

SHI Suhua, Ph.D.

Professor

School of Life Sciences
State Key Laboratory of Biocontrol

Office: He Dan Qing Hall 302 | **Phone:** +86 20 8411 3677 | **Fax:** +86 20 3402 2356 | **Email:**
lsssh@mail.sysu.edu.cn

Subject: Adaptive evolution, speciation mechanism, speciation genomics, evolutionary and ecological genomics, population genetics, phylogeography,

Website: <http://evolution.sysu.edu.cn>

Education and Academic Experience:

1982 B.S. (Biology), Jiangxi University, Nanchang, China
1986 M.S. (Botany), Sun Yat-Sen University, Guangzhou, China
1990 Ph.D.(Botany), Sun Yat-Sen University, Guangzhou, China
1990-1992-1995-present Lecture, Associate Professor, Professor, Sun Yat-Sen University
1996.3-1997.3 Visiting Scientist, Colorado State University, USA
2000.4-2000.7 Visiting Scientist, Yeungnam University, Korea
2000.9-2000.12 Visiting Scientist, Harvard University, USA
2004.11-2005.3 Visiting Scientist, University of Chicago, USA

Research Interests

Our current research focuses on adaptive evolution and speciation in mangroves. The aim of our research is to understand the molecular basis of adaptation and phenotypic variation by using genomic techniques. We are particularly interested in the evolutionary convergence among independently evolved species in the same biological community, as well as geographical mechanisms of speciation revealed by mangroves. Our research has shed considerable light on mangroves' emergence, which informs about mangroves' projected survival in the next century when the global sea level rises.

Honors/Awards

Winners of National Science Funds for Outstanding Young Scholars, Ministry of Science and Technology. 1999.

The Outstanding Young Scholar Award by Qiu Shi Science and Technologies Foundation. (Hong Kong) 2001.

1st Prize of Ministry Nature and Science Awards, Ministry of Education, China. 2002, 2008 (twice)

2nd Prize of National Nature and Science Awards, National Office for Science and Technology Awards, 2011.

The Corresponding Author of Botanical Society of America, 2017.

Professional Service (selected):

Serving on panels: NSFC (National Science Foundation of China)—1997-2000,2005-2009,2015-present; PNASA (Prize of National Nature and Science Awards, China)—2007,

2009-2010; PMNSA(Prize of Ministry Nature and Science Awards, Ministry of Education, China)—2006, 2010.

Organizing service: The International Mangrove Consortium (with the scientists from 15 countries and regions). We are de novo sequencing about 50 mangrove's and their close related inland species, including 5 major and typical mangroves groups, such as *Rhizophoraea*, *Avicennia*, *Sonneratia*, *Xylocarpus* and *Lumnitzera*. Population resequencing for several important species and transcriptome sequences from more than 40 mangrove species have been done too. All the data resources are available to the community of mangrove researches.

Sun Yat-sen University services: Advisor of 39 Ph.D, 27 M.S students (graduated) and 9 Ph.D, 4 M.S are studying. Two course for undergraduate students (Evolutionary Biology, Evolution of Genes and Genomics), and one course for graduate students (Molecular Systematics) for each year.

Editorial services: *Molecular Ecology*, 2019-; *Molecular Ecology Resource*, 2019-; *Evolution*, 2020-; *Journal of Systematics and Evolution*, 2008-; GGS (Genes and Genetic Systems, Japan), 2015-;

Professional societies: Botanical Society of China, Botanical Society of Guangdong Province, China. ASPT (American Society of Plant Taxonomists)

Major Grants (principal investigator):

