

## AINONG SHI

Associate Professor

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<https://scholar.google.com/citations?user=o4rwUWEAAAAJ&hl=en>

<https://loop.frontiersin.org/people/644493/overview>

### EDUCATION:

- Ph.D. – Plant Pathology and Crop Sciences. North Carolina State University, Raleigh, NC, USA. 1997.
- M.S. – Computer Systems. City University, Seattle, WA, USA. 2000.
- M.S. – Plant Genetics and Breeding. Graduate School of Chinese Academy of Agriculture Sciences, Beijing, China. 1986.
- B.S. – Plant Pathology and Entomology. Zhejiang University, Hangzhou, China. 1983.

### RESEARCH EXPERIENCE:

**Associate Professor** (07/2019 - ), **Assistant Professor** (06/2013- 06/2019), Dept. Horticulture, University of Arkansas, AR, USA.

- Lead and participate in classic and molecular breeding in vegetable crops such as arugula, spinach and cowpea for cultivars and germplasm development and release;
- conduct genetic and association mapping, single nucleotide polymorphism (SNP) discovery and genotyping, next-generation sequencing such as whole genome sequencing (WGS) and whole genome resequencing (WGRS), double digest restriction-site associated DNA sequencing (ddRADseq), genotyping by sequencing (GBS), whole genome bisulfite sequencing (WGBS), RNAseq, isoSeq, proteomics, and marker-assisted selection (MAS) and genomic selection (GS) in vegetable crops such as arugula, beans, cowpea, spinach and tomato.

**Scientist/Soy Genetic Project Lead**, Syngenta Seeds, Slater, IA, USA, 10/2009 – 05/2013.

- Implemented >10,000 F2/F3 MATS populations, developed a Visual Basic (VB) tool for marker implementation for trait selection in soybean molecular breeding.
- Analyzed, proposed, and implemented SNP markers for aphid resistance genes: Rag1, Rag2, rag1, rag3, and rag4 and assisted to select aphid resistant lines with stacked 2 – 3 aphid resistance genes.
- Led to develop and proposed 11 SNP markers associated with Rps1a, Rps1c, Rps1k, and rps1 of Phytophthora root rot resistance.
- Participated association analysis for SDS resistance and assisted to identify and validate 9 QTLs for SDS resistance in Syngenta soy lines.
- Analyze and summarized 17 populations for nine IDC QTL identification and validation.
- Analyzed and implemented >50 bi-parent GWS populations for data analysis and plant selection and high yield line development.
- Led and conducted QTL analysis and SNP marker development for rhg1 (SCN-qtIG), Rhg4 (SCNqtIA2), Rhg5 (SCN-qtIJ), SCN-qtIB1, SCN-qtID2, SCN-qtIG-2, SCN-qtIE, and SCN-qtIO of SCN resistance.

**Plant Geneticist**, Indiana Crop Improvement Association and Purdue University, IN, USA, 07/2008-09/2009.

- Conducted molecular marker identification, genetic mapping, association analysis and mapping, SNP discovery and genotyping for corn, soybean, and tomato.

**Postdoc**, Institute of Genomic Diversity, Cornell University, Ithaca, NY, USA, 12/2007-07/2008.

- Conducted association analysis in switchgrass and participated in nested association mapping of maize.

**Postdoc**, Dept. Crop, University of Arkansas, Fayetteville, AR, USA, 10/2005 – 11/2007.

- Identified molecular markers associated with seed quality and disease resistance; conducted genetic diversity, QTL analysis and association studies;
- Participated in soybean breeding.

**Postdoc**, Nursery Station, Tennessee State University, TN, USA, 04/2003 – 10/2005.

- Identified molecular markers associated with disease resistance, analyzed genetic diversity in dogwood, and detected pathogens in nursery crops.

**Postdoc**, Dept. of Crop, Washington State University, WA, USA, 10/1997 – 09/1998.

- Evaluated and identified disease resistance and participated in a wheat-breeding program for germplasm and cultivar release.

**Research Assistant**, Plant Pathology Department and Crop Science Department, North Carolina State University, Raleigh, NC, USA, 09/1993 – 09/1997.

- Evaluated and analyzed disease resistance and identified and mapped genes for disease resistance in wheat, and participated in a wheat-breeding program.

**Researcher**, Institute of Crop Breeding and Cultivar, Chinese Academy of Agriculture Sciences (CAAS), Beijing, China, 08/1986 – 08/1993.

- Performed germplasm identification for disease resistance and conducted genetic analysis of disease resistance in rice and wheat, and led a rice-breeding program for germplasm and cultivar release.

#### OTHER EXPERIENCE

- Software Test Engineer, Volt (Microsoft), Redmond, WA, USA, 09/2001-03/2003.
- Computer Lab Assistant, City University, Renton, WA, USA, 11/1998-08/2001.

#### PROFESSIONAL MEMBERSHIP:

- American Phytopathological Society; American Society for Horticultural Science; Crop Science Society of America; International Spinach Association; Gamma Sigma Delta.

#### JOURNAL EDITORIAL:

- Associate Editor: Agronomy, Crop Science, Frontiers in Plant Science, Vegetable Research

#### JOURNAL REVIEWER (44 Journals)

- Agronomy; Agrosystems, Geosciences & Environment; Biocatalysis and Agricultural Biotechnology; Biochemical Systematics and Ecology; Crop and Paster Science; Crop Journal; Crop Protection; Crop Science; DATABASE; Euphytica; Frontiers in Plant Science; Genetics; Genes; G3 (Genes, Genomics, Genetics); Genome; Genomics; Hopres (Crop Breeding, Genetics and Genomics); Horticulture Research; HortScience; HortTechnology; Journal of the American Society for Horticultural Science (JASHS); Journal of Agricultural and Food Chemistry; Journal of Agricultural Science and Technology; Journal of Biotechnology; Journal of Integrative Plant Biology; Journal of Plant Registrations; Journal of the Science of Food and Agriculture; Journal of Taibah University for Science; Legume Science; Molecular Biotechnology; Molecular Breeding; Molecular Genetics and Genomics; Nature Communications; Physiology and Molecular Biology of Plants; Plant Disease; Plant Breeding; Plant Healthy Progress; Plant Molecular Biology Reporter; Planta; PLoS ONE; Scientia Horticulturae; Scientific Reports; The Plant Genome; Theoretical and Applied Genetics; and Tropical Plant Biology.

#### TEACHING:

- HORT6033 Genetic Molecular Plant Breeding (<https://uark.box.com/s/v433qywabvbo3ng2h7y6yrb7lkq9vv18>).
- CEMB 590V Specific Topics in Cell and Molecular Biology.

#### GRANT AWARD (a total of \$6,027,358 budget, among which \$2,193,561 goes to Shi's lab)

- **Shi, A.** and Kai Ling. "Managing Emerging Tomato Brown Rugose Fruit Virus in Greenhouse Tomatoes Using Alternative Rootstock and Disinfection", NIFA CPPM Proposal Number: 2023-02996, 07/01/2023-06/30/2025, Total Funding Amount: \$323,001.

