BIOGRAPHICAL SKETCH

NAME:	**Ainong Shi**	POSITION TITLE: A s s o c i a t e P r o f e s s o r	

EDUCATION & TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Zhejiang University, China	BS	07/1983	Plant Pathology and Entomology
Chinese Academy Agri. Sci. China	MS	07/1986	Plant Breeding and Genetics
North Carolina State University, NC	PhD	12/1997	Plant Pathology and Crop Sciences

Appointments

04/2019–present: Associate Professor, Dept. Horticulture, University of Arkansas, AR.
06/2013–03/2019: Assistant Professor, Dept. Horticulture, University of Arkansas, AR.
10/2009–05/2013: Scientist/Soy Genetic Project Lead, Syngenta Seeds, Slater, IA.
07/2008–09/2009: Plant Geneticist, Indiana Crop and Purdue University, IN.
12/2007–07/2008: Postdoc, Cornell University, NY.
10/2005–11/2007: Postdoc, University of Arkansas, AR.

Publications (last four years and relevant) (*as corresponding author in all articles)

- 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.
- 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.
- 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.
- 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.
- Bhattarai, G.*, and **A. Shi***. 2021. Research advances and prospects of spinach breeding, genetics, and genomics, Vegetable Research 2021, 1: 9.
- 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.
- Bhattarai, G., **A. Shi*,** C. Feng, B. Dhillon, B. Mou*, J.C. Correll*. 2020. Genome-wide association studies in multiple spinach breeding populations refine downy mildew race 13 resistance genes. Frontiers in Plant Science, doi:10.3389/fpls.2020.563187.
- 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) 12:1375.
- **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, 9, uhac069.
- 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.
- Kandel, S.L., A.M. Hulse-Kemp, K. Stoffel, S.T. Koike, **A. Shi**, B. Mou, A. Van Deynze*, and S.J. Klosterman1*. 2020. Transcriptional analyses of resistant and susceptible spinach cultivars in response to the downy mildew pathogen, *Peronospora effuse*. Scientific Reports 10:6719.
- Kandel, S.L., B. Mou, N. Shishkoff, **A. Shi**, K.V. Subbarao, and S.J. Klosterman*. 2019. Spinach downy mildew: advances in our understanding of the disease cycle and prospects for disease management. Plant Disease 103:791-803.

Synergistic Activities

Service: As an associate editor for four journals: Agronomy, Crop Science, Frontiers in Plant Science, and Vegetable Research; as a reviewer for 44 academic journals, performed over 100 manuscripts reviewed; as USDA Cowpea and Vigna Crop Germplasm chair in 2019 and 2018; as ASHS Vegetable Breeding Interest Group chair in 2022 and Genetics and Germplasm (GG) Interest Group Chair in 2020; as the chair of Harvest & Plant Biotechnology section in 2018 Southern Region of American Society for Horticultural Science; as Vegetable Publication Award Committees (2014-17, 2020-2022) and as the chair in 2017; and as ASHS Graduate Student Activities Committee (2014-17).

Teaching and Advising: (1) Course teaching: HORT6033 Genetic Techniques in Plant Breeding (Molecular Plant Breeding); HORT5001 Graduate Student Seminar; and CEMB 590V Specific Topics in Cell and Molecular Biology. (2) Training: As a major professor advised 5 PhD and 3 MS graduated, and 3 undergraduate honors students; hosted for 3 postdoc and 8 visiting scholars; and currently advising 1 PhD, 3 MS, 1 Postdoc, 1 program associate, and 3 technician assistants; served on the advisory committee of over 20 graduate students (PhD+MS).

Grant award: 26 grants awarded from USDA and other agents with a total of $5,899,789 budget, among which $1,891,283 goes to Shi's lab. For example:
- **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" 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. "**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** and R. Dickson. "Evaluation and Genome-wide Study of Pythium Disease Resistance in Arugula and Spinach for Hydroponics and Indoor Farming" from Bowery Farming, 7/1/2022-6/30/2022 extended to 6/30/2027, $70,000 yearly.
- **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. 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.** 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.