- 1993-1995 The National Natural Science Foundation, China: The studies of molecular systematics on *Gnetum* (39200010)
- 1995-1997 The Ministry of Education Special Foundation, China: The studies of molecular character of ITS region in *Gnetum* and the phylogenetic significance (9455803)
- 1996-1998 The National Natural Science Foundation, China: The studies of molecular systematics on Hamamelidaceae (39570052)
- 1996-1998 The Natural Science and Technology Foundation of Guangdong Province, China: The studies of genetic diversity of yellow *Camellia* (950092)
- 1998-2000 The National Natural Science Foundation, China: Phylogeny of Hamamelidaceae Inferred from *matK* DNA sequences (39970057)
- 1998-2000 The Natural Science and Technology Foundation of Guangdong Province, China: The studies of the phylogeny of Hamamelidaceae based on *matK* DNA sequences (970190)
- 1999-2002 The National Nature Science Foundation, China ([The National Distinguishing Youth Project](#)): Studies on plant molecular systematics and evolution (39825104)
- 2000-2000 2000-2003 The Ministry of Education Special Program for the Excellent Young Teachers of Universities: Genetic diversity of two semi mangroves in coastal areas and inland.
- 2001-2003 The National Natural Science Foundation, China: Molecular phylogeny and evolution of Lythraceae *sensu lato* and related groups.(30070053)
- 2001-2003 The Natural Science and Technology Foundation of Guangdong Province, China: Studies on the genetic diversity of semi-mangroves in coastal areas and inland. (001223)

- 2002-2004 The Ministry of Education Special Foundation: The phylogeny and evolution of Sonneratiaceae and the relatives. (20010558013)
- 2005-2007 The National Natural Science Foundation, China: The molecular basis of speciation in *Sonneratia*. (30470119)
- 2007-2011 National Basic Research Program of China (973 project): Artificial Selection and Genome Evolution-Genomic Basis of the Evolution of Complicated Characters in Rice. (2007CB815701)
- 2008-2011 The National Natural Science Foundation, China (Key project): Mechanisms of adaptation and speciation at the genomic level in mangroves of the intertidal zones. (30730008)
- 2008-2010 The Ministry of Education Special Foundation, China: Evolutionary genomic study of loss of gene function in rice during domestication (20070558030)
- 2009-2011 National S&T Major Project of China (863 project): Development and application of a new transgene technology based on miRNAi. (2009ZX08010-017B)
- 2010-2012 The National Natural Science Foundation, China: Ecological and geographical distribution of a mangrove associate: *Hibiscus tiliaceus* in relation to adaptation to intertidal environments and the genomic mechanism. (40976081)
- 2012-2016 The National Natural Science Foundation, China (Key project): Processes and mechanisms of adaptation to the extreme environments of intertidal zone by mangroves. (41130208)
- 2014-2017 The National Natural Science Foundation, China (Key project): Adaptation and speciation in continually changing environments - Genomic mechanisms and their theoretical implications. (91331202)
- 2017-2021 The National Ministry of Science and Technology, National Key Research and Development Plan (R&D): Biological resources survey for the mangrove forest and DNA barcode library building of the important species. (2017FY100705)
- 2017-2019 The National Natural Science Foundation, China (Compositiv Key project): Genomic mechanisms and patterns of speciation with gene flow. (91731301)
- 2014-2017 The National Natural Science Foundation, China (Key project): Convergent adaptation among multiple mangrove taxa and the genomic mechanisms. (31830005)


Publications (selected)

- Shi, S.**, H. Chang, Y. Chen, L. Qu and J. Wen, 1998, Phylogenetic relationships of Hamamelidaceae: inferred from ITS regions of rDNA, *Biochemical and Systematic Evolution* 26: 55-69
- Wen J., **S. Shi**, R. K. Jansen, E. A. Zimmer, 1998. Phylogeny and biogeography of *Aralia* Sect. *Aralia* (Araliaceae), *American Journal of Botany* 85:866-875
- Shi, S***, H. Jin, Y. Zhong, X. He, Y. Huang, F. Tan, D. E. Boufford. 2000. Phylogenetic relationships of Magnoliaceae inferred from cpDNA *matK* sequences. *Theoretic and Applied Genetics*. 101 (5/6): 925-930
- Shi, S***, Y. Huang, F. Tan, X. He, D. E. Boufford. 2001. Phylogenetic analysis of the Sonneratiaceae and its relationship to Lythraceae based on ITS sequences of nrDNA. *Journal of Plant Research*. 113:253-258