- Mou, B., and **A. Shi**. “Enhancement of spinach and leafy vegetables for disease resistance and nutritional components using genome-wide association study and genomic prediction”, 07/01/2023 – 06/30/2025. A total of \$40,156.80 transferred from Mou’s lab to Shi’s for the collaborations.
- **Shi, A.** “Developing nutritious spinach and arugula for hydroponics and indoor farming with disease and pest tolerance” from Arkansas State Specialty Crop Block Grant Program, 10/01/2022-12/31/2024, a total of \$79,658.
- **Shi, A.** “Evaluation and Development of Spinach and Arugula Germplasm and Breeding Lines” from Bowery Farming, 05/2022-05/2023, a total of \$55,982.
- Joshi, V., **A. Shi**, M. Colley, and A. Formiga, “Streamlining Systems Approaches to Maximize Organic Spinach Productivity” from USDA Organic Agriculture Research and Extension Initiative (OREI), CONTRACT/GRANT/AGREEMENT NO: 2022-51300-37886 PROPOSAL NO: 2022-04068, 09/01/2022-08/31/2025, a total of \$453,789 in the first year and \$1,500,000 for three years.
- Ling, K. and **A. Shi**, “Evaluation and Genome-wide Association Study for Tomato Brown Rugose Fruit Virus Resistance in USDA Tomato Germplasm” from USDA Germplasm Evaluation, 9/1/2022-8/30/2023, a total of \$19,000. A new project “Evaluation and Genetic Study of Tomato, Spinach and Arugula under Controlled Environmental Conditions” with a total of \$30,000 (including the USDA CGC \$19,000).
- Viteri, D.M., **A. Shi**, and D. A. Linares “Evaluation and Genome-wide Association Study for Ashy Stem Blight (*Macrophomina phaseolina*) Resistance in USDA Common Bean (*Phaseolus vulgaris*) Germplasm” from USDA Germplasm Evaluation, 9/1/2022-8/30/2023, a total of \$19,000
- **Shi, A.**, B. Bluhm, G. Bhattarai, and H. Xiong, “Evaluation, Genome-wide Association Study and Genomic Prediction for Bacterial Wilt and Salt and Drought Tolerance in Tomato” from USDA Crop Germplasm Evaluation grant 58-8060-1-008, 8/1/2021-7/30/2023, a total of \$22,761.
- **Shi, A.**, B. Bluhm, H. Xiong, and G. Bhattarai, “Genome-wide Association Study and Genomic Prediction for Bacterial Wilt Disease Resistance in Tomato”. University of Arkansas Provost's Collaborative Research Grant, 10/01/2020-12/31/2021. \$4,900.
- **Shi, A.**, J. Correll, and Gehendra Bhattarai, “Evaluation and Association Analysis of resistance to Pythium on USDA Spinach Germplasm” from USDA Germplasm Evaluation grant 58-5030-0-047, 08/01/2020 – 08/31/2022, a total of \$24,500.
- **Shi, A.** “Genetic Analysis and Trait-Specific Molecular Marker Development in Sugarcane” from USDA-ARS with agreement number 58-6052-1-002, 06/01/2021-05/31/2023, a total of \$37,000. An extension of one year till 05/31/2024 was funded with \$15,000 extra budget, collaborated with Yong-bao Pan in USDA-ARS.
- **Shi, A.**, “Arugula Breeding and Genetics” from Bowery Farming, 04/2020-04/2021, a total of \$51,762.
- **Shi, A.** and W. Ravelombola, “Evaluation, Genome-wide Association Study and Genomic Selection of Salt Tolerance in USDA Cowpea Germplasm” from USDA Germplasm Evaluation 58-6046-9-004, 09/01/2020 – 08/31/2022, a total of \$23,256.
- **Shi, A.** and J. Correll, “Evaluation and Association Analysis of Leaf Spot Resistance for USDA Spinach Germplasm” from USDA Germplasm Evaluation grant 58-5030-9-051, 7/1/2019-6/30/2021, a total of \$19,380.
- **Shi, A.**, J. Qin, and W. Ravelombola, “Evaluation and Association Analysis of Drought Tolerance in USDA Cowpea Germplasm” from USDA Germplasm Evaluation grant 58-6046-9-004, 7/1/2019-6/30/2020, a total of \$19,380.
- **Shi, A.**, “Enhancing Vegetable Development for Quality and Abiotic and Biotic Stress Tolerance”, USDA, National Institute of Food and Agriculture Hatch project No. ARK0VG2018, Accession Number 1017337, 10/01/2018-09/30/2023.
- **Shi, A.**, “Genetic Improvement for Vegetable Crops in Arkansas”, USDA, National Institute of Food and Agriculture Hatch project No. ARK02440, Accession No. 1002423, 01/29/2014-09/30/2018.
- **Shi, A.**, J. Correll, B. Mou, C. Avila, L. Du Toit, C. Feng, L. Stein, and R. Hogan, “Developing Genetic and Molecular Resources to Improve Spinach Production and Management (GRANT12355010)” from USDA-SCRI

grant 2017-51181-26830, 09/01/2017-06/30/2022, a total of \$2,447,430.

- **Shi, A.**, J. Correll, and B. Mou, “Classic and Molecular Breeding for Downy Mildew Resistance in Spinach” from USDA-AMS SCMP grant 16SCCMAR0001, 10/01/2016-04/30/2021, a total of \$755,784.
- **Shi, A.** and J. Correll, “Evaluation and Association Analysis of White Rust Resistance for USDA Spinach Germplasm” from USDA Germplasm Evaluation grant 58-5030-6-076 second awarded, 7/1/2017-06/30/2019, a total of \$29,868.
- **Shi, A.**, J. Qin, and S. Chen, “Evaluation and Association Analysis of Soybean Cyst Nematode Resistance in USDA Common Bean (*Phaseolus vulgaris*) Germplasm” from USDA Germplasm Evaluation grant 58-2090-8-053, 7/1/2018-06/30/2020, a total of \$21,318.
- Chen, S., T. Michaels, and **A. Shi**. “Identification and Characterization of the Soybean Cyst Nematode Resistance in Dry Bean” from AGRI Minnesota Crop Research Grant Program, 1/1/2017- 12/31/ 2019, a total of \$289,174.
- **Shi, A.** and J. Correll, “Development of SNP Markers for White Rust Resistance and Genetic Diversity Analysis in Spinach” from Pop Vriend Seeds, Rijk Zwaan, and Sakata seed companies, 7/1/2016-6/30/2018, a total of \$118,827.
- **Shi, A.** “Evaluation and Association Analysis of Seed Protein Content in Cowpea”, University of Arkansas Provost Grant, 1/1/2017 – 12/31/2017, \$2,000.
- **Shi, A.** and J. Correll, “Molecular Research and Breeding through DNA Sequencing and SNP Development in Spinach”, Pop Vriend Seeds, 2016-2018, a total of \$9,500.
- **Shi, A.** and J. Correll, “Evaluation and Association Analysis of White Rust Resistance for USDA Spinach Germplasm” from USDA Germplasm Evaluation grant 58-5030-6-076, 7/1/2016-6/30/2019, a total of \$12,621.
- **Shi, A.**, “QTL and Association Analysis for White Rust Resistance in Spinach”, Texas Spinach Producers Board, 2016-2017, \$3,420.
- **Shi, A.**, “Evaluation and Association Analysis of Seed Protein Content in USDA Cowpea Germplasm” from USDA Germplasm Evaluation grant 58-6046-6-004, 7/1/2016-6/30/2017, \$11,650.
- **Shi, A.**, “QTL and Association Analysis for White Rust Resistance in Spinach”, Texas Spinach Producers Board, 2015-2016, \$5,000.
- **Shi, A.**, “Enhance Spinach Improvement for White Rust Resistance and Heat-tolerance with Slowing Bolting”, Texas Spinach Producers Board, 2014-2015, \$5,000.
- **Shi, A.**, “Association Analysis of Bacterial Blight Resistance in USDA Cowpea Germplasm Core Collection” from USDA Germplasm Evaluation grant 6607-21000-011-00D, 2014-2015, a total of \$12,686.
- **Shi, A.**, “Research in Teaching Grants”, U of A Global Campus, 2013-2014, \$3,500.

**PUBLICATION** (refereed:152; book chapter:1; non-refereed:15; submitted:7; abstract:156; presentation:201; and patent:5)

**Refereed** (\*as the corresponding author in all articles)

## 2023

1. Bhattarai, G.\*, **A. Shi**\*, B. Mou\*, and J. Correll\*. 2023. Skim resequencing of progeny population of Lazio and Whale crossed with Viroflay finely mapped downy mildew locus and identified resistance genes in spinach Horticulture Research, uhad076, <https://doi.org/10.1093/hr/uhad076> ; <https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad076/7128292>
2. Chen, Y., H. Xiong\*, W. Ravelombola, G. Bhattarai, T.C. Barickman, I. Alatawi, T.M. Phiri, K. Chiwina, B. Mou, S. Tallury, and **A. Shi**\*. 2023. Genome-wide association study and genomic prediction of seed protein content in cowpea (submitted to Plants).
3. Islam, ASM. F., J.J. Rameneni, C.A. Avila\*, and **A. Shi**\*. 2023. Improving Genomic Prediction of Vitamin C

content in Spinach using GWAS-derived Markers (Submitted to BMC Genomics).