Patent: (1) **Shi, A**. et al. 2022; 2021. Nematode resistance alleles in soybean, Patent number: 20220033886 and 11180795. (2)**Shi, A**. et al. 2016; 2020. Molecular markers linked to disease resistance in soybean. Patent number: 10655142. (3) Hamilton … **A. Shi**. 2015; 2017; 2018; 2020; 2022. Molecular markers associated with soy iron deficiency chlorosis. Patent numbers: 11236400, 10648041, 9879326, 9458504, 9708674, and 10544470. (4) Ju-Kyung … **A. Shi**, 2012; 2015; 2016; 2018. Soy gene cluster regions and methods of use. Patent number: 9307707 and 10045494. (5) Chen, S. and **A. Shi**. 2020. Identification of A major QTL for resistance to HG Type 2.5.7 and moderate resistance to HG Type 7 of soybean cyst nematode in soybean. Patent online: https://patents.justia.com/inventor/ainong-shi
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.

PUBLICATION (refereed: 151; book chapter: 1; non-refereed: 15; abstract: 142) **(listed 2023-2016)** (*as 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.

2. 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 Theoretical and Applied Genetics).

3. 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).

4. Riaz, A.*, Q. Raza, A. Kumar, D. Dean, K. Chiwina, T.M. Phiri, 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

5. Viteri, D.M*, A.M. Linares, Z. Miranda, and **A. Shi*.** 2022. Genome-wide study reveals a QTL region for ashy stem blight resistance in the Andean common bean line PRA154. Frontiers in Plant Science (Accepted, Manuscript ID: 1176967).

6. 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

7. Xiong*, H., Y. Chen, Y-B. Pan, J. Wang, **A. Shi*** and W. Lu*. 2023. A genome-wide association study and genomic prediction for *Phakopsora pachyrhizi* resistance in soybean. Frontiers in Plant Science (Accepted).

2022

8. 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

9. 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

10. 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

11. 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.

12. 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

13. 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.

14. 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

15. 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/1flPp3VH9X66HP

16. 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

17. 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

18. 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

19. 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

20. 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.

21. **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.

22. 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

23. 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 Inbreed 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

24. 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.

25. 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

26. 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

27. 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

28. 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

29. 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

30. 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

31. 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.

32. Olorunwa, O.J, **A. Shi**, and T. C. Barickman*. 2021. Varying Drought Stress Induces Morpho-Physiological Changes in Cowpea (*Vigna unguiculata* (L.) Genotypes. Plant Stress, Available online 11 September 2021, 100033. https://doi.org/10.1016/j.stress.2021.100033

33. Park, S., P. Kumar, **A. Shi**, and B Mou*. 2021. Population genetic and genome-wide association studies using genotyping by sequencing (GBS) provide an insight into the influence of selective breeding on genetic variation in lettuce. The Plant Genome 2021;e20086, https://doi.org/10.1002/tpg2.20086.

34. Ravelombola, W., A. Manley, C. Adams, C. Trostle, S. Ale, A. Shi, J. Cason. 2021. Genetic and Genomic Resources in Guar: A Review. Submission to Euphytica 217:199, https://doi.org/10.1007/s10681-021-02929-2.

35. Ravelombola, W.*, **A. Shi***, and B. Huynh*. 2021. Loci discovery, network-guided approach, and genomic prediction for drought tolerance index in a multi-parent advanced generation inter-cross (MAGIC) cowpea population. Horticulture Research (2021) 8:24, https://doi.org/10.1038/s41438-021-00462-w.

36. Ravelombola, W., L. Dong, T.C. Barickman, H. Xiong, D. Olaoye, G. Bhattarai, B. Zia, H. Alshaya Sr., I. Alatawi, and **A. Shi*.** 2021. Evaluation of Salt Tolerance in Cowpea at Seedling Stage. Euphytica 217, Article number: 116 (2021), https://doi.org/10.1007/s10681-021-02832-w

37. Ravelombola, W., J. Qin, **A. Shi**, J. Yuan, F. Wang, P. Chen, Q. Song, L. Yan, Y. Feng, T. Zhao, Y. Meng, C. Yang*, and M. Zhang*. 2021. Genome-wide association study and genomic selection for plant height, maturity, seed weight, and seed yield in soybean. PlosOne Published: August 13, 2021. https://doi.org/10.1371/journal.pone.0255761

38. **Shi, A.*,** P. Gepts, Q. Song, H. Xiong, T.E. Michaels, and S. Chen*. 2021. Genome-wide association study and genomic selection for soybean cyst nematode resistance in USDA common bean (*Phaseolus vulgaris*) core collection. Frontiers in Plant Science, 07 June 2021, https://doi.org/10.3389/fpls.2021.624156; https://www.frontiersin.org/articles/10.3389/fpls.2021.624156/full.