- Shi, S***, Y. Huang, Y. Zhong, Y. Du, Q. Zhang, H. Chang, D Boufford, 2001. Phylogeny of the Altingiaceae based on cpDNA *matK*, PY-IGS and nrDNA ITS sequences. *Plant Systematics and Evolution*. 230, 1-2: 13-24
- Huang, Y., **S. Shi***, 2002. Phylogenetics of Lythraceae sensu lato: A preliminary analysis based on chloroplast *rbcl* gene, *psaA-ycf3* spacer, and nuclear rDNA internal transcribed spacer (ITS) sequences. *International Journal of Plant Sciences*. 163 (2): 215-225.
- Shi S***, Y. Zhong, Y. Huang, X. Qiu, H. Chang, 2002. Phylogenetic relationships of the Rhizophoraceae in China based on sequences of the chloroplast gene *matK* and the ITS regions of nuclear ribosomal DNA. *Biochemical and Systematic Ecology* 30(4): 309-319.
- Zhong, Y., Q. Zhao, **S. Shi**, Y. Huang, M. Hasegawa, 2002. Detecting evolutionary rate heterogeneity among mangroves and their close terrestrial relatives. *Ecology Letters* 6(5): 1-6.
- Shi, S***, Y. Zhong, W. A. Hoch, 2002. Chapter 6: Distribution and commercial cultivation of Magnolia. In *Magnolias*, Ed. S.D. Sarker, Y. Maruyama. Harwood Pub. 156-180.
- Tan, F. S. **Shi***, Y. Zhong, X. Gong, Y. Wang, 2002. Phylogenetic relationships of Combretaceae (Combretaceae) inferred from plastid, nuclear and spacer sequences. *Journal of Plant Research* 115: 475-481
- Shi, S***, Y. Du, D. Boufford, X. Gong, Y. Huang, H. He, Y. Zhong, 2003. Phylogenetic position of *Schnabelia*, a genus endemic to China: evidence from sequences of cpDNA *matK* gene and nrDNA ITS regions. *Chinese Science Bulletin* 48 (11): 1177-1180
- Tang, T., Y. Zhong, S. Jian, **S. Shi*** 2003. Genetic diversity of *Hibiscus tiliaceus* (Malvaceae) in China using AFLP markers. *Annals of Botany* 92: 409-414
- Peng, Y., Z. Chen, X. Gong, Y. Zhong, **S. Shi***, 2003. Phylogenetic position of *Dipentodon sinicus*: evidence from DNA sequences of chloroplast *rbcl*, nuclear ribosomal 18S and mitochondria *matR* genes. *Botanical Bulletin of Academia Sinica* 44: 217-222
- Huang, Y., P. W. Fritsch, and **S. Shi**, 2003. A revision of the imbricate group of *Styrax* series *Cyrta* in Asia. *Annals of Missouri Botanical Garden*. 90:491-553
- Wu C.-I., **S. Shi**, Y. Zhang. 2004. A case for conservation. *Nature* 428: 213-214.
- Shi, S***, Y. Huang, K. Zeng, X. Tan, H. He, Y. Fu, 2005. Molecular phylogenetic analysis of mangroves: independent evolutionary origins of vivipary and salt secretion. *Molecular Phylogenetics and Evolution* 34: 159-166
- Tan, F., Y. Huang, X. Ge, **S. Shi***, 2005. Population genetic structure and conservation implications of *Ceriops decandra* in Malay Peninsula and North Australia. *Aquatic Botany* 81(2): 175-188.
- Zhou, R., **S. Shi***, C-I. Wu, 2005. Molecular criteria for determining new hybrid species - an application to the *Sonneratia* hybrids. *Molecular Phylogenetics and Evolution* 35: 595-601
- Lu J., T. Tang, H. Tang, J. Huang, **S. Shi***, C-I Wu*, 2006. The accumulation of deleterious mutations in the rice genomes: A hypothesis on the cost of domestication. *Trends in Genetics* 22: 126-131.
- Zeng K., **S. Shi**, Y-X Fu, C-I Wu. 2006. Statistical tests for detecting positive selection by utilizing high-frequency variants. *Genetics* 174: 1431-1439.
- Tang T., J. Lu, J. Huang, J. He, S. R. McCouch, Y. Shen, Z. Kai, M. D. Purugganan, **S. Shi***, C-I Wu*. 2006. Genomic variation in rice: Genesis of highly polymorphic linkage blocks during domestication. *PLOS Genetics* 2(11): e199.
- Zeng K., **Shi S.**, Wu C-I. 2007. Compound tests for the detection of hitchhiking under positive selection. *Molecular Biology and Evolution* 24: 1898-1908.