4. Olaoye, D., G. Bhattarai, C. Feng, J.C. Correll\*, and **A. Shi\***. 2023. Evaluation of downy mildew resistance in spinach (submitted to Euphytica). <https://doi.org/10.21203/rs.3.rs-3085075/v1>; <https://www.researchsquare.com/article/rs-3085075/v1>.
5. Ravelombola W\*, H. Xiong, G. Bhattarai, A. Manley, J. Cason, H. Pham, B. Zia, and **A. Shi\***. 2023. Genome-Wide Association Study for Drought Tolerance in Cowpea (*Vigna unguiculata* (L.) Walp.) at Seedling Stage Using a Whole Genome Resequencing Approach (submitted to Horticulture Research).
6. Ravelombola W\*, L. Dong, T.C. Barickman, H. Xiong, A. Manley, J. Cason, H. Pham, B. Zia, and **A. Shi\***. 2023. Genome-Wide Association Study for Salt Tolerance in Cowpea (*Vigna unguiculata* (L.) Walp.) at Seedling Stage Using a Whole Genome Resequencing Approach (Submitted to Frontiers in Plant Science; Manuscript ID: 1188918).
7. Riaz, A.\*, Q. Raza, A. Kumar, D. Dean, K. Chiwina, T.M. Phiri, J. Thomas, and **A. Shi**. 2023. GWAS and genomic selection for marker-assisted development of sucrose enriched soybean cultivars (submitted to Euphytica). <https://doi.org/10.1101/2023.04.16.537083>
8. Viteri, D.M\*, A.M. Linares, Z. Miranda, and **A. Shi\***. 2022. Genome-wide study reveals a QTL region for ashly stem blight resistance in the Andean common bean line PRA154. (Submitted to Theoretical and Applied Genetics).
9. Xiong, H., J. Chen, S. Gao, Y. Pan\*, and **A. Shi\***. 2023. Association Study and Genomic Prediction for Fiber and Sucrose Contents in a Mapping Population of LCP 85-384 Sugarcane. *Plants* 2023, 12, 1041. <https://doi.org/10.3390/plants12051041>; <https://www.mdpi.com/2223-7747/12/5/1041>
10. Xiong\*, H., Y. Chen, Y-B. Pan, J. Wang\*, W. Lu, and **A. Shi\***. 2023. A genome-wide association study and genomic prediction for *Phakopsora pachyrhizi* resistance in soybean. *Frontiers in Plant Science*, Volume 14 - 2023 | <https://doi.org/10.3389/fpls.2023.1179357>

## 2022

11. Bhattarai, G., **A. Shi\***, B. Mou, and J. Correll. 2022. Resequencing worldwide spinach germplasm identifies downy mildew field tolerance QTLs and genomic prediction tools. *Horticulture Research*, Published: 13 September 2022, uhac205, <https://doi.org/10.1093/hr/uhac205>; <https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhac205/6696976>
12. Bhattarai, G.\*, D. Olaoye, B. Mou\*, J. C. Correll\*, **A. Shi\***. 2022. Mapping and selection of downy mildew resistance in spinach cv. whale by low coverage whole genome sequencing. *Frontiers in Plant Science*, PUBLISHED 06 October 2022, <https://doi.org/10.3389/fpls.2022.1012923>
13. Guo, J., Y. Jiao, H Xiong, **A. Shi**, Y. Yang, L. Feng, L. Dong\*, and L. Shi\*. 2022. Impact of nutrient solutions under inorganic substrate soilless cultivation on plant growth, fruit yield and quality of tomato. *Technology in Horticulture* 2, Article number: 5 (2022). <https://doi.org/10.48130/TIH-2022-0005>; <https://www.maxapress.com/article/doi/10.48130/TIH-2022-0005>
14. Guo J., L. Dong, S.L. Kandel, Y. Jiao, L. Shi, Y. Yang, **A. Shi**, and B. Mou. 2022. Transcriptomic and Metabolomic Analysis Provides Insights into the Fruit Quality and Yield Improvement in Tomato under Soilless Substrate-based Cultivation. *Agronomy* 2022, 12(4), 923. <https://doi.org/10.3390/agronomy12040923>. <https://www.mdpi.com/2073-4395/12/4/923/htm>.
15. Joshi, V.\*, **A. Shi\***, A.K Mishra, H. Gill, and J. DiPiazza. 2022. Genetic dissection of nitrogen induced changes in the shoot and root biomass in spinach. *Scientific Reports* (2022) 12:13751 | <https://doi.org/10.1038/s41598-022-18134-7>
16. Kandel, S., A. Anchieta, **A. Shi**, B. Mou, and S.J. Klosterman. 2022. Crustacean meal elicits expression of

- growth and defense-related genes in roots of lettuce and tomato. *PhytoFrontiers*, 2:10-20. <https://doi.org/10.1094/PHYTOFR-03-21-0017-R>.
17. Kumar, P., R.L. Eriksen, I. Simko, **A. Shi**, and B. Mou. 2022. Insights into nitrogen metabolism in the wild and cultivated lettuce as revealed by transcriptome and weighted gene co-expression network analysis. *Scientific Reports*, 9852 (2022). <https://doi.org/10.1038/s41598-022-13954-z>
  18. Olorunwa, O.J., B. Adhikari, S. Brazel, S. C. Popescu, G.V. Popescu, A. Shi, T.C. Barickmana. 2022. Waterlogging during the reproductive growth stage causes physiological and biochemical modifications in the leaves of cowpea (*Vigna unguiculata* L.) genotypes with contrasting tolerance. *Plant Physiology and Biochemistry*, 190(1):133-144. <https://doi.org/10.1016/j.plaphy.2022.08.018>; <https://authors.elsevier.com/c/1fIPp3VH9X66HP>
  19. Olorunwa, O.J., B. Adhikari, S. Brazel, **A. Shi**, S. Popescu, G. Popescu, and T.C. Barickman\*. 2022. Growth and Photosynthetic Responses of Cowpea Genotypes under Waterlogging at the Reproductive Stage. *Plants* 2022, 11(17), 2315; <https://doi.org/10.3390/plants11172315>; <https://www.mdpi.com/2223-7747/11/17/2315>
  20. Olorunwa, O.J., A. Shi, and T. C. Barickman\*. 2022. Screening of Cowpea (*Vigna unguiculata* (L.) Genotypes for Waterlogging Tolerance Using Morpho-physiological Traits at Early Growth Stage. *Plant Science* 315, February 2022, 111136, <https://doi.org/10.1016/j.plantsci.2021.111136>
  21. Qin, J., F. Wang, Z.Q. Song, **A. Shi\***, T. Zhao, Q. Song, W. Ravelombola, H. An, L. Yan, C. Yang and M. Zhang. 2022. Mapping and Genomic Selection for Seed Protein in Soybean Breeding Pipeline. *Frontiers in Plant Science*, June 2022 | Volume 13 | Article 882732. <https://doi.org/10.3389/fpls.2022.882732>; <https://www.frontiersin.org/articles/10.3389/fpls.2022.882732>
  22. Ravelombola, W.\*, **A. Shi\***, B.L.Huynh, J. Qin, H. Xiong, A. Manley, L. Dong, D. Olaoye, G. Bhattarai, B. Zia, H. Alshaya, and I. Alatawi. 2022. Genetic architecture of salt tolerance in a multi-parent advanced generation inter-cross (MAGIC) cowpea population. *BMC Genomics* 23:100, <https://doi.org/10.1186/s12864-022-08332-y>
  23. Rice, A., K. Moldenhauer, A. Pereira, **A. Shi**, E. Shakiba\*. 2022. QTL Mapping of Panicle Architecture and Yield-Related Traits between Two U.S. Rice Cultivars ‘LaGrue’ and ‘Lemont’. *Euphytica* (2022) 218:7 <https://doi.org/10.1007/s10681-021-02940-7>.
  24. **Shi, A.\***, G. Bhattarai, H. Xiong, C.A. Avila\*, C. Feng, B. Liu, V. Joshi, L. Stein\*, B. Mou\*, L.J. du Toit\*, and J.C. Correll\*. 2022. Genome-wide association study and genomic prediction of white rust resistance in USDA GRIN Spinach Germplasm. *Horticulture Research*, Volume 9, 2022, uhac069, <https://doi.org/10.1093/hr/uhac069>.
  25. Usovsky, M., P. Chen\*, D. Li, A. Wang, A. Shi, C. Zheng, E. Shakiba, D. Lee, C.C. Vieira, Y. Lee, C. Wu, I. Cervantez, and D. Dong. 2022. Decades of genetic research on Soybean mosaic virus resistance in soybean. *Viruses* 2022, 14(6), 1122; <https://doi.org/10.3390/v14061122>
  26. Viteri, D.M\*, A.M. Linares, Z. Miranda, and **A. Shi\***. 2022. Identification of a QTL Region for Ashy Stem Blight Resistance Using Genome-wide Association and Linage Analysis in a Common Bean Recombinant Inbred Lines Derived from BAT 477 and NY6020-4. *Frontiers in Plant Science*. Accepted: 10 Oct 2022. <https://www.frontiersin.org/articles/10.3389/fpls.2022.1019263/full>; <https://doi.org/10.3389/fpls.2022.1019263>
  27. Xiong, H., J. Chen, S. Gao, Y. Pan\*, and **A. Shi\***. 2022. Population structure and genetic diversity analysis in sugarcane (*Saccharum* spp. hybrids) and six related *Saccharum* species. *Agronomy* 12(2) 412, <https://doi.org/10.3390/agronomy12020412>.
  28. Zia, B, **A. Shi\***, D. Olaoye, H. Xiong, W. Ravelombola, P. Gepts, H.F. Schwartz, M.A. Brick, K. Otto, B. Ogg, and S. Chen\*. 2022. Genome-wide association study and genomic prediction for common bean bacterial wilt resistance in common bean (*Phaseolus vulgaris*) core collection. *Frontiers in Genetics*, 31 May 2022 |



