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发表论文

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2018年发表

- 1.Zhao QT[†], Feng QT[†], Lu HY, Li Y, Wang AH, Tian QL, Zhan QL, Lu YQ, Zhang L, Huang T, Wang YC, Fan DL, Zhao Y, Wang ZQ, Zhou CC, Chen JY, Zhu CR, Li WJ, Weng QJ, Xu Q, Wang ZX, Wei XH, Han B, Huang XH^{*}(2018). Pan-genome analysis highlights the extent of genomic variation in cultivated and wild rice. **Nature Genetics**, 50(2):278-284. (**IF=27.125**)
- 2.Wang Q, Nian JQ, Xie XZ, Yu H, Zhang J, Bai JT, Dong GJ, Hu J, Bai B, Chen LC, Xie QJ, Feng J, Yang XL, Peng JL, Chen F, Qian Q^{*}, Li JY^{*}, Zuo JR^{*} (2018). Genetic variations in ARE1 mediate grain yield bymodulating nitrogen utilization in rice. **Nat Commun**, 9:735. (**IF=12.353**)
- 3.Yang YJ[†], Chen JM[†], Huang QN, Tang SQ, Wang JL, Hu PS^{*}, Shao GS^{*}(2018). Can liming reduce cadmium (Cd) accumulation in rice (*Oryza sativa*) in slightly acidic soils? A contradictory dynamic

equilibrium between Cd uptake capacity of roots and Cdimmobilisation in soils. ***Chemosphere***, 193:547-556. (IF=4.427)

4.Qi JF, Zhang M, Lu CK, C.Hettenhausen, Tan Q, Cao GY, Zhu XD, Wu GX, Wu JQ^{*}(2018). Ultraviolet-B enhances the resistance of multiple plant species to lepidopteraninsect herbivory through the jasmonic acid pathway. ***Sci Rep-UK***, 8:277.(IF=4.122)

5.Chen JY, Zhang HW, Zhang HL, Ying JZ, Ma LY^{*}, Zhuang JY^{*} (2018).Natural variation at qHd1 affects heading date acceleration at hightemperatures with pleiotropism for yield traits in rice. ***BMC Plant Biol***,18:112. (IF=3.930)

6.Qiu ZN[†], Kang SJ[†], He L, Zhao J, Zhang S, HuJ, Zeng DL, Zhang GH, Dong GJ, Gao ZY, Ren DY, Chen G, Guo LB, Qian Q^{*},Zhu L^{*} (2018). The newly identified *heat-stress sensitive albino1* gene affects chloroplast development in rice. ***Plant Sci***, 267:168-179.(IF=3.712)

7.He Y, Li LJ, Zhang ZH, Wu JL^{*} (2018). Identification and ComparativeAnalysis of Premature Senescence Leaf Mutants in Rice (*Oryza sativa* L.). ***Int J Mol Sci***, 19(1):140. (IF=3.687)

8.Chen G^{*}, Liu CL, Gao ZY, Zhang Y, Zhang AP, Zhu L, Hu J, Ren DY, Yu L, XuGH^{*}, Qian Q^{*} (2018). Variation in the Abundance of *OsHAK1*Transcript Underlies the Differential Salinity Tolerance of an indica and a *japonica* Rice Cultivar. ***Front Plant Sci***, 8:2216. (IF=3.678)

9.Zhu CQ, Zhang JH, Sun LM, Zhu LF, B.Abliz, Hu WJ, Zhong C, Bai ZG., H.Sajid, Cao XC^{*},Jin QY^{*} (2018). Hydrogen Sulfide Alleviates Aluminum Toxicity viaDecreasing Apoplast and Symplast Al Contents in Rice. ***Front Plant Sci***, 9:294. (IF=3.678)

10.Ye JT[†], Niu XJ[†], Yang YL, Wang S, Xu Q, Yuan XP, Yu HY, Wang YP, Wang S^{*}, Feng Y^{*}, Wei XH^{*} (2018).Divergent *Hd1*, *Ghd7*, and *DTH7* Alleles Control Heading Dateand Yield Potential of *Japonica* Rice in Northeast China. ***Front Plant Sci***, 9:35. (IF=3.678)

11.Lu QT[†], Niu XJ[†], Zhang MC, Wang CH, Xu Q,Feng Y, Yang YL, Wang S, Yuan XP, Yu HY, Wang YP, Chen XP, Liang XQ, Wei XH^{*}(2018). Genome-Wide Association Study of Seed Dormancy and the Genomic Consequences of Improvement Footprints in Rice (*Oryza sativa* L.). ***Front Plant Sci***, 8:2213. (IF=3.678)

12.Chen G^{*}, Liu CL, Gao ZY, Zhang Y, Zhu L, Hu J, Ren DY, Xu GH^{*},Qian Q^{*} (2018). Driving the expression of *RAA1* with adrought-responsive promoter enhances root growth in rice, its accumulation of potassium and its tolerance to moisture stress. ***Enviro Exp Bot***, 147:147-156. (IF=3.666)

- 13.Shen L[†], Wang C[†], Fu YP, Wang JJ, Liu Q, Zhang XM, Yan CJ^{*}, Qian Q^{*}, Wang KJ^{*} (2018). QTL editing confers opposing yield performance in different rice varieties. *J Integr Plant Biol*, 60(2):89-93. (IF=3.129)
- 14.Zhang XB[†], Feng BH[†], Wang HM, Xu X, Shi YF, HeY, Chen Z, A.P.Sathe, Shi L, Wu JL^{*} (2018). A substitution mutationin *OsPELOTA* confers bacterial blight resistance by activating thesalicylic acid pathway. *J Integr Plant Biol*, 60(2):160-172. (IF=3.129)
- 15.He L[†], Zhang S[†], Qiu ZN, Zhao J, Nie WD,Lin HY, Zhu ZG, Zeng DL, Qian Q^{*}, Zhu L^{*} (2018). *FRUCTOKINASE-LIKEPROTEIN 1* interacts with TRXz to regulate chloroplast development in rice. *J Integr Plant Biol*, 60(2):94-111. (IF=3.129)
- 16.Qian Q (2018). Genomics-assisted germplasm improvement. *J Integr Plant Biol*,60(2):82-84. (IF=3.129)
- 17.Meng XB[†], Hu XX[†], Liu Q, Song XG, Gao CX,Li JY^{*}, Wang KJ^{*} (2018). Robust genome editing of CRISPR-Cas9 at NAG PAMs in rice. *Sci China Life Sci*,61(1):122-125. (IF=3.085)
18. Zhang CX, Li GY, Chen TT, Feng BH, Fu WM, Yan JX, M.R.Islam, Jin QY, Tao LX^{*},Fu GF^{*} (2018). Heat stress induces spikelet sterility in rice anthesis through inhibition of pollen tube elongation interfering with auxin homeostasis in pollinated pistils. *Rice*, 11:14. (IF=3.039)
- 19.Zhang MC, Ye J, Xu Q, Feng Y, Yuan XP, Yu HY, Wang YP, Wei XH^{*}, Yang YL^{*}(2018). Genome-wide association study of cold tolerance of Chinese *indica* rice varieties at the bud burst stage. *Plant Cell Rep*, 37(3):529-539.(IF=2.989)
- 20.Zhong C[†], Cao XC[†], Bai ZG, Zhang JH, Zhu LF,Huang JL, Jin QY^{*} (2018). Nitrogen metabolism correlates with theacclimation of photosynthesis to short-term water stress in rice (*Oryzasativa* L.). *Plant Physiol Bioch*, 125:52-62. (IF=2.718)
- 21.Wu WX, Zhang YX, Zhang M, Zhan XD, Shen XH, Yu P, Chen DB, Liu QE, S.Sinumporn, K.Hussain,Cheng SH^{*}, Cao LY^{*} (2018). The rice CONSTANS-like protein OsCOL15 suppresses flowering by promoting *Ghd7* and repressing *RID1*. *Biochem Bioph Res Co*, 495(1):1349-1355. (IF=2.559)
- 22.Huang DR, Fan YY, Hu BL, Xiao YQ, Chen DZ, Zhuang JY^{*} (2018). Assessment and genetic analysis of heavy metal content in rice grain using an *Oryzasativa* × *O. rufipogon* backcross inbred line population. *J Sci Food Agr*, 98(4):1339-1345. (IF=2.379)
- 23.Y.M.N.Adedze,Feng BB, Shi L, Sheng ZH, Tang SQ, Wei XJ^{*}, Hu PS^{*} (2018). Further insight into the role of *KAN1*, a member of *KANADI* transcriptionfactor family in rice. *Plant Growth Regul*, 84(2):237-248. (IF=2.081)

- 24.Wang ZW, Lv J, Xie SZ, Zhang Y, Qiu ZN, Chen P, Cui YT, Niu YF, Hu SK, Jiang HZ, Ge SZ,H.Trinh, Lei KR, Bai WQ, Zhang Y*, Guo LB*, Ren DY* (2018).OsSLA4 encodes a pentatricopeptide repeat protein essential for early chloroplast development and seedling growth in rice. ***Plant Growth Regul***, 84(2):249-260. (**IF=2.081**)
- 25.Cao XC†, Zhu CQ†, Zhong C†, S.Hussain, Zhu LF, Wu LH,Jin QY* (2018). Mixed-nitrogen nutrition-mediated enhancement ofdrought tolerance of rice seedlings associated with photosynthesis, hormone balance and carbohydrate partitioning. ***Plant Growth Regul***, 84(3):451-465. (**IF=2.081**)
26. Huang FL, Wei XJ, He JW, Sheng ZH, Shao GN, Wang JL, Tang SQ, Xia SP, Xiao YH, Hu PS*(2018). Mapping of Quantitative Trait Loci Associated with Concentrations of Five Trace Metal Elements in Rice (*Oryza sativa*). ***Int J Agric Biol***, 20(3):554-560. (**IF=0.869**)
- 27.WangM†, Li WZ†, Fang C†, Xu F†, Liu YC†, Wang Z, Yang R, Zhang M, LiuSL, Lu SJ, Lin T, Tang JY, Wang YQ, Wang HR, Lin H, Zhu BG, Chen MS, Kong FJ, LiuBH, Zeng DL, Scott A. Jackson*, Chu CC*, Tian ZX*.Parallel selection on a dormancy gene during domestication of crops frommultiple families. ***Nat Genet***, 2018, 50(10):1435-1445. (**IF=27.125**)
- 28.ZhanN†, Wang C†, Chen LC, Yang HJ, Feng J, Gong XQ, Ren B, WuR, Mu JY, Li YS, Liu ZH, Zhou Y, Peng JL, Wang KJ, Huang X, Xiao S and Zuo JR*.S-Nitrosylation Targets GSNO Reductase for Selective Autophagy during HypoxiaResponses in Plants. ***Mol Cell***, 2018, 71(1),142-154. (**IF=14.248**)
29. Guo LB†, Qiu J†, Li LF, Lu BR, Kenneth Olsen, FanLJ*. Genomic Clues for Crop-Weed Interactions and Evolution. ***TrendsPlant Sci***, 2018, 23(12):1102-1115. (**IF=12.149**)
30. Ying JZ†,Ma M†, Bai C†, Huang XH, Liu JL, Fan YY, Song XJ*.TGW3, a major QTL that negatively modulates grain length and weight in rice. ***Mol Plant***, 2018, 11:750-753. (**IF=9.326**)
31. Hu SK, Hu XM, Hu J, Shang LG, Dong GJ, Zeng DL, Guo LB, Qian Q*.Xiaowei, a New Rice Germplasm for Large-Scale Indoor Research. ***Mol Plant***,2018, 11(11):1418-1420. (**IF=9.326**)
32. JiangPF†, Wang SL†, Zheng H, Li H, Zhang F, Su YH, Xu ZT, Lin HY, QianQ, Ding Y*. SIP1 participates in regulation of flowering time inrice by recruiting OsTrx1 to Ehd1. ***New Phytol***, 2018,219(1):422-435. (**IF=7.433**)
- 33.Cai YC†, Li SF†, Jiao GA, Sheng ZH,Wu YW, Shao GN, Xie LH, Peng C, Xu JF, Tang SQ, Wei XJ*, Hu PS*.OsPK2 encodes a plastidic pyruvate kinase involved in rice endospermstarch synthesis, compound granule formation and grain filling. ***Plant Biotechnol J***, 2018, 16(11):1878-1891. (**IF=6.305**)
- 34.Hong YB†, Zhang YX†, Sittipun Sinumporn†, Yu N, Zhan XD, Shen XH,Chen DB, Yu P, Wu WX, Liu QE, Cao ZY, Zhao CD, Cheng SH*, Cao LY*.Premature leaf senescence 3, encoding a methyltransferase,is required for melatoninbiosynthesis in rice. ***Plant J***, 2018, 95(5):877-891. (**IF=5.775**)

35. E ZG†, Li T†, Zhang HY†, Liu ZH, Deng H, Sandeep Sharma, Wei XF, Wang L, Niu BX, Chen C*. A group of nuclearfactor Y transcription factors are sub functionalized during endospermdevelopment in monocots. *J Exp Bot*, 2018, 69(10):2495-2510. (IF=5.354)
36. Ren DY†, Hu J†, Xu QK†, Cui YJ, Zhang Y, Zhou TT, Rao YC, Xue DW, Zeng DL, Zhang GH, Gao ZY, Zhu L, Shen L, Chen G, Guo LB, Qian Q*. FZP determines grain size and sterile lemma fate in rice. *J Exp Bot*, 2018, 69(20):4853-4866. (IF=5.354)
37. Guo F, Zhang HD, Liu W, Hu XM, Han N, Qian Q, Xu L*, Bian HW*. Callus initiationfrom root explants employs different strategies in rice and Arabidopsis. *Plant Cell Physiol*, 2018, 59(9):1782-1789. (IF=4.760)
38. Chen GQ, Yan Q, Fang Y, Wu LJ, Krell PJ, and Feng GZ*. The N terminus of *Autographa californica* multiple nucleopolyhedrovirus DNA polymerase is required for efficient viral DNA replication and virus and occlusion body production. *J Virol*, 2018, 92: JVI-00398. (IF=4.368)
39. Wu H, Xiang J*, Zhang YP, Zhang YK, Peng SB, Chen HZ* & Zhu DF*. Effects of Post-Anthesis Nitrogen Uptake and Translocation on Photosynthetic Production and Rice Yield. *Sci Rep-UK*, 2018, 8(1):12891. (IF=4.122)
40. Niu YF†, Chen P†, Zhang Y†, Wang ZW, Hu SK, Jin GL, Tang CX, Guo LB*. Natural variation among *Arabidopsis thaliana* accessions in tolerance to high magnesium supply. *Sci Rep-UK*, 2018, 8(1):13640. (IF=4.122)
41. Feng BH†, Zhang CX†, Chen TT, Zhang XF, Tao LX* and Fu GF*. Salicylic acid reverses pollen abortion of rice caused by heat stress. *BMC Plant Biol*. 2018, 18: 245. (IF=3.930)
42. Xu X, Chen Z, Shi YF, Wang HM, He Y, Shi L, Chen T, Wu JL*, Zhang XB*. Functional inactivation of OsGCNT induces enhanced disease resistance to *Xanthomonas oryzae* pv. *oryzae* in rice. *BMC Plant Biol*. 2018, 18: 264. (IF=3.930)
43. Chen G†*, Zhang Y†, Ruan BP, Guo LB, Zeng DL, Gao ZY, Zhu L, Hu J, Ren DY, Yu L, Xu GH*, Qian Q*. OsHAK1 controls the vegetative growth and panicle fertility of rice by its effect on potassium-mediated sugar metabolism. *Plant Sci*, 2018, 274:261-270. (IF=3.712)
44. GalalBakr Anis, Zhang YX, Wang HM, Li ZH, Wu WX, Sun LP, Aamir Riaz, Cao LY*, Cheng SH*. Genomic regions analysis of seedling root traits and their regulation in responses to phosphorus deficiency tolerance in CSSL population of elite super hybrid rice. *Int J Mol Sci*, 2018, 19(5):1460. (IF=3.687)
45. He Y, Zhang ZH, Li LJ, Tang SQ, Wu JL*. Genetic and physio-biochemicalcharacterization of a novel premature senescence leaf mutant in rice (*Oryza sativa* L.). *Int J Mol Sci*, 2018, 19(8):2339. (IF=3.687)

46. ChenG, Wu C, He L, Qiu ZN, Zhang S, Zhang Y, Guo LB, Zeng DL, Hu J, Ren DY, Qian Q*, Zhu L*. Knocking Out the Gene RLS1 Induces Hypersensitivity to Oxidative Stress and Premature Leaf Senescence in Rice. *Int J Mol Sci*, 2018, 19(10):2853. (IF=3.687)
47. ZhangY†, Lv Y†, Noushin Jahan, Chen G, Ren DY, Guo LB*. Sensing of Abiotic Stress and Ionic Stress Responses in Plants. *Int J Mol Sci*, 2018, 19(11):3298. (IF=3.687)
48. Chen Z, Chen T, Atul Prakash Sathe, He YQ, Zhang XB*, Wu JL*. Identification of a novel rice semi-dominant mutant with enhanced resistance to *Xanthomonas oryzae* pv. *oryzae*. *Int J Mol Sci*, 2018, 19(12):3766. (IF=3.687)
49. Nanda S, Wan PJ*, Yuan SY, Lai FX, Wang WX and Fu Q*. Differential responses of OsMPKs in IR56 rice to two BPH populations of different virulence levels. *Int J Mol Sci*, 2018, 19(12):4030. (IF=3.687)
50. Tong XH, Wang YF, Sun AQ, BelloBK, Ni S, Zhang J*. Notched Belly Grain 4, a Novel Allele of Dwarf11, Regulates Grain Shape and Seed Germination in Rice (*Oryza sativa*L.). *Int J Mol Sci*, 2018, 19(12):4069. (IF=3.687)
51. Zhu AK†, Zhang YX†, Zhang ZH, Wang BF, Xue P, Cao YR, Chen YY, Li ZH, Liu QE, Cheng SH*, Cao LY*. Genetic Dissection of qPCG1 for a Quantitative Trait Locus for Percentage of Chalky Grain in Rice (*Oryza sativa* L.). *Front Plant Sci*, 2018, 9:1173. (IF=3.678)
52. Zhu CQ, Zhang JH, Zhu LF, Abliz B, Zhong C, Bai ZG, Hu WJ, Hussain S, James AB, Cao XC*, and Jin QY*. NH4+ facilitates iron reutilization in the cell walls of rice (*Oryza sativa*) roots under iron-deficiency conditions. *Enviro Exp Bot*, 2018, 151, 21-31. (IF=3.666)
53. Chen TT†, Feng BH†, Fu WM, Zhang CX, Tao LX* and Fu GF*. Nodes protect against drought stress in rice (*Oryza sativa*) by mediating hydraulic conductance. *Enviro Exp Bot*. 2018, 155: 411-419. (IF=3.666)
54. ZhangCX†, Feng BH†, Chen TT, Fu WM, Li HB, Li GY, Jin QY, TaoLX* and Fu GF*. Heat stress-reduced kernel weight in rice at anthesis is associated with impaired source-sink relationship and sugars allocation. *Enviro Exp Bot*, 2018, 155, 718-733. (IF=3.666)
55. Li KL†, Yuan SY†, Nanda S, Wang WX, Lai FX, Fu Q and Wan PJ*. The roles of E93 and Kr-h1 in metamorphosis of *Nilaparvata lugens*. *Front Physiol*, 2018, 9:1677. (IF=3.394)
56. Wang WX, Wan PJ, Lai FX, Zhu TH, and Fu Q*. Double-stranded RNA targeting calmodulin reveals a potential target for pest management of *Nilaparvata lugens*. *Pest Manage Sci*, 2018, 74(7):1711-1719. (IF=3.249)
57. Zhu CQ, Zhu XF, Wang C, Dong XY, Shen RF*. Nitrate inhibits the remobilization of cell wall phosphorus under phosphorus-starvation conditions in rice (*Oryza sativa*). *Planta*, 2018, 248(1):185-196.

(IF=3.249)

58. Wang DY†, Xu CM†, Ye C, Chen S, Chu G, Zhang XF*. Low recovery efficiency of basal fertilizer-N inplants does not indicate high basal fertilizer-N loss from split-applied N intransplanted rice. *Field Crops Res*, 2018, 229: 8-16. **(IF=3.127)**
59. Li ZY,Wang YF, Bello BK, Ajadi AA, Tong XH, Chang YX*, Zhang J*. Constructionof a Quantitative Acetylomic Tissue Atlas in Rice (*Oryza sativa L.*). *Molecules*, 2018, 23(11):2843. **(IF=3.098)**
60. Chen F, Dong GJ, Ma XH,Wang F, Zhang YL, Xiong EH, Wu JH, Wang HZ, Qian Q, Wu LM*, Yu YC*.UMP kinase activity is involved in proper chloroplast development in rice. *Photosynth Res*, 2018, 137(1):53-67. **(IF=3.091)**
61. Qiu ZN†, Chen DD†, He L, Zhang S,Yang ZN, Zhang Y, Wang ZW, Ren DY, Qian Q, Guo LB*, Zhu L*.The rice white green leaf 2 gene causes defects in chloroplast development and affects the plastid ribosomal protein S9. *Rice*, 2018, 11:39. **(IF=3.039)**
62. Dong Q†, ZhangZH†, Wang LL, Zhu YJ, Fan YY, Mou TM, Ma LY*, Zhuang JY*.Dissection and fine-mapping of two QTL for grain size linked in a 460-kb regionon chromosome 1 of rice. *Rice*, 2018, 11:44. **(IF=3.039)**
63. Cao XC†,Zhong C†, Zhu CQ, Zhu LF, Zhang JH, Wu LH, Jin QY*.Ammonium uptake and metabolism alleviate PEG-induced water stress inriceseedlings. *Plant Physiol Bioch*, 2018, 132:128-137. **(IF=2.718)**
64. Zhu CQ, Cao XC, Zhu LF, Hu WJ, Hu AY, Bai ZG, Zhong C, Sun LM, Liang QD, Huang J,Yang SX, Zhang JH*, and Jin QY*. Ammonium mitigates Cdtoxicity in rice (*Oryza sativa*) via putrescine-dependental terations of cell wall composition. *Plant Physiol Bioch*, 2018,132:189-201. **(IF=2.718)**
65. Wang YL,Cui YT, Hu GH, Wang XD, Chen HZ, Shi QH, Xiang J, Zhang YK, Zhu DF*,Zhang YP*. Reduced bioactive gibberellin content in rice seeds underlow temperature leads to decreased sugar consumption and low seed germination rates. *Plant Physiol Bioch*, 2018,133:1-10. **(IF=2.718)**
66. Sun ZC, Zhu YJ, Chen JY,Zhang H, Zhang ZH, Niu XJ, Fan YY, Zhuang JY*. Minor-effect QTL forheading date detected in crosses between indica rice cultivar Teqing and nearisogenic lines of IR24. *Crop J*, 2018, 6: 291–298.**(IF=2.658)**
67. Wu LJ, Xiao W, Chen GQ, Song DW, Khaskheli MA, Li P, Zhang SY, and Feng GZ*.Identification of *Pseudomonas mosselii* BS011 gene clusters required forsuspension of Rice Blast Fungus *Magnaporthe oryzae*. *J Biotechnol*, 2018, 282: 1-9. **(IF= 2.533)**
68. Wang JH,Fang YX, Tian B, Zhang XQ, Zeng DL, Guo LB, Hu J*, Xue DW*.New QTLs identified for leaf correlative traits in rice seedlings under cadmiumstress. *Plant Growth Regul*, 2018, 85(2):329-335. **(IF=2.081)**

69. Chen PT†, Hu HT†, Zhang YT, Wang ZW, Dong GJ, Cui YT, Qian Q, Ren DY*, Guo LB*. Genetic analysis and fine-mapping of a new rice mutant, white and lesion mimic leaf1. *Plant Growth Regul*, 2018, 85(3):425-435. (IF=2.081)
70. Luo RJ, Cao RJ, Jiao GA, Lv YS, Zhong M, Tang SQ, Wei XJ*, Hu PS*. The involvement of long non-coding RNAs in the formation of high-temperature-induced grain chalkiness in rice. *Plant Growth Regul*, 2018, 86(2):263-271. (IF=2.081)
71. Hussain S, Zhong C, Bai ZG, Cao XC, Zhu LF, Hussain A, Zhu CQ, Fahad S, James, Zhang JH*, Jin QY*. Effects of 1-methylcyclopropene on rice growth characteristics and superior and inferior spikelet development under salt stress. *J Plant Growth Reg*, 2018, 37: 1368-1384. (IF=2.047)
72. Luo RJ, Jiang HW, Lv YS, Hu SK, Sheng ZH, Shao GN, Tang SQ, Hu PS, Wei XJ*. Chlorophyll deficient 3, Encoding a Putative Potassium Efflux Antiporter, Affects Chloroplast Development Under High Temperature Conditions in Rice (*Oryza sativa* L.). *Plant Mol Bio Rep*, 2018, 36(4):675-684. (IF=1.844)
73. Qin YB, Cheng P, Cheng YC, Feng Y, Huang DR, Huang TX, Song XJ*, Ying JZ*. QTL-seq identified a major QTL for grain length and weight in rice using near isogenic F2 population. *Rice Sci*, 2018, 25(3):121-131. (IF=1.521)
74. Fu SZ, Yin GK, Xin X, Wu SH, Wei XH*, Lu XX*. Levels of Crotonaldehyde and 4-hydroxy-(E)-2-nonenal and Expression of Genes Encoding Carbonyl-Scavenging Enzyme at Critical Node During Rice Seed Aging. *Rice Sci*, 2018, 25(3): 152-160. (IF=1.521)
75. E ZG, Li TT, Chen C, Wang L*. Genome-Wide Survey and Expression Analysis of P 1B -ATPases in Rice. *Rice Sci*, 2018, 25(4):208-217. (IF=1.521)
76. Islam MR†, Feng BH†, Chen TT, Tao LX* and Fu GF*. Role of abscisic acid in thermal acclimation of plants. *J Plant Biolo*, 2018, 61:255-264. (IF=1.459)
77. Yang YL†, Zhang MC†, Xu Q, Feng Y, Yuan XP, Yu HY, Wang YP, Wei XH*. Exploration of genetic selection in rice leaf length and width. *Botany*, 2018, 96(4):249-256. (IF=1.178)
78. Hu DW†, Sheng ZH†, Li QL, Chen W, Wei XJ, Xie LH, Jiao GA, Shao GN, Wang JL, Tang SQ, Hu PS*. Identification of QTLs associated with cadmium concentration in rice grains. *J Integ Agr*, 2018, 17(7):1563-1573. (IF=1.042)
79. Liu SH†, Yang BJ†, Wang AY, Luo J, Tang J*. The white gene in *Nilaparvata lugens* and its expression pattern under two different survival stresses. *J Asia-Pac Entomol*, 2018, 21:701-707. (IF=0.875)
80. Hussain S, Cao XC, Zhong C, Zhu LF, Khaskheli MA, Fiaz S, Zhang JH*, Jin QY*. Sodium chloride stress during early growth stages altered physiological and growth characteristics of rice. *Chil J Agr Res*, 2018, 78(2):183-197. (IF=0.775)