- Zeng K., S. Mano, **S. Shi**, C-I, Wu, 2007, Comparisons of site- and haplotype-frequency methods for detecting positive selection. *Molecular Biology and Evolution* 24: 1562-1574.
- Zhou R., K. Zeng, W. Wu, X. Chen, Z. Yang, **S. Shi***, C-I. Wu. 2007. Population Genetics of Speciation in Nonmodel Organisms: I. Ancestral polymorphism in Mangroves. *Molecular Biology and Evolution* 24: 2746-2754.
- Lu J., Y. Shen, Q. Wu, S. Kumar, B. He, **S. Shi**, R. W. Carthew, S. Wang, C-I Wu. 2008. The birth and death of microRNA genes in *Drosophila*. *Nature Genetics* 40: 351-355.
- Zhou R., X. Gong, D. Boufford, C-I Wu, **S. Shi*** 2008. Testing hypothesis of unidirectional hybridization in plants: observations on *Sonneratia*, *Bruguiera* and *Ligularia*. *BMC Evolutionary Biology* 8:149.
- Yu Y., Tang T., Qian Q., Wang Y., Yan M., Zeng D., Han B., Wu C-I, **Shi S***, Li J*.2008. Independent losses of function in a polyphenol oxidase in rice: differentiation in grain discoloration between subspecies and the role of positive selection under domestication. *Plant Cell* 20: 2946-2959.
- Bao H., H. Guo, J. Wang, R. Zhou, X. Lu, **S. Shi***, 2009. MapView: visualization of short reads alignment on a desktop computer. *Bioinformatics* 25: 1554-1555.
- Bao H., Y. Xiong, H. Guo, R. Zhou, X. Lu and **S. Shi***, 2009. MapNext: A software tool for spliced and unspliced alignments and SNP detection of short sequence reads. *BMC Genomics* 10 (Suppl 3): S13.
- Tang, T.,S. Kumar, Y.Shen, J. Lu, M-L. Wu, **S. Shi**, W-H.Li, C-I Wu. 2010. Adverse interactions between micro-RNAs and target genes from different species. *PNAS* 107 (29) : 12935-12940.
- Zhou R., S. Ling, W. Zhao, Naoki Osada, S. Chen, M. Zhang, Z. He, H. Bao, C. Zhong, B. Zhang, X. Lu, David Turissini, Norman C. Duke, J. Lu, **S. Shi***, C-I Wu*. 2011. Population genetics in non-model organisms: II. Natural selection in marginal habitats revealed by deep sequencing on dual platforms. *Molecular Biology and Evolution* 28: 2833-2842.
- He Z, Zhai W, Wen H, Tang T, Wang Y, **S. Shi***, C-I Wu*. 2011. Two evolutionary histories in the genome of rice: the roles of domestication genes. *PLoS Genet* 7: e1002100.
- Shen, Y., Y. Lv, W. Liu, M. Wen, T. Tang, R. Zhang, E. Hungate, **S. Shi***, C-I. Wu*, 2011. Testing hypotheses on the rate of molecular evolution in relation to gene expression using microRNAs. *PNAS* 108: 15942-15947.
- Liang, S., L. Fang, R. Zhou, T. Tang, S. Deng, S. Dong, Y. Huang, C. Zhong, **S. Shi***, 2012. Transcriptional homeostasis of a mangrove species, *Ceriops tagal*, in saline environments, as revealed by microarray analysis. *PLoS One* 7(5): e36499
- He, Z., X. Li, S. Ling, Y. Fu, E. Hungate, **S. Shi*** and C-I Wu. 2013. Estimating DNA polymorphism from next generation sequencing data with high error rate by dual sequencing applications. *BMC Genomics* 14:535
- Guo, W., Y. Huang, Z. He, Y. Yan, R. Zhou and **S Shi***. 2013. Development and characterization of microsatellite loci for smooth cordgrass, *Spartina alterniflora* (Poaceae). *Applications in Plant Sciences* 1: 1200211
- Huang, L., X. Li, Y. Huang, **S Shi***, and Renchao Zhou. 2014. Molecular evidence for natural hybridization in the mangrove genus *Avicennia*. *Pak. J. Bot.*, 46(5): 1577-1584
- Yang, Y., S. Yang, J. Li, Y. Deng, Z. Zhang, S. Xu, W. Guo, C. Zhong, R. Zhou*, **S. Shi***. 2015. Transcriptome analysis of the holly mangrove *Acanthus ilicifolius* and its terrestrial relative,