<https://doi.org/10.3389/fgene.2022.853114>.

## 2021

29. Awika, H.O., J. Solorzano, U.C. Rivera, **A. Shi**, J. Enciso, and C.A. Avila\*. 2021. Prediction modeling for yield and water-use efficiency in spinach using remote sensing via an unmanned aerial system. *Smart Agriculture Technology* 1 (2021) 100006. <https://doi.org/10.1016/j.atech.2021.100006>
30. Bhattarai, G.\*, and **A. Shi**\*. 2021. Research advances and prospects of spinach breeding, genetics, and genomics, *Vegetable Research* 2021, 1: 9. <http://www.maxapress.com/article/doi/10.48130/VR-2021-0009>. <https://doi.org/10.48130/VR-2021-0009>
31. Bhattarai, G., W. Yang, **A. Shi**\*, C. Feng, B. Dhillon, J.C. Correll\*, and B. Mou\*. 2021. Mapping and candidate gene identification of downy mildew race 16 resistance in spinach. *BMC Genomics* 22-478, <https://doi.org/10.1186/s12864-021-07788-8>
32. Bhattarai, G., **A. Shi**\*, D.R. Kandel, N. Solís-Gracia, J.A. da Silva, and C.A. Avila\*. 2021. Genome-wide simple sequence repeats (SSR) markers discovered from whole-genome sequence comparisons of multiple spinach accessions. *Scientific Reports*, 11, Article number: 9999 (2021), <https://doi.org/10.1038/s41598-021-89473-0>; <https://www.nature.com/articles/s41598-021-89473-0>
33. Gyawali, S., G. Bhattarai, **A. Shi**\*, C. Kik, and L. du Toit\*. 2021. Early stages of allopatric speciation in *Spinacia turkestanica* and the domestication of cultivated spinach. *Frontiers in Genetics*. 08 December 2021 | <https://doi.org/10.3389/fgene.2021.740437>
34. Moseley, D., L. Mozzoni\*, A. Kaler, E. Mason, **A. Shi**, M. Orazaly, L. Lara, and P. Chen. 2021. Evaluation of Genetic diversity and association mapping for seed weight and size in vegetable soybean [*Glycine max* (L.) Merr.] Germplasm. *Crop Science* First published: 21 June 2021 <https://doi.org/10.1002/csc2.20588>.
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## ABSTRACTS PUBLISHED:

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  12. Gehendra Bhattarai, **Ainong Shi**, Beiquan Mou and James C. Correll. 2022. Molecular Breeding Effort Using Genome Resequencing in Spinach for Resistance to Economically Important Pathogens. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
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  14. Haizheng Xiong, Yilin Chen, **Ainong Shi** and Yong-Bao Pan. 2022. A Genome-Wide Association Study and Genomic Prediction for Fiber and Sucrose Contents in Sugarcane. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
  15. Ibtisam Alatawi, Gehendra Bhattarai, Haizheng Xiong, Waltram Ravelombola, Theresa Makawa Phiri, Kenani Chiwina, Yilin Chen, Burt Bluhm, Neelendra Joshi, Dilip Panthee and **Ainong Shi**. 2022. Evaluation of Tomato Germplasm for Salt Tolerance at Seedling Stage. 2022 ASHS annual conference July 30 – August 3, Chicago, IL,
  16. Ibtisam Alatawi, Gehendra Bhattarai, Haizheng Xiong, Theresa Makawa Phiri, Kenani Chiwina, Yilin Chen, Burt Bluhm, Neelendra Joshi, Dilip Panthee and **Ainong Shi**. 2022. Characterization of Genetic Diversity of Tomato Germplasm Accessions. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
  17. Kenani Chiwina, Gehendra Bhattarai, Haizheng Xiong, Theresa Makawa Phiri, Yilin Chen, Ibtisam Alatawi, Burt Bluhm, Neelendra Joshi, Ryan Dickson and **Ainong Shi**. 2022. Evaluation of Drought Tolerance in USDA Tomato Accessions. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
  18. Omolayo Joshua Olorunwa, Bikash Adhikari, **Ainong Shi** and T. Casey Barickman. 2022. Shoot Biomass, Photosynthesis, and Chlorophyll Fluorescence Parameters of Tolerant and Sensitive Cowpea Genotypes Under Waterlogging at the Reproductive Growth Stage. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
  19. Omolayo Joshua Olorunwa, Bikash Adhikari, **Ainong Shi** and T. Casey Barickman. 2022. Waterlogging Induces

- Physiological and Biochemical Changes in Cowpea (*Vigna unguiculata* L.) Genotypes with Contrasting Tolerance at Different Growth Stages Under Field Conditions. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
20. Theresa Makawa Phiri, Gehendra Bhattarai, **Ainong Shi** and Yong-Bao Pan. 2022. A Genomic Wide Association Study of Yield-Related Traits in Sugarcane. 2022 ASHS annual conference July 30 – August 3, Chicago, IL,
  21. Yilin Chen, Haizheng Xiong, Gehendra Bhattarai, Waltram Ravelombola, T. Casey Barickman, Ibtisam Alatawi, Theresa Makawa Phiri, Kenani Chiwina, Beiquan Mou and **Ainong Shi**. 2022. A Genome-Wide Association Study Reveals Region Associated with Seed Protein Content in Cowpea. 2022 ASHS annual conference July 30 – August 3, Chicago, IL.
  22. **Ainong Shi**, James C. Correll, Gehendra Bhattarai, Bo Liu, Chunda Feng, Henry O. Awika, Carlos A. Avila, and Beiquan Mou. 2020. Evaluation and Genome-Wide Association Study for White Rust Resistance in USDA Spinach Germplasm. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  23. Bazgha Zia and **Ainong Shi**. 2020. Differential Gene Expression to Identify Potential Genetic Elements Involved in Disease Resistance to Downy Mildew Pathogen in Spinach Cultivars. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  24. Dotun Olaoye, Gehendra Bhattarai, Chunda Feng, James C. Correll and **Ainong Shi**. 2020. Genome-Wide Association Study and Genomic Selection for Downy Mildew Resistance in Spinach. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  25. Dotun Olaoye, Waltram Second Ravelombola, Gehendra Bhattarai, Haizheng Xiong, and **Ainong Shi**. 2020. Comparative Transcriptional Characterization for Drought Tolerance in Common Bean. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  26. Gehendra Bhattarai, **Ainong Shi**, James C. Correll, Chunda Feng, and Beiquan Mou. 2020. Field Evaluation and Genome-Wide Association Analysis of Downy Mildew Resistance in Spinach. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  27. Gehendra Bhattarai, Bo Liu, Ainong Shi, Chunda Feng and James C. Correll. 2020. Genome-Wide Association of Leaf Spot (*Stemphylium vesicarium*) Resistance in USDA Spinach Germplasm. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  28. Gehendra Bhattarai, **Ainong Shi**, Carlos A. Avila, and Larry A. Stein. 2020. GWAS on USDA Spinach Germplasm Evaluated for Downy Mildew in the Texas' Wintergarden Production Area. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  29. Gehendra Bhattarai, **Ainong Shi**, James C. Correll, and Bindu Poudel. 2020. Identification of Genomic Regions Associated with Bolting and Flowering Time in Spinach. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  30. Haizheng Xiong, **Ainong Shi**, Waltram Second Ravelombola, Gehendra Bhattarai, Beiquan Mou and Sora Imamura. 2020. GWAS of Yield Related Traits and Genetic Diversity in Cowpea. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  31. Huda Alshaya, Ibtisam Alatawi, Neel Joshi, Waltram Ravelombola, **Ainong Shi**, and Haizheng Xiong. 2020. Evaluation of Drought Tolerance in Tomatoes at Seedling Stage. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  32. Waltram Second Ravelombola, Haizheng Xiong and **Ainong Shi**. 2020. Variation of Salt Tolerance at Seedling Stage in a Cowpea Biparental Population Derived from the Cross between 09\_529 and 15\_07\_86. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  33. Waltram Second Ravelombola, Haizheng Xiong and **Ainong Shi**. 2020. Genetic Architecture of Drought Tolerance in Cowpea. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  34. Waltram Second Ravelombola, Haizheng Xiong and **Ainong Shi**. 2020. Genetic Architecture of Salt Tolerance in Cowpea. 2020 ASHS Annual Conference, August 9 – 13 at Orlando, Florida.
  35. Neil D. Adhikari, Renée L. Eriksen, **Ainong Shi**, and Beiquan Mou. 2020. Proteomics analysis suggests a higher flux through major metabolic pathways in *Lactuca sativa* cv. Salinas than *Lactuca serriola* accession