81. Hu Y, Dai CG, He JC, ZhengYL Fu Q*. A Technique for Determining the Mating Status of *Chilosuppressalis* (Lepidoptera: Crambidae) Males1. *J Entomol Sci*, 2018, 53(1):11-16. (IF=0.677)
82. Wang ZZ†, Ye XQ†, Shi M†, Li F†, Wang ZH†, Zhou YN, Gu QJ, Wu XT, Yin CL, Guo DH, Hu RM, Hu NN, Chen T, Zheng BY, Zou JN, Zhan LQ, Wei SJ, Wang YP, Huang JH, Fang XD, StrandMR, Chen XX*. Parasitic insect-derived miRNAs modulate hostdevelopment. *Nat Commun*, 2018, 9(1): 2205. (IF=12.353)
83. Chen Y*†, Wang J†, Yang N, WenZY, Sun XP, Chai YR and Ma ZH*. Wheat microbiome bacteria can reduce virulenceof a plant pathogenic fungus by altering histone acetylation. *Nat Commun*, 2018, 9:3429. (IF =12.353)
84. Lu HP†, Luo T†, Fu HW†, Wang L, Tan YY, Huang JZ, Wang Q, Ye GY, Gatehouse AMR, Lou YG* and Shu QY*. Resistance of rice to insect pestsmediated by suppression of serotonin biosynthesis. *Nat Plants*, 2018, 4(6):338-344. (IF=11.471)
85. Pan PL†,Ye YX†,Lou YH, Lu JB, Cheng C, Shen Y, Moussian B, Zhang CX*. A comprehensive omics analysisand functional survey of cuticular proteins in the brown planthopper. *P Natl Acad Sci USA*, 2018, 115:5175-5138. (IF=9.504)
86. Fu S, Xu Y, Li CY, Li Y, Wu JX and Zhou XP. Rice stripe virus interferes withS-acylation of remorin and induces its autophagic degradation to facilitatevirus infection. *Mol Plant*, 2018, 11, 269-287. (IF=9.326)
87. Hu LF†, Ye M†, Kuai P, Ye MF, Erb M and Lou YG*. OsLRR-RLK1,an early responsive leucine-rich repeat receptor like kinase, initiates ricedefense responses against a chewing herbivore. *New Phytol*, 2018, 219(3):1097-1111. (IF=7.433)
88. Yin YN, Wang ZH, Cheng DN, Chen X, Chen Y and Ma ZH*.The ATP-binding protein FgArb1 is essential for penetration, infectious andnormal growth of *Fusarium graminearum*.*New Phytol*, 2018, 219: 1447–1466. (IF=7.433)
89. Tang GF†, Chen Y†, Xu JR,Kistler H. C, and Ma ZH*. The fungal myosin I is essential for *Fusarium* toxinsome formation. *PLoS Pathog*, 2018, 14(1): e1006827. (IF=6.158)
90. Lindsey ARI*, Kelkar YD, Wu X, Sun D, Martinson EO, Yan ZC, Rugman-Jones PF, Hughes DST, Murali SC, Qu JX, Dugan SN, Lee SL, Chao H, Dinh H, Y, Doddapaneni HV, Worley KC, Muzny DM, Ye GY, Gibbs RA, Richards S, Yi SV, Stouthamer R*†, Werren JH*†.Comparative genomics of the miniature wasp and pest control agent *Trichogramma pretiosum*. *BMC Biol*, 2018, 16: 54. (IF=5.77)
91. Zhu XM, Liang S, Shi HB, Lu JP, Dong B, Liao QS, Lin FC,Liu XH*. VPS9 domain-containing proteins are essential forautophagy and endocytosis in *Pyricularia oryzae*. *Environ Microbiol*, 2018,20(4):1516-1530. (IF=4.974)

92. Chen Y*, Zheng SY, Ju ZZ, Zhang CQ, Tang GF, Wang J, Wen ZY, Chen W, and Ma ZH. Contribution of peroxisomal docking machinery to mycotoxin biosynthesis, pathogenicity and pexophagy in the plant pathogenic fungus *Fusarium graminearum*. *Environ Microbiol*, 2018, 9(20):3224-3245. (IF=4.974)
93. Cao HJ, Huang PY, Yan YX, Shi YK, Dong B, Liu XH, Ye LD, Lin FC, Lu JP*. The basic helix-loop-helix transcription factor Crf1 is required for development and pathogenicity of the rice blast fungus by regulating carbohydrate and lipid metabolism. *Environ Microbiol*, 2018, 20(9):3427-3441. (IF=4.974)
94. Zheng BY, Cao LJ, Tang P, van Achterberg K, Hoffmann AA, Chen HY, Chen XX*, Wei SJ*. Gene arrangement and sequence of mitochondrial genomes yield insights into the phylogeny and evolution of bees and sphecid wasps (Hymenoptera: Apoidea). *Mol Phylogenet Evol*, 2018, 124: 1-9. (IF=4.412)
95. Shi XX†, Huang YJ†, Begum MA, Zhu MF, Li FQ, Zhang MJ, Zhou WW*, Mao CG*, Zhu ZR*. A neutral ceramidase, NICDase, is involved in the stress responses of brown planthopper, *Nilaparvata lugens* (Stål). *Sci Rep-UK*, 2018, 8:1130. (IF=4.122)
96. Wang GY†, Zhu JL, Zhou WW, Liu S, Khairul QM, Ansari NA, Zhu ZR*. Identification and expression analysis of putative chemoreception genes from *Cyrtorhinus lividipennis* (Hemiptera: Miridae) antennal transcriptome. *Sci Rep-UK*, 2018, 8:12981. (IF=4.122)
97. Chen JN, Zhou SC, Wang Y, Shi M, Chen XX*, Huang JH*. Biocontrol characteristics of the fruit fly pupal parasitoid *Trichopria drosophilae* (Hymenoptera: Diapriidae) emerging from different hosts. *Sci Rep-UK*, 2018, 8(1): 13323. (IF=4.122)
98. Xu C, Cheng JH, Lin HY, Lin CY, Gao JH, Shen ZC*. Characterization of transgenic rice expressing fusion protein Cry1Ab/Vip3A for insect resistance. *Sci Rep-UK*, 2018, 8(1):15788. (IF=4.122)
99. Zhu XM, Li L, Wu M, Liang S, Shi HB, Liu XH, Lin FC*. Current opinions on autophagy in pathogenicity of fungi. *Virulence*, 2018:1-9. (IF=3.947)
100. Li Q, Wang XX, Chen XX, Han BY*. Complete mitochondrial genome of the tea looper caterpillar, *Ectropis obliqua* (Lepidoptera: Geometridae) with a phylogenetic analysis of Geometridae. *Int J Biol Macromol*, 2018, 118:491-496. (IF=3.909)
101. Zhu JC, Tang P, Zheng BY, Wu Q, Wei SJ, Chen XX*. The first two mitochondrial genomes of the family Aphelinidae with novel gene orders and phylogenetic implications. *Int J Biol Macromol*, 2018, 118:386-396. (IF=3.909)
102. Yan ZC, Fang Q, Tian Y, Wang F, Chen XX, Werren JH, Ye GY*. Mitochondrial DNA and their nuclear copies in the parasitic wasp *Pteromaluspuparum*: A comparative analysis in Chalcidoidea. *Int J Biol Macromol*, 2019, 121:572-579. (IF=3.909)

103. Liu XL, Li JC, Xu LP, Wang Q and Lou YG*. Expressing OsMPK4Impairs Plant Growth but Enhances the Resistance of Rice to the Striped StemBorer Chilo suppressalis. *Int J Mol Sci*, 2018, 19(4): E1182. (IF=3.687)
104. Zhou PY†, Mo XC†, Wang WW, Chen X and Lou YG*. The CommonlyUsed Bactericide Bismerthiazol Promotes Rice Defenses against Herbivores. *Int J Mol Sci*, 2018, 19(5): E1271. (IF=3.687)
105. Chen L†, Cao TT†, Zhang J and Lou YG*. Overexpression of OsGID1 Enhances the Resistance of Riceto the Brown Planthopper Nilaparvatalugens. *Int J Mol Sci*, 2018, 19(9): E2744. (IF=3.687)
106. Shi YK, Wang H, Yan YX, Cao HJ, Liu XH, Lin FC, Lu JP*. Glycerol-3-Phosphate Shuttle Is Involved in Development and Virulence in theRice Blast Fungus Pyricularia oryzae. *Front Plant Sci*, 2018, 9:687. (IF=3.678)
107. Xue WH, Xu N, YuanXB, Chen HH, Zhang JL, Fu SJ, Zhang CX, Xu HJ*. CRISPR/Cas9-mediated knockout of two eye pigmentation genes in the brownplanthopper, Nilaparvata lugens (Hemiptera: Delphacidae). *Insect Biochem Molec*, 2018, 93:19-26. (IF=3.562)
108. Lu JB, Lou XM, Zhang XY, Pan PL, Zhang CX*. An ungrouped cuticular protein isessential for normal endocuticle formation in the brown planthopper. *Insect Biochem Molec*, 2018, 100:1-9. (IF=3.562)
109. Zhuo JC, Hu QL, Zhang HH, Zhang MQ, Bok JO, Zhang CX*. Identification and functionalanalysis of the doublesex gene in a hemimetabolous insect, the brownplanthopper. *Insect Biochem Molec*, 2018, 102:31-42. (IF=3.562)
110. Zhou CG, Tan YY, Gossner S, Li YF, Shu QY, Engel KH*. Stability of the metabolite signature resulting from the ossultr3;3 mutation in low phytic acid rice (*Oryza sativa* L.) seeds uponcross-breeding. *J Agr Food Chem*, 2018, 66 (35):9366-9376. (IF = 3.412)
111. Jiang YD†, Yuan X†, Zhou WW, Bai YL, Wang GY, Zhu ZR*. Cryptochromeregulates circadian locomotor rhythms in the small brown planthopper *Laodelphax striatellus* (Fallén). *Front Physiol*, 2018, 9:149. (IF=3.394)
112. Lu LN, Wu SL, Jiang J, Liang JT, Zhou XP and Wu JX*. Whole genome deep sequencing revealed host impact on populationstructure, variation and evolution of Rice stripe virus. *Virology*, 2018, 524:32-44. (IF=3.374)
113. Tian JC, Wang GW, Han HL, Romeis J, Zhang FC, Ye GY, Xie MC, Wang GY and Lu ZX. The rice planthopper parasitoid *Anagrus nilaparvatae* is not at risk when feeding on honeydewderived from *Bacillus thuringiensis*(Bt) rice. *Pest Manag Sci*, 2018, 74(8): 1854-1860. (IF=3.249)

114. Ye XQ, Shi M, HuangJH, Chen, XX*. Parasitoid polydnaviruses and immune interaction withsecondary hosts. *Dev Comp Immunol*, 2018,83:124-129. (IF=2.913)
115. Wang ZZ, Zhan LQ,Chen XX*. Two types of lysozymes from the whitefly Bemisia tabaci: Molecular characterization and functionaldiversification. *Dev Comp Immunol*, 2018, 81:252-261. (IF=2.913)
116. Wang QJ, Li JJ,Dang C, Chang XF, Fang Q, Stanley D and Ye GY*. Rice dwarf virus infectionalters green rice leafhopper host preference and feeding behavior. *PLoS ONE*, 2018, 13(9): e0203364. (IF=2.766)
117. Wang ZH, Hu RM, Ye XQ, Huang JH, Chen XX*,Shi M*. Laccase 1 gene from *Plutellaxylostella* (PxLac1) and its functions in humoral immune response. *J Insect Physiol*, 2018,107:197-203. (IF=2.733)
118. Mao LJ, Chen JJ, Xia CY, Feng XX, Kong DD, Qi ZY, Liu F,Che D, Lin FC, Zhang CL*. Identification and characterization of new Muscodorendophytes from gramineous plants in Xishuangbanna, China. *Microbiology Open*, 2018, e00666. (IF=2.682)
119. Lou YH, Pan PL, Ye YX, Chen C, Xu HJ, Zhang CX*.Identification and functional analysis of a novel chorion protein essential foregg maturation in the brown planthopper. *Insect Mol Biol*, 2018,27(3), 393–403. (IF=2.492)
120. Sun J, Wang Y, Zhang XQ, Rasmussen SK, Jiang XT,Song WJ*, Wu DX, Shu XL*. Dependence ofphysiochemical, functional and textural properties of high-resistant starch rice on endogenous nonstarch polysaccharides. *Int J Food Sci Tech*, 2018, 53(4):1079-1086. (IF=2.383)
121. Zhang MH, Chen R, Zhou XP and Wu JX*.Monoclonal antibody-based serological detection methods for Wheat dwarf virus. *Virologica Sinica*, 2018,33:162-172. (IF=2.357).
122. Kakar KU, Nawaz Z, Cui Z, Almoneafy AA, Ullah R, Shu QY*.Rhizosphere-associated Alcaligenes and Bacillus strains that induce resistance against blast and sheath blight diseases, enhance plant growth and improvemineral content in rice. *J Appl Microbiol*, 2018,124(3):779-796. (IF=2.16)
123. Amarasinghe GK, CeballosNG, Banyard AC, Basler CF, Bavari S, Bennett AJ, Blasdell KR, Briese T,Bukreyev A, Cai YY, Calisher CH, Lawson CC, Chandran K, Chapman CA, Chiu CY,Choi KS, Collins PL, Dietzgen RG, Dolja VV, Dolnik O, Domier LL, Durrwald R,Dye JM, Easton AJ, Ebihara H, Echevarria JE, Fooks AR, Formenty PBH, FouchierRAM, Freuling CM, Ghedin E, Goldberg TL, Hewson R, Horie M, Hyndman TH, JiangDH, Kityo R, Kobinger GP, Kondo H, Koonin EV, Krupovic M, Kurath G, Lamb RA,Leroy EM, Maes P, Maisner A, Marston DA, Mor SK, Muller T, Muhlberger E,Ramirez VMN, Netesov SV, Ng TFF, Nowotny N, Palacios G, Patterson JL, PaweskaJT, Payne SL, Prieto K, Rima BK, Rota P, Rubbenstroth D, Schwemmle M, SiddellS, Smithers S, Song QS, Song T, Stenglein MD, Stone DM, Takada A, Tesh RB,Thomazelli LM, Tomonaga K, Tordo N, Towner JS, Vasilakis N, Vazquez-Moron S,Verdugo C, Volchkov VE, Wahl V, Walker PJ, Wang D, Wang LF, Wellehan JFX, WileyMR, Whitfield AE,

- Wolf YI, Ye GY, Zhang YZ and Kuhn JH*. Taxonomy of the order Mononegavirales: update. *Arch Virol*, 2018, 163(8): 2283-2294. (IF=2.16)
124. Masum MM†, Liu L†, Yang M, Hossain MM, Siddiq MM, Supty ME, Ogunyemi SO, Hossain A, An QL and LiB*. Halotolerant bacteria belonging to operational group *Bacillus amyloliquefaciens* in biocontrol of the rice brown stripe pathogen *Acidovorax oryzae*. *J Appl Microbiol*, 2018, 125:1852-1867. (IF=2.16)
125. Huang LY, Wu M, Yu XY, Li L, Lin FC, Liu XH*. Physical interactions and mutational analysis of MoYpt7 in *Magnaporthe oryzae*. *J Zhejiang Univ Sci B*, 2018, 19(1):79-84. (IF=1.815)
126. Li S, Liu SM, FuHW, Huang JZ, Shu QY*. High-resolution melting-based tilling of γ-ray-induced mutations in rice. *J Zhejiang Univ Sci B*, 2018, 19(8):620-629. (IF=1.815)
127. Shi YK, Wang H, Wang J, Liu XH, Lin FC, Lu JP*. N6-methyladenosine RNA methylation is involved in virulence of the rice blastfungus *Pyricularia oryzae* (syn. *Magnaporthe oryzae*). *Fems Microbiol Lett*, 2018, 366(1):fny286. (IF=1.735)
128. Li B*, Wang XX, ChenJ, Liu H, Khattak Arif Ali, Wang YL, Qiu W and Sun GC. IcmF and DotU are required for the virulenceof *Acidovorax oryzae* strain RS-1. *Arch Microbiol*, 2018, 200:897-910. (IF=1.607)
129. Tian HW, vanAchterberg C, Chen XX*. The genera *Areopraon* Mackauer, 1959 and *Pseudopraon*Stary, 1975 (Hymenoptera, Braconidae, Aphidiinae) from China, with keys tospecies. *Zookeys*, 2018, 780:61-70. (IF=1.079)
130. Bao YY*, Zhang CX*. Recent advances inmolecular biology research of a rice pest, the brown planthopper. *J Integr Agr*, 2018, 17:60345-7. (IF=1.042)
131. Liu Z, He JH, ChenXX*. The laevigata-groupof the genus *Dolichogenidea* Mason,1981 from China, with descriptions of 26 new species. *Zootaxa*, 2018,4436(1):1-74. (IF=0.931)
132. Zhu JC, vanAchterberg C, Chen XX*. Review of the genus *Hylcalosia* Fischer (Hymenoptera, Braconidae, Alysiinae), withdescription of four new species from China. *Zootaxa*, 2018,4462(4):547-565. (IF=0.931)
133. Zhu JC, vanAchterberg C, Chen XX*. Review of the genus *Alysia* Latreille (Hymenoptera, Braconidae, Alysiinae), withdescription of six new species from China. *Zootaxa*, 2018,4500(1):1-42. (IF=0.931)
134. Tang P, vanAchterberg C, Chen XX*. Review of the genus *Earinus* Wesmael (Hymenoptera, Braconidae, Agathidinae) from China. *Zootaxa*, 2018,4504(3):345-358. (IF=0.931)
135. Li S, Liu SM, Liu YH, Tan YY, Huang JZ, Wei PC, Shu QY*. HRM-facilitated rapididentification and genotyping of mutations induced by CRISPR/Cas9 mutagenesisin rice. *Crop Breed Appl Biot*,

2018,18(2):184-191. (IF=0.806)

2017年发表

- 1.Deng YW, Zhai KR, Xie Z, Yang DY, Zhu XD,Liu JZ, Wang X, Qin P, Yang YZ, Zhang GM,Li Q, Zhang JF, Wu SQ, Joëlle M, Mao BZ,Wang ET, Xie HA, Didier Tharreau, He ZH* (2017). Epigenetic regulation of antagonistic receptors confers rice blast resistance with yield balance. *Science*,355(6328):962-965. (IF=37.205)
- 2.Wang SS†, Wu K†, Qian QT†, Liu Q, Li Q, Pan YJ, Ye YF,Liu XY, Wang J, Zhang JQ, Li S, Wu YJ, Fu XD* (2017). Non-canonical regulation of SPL transcription factors by a human OTUB1-like deubiquitinase defines a new plant type rice associated with higher grain yield. *Cell Res*, 27:1142-1156. (IF=15.606)
- 3.Zeng DL†, Tian ZX†, Rao YC, Dong GJ, Yang YL, Huang LC, LengYJ, Xu J, Sun C, Zhang GH, Hu J, Zhu L, Gao ZY, Hu XM, Guo LB, Xiong GS, Wang YH, Li JY* and Qian Q* (2017). Rational design of high-yield and superior-quality rice. *Nature Plants*,doi:10.1038/nplants.2017.31. (IF=10.3)
- 4.Duan PG†, Xu JST†, Zeng DL, Zhang BL, Geng MF,Zhang GZ, Huang K, Huang LJ, Xu R, Ge S, Qian Q, Li YH* (2017). Natural Variation in the Promoter of GSE5 Contributes to Grain Size Diversity in Rice. *Mol Plant*,10(5):685-694. (IF=8.827)
- 5.Gong JY†, Miao JST†, Zhao Y, Zhao Q, Feng Q,Zhan QL, Cheng BY, Xia JH, Huang XH*, Yang SH*, Han B* (2017). Dissecting the Genetic Basis of Grain Shape and Chalkiness Traitsin Hybrid Rice Using Multiple Collaborative Populations. *Mol Plant*,10(10):1353-1356. (IF=8.827)
- 6.Liu QE†, Ning YS†, Zhang YX†, Yu N, Zhao CD, Zhan XD, Wu WX,Chen DB, Wei XJ, Wang GL*,Cheng SH*, Cao LY* (2017). OsCUL3 a Negatively Regulates Cell Death and Immunity by Degrading OsNPR1 in Rice. *Plant Cell*, 29(2):345-359. (IF=8.688)
- 7.Ren DY†, Yu HP†, Rao YC†, Xu QK, Zhou TT, Hu J,Zhang Y, Zhang GH, Zhu L, Gao ZY, Chen G, Guo LB, Zeng DL*, Qian Q*(2017). 'Two-floret spikelet' as a novel resource has the potential to increase rice yield. *Plant Biotechnol J*, doi:10.1111/pbi.12849. (IF=7.443)
- 8.Hu XX†,Meng XB†, Liu Q, Li JY*, Wang KJ* (2017). Increasing the efficiency of CRISPR-Cas9-VQR precise genome editing in rice. *Plant Biotechnol J*, DOI:10.1111/pbi.12771 . (IF=7.443)
- 9.Kou YJ, Tan YH, Ravikrishna Ramanujam, Naweed I Naqvi* (2017). Structure-function analyses of the Pth11 receptor reveal an important role for CFEM motif and redox regulationin rice blast. *New Phytol*, 214(1):330-342.(IF=7.33)

- 10.Leng YJ[†], Yang YL[†], Ren DY[†], Huang LC, Dai LP, Wang YQ, Chen L, Tu ZJ, Gao YH, Li XY, Zhu L, Hu J, Zhang GH, Gao ZY, Guo LB, Kong ZS, Lin YJ, Qian Q^{*}, Zeng DL^{*} (2017). A Rice *PECTATE LYASE-LIKE* Gene Is Required for Plant Growth and Leaf Senescence. *Plant Physiol*, 174(2):1151-1166. (IF=6.456)
- 11.Xu YH[†], Julien Sechet[†], Wu YB[†], Fu YP, Zhu LF, Li JC, Zhang YP, Emilie Gineau, Cyril Gaertner, Zhou J, Fan XR, Liu Y, Zhou L, Grégory Mouille^{*}, Lin XC^{*} (2017). Rice Sucrose Partitioning Mediated by a Putative Pectin Methyltransferase and HomogalacturonanMethylesterification. *Plant Physiol*, 174(3):1595-1608. (IF=6.456)
- 12.Lu YS[†], Shao GN[†], Qiu JH, Jiao GA, Sheng ZH, Xie LH, Wu YW, Tang SQ, Wei XJ^{*}, Hu PS^{*} (2017). *White Leaf and Panicle 2*, encoding a PEP-associated protein, is required for chloroplast biogenesis under heat stress in rice. *J Exp Bot*, 68(18):5147-5160. (IF=5.830)
- 13.Ma QX[†], Cao XC[†], Xie YN, Gu Y, Feng Y, Mi WH, Yang X, Wu LH^{*} (2017). Effect of pH on the uptake and metabolism of glycine in pak choi (*Brassica chinensis* L.). *Environ Exp Bot*, 133:139-150. (IF=4.369)
- 14.Ma QX[†], Cao XC[†], Tan XL, Si LL, Wu LH^{*} (2017). Effects of cadmium stress on pakchoi (*Brassica chinensis* L.) growth and uptake of inorganic and organic nitrogenous compounds. *Environ Exp Bot*, 137:49-57. (IF=4.369)
- 15.Zhao X[†], Chen TT[†], Feng BH, Zhang CX, Peng SB, Zhang XF, Fu GF^{*}, Tao LX^{*} (2017). Non-photochemical quenching plays a key role in light acclimation of rice plants differing in leaf color. *Front Plant Sci*, 7:1968. (IF=4.298)
- 16.Yu HP[†], Ruan BP[†], Wang ZW[†], Ren DY^{*}, Zhang Y, Leng YJ, Zeng DL, Hu J, Zhang GH, Zhu L, Gao ZY, Chen G, Guo LB, Chen WF^{*}, Qian Q^{*} (2017). Fine Mapping of a Novel *defective glume 1 (dg1)* Mutant, Which Affects Vegetative and Spikelet Development in Rice. *Front Plant Sci*, 8:486. (IF=4.298)
- 17.Hou YX[†], Qiu JH[†], Wang YF, Li ZY, Zhao J, Tong XH, Lin HY, Zhang J^{*} (2017). A Quantitative Proteomic Analysis of Brassinosteroid-induced Protein Phosphorylation in Rice (*Oryza sativa* L.). *Front Plant Sci*, 8:514. (IF=4.298)
- 18.Zhang MC[†], Lu Q[†], Wu W, Niu XJ, Wang CH, Feng Y, Xu Q, Wang S, Yuan XP, Yu HY, Wang YP, Wei XH^{*} (2017). Association Mapping Reveals Novel Genetic Loci Contributing to Flooding Tolerance during Germination in *Indica* Rice. *Front Plant Sci*, 8:678. (IF=4.298)
- 19.Zhong C[†], Cao XC[†], Hu JJ, Zhu LF, Zhang JH, Huang JL, Jin QY^{*} (2017). Nitrogen Metabolism in Adaptation of Photosynthesis to Water Stress in Rice Grown under Different Nitrogen Levels. *Front Plant*

***Sci*, 8:1079. (IF=4.298)**

20.Zeng YH, Zhang YP^{*}, Xiang J, Norman T.Uphoff, Pan XH, Zhu DF^{*} (2017). Effects of Low Temperature Stress on Spikelet-Related Parameters during Anthesis in Indica-Japonica Hybrid Rice. ***Front Plant Sci***, 8:1350. (IF=4.298)

21.Zheng ZG, Yang XM, Fu YP, Zhu LF, Wei HT, Lin XC^{*} (2017). Over expression of *PvPin1*, a Bamboo Homolog of *PIN1*-Type *Parvulin 1*, Delays Flowering Time in Transgenic *Arabidopsis* and Rice. ***Front Plant Sci***, 8:1526.(IF=4.298)

22.Zhang PP[†], Zhang YX[†], Sun LP, Sittipun Sinumporn, Yang ZF, SunB, Xuan DD, Li ZH, Yu P, Wu WX, Wang KJ, Cao LY^{*}, Cheng SH^{*} (2017). The Rice AAA-ATPase OsFIGNL1 Is Essential for Male Meiosis. ***Front Plant Sci***, 8:1639. (IF=4.298)

23.Chen G[†], Liu CL[†], Gao ZY, Zhang Y, Jiang HZ, Zhu L, Ren DY, YuL, Xu GH^{*}, Qian Q^{*} (2017). *OsHAK1*, a High-Affinity Potassium Transporter, Positively Regulates Responses to Drought Stress in Rice. ***Front Plant Sci***, 8:1885. (IF=4.298)

24.Li SF[†], Wei XJ[†], Ren YL, Qiu JH, Jiao GA, Guo XP, Tang SQ, Wan JM*, Hu PS* (2017). *OsBT1* encodes an ADP-glucose transporter involved in starch synthesis and compound granule formation in rice endosperm. ***Sci Rep-UK***, 7:40124. (IF=4.259)

