Curriculum Vitae

Jianxin Shi, Ph. D, Professor

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Personal Information

Gender: Male Birth Place: Jiangsu Marital: Married
Birth Date: 1966.09

Research Interests

- Regulatory mechanisms underlying plant cuticle metabolism and its effects on plant development and stress response
- Development and application of methods for molecular characterization of genetically modified and genome edited crops
- Molecular mechanisms behind seed development and quality formation

Education

- 2001.12-2007.01 Ph. D The Hebrew University of Jerusalem, Israel
- 1988.09-1991.06 M Sci Southwest University, China
- 1984.09-1988.06 B Sci Shanxi Agricultural University, China

Overseas Research Experience

- 2019.06-2020.07 **Visiting Scientist** Food and Agriculture Organization, Italy
- 2013.01-2013.02 **Visiting Scientist** Max Planck Institute for Molecular Plant Physiology, Germany Plant hormone detection using GC-MS
- 2012.06-2012.07 **Visiting Scientist** Department of Plant Biology, University of Strasbourg, France In vitro enzyme activity assay of plant CYP450s
- 2011.02-2011.03 **Visiting Scholar** Department of Plant Ecology, University of Bonn, Germany GC-MS determination of plant waxes, cutin and suberin
- 2007.01-2010.09 **Postdoctoral fellow** Department of Plant Sciences, Weizmann Institute of Science, Israel Transcriptional regulation of the cuticle biosynthesis in plants
- 2008.09-2008.10 **Visiting Scholar** Department of Plant Ecology, University of Bonn, Germany
- 2001.12-2007.01 **Ph. D** Faculty of Agricultural, Environmental and Food Science, the Hebrew University of Jerusalem, Israel Physiological and molecular responses of citrus fruit to anaerobic stress

- 2000.10-2001.06 **Visiting Scholar** Faculty of Agricultural, Environmental and Food Science, the Hebrew University of Jerusalem, Israel Controlling ethylene responses in horticultural crops with 1-MCP and its analogues

Domestic Research Experience

- 2021.12-Current Professor School of Life Sciences and Biotechnology, Shanghai Jiao Tong University
- 2012.02-2021.12 **Associate Professor** School of Life Sciences and Biotechnology, Shanghai Jiao Tong University
- 1991.06-2011.08 **Research Assistant, Assistant Researcher Fellow, associated Researcher Fellow** Postharvest Physiology Laboratory, Institute of Storage of Farm Products, Shanxi Academy of Agricultural Sciences (SAAS)
- 1995.05-2001.12 **Director,** Postharvest Physiology Laboratory

Honors and Awards

- 2018, Environmental safety evaluation and detection technology of genetically modified canola, the 1st Prize of Science and Technology, China Federation of Commerce (3/12)
- 2013, Rapid detection method of genetically modified products based on gene technology, the 2nd Prize of Science and Technology, China Association for Analysis and Testing (8/10)
- 2012, The detection methods of endogenous reference genes and their standardization for genetically modified products of rice, corn and canola, the 1st Prize of Science and Technology, Shanghai Municipal Government (11/12)
- 2002, 2004, 2005, Scholarship, Israel-China Friendship Association
- 1997, Insulated and Ventilated Container for Fruit Transportation, the 3rd Prize of Science and Technology, Shanxi Municipal Government（3/5）
- 1996, Outstanding CPC Member, SAAS
- 1993, Excellent Staff, SAAS

Publications in English （#Co-First author，*Correspondence）

2022

1. Hong J#, Rosental L#, Xu Y#, Xu D, Orf I, Wang W, Hu Z, Su S, Bai S, Ashraf M, Hu C, Zhang C, Li Z, Xu J, Liu Q, Zhang H, Zhang F, Luo Z, Chen M, Chen X, Betts N, Fernie A, Liang W, Chen G*, Brotman Y*, Zhang D*, **Shi J***. Genetic architecture of seed glycerolipids in Asian cultivated rice. ***Plant Cell and Environment***, 2022, doi: 10.1111/pce.14378.
2. Sun W, Shi J, Hong J, Zhao G, Wang W, Zhang D, Zhang W*, **Shi J***. Natural variation and underlying genetic loci of γ-oryzanol in Asian cultivated rice seeds. ***Plant Genome***, 2022, 15: e20201
3. Shi L#, Chen Y#, Hong J, Shen G, Schreiber L, Cohen H, Zhang D, Aharoni A*, **Shi J***. AtMYB31 is a wax regulator associated with reproductive development in Arabidopsis. ***Planta***, 2022, 256: 28.