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36. **Ainong Shi**, Jim Correll, Gehendra Bhattarai, Bo Liu, Chunda Feng, Henry Awika, Carlos A. Avila, and Beiquan Mou. 2020. Evaluation and Genome-wide Association Study for White Rust Resistance in USDA Spinach Germplasm. ASHS 2020 Annual Conference. August 9-13, 2020, Orlando, FL.
37. Gehendra Bhattarai, Bo Liu, **Ainong Shi**, Chunda Feng, and James C. Correll. 2020. Genome-wide Association of Leaf Spot (*Stemphylium vesicarium*) Resistance in USDA Spinach Germplasms. ASHS 2020 Annual Conference. August 9-13, 2020, Orlando, FL.
38. Gehendra Bhattarai, **Ainong Shi**, James C. Correll, Chunda Feng, and Beiquan Mou. 2020. Field evaluation and genome-wide association analysis of downy mildew resistance in spinach. ASHS 2020 Annual Conference. August 9-13, 2020, Orlando, FL.
39. Yubo Yang, Lingdi Dong, Linqi Shi, Jinghua Guo, Yonggang Jiao, Jun Qin, Ryan William Dickson and **Ainong Shi**. 2019. Effects of Low Temperature and Weak Light on Physiology of Tomato Seedlings. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
40. **Ainong Shi**, Jun Qin, Yuejin Weng, Waltram Ravelombola, Haizheng Xiong, Gehendra Bhattarai, Stephen Eaton, Senyu Chen and Beiquan Mou. 2019. Enhancement of Cowpea Breeding through Molecular Breeding in Cowpea. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
41. Qirui Cui, Yufeng Yang, Sora Imamura, Jossie Santamaria Archbold and **Ainong Shi**. 2019. Evaluation of Drought Tolerance in Arkansas Cowpea Lines at Seedling Stage. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
42. Yufeng Yang, Qirui Cui, Jun Qin, Waltram Ravelombola, Gehendra Bhattarai, Bazgha Zia, Olaoye Dotun Samuel, Sora Imamura, Jossie Santamaria Archbold and **Ainong Shi**. 2019. Evaluation of Drought Tolerance in Common Bean at Seedling Stage. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
43. Dotun Olaoye, Gehendra Bhattarai, Chunda Feng, **Ainong Shi** and Jim Correll. 2019. Evaluation of Incomplete Dominance in a Spinach Downy Mildew Resistance Locus. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
44. Sora Imamura, Qirui Cui, Jossie Santamaria Archbold and **Ainong Shi**. 2019. Evaluation of Morphological Traits of Pod Length, Pod Seed Number, Seed Weight, Seed Density and Seed Color in Cowpea (*Vigna unguiculata*). 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
45. Gehendra Bhattarai, **Ainong Shi**, James C Correll and Beiquan Mou. 2019. Mapping Resistance to Race of Downy Mildew in Multiple Spinach Populations. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
46. Adam Rice, Karen Moldenhauer, Andy Pereira, **Ainong Shi** and Ehsan Shakiba. 2019. QTL Mapping of Panicle Architecture and Yield Related Traits in Two US Rice Cultivars ‘Lagrué’ and ‘Lemont’. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
47. Jinghua Guo, Yan Yan, Lingdi Dong, Yonggang Jiao, Haizheng Xiong, Linqi Shi, Yu Tian, Yubo Yang and **Ainong Shi**. 2019. Quality Control Techniques and Related Factors for Hydroponic Leafy Vegetables. 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas.
48. **Ainong Shi**. 2019. Evaluation and Genome Wide Association Study for Seed Quality, Abiotic and Biotic Traits in USDA Cowpea Germplasm. USDA Vigna Germplasm Evaluation Workshop, organized by Ainong Shi and Shyam Tallury. Jointed with 2019 ASA-CSSA-SSSA International Annual Meeting | Nov. 10-13 | San Antonio, Texas. <https://scisoc.confex.com/scisoc/2019am/meetingapp.cgi/Session/19560>
49. **Ainong Shi**, Jun Qin, Senyu Chen, and Thomas Michaels. 2019. Genetic Diversity and Association Study of SCN Resistance in Common Bean. Bean Improvement Cooperative (BIC), November 3-6, 2019 and North American Pulse Improvement Association (NAPIA), November 6-8, 2019, Fargo, North Dakota.
50. **Ainong Shi**, Jun Qin, Yuejin Weng, Waltram Ravelombola, Haizheng Xiong, Gehendra Bhattarai, Stephen Eaton, Senyu Chen and Beiquan Mou. 2019. Enhancement of Cowpea Breeding through Molecular Breeding in Cowpea. Bean Improvement Cooperative (BIC), November 3-6, 2019 and North American Pulse Improvement



Association (NAPIA), November 6-8, 2019, Fargo, North Dakota.

51. **Ainong Shi**, James Correll, Chunda Feng, Beiquan Mou, Carlos A. Avila, Larry A. Stein, Rob Hogan, Lindsey du Toit, Jun Qin, Gehendra Bhattarai, Henry Awika, Sanjaya Gyawali and Shyam Kandel. 2019. Progress at Developing Genetic and Molecular Resources to Improve Spinach Production and Management. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
52. Gehendra Bhattarai, Chunda Feng, Braham Dhillon, **Ainong Shi** and James C. Correll. 2019. Evaluation of a Detached Leaf Inoculation Method to Screen for Resistance to Downy Mildew in Spinach. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
53. Gehendra Bhattarai, **Ainong Shi**, James Correll and Beiquan Mou. 2019. Mapping of Resistance to Downy Mildew Race 16 in Spinach Cultivar 'Whale'. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
54. Gehendra Bhattarai, **Ainong Shi**, James C. Correll, Chunda Feng, Braham Dhillon, Jun Qin and Beiquan Mou. 2019. Field Evaluation, Association Mapping, and QTL Analysis to Dissect Downy Mildew Resistance in Spinach. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
55. Jun Qin, **Ainong Shi**, Thomas E. Michaels and Senyu Chen. 2019. Genetic Diversity and Population Structure Analysis of Common Bean. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
56. Jun Qin, **Ainong Shi**, James Correll, Carlos A. Avila, Chunda Feng, Bo Liu, Gehendra Bhattarai, Bazgha Zia and Waltram Ravelombola. 2019. Genome-Wide Association Study and Genomic Selection for White Rust Resistance in Spinach. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
57. Ravelombola, W., and **A. Shi**. 2019. Assessment of the Variation in Reduction in above ground Traits in a Set of Genetically Diverse Cowpea Genotypes Under Salt Stress. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
58. Ravelombola, W., and **A. Shi**. 2019. In Vivo and in Vitro Assessment of Na<sup>+</sup> and Cl<sup>-</sup> Contents in Cowpea Under Salt Stress Using Micro Ion Electrodes. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
59. Ravelombola, W., and **A. Shi**. 2019. Evaluation of Reduction in Plant Height, Stem Diameter, and Chlorophyll Content Among 331 Cowpea Genotypes Under Drought Stress at Early Vegetative Stage. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
60. Ravelombola, W., and **A. Shi**. 2019. Genome-Wide Association Study (GWAS) and Genomic Selection (GS) for Drought Tolerance in Cowpea at Early Vegetative Stage. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
61. Ravelombola, W., and **A. Shi**. 2019. Salt Leaf Injury Score and Chlorophyll Content Variation Under Salt Stress in Cowpea Seedlings. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
62. Ravelombola, W., and **A. Shi**. 2019. Variation in Plant Greenness Score, Wilting Status, and Leaf-Related Traits in a Diverse Set of Cowpea Genotypes under Drought Conditions. ASHS 2019 Annual Conference. July 21-25, Las Vegas Nevada.
63. **Ainong Shi**. 2019. Cowpea breeding program in University of Arkansas. Legume workshop, March 4-5, The Samuel Roberts Noble Foundation, Ardmore, OK.
64. Jun Qin, **Ainong Shi**, Jim Correll, Gehendra Bhattarai, Bazgha Zia, Waltram Second Ravelombola. 2019. Genome-wide study for white rust resistance in spinach. 2019 Plant & Animal Genomics XXVI on January 12-16, 2019 at San Diego, CA, USA.
65. **Ainong Shi**, Jim Correll, Chunda Feng, Beiquan Mou, Carlos Avila, Lindsey du Toit, Larry Stein, Rob Hogan, Jun Qin, Wei Zhou, Gehendra Bhattarai, Bazgha Zia, Waltram Ravelombola, Yuejin Weng, Bo Liu, Sanjaya Gyawali, and Shyam Kandel. 2018. Developing Genetic and Molecular Resources to Improve Spinach Production and Management. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
66. **Ainong Shi**, Jun Qin, Jim Correll, Wei Zhou, Gehendra Bhattarai, Bazgha Zia, Waltram Ravelombola, Yuejin Weng, Chunda Feng, Bo Liu, Carlos Avila, and Beiquan Mou. 2018. Genome-wide Association Study and Genomic Selection for White Rust in Spinach. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.