25.Wan PJ^{*}, Tang YH, Yuan SY, He JC, Wang WX, Lai FX, Fu Q^{*} (2017). Reference genes for quantitative real-time PCR analysis in symbiont *Entomomycesdelphacidicola* of *Nilaparvata lugens* (Stål). ***Sci Rep-UK***, 7:42206. (IF=4.259)

26.Zhang YX[†], Zhou LY[†], Shen XH, Chen DB, Wu WX, Zhan XD, Liu QE,Zhu AK, Lou XY, Xu HM, Cheng SH^{*}, Cao LY^{*} (2017). Genetic dissection of yield traits in super hybrid rice Xieyou 9308 using both unconditional and conditional genome-wide association mapping. ***Sci Rep-UK***, 7:824. (IF=4.259)

27.Guo L, Qiu FL, Harish Gandhi, Suresh Kadaru, Erik Jon De Asis, Zhuang JY^{*}, Xie FM^{*} (2017). Genome-wide association study of outcrossing in cytoplasmic male sterile lines of rice. ***Sci Rep-UK***, 7:3223. (IF=4.259)

28.Ge CW[†], Wang L[†], Ye WJ, Wu LW, Cui YT, Chen P, Pan JJ, Zhang D, Hu J, Zeng DL, Dong GJ, Qian Q, Guo LB^{*}, Xue DW^{*} (2017). Single-point Mutation of an Histidine-aspartic Domain-containing Gene involving in Chloroplast Ribosome Biogenesis Leads to White Fine Stripe Leaf in Rice. ***Sci Rep-UK***, 7:3298. (IF=4.259)

- 29.Zhu YJ[†], Fan YY[†], Wang K, Huang DR, Liu WZ, Ying JZ, Zhuang JY^{*}(2017). *Rice Flowering Locus T1* plays an important role in heading date influencing yield traits in rice. ***Sci Rep-UK***, 7:4918. (IF=4.259)
- 30.Zhang XQ[†], Jiang H[†], Wang H, Cui J, Wang JH, Hu J, Guo LB, QianQ^{*}, Xue DW^{*} (2017). Transcriptome Analysis of Rice Seedling Roots in Response to Potassium Deficiency. ***Sci Rep-UK***,7:5523. (IF=4.259)
- 31.Chen H[†], Luo J[†], Zheng P, Zhang XB, Zhang CC, Li XY, Wang MG, HuangYQ, Liu XJ, Mehmood Jan, Liu YJ, Hu PS^{*}, Tu JM^{*} (2017). Application of Cre-lox gene switch to limit the Cry expression in rice green tissues. ***Sci Rep-UK***, 7:14505. (IF=4.259)
- 32.Liu CL,Chen G, Li YY, Peng YL,Zhang AP, Hong K, Jiang HZ, Ruan BP, Zhang B, Yang SL, Gao ZY^{*}, Qian Q^{*} (2017). Characterization of a major QTL for manganese accumulation in rice grain. ***Sci Rep-UK***, 7:17704. (IF=4.259)
- 33.Hu XX[†], Wang C[†], Liu Q, Fu YP, Wang KJ^{*}(2017). Targeted mutagenesis in riceusing CRISPR-Cpf1 system. ***J Genet Genomics***, 44(1):71-73. (IF=4.051)
- 34.Hua YF[†], Wang C[†], Huang J[†],Wang KJ^{*} (2017). A simple and efficient method for CRISPR/Cas9-induced mutant screening. ***J Genet Genomics***, 44(4):207-213. (IF=4.051)
- 35.Ma QX, Cao XC, Xie YN, Xiao H, Tan XL, Wu LH^{*} (2017). Effects of glucoseon the uptake and metabolism of glycine in pakchoi (*Brassica chinensis*L.) exposed to various nitrogen sources. ***BMC Plant Biol***, 17:58. (IF=3.964)
- 36.Wei XJ[†],Jiao GA[†], Lin HY, Sheng ZH, Shao GN, Xie LH, Tang SQ, Xu QG^{*},Hu PS^{*}(2017). *GRAIN INCOMPLETEFILLING* 2 regulates grain filling and starch synthesis during rice caryopsis development. ***J Integr Plant Biol***, 59(2):134-153. (IF=3.962)
- 37.Wei XJ[†], Song XW[†], Wei LY[†], Tang SQ, Sun J, Hu PS^{*},Cao XF^{*} (2017). An epiallele of rice *AK1* affects photosynthetic capacity. ***J Integr Plant Biol***, 59(3):158-163. (IF=3.962)
- 38.Ma QX[†], Cao XC[†], Ma JZ, Tan XL, Xie YN, Xiao H, Wu LH^{*} (2017). Hexavalent chromiumstress enhances the uptake of nitrate but reduces the uptake of ammonium and glycine in pak choi (*Brassica chinensis* L.). ***Ecotox Environ Saf***, 139:384-393. (IF=3.743)
- 39.Zhou FY^{†*}, Zhang Y[†], Tang W, Wang M, Gao TC (2017). Transcriptomic sanalysis of the flowering regulatory genes involved in the herbicide resistance of Asia minor bluegrass (*Polypogon fugax*). ***BMC Genomics***, 18:953.(IF=3.729)

40. Mei JS[†], Li FF[†], Liu XR, Hu GC, Fu YP, Liu WZ^{*} (2017). Newly identified *CSP41b* gene localized in chloroplasts affects leaf color in rice. *Plant Sci*, 256:39-45. (IF=3.437)
41. Bi ZZ[†], Zhang YX[†], Wu WX, Zhan XD, Yu N, Xu TT, Liu QN, Li Z, Shen XH, Chen DB, Cheng SH^{*}, Cao LY^{*} (2017). *ES7*, encoding a ferredoxin-dependent glutamate synthase, functions in nitrogen metabolism and impacts leaf senescence in rice. *Plant Sci*, 259:24-34. (IF=3.437)
42. Wu WX[†], Zheng XM[†], Chen DB, Zhang YX, Ma WW, Zhang H, Sun LP, Yang ZF, Zhao CD, Zhan XD, Shen XH, Yu P, Fu YP, Zhu SS, Cao LY^{*}, Cheng SH^{*} (2017). *OsCOL16*, encoding a CONSTANS-like protein, represses flowering by up-regulating *Ghd7* expression in rice. *Plant Sci*, 260:60-69. (IF=3.437)
43. Qian WJ[†], Wu C[†], Fu YP, Hu GC, He ZQ^{*}, Liu WZ^{*} (2017). Novel rice mutants overexpressing the brassinosteroid catabolic gene *CYP734A4*. *Plant Mol Biol*, 93(1):197-208. (IF=3.356)
44. Wang YF, Tong XH, Qiu JH, Li ZY, Zhao J, Hou YX, Tang LQ, Zhang J^{*} (2017). A phosphoproteomic landscape of rice (*Oryza sativa*) tissues. *Physiol Plantarum*, 160(3):458-475. (IF=3.330)
45. Qiu JH[†], Hou YX[†], Wang YF, Li ZY, Zhao J, Tong XH, Lin HY, Wei XJ, Ao HJ, Zhang J^{*} (2017). A Comprehensive Proteomic Survey of ABA-Induced Protein Phosphorylation in Rice (*Oryza sativa* L.). *Int J Mol Sci*, 18:60. (IF=3.226)
46. Wang YF, Hou YX, Qiu JH, Li ZY, Zhao J, Tong XH, Zhang J^{*} (2017). A Quantitative Acetylomic Analysis of Early Seed Development in Rice (*Oryza sativa* L.). *Int J Mol Sci*, 18:1376. (IF=3.226)
47. Zhong M, Li SF, Huang FL, Qiu JH, Zhang J, Sheng ZH, Tang SQ, Wei XJ^{*}, Hu PS^{*} (2017). The Phosphoproteomic Response of Rice Seedlings to Cadmium Stress. *Int J Mol Sci*, 18:2055. (IF=3.226)
48. Leng YJ, Ye GY^{*}, Zeng DL^{*} (2017). Genetic Dissection of Leaf Senescence in Rice. *Int J Mol Sci*, 18(12):2686. (IF=3.226)
49. Xiang J[†], Wu H[†], Zhang YP, Zhang YK, Wang YF, Li ZY, Lin HY, Chen HZ^{*}, Zhang J^{*}, Zhu DF^{*} (2017). Transcriptomic Analysis of Gibberellin- and Paclobutrazol-Treated Rice Seedlings under Submergence. *Int J Mol Sci*, 18(10):2225. (IF=3.226)
50. Zeng YX[†], Shi JS[†], Ji ZJ, Wen ZH, Liang Y, Yang CD^{*} (2017). Genotype by Environment Interaction: The Greatest Obstacle in Precise Determination of Rice Sheath Blight Resistance in the Field. *Plant Dis*, 101(10):1795-1801. (IF=3.173)

- 51.Wang DY[†], Xu CM[†], Yan JX, Zhang XG, Chen S, BhagirathS. Chauhan, Wang L, Zhang XF^{*}(2017). ¹⁵N tracer-based analysis of genotypic differences in the uptake and partitioning of N applied at different growth stages in transplanted rice. *Field Crop Res*, 211:27-36. (**IF=3.048**)
- 52.Niu YF[†], Ye CY, He J, Han F, Guo LB,Zheng HF^{*}, Chen GB^{†*}(2017). Reproduction and In-Depth Evaluation of Genome-Wide Association Studies and Genome-Wide Meta-analyses Using Summary Statistics. *g3-Genes Genom Ge*, 7(3):943-952. (**IF=2.861**)
- 53.Wang WX, Li KL, Wan PJ, Lai FX, Fu Q^{*}, Zhu TH^{*} (2017). Ras-like family small GTPases genes in *Nilaparvata lugens*: Identification, phylogenetic analysis, gene expression and function in nymphal development. *Plos One*, 12(2):DOI:10.1371/journal.pone.0172701. (**IF=2.806**)
- 54.Ying JZ[†], Zhao J[†], Hou YX, Wang YF, Qiu JH,Li ZY, Tong XH, Shi ZM, Zhu J, Zhang J^{*} (2017). Mapping the N-linked glycosites of rice (*Oryza sativa L.*) germinating embryos. *Plos One*, 12(3):DOI:10.1371/journal. pone. 0173853. (**IF=2.806**)
- 55.He JW[†], Shao GN[†], Wei XJ, Huang FL, Sheng ZH,Tang SQ, Hu PS^{*} (2017). Fine mapping and candidategene analysis of *qTAC8*, a major quantitative trait locus controlling tiller angle in rice (*Oryza sativa L.*). *Plos One*, 12(5): DOI:10.1371/journal.pone.0178177. (**IF=2.806**)
- 56.Zeng YX[†], Shi JS[†], Ji ZJ, Wen ZH, Liang Y,Yang CD^{*}(2017). Combination of twelve alleles at six quantitative trait loci determines grain weight in rice. *Plos One*, 12(7):DOI: 10.1371/journal.pone.0181588. (**IF=2.806**)
- 57.Sheng ZH[†], Lv YS[†], Li W, Luo RJ, Wei XJ, XieLH, Jiao GA, Shao GN, Wang JL, Tang SQ^{*}, Hu PS^{*} (2017). *Yellow-Leaf 1* encodes amagnesium-protoporphyrin IX monomethyl ester cyclase, involved in chlorophyll biosynthesis in rice (*Oryza sativa L.*). *Plos One*, 12(5):doi.org/10.1371/journal.pone.0177989. (**IF=2.806**)
- 58.Zhang YK, Chen HZ, Zhang YP, Xiang J, Ji GM, Zhu DF^{*} (2017). Root morphology in responseto nitrogen supply in mid-season *indica* rice cultivars released indifferent decades. *Sci China Life Sci*, 60(4):439-442. (**IF=2.781**)
- 59.Shen L[†], Hua YF[†], Fu YP[†], Li J[†], Liu Q, Jiao XZ, Xin GW,Wang JJ, Wang XC, Yan CJ^{*}, Wang KJ^{*} (2017). Rapid generation of genetic diversity by multiplex CRISPR/Cas9 genome editing in rice. *Sci China Life Sci*, 60(5):506-515. (**IF=2.781**)
- 60.Cao XC[†], Zhong C[†], Zhu LF, Zhang JH, Sajid Hussain, Wu LH, Jin QY^{*}(2017). Glycine increases cold tolerance in rice via the regulation of N uptake, physiological characteristics, and photosynthesis. *Plant*

***Physiol Bio*, 112:251-260. (IF=2.724)**

- 61.Wang YF[†], Lin HY[†], Tong XH, Hou YX, Chang YX,Zhang J^{*}(2017). DNA demethylation activates genes in seed maternal integument development in rice (*Oryza sativa L.*). ***Plant Physiol Bio***,120:169-178. **(IF=2.724)**
- 62.Su Y, Hu SK, Zhang B, Ye WJ, Niu YF, Guo LB^{*}, Qian Q^{*}(2017). Characterization and fine mapping of a new early leaf senescence mutant es3(t) in rice. ***Plant Growth Regu***, 81:419-431. **(IF=2.646)**
- 63.Xu JT[†], Wang LT[†], Zhou MY, Zeng DL, Hu J,Zhu L, Ren DY, Dong GJ, Gao ZY, Guo LB, Qian Q^{*}, Zhang WZ^{*}, Zhang GH^{*}(2017). *Narrow albino leaf 1* is allelic to *CHR729*, regulates leaf morphogenesis and development by affecting auxin metabolism in rice. ***Plant Growth Regu***, 82:175-186. **(IF=2.646)**
- 64.Yu HP, Qiu ZN, Xu QK, Wang ZW, Zeng DL, Hu J, Zhang GH, Zhu L, Gao ZY, Chen G, Guo LB, Qian Q^{*}, Ren DY^{*}(2017). Fine mapping of *LOW TILLER 1*, a gene controlling tillering and panicle branching in rice. ***Plant Growth Regu***, 83:93-104. **(IF=2.646)**
- 65.Zhang CX[†], Feng BH[†], Chen TT, Zhang XF, Tao LX^{*},Fu GF^{*} (2017). Sugars, antioxidant enzymes and IAA mediate salicylic acid to prevent rice spikelet degeneration caused by heat stress. ***Plant Growth Regu***, 83:313-323. **(IF=2.646)**
- 66.Wu LJ, Chen GQ, Feng GZ^{*} (2017). Complete genome sequence of *Streptomyces griseochromogenes* ATCC 14511T, a producer of nucleoside compounds and diverse secondary metabolites. ***J Biotechnol***, 249:16-19. **(IF=2.599)**
- 67.Liu RF[†], Zhang YT[†], Chen PT[†], Lin HY, Ye GY, Wang ZW, GeCW, Zhu B^{*}, Ren DY^{*} (2017). Genomic and phenotypic analyses of *Pseudomonas psychrotolerans* PRS08-11306 reveal a turnerbactin biosynthesis gene cluster that contributes tonitrogen fixation. ***J Biotechnol***, 253:10-13. **(IF=2.599)**
- 68.Zhang JH, Hussain S, Zhao FT, Zhu LF, Cao XC, Yu SM, Jin QY^{*}(2017). Effects of *Azospirillumbrasilense* and *Pseudomonas fluorescens* on nitrogen transformation and enzyme activity in the rice rhizosphere. ***J Soil Sediment***, doi.org/10.1007/s11368-017-1861-7. **(IF=2.522)**
- 69.Zhang PT^{*}, Zhong KZ[†], Zhong ZZ, Tong HH^{*} (2017). Identifying aluminum tolerance in rice with a molecular marker. ***Mol Breeding***, 37:1-4. **(IF=2.465)**
- 70.Chen GQ[†], Fang YT[†], Wu LJ, Yan Q, Peter J.Krell, Feng GZ^{*} (2017). A betabaculovirus DNA polymerase cannot substitute for the DNA polymerase of the alphabaculovirus *Autographa californica*

nucleo polyhedrovirus. *Arch Virol*, 162(11):3487-3492. (IF=2.058)

71.Liu SH[†], Luo J[†], Yang BJ, Wang AY and Tang J^{*}(2017). *karmoisin* and *cardinal*ortholog genes participate in the ommochrome synthesis of *Nilaparvata lugens*(Hemiptera:Delphacidae). *Insect sci*, Doi: 10.1111/1744-7917. 12501. (IF=2.026)

72.Tang W, Chen J, Zhang JP, Lu YL^{*}(2017). Seed Germination, Seedling Emergence, and Response to Herbicides of Triquetrous Murdannia (*Murdannia triquetra*) in Rice. *Weed Sci*, 65(1):141-150. (IF=1.862)

73.Zhang AP[†], Liu CL[†], Chen G, Hong K, Gao Y,Tian P, Peng YL, Zhang B, Ruan BU, Jiang HZ, Guo LB, Qian Q, Gao ZY^{*}(2017). Genetic analysis for rice seedling vigor and fine mapping of a major QTL *qSSL1b* for seedling shoot length. *Breeding Sci*, 67(3):307-315. (IF=1.792)

74.Zhang JP, Fu F, Liu C, Lin ZX, Wang YY, Ye CY, Lu YL^{*}(2017). Chloroplast DNA markers for *Echinochloataxa*. *Weed Res*, 57:355-360. (IF=1.782)

75.Wang WX, Zhu TH, Li KL, Chen LF, Lai FX^{*}, Fu Q^{*}(2017). Molecular characterization, expression analysis and RNAi knock-down of elongation factor 1 α and 1 γ from *Nilaparvatalugens* and its yeast-like symbiont. *B Entomol Res*,107:303-312. (IF=1.758)

76.Chen TT[†], Zhao X[†], Zhang CX, Yang YJ, Feng BH,Zhang XF, Fu GF^{*}, Tao LX^{*}(2017). Application of Salicylic Acid Improves Filling of Inferior Grains of Rice during Late Maturity under Mild Cold Stress. *Crop Sci*, 57:1-13. (IF=1.629)

77.Sheng ZH[†], Li QL[†], Li W, Chen W, Wei X, Xie LH,Jiao GA, Shao GN, Wang JL, Tang SQ^{*}, Hu PS^{*} (2017). Identification of a three-base deletion in the *Pi2* locus, and development of functional marker for marker-assisted resistance election. *Euphytica*, 213:302. (IF=1.626)

78.Tondi Yacouba Nassirou, He WC, Chen CJ, Adedze Y. M. Nevame, Athanase Nsabiyumva, Dong XL, Yin YL, Rao QQ, Zhou W, Shi H, Zhao WB, Jin DM^{*}(2017). Identification of inter specific heterotic loci associated with agronomic traits in rice introgression lines carrying genomic fragments of *Oryza glaberrima*. *Euphytica*, 213:176. (IF=1.626)

79.Zhang M[†], Zhang HL[†], Dai DQ, Li XM, Chen JY,Bao JS^{*}, Ma LY^{*}(2017). Identification of QTLs for rice flower opening time in two environments. *Euphytica*, 213:181. (IF=1.626)

80.Y.M.N.Adedze, Wei XJ, Sheng ZH, Jiao GA, Tang SQ^{*}, Hu PS^{*} (2017). Characterization of a rice *dwarf and narrow leaf 2* mutant. *Biol Plantarum*, 61(1):85-94. (IF=1.551)

- 81.Yuan SY, Li GQ^{*}, Wan PJ^{*}, Fu Q, Lai FX and Mu LL(2017). Knockdown of a putative argininosuccinate lyase gene reduces arginine content and impairs nymphal development in *Nilaparvata lugens*. **Arch Insect Biochem Physiol**, 95(1): e21385. (IF=1.530)
- 82.He Y, Shi YF, Zhang XB, Wang HM, Xu X, Wu JL^{*}(2017). Identification of a Gravitropism-Deficient Mutant in Rice. **Rice Science**, 24(2):109-118. (IF=1.521)
- 83.Liang Y, Yan BY, Peng YL, Ji ZJ, Zeng YX, Wu HL, Yang CD^{*}(2017). Molecular Screening of Blast Resistance Genes in Rice Germplasms Resistant to Magnaporthe oryzae. **Rice Science**, 24(1):41-47. (IF=1.521)
- 84.Cao XC[†], Zhong C[†], Ma QX, Zhu LF, Zhang JH, Jin QY^{*}, Wu LH^{*}, Zhu YH (2017). Concentration and composition of soil amino compounds in major Chinese croplands. **Chem Ecol**, 33(2):156-170. (IF=1.463)
- 85.Ruan BP[†], Gao ZY[†], Zhao J, Zhang B, Zhang AP, Hong K, Yang SL, Jiang HZ, Liu CL, Chen G, Peng YL, Dong GJ, Guo LB, Xu ZJ, Qian Q^{*}(2017). The rice *YGL* gene encoding an Mg²⁺-chelatase ChID subunit is affected by temperature for chlorophyll biosynthesis. **J Plant Biol**, 60(4):314-321.(IF=1.437)
- 86.Cao XC^{†*}, Zhong C[†], Hussain Sajid, Zhu LF, Zhang JH, Wu LH, Jin QY^{*}(2017). Effects of watering regime and nitrogen application rate on the photo synthetic parameters, physiological characteristics, and agronomic traits of rice. **Acta Physiol Plant**, 39:135. (IF=1.364)
87. Zhao X, Feng BH, Chen TT, Zhang CX, Tao LX^{*}, Fu GF^{*}(2017). Transcriptome analysis of pale green leaf rice reveals photosynthetic regulatory pathways. **Acta Physiol Plant**, 39:274. (IF=1.364)
88. Xie LH[†], Tang SQ[†], Luo J, Wei XJ, Shao GN, Jiao GA, Sheng ZH, Hu PS^{*} (2017). Physicochemical properties of rice starch for production of vermicelli with premium quality. **J Food Sci Technol**, 54(12):3928-3935. (IF=1.262)
89. Chen X, Li GQ^{*}, Wan PJ^{*} and Fu Q(2017). Efficient RNA interference for three neuronally-expressed genes in *Nilaparvata lugens* (Stål) (Hemiptera: Delphacidae). **J Asia-Pac Entomol**, 20(2): 513-519. (IF=1.046)
90. Liu SH[†], Wang AY[†], Yang BJ, Luo J, Tang J^{*}(2017). Knockdown of an ABC transporter leads to bright red eyes in the brown planthopper, *Nilaparvatalugens* (Stål) (Hemiptera: Delphacidae). **J Asia-Pac Entomol**, 20: 421-428. (IF=1.046)
91. Wang Z[†], Chen JY[†], Zhu YJ, Fan YY, Zhuang JY^{*}(2017). Validation of *qGS10*, a quantitative trait locus for grain size on the long arm of chromosome 10 in rice (*Oryza sativa* L.). **J Integr Agr**, 16(1): 16-26. (IF=1.042)

- 92.Yao Q, Chen GT, Wang Z, Zhang C, Yang BJ, Tang J^{*} (2017). Automated detection and identification of white-backed planthoppers in paddy fields using image processing. *J Integr Agr*,16(7): 1547-1557. (IF=1.042)
93. Sajid Hussain, Zhang JH^{*},Zhong C, Zhu LF, Cao XC, Yu SM, Allen Bohr James, Hu JJ, Jin QY^{*} (2017). Effects of salt stress on rice growth and development characteristics and the regulating ways: A review. *J Integr Agr*, 16(11):2357-2374. (IF=1.042)
94. Cao XC, Wu LH^{*}, Ma QX, Yuan L, ZhuYH, Jin QY (2017). Effects of nitrogen rate and nitrogen form on glycine uptake by pakchoi (*Brassica chinensis* L.) understerile culture. *J Plant Nutri*, 40(4):476-485. (IF=0.618)

2016年发表

- 1.Huang XH^{†*}, Yang SH[†], Gong JY[†], Zhao Q,Feng Q, Zhan QF, Zhao Y, Li WJ, Cheng BY, Xia JH, Chen N, Huang T, Zhang L, Fan DL, Chen JY, Zhou CC, Lu YQ, Weng QJ, Han B^{*}(2016). Genomicarchitecture of heterosis for field traits in rice. *Nature*, 2016,537:629-633. (IF=38.138)
- 2.Zhou HJ, Wang LJ, Liu GF,Meng XB, Jing YH, Shu XL, Kong XL, Sun J, Yu H, Smith SM, Wu DX^{*}, LiJY^{*} (2016). Critical roles of soluble starch synthase SSIIIa andgranule-bound starch synthase Waxy in synthesizing resistant starch in rice. *P Natl Acad Sci USA*, DOI:10.1073/pnas.1615104113. (IF=9.423)
- 3.Zhu B[†], Ibrahim M[†], Cui ZQ, Xie GL, Jin GL, KubeM, Li B^{*}, Zhou XP^{*} (2016). Multi-omics analysis of nichespecificity provides new insights into ecological adaptation in bacteria. *ISME J*, 10(8):2072-2075. (IF=9.328)
- 4.Jackson AO, Li ZH^{*} (2016). Developmentsin plant negative-strand RNA virus reverse genetics. *Annu Rev Phytopathol*, 54:469-498. (IF=9.308)
- 5.Qi YX[†], Huang JT^{*},Li MQ, Wu YS, Xia RY, Ye GY^{*} (2016). Serotoninmodulates insect hemocyte phagocytosis via two different serotonin receptors. *eLife*, 5:e12241. (IF=8.303)
- 6.Qian Q, Guo LB, Steven SM^{*}, Li JY^{*} (2016). Breeding high-yield superior quality hybrid super rice by rational design. *Natl Sci Rev*, 3(3):283-294. (IF=8)
- 7.Zhao HJ[†], Frank T[†],Tan YY[†], Zhou CG, Jabnoune M, Bulak AA, Cui HR, Huang JZ, HeZH, Yves P^{*}, Engel KH^{*} , Shu QY^{*} (2016). Disruptionof OsSULTR3:3 reduces phytate andphosphorus concentrations and alters the metabolite profile in rice grains. *New Phytol*, 211:926-939. (IF=7.21)