4. Shen G, Sun W, Chen Z, Shi L, Hong J, **Shi J***. Plant GDSL esterases/lipases: evolutionary, physiological and molecular functions in plant development. ***Plants***, 2022, 11: 468.
5. Yang Y, **Shi J**, Chen L, Xiao W, Yu J*. ZmEREB46, a maize ortholog of Arabidopsis WAX INDUCER1/SHINE1, is involved in the biosynthesis of leaf epicuticular very-long-chain waxes and drought tolerance. ***Plant Science***, 2022, 321: 111256.
6. Chang S, Ren Z, Liu C, Du P, Li J, Liu Z, Zhang F, Hou H, **Shi J**, Liang W, Yang L, Ren H, Zhang D*. OsFH3 encodes a type II formin required for rice morphogenesis. ***International Journal of Molecular Science***, 2022, 22: 13250.
7. Mao F, Wu D, Lu F, Yi X, Gu Y, Liu B, Liu F, Tang T, **Shi J**, Zhao X, Liu L*, Ji L*. QTL mapping and candidate gene analysis of low temperature germination in rice (*Oryza sativa* L.) using a genome wide association study. ***PeerJ***, 2022, 10: e13407, DOI 10.7717/peerj.13407
8. Kim J, Silva J, Park C, Kim Y, Park N, Sukweenadhi J, Yu J, **Shi J**, Zhang D, Kim K, Son HJ, Park HC, Hong CO, Lee KM, Kim YJ*. Overexpression of the Panax ginseng CYP703 alters cutin composition of reproductive tissues in Arabidopsis. ***Plants***, 2022, 11, 382.
9. Xiao Y, Zhou Y, **Shi J**, Zhang D. OsGAMYL12 is required for pollen maturation and germination in rice. ***Reproduction and Breeding***, 2022, 2: 1-8.

- **2021**

1. Ashraf M, Mao Q, Hong J, Shi L, Ran X, Liaquat F, Uzair M, Liang W, Fernie AR, **Shi J***. HSP70-16 and VDAC3 jointly inhibit seed germination under cold stress in Arabidopsis. ***Plant Cell and Environment***, 2021, 44: 3616-3627.
2. Biswas S, Zhang D, **Shi J***. Crispr/Cas systems: opportunities and challenges for crop breeding. ***Plant Cell Reports***, 2021, 40: 979–998.
3. Shi J, **Shi J**, Liang W, Zhang D. Integrating GWAS and transcriptomics to identify genes involved in seed dormancy in rice. ***Theoretical and Applied Genetics,*** 2021, 134: 3553–3562.
4. Liaquat F, Liu Q, Arif S, Haroon U, Saqib S, Zaman W, **Shi J**, Che S, Lv, XL, Akbar M, Munis MFH. Isolation and characterization of pathogen causing brown rot in lemon and its control by using ecofriendly botanicals. ***Physiological and Molecular Plant Pathology***, 2021, 114: 101639.
5. Liaquat F, Munis MFH, Arif S, Haroon U, **Shi J**, Saqib S, Zaman W, Che S, Liu Q. PacBio single-molecule long-read sequencing reveals genes tolerating manganese stress in *Schima superba* saplings. ***Frontiers in Genetics***, 2021, 12: 635043.
6. Pan J$^\#$, Zhang L$^\#$, Chen G, Wen H, Chen Y, Du H, Zhao J, He H, Lian H, Chen H, **Shi J**, Cai R, Wang G*, Pan J*. Study of micro-trichome (mict) reveals novel connections between transcriptional regulation of multicellular trichome development and specific metabolism in cucumber. ***Horticulture Research***, 2021, 8: 21.
7. Sun W, Chen Z, Hong J, **Shi J***. Promoting human nutrition and health through plant metabolomics: current status and challenges. ***Biology,*** 2021, 10: 20.
8. Hong J$^\#$, Shi Q$^\#$, Biswas S, Jiang SC, **Shi J***. Moving genome edited crops forward from the laboratory bench to the kitchen table. ***Food Control***, 2021, 122:107790.