67. Bazgha Zia, Gehendra Bhattarai, Chunda Feng, Wei Zhou, Jun Qin, Maria Isabel Villarroel-Zeballos, Yuejin Weng, Waltram Ravelombola, Jim Correll, **Ainong Shi**, and Beiquan Mou . 2018. Evaluation and Association Analysis of Downy Mildew Resistance in USDA Spinach Germplasm. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
68. Gehendra Bhattarai, Bazgha Zia, Wei Zhou, Chunda Feng, Jun Qin, Waltram Ravelombola, Yuejin Weng, Jim Correll, **Ainong Shi**, and Beiquan Mou. 2018. Field phenotyping and genome wide association analysis for downy mildew resistance in USDA spinach germplasm. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
69. Gehendra Bhattarai, Bazgha Zia, Wei Zhou, Jun Qin, Waltram Ravelombola, Yuejin Weng, Chunda Feng, Jim Correll, **Ainong Shi**, and Beiquan Mou. 2018. Development of Genome-wide Simple Sequence Repeat (SSR) Markers in Spinach. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
70. Jun Qin, **Ainong Shi**, Wei Zhou, Yuejin Weng, Waltram Ravelombola, Gehendra Bhattarai, and Bazgha Zia. 2018. A SNP Set for Spinach Cultivar Determination. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
71. Lingdi Dong, Waltram Ravelombola, Yuejin Weng, Jun Qin, Wei Zhou, Gehendra Bhattarai, Bazgha Zia, Wei Yang, and **Ainong Shi**. 2018. Assessment of Leaf Chlorophyll Content under Salt Conditions in Cowpea Seedlings over Time. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
72. Waltram Ravelombola, Yuejin Weng, Jun Qin, Wei Zhou, Gehendra Bhattarai, Bazgha Zia, and **Ainong Shi**. 2018. Genetic Architecture of Abiotic Stress Tolerance in Cowpea through Multiple Genomic Selection Models. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
73. Waltram Ravelombola, Jun Qin, Gehendra Bhattarai, Yuejin Weng, Wei Zhou, Bazgha Zia, and **Ainong Shi**. 2018. Genomic Selection-Based Approach for Resistance to Aphids and Cowpea Mosaic Virus in Cowpea. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
74. Wei Zhou, Yuejin Weng, Bo Liu, Gehendra Bhattarai, Jun Qin, Bazgha Zia, Waltram Ravelombola, Chunda Feng, Jim Correll, and **Ainong Shi**. 2018. Identification and evaluation of white rust resistance in spinach germplasm. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
75. Yuejin Weng, Jun Qin, Wei Yang, Waltram Ravelombola, Haizheng Xiong, Gehendra Bhattarai, Bazgha Zia, Wei Zhou, **Ainong Shi**, and Beiquan Mou. 2018. Evaluation and Association Analysis of Seed Protein Content in USDA Cowpea Germplasm. 2018 ASHS Annual Conference on July 30-August 3, Washington, DC.
76. **Shi, A.** 2018. Genome-wide association study and genomic selection in spinach. Gust talk on February 23, 2018 at ABL, Arkansas State University, Jonesboro, AR.
77. **Ainong Shi**, Jun Qin, Yuejin Weng, Jim Correll, Chunda Feng, Gehendra Bhattarai, Waltram Ravelombola, Bazgha Zia, Wei Zhou, and Beiquan Mou. 2018. Genetic diversity, genome-wide association study and genomic selection in spinach. The 2018 International Spinach Conference, 02/14-02/15, 2018 in Murcia, Spain.
78. Chunda Feng, Bo Liu, Braham Dhillon, Maria Villarroel-Zeballos, Burt Bluhm, **Ainong Shi**, James Correll. 2018. Molecular markers for spinach sex determination gene. The 2018 International Spinach Conference, 02/14-02/15, 2018 in Murcia, Spain.
79. Jim Correll, Chunda Feng, and **Ainong Shi**. 2018. White rust: beyond borders. The 2018 International Spinach Conference, 02/14-02/15, 2018 in Murcia, Spain.
80. Braham Deep Singh Dhillon, Chunda Feng, **Ainong Shi**, Quighua Pan, and Jim Correll. 2018 Spinach genome sequence overview including NIL1 and candidate resistance genes. The 2018 International Spinach Conference, 02/14-02/15, 2018 in Murcia, Spain.
81. **Ainong Shi**, Jun Qin, Yuejin Weng, Gehendra Bhattarai, Waltram Ravelombola, Bazgha Zia, Wei Zhou, Jim Correll, and Beiquan Mou. 2018. Genetic diversity and genome-wide association study in spinach. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
82. **Ainong Shi**, Jun Qin, Beiquan Mou, Yuejin Weng, Waltram Ravelombola, Haizheng Xiong, and Gehendra Bhattarai. 2018. Genetic Diversity, Population Structure and Genome-wide Association Study in Cowpea. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.