- 8.Cao HJ[†], Huang PY[†], Zhang LL, Shi YK, Sun DD, Yan YX, Liu XH, Dong B, Chen GQ, Snyder JH, Lin FC,Lu JP^{*} (2016). Characterization of 47Cys2-His2 zinc finger proteins required for the development and pathogenicity of the rice blast fungus *Magnaporthe oryzae*. *New Phytol*, 211:1035-1051. (IF=7.21)
- 9.Shen QT, Hu T, Bao M, Cao LG, Zhang HW, Song FM, Xie Q, Zhou XP^{*} (2016). Tobacco RING E3 ligase NtRFP1 mediate sububiquitination and proteasomal degradation of a geminivirus-encoded βC1. *Mol Plant*, 9(6):911-925. (IF=7.142)
- 10.Hu XX[†], Wang CT[†], Fu YP[†],Liu Q, Jiao XZ, Wang KJ^{*} (2016). Expanding the Range of CRISPR/Cas9 Genome Editing in Rice. *Mol Plant*,9(6): 943-945. (IF=7.142)
- 11.Wu LW[†], Ren DY[†], Hu SK[†], Li GM[†], Dong GJ, Jiang L, Hu XM, Ye WJ,Cui YT, Zhu L, Hu J, Zhang GH, Gao ZY, Zeng DL, Qian Q^{*}, Guo LB^{*}(2016). Down-regulation of a nicotinate phosphoribosyl transferase gene, *OsNaPRT1*, leads to withered leaf tips. *Plant Physiol*, 171(2): 1085-1098. (IF=6.28)
- 12.Shi HB[†], Chen GQ[†],Chen YP, Dong B, Lu JP, Liu XH^{*}, Lin FC^{*} (2016). MoRad6-mediated ubiquitination pathways areessential for development and pathogenicity in *Magnaporthe oryzae*. *Environ Microbiol*, 18(11):4170-4187. (IF=5.932)
- 13.Chen F[†], Dong GJ[†], Wu LM[†], Wang F, YangXZ, Ma XH, Wang HL, Wu JH, Zhang YL, Wang HZ, Qian Q^{*}, Yu YC^{*} (2016).A nucleus-encoded chloroplast protein YL1 is involved in chloroplast development and efficient biogenesis of chloroplast ATP synthase in rice. *Sci Rep-UK*, DOI: 10.1038/srep32295. (IF=5.228)
- 14.Zhou LY, Liu SY, Wu WX, Chen DB, Zhan XD, Zhu AK,Zhang YX, Cheng SH, Cao LY, Lou XY, Xu HM^{*} (2016). Dissectionof genetic architecture of rice plant height and heading date bymultiple-strategy-based association studies. *Sci Rep-UK*, 6(29718):1-10. (IF=5.228) (参与)
- 15.Li B^{*†}, Ge MY[†], Zhang Y, Wang L,Ibrahim M, Wang YL, Sun GC, Chen GY^{*} (2016). Newinsights into virulence mechanisms of rice pathogen Acidovorax avenae subspavenae strain RS-1 following exposure to beta-lactam antibiotics. *Sci Rep-UK*, 6:22241. (IF=5.228)
- 16.Ma QX[†], Cao XC[†], Wu LH^{*}, Mi WH, Feng Y (2016). Light intensity affects the uptake andmetabolism of glycine by pakchoi (*Brassica chinensis* L.). *Sci Rep-UK*, 6, 21200. (IF=5.228)
- 17.Xie L, Shang WN, Liu CK, Zhang QF, Sunter G, Hong J^{*}, Zhou XP^{*}(2016). Mutual association of broad bean wilt virus 2 VP37-derivedtubules and plasmodesmata obtained from cytological observation. *Sci Rep-UK*, 6:21552. (IF=5.228)

- 18.Su X[†], Fu S[†], Qian YJ, Zhang LQ, Xu Y^{*}, Zhou XP^{*} (2016). Discovery and small RNA profile of pecan mosaic-associatedvirus, a novel potyvirus of pecan trees. *Sci Rep-UK*, 6:26741. (**IF=5.228**)
- 19.Liu XH, Ning GA, Huang LY, Zhao YH, Dong B, Lu JP, Lin FC^{*} (2016). Calpains are involved inasexual and sexual development, cell wall integrity and pathogenicity of therice blast fungus. *Sci Rep-UK*, 6:31204. (**IF=5.228**)
- 20.Zhang HJ, Hong YB, Huang L, Li DY, Song FM^{*} (2016). Arabidopsis AtERF014 acts as a dual regulatorthat differentially modulates immunity against *Pseudomonas syringae* pv. *tomato*and *Botrytis cinerea*. *Sci Rep-UK*, 6:30251. (**IF=5.228**)
- 21.Deng SZ, Gu ZK, Yang N, Li L, Yue XF, Que YW, Sun GC,Wang ZY^{*}, Wang JY^{*} (2016). Identificationand characterization of the peroxin 1 gene *MoPEX1*required for infection related morphogenesis and pathogenicity in *Magnaporthe oryzae*. *Sci Rep-UK* , 6, 36292,DOI:10.1038/srep36292. (**IF=5.228**)
- 22.Gao F, Gu QJ, Pan J, Wang ZH, Yin CL, Li F, Song QS,Strand MR, Chen XX, Shi M^{*} (2016). *Cotesia vestalis* teratocytes express a diversity of genes andexhibit novel immune functions in parasitism. *Sci Rep-UK*, 6:e26967. (**IF=5.228**)
- 23.Song SN, Tang P, Wei SJ^{*}, Chen XX^{*} (2016). Comparative and phylogenetic analysis of themitochondrial genomes in basal hymenopterans. *Sci Rep-UK*, 6:e20972. (**IF=5.228**)
- 24.Xu G, Gu GX, Teng ZW, Wu SF, Huang J, Song QS, Ye GY,Fang Q^{*} (2016). Identification andexpression profiles of neuropeptides and their G protein-coupled receptors inthe rice stem borer *Chilo suppressalis*. *Sci Rep-UK*, 6:28976. (**IF=5.228**)
- 25.Yan ZC, Fang Q, Wang L, Liu JD, Zhu Y, Wang F, Li F, Werren JH, Ye GY^{*} (2016). Insightsinto the venom composition and evolution of an endoparasitoid wasp by combiningproteomic and transcriptomic analyses. *Sci Rep-UK*, 6:19604. (**IF=5.228**)
- 26.Liu XH, Xu F, Snyder JH, Shi HB, Lu JP, Lin FC^{*} (2016). Autophagy in plant pathogenic fungi. *Semin Cell Dev Biol*, 27:128-137. (**IF=5.181**)
- 27.Zhang T, XB Xu, Huang CJ, Qian YJ, Li ZG, Zhou XP^{*} (2016). A novel DNA motifcontributes to selective replication of a geminivirus-associated betasatelliteby a helper virus-encoded replication-related protein. *J Virol*, 90(4): 2077-89. (**IF=4.606**)
- 28.Zhang P, Zhong KZ, Tong HH, Shahid MQ, Li JQ^{*} (2016). Association Mapping for Aluminum Tolerance in aCore Collection of Rice landraces. *Front. Plant Sci*, doi:10.3389/fpls.2016.01415.

(IF=4.495)

29.Zhang PT^{*}, Zhong KZ[†], Shahid MQ, Tong HH^{*} (2016). Association analysis in rice: From application to utilization. ***Front. Plant Sci.***, doi:10.3389/fpls.2016.01202. **(IF=4.495)**

30.Fu GF[†], Feng BH[†], Zhang CX, Yang YJ, Yang XQ, Chen TT, Zhao X, Zhang XF, Jin QY^{*}, Tao LX^{*} (2016). Heat stress is more damaging to superiorspikelets than inferiors of rice (*Oryza sativa L.*) due to their different organ temperatures. ***Front. Plant Sci.***, DOI:10.3389/fpls.2016.01637. **(IF=4.495)**

31.Ouyang ZG, Liu SX, Huang LH, Hong YB, Li XH, Huang L, Zhang YF, Zhang HJ, Li DY, Song FM^{*} (2016). Tomato SIERF.A1, SIERF.B4, SIERF.C3 and SIERF.A3, members of B3 group of ERF family, are required for resistance to *Botrytiscinerea*. ***Front. Plant Sci.***, 7:1964. **(IF=4.495)**

32.Hong YB, Zhang HJ, Huang L, Li DY, Song FM^{*} (2016). Overexpression of a stress-responsive NAC transcription factor gene ONAC022 improves drought and salt tolerance in rice. ***Front Plant Sci.***, 7:4. **(IF=4.495)**

33.Begum MA, Shi XX, Tan Y, Zhou WW, Hannun Y, Obeid L, Mao CG^{*}, Zhu ZR^{*} (2016). Molecular Characterization of Rice OsLCB2a1 Gene and Functional Analysis of its Role in Insect Resistance. ***Front Plant Sci.***, 7:1789. **(IF=4.495)**

34.Ren DY[†], Rao YC[†], Leng YJ[†], Li ZZ, Xu QK, Wu LW, Qiu ZN, Xue DW, Zeng DL, Hu J, Zhang GH, Zhu L, Gao ZY, Chen G, Dong GJ, Guo LB^{*} and Qian Q^{*} (2016). Regulatory Role of OsMADS34 in the Determination of Glumes Fate, Grain Yield, and Quality in Rice. ***Front Plant Sci.***, doi: 10.3389/fpls.2016.01853. **(IF=4.495)**

35.Sun DD[†], Cao HJ[†], Shi YK[†], Huang PY, Dong B, Liu XH, Lin FC, Lu JP^{*} (2016). The regulatory factor X protein MoRfx1 is required for development and pathogenicity in the rice blast fungus *Magnaporthe oryzae*. ***Mol Plant Pathol.***, 19, DOI: 10.1111/mpp.12461. **(IF=4.335)**

36.Li B^{*}, Zhang Y, Yang YZ, Qiu W, Wang XX, Liu BP, Wang YL, Sun GC (2016). Synthesis, characterization, and antibacterial activity of chitosan/TiO₂ nanocomposite against *Xanthomonas oryzae* pv. *oryzae*. ***Carbohydr Polym.***, 152:825-831. **(IF=4.219)**

37.Huang HJ, Liu CW, Huang XH, Zhou X, Zhuo JC, Zhang CX, Bao YY^{*} (2016). Screening and Functional Analyses of *Nilaparvata lugens* Salivary Proteome. ***J Proteome Res.***, 15:1883-1896. **(IF=4.173)**

38.Dai Y, Cao ZY, Huang L, Liu SX, Shen ZH, Wang YY, Wang H, Zhang HJ, Li DY, Song FM^{*} (2016). CCR4-Not complex subunit Not2 plays critical roles in vegetative growth, conidiation and virulence in

watermelon Fusarium wilt pathogen *Fusariumoxysporum* f.sp.*niveum*. ***Front Microbiol***, 7:1449. (IF=4.165)

39.Lin HY[†], Hu SK[†], Liu RF, Chen P, Ge CW, Zhu B, GuoLB^{*} (2016). Genome Sequence of *Pseudomonas koreensis* CRS05-R5, an Antagonistic Bacterium Isolated from Rice Paddy Field. ***Front Microbiol***, 2016,7:1756. (IF=4.165)

40.Qian YJ[†], Hou HW[†], Shen QT, Cai XZ, Sunter G, ZhouXP^{*} (2016). RepA protein encoded by *Oat dwarf virus* elicits a temperature-sensitive hypersensitiveresponse-type cell death that involves jasmonic acid-dependent signaling. ***Mol Plant Microbe In***, 29(1):5-21. (IF=4.145)

41.Li QT[†], Wei SJ[†], Tang P, Wu Q, Shi M, Sharkey MJ, Chen XX^{*} (2016). Multiplelines of evidence from mitochondrial genomes resolve phylogenetic relationshipsof parasitic wasps in Braconidae. ***Genome Biol Evol***, 8(9):2651-2662. (IF=4.098)

42.Xie QJ[†], Liang YT[†], Zhang J, Zheng HK, Dong GJ,Qian Q^{*}, Zuo JR^{*} (2016). Involvement of a putative bipartite transit peptide in targeting rice pheophorbide α oxygenase intochloroplasts for chlorophyll degradation during leaf senescence. ***J Genet Genomics***, 2016, 43(3):145-154. (IF=3.981)

43.Sun B[†], Zhan XD[†],Lin ZC, Wu WX, Yu P, Zhang YX, Sun LP, Cao LY*, Cheng SH* (2016). Fine mapping and candidate GENE analysis of qHD5, a novelmajor QTL with pleiotropism for yield-related traits in rice (*Oryza sativa L.*). ***Theor Appl Genet***, DOI: 10.1007/s00122-016-2787-y. (IF=3.9)

44.Yu B, Li DT, Lu JB, Zhang WX, Zhang CX^{*}(2016). Seminal fluid protein genes of the brown planthopper, *Nilaparvatalugens*. ***BMC Genomics***,17:65. (IF=3.867)

45.Yang YJ[†], Xiong JT^{*}, Chen RJ, FuGF, Chen TT, Tao LX^{*} (2016). Excessive nitrate enhances cadmium (Cd)uptake by up-regulating the expression of *OsIRT1* in rice (*Oryzasativa*). ***Environ Exp Bot***, 122:141-149. (IF=3.712)

46.Huang QN, Shi YF, Zhang XB, Song LX, Feng BH, Wang HM,Xu X, Li XH, Guo D, Wu JL^{*} (2016). Single base substitution in *OsCDC48* isresponsible for premature senescence and death phenotype in rice. ***JIntegr Plant Biol***, 58(1):12-28. (IF=3.67)

47.Huang L, Hong YB, Zhang HJ, Li DY, Song FM^{*} (2016).Rice NAC transcription factor ONAC095 plays opposite roles in drought and coldstress tolerance. ***BMC Plant Biol***, 16:203. (IF=3.631)

48.Wang SZ[†], Chen WY[†], Yang CD, Yao J, Xiao WF, XinY, Qiu JR, Hu WM, Yao HG, Ying W, Fu YP, Tong JX, Chen ZZ, Ruan SL^{*},Ma HS^{*} (2016). Comparative proteomic analysis reveals alterations

in development and photosynthesis-related proteins in diploid and triploid rice. *BMC Plant Biol.*, 16: 199. (IF=3.631)

49. Fang Q, Wang BB, Ye XH, Wang F, Ye GY^{*} (2016). Venom of parasitoid *Pteromaluspuparum* impairs host humoral antimicrobial activity by decreasing host cecropin and lysozyme gene expression. *Toxins*, 8:52. (IF=3.571)

50. Meng LJ, Guo LB, Ponce K, Zhao XQ, Ye GY^{*} (2016). Characterization of three Indica rice multi-parent advanced generation intercross (MAGIC) populations for QTL identification. *Plant Genome-US*, DOI: 10.3835/plant_genome 2015.10.0109. (参与) (IF=3.509)

51. Ren DY[†], Rao YC[†], Huang LC, Leng YJ, Hu J, Lu M, Zhang GH, Zhu L, Gao ZY, Dong GJ, Guo LB, Qian Q^{*}, Zeng DL^{*} (2016). Fine Mapping Identifies a New QTL for Brown Rice Rate in Rice (*Oryza Sativa*L.). *Rice*, DOI: 10.1186/s12284-016-0076-7. (IF=3.417)

52. Gao YT[†], Liu CL[†], Li YY, Zhang AP, Dong GJ, Xie LH, Zhang B, Ruan BP, Hong K, Xue DW, Zeng DL, Guo LB, Qian Q, Gao ZY^{*} (2016). QTL analysis for chalkiness of rice and fine mapping of a candidate gene for *qACE9*. *Rice*, 9:41. (IF=3.417)

53. Gao L, Chang JD, Chen RJ, Li HB, Lu HF, Tao LX, Xiong J^{*} (2016). Comparison on cellular mechanisms of iron and cadmium accumulation in rice: prospects for cultivating Fe-rich but Cd-free rice. *Rice*, 9:39. (参与) (IF=3.417)

54. Huangfu JY, Li JC, Li R, Ye M, Kuai P, Zhang TF, Lou YG^{*} (2016). The Transcription Factor OsWRKY45 Negatively Modulates the Resistance of Rice to the Brown Planthopper *Nilaparvata lugens*. *Int J Mol Sci*, 17(6):697, DOI:10.3390/ijms17060697. (IF=3.257)

55. Lu Q, Zhang MC, Niu XJ, Wang CH, Xu Q, Feng Y, Wang S, Yuan XP, Yu HY, Wang YP, Wei XH^{*} (2016). Uncovering novel loci for mesocotyl elongation and shoot length in indica rice through genome-wide association mapping. *Planta*, 243(3):645-657. (IF=3.239)

56. Feng YT[†], Lu QT[†], Zhai RR, Zhang MC, Xu Q, Yang YL, Wang S, Yuan XP, Yu HY, Wang YP, Wei XH^{*} (2016). Genomewide association mapping for grain shape traits in indica rice. *Planta*, 244(4):819-830. (IF=3.239)

57. Wan PJ, Tang YH, Yuan SY, Wang WX, Lai FX, Yu XP^{*}, Fu Q^{*} (2016). ATP phosphoribosyl transferase from symbiont *Entomomyces delphacidicola* involved in histidine biosynthesis of *Nilaparvata lugens* (Stål). *Amino Acids*, 48(11):2605-2617. (IF=3.196)

- 58.Wang SL, Cheng RL, Lu JB, Yu XP, Zhang CX^{*} (2016). A Cripavirus in the brown planthopper, *Nilaparvata lugens*. *J Gen Virol*, 97:706-714. (IF=3.192)
- 59.Chen GQ, Fang Y, Hu ZY, Krell PJ, Feng GZ^{*} (2016). Autographa californica multiplenucleopolyhedrovirus with DNA polymerase (DNA pol) of *Spodoptera litura* nucleopolyhedrovirus (SplNPV) and identification of a nuclear localization signal in SplNPV DNAPol. *J Gen Virol*, 97(8):1968-1980. (IF=3.192)
- 60.Zeng YX, Ji ZJ, Wen ZH, Liang Y, Yang CD^{*} (2016). Combination of Eight Alleles at Four Quantitative Trait Loci Determines Grain Length in Rice. *Plos One*, DOI:10.1371/journal.pone.0150832. (IF=3.057)
- 61.Niu YF, Ahammed GJ, Tang CX, Guo LB^{*}, Yu JQ^{*} (2016). Physiological and Transcriptome Responses to Combinations of Elevated CO₂ and Magnesium in *Arabidopsis thaliana*. *PLoS One*, DOI:10.1371/journal.pone.0149301. (IF=3.057)
- 62.Cao XC[†], Ma QX[†], Zhong CT[†], Yang X, Zhu LF, Zhang JH, Jin QY^{*}, Wu LH^{*} (2016). Elevational Variation in Soil Amino Acid and Inorganic Nitrogen Concentrations in Taibai Mountain, China. *PLoS One*, 11(6): e0157979. (IF=3.057)
- 63.Li ZY, Tang LQ, Qiu JH, Zhang W, Wang YF, Tong XH, Wei XJ, Hou YX, Zhang J^{*} (2016). Serine carboxypeptidase 46 regulates grain filling and seed germination in rice (*Oryza sativa L.*). *PLoS One*, 11(7):e0159737. (IF=3.057)
- 64.Xu XH, He Q, Chen C^{*}, Zhang CL^{*} (2016). Differential communications between fungi and host plants revealed by secretomeanalysis of phylogenetically related endophytic and pathogenic fungi. *PLoS One*, 11(9):e0163368. (IF=3.057)
- 65.Jiang YT[†], Wang JL[†], Chen J, Mao LJ, Feng XX, Zhang CL^{*}, Lin FC^{*} (2016). *Trichoderma* biodiversity of agricultural fields in East China reveals a gradient distribution of species. *PLoS One*, 11(8):e0160613. (IF=3.057)
- 66.Xiong HZ, Shi AN^{*}, Mou BQ^{*}, Qin J, Motes D, Lu WG, Ma JB, Weng YJ, Yang W, Wu DX (2016). Genetic Diversityand Population Structure of Cowpea (*Vigna unguiculata L. Walp*). *PLoS One*, DOI:10.1371/journal.pone.0160941. (IF=3.057)
- 67.Liu XB[†], Wei XJ[†], Sheng ZH, Jiao GA, Tang SQ, Luo J^{*}, Hu PS^{*} (2016). Polycomb Protein OsFIE2 Affects Plant Height and Grain Yield in Rice. *PLoS One*, 11(10):e0164748ice. (IF=3.057)
- 68.Liang SS, Wu LW, Ren GJ, Zhao XQ, Zhou MX, McNeil D, Ye GY^{*} (2016).Genome-wide association study of grain yield and related traits using a collection of advanced Indica rice breeding lines for irrigated

ecosystems. *Field Crop Res*, 193:70-86. (参与) (**IF=2.927**)

69.Xia RY, Li MQ, Wu YS, Qi YX, Ye GY, Huang J^{*}(2016). A new family of insect muscarinic acetylcholinereceptors. *Insect Mol Biol*, 25:362-369. (**IF=2.866**)

70.Yu B, Li DT, Wang SL, Xu HJ, Bao YY, Zhang CX^{*}(2016). Ion transport peptide(ITP) regulates wing expansion and cuticle melanism in the brown planthopper, *Nilaparvata lugens*. *Insect Mol Biol*, 25(6)778-787. (**IF=2.866**)

71.Wang XQ, Wang GH, Zhu ZR, Tang QY, Hu Y, Qiao F, HeongKL, Cheng JA*(2016). Spider (Araneae) Predations on White-backed Planthopper *Sogatella furcifera* in Subtropical Rice Ecosystems, China. *Pest Manag Sci*, 37(8). (**IF=2.811**)

72.Liu N, Ning GA, Liu XH, Feng XX, Lu JP, Mao LJ, Su ZZ,Wang Y, Zhang CL^{*}, Lin FC^{*} (2016). An autophagy gene, *HoATG5*, is involved in sporulation, cell wall integrity and infection of wounded barley leaves. *Microbiol Res*,192:326-335. (**IF=2.723**)

73.Wu LW, Liu RF, Niu YF, Lin HY, Ye WJ, Guo LB^{*}, Hu XM^{*} (2016). Whole genome sequence of *Pantoea ananatis* R100, an antagonistic bacterium isolated from rice seed. *J Biotechnol*, 225, 1-2. (**IF=2.667**)

74.Fang Y[†], Wu L^J[†], Chen GQ, Feng GZ*(2016). Complete genome sequence of *Pseudomonas azotoformanans* S4, a potential biocontrol bacterium. *J Biotechnol*, 227:25-26. (**IF=2.667**)

75.Xu G, Wu SF, Teng ZW, Yao HW, Fang Q, Huang J, Ye GY^{*}(2016). Molecular characterization and expression profiles of nicotinic acetylcholine receptors in the rice striped stem borer, *Chilo suppressalis* (Lepidoptera: Crambidae). *Insect Sci*, DOI: 10.1111/1744-7917. (**IF=2.551**)

76.Han JB, Li GQ^{*} , Wan PJ^{*} , Zhu TT, Meng QW (2016). Identification of glutathione S-transferase genes in *Leptinotarsa decemlineata* and their expression patterns under stress of three insecticides. *Pestic Biochem Phys*,133:26-34. (**IF=2.388**)

77.Wang B, Wang LL, Chen FY, Yang XL, Ding M, Zhang ZK, Liu SS, Wang XW,Zhou XP^{*} (2016). MicroRNA profiling of the whitefly *Bemisia tabaci* Middle East-Aisa Minor following the acquisition of *Tomato yellow leaf curl China virus*. *Virol J*, 13:20. (**IF=2.362**)

78.Teng ZW, Xu G, Gan SY, Chen X, Fang Q, Ye GY*(2016). Effects of the endoparasitoid *Cotesia chilonis*(Hymenoptera: Braconidae) parasitism, venom and calyx fluid on cellular and humoral immunity of its host *Chilo suppressalis* (Lepidoptera: Crambidae) larvae. *J Insect Physiol*, 85:46-56. (**IF=2.267**)

79.Chen S, Cao LG, Huang QQ, Qian YJ^{*} , Zhou XP (2016).The complete genome sequence of a novel maize-associated totivirus. *Arch Virol*, 161(2):487-490. (**IF=2.255**)

- 80.Kakar KU, Ren X, Nawaz Z, Cui ZQ, Li B^{*},Xie GL, Hassan MA, Ali E, Sun GC^{*}(2016). A consortium of rhizobacterial strains and biochemical growth elicitors improve cold and drought stress tolerance in rice(*Oryza sativa L.*). ***Plant Biology***, 18:471-483. **(IF=2.216)**
- 81.Cui ZQ, Ojaghian MR, Tao ZY, Kakar KU, Zeng J, Zhao WJ, Duan YP, Cruz CMV, Li B, Zhu B^{*}, Xie GL^{*} (2016). Multiplex PCR assay for simultaneous detection of six major bacterial pathogens of rice. ***Appl Microbiol***, 120: 1357-1367. **(IF=2.156)**
- 82.Zhang HW, Fan YY, Zhu YJ, Chen JY, Yu SB, Zhuang JY^{*} (2016). Dissection of the *qTGW1.1* region into two tightly-linked minor QTLs having stable effects for grain weight in rice. ***BMC Genet***, 17:98, DOI:10.1186/s12863-016-0410-5. **(IF=2.152)**
- 83.Xu QT[†], Yuan XP[†], Wang S, Feng Y, Yu HY, Wang YP, Yang YL, Wei XH^{*}, Li XM^{*}(2016). The genetic diversity and structure of indica rice in China as detected by single nucleotide polymorphism analysis. ***BMC Genet***, 17:53. **(IF=2.152)**
- 84.Zhou ZS, Wang ZY, Liu YX, Liang GM, Shu CL, Song FP, Zhou XP, Bravo A, Soberón M, Zhang J^{*} (2016). Identification of ABCC2 as a binding protein of Cry1Ac on brush border membrane vesicles from *Helicoverpa armigera* by an improved pull-down assay. ***Microbiology Open***, 5(4):659-69. **(IF=2.148)**
- 85.Zhang ZH, Cao LY, Chen JY, Zhang YX, Zhuang JY^{*}, Cheng SH^{*} (2016). Effects of *Hd2* in the presence of the photoperiod-insensitive functional allele of *Hd1* in rice. ***Biol Open***, 5: 1719-1726. **(IF=2.135)**
- 86.RoyChowdhury M, Li XB^{*}, Qi HY, Li WX, Sun J, Huang C, Wu DX^{*} (2016). Functional characterization of 9-/13-LOXs in rice and silencing their expressions to improve grain qualities. ***BioMed Res Int***, <http://dx.doi.org/10.1155/2016/4275904>. **(IF=2.134)**
- 87.Ye WJ, Hu SK, Wu LW, Ge CW, Cui YT, Chen P, Wang XQ, Xu J, Ren DY, Dong GJ, Qian Q^{*}, Guo LB^{*} (2016). *White stripe leaf 12*(WSL12), encoding a nucleoside diphosphate kinase 2(OsNDPK2), regulates chloroplast development and abiotic stress response in rice. ***Mol Breeding***, 36:57. **(IF=2.108)**
- 88.Zhu YJ, Huang DR, Fan YY, Zhang ZH, Ying JZ, Zhuang JY^{*} (2016). Detection of QTLs for yield heterosis in rice using a RIL population and its testcross population. ***Int J Genomic***, Article ID 2587823, 9 pages, DOI:10.1155/2016/2587823. **(IF=1.83)**
- 89.Song SN, Chen PY, Wei SJ, Chen XX^{*} (2016). The mitochondrial genome of *Polistes jokahamae* and a phylogenetic analysis of the Vespoidea(Insecta: Hymenoptera). ***Mitochondrial DNA***, 27(4):2783-2784. **(IF=1.76)**