■ 2020

1. Liaquat F, Munis MFH, Haroon U, Arif S, Saqib S, Zaman W, Khan AR, **Shi J,** Che S, Liu Q. Evaluation of metal tolerance of fungal strains isolated from contaminated mining soil of Nanjing, China. ***Biology***, 2020, 9: 469.
2. Biswas S, Li R, Hong J, Zhao X, Yuan Z, Zhang D, **Shi J***. Effective identification of CRISPR/Cas9-induced and naturally occurred mutations in rice using a multiplex ligation-dependent probe amplification-based method. ***Theoretical and Applied Genetics***, 2020, 133: 2323–2334.
3. Biswas S, Tian J, Li R, Chen X, Luo Z, Chen M, Zhao X, Zhang D, Persson S, Yuan Z*, **Shi J***. Investigation of CRISPR/Cas9-induced SD1 rice mutants highlights the importance of molecular characterization in plant molecular breeding. ***Journal of Genetics and Genomics***, 2020, 47: 273-280.
4. Cui D, Hu C*, Zou Z, Sun X, **Shi J**, Xu N*. Comparative transcriptome analysis unveils mechanisms underlying the promoting effect of potassium iodide on astaxanthin accumulation in haematococcus pluvialis under high light stress. ***Aquaculture***, 2020, 525, 735279.
5. Hu C, Cui D, Sun X, **Shi J**, Xu N*. Primary metabolism is associated with the astaxanthin biosynthesis in the green algae *Haematococcus pluvialis* under light stress. ***Algal Research-Biomass Biofuels and Bioproducts***, 2020, 46, 101768.
6. Hu C, Rao J, Song Y, Chan SA, Tohge T, Cui B, Lin H, Fernie AR, Zhang D, **Shi J***. Dissection of flag leaf metabolic shifts and their relationship with those occurring simultaneously in developing seed by application of non-targeted metabolomics. ***PLoS One***, 2020, 15: e0227577.
7. Jiang HL[#], Hong J[#], Jiang YT, Yu SX, Zhang YJ, **Shi JX**, Lin WH*. Genome-wide association analysis identifies candidate genes regulating seed number per silique in *Arabidopsis thaliana*. ***Plants-Basel***, 2020, 9: 585.
8. Khizar M, **Shi J**, Saleem S, Liaquat F, Ashraf M, Latif S, Haroon U, Hassan SW, Rehman SU, Chaudhary HJ, Quraishi UM*. Resistance associated metabolite profiling of Aspergillus leaf spot in cotton through non-targeted metabolomics. **PLoS One**, 2020, 15: e0228675.
9. Mondol PC, Xu D, Duan L, **Shi J**, Wang C, Chen X, Chen M, Hu J, Liang W*, Zhang D*. Defective Pollen Wall 3 (DPW3), a novel alpha integrin - like protein, is required for pollen wall formation in rice. ***New Phytologist***, 2020, 225: 807-822.
10. Ran X, Chen X, Shi L, Ashraf M, Yan F, Chen Y, Xu J*, **Shi J***. Transcriptomic insights into the roles of HSP70-16 in sepal's responses to developmental and mild heat stress signals. ***Environmental and Experimental Botany***, 2020, 179: 104225.
11. Silva J, Sukweenadhi J, Myagmarjav D, Mohanan P, Yu, J, **Shi J**, Jung K, Zhang D, Yang DC, Kim Y. Overexpression of a novel cytochrome P450 monooxygenase gene, CYP704B1, from Panax ginseng increase biomass of reproductive tissues in transgenic Arabidopsis. ***Molecular Biology Reports***, 2020, 47: 4507-4518.
12. Uzair M, Xu D, Schreiber L, **Shi J,** Liang W, Jung KH, Chen M, Luo Z, Zhang Y, Yu J, Zhang D*. PERSISTENT TAPETAL CELL2 is required for normal tapetal programmed cell death and pollen wall patterning. ***Plant Physiology***, 2020, 182: 962-976.