83. Waltram Ravelombola, Jun Qin, **Ainong Shi**, Yuejin Weng, Gehendra Bhattarai, Lingdi Dong, and J. Bradley Morris. A SNP-based association analysis for plant growth habit in worldwide cowpea germplasm. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
84. Waltram Ravelombola, Jun Qin, Yuejin Weng, Gehendra Bhattarai, and **Ainong Shi**. 2017. Evaluation of drought tolerance in cowpea. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
85. Waltram Ravelombola, Yuejin Weng, Jun Qin, and **Ainong Shi**. 2017. Phenomics of Cowpea at Seedling Stage under Salt Stress. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
86. Waltram Ravelombola, Yuejin Weng, Jun Qin, and **Ainong Shi**. 2017. A rapid approach for salt tolerance evaluation in cowpea at seedling stage. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
87. Ravelombola, W., J. Qin, **A. Shi**, J.C. Miller, Jr., D. Scheuring, Y. Weng, G. Bhattarai, L. Dong, and W. Yang, 2017. Association analysis for iron deficiency chlorosis tolerance in cowpea. 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
88. Yuejin Weng, Jun Qin, Gehendra Bhattarai, Waltram Ravelombola, Bazgha Zia, Wei Zhou, and **Ainong Shi**. 2018. Study on photoperiodism in spinach (*Spinacia oleracea* L.). 2018 SR-ASHS conference on February 2-4, Jacksonville, FL.
89. **Ainong Shi**, Jun Qin, Beiquan Mou, and Jim Correll. 2018. Phenotypic and genetic diversity of spinach USDA germplasm accessions. 2018 Plant & Animal Genomics XXVI on January 13-17, 2018 at San Diego, CA, USA.
90. Jun Qin, **Ainong Shi**, Beiquan Mou, and Michael Grusak. 2018. Phenotypic and genetic diversity and association study of mineral components in spinach. 2018 Plant & Animal Genomics XXVI on January 13-17, 2018 at San Diego, CA, USA.
91. Jun Qin, **Ainong Shi**, and Senyu Chen. 2018. Genome-wide association study (GWAS) of soybean cyst nematode resistance in soybean. 2018 Plant & Animal Genomics XXVI on January 13-17, 2018 at San Diego, CA, USA.
92. **Ainong Shi**, Jun Qin, Yuejin Weng, Beiquan Mou, Senyu Chen, Waltram Ravelombola, Dennis Motes, Haizheng Xiong, Lingdi Dong, Wei Yang, and Gehendra Bhattarai. 2017. Genome-wide association study (GWAS) in cowpea. ASA, CSSA & SSSA International Annual Meetings: Oct. 22-25, 2017, Tampa, FL, USA.
93. Jun Qin, **Ainong Shi**, Senyu Chen, Thomas E Michaels, Yuejin Weng. 2017. Whole genome sequencing and resequencing for genome-wide study in common bean. ASA, CSSA & SSSA International Annual Meetings: Oct. 22-25, 2017, Tampa, FL, USA.
94. Jun Qin, Qijian Song, **Ainong Shi**, Song Li, Mengchen Zhang and Bo Zhang. 2017. Genome-wide association study of resistance to five races of *Phytophthora sojae* in soybean. ASA, CSSA & SSSA International Annual Meetings: Oct. 22-25, 2017, Tampa, FL, USA.
95. Waltram Ravelombola, **Ainong Shi**, Yuejin Weng, Beiquan Mou, Dennis Motes, John R. Clark, Pengyin Chen, Vibha Srivastava, Jun Qin, Lingdi Dong, Wei Yang, Gehendra Bhattarai and Yuichi Sugihara. 2017. Evaluation of association analysis of salt tolerance in cowpea. 2017 ASHS Annual Meeting, September 19-22, Waikoloa, Hawaii, USA.
96. Waltram Ravelombola, **Ainong Shi**, Yuejin Weng, Beiquan Mou, Dennis Motes, John Clark, Pengyin Chen, Vibha Srivastava, Jun Qin, Lingdi Dong, Wei Yang, Gehendra Bhattarai, and Yuichi Sugihara. Evaluation an Association Mapping for Cowpea Salt Tolerance. Presented during the Plant Science Symposium in Florida, on April 13, 2017, Gainesville, FL.
97. Waltram Ravelombola, **Ainong Shi**, Yuejin Weng, Beiquan Mou, Dennis Motes, John Clark, Pengyin Chen, Vibha Srivastava, Jun Qin, Lingdi Dong, Wei Yang, Gehendra Bhattarai, and Yuichi Sugihara. Evaluation and Association Mapping for Cowpea Salt Tolerance Using a Genotyping-By-Sequencing Approach. Presented on February 15, 2017 during the Horticulture Seminar, University of Arkansas, Fayetteville, AR.
98. Haizheng Xiong, Jun Qin, **Ainong Shi**, Beiquan Mou, Dianxing Wu, Jian Sun, Xiaoli Shu, Zhixue Wang, Weiguo Lu, Jianbing Ma, Yuejin Weng and Wei Yang. 2017. Genetic and Phenotypic Diversity Analysis in Cowpea. 2017 ASHS Annual Meeting, 09/19-22, Waikoloa, Hawaii, USA.
99. Jun Qin, **Ainong Shi**, Beiquan Mou, Michael A. Grusak, Jim Correll, Yuejin Weng, Dennis Motes, Lingdi Dong,

- Wei Yang, Gehendra Bhattarai, Waltram Second Ravelombola, Haizheng Xiong and Jianbing Ma. 2017. Genetic Diversity and Association Analysis of Mineral Components in Spinach. 2017 ASHS Annual Meeting, September 19-22, Waikoloa, Hawaii, USA.
100. **Ainong Shi**, Jun Qin, Beiquan Mou, Jim Correll, Yuejin Weng, Chunda Feng, Dennis Motes, Wei Yang, Gehendra Bhattarai, Waltram Second Ravelombola, Lingdi Dong and Yuichi Sugihara. 2017. Genome-Wide Association Study Using Next Generation Sequencing in Spinach. 2017 ASHS Annual Meeting, September 19-22, Waikoloa, Hawaii, USA.
  101. **Ainong Shi**, Jun Qin, Yuejin Weng, Waltram Ravelombola, Dennis Motes, Haizheng Xiong, Lingdi Dong, Wei Yang, Gehendra Bhattarai and Beiquan Mou. 2017. Whole Genome Sequencing and Resequencing for Genome-Wide Study in Cowpea. 2017 ASHS Annual Meeting, September 19-22, Waikoloa, Hawaii, USA.
  102. Gehendra Bhattarai, Jun Qin, Yuejin Weng, L. John Bradley Morris, Waltram Ravelombola, Wei Yang, and **Ainong Shi**. 2017. Association analysis of cowpea mosaic virus resistance in the USDA cowpea germplasm collection (Submitted to The National Association of Plant Breeders (NAPB) 2017 Annual Meeting, August 7-10, 2017, University of California, Davis, CA, USA.
  103. **Ainong Shi**. 2017. Cowpea Breeding and Genetic Research. Presented on the Horticultural Department Seminar on September 27, 2017, PTSC 009, and University of Arkansas Campus.
  104. **Ainong Shi**. 2017. Whole genome sequencing and genotyping by sequencing for crop improvement. Presented on the Cell and Molecular Biology (CEMB) Program Seminar on April 7, 2017, University of Arkansas Campus.
  105. **Shi, A.**, and J. Correll. 2017. Spinach molecular breeding. Presented on the International Working Group on *Peronospora farinosa* (IWGP) conference on February 1, 2017 in Netherland.
  106. **Shi, A.**, B. Mou, J. Ma, J. Correll, J. Qin, Y. Weng, D. Motes, and W. Yang. 2017. Genetic diversity and association analysis in spinach. 2017 Plant & Animal Genomics XXV on January 14-18, 2017 at San Diego, CA, USA.
  107. Qin, J., A. Shi. 2017. Association analysis of seed antioxidant content and aphid tolerance in cowpea. 2017 Plant & Animal Genomics XXV on January 14-18, 2017 at San Diego, CA, USA.
  108. **Shi, A.** 2016. Spinach molecular breeding. Gust talk on September 15, 2016 at ABI, Arkansas State University, Jonesboro, AR.
  109. **Shi, A.**, B. Mou, J. Ma, J. Correll, D. Motes, C. Feng, J. Ma, Y. Weng, J. Qin, W. Yang, G. Bhattarai, W. Ravelombola, J. Chitwood, H., Xiong, and W. Lu. 2016. Molecular breeding in spinach. The 2016 International Spinach Conference, 11/30 – 12/1, 2016 in San Antonio, TX.
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#### GENEBANK SUBMITTED:

- AY789478, AY870864, AY870865, DQ062668-DQ062675, DQDQ066421, DQ023289-DQ023292, FJ686039-FJ686046, FJ809919-FJ809928, FJ985979-FJ985984, and FJ817592-AF536200.