- 90.Song SN, Wang ZH, Li Y, Wei SJ, Chen XX^{*}(2016). The mitochondrial genome of *Tenthredo tienmushana* (Takeuchi) and a related phylogenetic analysis of the sawflies (Insecta: Hymenoptera). *Mitochondrial DNA*, 27(4):2860-2861. (IF=1.76)
- 91.Wang HK, Cao YC, Lin FC^{*}(2016). Two novel *Eupenicillium* species isolated from soil in China. *J Microbiol Biotechn*, 5(1):72-77. (IF=1.685)
- 92.Ji ZJ, Zeng YX, Liang Y, Qian Q^{*}, Yang CD^{*} (2016). Transcriptomic dissection of the rice-*Fusariumfujikuroi* interaction by RNA-Seq. *Euphytica*, 211:123–137. (IF=1.618)
- 93.Yang YJ, Chen RJ, Fu GF, Xiong J^{*}, Tao LX^{*}(2016). Phosphate deprivation decreases cadmium (Cd) uptake but enhances sensitivity to Cd by increasing iron (Fe) uptake and inhibiting phytochelatins synthesis in rice (*Oryza sativa*). *Acta Physiol Plant*, 38:28. (IF=1.563)
- 94.Dai LP, Wang L, Leng YJ, Yang YL, Huang LC, Chen L, Wang YQ, Ren DY, HuJ, Zhang GH, Zhu L, Guo LB, Qian Q^{*}, Zeng DL^{*} (2016). Quantitative Trait Loci Mapping for Appearance Quality in Short-Grain Rice. *CropSci*, 56(4):1484-1492. (IF=1.55)
- 95.Nguyen H, Chen XY, Jiang M, Wang Q, Deng L, Zhang WZ, Shu QY^{*}(2016). Development and molecular characterization of a doubled haploid population derived from a hybrid between japonica rice and wide compatible indica rice. *Breeding Sci*, 66:552-559. (IF=1.543)
- 96.Lu ZB, Dang C, Han NS, Shen ZC, Peng YF, Stanley DW, Ye GY^{*}(2016). The new transgenic cry1Ab/vip3H rice poses no unexpected ecological risks to arthropod communities in rice agroecosystems. *Environ Entomol*, 45:518-525. (IF=1.315)
- 97.Ren SP, Yang F, Gao MQ, Pu DQ, Shi M, Ye GY, Shen ZC, Chen XX^{*}(2016). Effects of transgenic Bt rice on nontarget *Rhopalosiphum maidis* (Homoptera: Aphididae). *Environ Entomol*, 45(4):1090-1096. (IF=1.315)
- 98.Yuan XT[†], Jiang YD[†], Wang GY, Yu H, Zhou WW, Liu S, Yang MF, Cheng JA, Gurr GM, Way MO, Zhu ZR^{*}(2016). Odorant-Binding Proteins and Chemosensory Proteins from an Invasive Pest *Lissorhoptrus oryzophilus* (Coleoptera: Curculionidae). *Environ Entomol*, 45(5):1276–1286. (IF=1.315)
- 99.Lu HP, Pang WQ, Li WX, Tan YY, Wang Q, Zhao HJ, Shu QY^{*} (2016). Tissue-specific expression, developmentally and spatially regulated alternative splicing, and protein subcellular localization of OsLpa1 in rice. *J Zhejiang Univ Sci B*, 17:100-109. (IF=1.303)
- 100.Cao XC[†], Ma QX[†], Wu LH^{*}, Zhu LF, Jin QY (2016). Effects of ammonium application rate on uptake of soil adsorbed amino acids by rice. *J Zhejiang Univ Sci B*, 17(4):294-302. (IF=1.303)

- 101.Li S, Zheng YC, Cui HR, Fu HW, Shu QY, Huang JZ^{*} (2016). Frequency and type of inheritable mutations induced by gamma rays in rice as revealed by whole genome sequencing. *J Zhejiang Univ-Sci B*, 17(12):905-915. (**IF=1.303**)
- 102.Li WX, Wu SL, Liu YH, Jin GL, Zhao HJ, Shu QY^{*} (2016). Genome-wide profiling of genetic variation in *Agrobacterium*-transformed rice plants. *J Zhejiang Univ-Sci B*, 17(12):992-996. (**IF=1.303**)
- 103.Mao N, Tang P, Tian HW, Shi Min, Chen XX^{*} (2016). General morphology and ultra structure of the female reproductive apparatus of *Trichomalopsisshirakii* Crawford (Hymenoptera, Pteromalidae). *Microsc Res Techniq*, 79(7):625-636. (**IF=1.13**)
- 104.Yu P[†], Wang XM[†], Yuan XP, Wang CH, Xu Q, Feng Y, Yu HY, Wang YP, Wei XH^{*} (2016). Sequence variations and haplotypes of the bacterial blight resistance Gene *xa13* in rice. *J Plant Pathol*, 98(1):167-170. (**IF=1.038**)
- 105.Li Y, He JH, Chen XX^{*} (2016). The genus *Eurobracon* Ashmead (Hymenoptera, Braconidae, Braconinae) in China, with description of three new species. *Zootaxa*, 4132(3):83-392. (**IF=0.994**)
- 106.Liu Z, He JH, Chen XX^{*} (2016). The genus *Pholetesor* Mason, 1981 (Hymenoptera, Braconidae, Microgastrinae) from China, with descriptions of eleven new species. *Zootaxa*, 4150(4):351-387. (**IF=0.994**)
- 107.Li Y, He JH, Chen XX^{*} (2016). Four subgenera of *Bracon* Fabricius (Hymenoptera, Braconidae, Braconinae) newly recorded from China, with description of five new species. *Zootaxa*, 4208(5):459-473. (**IF=0.994**)
- 108.Elshakh ASA, Anjum SI, Qiu W, Almoneafy AA, Wang L, Zhang Y, Cui ZQ, Li B, Sun GC, Xie GL^{*} (2016). Controlling and defence-related mechanisms of *Bacillus* Strains against bacterial leaf blight of rice. *J Phytopathol*, 164(7-8):534-546. (**IF=0.945**)
- 109.Yang PP, Shi WX, Wang HK*, Liu HM (2016). Screening of freshwater fungi for decolorizing multiple synthetic dyes. *Braz J Microbiol*, (47):828-834. (**IF=0.865**)
- 110.Qiao F, Zhu QZ, Wang XQ, Wang GY, Gurr GM, Zhu ZR, Heong KL, Cheng JA^{*} (2016). Reciprocal Intraguild Predation Between Two Mirid Predators, *Cyrtorhinuslividipennis* and *Tytthus chinensis* (Hemiptera: Miridae). *Biocontrol Sci Technol*, 26(9):1267-1284. (**IF=0.848**)
- 111.Zeng YH[†], Zhang YP[†], Xiang J, Wu H, Chen HZ, Zhang YK, Zhu DF^{*} (2016). Effects of chilling tolerance induced by spermidine pretreatment on antioxidative activity, endogenous hormones and ultrastructure of indica-japonica hybrid rice seedlings. *J Integr Agr*, 15(2):295-308. (**IF=0.724**)

- 112.Ji ZJ[†], Yang SD[†], Zeng YX, Liang Y, Yang CD^{*},Qian Q^{*} (2016). Pyramiding blast, bacterial blight and brown planthopper resistance genes in rice restorer lines. *J Integr Agr*,15(7):1432–1440. (**IF=0.724**)
- 113.Gao X[†], Zhu XD[†], Fang N[†],Duan PG, Wu YB, Luo YH^{*}, Li YH(2016). Identificationof QTLs for grain size and characterization of the beneficial alleles of grainsize genes in large grain rice variety BL129. *J Integr Agr*,15(1): 1-9. (**IF=0.724**)
- 114.Akhtar ZR, Dang C, Wang F, Peng YF, Ye GY^{*}(2016). Thrips-mediated impacts from transgenic rice expressing Cry1Ab on ecological fitness of non-target predator *Orius tantillus* (Hemiptera: Anthocoridae). *J Integr Agr*, 15: 2059-2069. (**IF=0.724**)
- 115.Li XB^{*} , Yan WG, Agrama H, Jackson A, Jia M, Jia LM,Moldenhauer K, Correa F, Wu DX^{*}(2016). Genetic analysis of genetic basis of a physiological disorder “straighthead” in rice (*Oryza sativa* L.). *Genes Genom*, 38(5):453-457. (**IF=0.692**)
- 116.Hu BL, Huang DR, Xiao YQ, Fan YY, Chen DZ, Zhuang JY^{*} (2016). Mapping QTLs for mineral element contents inbrown and milled rice using an *Oryza sativa* x *O. rufipogon* backcross in bred line population. *Cereal Res Commun*,44: 57-68. (**IF=0.528**)
- 117.Liu SX, Deng LM, Fu YP, Hu GC, Liu WZ^{*} , Zhao X^{*} (2016).Identification and Characterization of the yls Mutation in Rice (*Oryzasativa* L.) with Lower Photosynthetic Pigment Content. *Czech J Genet Plant*, 52:101-107. (参与) (**IF=0.476**)
- 118.Yu HP, Ren DY, Zhu YZ, Xu JM, Wang YX, Liu RF, Fang YX, Shi ZY, Pan JJ,Lu M, Ma BJ, Hu J^{*} , Rao YC^{*} (2016). *MULTI-TILLERINGDWARF1*, a new allele of *BRITTLE CULM 12*, affects plant height and tiller in rice. *Sci Bull*, DOI:10.1007/s11434-015-0981-y. (**IF=4**)
- 119.Wan PJ, Yuan SY, Wang WX, Chen X, Lai FX, Fu Q^{*} (2016). A genome-wide identification and analysis of the basic helix-loop-helix transcription factors in brown planthopper, *Nilaparvatalugens*. *Genes*, 7(11):100. (**IF=3.6**)
- 120.Hu LF, YeM, Li R, Lou YG^{*}(2016). OsWRKY53,a versatile switch in regulating herbivore-induced defense responses in rice. *Plant Signaling & Behavior*,11(4):e1169357. (**IF=0**)
- 121.Liu Z, Chen Z, Hong J, Wang XF, Zhou CY, Zhou XP, JX Wu^{*} (2016).Monoclonal antibody-based serological methods for detecting *Citrus tristeza virus* in citrus groves. *Virologica Sinica*, 31(4):324-330. (**IF=0**)
- 122.Xu X, Zhang XB, Shi YF, Wang HM, Feng BH, Li XH, HuangQN, Song LX, Guo D, He Y, Wu JL^{*} (2016). A point mutation in an F-box domain-containing protein is responsible for brownhull phenotype in

rice. *Rice Science*, 23(1):1-8. (IF=0)

2015年发表

- 1.Xu HJ , Xue J , LuB , Zhang XC , Zhuo JC , He SF , Ma XF , Jiang YQ , Fan HW , Xu JY , Ye YX ,Pan PL , Li Q , Bao YY , Nijhout HF , Zhang CX (2015). Two insulin receptors determine alternative wing morphs in planthoppers. *Nature*, 519(7544):464-467. (IF=41.456)
- 2.Ma Y, Dai XY,Xu YY, Luo W, Zheng XM, Zeng DL, Pan YJ, Lin XL, LiuHH, Zhang DJ, Xiao J, Guo XY, Xu SJ, Niu YD, Jin JB, Zhang H, Xu X, Li LG, WangW, Qian Q, Ge S, and Chong K* (2015). COLD1 Confers Chilling Tolerance in Rice. *Cell*. 160, 1–13. (参与) (IF=33.116)
- 3.Wang YX, Xiong GS, Hu J, Jiang L, Yu H, Xu J, Fang YX, Zeng LJ, Xu EB, Xu J, Ye WJ, Meng XB, LiuRF, Chen HQ, Jing YH, Wang YH, Zhu XD*, Li JY* & Qian Q* (2015). Copynumber variation at the GL7 locus contributes to grain size diversity in rice. *Nature Genetics*, 47(8):944-948. (IF=29.352)
- 4.Huang XH*, Yang SH*, Gong JY*, Zhao Y*, Feng Q, Gong H, Li WJ, Zhan QL, Cheng BY, Xia JH, Chen N,Hao ZN, Liu KY, Zhu CR, Huang T, Zhao Q, Zhang L, Fan DL, Zhou CC, Lu YQ, WengQJ, Wang ZX, Li JY & Han B (2015). Genomic analysis of hybrid rice varieties reveals numerous superior alleles that contribute to heterosis. *Nature Communications*. DOI:10.1038/ncomms7258. (IF=11.47)
- 5.Li R, Zhang J, Li JC,Zhou GX, Wang Q, Bian WB, Erb M, Lou YG* (2015). Prioritizing plant defence over growth through WRKY regulation facilitates infestation by non-target herbivores. *eLife*, 4:e04085. (IF=9.322)
- 6.Xiong J*, Yang YJ,Fu GF, Tao LX* (2015). Novel roles of hydrogen peroxide (H_2O_2) in regulating pectin synthesis and demethylesterification in the cell wall of rice (*Oryza sativa*) root tips. *New Phytologist*, 206:118–126. (IF=7.672)
- 7.Li FF, Xu XB, Gu ZH, Cao LG, Hu T, Li ZH*, Zhou XP* (2015). The AC5 protein encoded by Mungbean yellow mosaic India virus is a pathogenicity determinant that suppresses RNA silencing-based antiviral defenses. *New Phytologist*, 208(10):555–569. (IF=7.672)
- 8.Wang Q, Ma XN, QianSS, Zhou X, Sun K, Chen XL, Zhou XP, Jackson AO, Li ZH* (2015). Rescue of a plant negative strand virus from cloned cDNA: insights into enveloped plantvirus movement and morphogenesis. *PLoS Pathogens*, 11(10):e1005223. (IF=7.562)
- 9.Rao YC, Yang YL, Xu JL, Li XJ,Leng YJ, Dai LP, Huang LC, Shao GS, Ren DY, Hu J, Guo LB, Pan JW, and Zeng DL (2015).Early Senescence1 encodes a Scar-like protein that affects water loss in rice. *Plant Physiology*, 169: 1225–1239. (IF=6.841)
- 10.Hu LF, Ye M, ZhangTF, Li R, Zhou GX, Wang Q, Lu J, Lou YG* (2015). The rice transcription factorWRKY53 suppresses herbivore-induced defenses by acting as a negative feedbackmodulator of

map kinase activity. *Plant Physiology*, DOI:10.1104/pp.15.01090. (IF=6.841)

11.Hu J,Wang Y, Fang Y, Zeng L, Xu J, Yu H, Shi Z, Pan J, Zhang D, Kang S, Zhu L, DongG, Guo L, Zeng D, Zhang G, Xie L, Xiong G, Li J, Qian Q (2015). A rare allele of GS2 enhances grain size and grain yield in rice. *Molecular Plant*, 8(10): 1455-1465. (IF=6.337)

12.Wang KJ*, Wang C,Liu Q, Liu WZ and Fu YP (2015). Increasing the Genetic Recombination Frequency by Partial Loss of Function of the Synaptonemal Complex in Rice. *Molecular Plant*, doi.org/10.1016/j.molp. (IF=6.337)

13.Liu XH, Chen SM,Gao HM, Ning GA, Shi HB, Wang Y, Dong B, Qi YY, Zhang DM, Lu GD, Wang ZH, ZhouJ* and Lin FC *(2015). The small GTPase MoYpt7 is required for membrane fusionin autophagy and pathogenicity of Magnapor the oryzae. *Environmental Microbiology*,17(11):4495-4510. (IF=6.201)

14.Guo LB[†],Qiu J[†], Han ZJ[†], Ye ZH[†], Chen C[†],Liu CJ, Xin XF, Ye CY, Wang YY, Xie HQ, Wang Y, Bao JD, Tang S, Xu J, Gui YJ,Fu F, Wang WD, Zhang XC, Zhu QH, Guang XM, Wang CZ, Cui HF, Cai DG, Ge S,Tuskan GA, Yang XH, Qian Q, He SY, Wang J*, Zhou XP* and Fan LJ* (2015). A hostplant genome (*Zizania latifolia*) after a century-longendophyte infection. *The Plant Journal*, 83(4):600-609. (IF=5.972)

15.Qi T, Cao YJ, CaoLY, Gao YM, Zhu SJ, Lou XY and Xu HM* (2015). Dissecting Genetic Architecture Underlying Seed Traits in Multiple Environments. *Genetics*,199:61–71.(参与) (IF=5.963)

16.Huang HJ, Bao YY*,Lao SH, Huang XH, Ye YZ, Wu JX, Xu HJ, Zhou XP, Zhang CX (2015). Rice raggedstunt virus-induced apoptosis affects virus transmission from its insectvector, the brown planthopper to the rice plant. *Sci Rep*, 5:11413. (IF=5.578)

17.Wu, SF, Xu, G,Stanley, D, Huang, J and Ye, GY (2015). Dopamine modulates hemocyte phagocytosis via a D1-like receptor in the rice stem borer. *Sci Rep*,5:12247. (IF=5.578)

18.Xu XH, Wang C, LiSX, Su ZZ, Zhou HN, Mao LJ, Feng XX, Liu PP, Chen X, Snyder JH, Kubicek CP,Zhang CL*, Lin FC (2015). Friend or foe: differential responses of rice toinvasion by mutualistic or pathogenic fungi revealed by RNAseq and metabolite profiling. *Sci Rep*, 5:13624. (IF=5.578)

19.Yang YL, Xu J,Huang LC, Leng YJ, Dai LP, Rao YC, Chen L, Wang YQ, Tu ZJ, Hu J, Ren DY, ZhangGH, Zhu L, Guo LB, Qian Q,* and Zeng DL* (2015). *PGL*, encodingchlorophyllide a oxygenase 1, impacts leaf senescence and indirectly affects grain yield and quality in rice. *Journal of Experimental Botany*, DOI:10.1093/jxb/erv529. (IF=5.526)

20.Ouyang ZG, Li XH,Huang L, Hong YB, Zhang YF, Zhang HJ, Li DY, Song FM (2015). Elicitin-likeproteins Oli-D1 and Oli-D2 from Pythium oligandrum trigger hypersensitive response in Nicotiana benthamiana and induce resistance against Botrytiscinerea in tomato. *Molecular Plant Pathology*, 16(3):238–250. (IF=4.724)

- 21.Xu Y, Wu JX, Fu S, Li CY, Zhu ZR, Zhou XP* (2015). *Rice stripe Tenuivirus* nonstructuralprotein 3 hijacks the 26S proteasome of the small brown planthopper, via directinteraction with regulatory-particle non-ATPase subunit 3. *Journal of Virology*, 89(8):4296-4310. (IF=4.439)
- 22.Qi, YX, Xia, RY,Wu, YS, Stanley, D, Huang, J and Ye, GY (2015). Larvae of the small whitebutterfly, *Pieris rapae*, express a novel serotonin receptor. *J. Neurochem*,131(6):767-777. (IF=4.281)
- 23.Qiu JH,Hou YX, Tong XH, Wang YF, Lin HY, Liu Q, Zhang W, Li ZY, Nallamilli BR, Zhang J(2015). Quantitative phosphoproteomic analysis of early seed development in rice(*Oryza sativa L.*). *Plant Molecular Biology*, DOI: 10.1007/s11103-015-0410-2. (IF=4.257)
- 24.Xu, G,Wu, SF, Wu, YS, Gu, GX, Fang, Q and Ye, GY (2015). De novo assembly and characterization ofcentral nervous system transcriptome reveals neurotransmitter signaling systemsin the rice striped stem borer, *Chilo suppressalis*. *BMC Genomics*,16(1):525. (IF=3.986)
- 25.Li DY,Fu FY, Zhang HJ, Song FM (2015). Genome-wide systematic characterization of thebZIP transcriptional factor family in tomato (*Solanum lycopersicum L.*). *BMC Genomics*, 16:771. (IF=3.986)
- 26.Huang LZ, Li ZF, Wu JX, Yang XL, Fan LJ, Fang RX*, Zhou XP* (2015). Analysis ofgenetic variation and diversity of rice stripe virus populations throughhigh-throughput sequencing. *Frontiers in Plant Science*, (6): 176.(IF=3.948)
- 27.Li XH,Zhang HJ, Tian LM, Huang L, Liu SX, Li DY, Song FM (2015). Tomato SIRbohB, amember of the NADPH oxidase family, is required for disease resistance againstBotrytis cinerea and tolerance to drought stress. *Frontiers in PlantScience*, (6): 463. (IF=3.948)
- 28.Zhang HJ, Huang L, Dai Y, Liu SX, Hong YB, Tian LM, Huang LH, Cao ZY, Li DY and Song FM (2015). Arabidopsis *AtERF15* positively regulates immunity against Pseudomonas syringae pv. tomato DC3000 and Botrytis cinerea. *Frontiers in Plant Science*, (6): 686. (IF=3.948)
- 29.Li XH,Huang L, Hong YB, Zhang YF, Liu SX, Li DY, Zhang HJ, Song FM (2015). Co-silencingof tomato S-adenosylhomocysteine hydrolase genes confers increased immunityagainst Pseudomonas syringae pv. tomato DC3000 and enhanced tolerance todrought stress. *Frontiers in Plant Science*, (6): 717. (IF=3.948)
- 30.Yue XF,Que YW, Xu L, Deng SZ, Peng YL, Talbot NJ, Wang ZY (2015). *ZNF1* encodes a putative C2H2 zinc fingerprotein essential for appressorium differentiation by the rice blast fungus *Magnaporthe oryzae*. *Mol Plant Microbe Interact*, DOI:10.1094/MPMI-09-15-0201-R. (IF=3.944)
- 31.Zhang B[†],Ye WJ[†], Ren DY, Tian P, Peng YL, Gao Y, Ruan BP, Wang L, Zhang GH, GuoLB, Qian Q and Gao ZY* (2015). Genetic analysis of flag leaf size and candidate genes determination of a major QTL for flag leaf width in rice. *Rice*,DOI:10.1186/s12284-014-0039-9. (IF=3.919)

- 32.Li DY, Zhang HJ, Song QM, Wang L, Liu SX, Hong YB, Huang L and Song FM (2015). Tomato SI3-MMP, amember of the Matrix metalloproteinase family, is required for disease resistance against Botrytis cinerea and Pseudomonas syringae pv. tomato DC3000,**BMC Plant Biology**, 15:143. (IF=3.813)
- 33.Zhang YF, Li DY,Zhang HJ, Hong YB, Huang L, Liu SX, Li XH, Ouyang ZG, Song FM (2015). Tomato histone H2B monoubiquitination enzymes SIHUB1 and SIHUB2 contribute to disease resistance against Botrytis cinerea through modulating the balance between SA-and JA/ETmediated signaling pathways. **BMC Plant Biology**, 15:252.(IF=3.813)
- 34.Chen TT, Xu GW,Wang ZQ, Zhang H, Yang JC* and Zhang JH* (2015). Expressions of proteins insuperior and inferior spikelets of rice during grain filling and theirregulation by irrigation regimes. **Proteomics**, DOI10.1002/pmic.201500070. (IF=3.807)
- 35.Wang C,Shen L, Fu YP, Yan CJ and Wang KJ* (2015). A Simple CRISPR/Cas9 System for Multiplex Genome Editing in Rice. **Journal of Genetics and Genomics**,doi:10.1016/j.jgg.2015.09.011. (IF=3.585)
- 36.Yang YJ, Xiong J,Chen RJ, Fu GF, Chen TT, Tao LX* (2015). Nitrate Enhances Cadmium Uptake by Increasing Iron-transporters of Nramp1 and IRT1 in Rice (*Oryza sativa*). **Environmental and Experimental Botany**, (2016)122:141-149. (IF=3.359)
- 37.Huang QN, Shi YF,Zhang XB, Song LX, Feng BH, Wang HM, Xu X, Li XH, Guo D, Wu JL* (2015). Singlebase substitution in *OsCDC48* is responsible for premature senescence and deathphenotype in rice. **J Integr Plant Biol**, DOI: 10.1111/jipb.12372. (IF=3.335)
- 38.Qi JF, Li JC, HanX, Li R, Wu JQ, Yu HX, Hu LF, Xiao YT, Lu J, Lou YG* (2015). Jasmonic acidcarboxyl methyltransferase regulates development and herbivory-induced defense response in rice. **J Integr Plant Biol**, DOI:10. 1111/jipb.12436. (IF=3.335)
- 39.Ren DY, Rao YC, Wu LW, Xu QK, Li ZZ, Yu HP, Zhang Y, Leng YJ, Hu J, Zhu L, Gao ZY, Dong GJ, Zhang GH, Guo LB, Zeng DL, Qian Q (2015). The pleiotropic *ABNORMAL FLOWER AND DWARF1* affects plant height, floral development and grain yield in rice. **J Integr Plant Biol**, DOI:10.1111/jipb.12441. (IF=3.335)
- 40.Wang CY, Zhang QF,Gao YZ, Zhou XP, Ji G, Huang XJ, Hong J*, Zhang CX* (2015). Insight into the three-dimensional structure of maize chloroticmottle virus revealed by Cryo-EM single particle analysis. **Virology**, 485:171-178. (IF=3.321)
- 41.Wan PJ, Fu KY, LüFG, Guo WC and Li GQ* (2015). Knockdown of a putative alanine amino transferase gene affects amino acid content and flight capacity in the Colorado potato beetle *Leptinotarsa decemlineata*. **Amino Acids**, 47(7):1445-1454. (IF=3.293)
- 42.Wan PJ, Yang L,Yuan SY, Tang YH, Fu Q*, Li GQ* (2015). Pathways of Amino Acid Degradation in*Nilaparvata lugens* (Stål) with Special Reference to Lysine-Ketoglutarate Reductase/Sac charopine

Dehydrogenase(LKR/SDH). **PLoS ONE**, 10(5):e0127789. (IF=3.234)

43.Virk N, Li DY, TianLM, Huang L, Hong YB, Li XH, Zhang YF, Liu B, Zhang HJ, Song FM (2015). ArabidopsisRaf-Like Mitogen-Activated Protein Kinase Kinase Kinase Gene *Raf43* Is Requiredfor Tolerance to Multiple Abiotic Stresses. **PLoS ONE**, 10(7): e0133975. (IF=3.234)

44.Li KL, Wan PJ, WangWX, Lai FX, Fu Q* (2015). Ran Involved in the Development and Reproduction Is a Potential Target for RNA-Interference-Based Pest Management in Nilaparvatalugens. **PLoS ONE**, 10(11):e0142142. (IF=3.234)

45.Lv XG, Shi YF, XuX, Wei YL, Wang HM, Zhang XB, Wu JL* (2015). *Oryza sativa* chloroplast signal recognition particle 43 (OscpSRP43) is required for chloroplast development and photosynthesis. **PLoS ONE**, 10(11):e0143249. (IF=3.234)

46.Zhang YK, Zhu DF*,Zhang YP, Chen HZ, Xiang J, Lin XQ (2015). Low pH-induced changes of antioxidant enzyme and ATPase activities in the roots of rice(*Oryza sativa* L.) seedlings. **PLoS ONE**, DOI:10.1371/journal. pone. 0116971. (IF=3.234)

47.Zhao J, Qiu Z, RuanB, Kang S, He L, Zhang S, Dong G, Hu J, Zeng D, Zhang G, Gao Z, Ren D, Hu X,Chen G, Guo L, Qian Q, Zhu L (2015). Functional Inactivation of Putative Photosynthetic Electron Acceptor Ferredoxin C2 (FdC2) Induces Delayed HeadingDate and Decreased Photo synthetic Rate in Rice. **PLoS One**. Nov24;10(11):e0143361. (IF=3.234)

48.Zhang JH, Lin YJ,Zhu LF, Yu SM, Kundu SK, Jin QY (2015). Effects of 1-methylcyclopropene on function of flag leaf and development of superior and inferior spikelets in rice cultivars differing in panicle types. **Field Crops Research**, 177,64-74. (IF=2.976)

