editorial Board member for Scientific Reports
2018-present	Editorial Board member for Crop Journal
2018-present	Member of University Graduate Council at KSU
2020-present	Departmental Committee on Planning
2020-present	Graduate student scholarship committee

Affiliations

- Interdepartmental Genetics Program, Faculty
- Member of AAAS
- Member of GSA

Training workshops

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

Outreach

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