2020

39. Adhikari, N.D., R.L. Eriksen, **A. Shi,** and B. Mou*. 2020. Proteomics Analysis Indicates Greater Abundance of Proteins Involved in Major Metabolic Pathways in *Lactuca sativa* cv. Salinas than *Lactuca serriola* Accession US96UC23. Proteomics, 20, 1900420, https://doi.org/10.1002/pmic.201900420.

40. Bhattarai, G., **A. Shi*,** C. Feng, B. Dhillon, B. Mou*, J.C. Correll*. 2020. Genome-wide association studies in multiple spinach breeding populations refine downy mildew race 13 resistance genes. Frontiers in Plant Science, doi:10.3389/fpls.2020.563187. https://doi.org/10.3389/fpls.2020.563187; https://www.frontiersin.org/articles/10.3389/fpls.2020.563187/full.

41. Bhattarai, G., C. Feng, B. Dhillon, **A. Shi,** M. Villarroel-Zeballos, J.C. Correll*. 2020. Detached leaf inoculation assay for evaluating resistance to the spinach downy mildew pathogen. European Journal

of Plant Pathology, 158:511–520, https://doi.org/10.1007/s10658-020-02096-5.

42. Cui, Q., H. Xiong, Y. Yang, S. Eaton, S. Imamura, J. Santamaria, W. Ravelombola, R.E. Mason, L. Wood, L.A. Mozzoni, and **A. Shi***. 2020. Evaluation of drought tolerance in Arkansas cowpea lines at seedling stage. HortScience 55:1132–1143, https://doi.org/10.21273/HORTSCI15036-20.

43. Kandel, S.L., A.M. Hulse-Kemp, K. Stoffel, S.T. Koike, **A. Shi**, B. Mou, A. Van Deynze*, and S.J. Klosterman1*. 2020. Transcriptional analyses of resistant and susceptible spinach cultivars in response to the downy mildew pathogen, *Peronospora effuse*. Scientific Reports 10:6719 | https://doi.org/10.1038/s41598-020-63668-3.

44. Park, S., **A. Shi**, and B. Mou*. 2020. Genome-wide identification and expression analysis of the CBF/DREB1 gene family in lettuce. Scientific Reports 10:5733, https://doi.org/10.1038/s41598-020-62458-1.

45. Ravelombola, W., J. Qin, **A. Shi***, L. Nice, Y. Bao, A. Lorenz, J. H. Orf, N. D. Young, and S. Chen*. 2020. Genome-wide association study and genomic selection for tolerance of soybean biomass reduction under to soybean cyst nematode infestation. PlosOne, Published: July 16, 2020. https://doi.org/10.1371/journal.pone.0235089.

46. Ravelombola, W., **A. Shi*,** S. Chen, H. Xiong, Y. Yang, Q. Cui, D. Olaoye, and B. Mou*. 2020. Evaluation of cowpea for drought tolerance at seedling stage. Euphytica 216:123, https://doi.org/10.1007/s10681-020-02660-4.

47. Yang, Y., L. Dong*, L. Shi, J. Guo, Y. Jiao, H. Xiong, R.W. Dickson, and **A. Shi**. 2020. Effects of low temperature and weak light on physiology of tomato seedlings. American Journal of Plant Science 11: 162-https://doi.org/10.4236/ajps.2020.112013; ; https://www.scirp.org/journal/paperinformation.aspx?paperid=98358

48. Yang, Y., D. Shi, Y. Wang, L. Zhang, X. Chen, X. Yang, H. Xiong, G. Bhattarai, W. Ravelombola, D. Olaoye, G. Yang*, and **A. Shi*.** 2020. Involvement of WRKY transcription factors and glucose metabolism in the regulation of sweet potato skin color as revealed by the transcript profiling of Sushu 8 and Zhengshu 20. Plant Physiology and Biochemistry 148:1-9. https://doi.org/10.1016/j.plaphy.2019.12.035.