49.Nawaz Z, Kakar KU,Li XB, Li S, Zhang B, Shou HX, Shu QY* (2015). Genome-wide Association Mappingof Quantitative Trait Loci (QTLs) for Contents of Eight Elements in Brown Rice(*Oryza sativa* L.). **J Agric Food Chem**, 63:8008-8016. (IF=2.912)

50.Fang YX, Lin HY, Wu LW, Ren DY, Ye WJ, Dong GJ, Zhu L, Guo LB (2015). Genome sequence of *Xanthomonas sacchari* R1, a biocontrol bacteriumisolated from the rice seed. **Journal Biotechnology**, 206: 77-78. (IF=2.871)

51.Li GM, Xu J, Wu LW,Ren DY, Ye WJ, Dong GJ, Zhu L, Zeng DL, Guo LB (2015). Full genome sequence of *Brevibacillus laterosporus* strain B9, a biological control strain isolated from Zhejiang, China. **Journal Biotechnology**, 207:77-78. (IF=2.871)

52.Shi ZY, Ren DY, HuSK, Hu XM, Wu LW, Lin HY, Hu J, Zhang GH, Guo LB (2015). Whole genome sequence of *Pseudomonas aeruginosa* F9676, an antagonistic bacterium isolated from rice seed. **Journal Biotechnology**, 211:77-78. (IF=2.871)

- 53.Sun LJ, Huang L,Hong YB, Zhang HJ, Song FM, Li DY (2015). Comprehensive Analysis Suggests Overlapping Expression of Rice ONAC Transcription Factors in Abiotic and Biotic Stress Responses. *International Journal of Molecular Sciences*, 16:4306-4326. (**IF=2.862**)
- 54.Huang L, Zhang HJ,Hong YB, Liu SX, Li DY and Song FM (2015). Stress-Responsive Expression,Subcellular Localization and Protein–Protein Interactions of the Rice Metacaspase Family. *International Journal of Molecular Sciences*,16:16216-16241. (**IF=2.862**)
- 55.Lu, ZB, Liu, YE,Han, NS, Tian, JC, Peng, YF, Hu, C, Guo, YY and Ye, GY (2015). Transgenic cry1C or cry2A rice has no adverse impacts on the life-tableparameters and population dynamics of the brown planthopper, Nilaparvata lugens (Hemiptera: Delphacidae). *Pest Management Science*, 71(7):937-945. (**IF=2.694**)
- 56.Wan PJ, Fu KY, Lü FG, Wang XX, Guo WC and Li GQ* (2015). Knocking down a putative Δ1-pyrroline-5-carboxylate dehydrogenase gene by RNA interference inhibits flight and causes adultlethality in the Colorado potato beetle Leptinotarsa decemlineata (Say). *Pest Management Science*, 71(10):1387-1396. (**IF=2.694**)
- 57.Li Y, Que YW, Liu YT,Yue XF, Meng XL, Zhang ZG, Wang ZY (2015). The putative G-gmma subunit gene *MGG1* is required for conidiation, appressorium formation, mating and pathogenicity in Magnaporthe oryzae. *Current Genetics*, 61(4):641-651. (**IF=2.682**)
- 58.Arca M, Mougel F,Guillemaud T, Dupas S, Rome Q, Perrard A, Muller F, Fossoud A,Capdevielle-Dulac C, Torres-Leguizamon M, Chen XX, Tan JL, Jung C, Villemant C, Arnold G, Silvain JF (2015). Reconstructing the invasion and the demographichistory of the yellow-legged hornet, Vespa velutina, in Europe. *Biological Nvasions*, 17(8):2357-2371. (**参与**) (**IF=2.586**)
- 59.Khan IA, Ning GA,Liu XH, Feng XX, Lin FC, Lu JP* (2015). Mitochondrial fission protein *MoFis1* mediates conidiation and is required for full virulence of the rice blastfungus Magnaporthe oryzae. *Microbiological Research*, 178:51-58. (**IF=2.561**)
- 60.Liu N, Chen GQ,Ning GA, Shi HB, Zhang CL, Lu JP, Mao LJ, Feng XX, Liu XH, Su ZZ*, Lin FC* (2015).*MoARG1*, *MoARG5,6* and *MoARG7* involved in arginine biosynthesis areessential for growth, conidiogenesis, sexual reproduction, and pathogenicity in*Magnaporthe oryzae*. *Microbiological Research*,180:11-22. (**IF=2.561**)
- 61.Liu N, Chen GQ,Ning GA, Shi HB, Zhang CL, Lu JP, Mao LJ, Feng XX, Liu XH, Su ZZ*, Lin FC*(2016). Agrobacterium tumefaciens-mediated transformation:an efficient toolfor insertional mutagenesis and targeted gene disruption in Harpophora oryzae. *Microbiological Research*,182:40-48. (**IF=2.561**)
- 62.Zhang YF, Jin XY,Ouyang ZG, Li XH, Liu B, Huang L, Hong YB, Zhang HJ, Song FM, Li DY (2015). Vitamin B6 contributes to disease resistance against Pseudomonas syringae pv. tomatoDC3000 and

- Botrytis cinerea in *Arabidopsis thaliana*. *Journal of Plant Physiology*, 175:21-25. (IF=2.557)
- 63.Wu SF, Xu G and YeGY (2015). Characterization of a tyramine receptor type 2 from hemocytes of rice stem borer, *Chilo suppressalis*. *J Insect Physiol*, 75: 39-46. (IF=2.47)
- 64.Zhang CX, Fu GF, Yang XQ, Yang YJ, Zhao X, Chen TT, Zhang XF, Jin QY, Tao LX* (2015). Heat stress is damaging to the spikelets than to the flag leaves because of their different dissipation abilities. *Journal of Agronomy and Crop Science*, DOI:10.1111/JAC.12138. (IF=2.444)
- 65.He XR, Yu ZN, Jiang SJ, Zhang PZ, Shang ZC, Lou YG*, Wu J* (2015). Finding new elicitors that induce resistance in rice to the white-backed planthopper *Sogatella furcifera*. *Bioorganic & Medicinal Chemistry Letters*, 25: 5601-5603. (IF=2.42)
- 66.Huang LC, Dai LP, Wang L, Leng YJ, Yang YL, Xu J, Hu J, Rao YC, Zhang GH, Zhu L, Dong GJ, Guo LB, Qian Q, Zeng DL (2015). Genetic Dissection for Chlorophyll Content of the Top Three Leaves During Grain Filling in Rice (*Oryza sativa* L.). *J Plant Growth Regul*, 34:381–391. (IF=2.237)
- 67.Su X, Fu S, Qian YJ, Xu Y*, Zhou XP* (2015). Identification of Hop stunt viroid from infecting Citrus limon in China using small RNAs deep sequencing approach. *Virology Journal*, 12(1):103. (IF=2.181)
- 68.Li N, Chen Z, Liu Y, Liu Y, Zhou XP*, Wu JX* (2015). Development of monoclonal antibodies and serological assays specific for Barley yellow dwarf virus GAV strain. *Virology Journal*, 12(1):136. (IF=2.181)
- 69.Xu J¹, Liu CL¹, Li MR, Hu J, Zhu L, Zeng DL, Yang YL, Peng YL, Ruan BP, Guo LB*, Li HQ* (2015). A rice DEAD-box RNA helicase protein, OsRH17, suppresses 16S ribosomal RNA maturation in *Escherichia coli*. *Gene*, 555: 318–328. (IF=2.138)
- 70.Zhan XD¹, Sun B¹, Lin ZC¹, Gao ZQ, Yu P, Liu QE, Shen XH, Zhang YX, Chen DB, Cheng SH*, Cao LY* (2015). Genetic mapping of a QTL controlling source–sink size and heading date in rice. *Gene*, 571: 263–270. (IF=2.138)
- 71.Wan PJ, Yuan SY, Tang YH, Li KL, Yang L, Fu Q*, Li GQ* (2015). *Bulletin of Entomological Research*, 105-113. (IF=1.91)
- 72.Yang YL, Xu J, Rao YC, Zeng YJ, Liu HJ, Zheng TT, Zhang GH, Hu J, Guo LB, Qian Q, Zeng DL, Shi QH (2015). Cloning and functional analysis of pale-green leaf (*PGL10*) in rice (*Oryza sativa* L.). *Plant Growth Regul*, DOI:10.1007/s10725-015-0075-5. (IF=1.672)
- 73.Fang YX, Wu WM, Zhang XQ, Jiang H, Lu WY, Pan JJ, Hu J, Guo LB, Zeng DL, Xue DW* (2015). Identification of quantitative trait loci associated with tolerance to low potassium and related ion concentrations at seedling stage in rice (*Oryza sativa* L.). *Plant Growth Regul*. DOI 10.1007/s10725-015-0047-9. (参与) (IF=1.672)

74. Ge CW, E ZG, Pan JJ, Jiang H, Zhang XQ, Zeng DL, Dong GJ, Hu J*, Xue DW* (2015). Map-based cloning of a spotted-leaf mutant gene *OsSL5* in Japonica rice. *Plant Growth Regul.* 75(3):595-603. (IF=1.672)
75. Wang L, Xu J, NianJQ, Shen NW, Lai KK, Hu J, Zeng DL, Ge CW, Zhu L, Qian Q, Zhang GH (2015). Characterization and fine mapping of the rice gene *OsARVL4* regulating leaf morphology and leafvein development. *Plant Growth Regul.*, DOI10.1007/s10725-015-0097-z. (IF=1.672)
76. Wang BH, Zhou GX, Xin ZJ, Ji R, Lou YG (2015). (Z)-3-hexenal, one of the green leaf volatiles, increases susceptibility of rice to the white-backed planthopper *Sogatellafurcifera*. *Plant Molecular Biology Reporter*, 33:377-387. (IF=1.656)
77. Li YY, Tao HJ, Xu J, Shi ZY, Ye WJ, Wu LW, Zeng DL, Gao ZY, Guo LB (2015). QTL analysis for cooking traits of super rice with a high-density SNP genetic map and finemapping of a novel boiled grain length locus. *Plant Breeding*, 134:535-541. (IF=1.598)
78. Shi ZY, Rao YC, Xu J, Hu SK, Fang YX, Yu HP, Pan JJ, Liu RF, Ren DY, Wang XH, Zhu Y, Zhu L, Dong GJ, Zhang GH, Zeng DL, Guo LB, Hu J*, Qian Q* (2015). Characterization and cloning of *SMALL GRAIN 4*, a novel *DWARF11* allele that affects brassinosteroid biosynthesis in rice. *Science Bulletin*, 60(10):905–915. (IF=1.579)
79. Kang SJ, Fang YX, Zou GX, Ruan BP, Zhao J, Dong GJ, Yan MX, Gao ZY, Zhu L* (2015). White-Green Leaf Gene Encoding Protochlorophyllide Oxidoreductase B Is Involved in Chlorophyll Synthesis of Rice. *Crop Science*, 55:284-293. (IF=1.575)
80. Wang LL, Chen YY, Guo L, Zhang HW, Fan YY, Zhuang JY* (2015). Dissection of *qTGW1.2* to three QTLs for grain weight and grain size in rice (*Oryza sativa L.*). *Euphytica*, 202:119–127. (IF=1.385)
81. Zeng YX, Ji ZJ, Yang CD* (2015). The way to a more precise sheath blight resistance QTL in rice. *Euphytica*, 203:33–45. (IF=1.385)
82. Sheng ZH, Tang LQ, Shao GN, Xie LH, Jiao GA, Tang SQ, Hu PS (2015). The rice thermo-sensitive genic male sterility gene *tms9*: pollen abortion and gene isolation. *Euphytica*, 203:145–152. (IF=1.385)
83. Cao XC, Wu LH, Yuan L, Li XY, Zhu YH, Jin QY (2015). Uptake and uptake kinetics of nitrate, ammonium and glycine by pakchoi seedlings (*Brassica Campestris L. ssp. Chinensis L. Makino*). *Scientia Horticulturae*, 186:247-253. (IF=1.365)
84. Lu HP, Edwards M, Wang QZ, Zhao HJ, Fu HW, Huang JZ, Gatehouse A, Shu QY* (2015). Expression of cytochrome P450 CYP81A6 in rice: tissue specificity, protein subcellular localization, and response to herbicide application. *Journal of Zhejiang University SCIENCE B*, 16(2):113-122. (IF=1.278)

- 85.Zhao QC, Liu MH,Zhang XW, Lin CY, Zhang Q, Shen ZC (2015). Generation of insect-resistant and glyphosate-tolerant rice by introduction of a T-DNA containing two Btinsecticidal genes and an *EPSPS* gene. *Journal of Zhejiang University SCIENCE B*, 16(10):824-831. (**IF=1.278**)
- 86.Li Q, Wei SJ, ShiM, Chen XX* (2015). Complete mitochondrial genome of *Neochauliodes bowringi*(MacLachlan) (Megaloptera: Corydalidae). *Mitochondrial DNA*, 26(1):112-113. (**IF=1.209**)
- 87.Li Q, Wei SJ, ShiM, Chen XX* (2015). The mitochondrial genome of *Diadromus collaris*(Hymenoptera: Ichneumonidae). *Mitochondrial DNA*, 26(2):303-304. (**IF=1.209**)
- 88.Li Q, Wei SJ, ShiM, Chen XX* (2015). The complete mitochondrial genome of *Neopanorpa pulchra*(Mecoptera: Panorpidae). *Mitochondrial DNA*, 26(2):305-306. (**IF=1.209**)
- 89.Liu S, Shi XX, Jiang YD Zhu ZJ, Qian P, Zhang MJ, Yu H, Zhu QZ, Gong ZJ and Zhu ZR* (2015). Denovo analysis of the *Tenebrio molitor* (Coleoptera:Tenebrionidae) transcriptome and identification of putative glutathione S-transferase genes. *Applied Entomology & Zoology*, 50:63–71. (**IF=1.144**)
- 90.Wang WX, Li KL,Chen Y, Lai FX, Fu Q* (2015). Identification and Function Analysis of enolase Gene *NIEno1* from *Nilaparvata lugens* (Stål) (Hemiptera:Delphacidae). *J Insect Sci*, 15(1): 66; DOI: 10.1093/jisesa/iev046. (**IF=1.025**)
- 91.Wang L, Zhu JY, Qian C, Fang Q and Ye GY (2015). Venom of the parasitoid wasp *Pteromaluspuparum* contains anodorant binding protein. *Arch Insect Biochem Physiol*, 88(2): 101-110. (**IF=1.021**)
- 92.Qi Y, Teng Z, GaoL, Wu S, Huang J, Ye G and Fang Q (2015). Transcriptome analysis of anendoparasitoid wasp *Cotesia chilonis* (Hymenoptera: Braconidae) reveals genesinvolved in successful parasitism. *Arch Insect Biochem Physiol*, 88(4): 203-221. (**IF=1.021**)
- 93.Gong ZJ, Liu S,Jiang YD, Zhou WW, Liang QM, Cheng J, Zhang CX, Zhu ZR* and Geoff M G (2015). Constructionand Analysis of Antennal cDNA Library From Rice Striped Stem Borer, *Chilo Supressalis*(Walker) (Lepidoptera: Pyralidae),and Expression Profiles of Putative Odorant-Binding Protein and Chemosensory Protein Genes. *Arch Insect Biochem Physiol*, 89(1):35-53. (**IF=1.021**)
- 94.Zhu Y, Fang Q, LiuY, Gao LF, Yan ZC and Ye GY (2015). THE ENDOPARASITOID *Pteromalus puparuml* NFLUENCES HOST GENE EXPRESSION WITHIN FIRST HOUR OF PARASITIZATION. *Arch Insect Biochem Physiol*, 90(3):140-153. (**IF=1.021**)
- 95.Liu S, Shi XX, ZhuQZ, Jiao WJ, Zhu ZJ, Yu H, Wang GY, Zhu ZR* (2015). Identification and expression profiles of putative chemosensory protein genes in *Cnaphalocrocis medinalis* (Lepidoptera: Pyralidae). *Journal of Asia-Pacific Entomology*,18(1):99-105. (**IF=0.946**)

- 96.Zhou WW, Yuan X, Qian P, Cheng JA, Zhang CX, Gurr M G and Zhu ZR* (2015). Identification and expression profiling of putative chemosensory protein genes in two rice planthoppers, *Laodelphax striatellus* (Fallén) and *Sogatella furcifera* (Horváth). *Journal of Asia-Pacific Entomology*, 18(4):771-778. **(IF=0.946)**
- 97.Liu Z, He JH, Chen XX* (2015). The *lacteus*-, *laspeyresiella*- and *mycetophilus*-groups of *Apanteles* Foerster, 1862 (Hymenoptera, Braconidae, Microgastrinae) in China, with descriptions of eight new species. *Zootaxa*, 3949(3):370–392. **(IF=0.906)**
- 98.Tang P, Belokobylskij SA, Chen XX* (2015). Spathius Nees, 1818 (Hymenoptera:Braconidae, Doryctinae) from China with a key to species. *Zootaxa*, 3960 (1): 1–132. **(IF=0.906)**
- 99.Mao J, He JH, Chen XX* (2015). The discovery of the genus *Protodacnusa* Griffiths, 1964(Hymenoptera: Braconidae, Alysiinae) in China, with descriptions of six newspecies. *Zootaxa*, 3990 (3): 355–368. **(IF=0.906)**
- 100.Tu BB, Lelej AS, Chen XX* (2015). Review of the genus *Taiwanomyrme* Tsuneki, 1993(Hymenoptera, Mutillidae, Mutillinae), with description of two new species from China. *Zootaxa*, 4020 (3): 588–600. **(IF=0.906)**
- 101.Zeng YX*, Xia LZ*, WenZH*, Ji ZJ, Zeng DL, Qing Q, Yang CD (2015). Mapping resistant QTLs for rice sheath blight disease with a doubled haploid population. *Journal of Integrative Agriculture*, 14(5): 801–810. **(IF=0.833)**
- 102.Chen Y, Lai FX, SunYQ, Hong LY, Tian JC, Zhang ZT, Fu Q* (2015). Cry1Ab rice does not impact biological characters and functional response of *Cyrtorhinus lividipennis* preying on *Nilaparvata lugens* eggs. *Journal of Integrative Agriculture*, 14(10):2011–2018. **(IF=0.833)**
- 103.Wen ZH¹, Zeng YX¹, Ji ZJ and Yang CD* (2015). Mapping quantitative trait locifor sheath blight disease resistance in Yangdao 4 rice. *Genetics and Molecular Research*, 14 (1): 1636-1649. **(IF=0.775)**
- 104.Wang K, Zhuang JY, Huang DR, Ying JZ, Fan YY* (2015). Genome-wide polymorphisms between the parents of an elite hybrid rice andthe development of a novel set of PCR-based InDel markers. *Genetics and Molecular Research*, 14(2):3209-3222. **(IF=0.775)**
- 105.Zhang YP, E ZG, JiangH, Wang L, Zhou J, Zhu DF* (2015). A comparative study of stress-related gene expression under single stress and intercross stress in rice. *Genetics and Molecular Research*, 14(2):3702-3717. **(IF=0.775)**
- 106.Cai J, Zhang M, GuoLB, Li XM, Bao JS* and Ma LY* (2015). QTLs for rice flag leaf traits in doubled haploid populations indifferent environments. *Genetics and Molecular Research*, 14(2):6786-6795. **(IF=0.775)**

2014年发表

- 1.Sun HY+, Qian Q+, Wu K+, Luo JJ+, Wang SS+, Zhang CW, MaYF, Liu Q, Huang XZ, Yuan QB, Han RX, Zhao M, Dong GJ, Guo LB, Zhu XD, Gou ZH,Wang W, Wu YJ, Lin HX, Fu XD*(2014). Heterotrimeric G proteins regulate nitrogen-use efficiency in rice. *Nature Genetics*, 46(4):652-657. (IF=29.352)
- 2.Xue J, Zhou X, Zhang CX, Yu LL, Fan HW, Wang Z, Xu HJ, Xi Y, Zhu ZR, Zhou WW, Pan PL, Li BL, Colbourne JK, Noda K, Suetsugu Y, Kobayashi T, Zheng Y, Liu SL, Zhang R, Liu Y, Luo YD, Fang DM, Chen Y, Zhan DL, Lv XD, Cai Y, Wang ZB, Huang HJ, Cheng RL, Zhang XC, Lou YH, Yu B, Zhuo JC, Ye YX,Zhang WQ, Shen ZC, Yang HM, WangJ, Wang J, Bao YY and Cheng JA (2014). Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. *Genome Biology*,15:521.(IF=10.81)
- 3.Sang DJ+, Chen DQ+, Liu GF, Liang Y, Huang LZ, Meng XB, Chu JF, Sun XH, Dong GJ, Qian Q, Yuan YD, Li JY*, Wang YH* (2014). Strigolactones regulate rice tiller angle by attenuating shoot gravitropismthrough inhibiting auxin biosynthesis. *PNAS*, 111(30):11199-11204.(IF=9.674)
- 4.Tong H, Xiao Y, Liu D, Gao S, Liu L, Yin Y, Jin Y, Qian Q, Chu C (2014). Brassinosteroid Regulates Cell Elongation by Modulating Gibberellin Metabolism in Rice. *Plant Cell*,
doi:<http://dx.doi.org/10.1105/tpc.114.132092>. (IF=9.339)
- 5.Wang SK+, Zhang SN+, Sun CD, Xu YX,Chen Y, Yu CL, Qian Q, Jiang DA, Qi YH (2014). Auxin response factor (*OsARF12*), a novel regulator for phosphate homeostasis in rice (*Oryza sativa*). *New Phytologist*, 201(1):91-103. (IF=7.672)
- 6.Li FF, Huang CJ, Li ZH^{1*}, Zhou XP* (2014). Suppression of RNA Silencing by a Plant DNA Virus Satellite Requires a Host Calmodulin-Like Protein to Repress RDR6 Expression. *PLoS Pathogens*,10(2):e1003921. (IF=7.562)
- 7.Kong LF, Wu JX, Lu LN, Xu Y, Zhou XP (2014). Interaction between Rice stripe virus disease-specific protein and host PsbP enhances virus symptoms. *Molecular Plant*, 7(4): 691-708. (IF=6.337)
- 8.Lu J, Li JC, Ju HP, Liu XL, Erb M, Wang X, Lou YG (2014).Contrasting effects of ethylene biosynthesis on induced plant resistance against a chewing and a piercing-sucking herbivore in rice. *Molecular Plant*, 7(11):1670-1682. (IF=6.337)
- 9.Zhang GH⁺, Li SY⁺, Wang L⁺,Ye WJ, Zeng DL, Rao YC, Peng YL, Yang YL, Hu J, Xu J, Gao ZY, Zhu L, Dong GJ,Hu XM, Yan MX, Guo LB, Li CY, Qian Q* (2014). *LSCHL4* from Japonica Cultivar, Which Is Allelic to *NAL1*, Increases Yield of Indica Super Rice 93-11. *Molecular Plant*, 7(8):1350-1364. (IF=6.337)
- 10.Xu YX⁺, Zhang SN⁺, Wang SK, Xu LG¹,Li CY, Qian Q, Chen F, Markus, Qi YH*, Jiang DA* (2014). *OsABCB14* functions in auxin transport and iron homeostasis in rice (*Oryza sativa* L.). *The Plant*

***Journal*, 79(1):106-117. (参与)(IF=5.972)**

- 11.Wang SK⁺, Xu YX⁺, Li ZL⁺,Zhang SN, Lim JM, Oh Lee K, Li CY, Qian Q, Jiang DA¹, Qi YH* (2014). OsMOGS is required for N-glycan formation and auxin-mediated root development in rice (*Oryza sativa* L.). ***The Plant Journal***, 78(4):632-645. (参与)(IF=5.972)
- 12.Duan PG⁺, Rao YC⁺, Zeng DL⁺,Yang YL, Xu R, Zhang BL, Dong GJ, Qian Q*, Li YH* (2014). SMALL GRAIN 1, which encodes a mitogen-activated protein kinase kinase 4, influences grain size in rice. ***The Plant Journal***, 77(4):547-557. (IF=5.972)
- 13.Yang Y, Wang DF, Zhang XW, Fang J, Shen ZC (2014). Transgenic rice asbioreactor for production of the candida antarctica lipase B. ***Plant Biotechnology Journal***, 12: 963-970. (IF=5.752)
- 14.Xu XH, Su ZZ, Wang C, Kubicek CP, Feng XX, Mao LJ, Wang JY, Chen C, Lin FC, Zhang CL (2014). The rice endophyte *Harpophora oryzae* genome reveals evolution from a pathogen to a mutualistic endophyte. ***SCIENTIFIC REPORTS***, 4:5783. (IF=5.578)
- 15.Li B*, Ibrahim M, Ge MY, Cui ZQ, Sun GC, Xu F & KubeM (2014). Transcriptome analysis of *Acidovorax avenae* subsp. *avenae* cultivated in vivo and co-culture with *Burkholderia seminalis*. ***SCIENTIFIC REPORTS***, 4:5698. (IF=5.578)
- 16.Pu DQ, Shi M, Wu Q, Gao MQ, Liu JF, Ren SP, Yang F, Tang P, Ye GY, Shen ZC, He JH, Yang D, Bu WJ, Zhang CT, Song QS, Xu D, Strand MR and Chen XX (2014). Flower-visiting insects and their potential impact on transgene flow in rice. ***JOURNAL OF APPLIED ECOLOGY***, 51(5):1357-1365. (IF=4.564)
- 17.Xue DW⁺, Jiang H⁺, Deng XX, Zhang XQ, Wang H, Xu XB, Hu J, Zeng DL, Guo LB, Qian Q (2014). Comparative proteomic analysis provides new insights into cadmium accumulation in rice grain under cadmium stress. ***Journal of Hazardous Materials***, 280:269-278. (IF=4.529)
- 18.Yao M, Liu XF, Li S, Xu Y, Zhou YJ, Zhou XP*, Tao XR*(2014). Rice stripe tenuivirus NSvc2 glycoproteins targeted to golgi body by N-terminal transmembrane domain and adjacent cytosolic 24 amino-acids via COPI- and COP II-dependent secretion pathway. ***Journal of Virology***, 88(6):3223-3234. (IF=4.439)
- 19.Feng GZ, Krell PJ* (2014). *Autographa californica* Multiple Nucleopolyhedrovirus DNA Polymerase C Terminus Is Required for Nuclear Localization and Viral DNA Replication. ***Journal of Virology***, 88(18):10918-10933. (IF=4.439)
- 20.Wu SF, Xu G, Qi YX, Xia RY, Huang J, Ye GY (2014). Two splicing variants of a novel family of octopamine receptors with different signaling properties. ***J Neurochem***, 129(1): 37-47. (IF=4.281)