- Acanthus leucostachyus*, provides insights into adaptation to intertidal zones. BMC Genomics 16:605 DOI: 10.1186/s12864-015-1813-9
- Yang, Y., S. Yang, L. Fang, J. Li, C. Zhong, R. Zhou*, **S. Shi***. 2015. Phylogenetic position of *Sonneratia griffithii* based on sequences of the nuclear ribosomal internal transcribed spacer and 13 nuclear genes. Journal of Systematics and Evolution 53: 47-52
- Yang, Y., S. Yang, J. Li, X. Li, C. Zhong, Y. Huang, R. Zhou, **S. Shi***. 2015. De novo assembly of the transcriptomes of two yellow mangroves, *Ceriops tagal* and *C. zippeliana*, and one of their terrestrial relatives, *Pellacalyx yunnanensis*. Marine Genomics 23: 33–36
- He, Z., Z. Zhang , W. Guo, Y. Zhang, R. Zhou, **S. Shi***. 2015. De Novo assembly of coding sequences of the mangrove palm (*Nypa fruticans*) using RNA-Seq and discovery of whole-genome duplications in the ancestor of palms. PLoS ONE 10(12): e0145385
- Chen Y., Y. Hou, Z. Guo, W. Wang, C. Zhong, R. Zhou, **S. Shi***. (2015) Applications of multiple nuclear genes to the molecular phylogeny, population genetics and hybrid Identification in the mangrove genus *Rhizophora*. PLoS ONE 10(12): e0145058
- Guo Z., Y. Huang, Y. Chen, N. C. Duke, C. Zhong., **Shi S***. 2016 Genetic discontinuities in a dominant mangrove *Rhizophora apiculata* (Rhizophoraceae) in the Indo-Malesian region. Journal of Biogeography 43: 1856–1868
- Li J., Y. Yang, Q. Chen, L. Fan, Z. He, W. Guo, S. Qiao, Z. Wang, M. Guo., C. Zhong, R. Zhou, **S. Shi***. 2016 Pronounced genetic differentiation and recent secondary contact in the mangrove tree *Lumnitzera racemosa* revealed by population genomic analyses. Scientific Reports 6: 29486 | DOI:10.1038/srep 29486
- Yang Y., N. C. Duke, F. Peng, J. Li, S. Yang, C. Zhong, R. Zhou, **S. Shi*** 2016 Ancient Geographical Barriers Drive Differentiation among *Sonneratia caseolaris* Populations and Recent Divergence from *S. lanceolata*. Frontiers in Plant Science doi: 10.3389/fpls.2016.01618
- Zhang Z., Z. He, S. Xu, X. Li, W. Guo, Y. Yang, C. Zhong, R. Zhou, **S. Shi*** 2016 Transcriptome analyses provide insights into the phylogeny and adaptive evolution of the mangrove fern genus *Acrostichum*. Scientific Report 6:35634 | DOI: 10.1038/srep35634
- Li, X., N. C. Duke, Y. Yang, L. Huang, Y. Zhu, Z. Zhang, R. Zhou, C. Zhong, Y. Huang*, **S. Shi***. 2016. Re-evaluation of phylogenetic relationships among species of the mangrove genus *Avicennia* from Indo-West Pacific Based on Multi locus Analyses. PLoS ONE 11(10): e0164453
- Fang, L., Y. Yang, W. Guo, J. Li, C. Zhong, Y. Huang, R. Zhou, **S. Shi***. De novo assembly of the transcriptome of *Aegiceras corniculatum*, a mangrove species in the Indo-West Pacific region Marine Genomics 28: 49-52
- Li, J., Y. Yang, S. Yang, Z. Zhang, S. Chen, C. Zhong, R. Zhou, **S. Shi*** 2016. Comparative transcriptome analyses of a mangrove tree *Sonneratia caseolaris* and its non-mangrove relatives, *Trapa bispinosa* and *Duabanga grandiflora*. Marine Genomics 31: 13-15
- Yang, Y., J. Li, S. Yang, X. Li, L. Fang, C. Zhong, N. C. Duke, R. Zhou*, S. Shi* 2017 Effects of Pleistocene sea-level fluctuations on mangrove population dynamics: A lesson from *Sonneratia alba*. BMC Evolutionary Biology 17:22 DOI 10.1186/s12862-016-0849-z
- Xu, S., Z. He, Z. Guo, Z. Zhang, J. G. Wyckoff, A. Greenberg, Cl. Wu, **S. Shi*** 2017 Genome-wide convergence during evolution of mangroves from woody plants. Molecular Biology and Evolution 34: 1008-1015
- Yang, M., Z. He, **S. Shi***, Cl. Wu *. 2017 Can genomic data alone tell us whether speciation