#### PATENT:

**JUSTIA PATEN list:** <https://patents.justia.com/inventor/ainong-shi>

1. **Nematode resistance alleles in soybean.** **Patent number:** 20220033886 and 11180795. **Abstract:** Methods for conveying soy cyst nematode (SCN) resistance into non-resistant soybean germplasm are provided. In some embodiments, the methods include introgression SCN resistance into a non-resistant soybean using one or more nucleic acid markers for marker-assisted breeding among soybean lines to be used in a soybean breeding program, wherein the markers are linked to and/or associated with SCN resistance. Also provided are single nucleotide polymorphisms (SNPs) associated with resistance to SCN. Soybean plants and seeds produced by any of the disclosed methods are provided. **Type:** Grant. (1) Filed: October 19, 2021, Publication date: February 3, 2022; (2) **Filed:** June 2, 2016. **Date of Patent:** November 23, 2021. **Assignee:** Syngenta Participations AG. **Inventors:** Ainong Shi, Becky Welsh Breitingner, Ju-Kyung Yu, Azhaguvel Perumal. <https://patents.justia.com/patent/20220033886>; <https://patents.justia.com/patent/11180795>
2. **Molecular markers linked to disease resistance in soybean.** **Patent number:** 10655142; <https://patents.justia.com/patent/10655142>; **Abstract:** The present invention relates to methods and compositions for identifying, selecting and/or producing a soybean plant or germplasm having a Rps1 resistance allele and resistance to Phytophthora sojae. A soybean plant, part thereof and/or germplasm that has been identified, selected and/or produced by any of the methods of the present invention is also provided. **Type:** Grant; **Filed:** January 19, 2016; **Date of Patent:** May 19, 2020; **Assignee:** Syngenta Participations AG. **Inventors:** Ainong Shi, Harish T. Gandhi, Becky Welsh Breitingner, Zhanyou Xu, Roger L. McBroom, Harikrishnan Ramasubramaniam. <https://patents.google.com/patent/US10655142B1/en>
3. **Molecular markers associated with soy iron deficiency chlorosis.** **Patent number:** 11236400; <https://patents.justia.com/patent/11236400>; 10648041; <https://patents.justia.com/patent/10648041>; **Patent number:** 9879326; <https://patents.justia.com/patent/9879326>. **Abstract:** The present invention relates to methods and compositions for identifying, selecting and/or producing a soybean plant or germplasm having iron deficiency chlorosis tolerance. A soybean plant, part thereof and/or germplasm, including any progeny and/or seeds derived from a soybean plant or germplasm identified, selected and/or produced by any of the methods of the present invention is also provided. **Type:** Grant; **Filed:** December 3, 2015; December 15, 2017; April 2, 2020; **Date of Patent:** January 30, 2018; May 12, 2020; February 1, 2022. **Assignee:** Syngenta Participations AG. **Inventors:** Mark Charles Hamilton, Craig Lynn Davis, Jean Robert Gelin, Elhan Sultan Ersoz, Ju-Kyung Yu, Thomas Joseph Curley, Baohong Guo, Ainong Shi, <https://patents.google.com/patent/US10648041B1/en>; <https://patents.google.com/patent/US9879326B1/en>.
4. **Resistance alleles in soybean.** **Patent number:** 9458504; <https://patents.justia.com/patent/9458504>; **Patent number:** 9708674; <https://patents.justia.com/patent/9708674>; **Patent number:** 10544470; <https://patents.justia.com/patent/10544470>. **Abstract:** The present invention relates to methods and compositions for identifying, selecting and/or producing a soybean plant or germplasm having iron deficiency chlorosis tolerance. A soybean plant, part thereof and/or germplasm, including any progeny and/or seeds derived from a soybean plant or germplasm identified, selected and/or produced by any of the methods of the present invention is also provided. **Type:** Grant; **Filed:** April 30, 2012; September 1, 2016; June 13, 2017; **Date of Patent:** October 4, 2016; July 18, 2017; January 28, 2020; **Assignee:** Syngenta Participations AG

**Inventors:** Mark Charles Hamilton, Harish Gandhi, [Ainong Shi](#), Craig Lynn Davis, Thomas Joseph Curley, Jr., Baohong Guo, <https://patents.google.com/patent/US9458504B1/en>; <https://patents.google.com/patent/US9708674B2/en>; <https://patents.google.com/patent/US10544470B2/en>.

5. Soy gene cluster regions and methods of use. Patent number: 20220312708, <https://patents.justia.com/patent/20220312708>; patent number: 11382290; <https://patents.justia.com/patent/11382290>; Patent number: 9307707; <https://patents.justia.com/patent/10655142>; Patent number: 10045494; <https://patents.justia.com/patent/10045494>. **Abstract:** Methods for conveying pathogen resistance into non-resistant soybean germplasm are provided. In some embodiments, the methods include introgressing pathogen resistance into a non-resistant soybean using one or more nucleic acid markers for marker-assisted breeding among soybean lines to be used in a soybean breeding program, wherein the markers are linked to and/or associated with pathogen resistance. Also provided are single nucleotide polymorphisms (SNPs) associated with resistance to pathogens; soybean plants, seeds, and tissue cultures produced by any of the disclosed methods; seed produced by the disclosed soybean plants; and compositions including amplification primer pairs capable of initiating DNA polymerization by a DNA polymerase on soybean nucleic acid templates to generate soybean marker amplicons. **Type:** Grant; **Filed:** November 28, 2012; December 14, 2015; **Date of Patent:** April 12, 2016; August 14, 2018; **Assignee:** Syngenta Participations AG. **Inventors:** Ju-Kyung Yu, Becky Welsh Breitingner, David Plunkett, [Ainong Shi](#), Daniel Dyer, <https://patents.google.com/patent/US20180310501A1/en>; <https://patents.google.com/patent/US20180310501A1/en>;
6. Murphy P., S. Leath, R.A. Navarro, [A. Shi](#), D. Huynh. 1998. PI 597348, PI 597349, PI 597350, PI 599034, PI 599035, and PI 599036 of *Triticum aestivum* accessions. Plant Inventory No. 206, Part I. Plant Materials Introduced January 1 to June 30, 1997 (Nos. 596294 to 599110) edited by R.A. Norris. USDA-ARS, June 1998. [https://www.ars-grin.gov/npgs/pi\\_books/scans/pi206pt1.pdf](https://www.ars-grin.gov/npgs/pi_books/scans/pi206pt1.pdf).
7. Chen\*, S. and **A. Shi\***. 2020. "Identification of A major QTL for resistance to soybean cyst nematode (*Heterodera glycines*) in soybean and methods of use" for which provisional patent application No. 63/011,633 was filed Aril 17, 2020 (Atty. File No. 920171.00331) (Hereinafter the "International Paten Application and United States Patent Application").

**Intellectual Property:** Cowpea varieties, 'AR 10-ES01', 'AR07-303', 'AR09-393', and 'AR09-692'.

Arkansas cowpea cultivars/breeding lines for high drought tolerance: AR Blackeye#1, AR17-40, AR17-61, AR17-81, AR17-86, AR17-131, Early Scarlet, and Empire; for salt tolerance: AR09-671, AR09-529, and AR09-470; for high seed protein content: Early Scarlet, AR09-204, and AR01-1781; and for high seed sugar content: Empire and AR09-655.

#### SKILLS/KNOWLEDGE:

- Extensive experience in plant pathology, plant breeding and genetics including field, greenhouse and lab experiments. Strong skills in experimental design and statistical data analysis using JMP and SAS. Experience in project management (organizing, supervising, proposal writing and execution).
- Wet-bench experience in molecular technology including DNA extraction and RNA isolation, southern transferring and hybridization, electrophoresis, DNA amplification, cloning, isolation and sequencing. Skills in PCR primer and assay designing, DNA polymorphism, molecular marker analysis (AFLP, PCR, RAPD, SNP, SSR, and RFLP), and next generation sequencing including RNA sequencing (RNAseq), isoSeq, GBS, ddRADseq, whole genome sequencing and resequencing.
- Experience in QTL mapping, genetic diversity, genome-wide association study (GWAS), and genomic prediction (GP) with a variety of software and computer tools such as Arlequin, BLINK, FarmCPU, GAPIT, GenSel, Paup, NTSys, Phylip, Structure 2, Mega 7/X, Tassel 5, Haploview, JoinMap 4, MSTmap, Qgene, PowerMarker, rrBLUP/gBLUP/cBLUP/Bayers, WinQTLCartographer 2.5, QTLNetwork 2.1, and MapChart.
- Strong abilities in bioinformatics and proficient in the use of software and tools such as Assay Design, Blast, BioEdit, ClustalW/ClustalX, MAGA 7/x, Primer3/BatchPrimer3, SSRLocator, TreeView, and ExPASy tools etc. and database

sources such as FASTA, GenBank, PDB, PubMed, and Soybase.

- Proficient computer user including Word, Excel, Access, PowerPoint, Outlook, MS FrontPage and programming including VB/VBA, C/C++, HTML, Java, Perl, and SQL, and database management such as MySQL and MS SQL Server.
- Certification: MCP, MCSE, and MCDBA from Microsoft, 2000; Java 2 programming: University of Washington and Sun Microsystems, 2000; C, C++, HTML, Java 2, JavaScript.