13. Xu D, Mondol PC, Ishiguro S, **Shi J**, Zhang D, Liang, W. NERD1 is required for primexine formation and plasma membrane undulation during microsporogenesis. ***aBIOTECH***, 2020, 1: 205–218.
14. Zafar SA, Patil SB, Uzair M, Fang J, Zhao J, Guo T, Yuan S, Uzair M, Luo Q, **Shi J**, Schreiber L, Li X*. DEGENERATED PANICLE AND PARTIAL STERILITY 1 (DPS 1) encodes a cystathionine β-synthase domain containing protein required for anther cuticle and panicle development in rice. ***New Phytologist***, 2020, 225: 356-375.
15. Zhu B, Li H, Xia X, Meng Y, Wang N, Li L, **Shi J**, Pei Y, Lin M, Niu L, Lin H. ATP-binding cassette G transporters SGE1 and MtABCG13 control stigma exsertion. ***Plant Physiology***, 2020, 184: 223–235.
16. Zhu L, He S, Liu Y, **Shi J***, Xu J*. Arabidopsis FAX1 mediated fatty acid export is required for the transcriptional regulation of anther development and pollen wall formation. ***Plant Molecular Biology,*** 2020, 104: 187-201.

■ 2019

17. Zafar SA, Patil SB, Uzair M, Fang J, Zhao J, Guo T, Yuan S, Uzair M, Luo Q, **Shi J**, Schreiber L, Li X. Degenerated panicle and partial sterility 1 (DPS1) encodes a CBS domain containing protein required for anther cuticle and panicle development in rice. ***New Phytologist***, (2019), doi:10.1111/nph.16133
18. Xu D, Qu S, Tucker MR, Zhang D, Liang W, **Shi J***. OsTKPR1 functions in anther cuticle development and pollen wall formation in rice. ***BMC Plant Biology***, 2019 19:104.
19. Duan S, Wu Y, Fu R, Wang L, Chen Y, Xu W, Zhang C, Ma C, **Shi J***, Wang S*. Comparative metabolic profiling of grape skin tissue along grapevine berry developmental stages reveals systematic influences of root restriction on skin metabolome. ***International Journal of Molecular Science***, 2019, 20, 534: doi:10.3390/ijms20030534
20. Hu C#, Zhao H#, **Shi J**, Li J, Nie X, Yang G. Effects of 2,4-dichlorophenoxyacetic acid on cucumber fruit development and metabolism. ***International Journal of Molecular Science***, 2019, 20, 1126; doi:10.3390/ijms20051126.
21. Biswas S, Li R, Yuan Z, Zhang D, Zhao X*, **Shi J***. Development of methods for effective identification of CRISPR/Cas9-induced indels in rice. ***Plant Cell Reports***, 2019, 38(4): 503-510. https://doi.org/10.1007/s00299-019-02392-3.
22. Li R, **Shi J**, Liu B, Wang C, Zhang D, Zhao X, Yang L. Inter-laboratory validation of visual loop-mediated isothermal amplification assays for GM contents screening. ***Food Chemistry***, 2019, 274: 659–663.
23. Zhao G, Zhang Y, Sun S, Xie M, Hu C, Shi Y, **Shi J**, Li J. Identification of the biochemical characteristics of developing giant embryo rice grains using non-targeted metabolomics. ***Journal of Cereal Science***, 2019, 85: 70–76.
24. Chen X#, Shi L#, Chen Y, Zhu L, Zhang D, Xiao S, Aharoni A, **Shi J***, Xu J*. Arabidopsis HSP70-16 is required for flower opening under normal or mild heat stress temperatures. ***Plant Cell and Environment***, 2019; 42:1190–1204. https://doi.org/10.1111/pce.13480
25. Siddique K, Wei J, Li R, Zhang D, **Shi J***. Identification of T-DNA insertion site and flanking sequence of a genetically modified maize event IE09S034 using next-

generation sequencing technology. ***Molecular Biotechnology***, 2019, https://doi.org/10.1007/s12033-019-00196-0.