- happened with gene flow? *Molecular Ecology* 26: DOI: 10.1111/mec.14117
- Yang, M., Z. He, Y. Huang, L. Lu, Y. Yan, L. Hong, H. Shen, Y. Liu, Q. Guo, L. Jiang, Y. Zhang, A. J. Greenberg, R. Zhou, X. Ge, X., C-I. Wu, **S. Shi*** 2017, The emergence of the hyper-invasive vine, *Mikania micrantha* (Asteraceae), via admixture and founder events inferred from population transcriptomics. *Molecular Ecology* 26: doi:10.1111/mec.14124
- Xu, S., Z. He, Z. Zhang, Z. Guo, W. Guo, H. Lyu, J. Li, M. Yang, Z. Du, Y. Huang, R. Zhou, C. Zhong, D. E. Boufford, M. Lerdau, C-I. Wu, N. C. Duke, The International Mangrove Consortium, **S. Shi***. 2017. The origin, diversification and adaptation of a major mangrove clade (Rhizophoreae) revealed by whole genome sequencing. *National Science Review*, 4: 721-734
- Guo, Z., X. Li, Z. He, Y. Yang, W. Wang, C. Zhong, A. Greenberg, C-I. Wu, N. C. Duke, **S. Shi***. 2018. Extremely low genetic diversity across mangrove taxa reflects past sea level changes and hints at poor future responses. *Global Change Biology*, 24:1741–1748
- Lyu, H., Z. He, C-I. Wu*, **S. Shi***. 2018. Convergent adaptive evolution in marginal environments: unloading transposable elements as a common strategy among mangrove genomes. *New Phytologists*, 217: 428–438
- Liu, L., Z. Guo, C. Zhong, **S. Shi***. 2018. DNA barcoding reveals insect diversity in the mangrove ecosystems of the Hainan Island, China. *Genome*. 61(11): 797-806
- Yang, Y., W. Guo, X. Shen, J. Li, S. Yang, S. Chen, Z. He, R. Zhou*, **S. Shi***. 2018. Identification and characterization of evolutionarily conserved alternative splicing events in a mangrove genus *Sonneratia*. *Scientific Reports* 8:4425
- Liu, Z, G. Chen, T. Zhu, Z. Zeng, Z. Lyu, J. Wang, K. Messenger, A. J. Greenberg, Z. Guo, Z. Yang, **S. Shi***, Y. Wang*. 2018. *Molecular Phylogenetics and Evolution* 127: 723-731
- He, Z., X Li, M. Yang, X. Wang, C. Zhong, N. C. Duke, C-I. Wu*, **S. Shi***. 2019. Speciation with gene flow via cycles of isolation and migration: Insights from multiple mangrove taxa. *National Science Review*. 6: 275–288
- He, Z., S. Xu, Z. Zhang, W. Guo, H. Lyu, C. Zhong, D. Boufford, N. Duke, The International Mangrove Consortium , **S. Shi***. 2020. Convergent adaptation of the genomes of woody plants at the land-sea interface. *National Science Review*. 7: 978-993
- Wang, X., Z. He, S. Shi*, C-I Wu*. 2020. Genes and speciation: is it time to abandon the biological species concept? *National Science Review*. 7: 1387–1397
- Feng, X., S. Xu, J. Li, Y. Yang, Q. Chen, H. Lyu, C. Zhong, Z. He* & **S. Shi***. 2020. Molecular adaptation to salinity fluctuation in tropical intertidal environments of a mangrove tree *Sonneratia alba*. *BMC Plant Biology* 20:178 (doi.org/10.1186/s12870-020-02395-3)
- Xie, W., C. Zhong, X. Li, Z. Guo*, S. Shi. 2020. Hybridization with natives augments the threats of introduced species in *Sonneratia* mangroves. *Aquatic Botany* 160: 103166 (doi: 10.1016/j.aquabot.2019.103166)
- Xu, S., J. Wang, Z. Guo, Z. He*, **S. Shi***. 2020. Genomic Convergence in the Adaptation to Extreme Environments. *Plant Communications*. 100117 (doi: 10.1016/j.xplc.2020.100117)
- Feng, X., G. Li, S. Xu, W. Wu, Q. Chen, S. Shao, M. Liu, N. Wang, C. Zhong, Z. He, **S. Shi**. 2021. Genomic insights into molecular adaptation to intertidal environments in the mangrove *Aegiceras corniculatum*. *New Phytologist*. 231: 2346-2358 (doi: 10.1111/nph.17551)
- Xu, S., Z. Guo, X. Feng, S. Shao, Y. Yang, J. Li, C. Zhong, Z. He*, **S. Shi***. 2021. Where whole-genome duplication is most beneficial: Adaptation of mangroves to a wide salinity