- 21.Song J, Wei XJ, Shao GN, Sheng ZH, Chen DB, Liu CL, JiaoGA, Xie LH, Tang SQ*, Hu PS* (2014). The rice nuclear gene *WLP1* encoding a chloroplastribosome L13 protein is needed for chloroplast development in rice grown under low temperature conditions. *Plant Molecular Biology*, 84(3):301-314. (IF=4.257)
- 22.Liu H, Yang CL, Ge MY, Ibrahim M, Li B, Zhao WJ, Chen GY,Zhu B, Xie GL* (2014). Regulatory role of tetR gene in a novel gene cluster of Acidovorax avenae subsp. avenae RS-1 under oxidative stress. *Front Microbiology*, 5:547. (IF=3.989)
- 23.Zhang YF, Liu B, Li XH, Ouyang ZG, Huang L, Hong YB,Zhang HJ, Li DY, Song FM (2014). The denovo biosynthesis of vitamin B6 isrequired for disease resistance against Botrytis cinerea in tomato. *Molecular Plant Microbe Interactions*, 27:688-699. (IF=3.944)
- 24.Huang JZ, Zhang HL, E ZG, Shu QY (2014). Workable malesterility systems for hybrid rice: Genetics, biochemistry, molecular biology, and utilization. *Rice*,7:13. (IF=3.919)
- 25.Guo LB, Gao ZY, Qian Q* (2014). Application of resequencing to rice genomics, functional genomics and evolutionary analysis. *Rice*,7(4):1-10. (IF=3.919)
- 26.Wei SJ, Li Q, van AK, Chen XX (2014). Two mitochondrial genomes from the families Bethylidae and Mutillidae:Independent rear rangement of protein-coding genes and higher-level phylogeny of the Hymenoptera. *MOLECULAR PHYLOGENETICS AND EVOLUTION*, 77,1-10. (IF=3.916)
- 27.Li XH, Huang L, Zhang YF, Ouyang ZG, Hong YB, Zhang HJ,Li DY, Song FM (2014). Tomato SR/CAMTA transcription factors SISR1 and SISR3L negatively regulate disease resistance response and SISR1L positively modulates drought stress tolerance. *BMC Plant Biology*,14:286. (IF=3.813)
- 28.Li XH, Zhang YF, Huang L, Ouyang ZG, Hong YB, Zhang HJ,Li DY, Song FM (2014). Tomato SIMKK2 and SIMKK4 contribute to disease resistance against Botrytis cinerea. *BMC Plant Biology*, 14:166. (IF=3.813)
- 29.Wang CH, Yang YL, Yuan XP, Xu Q, Feng Y, Yu HY, Wang YP andWei XH (2014). Genome-wide association study of blast resistance in indicarice. *BMC Plant Biology*, 14:311. (IF=3.813)
- 30.Yang YL⁺, Xu J⁺, Leng YJ, Xiong GS,Hu J, Zhang GH, Huang LC, Wang L, Guo LB, Li JY, Chen F, Qian Q, Zeng DL* (2014).Quantitative trait loci identification, fine mapping and gene expressionprofiling for ovicidal response to white backed planthopper (*Sogatella furcifera*Horvath) in rice (*Oryza sativa* L.). *BMC Plant Biology*, 14(145):1-16.(IF=3.813)
- 31.Wang CH, Zheng XM, Xu Q, Yuan XP, Huang L, Zhou HF, Wei XH, Ge S (2014). Genetic diversity and classification of *Oryza sativa* with emphasis on Chinese rice germplasm. *Heredity*,112: 489-496. (IF=3.805)

- 32.Chen JY, Guo L, Ma H, Chen YY, ZhangHW, Ying JZ, Zhuang JY (2014). Fine mapping of *qHd1*, a minor heading date QTL with pleiotropism for yield traits in rice (*Oryza sativa* L.). *Theor Appl Genet*, 127:2515-2524. (IF=3.79)
- 33.Li RQ, Huang JZ, Zhao HJ, Fu HW, Li YF, Liu GZ, Shu QY (2014).A down-regulated epi-allele of the genomes uncoupled 4 gene generates a xanthamarker trait in rice. *THEORETICAL AND APPLIED GENETICS*,127(11) : 2491-2501. (IF=3.79)
- 34.Liu B, Hong YB, Zhang YF, Li XH, Huang L, Zhang HJ, Li DY,Song FM (2014). Tomato WRKY transcriptional factor SIDRW1 is required for disease resistance against *Botrytis cinerea* and tolerance to oxidative stress. *Plant Science*, 227:145-156. (IF=3.607)
- 35.Hu J⁺, Dong GJ⁺, Fang YX⁺,Rao YC, Xu J, Xue DW, Yu HP, Ge CW, Shi ZY, Pan JJ, Zhu L, Zeng DL, Zhang GH,Guo LB, Qian Q* (2014). A New-Nipponbare Rice Germplasm with High Seed-Setting Rate. *Journal of Genetics and Genomics*, 41(10):549-552. (IF=3.585)
- 36.Shu XL, Sun J, Wu DX (2014). Effects of grain development on formation of resistant starch in rice. *Food Chemistry*, 164:89-97. (IF=3.391)
- 37.Xie LH⁺, Tang SQ⁺, Chen N, Luo J,Jiao GA, Shao GN, Wei XJ, Hu PS* (2014). Optimisation of near-infrared reflectance model in measuring protein and amylose content of rice flour. *Food Chemistry*, 142(1):92-100. (IF=3.391)
- 38.Fang YX, Hu J, Xu J, Yu HP, Shi ZY, XiongGS, Zhu L, Zeng DL, Zhang GH, Gao ZY, Dong GJ, Yan MX, Guo LB, Wang YHand Qian Q* (2014). Identification and characterization of *Min1*, a generegulating rice shoot development. *JIPB*, DOI: 10.1111/jipb.12230.(IF=3.335)
- 39.Chen SL, Liu RF, Koyanagi KO, Kishima Y* (2014). Rice genomes recorded ancient pararetrovirus activities: Virus genealogy and multiple origins of endogenization during rice speciation. *Virology*, 471-473(0):141-152.(IF=3.321)
- 40.Yu HX, Ji R, Ye WF, Chen HD, Lai FX, Fu Q, Lou YG (2014).Transcriptome analysis of fat bodies from two brown planthopper (*Nilaparvatalugens*) populations with different virulence levels in rice. *PLoS One*,9(2) e88528. doi:10.1371/journal.pone. 0088528. (IF=3.234)
- 41.Zeng XQ, Chen GQ, Liu XH, Dong B, Shi HB, Lu JP, Lin FC (2014).Crosstalk between *SNF1* pathway and the peroxisome-mediated lipid metabolism inMagnaporthe oryzae. *PLoS One*, e103124. (IF=3.234)
- 42.Li Y, Yue XF, Que YW, Yan X, Ma ZH, Talbot NJ, Wang ZY (2014).Characterisation of four LIM protein-encoding genes involved ininfection-related development and pathogenicity by the rice blast fungus Magnapor the oryzae. *PLoS One*, 9(2): e88246. (IF=3.234)

- 43.Liu B, Ouyang ZG, Zhang YF, Li XH, Hong YB, Huang L, LiuSX, Zhang HJ, Li DY, Song FM (2014). Tomato NAC transcription factor SISRN1 positively regulates defense response against biotic stress but negatively regulates abiotic stress response. *PLoS One*, 9(7):e102067. (IF=3.234)
- 44.Xu X, Bai H, Liu C, Chen E, Chen Q, Zhuang J (2014). Genome-wide analysis of micro RNAs and their target genes related to leafsenescence of rice. *PLoS One*, 9(12): e114313. (IF=3.234)
- 45.Wang CH, Liu XJ, Peng ST, Xu Q, Yuan XP, Feng Y, Yu HY,Wang YP, Wei XH (2014). Development of novel microsatellite markers for the BBCC Oryza genome (Poaceae) using high-throughput sequencing technology. *PLoS One*, 9 (3): e91826. (IF=3.234)
- 46.Zhang P, Liu XD, Tong HH, Lu YG*, Li JQ* (2014). Association Mapping for Important Agronomic Traits in Core Collection of Rice(*Oryza sativa* L.) with SSR Markers. *PLoS One*, 9(10):e111508:1-16. (IF=3.234)
- 47.Wang DY, Chen S, Wang ZM, Ji CL, XuCM, Zhang XF* (2014). Optimizing Hill Seeding Density for High-Yielding HybridRice in a Single Rice Cropping System in South China. *PLoS One*, 9(10):e109417:1-14. (IF=3.234)
- 48.Zhou GX, Ren N, Qi JF, Lu J, Xiang CY, Ju HP, Cheng JA, Lou YG (2014). The 9-lipoxygenase Osr9-LOX1 interacts with the 13-lipoxygenase-mediated pathway to regulate resistance to chewing and piercing-sucking herbivores in rice. *Physiologia Plantarum*, 152:59–69. (IF=3.138)
- 49.Zhang HJ, Jin XY, Huang L, Hong YB, Zhang YF, Ouyang ZG,Li XH, Song FM (2014). Molecular characterization of ricesphingosine-1-phosphate lyase gene *OsSPL1* and functional analysis of its role in disease resistance response. *Plant Cell Reports*, 33:1745-1756. (IF=3.071)
- 50.Peng YL, Gao ZY, Zhang B, Liu CL, Xu J, Ruan BP, Hu J,Dong GJ, Guo LB, Liang GH, Qian Q* (2014). Fine mapping and candidate geneanalysis of a major QTL for panicle structure in rice. *Plant Cell Reports*, 33(11):1843-1850. (IF=3.071)
- 51.Rao YC, Li YY, Qian Q* (2014). Recent progress on molecular breeding of rice in China. *Plant Cell Reports*, 33(4), SI:551-564. (IF=3.071)
- 52.Wu WM, Cheng SH (2014). Root genetic research, an opportunity and challenge to rice improvement. *Field Crops Research*,165:111-124. (IF=2.976)
- 53.Ojaghian MR, Wang L, Cui ZQ, Yang CL, Tao ZY, Xie GL* (2014). Antifungal and SAR potential of crude extracts derived from neemandginger against storage carrot rot caused by *Sclerotinia sclerotiorum*. *Industrial Crops and Products*, 55:130-139. (IF=2.837)
- 54.Li Z⁺, Zhang YX⁺, Liu L, Liu QE, BiZZ, Yu N, Cheng SH*, Cao LY* (2014). Fine mapping of the *lesion mimic and earlysenescence 1 (lmes1)* in rice (*Oryza sativa*). *Plant Physiology and Biochemistry*, 80(0):300-307. (IF=2.756)

- 55.Wan PJ, Fu KY, Lü FG, Wang XX, Guo WC, Li GQ (2014). Knocking down a putative Δ1-pyrroline-5-carboxylate dehydrogenase gene by RNA interference inhibits flight and causes adult lethality in the Colorado potato beetle *Leptinotarsa decemlineata* (Say). *Pest Management Science*, doi:10.1002/ps.3941. (IF=2.694)
- 56.Wan PJ, Yang L, Wang WX, Fan JM, Fu Q and Li GQ (2014). Constructing the major biosynthesis pathways for amino acids in the brown planthopper, *Nilaparvatalugens* (Stål) (Hemiptera: Delphacidae) based on the transcript omedata. *Insect Molecular Biology*, 23(2):152-164. (IF=2.589)
- 57.Cui ZQ, Ibrahim M, Yang CL, Fang Y, Annam H, Li B*, WangYL, Xie GL, Sun GC (2014). Susceptibility of Opportunistic Burkholderia glumae to Copper Surfaces Following Wet or Dry Surface Contact. *Molecules*, 19:9975-9985. (IF=2.416)
- 58.Ye HX, Harasymow S, Zhang XQ, Paynter B, Wu DX, Jones M, Shu XL, Li CD (2014). Sequence variation and haplotypes of lipoxygenase gene *LOX-1* in the Australian barley varieties. *BMC Genetics*, 34(4): 2081-2089. (IF=2.387)
- 59.Nawaz Z, Kakar KU, Saand MA, Shu QY (2014). Cyclic nucleotide-gated ion channel gene family in rice, identification, characterization and experimental analysis of expression response to plant hormones, biotic and abiotic stresses. *BMC Genomics*, 15:853. (IF=2.387)
- 60.Xu Y, Huang LZ, Wang ZC, Fu S, Che J, Qian YJ, Zhou XP (2014). Identification of Himetobi P virus infection in the small brown planthopper by deep sequencing and assembly of virus-derived small interfering RNAs. *Virus Research*, 179:235-240. (IF=2.324)
- 61.Wang Y, Gupta S, Wallwork H, Zhang XQ, Zhou GF, Broughton S, Loughman R, Lance R, Wu DX, Shu XL, Li CD (2014). Combination of seedling and adult plant resistance to leaf scald for stable resistance in barley. *Molecular Breeding*, 15(1): 36-41. (IF=2.246)
- 62.Zhang HL, Huang JZ, Liu QL, Nawaz Z, Lu HP, Gong JY, Zhu YJ, Yan WG, Shu QY (2014). Characterization of an RNase Z nonsense mutation identified exclusively in environment-conditioned genic male sterile rice. *Molecular Breeding*, 34(2): 481-489. (IF=2.246)
- 63.Zhang JH, Zhu LF, Yu SM, Jin QY* (2014). Involvement of 1-Methylcyclopropene in Plant Growth, Ethylene Production, and Synthase Activity of Inferior Spikelets in Hybrid Rice Differing in Panicle Architectures. *Journal of Plant Growth Regulation*, 33(3):551-561. (IF=2.237)
- 64.Liu SH, Yao J, Yao HW, Jiang PL, Yang BJ, Tang J* (2014). Biological and biochemical characterization of a red-eye mutant in *Nilaparvatalugens* (Hemiptera: Delphacidae). *Insect Science*, 21(4):469-476. (IF=2.144)
- 65.Xu J, Liu CL, Li MR, Hu J, Zhu L, Zeng DL, Yang YL, Peng YL, Ruan BP, Guo LB, Li HQ (2014). A rice DEAD-box RNA helicase protein, OsRH17, suppresses 16S ribosomal RNA maturation in *Escherichia coli*.

GENE, 555:318-328. (IF=2.138)

66.Li WX, Huang JZ, Zhao HJ, Tan YY, Cui HR, Poirier Y, ShuQY (2014). Production of low phytic acid rice by hairpin RNA- and artificial microRNA-mediated silencing of OsMIK in seeds. **Plant Cell Tissue and Organ Culture**, 119:15–25. (IF=2.125)

67.Ojaghian MR, Chen Y, Chen SY, Cui ZQ, Xie GL* & Zhang JZ (2014). Antifungal and enzymatic evaluation of plant crude extracts derived from cinnamon and rosemary against *Sclerotinia* carrot rot. **Ann Appl Biol**, 164:415-429. (IF=2.0)

68.Wu JX, Ni YQ, Liu H, Ding M, Zhou XP* (2014). Monoclonal antibody-based serological assays and immunocapture-RT-PCR for detecting Rice dwarf virus in field rice plants and leaf hopper vectors. **Journal of Virological Methods**, 195(1):134-140. (IF=1.781)

69.Kakar KU, Nawaz Z, Cui ZQ, Almoneafy A, Zhu B, Xie GL* (2014). Characterizing the mode of action of *Brevibacillus laterosporus* B4 for control of bacterial brown spot of rice caused by *A. avenae* subsp. *avenae* RS-1. **World J Microbiol Biotechnol**, 30:469–478. (IF=1.779)

70.Wang JY, Xu XH, Mao LJ, Lao JP, Lin FC, Yuan ZL, Zhang CL (2014). Endophytic Diaporthe from Southeast China are genetically diverse based on multi-locus phylogeny analyses. **World journal of Microbiology & Biotechnology**, 30(1): 237-243. (IF=1.779)

71.Ibrahim M, Tao ZY, Annam H, Yang CL, Mehmoona I, AbdulW, Fang Y, Li B, Xie GL* (2014). Deciphering the role of *Burkholderia cenocepacia* membrane proteins in antimicrobial properties of chitosan. **Arch Microbiol**, 196:9-16. (IF=1.667)

72.Xin ZJ, Wang Q, Yu ZN, Hu LC, Li JC, Xiang CY, Wang BH, Lou YG (2014). Overexpression of a xylanase inhibitor gene, *OsHI-XIP*, enhances resistance in rice to herbivores. **Plant Molecular Biology Reporter**, 32(2): 465–475. (IF=1.656)

73.Wang BH, Zhou GX, Xin ZJ, Ji R, Lou YG (2014). (Z)-3-hexenal, one of the green leaf volatiles, increases susceptibility of rice to the white-backed planthopper *Sogatella furcifera*. **Plant Molecular Biology Reporter**, DOI:10.1007/s11105-014-0756-7. (IF=1.656)

74.Li DY, Zhang HJ, Hong YB, Huang L, Li XH Li, Zhang YF, Ouyang ZG, Song FM (2014). Genome-wide identification, biochemical characterization, and expression analyses of the YTH domain-containing RNA-binding protein family in *Arabidopsis* and rice. **Plant Molecular Biology Reports**, 32:1169-1186. (IF=1.656)

75.Chen XX (2014). Taxonomy of parasitoid wasps in China: An overview. **BIOLOGICAL CONTROL**, 68, 57-72. (IF=1.635)

- 76.Kakar K, Duan YP, Nawaz Z, Sun GC, Almoneafy A, Annam H, Elshakh A, Li B, Xie GL* (2014). A novel rhizobacterium Bk7 for biological control of brown sheath rot of rice caused by *Pseudomonas fuscovaginae* and its mode of action. *Eur J Plant Pathol*, 138:819-834. (**IF=1.49**)
- 77.Almoneafy A, Kakar K, Nawaz Z, Li B, Saand M, Yang CL, Xie GL* (2014). Tomato plant growth promotion and antibacterial-related-mechanisms of four rhizobacterial *Bacillus* strains against *Ralstonia solanacearum*. *Symbiosis*, 63:59-70. (**IF=1.438**)
- 78.Leng YJ, Xue DW, Yang YL, Hu SK, Su Y, Huang LC, Wang L, Zheng TT, Zhang GH, Hu J, Gao ZY, Guo LB, Qian Q*, Zeng DL* (2014). Mapping of QTLs for eating and cooking quality-related traits in rice(*Oryza sativa* L.). *Euphytica*, 197(1):99-108. (**IF=1.385**)
- 79.Zeng YX, Ji ZJ, Yang CD* (2014). The way to amore precise sheath blight resistance QTL in rice. *Euphytica*, DOI:10.1007/s10681-014-1246-6. (**IF=1.385**)
- 80.Lu ZB, Tian JC, Wang W, Xu HX, Hu C, Guo YY, Peng YF, Ye GY (2014). Impacts of Bt Rice Expressing Cry1C or Cry2A Protein on the Performance of Nontarget Leafhopper, *Nephrotettix cincticeps*(Hemiptera:Cicadellidae), Under Laboratory and Field Conditions. *Environmental Entomology*, 43(1):209-217. (**IF=1.295**)
- 81.Lu ZB, Tian JC, Han NS, Hu C, Peng YF, Stanley D, Ye GY(2014). No Direct Effects of Two Transgenic Bt Rice Lines, T1C-19 and T2A-1, on the Arthropod Communities. *Environmental Entomology*, 43(5): 1453-1463. (**IF=1.295**)
- 82.Jiao GA, Wei XJ, Shao GN, Xie LH, Sheng ZH, Tang SQ*, Hu PS* (2014). Impact of Rice Flour Cold-Water-Soluble Fraction Removal on Gelatinization and Pasting Properties. *Cereal Chemistry*, 91(5):473-481. (**IF=1.231**)
- 83.Ke YG, Yang ZJ, Yu SW*, Li TF, Wu JH, Gao H, Fu YP, Luo LJ* (2014). Characterization of *OsDREB6* Responsive to Osmotic and Cold Stresssesin Rice. *Journal of Plant Biology*, 57(3):150-161. (**IF=1.208**)
- 84.Tang P, Belokobylskij S, Chen XX (2014). The genus Polystenus (Hymenoptera: Braconidae: Doryctinae) in China, with descriptions of two new species. *Journal of Insect Science*, 14,66. (**IF=1.025**)
- 85.Ysn CJ, He JH, Chen XX (2014). The discovery of the genus Spasskia Belokobylskij, 1989 (Hymenoptera: Braconidae) in China, with description of a newspecies. *Journal of Insect Science*, 14,119. (**IF=1.025**)
- 86.Yang YL⁺, Rao YC⁺, Xu J⁺,Shao GN, Leng YJ, Huang LC, Wang L, Dai LP, Zhang GH, Hu J, Zhu L, Li C, Gao Z,Guo LB, Qian Q*, Zeng DL* (2014). Genetic analysis of sugar-related traits in rice grain. *South African Journal of Botany*, 93:137-141. (**IF=0.987**)

- 87.Zhao J, Fang YX, Kanga S, Ruan BP, Xu J, Dong GJ, Yan MX, Hu J, Zeng DL, Zhang GH, Gao GY, Guo LB, Qian Q, Zhu L (2014). Identification and characterization of a new allele for *ZEBRA LEAF 2*, a gene encoding carotenoid isomerase in rice. *South African Journal of Botany*, 95:102-111. (IF=0.987)
- 88.Fan JM, Wan PJ, Fu Q, Li N, Mu LL, Li GQ (2014). Molecular cloning and characterization of two alanine amino transferase genes in the white-backed planthopper *Sogatella furcifera*. *Journal of Asia-Pacific Entomology*, 7:355–361. (IF=0.946)
- 89.Hu Y, Cheng JA, Zhu ZR, Heong KL, Fu Q, He JC (2014). Acomparative study on population development patterns of *Sogatella furcifera* between tropical and subtropical areas. *Journal of Asia-Pacific Entomology*, 17: 845–851. (IF=0.946)
- 90.Zhang JP, Peng G, Duan GF, Zhou YJ, Yang S & Yu LQ(2014). Bipolaris eleusines, a potential mycoherbicide candidate for control of barnyard grass (*Echinochloa crus-galli*). *Biocontrol Science and Technology*, 24(7): 839-846. (IF=0.938)
- 91.Tu BB, Lelej AS, Chen XX (2014). Review of the genus *Cystomutilla* André, 1896 (Hymenoptera: Mutillidae: Sphaeropthalminae:Sphaeropthalmini), with description of the new genus *Hemutilla* gen. nov. and four new species from China. *ZOOTAXA*, 3889(1), 071–091. (IF=0.906)
- 92.Song SN, He JH, Chen XX (2014). The subgenus *ChoerasMason*, 1981 of genus *Apanteles* Foerster, 1862 (Hymenoptera, Braconidae, Microgastrinae) from China,with descriptions of eighteen new species. *ZOOTAXA*, 3754(5),501-554. (IF=0.906)
- 93.Liu Z, He JH, Chen XX (2014). The grandiculus- and metacarpalis-group of the genus *Apanteles* Foerster, 1862 (Hymenoptera,Braconidae, Microgastrinae) from China, with descriptions of eight new species.*ZOOTAXA*, 3765(5), 435-457.(IF=0.906)
- 94.Wu Q, H JH, Chen XX (2014). The genus *Ademon* Haliday (Hymenoptera: Braconidae: Opiinae) from China, with descriptions of two newspecies. *ZOOTAXA*, 3794(2), 294-298. (IF=0.906)
- 95.Shen HC+, Shi YF+, Feng BH, Wang HM, Xu X, Huang QN, Lü XG,Wu JL* (2014). Identification and Genetic Analysis of a Novel Rice Spotted-LeafMutant with Broad-Spectrum Resistance to *Xanthomonas oryzae* pv.*oryzae*. *Journal of Integrative Agriculture*, 13(4):713-721. (IF=0.833)
- 96.Yao Q*, Xian DX, Liu QJ, Yang BJ, Diao GQ, Tang J (2014). Automated Counting of Rice Planthoppers in Paddy Fields Based on ImageProcessing. *Journal of Integrative Agriculture*, 13(8):1736-1745. (IF=0.833)
- 97.Ji ZJ, Shi JY, Zeng YX, Qian Q*, Yang CD* (2014). Application of a simplified marker-assisted backcross technique for hybrid breeding in rice. *Biologia*, 69(4):463-468. (IF=0.827)

- 98.E ZG, Zhang YP, Zhou JH, Wang L* (2014).Mini review roles of the bZIP gene family in rice. ***Genetics and Molecular Research***,13(2):3025-3036. (**IF=0.775**)
- 99.Liu M, Wang BJ, Jiang KY, Gong K, Sun SJ, Wang L*, Liu WZ*,Fu YP (2014). Rice Bran Expressing a Shrimp Antimicrobial Peptide Confers Delayed Spoilage of Fish Feed and Resistance of Tilapia to Aeromonashydrophila. ***Journal of the World Aquaculture Society***, 45(3):269-278. (**IF=0.732**)
- 100.Nawaz Z, Shu QY (2014). Molecular nature of chemically and physically induced mutants in plants:are view. ***PLANT GENETIC RESOURCES-CHARACTERIZATION AND UTILIZATION***, 12:S74-S78. (**IF=0.58**)
- 101.Weng LS, Deng LH, Lai FX, Xiao GY (2014).Optimization of the Cry2Aa Gene and Development of Insect-resistant andHerbicide-tolerant Photoperiod-sensitive Genic Male Sterile Rice. ***Czech J Genet Plant Breed***, 50 (1): 19–25. (**IF=0.364**)
- 102.Ma YQ, Zhang M, Li YL, Shui JF, Zhou YJ (2014). Allelopathy of rice (*Oryza sativa L.*) root exudates and its relations with *Orobanche cumana* Wallr. and *Orobanche minor* Sm. germination. ***Journal of Plant Interactions***, 9(1):722-730. (**IF=0.00**)

2013年发表

- 1.Gao ZY, Zhao SC, He WM, Guo LB, Peng YL, Wang JJ, Guo XS, Zhang XM, Rao YC, Zhang C, Dong GJ, Zheng FY, LuCX, Hu J, Zhou Q, Liu HJ, WuHY, Xu J, Ni PX, Zeng DL, Liu DH, Tian P, Gong LH, Ye C, Zhang GH, Wang J, TianFK, Xue DW, Liu Y, Zhu L, Chen MS, Li JY, Cheng SH, Zhang GY, Wang J, Qian Q*(2013).Dissecting yield-associated loci in super hybrid rice by resequencing recombinant inbred lines and improving parental genome sequences. ***P Natl Acad Sci USA***,110(35):14492-14497. (**IF=9.737**)
- 2.Li SY, Zhao BR, YuanDY, Duan MJ, Qian Q, Tang L, Wang B, Liu XQ, Zhang J, Wang J, Sun JQ, Li CY (2013). Rice zinc finger protein DST enhances grain production through controlling *Gn1a/OsCKX2* expression. ***P Natl Acad Sci USA***, doi:10.1073/pnas.1300359110.(参与) (**IF=9.737**)
- 3.Lu Z, Yu H, Xiong G, Wang J, Jiao Y, Liu G, Jing Y, Meng X,Hu X, Qian Q, Fu X, Wang YH, Li JY* (2013). Genome-Wide Binding Analysis of the Transcription Activator *IDEAL PLANT ARCHITECTURE1* Reveals a Complex Network Regulating Rice Plant Architecture. ***Plant Cell***, 25(10):3743-3759. (参与) (**IF=9.251**)
- 4.Liu L, Shang-Guan K, Zhang B, Liu X, Yan M, Zhang L, Shi Y,Zhang M, Qian Q, Li J, Zhou YH* (2013). *Brittle Culm1*, a COBRA-like protein,functions in cellulose assembly through binding cellulose microfibrils. ***PLoS Genet***. 9(8):e1003704. (参与) (**IF=8.517**)
- 5.Hu XM, Qian Q,Xu T, Zhang YE, Dong GJ, Gao T, Xie Q, Xue YB*(2013). The U-Box E3 Ubiquitin Ligase TUD1 Functions with a Heterotrimeric G α Subunit to Regulate Brassinosteroid-Mediated Growth in Rice.***PLoS Genet***, 9(3): 1-13. (参与) (**IF=8.517**)