■ 2018

1. Bi H, **Shi J**, Kovalchuk N, Luang S, Bazanova N, Chirkova L, Zhang D, Shavrukov Y, Stepanenko A, Tricker P, Langridge P, Hrmova M, Lopato S, Borisjuk N. Overexpression of the TaSHN1 transcription factor in bread wheat leads to leaf surface modifications, improved drought tolerance and no yield penalty under controlled growth conditions. ***Plant Cell and Environ***, 2018, 41: 2549–2566.
2. Borisjuk N*, Peterson AA, Lv J, Qu G, Luo Q, Shi L, Chen G, Kishchenko O, Zhou Y and **Shi J***. Structural and biochemical properties of duckweed surface cuticle. ***Frontiers in Chemistry***, 2018, 6:317. doi: 10.3389/fchem.2018.00317.
3. Li R, **Shi J**, Liu B, Zhang D, Zhao X, Yang L*. International collaborative ring trial of four gene-specific loop-mediated isothermal amplification assays in GMO analysis. ***Food Control***, 2018, 84：278-283.
4. Hu C, Zhao H, Wang W, Xu M, **Shi J**, Nie X, Yang G*. Identification of conserved and diverse metabolic shift of the stylar, intermediate and peduncular segments of cucumber fruit during development. ***International Journal of Molecular Sciences***, 2018. 19(1): 135.
5. Wang W$^{\#}$, Mauleon R$^{\#}$, Hu Z$^{\#}$, Chebotarov D$^{\#}$, Tai S$^{\#}$, Wu Z$^{\#}$, Li M$^{\#}$, Zheng T$^{\#}$, Fuentes RR$^{\#}$, Zhang F$^{\#}$, Mansueto L$^{\#}$, Copetti D$^{\#}$, Sanciangco M, Palis KC, Xu J, Sun C, Fu B, Zhang H, Gao Y, Zhao X, Shen F, Cui X, Yu H, Li Z, Chen M, Detras J, Zhou Y, Zhang X, Zhao Y, Kudrna D, Wang C, Li R, Jia B, Lu J, He X, Dong Z, Xu J, Li Y, Wang M, **Shi J**, Li J, Zhang D, Lee S, Hu W, Poliakov1 A, Dubchak I, Ulat VJ, Borja FN, Mendoza RJ, Ali J, Li Jing, Gao Q, Niu Y, Yue Z, Naredo MEB, Talag J, Wang X, Li J, Fang X, Yin Y, Glaszmann JC, Zhang J, Li J, Hamilton RS, Wing RA*, Ruan J*, Zhang G*, Wei C*, Alexandrov N*, McNally KL*, Li Z*, Leung H. Genomic variation in 3,010 diverse accessions of Asian cultivated rice. ***Nature***, 2018, 557: 43-49.
6. Arulandhu AJ, van Dijka J, Staats M, Hagelaar R, Voorhuijzen M, Molenaar B, van Hoof R, Li R, Yang L, **Shi J**, Scholtens I, Kok E. NGS-based amplicon sequencing approach; towards a new era in GMO screening and detection. ***Food Control***, 2018, 93: 201–210.
7. Hu Z, Wang W, Wu Z, Sun Chen, Li M, Lu J, Fu B, **Shi J**, Xu J, Ruan J, Wei C, Li Z. Data Descriptor: Novel sequences, structural variations and gene presence variations of Asian cultivated rice. ***Scientific Data***, 2018, 5:180079
8. Kim Y, Joo S, **Shi J**, Hu C, Quan S, Hu J, Sukweenadhi J, Mohanan P, Yang D, Zhang D. Metabolic dynamics and physiological adaptation of Panax ginseng during development. ***Plant Cell Reports***, 2018, 7:393–410