49. Zhu, S.*, E. Niu, W. Wang, and A. Shi.2020. Identification and evaluation of SNP core loci for olive germplasm. Molecular Plant Breeding 18(5):10. https://doi.org/10.13271/j.mpb.018.001548; https://xueshu.baidu.com/usercenter/paper/show?paperid=1c3m08r0s3660pc0pj1u0rp09b289728

2019

50. Bauchet, G., K. Bett, C. Cameron, J. Campbell, E. Cannon, S. Cannon*, J. Carlson, A. Chan, A. Cleary, T. Close, D. Cook, A. Cooksey, C. Coyne, S. Dash, R. Dickstein, A. Farmer, D. Fernandez-Baca, S. Hokin, E. Jones, Y. Kang, M. Monteros, M. Muñoz-Amatriaín, K. Mysore, C. Pislariu, C. Richards, **A. Shi,** C. Town, M. Udvardi, E. von Wettbert, N. Young, and P. Zhao. 2019. The future of legume genetic data resources: challenges, opportunities, and priorities. Legume Science, 2019;e16; https://doi.org/10.1002/leg3.16.

51. Dong, L., W. Ravelombola, Y. Weng, J. Qin, G. Bhattarai, B. Zia, W. Zhou, B. Mou, and **A. Shi*.** 2019. Seedling salt tolerance for above ground-related traits in cowpea (*Vigna unguiculata* (L.) Walp). Euphytica 215:53, https://doi.org/10.1007/s10681-019-2379-4.

52. Dong, L., W. Ravelombola, Y. Weng, J. Qin, W. Zhou, G. Bhattarai, B. Zia, W. Yang, and **A. Shi***. 2019. Change in chlorophyll content over time well differentiated salt-tolerant, moderately salt-tolerant, and salt-susceptible cowpea genotypes. HortScience 54(9):1477-1484. https://doi.org/10.21273/HORTSCI13853-18

53. Guo, J., L. Dong*, Y. Jiao, H. Xiong, L. Shi, Y. Tian, Y. Yang, and **A. Shi**. 2019. Quality control techniques and related factors for hydroponic leafy vegetables. HortScience 54:1330-1337. https://doi.org/10.21273/HORTSCI13853-18.

54. Kandel, S.L., B. Mou, N. Shishkoff, **A. Shi**, K.V. Subbarao, and S.J. Klosterman*. 2019. Spinach downy mildew: advances in our understanding of the disease cycle and prospects for disease management. Plant Disease 103:791-803. https://doi.org/10.1094/PDIS-10-18-1720-FE.

55. Kandel, S.L, K.V. Subbarao, **A. Shi**, B. Mou*, and S.J. Klosterman*. 2019. Evaluation of biopesticides for managing downy mildew of spinach in organic production systems in California, 2017 and 2018. Plant Disease Management Reports, Report No. 13:V171.

56. Ravelombola, W., J. Qin, **A. Shi***, L. Nice, Y. Bao, A. Lorenz, J. H. Orf, N. D. Young, and S. Chen*. 2019. Genome-wide association study and genomic selection for soybean chlorophyll content associated with soybean cyst nematode. BMC Genomics (2019) 20:904; https://doi.org/10.1186/s12864-019-6275-z.

57. Ravelombola, W., J. Qin, Y. Weng, B. Mou*, **A. Shi*.** 2019. A simple and cost-effective approach for salt tolerance evaluation in cowpea (*Vigna unguiculata*) seedlings. HortScience 54:1280-1287. DOI: https://doi.org/10.21273/HORTSCI14065-19.

58. Qin, J., **A. Shi**, Q. Song, S. Li, F. Wang, Y. Cao, W. Ravelombola, C. Yang, and M. Zhang*. 2019. Genome wide association study and genomic selection of amino acid contents in soybean seeds. Frontiers in Plant Science, 10:1445. https://doi.org/10.3389/fpls.2019.01445.

59. Weng, Y, J. Qin, S. Eaton, Y. Yang, W. Ravelombola, and **A. Shi***. 2019. Evaluation of seed protein content in USDA cowpea germplasm. HortScience 54(5):814–817. https://doi.org/10.21273/HORTSCI13929-19.