- range between land and sea. *Molecular Ecology*. (doi: 10.1111/mec.16320)
- Chen, Qipian, H. Yang, X. Feng, Qingjian Chen, **S. Shi***, C-I. Wu*, Z. He*. 2021. Two decades of suspect evidence for adaptive molecular evolution — negative selection confounding positive selection signals. *National Science Review*. (doi: 10.1093/nsr/nwab217)
- Zhang, R., Z. Guo*, L. Fang, C. Zhong, N. Duke, **S. Shi***. 2022. Population subdivision promoted by a sea-level-change-driven bottleneck: A glimpse from the evolutionary history of the mangrove plant *Aegiceras corniculatum*. *Molecular Ecology*. 31: 780-797 (doi: 10.1111/mec.16290)
- He, Z., X. Feng, Q. Chen, L. Li, S. Li, K. Han, Z. Guo, J. Wang, M. Liu, C. Shi, S. Xu, S. Shao, X. Liu, X. Mao, W. Xie, X. Wang, R. Zhang, G. Li, W. Wu, Z. Zheng, C. Zhong, N. Duke, D. Boufford, G. Fan, C-I. Wu, R. Ricklefs, **S. Shi***. 2022. Evolution of coastal forests based on a full set of mangrove genomes. *Nature Ecology & Evolution*. (doi: 10.1038/s41559-022-01744-9)