■ 2017

1. Liu H$^{\#}$, Cui B$^{\#}$, Xu Y, Hu C, Liu Y, Qu G, Li D, Wu Y, Zhang D, Quan S*, **Shi J*.** Ethyl carbamate induces cell death through its effects on multiple metabolic pathways. ***Chemico-Biological Interactions***, 2017, 277: 21-32.

2. Zhu X, Yu J, **Shi J**, Tohge T, Fernie AR, Meir S, Aharoni A, Xu D, Zhang D, Liang W. The polyketide synthase OsPKS2 is essential for pollen exine and Ubisch body patterning in rice. ***Journal of Integrative Plant Biology***, 2017, 59 (9): 612–628.
3. Liu, Ze, Lin S, **Shi J**, Yu J, Zhu L, Yang X, Zhang D, Liang W*. Rice No Pollen 1 (NP1) is required for anther cuticle formation and pollen exine patterning. ***The Plant Journal***, 2017, 91(2):263-277.
4. Yang X, Liang W, Chen M, Zhang D, Zhao X, **Shi J***. Rice fatty acyl-CoA synthetase OsACOS12 is required for tapetum programmed cell death and male fertility. ***Planta***, 2017, 246:105–122.
5. Xu D, **Shi J,** Rautengarten C, Yang L, Qian X, Uzair M, Zhu L, Luo Q, An G, Wabmann F, Schreiber L, Hu j, Zhang D, Liang W. Defective Pollen Wall 2 (DPW2) encodes an acyl transferase required for rice pollen development. ***Plant Physiology***, 2017, 173(1): 240-255.
6. Hu Z, Sun C, Lu KC, Chu X, Zhao Y, Lu J, **Shi J***, Wei C*. EUPAN enables pan-genome studies of a large number of eukaryotic genomes. ***Bioinformatics***, 2017, 33(15):2408-2409.
7. Li R#, Quan S#, Yan X, Biswas S, Zhang D, **Shi J***. Molecular characterization of genetically-modified crops: Challenges and strategies. ***Biotechnology Advance***, 2017, 35(2):302-309.
8. Men X, **Shi J**, Liang Wan, Zhang Q, Lian G, Quan S, Zhu L, Luo Z, Chen M, Zhang D*. Glycerol-3-Phosphate Acyltransferase 3 (OsGPAT3) is required for anther development and male fertility in rice. ***Journal of Experimental Botany***, 2017, 68(3):513-526.
9. Sun C, Hu Z, Zheng T, Lu K, Zhao Y, Wang W, **Shi J**, Wang C, Lu J, Zhang D, Li Z, Wei C*. RPAN: rice pan-genome browser for ~3000 rice genomes. ***Nucleic Acids Research***, 2017, 45(2):597-605.
10. Bao S, **Shi J**, Luo F, Ding B, Hao J, Xie X, Sun SJ*. Overexpression of Sorghum WINL1 gene confers drought tolerance in Arabidopsis thaliana through the regulation of cuticular biosynthesis. ***Plant Cell, Tissue and Organ Culture***, 2017, 128(2), 347-356
11. Ye Z, Xu J, **Shi J**, Zhang D, Chye M. Kelch-motif containing acyl-CoA binding proteins AtACBP4 and AtACBP5 are differentially expressed and function in floral lipid metabolism. ***Plant Molecular Biology***, 2017, 93(1-2):209-225.
12. Sekse C, Holst-Jensen A, Dobrindt U, Johannessen GS, Li W, Spilsberg B, **Shi J**. High throughput sequencing for detection of foodborne pathogens. ***Frontiers in Microbiology***, 2017, 8: 2029.