60. Zhu, S.*, E. Niu, E., **A. Shi**, and B. Mou. 2019. Genetic diversity analysis of olive germplasm (*Olea europaea* L.) with genotyping-by-sequencing technology. Frontiers in Genetics 10:755. https://doi.org/10.3389/fgene.2019.00755.

2018

61. Feng, C., B.H. Bluhm, **A. Shi**, J.C. Correll*. 2018. Molecular markers linked to three spinach downy mildew disease resistance loci. Euphytica 214: 174. https://doi.org/10.1007/s10681-018-2258-4.

62. Ravelombola, W., **A. Shi***, Y. Weng, B. Mou, D. Motes, J. Clark, P. Chen, V. Srivastava, J. Qin, L. Dong, W. Yang, G. Bhattarai, and Y. Sugihara. 2018. Association analysis of salt tolerance in cowpea at germination and seedling stages. Theoretic and Applied Genetics 131(1):79–91. https://doi.org/10.1007/s00122-017-2987-0.

63. Ravelombola, W., **A. Shi*,** J. Qin, Y. Weng, G. Bhattarai, B. Zia, W. Zhou, and B. Mou. 2018. Investigation on various above-ground traits to identify drought tolerance in cowpea seedlings. HortScience 53(12):1757–1765. https://doi.org/10.21273/HORTSCI13278-18.

64. Ravelombola, W., J. Qin, **A. Shi***, J.C. Miller, Jr., D. Scheuring, Y. Weng, G. Bhattarai, L. Dong, and W. Yang, 2018. Population structure analysis and association mapping for iron deficiency chlorosis in worldwide cowpea germplasm. Euphytica 214:96. https://doi.org/10.1007/s10681-018-2176-5.

65. Weng, Y., W. Ravelombola, J. Qin, W. Yang, W. Zhou, Y. Wang, Z. Young, and **A. Shi***. 2018. Evaluation of soluble sugar content in cowpea seeds. American Journal of Plant Sciences 9:1455-1466. https://doi.org/10.4236/ajps.2018.97106

66. Xiong, H., **A. Shi,** D. Wu, Y. Weng, J. Qin, W. Ravelombola, X. Shu, and W. Zhou*. 2018. Genome-wide identification, classification and evolutionary expansion of KNOX gene family in Rice (*Oryza sativa*) and Populus (*Populus trichocarpa*). American Journal of Plant Sciences 9:1071-1092. https://doi.org/10.4236/ajps.2018.96082

67. Xiong, H., J. Qin, A. Shi*, B. Mou, D. Wu, J. Sun, X. Shu, Z. Wang, W. Lu, J. Ma, Y. Weng, and W. Yang. 2018. Genetic differentiation and diversity upon genotype and phenotype in cowpea. Euphytica, 214:4; DOI: https://doi.org/10.1007/s10681-017-2088-9

68. Yang, W., A. Shi*, J. Ma, J. Correll, M. Evans, D. Motes, H. Xiong, Y. Weng, and J. Qin. 2018. Identification of the pathogen of powdery mildew disease on dandelions. Australasian Plant Disease Notes 13: 12. https://doi.org/10.1007/s13314-018-0296-3.

2017

69. Bhattarai, G., **A. Shi***, J. Qin, Y. Weng, J.B. Morris, D. Pinnow, B. Buckley, W. Ravelombola, W. Yang, and L. Dong. 2017. Association analysis of cowpea mosaic virus (CPMV) resistance in the USDA cowpea germplasm collection. Euphytica 213(10). DOI: http://doi.org/10.1007/s10681-017-2015-0.

70. Klepadlo, M., P. Chen*, **A. Shi**, R.E. Mason, K.L. Korth, V. Srivastava and C. Wu. 2017. Two tightly linked genes for soybean mosaic virus resistance in soybean. Crop Sci. 57(4):1844-1853. doi: https://doi.org/10.2135/cropsci2016.05.0290.

71. Klepadlo, M., P. Chen*, **A. Shi**, R. E. Mason, K. L. Korth, and V. Srivastava. 2017. Single nucleotide polymorphism markers for rapid detection of the Rsv4 locus for soybean mosaic virus resistance in diverse germplasm. Mol Breeding 37: 10. https://doi.org/10.1007/s11032-016-0595-3.

