

个人简历

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个人信息

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研究兴趣

- 代谢与植物的生长发育和逆境反应
- 转基因（包括基因编辑）作物安全评价
- 种子发育及品质形成的分子机制

学习经历

- 2001.12-2007.01 博士 耶路撒冷希伯来大学, REHOVOT, 以色列
- 1988.09-1991.06 硕士 西南农业大学, 重庆, 中国
- 1984.09-1988.06 学士 山西农业大学, 太谷, 中国

国外科研经历

- 2019.06-2020.07 访问专家 联合国粮农组织
- 2013.01-2013.02 访问学者 德国马普分子植物生理研究所
- 2012.06-2012.07 访问学者 法国斯特拉斯堡大学植物生物学系
- 2011.02-2011.03 访问学者 德国波恩大学植物生态系
- 2007.01-2010.09 博士后 以色列威兹曼科学院植物科学系 研究
课题：植物角质层生物合成的转录调控 (Transcriptional regulation of the cuticle biosynthesis in plants)
- 2008.09-2008.10 访问学者 德国波恩大学植物生态系
- 2001.12-2007.01 博士生 以色列耶路撒冷希伯来大学农学院 研究
课题：柑桔果实对无氧逆境的生理和分子生物学反应 (Physiological and molecular responses of citrus fruit to anaerobic stress)
- 2000.10-2001.06 访问学者 以色列耶路撒冷希伯来大学农学院 研究
课题：应用 1-MCP 及其同系物调控园艺产品对乙烯的反应 (Controlling

ethylene responses in horticultural crops with 1-MCP and its analogues)

国内科研经历

- 2021.12-现在 研究员, 上海交通大学生命科学技术学院
- 2012.02-2012.12 副研究员, 上海交通大学生命科学技术学院。
- 1991.06-2011.08 研究实习员, 助理研究员, 副研究员, 山西省农业科学院农产品贮藏保鲜研究所采后生理实验室
- 1995.05-2001.12 采后生理实验室主任(山西农科院农产品贮藏保鲜研究所)

荣誉和奖励

- 2018, 转基因油菜环境安全评价与转基因检测技术, 中国商业联合会科学技术奖一等奖(3/12)
- 2013, 基于基因技术的转基因产品快速检测方法, 中国分析测试学会科技二等奖(8/10)
- 2012, 水稻、玉米、油菜转基因产品内标准基因检测方法及标准化, 上海市科技进步一等奖(11/12)
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- 1997, 水果运输隔热通风集装箱, 山西省科技进步三等奖(3/5)
- 1996, 优秀共产党员, 山西省农业科学院
- 1993, 先进工作者, 山西省农业科学院

发表的 SCI 论文 (#共同第一作者, *通讯作者)

■ 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.
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 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
1. 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.
 2. 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:
 3. 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.
 4. 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: 503-510.
 5. 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.
 6. 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.
 7. 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.
 8. 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, 61: 694–702.
- 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.

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.
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6. Arulandhu AJ, van Dijken 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.

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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.
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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
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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.
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- 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.
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 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

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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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获得国家发明专利

- 张大兵, 石建新, 胡朝阳。用种子代谢物含量鉴定粳籼稻品种的方法, 中国发明专利号: ZL 2013 1 0419783. 2, 授权公告日: 2015 年 1 月 21 日。
- 张大兵, 石建新, 胡朝阳。用自然变异分析转基因水稻代谢组差异的方法, 中国发明专利号: ZL 2013 1 0429856. 6, 授权公告日: 2015 年 3 月 11 日
- 张大兵, 杨立桃, 石建新, 郭金超, 饶军。移植酸酶基因玉米 BVLA430101 品系特异性定量 PCR 检测方法, 中国发明专利号: ZL 2013 1 0429846. 2, 授权公告日: 2015 年 1 月 14 日
- 张大兵, 杨立桃, 石建新, 郭金超, 饶军。移植酸酶基因玉米外源基因插入位点旁侧序列及检测方法。授权公告日: 2016 年 6 月 1 日, 专利号: ZL 2013 1 0430113. 0

教学 (双语)

- 本科生: 生物安全导论, 生化分析原理和方法, 植物生物技术
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发表的中文论文 (英文摘要)

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4. 金蕾, 张大生, 刘卓星, 石建新, 许杰, 王纪忠*, 崔丽洁. 植物花香产生的代谢途径和分子机制研究进展. *江苏农业科学*, 2020, 48(23): 51-59.
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7. 刘会昌, 石建新*. 氨基甲酸乙酯诱导人体细胞凋亡分子机制研究. *食品科学*

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