■ 2016

1. Hu C$^{\#}$, Li Q$^{\#}$, Shen X, Quan S, Lin H, Duan L, Wang Y, Luo Q, Qu G, Han Q, Lu Y, Zhang D, Yuan Z* and **Shi J***. Characterization of factors underlying the metabolic shifts in developing kernels of colored maize. ***Scientific Reports***, 2016, 6:35479.
2. Biswas S$^{\#}$, Fan W$^{\#}$, Li R, Li S, Ping W, Li S, Naumova A, Peelen T, Kok E, Yuan Z, Zhang D, **Shi J***. The development of DNA based methods for the reliable and efficient identification of *Nicotiana tabacum* in tobacco and its derived products. ***International Journal of Analytical Chemistry***, 2016, Article ID 4352308.

3. Chen M, Xu J, Devis DL, **Shi J**, Ren K, Searle I, Zhang D*. Origin and functional prediction of pollen allergens in plants. ***Plant Physiology***, 2016, 172(1): 341-357.
4. Arulandhu AJ, van Dijk JP, Dobnik D, Holst-Jensen A, **Shi J**, Zel J, Kok EJ*****. DNA enrichment approaches to identify unauthorized genetically modified organisms (GMOs). ***Analytical and Bioanalytical Chemistry***, 2016, 408(17):4575-4593.
5. Holst-Jensen A*****, Spilsberg B, Arulandhu AJ, Kok E, **Shi J**, Zel J (2016). Application of whole genome shotgun sequencing for detection and characterization of genetically modified organisms and derived products. ***Analytical and Bioanalytical Chemistry***, 2016, 408(17): 4595-4614.
6. Hong J, Yang L, Zhang D, **Shi J***. Plant metabolomics: an indispensable system biology tool for plant science. ***International Journal of Molecular Science***, 2016, 17(6), 767.
7. Hu C, Tohge T, Chan SA, Song Y, Rao J, Cui B, Lin H, Wang L, Fernie AR, Zhang D, **Shi J***. Identification of conserved and diverse metabolic shifts during rice grain development. ***Scientific Reports***, 2016, 6: 20942.
8. Kim YJ, Silva J, Zhang D, **Shi J**, Joo SC, Jang MG, Kwon WS, Yan DC*****. Development of interspecies hybrids to increase ginseng biomass and ginsenoside yield. ***Plant Cell Report***, 2016, 35(4):779-790.
9. Liu Y[#], Ran R[#], Hu C, Cui B, Xu Y, Liu H, Quan S, Li D, Li X, Wu Y, Zhang D, **Shi J***. The metabolic responses of HepG2 cells to the exposure of mycotoxin deoxynivalenol. ***World Mycotoxin Journal***, 2016, 9(4): 577-586.
10. Rao J, Yang L, Guo J, Quan S, Chen G, Zhao X, Zhang D, **Shi J***. Metabolic changes in transgenic maize mature seeds over-expressing the Aspergillus niger phyA2. ***Plant Cell Report***, 2016, 35(2), 429-437.
11. Rao J, Yang L, Guo J, Quan S, Chen G, Zhao X, Zhang D. **Shi J***. Development of event-specific qualitative and quantitative PCR detection methods for the transgenic maize BVLA430101. ***European Food Research and Technology***, 2016, 242(8), 1277-1284.
12. Zhao G, **Shi J**, Liang W, Zhang D*. ATP binding cassette G transporters and plant male reproduction, ***Plant Signaling & Behavior***, 2016, 11:3, e1136764

■ 2015

1. Li R, Wang C, Ji L, Zhao X, Liu M, Zhang D, **Shi J***. Loop-mediated isothermal amplification (LAMP) assay for GMO detection: recent progresses and future perspectives. ***Open Access Library Journal***, 2015, 2: e1264. http://dx.doi.org/10.4236/oalib.1101264.
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3. Wang C, Li R, Quan S, Shen P, Zhang D, **Shi J**, Yang L*****. GMO detection in food and feed through screening by visual loop-mediated isothermal amplification assays. ***Analytical and Bioanalytical Chemistry***, 2015, 407(16): 4829-4834.
4. Xie L, Chen Q, Chen M, Yu L, Huang L, Chen L, Wang F, Xia F, Zhu T, Wu J, Yin J, Liao B, **Shi J**, Zhang J, Aharoni, A, Yao N, Shu W, Xiao S*****. Unsaturation of very-long-chain ceramides protects plant from hypoxia-induced damages by modulating ethylene signaling in Arabidopsis. ***PLoS Genetics***, 2015, 11(3): e1005143. doi:10.1371/journal.pgen.1005143.