72. Qin, J., **A. Shi***, B. Mou, G. Bhattarai, W. Yang, Y. Weng, and D. Motes. 2017. Association mapping of aphid resistance in USDA cowpea core collection using SNPs. Euphytica 213:36. doi: http://doi.org/10.1007/s10681-016-1830-z.

73. Qin, J.*, **A. Shi***, B. Mou, M.A, Grusak, Y. Weng, W. Ravelombola, G. Bhattarai, L. Dong, and W. Yang. 2017. Genetic diversity and association mapping of mineral element concentrations in spinach leaves. BMC Genomics 18:941. https://doi.org/10.1186/s12864-017-4297-y.

74. Qin, J., Q. Song, **A. Shi,** S. Li, M. Zhang, Bo Zhang*. 2017. Genome-wide association mapping of resistance to *Phytophthora sojae* in a soybean germplasm panel from maturity groups IV and V. PLoS ONE 12(9):e0184613. DOI: https://doi.org/10.1371/journal.pone.0184613.

75. Qin, J., J. Zhang, F. Wang, J. Wang, Z. Zheng, C. Yin, H. Chen, **A. Shi**, B. Zhang, P. Chen, M. Zhang*. 2017. iTRAQ protein profile analysis of developmental dynamics in soybean leaves. PLoS ONE 12(9):e0181910. https://doi.org/10.1371/journal.pone.0181910.

76. Ravelombola, W., **A. Shi*,** Y. Weng, J. Clark, D. Motes, P. Chen, and V. Srivastava. 2017. Evaluation of salt tolerance at germination stage in cowpea. HortScience 52(9):1168-1176. DOI: https://doi.org/10.21273/HORTSCI12195-17

77. Ravelombola, W., J. Qin, **A. Shi*,** W. Lu, Y. Weng, H. Xiong, W. Yang, G. Bhattarai, S. Mahamane, W.A. Payne, J.C. Miller, Jr., D. Scheuring. 2017. Association mapping revealed SNP markers for adaptation to low phosphorus conditions and rock phosphate response in USDA cowpea germplasm. Euphytica 213:183 (DOI: https://doi.org/10.1007/s10681-017-1971-8

78. Ravelombola, W., J. Qin, **A. Shi*,** Y. Weng, G. Bhattarai, L. Dong, J.B. Morris. 2017. A SNP-based association analysis for plant growth habit in worldwide cowpea (*Vigna unguiculata* (L.) Walp) germplasm. Euphytica 213:284. First Online: 22 November 2017, https://doi.org/10.1007/s10681-017-2077-z ; https://link.springer.com/article/10.1007%2Fs10681-017-2077-z

79. **Shi, A*.,** J. Qin, B. Mou, J. Correll, Y. Weng, D. Brenner, C. Feng, D. Motes, W. Yang, L. Dong, and G. Bhattarai, and W. Ravelombola. 2017. Genetic diversity and population structure analysis of spinach by single-nucleotide polymorphisms identified through genotyping-by-sequencing. PLOS ONE, 12(11): e0188745, https://doi.org/10.1371/journal.pone.0188745

80. Weng, Y., **A. Shi***, W. Ravelombola1, W. Yang, J. Qin, D. Motes, D.O. Moseley, and P. Chen. 2017. A Rapid methods for measuring seed protein content in cowpea (*Vigna unguiculata* (L.) Walp). American J. of Plant Science 8(10): 2387-2396. https://doi.org/10.4236/ajps.2017.810161

81. Zeng, A., P. Chen*, K. Korth, F. Hancock, A. Pereira, K. Brye, C. Wu, and **A. Shi**. 2017. Genome-wide association study (GWAS) of salt tolerance in worldwide soybean germplasm lines. Mol Breeding 37: 30. doi: http://doi.org/10.1007/s11032-017-0634-8

2016

82. Chitwood, J, **A. Shi***, B. Mou, M. Evans, J. Clark, D. Motes, P. Chen, and D. Hensley. 2016 Population structure and association analysis of bolting, plant height, and leaf erectness in spinach. HortScince 51(5):481–486. https://doi.org/10.21273/HORTSCI.51.5.481

83. Chitwood, J., **A. Shi*,** M. Evans, C. Rom, D. Motes, P. Chen, and D. Hensley. 2016. Temperature effect on seed germination in spinach (*Spinacia oleracea* L.). HortScience 51(12):1475–1478. DOI: https://doi.org/10.21273/HORTSCI11414-16

84. Lyon, R., J. Correll, C. Feng, B. Bluhm, S. Shrestha, **A. Shi**, K. Lamour*. 2016. Population Structure of *Peronospora effusa* in the Southwestern United States. PlosOne 11(2): e0148385. https://doi.org/10.1371/journal.pone.0148385

85. Ma, J, **A. Shi***, B. Mou, M. Evans, J. Clack, D. Motes, J. Correll, H. Xiong, J. Qin, J. Chitwood, Y.

Weng. 2016. Association mapping of leaf traits in spinach. Plant Breed. 135:399–404 (doi: https://doi.org/10.1111/pbr.12369

86. Qin, J., **A. Shi***, H. Xiong, B. Mou, D. Motes, W. Lu, J.C. Miller, D.C. Scheuring, M.N. Nzaramba, Y. Weng, and W. Yang. 2016. Population structure analysis and association mapping of seed antioxidant content in USDA cowpea (*Vigna unguiculata* L. Walp.) core collection using SNPs. Canadian J Plant Science 96(6): 1026-1036. https://cdnsciencepub.com/doi/10.1139/CJPS-2016-0090 ; https://doi.org/10.1139/cjps-2016-0090

87. Ravelombola, W., **A. Shi*,** Y. Weng, D. Motes, P. Chen, V. Srivastava, and C. Wingfield. 2016. Evaluation of total seed protein content in eleven Arkansas cowpea genotypes. American J. Plant Science 7(15): 2288-2296. DOI: 10.4236/ajps.2016.715201. https://www.scirp.org/journal/paperinformation.aspx?paperid=72042

88. **Shi, A.*,** B. Buckley, B. Mou, D. Motes, J.B. Morris, J. Ma, H. Xiong, J. Qin, W. Yang, J. Chitwood, Yuejin Weng, W. Lu. 2016. Association analysis of cowpea bacterial blight resistance in USDA cowpea germplasm. Euphytica 208:143-155. https://doi.org/10.1007/s10681-015-1610-1 ; https://link.springer.com/article/10.1007/s10681-015-1610-1

89. **Shi, A.*,** and B. Mou. 2016. Genetic diversity and association analysis of leafminer (*Liriomyza spp*.) resistance in spinach (*Spinacia oleracea*). Genome 59(8):581-8, https://doi.org/10.1139/gen-2016-0075

90. **Shi, A.*,** B. Mou, J. Correll. 2016. Association analysis for oxalate concentration in spinach. Euphytica 212:17-28. https://doi.org/10.1007/s10681-016-1740-0.

91. **Shi, A.*,** B. Mou, J. Correll, D. Motes, Y. Weng, J. Qin, and W. Yang. 2016. SNP association analysis of resistance to Verticillium wilt (*Verticillium dahliae* Kleb.) in spinach. Australian Journal of Crop Science 10(8): 1188-1196. https://search.informit.com.au/documentSummary;dn=502343349346669;res=IELHSS.

92. **Shi, A.*,** B. Mou, J. Correll, S.T. Koike, D. Motes, J. Qin, Y. Weng, and W. Yang. 2016. Association analysis and identification of SNP markers for Stemphylium leaf spot (*Stemphylium botryosum* f. sp. *spinacia*) resistance in spinach (*Spinacia oleracea*). American Journal of Plant Sciences 7: 1600-1611. **DOI:** 10.4236/ajps.2016.712151 ; https://www.scirp.org/journal/paperinformation.aspx?paperid=69917

93. Xiong, H., **A. Shi**, J. Sun, Y. Wang, X. Shu, D. Wu. 2016. Genetic diversity of agronomic traits in global cowpea resource. Bulletin of Science and Technology 10:48-52. 10.3969/j.issn.1001-7119.2016.10.012; https://xueshu.baidu.com/usercenter/paper/show?paperid=8d0cf6dbd9f83cd21d2376139f7f4420

94. Xiong, H., **A. Shi***, B. Mou, J. Qin, D. Motes, W. Lu, J. Ma, Y. Weng, W. Yang. 2016. Genetic diversity and population structure of cowpea. PLoS ONE 11(8): e0160941. https://doi.org/10.1371/journal.pone.0160941.