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2014

1. Qu G, Quan S, Mondol P, Xu J, Zhang D, **Shi J***. Comparative metabolomic analysis of wild type and mads3 mutant rice anthers. ***Journal of Integrative Plant Biology***, 2014, 56(9): 849–863.
2. Lin H, Rao J, **Shi J**, Hu C, Cheng F, Wilson ZA, Zhang D, Quan S. Seed metabolomic study reveals significant metabolite variations and correlations among different soybean cultivars. ***Journal of Integrative Plant Biology***, 2014, 56(9): 826–836.
3. Xu J, Ding Z, Vizcay-Barrena G, **Shi J**, Liang W, Yuan Z, Werck-Reichhart D, Schreiber L, Wilson ZA, Zhang D. ABORTED MICROSPORES acts as a master regulator of pollen wall formation in Arabidopsis. ***The Plant Cell***, 2014, 26 (4): 1544-1556.
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5. Xu Y, Cui B, Ran R, Liu Y, Chen H, Kai G, **Shi J***. Risk assessment, formation, and mitigation of dietary acrylamide: Current status and future prospects. ***Food and Chemical Toxicology***, 2014, 69: 1–12
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7. Rao J, Cheng F, Hu C, Quan S, Lin H, Wang J, Chen G, Zhao X, Alexander D, Guo L, Wang G, Lai J, Zhang D, **Shi J***. Metabolic map of mature maize kernels. ***Metabolomics***, 2014, 10 (5): 775-787.
8. Cui B, Zhang W, Ran R, Xu Y, Wu A, Li D, Zhang D, **Shi J***, Chen H*. The Absorption and Accumulation Characteristics of Ethyl Carbamate in Human HepG2 Cells Revealed by. ***Life Science Journal***, 2014, 11: 10.

2013

1. Sela D, Buxdorf K, **Shi J**, Feldmesser E, Schreiber L, Aharoni A, Levy M*. Overexpression of AtSHN1/WIN1 provokes unique defense responses. ***PLoS ONE,*** 2013, 8(7): e70146.
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Book Chapter

Zhang D*, Shi J, Yang X. Role of Lipid Metabolism in Plant Pollen Exine Development. In ***Lipids in Plant and Algae Development*** (pp.315-337). 2016. Springer International Publishing.

Teaching (bilingual)

- **Undergraduate:** Introduction to Biosafety; Principles and Methods of Biochemical Analysis; Plant Biotechnology
- **Graduate student**: Biosafety (English), Principles and Applications of Biochemical Techniques; Signal Transduction of Animals, Plants and Microorganisms

Professional and social part-time jobs

- 2018-2020 Tutor of Shanghai High School Top Innovative Talents Early Training Project
- 2015 Shanghai Community College (School) Specially Invited Science Popularization Teacher
- 2013-present Spark expert, MOST
- 2012-present Reviewers of <Trends in Plant Sciences>, <Trends in Genetics>, <Plant Biotechnology Journal>, <Molecular Plant>, <Plant Physiology>, <New Phytologist>, <Journal of Experimental Botany>, <Plant Cell and Environment>, <BMC Plant Biology>, <Plant Cell Reports>, <Journal of Genetics and Genomics>, <Planta>, <Journal of Integrative Plant Biology>, <Plant Signaling & Behavior>, <Scientific Report>, <Journal of Agricultural and Food Chemistry>, <Food Chemical Toxicology>, and <Journal of Food Processing & Technology>.