- 6.Nallamilli BR, Zhang J,Mujahid HN, Malone BM, Bridges SM, Peng ZH (2013). Polycomb Group Gene *OsFIE2* Regulates Rice (*Oryza sativa*) Seed Development and Grain Filling via a Mechanism Distinct from *Arabidopsis*. *PLoS Genetics*, 9(3): e1003322. (参与) (IF=8.517)
- 7.Sun J, Qian Q, Ma DR, Xu ZJ, Liu D, Du HB, Chen WF* (2013). Introgression and selection shaping the genome and adaptive loci of weedy rice in northern China. *New Phytol*, 197(1): 290-9. (IF=6.736)
- 8.Wang S, Zhang S, Sun C, Xu Y, Chen Y, Yu C, Qian Q, Jiang DA*,Qi Y*(2014). Auxin response factor (OsARF12), a novel regulator for phosphatehomeostasis in rice (*Oryza sativa*). *New Phytol*, 201(1): 91-103. (参与)(IF=6.736)
- 9.Wu XR, Tang D, Li M, Wang KJ,Cheng ZK(2013). *Loose plant architecture 1*, an INDETERMINATE domain protein involved in shoot gravitropism, regulates plant architecture in rice. *Plant Physiol*, 61(1): 317-29.(参与)(IF=6.555)
- 10.Chen L, Xiong G, Cui X, Yan M, Xu T,Qian Q, Xue Y, Li J, Wang Y* (2013). *OsGRAS19* may be a novel component involved in the brassinosteroid signaling pathway in rice. *Mol Plant*. 6(3): 988-91. (参与) (IF=6.126)
- 11.Kong LF, Wu JX, Lu LN, Xu Y, Zhou XP*(2013). Interaction between Rice stripe virus disease-specific protein and host PsbP enhances virus symptoms. *Mol Plant*, doi: 10.1093/mp/sst158. (IF=6.126)
- 12.Wang J, Hu J, Qian Q, Xue HW(2013). *LC2* and *OsVIL2* Promote Rice Flowering by Photoperiod-induced Epigenetic Silencing of *OsLF*. *Mol Plant*, 6(2):514-527. (参与) (IF=6.126)
- 13.Zhang YM, Zhang G, Xiao N, Wang LN, FuYP, Sun ZX, Fang RX* (2013). The rice 'nutrition response and root growth' (NRR) gene regulates heading date. *Mol Plant*, 6(2): 585-588. (参与) (IF=6.126)
- 14.Luo Q, Tang D, Wang M, Luo WX, Zhang L, Qin BX, Shen Y, Wang KJ, Li YF, Cheng ZK (2013). The role of *OsMSH5* in cross over formation during rice meiosis. *Mol Plant* , 6(3): 729-742. (参与) (IF=6.126)
- 15.Xin ZJ, Wang Q, Yu ZN, Hu LC, Li JC, Xiang CY, Wang BH, Lou YG (2013)*. Overexpression of a xylanase inhibitor gene, *OsHI-XIP*, enhances resistance in rice to herbivores. *Plant Molecul Biol Rep*, DOI10.1007/s11105-013-0661-5. (IF=5.319)
- 16.Shen C, Wang S, Zhang S, Xu Y, Qian Q, Qi Y*, Jiang de A* (2013). OsARF16 a transcription factor, is required for auxin and phosphatestarvation response in rice (*Oryza sativa* L.). *Plant Cell Environ*, 36(3):607-20. (参与)(IF=5.135)
- 17.Ma L, Liu SM, Shi M, Chen XX*, Li S (2013). Ras1CA-upregulated bcpi inhibits cathepsin activity to prevent tissuedestruction of the Bombyx posterior silk gland.*J Proteome Res*, 12 (4):1924-1934. (IF=5.056)

- 18.Zhai RR, Feng Y, Wang HM, Zhan XD, Shen XH, Wu WM, Zhang YX, Chen DB, Dai GX, Yang ZL, Cao LY*, Cheng SH* (2013). Transcriptome analysis of rice root heterosis by RNA-Seq. **BMC Genomics**, 14:19. (**IF=4.397**)
- 19.Yu P, Wang CH, Xu Q, Feng Y, Yuan XP, Yu HY, Wang YP, Tang SX, Wei XH* (2013). Genome-wide copy number variations in *Oryza sativa* L. **BMC Genomics**, 14:649. (**IF=4.397**)
- 20.Wang CH, Zheng XM, Xu Q, Yuan XP, Huang L, Zhou HF, Wei XH*, Ge S* (2013). Genetic diversity and classification of *Oryza sativa* with emphasis on Chinese rice germplasm. **Heredity**, (in press). (**IF=4.11**)
- 21.Li B, Shan CL, Zhou Q, Fang Y, Wang YL, Xu F, Han LR, Ibrahim M, Guo LB*, Xie GL, Sun GC* (2013). Synthesis, characterization, and antibacterial activity of cross-Link chitosan-Glutaraldehyde. **Mar. Drugs**, 11: 1534-1552. (**IF=3.978**)
- 22.Feng BH, Yang Y, Shi YF, Shen HC, Wang HM, Xu X, Huang QN, Lv XG, Wu JL* (2013). Characterization and genetic analysis of a novel rice spotted-leaf mutant HM47 with broad-spectrum resistance to *anthomonas oryzae* pv.*oryzae*. **J Integr Plant Biol**, 55(5): 473-483. (**IF=3.75**)
- 23.Li W, Wu C, Hu GC, Xing L, Qian WJ, Si HM, Sun ZX, Wang XC, Fu YP*, Liu WZ* (2013). Characterization and Fine Mapping of a Novel Rice Narrow Leaf Mutant *nal9*. **J Integr Plant Biol**, 55(11): 1016-1025. (**IF=3.75**)
- 24.Zhai RR, Feng Y, Zhan XD, Shen XH, Wu WM, Yu P, Zhang YX, Chen DB, Wang HM, Lin ZC, Cao LY*, Cheng SH* (2013). Identification of transcriptome SNPs for assessing allele-specific gene expression in a super-hybrid rice Xieyou 9308. **PLoS ONE**, 8(4):1-6. (**IF=3.73**)
- 25.Wu SF, Sun FD, Qi YX, Yao Y, Fang Q, Huang J, Stanley D, Ye GY (2013). Parasitization by *Cotesia chilonis* influences gene expression in fat body and hemocytes of *Chilosuppressalis*. **PLoS ONE**, 8:e74309. (**IF=3.73**)
- 26.Ji R, Yu HX, Fu Q, Chen HD, Ye WF, Li SH, Lou YG* (2013). Comparative Transcriptome Analysis of Salivary Glands of Two Populations of Rice Brown Planthopper, *Nilaparvata lugens*, That Differ in Virulence. **PLoS ONE**, 8(11): e79612. (**IF=3.73**)
- 27.Su ZZ, Mao LJ, Li N, Feng XX, Yuan ZL, Wang LW, Lin FC, Zhang CL* (2013). Evidence for biotrophic life style and biocontrol potential of dark septate endophyte *Harpophora oryzae* to rice blast disease. **PLoS ONE**, 8(4): e61332. (**IF=3.73**)
- 28.Yan X, Que YW, Wang H, Wang CC, Li Y, Yue XF, Ma ZH, Talbot NJ, Wang ZY* (2013). The *MET13* methylene tetrahydrofolatereductase gene is essential for infection-related morphogenesis in the rice blast fungus *Magnapor the oryzae*. **PLoS ONE**, 8(10):e76914. (**IF=3.73**)

- 29.Li W, Rokni-Zadeh H, Vleeschouwer MD, Ghequire MG. K., Sinnaeve D, Xie GL, Rozenski J, Madder A, Martins J, Mot RD (2013). The Antimicrobial Compound Xantholys in Defines a New Group of *Pseudomonas* cyclic Lipopeptides. *PLoS ONE*, 8(5):e62946. (IF=3.73)
- 30.Chen GQ, Liu XH, Zhang LL, Cao HJ, Lu JP, Lin FC* (2013). Involvement of MoVMA11, a putative vacuolar ATPase c' subunit, in vacuolar acidification and infection-related morphogenesis of *Magnaporthe oryzae*. *PLoS ONE*, 8(6):e67804. (IF=3.73)
- 31.Shi M, Wang YN, Zhu N, Chen XX* (2013). Four heat shock protein genes of the endoparasitoid wasp, *Cotesia vestalis*, and their transcriptional profiles in relation to developmental stages and temperature. *PLoS ONE*, 8(3): e59721. (IF=3.73)
- 32.Wei SJ*, Shi BC, Gong YJ, Jin GH, Chen XX, Meng XF (2013). Genetic structure and demographic history reveal migration of the diamond back moth *Plutellaxylostella* (Lepidoptera: Plutellidae) from the southern to northern regions of China. *PLoS ONE*, 8(4): e59654. (IF=3.73)
- 33.Zhao HJ, Cui HR, Xu XH, Tan YY, Fu JJ, Liu GZ, Poirier Y, ShuQY* (2013). Characterization of OsM1K in a rice mutant with reduced phytate content reveals an insertion of a rearranged retrotransposon. *Theor Appl Genet*, 126(12):3009-3020. (IF=3.658)
- 34.Li R, Afsheen S, Xin ZJ, Han X, Lou YG* (2013). OsNPR1 negatively regulates herbivore-induced JA and ethylene signaling and plant resistance to a chewing herbivore in rice. *Physiol Plant*, 147(3): 340-51. (IF=3.656)
- 35.Sun L, Zhang H, Li D, Huang L, Hong Y, Ding XS, Nelson RS, Zhou X, Song F (2013). Functions of rice NAC transcriptional factors, ONAC122 and ONAC131, in defense responses against *Magnaporthe grisea*. *Plant Mol Biol*, 81(1): 41–56. (IF=3.518)
- 36.Ji J, Tang D, Wang M, Li Y, Zhang L, Wang KJ, Li M, Cheng Z (2013). *MRE11* is required for homologous synapsis and DSB processing in rice meiosis. *Chromosoma*, 122: 363-376. (参与) (IF=3.34)
- 37.Wu SF, Wang F, Huang J, Fang Q, Ye GY (2013). Molecular and cellular analyses of a ryanodine receptor from hemocytes of *Pieris rapae*. *Dev & Comp Immunol*, 41(1):1-10. (IF=3.3)
- 38.Tan YY, Fu HW, Zhao HJ, Lu S, Fu JJ, Li YF, Cui HR, Shu QY* (2013). Functional molecular markers and high-resolution melting curve analysis of lowphytic acid mutations for marker-assisted selection in rice. *Mol Breeding*, 31(3): 517-528. (IF=3.251)
- 39.Zhou Y, Lin XW, Zhang YR, Huang YJ, Zhang CH, Yang Q, Li HY, Yuan JQ, Cheng JA, Xu R, Mao C, Zhu ZR* (2013). Identification and biochemical characterization of Laodelphax striatellusneutral ceramidase. *Insect Mol Biol*, 22(4): 366-375. (IF=3.044)
- 40.Shao GN, Tang SQ, Chen ML, Wei XJ, He JW, Luo J, Jiao GA, HuYC, Xie LH, Hu PS (2013). Haplotype variation at Badh2, the gene determining fragrance in rice. *Genomics*, 101: 157-162. (IF=3.01)

- 41.Gao HM, Liu XG, Shi HB, Lu JP, Yang J, Lin FC, Liu XH* (2013). *MoMon1* is required for vacuolar assembly, conidiogenesis and pathogenicity in the rice blast fungus *Magnaporthe oryzae*. ***Res Microbiol***, 164:300-309. (IF=2.889)
- 42.Xu Y, Huang LZ, Wang ZC, Fu S, Jing Che, Qian YJ, Zhou XP* (2013). Identification of Himetobi P virus infection in the small brown planthopper by deep sequencing and assembly of virus-derived small interfering RNAs. ***Virus Res***, doi:10.1016/j.virusres. (IF=2.745)
- 43.Wei XJ, Zhang XW, Shao GN, He JW, Jiao GA, Xie LH, Sheng ZH, Tang SQ*, Hu PS* (2013). Fine mapping of *BH1*, a gene controlling lemma and palea development in rice. ***Plant Cell Reports***, 32:1455-1463. (IF=2.509)
- 44.Li S, Yan S, Wang AH, Zou G, Huang X, Han B, Qian Q*, Tao Y* (2013). Identification of QTL associated with tissue culture response through sequencing-based genotyping of RILs derived from 93-11× Nipponbare in rice (*Oryza sativa*). ***Plant Cell Rep***, 32(1):103-16. (IF=2.509)
- 45.Wang Q, Li JC, Hu LF, Zhang TF, Zhang GR, Lou YG* (2013). OsMPK3 positively regulates the JA signaling pathway and plant resistance to a chewing herbivore in rice. ***Plant Cell Rep***, 32:1075-1084. (IF=2.509)
- 46.Zhang H, Li L, Yu Y, Mo J, Sun L, Liu B, Li D, Song F(2013). Cloning and characterization of two rice long-chain base kinase genes and their function in disease resistance and cell death. ***Mol Biol Rep***, 40(1):117–127. (IF=2.506)
- 47.Ojaghian MR, Almoneafy AA, Cui ZQ, Xie GL*, Zhang JZ, Shang CL, Li B (2013). Application of acetyl salicylic acid and chemically different chitosans against storage carrot rot. ***Postharvest Biology and Technology***, 84: 51-60. (IF=2.454)
- 48.Mujahid Hana, Tan F, Zhang J, Nallamilli BR, Pendarvis K, Peng ZH (2013). Nuclear proteome response to cell wall removal in rice (*Oryza sativa*). ***Proteome Sci***, 11:26. (参与) (IF=2.42)
- 49.Hu SK, Dong GJ, Xu J, Qian Q, Zeng DL, Guo LB* (2013). A point mutation in the zinc finger motif of RID1/EHD2/OsID1 protein leads to outstanding yield-related traits in *japonica* rice variety Wuyunjing 7. ***Rice***, 6(1): 24. (IF=2.381)
- 50.Chen XF, Fu SF, Zhang PH, Gu ZM, Liu JZ, Qian Q, Ma BJ (2013). Proteomic analysis of a disease-resistance-enhanced lesion mimic mutant spotted leaf 5 in rice. ***Rice***, 6:1. (参与) (IF=2.381)
- 51.Wei SJ*, Shi BC, Gong YJ, Li Q, Chen XX (2013). Characterization of the mitochondrial genome of the diamond back moth *Plutella xylostella* (Lepidoptera: Plutellidae) and phylogenetic analysis of advanced moths and butterflies. ***DNA Cell Biol***, 32(4):173-187. (IF=2.344)
- 52.Wang YL, Liu SY, Mao XQ, Zhang Z, Jiang H, Chai RY, Qiu HP, Wang JY, Du XF, Li B*, Sun GC (2013). Identification and characterization of rhizosphere fungal strain MF-91 antagonistic to rice blast

- and sheath blight pathogens. *Journal of Applied Microbiology*, 114:1480-1490. (IF=2.337)
- 53.Zhu B, Zhou Q, Lin L, Hu CJ, Shen P, Yang LT, An QL*, Xie GL*, Li YR* (2013). *Enterobacter sacchari* sp. nov., anitrogen-fixing bacterium associated with sugar cane(*Saccharum officinarum* L.). *Int J Syst Evol Microbiol*, 3:2577-2582. (IF=2.268)
- 54.Li B,Liu BP, Shan CL, Ibrahim M, Lou YH, Wang YL, Xie GL, Li HY, Sun GC (2013). Antibacterial activity of two chitosan solutions and their effect on rice bacterial leaf blight and leaf streak. *Pest Management Science*, DOI: 10.1002/ps.3399. (IF=2.251)
- 55.Tang SQ, Shao GN, Wei XJ, Chen ML, Sheng ZH, Luo J, Xie LH,Jiao GA, Hu PS* (2013). QTL mapping of grain weight in rice and the validationof the QTL *qTGW3.2* *Gene*, 527(1): 201-206. (IF=2.196)
- 56.Wu JX, Ni YQ, Liu H, Rao LX, Zhou YJ, Zhou XP (2013).Development and use of three monoclonal antibodies for the detection of Rice black-streaked dwarf virus in field plants and planthopper vectors. *Virol J*,10:114. (IF=2.092)
- 57.Du J, Zeng D, Wang B, Qian Q, Zheng S, Ling HQ* (2013). Environmental effects on mineral accumulation in rice grains and identification of ecological specific QTLs. *Environ Geochem Health*, 35(2):161-70. (IF=2.076)
- 58.Liu S, Liang QM, Huang YJ, Qiao F, Zhou WW, Gong ZJ, Cheng JA, Gurr GM, Zhu ZR* (2013). Cloning, functional characterization, andexpression profiles of NADPH-cytochrome P450 reductase gene from the rice striped stem borer, *Chilo suppressalis*(Lepidoptera:Pyralidae). *Comp Biochem Physiol B: Biochem Mol Biol*,166(3-4):225-231. (IF=2.069)
- 59.Chen XX*, Tang P, Zeng J, van AchterbergC, He HJ (2014). Taxonomy of parasitoid wasps in China: an overview. *Biological Control*, 68:57-72. (IF=1.917)
- 60.Lou YG*, Zhang GR, Zhang WQ, HuY, Zhang J (2013). Biological control of rice insect pests in China.*Biological Control*, 67: 8-20. (IF=1.917)
- 61.Ibrahim M ,Tao ZY, Hussain A, Yang CL, Ilyas M,Waheed A,Yuan F, Li B, Xie GL (2013). Decipheringthe role of *Burkholderia cenocepacia* membrane proteins in antimicrobial properties of Chitosan. *Archives of Microbiology*, DOI:10.1007/s00203-013-0936-0. (IF=1.905)
- 62.Kakar K, Li B, Xie GL (2013). A novel rhizobacterium Bk7 for biological control of brown sheath rot of rice caused by *Pseudomonas fuscovaginae* and its mode of action. *European J Plant Pathology*. (IF=1.61)
- 63.Wang JY, Xu XH, Mao LJ, Lao JP, Lin FC, Yuan ZL, Zhang CL* (2013).Endophytic Diaporthe from Southeast China are genetically diverse based on multi-locus phylogeny analyses. *World J Microbiol Biotechnol*, DOI: 10.1007/s11274-013-1446-6. (IF=1.551)

- 64.Liu S, Zhang YR, Zhou WW, Liang QM, Yuan X, Cheng J, Zhu ZR*,Gong ZJ (2013). Identification and characterization of two sensory neuron membrane proteins from *Cnaphalocrocis medinalis* (Lepidoptera:Pyralidae). *Arch Insect Biochem Physiol*, 82(1): 29-42. (**IF=1.515**)
- 65.Virk N, Liu B, Zhang H, Li X, Zhang Y, Li D, Song F (2013). Tomato *SIMPK4* is required for resistance against *Botrytis cinerea* and tolerance to drought stress. *Acta Physiol Plant*, 35(4):1211-1221. (**IF=1.305**)
- 66.Kakar K, NawazZ, Cui Z., Almoneafy A, Zhu B, Xie GL (2013). Characterizing the mode of action of *Brevibacillus laterosporus* B4 for control of bacterial brown spot of rice caused by *A. avenae*subsp.*avenae*RS-1. *World J Microbiol Biotechnol*, DOI 10.1007/s11274-013-1469-z. (**IF=1.262**)
- 67.Zhang JH, Liu JL, Zhang JB*, Cheng YN, Wang WP (2013). Nitrate-nitrogen dynamics and nitrogen budgets in rice-wheat rotations in Taihu Lake region, China. *Pedosphere*, 23(1): 59-69.(参与) (**IF=1.232**)
- 68.Liu S, Qiao F, Liang QM, Huang YJ, Zhou WW, Gong ZJ, Cheng J,Zhu ZR* (2013). Molecular characterization of two sensory neuron membrane proteins from *Chilo suppressalis* (Lepidoptera: Pyralidae). *Ann Entomol Soc Am*, 106(3): 378-384. (**IF=1.196**)
- 69.Fu BX, Zhu ZR, Rong NH, Hong J, Zhang CX, Cheng JA (2013). Phase-related developmental characteristics of antennal sensilla of nymphal *Laodelphax striatellus* (Hemiptera: Delphacidae), a serious virus-transmitting insect vector of graminaceous crops. *Ann Entomol Soc Am*,106(5):626-636. (**IF=1.196**)
- 70.Yang J, Wang J, Fan FJ, Zhu JY, Chen T, Wang CL, Zheng TQ, ZhangJ, Zhong WG (2013). Development of AS-PCR marker based on a keymutation confirmed by re-sequencing of Wx-mp in Milk Princess and its application in japonica soft rice (*Oryza sativa L.*) breeding. *Plant Breeding*, DOI: 10.1111/pbr.12088. (参与) (**IF=1.175**)
- 71.Huang LZ, Rao LX, Zhou XP, Wu JX (2013). Genetic variability and evolution of Rice stripe virus. *J Zhejiang Univ-Sci B (Biomed &Biotechnol)*,14(10):875-885. (**IF=1.108**)
- 72.Wang HM, Xu XM, Zhan XD, Zhai RR, Wu WM, Shen XH, Dai GX, Cao LY, Cheng SH (2013).Identification of *qRL7*, a major quantitative trait locus associated with rice root length in hydroponic conditions. *Breeding Sci*, 63(3): 267-274. (**IF=1.04**)
- 73.Li D, Wang F, Liu B, Zhang Y, Huang L, Zhang H, Song F (2013).Ectopic Expression of Rice OsBIANK1, Encoding an Ankyrin Repeat-Containing Protein, in Arabidopsis Confers Enhanced Disease Resistance to *Botrytis cinerea* and *Pseudomonas syringae*. *J Phytopathol*,161(1):27-34. (**IF=1**)
- 74.Wei XJ, Tang SQ, Shao GN, Chen ML, Hu YC, Hu PS* (2013). Fine mapping and characterization of a novel dwarf and narrow leaf rice mutant *dn1* in rice. *Genet Mol Res*, 12(3)3845-3855. (**IF=0.994**)
- 75.Zeng YX, Wen ZH, Ma LY, Ji ZJ, Li XM, Yang CD* (2013). Development of 1047 insertion-deletion markers for rice genetic studies and breeding. *Genet Mol Res*, 12(4): 5226-5235. (**IF=0.994**)

- 76.Belokobylskij S, Tang P, Chen XX(2013). *Asiaontsira* gen. nov, a new tropical genus of subfamily Doryctinae (Hymenoptera, Braconidae) from Vietnam and South-Eastern China. *Entomol Sci*, 16: 309-315. (**IF=0.981**)
- 77.Liu JX, He JH, Chen XX* (2013). The discovery of genus *Fredegunda* Fitton, Shaw & Gauld in China, with description of a new species (Hymenoptera, Ichneumonidae, Pimplinae). *Zootaxa*, 3637 (1): 79-83. (**IF=0.974**)
- 78.Tang P, Belokobylskij S, Chen XX*(2013).The discovery of the genus *Guaygata* Marsh (Hymenoptera, Braconidae, Doryctinae) from China, with description of a new species. *Zootaxa*, 3637 (1): 084-088. (**IF=0.974**)
- 79.Tang P, Belokobylskij SA, He JH, Chen XX* (2013). *Heterospilus* Haliday, 1836(Hymenoptera: Braconidae, Doryctinae) from China with a key to species. *Zootaxa*,3683(3): 201-246. (**IF=0.974**)
- 80.Yan CJ, HE JH, Chen XX* (2013). Two genera *Foersteria* Szépligeti, 1896 and *Polydegnon* Foerster, 1862 (Hymenoptera, Braconidae, Brachistinae) from China, with description of a new species. *Zootaxa*, 3683 (2): 178-184. (**IF=0.974**)
- 81.Yan CJ, He JH, Chen XX* (2013). The genus *Brulleia* Szépligeti (Hymenoptera, Braconidae, Helconinae) from China, with descriptions of four new species. *Zookeys*, 257:17-31. (**IF=0.864**)
- 82.Belokobylskij S, Tang P, Chen XX (2013).The Chinese species of the genus *Ontsira* Cameron (Hymenoptera, Braconidae, Doryctinae). *ZooKeys*, 45: 73-96. (**IF=0.864**)
- 83.Belokobylskij S*, Tang P, Chen XX (2013). Chinese species of the genus *Neurocrassus* Šnoflak, 1945 (Hymenoptera, Braconidae, Doryctinae) with a key to Asian species. *Annales Zoologici (Warszawa)*, 63(2): 235-249. (**IF=0.66**)
- 84.Fang Y, Liu JZ, Li B*, Wang YL, Sun GC (2013). Effect of storage methods on virulence variation of *Xanthomonas oryzae* pv.*oryzae*. *J Food Agr. Enviro*, 11(3&4):1134-1136. (**IF=0.517**)
- 85.Abdulwareeth A. A, Ojaghian MR, Xu SF, Ibrahim M, Xie GL, Shi Y, Tian WX, Li B (2013). Synergistic effect of Acetyl salicylic acid and DL-Beta-aminobutyric acid on biocontrol efficacy of *Bacillus* strains against tomato bacterial wilt. *Tropical Plant Pathology*,38(2):102-113. (**IF=0.513**)
- 86.Zeng YX, Ma LY, Ji ZJ, Wen ZH, Li XM, Shi CH*, Yang CD* (2013). Fine mapping and candidate gene analysis of *LM3*, a novel lesion mimic gene in rice. *Biologia*, 68(1):82-90. (**IF=0.506**)
- 87.Shi M, Zhu N, Yin Y, Chen XX* (2013). Four serine protease cDNAs from the midgut of *Plutella xylostella* and their proteinase activity are influenced by the endoparasitoid, *Cotesia vestalis*. *Arch Insect Biochem Physiol*,83(2):101-114. (**IF=1.515**)
- 88.Li B, Shan CL, Qiu H, Fang Y, Ge MY, Wang YL, Guo LB, Wu GX, Ibrahim M, Xie GL, Sun GC (2013). Characterization of Chinese cabbage club root by Fourier transform infrared spectra. *Asia J Chem*,

25(15): 8460-8462. (IF=0.266)

89.Fang Y, Li B, Wang YL, Guo LB, Sun GC (2013). Rapid comparative analysis of *Burkholderia seminalis* from apricot, water and rice rhizosphere by FTIR. *Asian J Chem*, 25(17) in press. (IF=0.266)

90.Li B, Shan CL, Ge MY, Fang Y, Wang YL, Xie GL, Sun GC (2013). Antibacterial mechanism of chitosan and its application in protection of plantfrom bacterial disease. *Asian J Chem*. 25(17) in press. (IF=0.266)

91.Li B*, Fang Y, Shan CL, Ibrahim M, Xie GL, Wang YL, Sun GC (2013). Differential effect of metal ions on antibacterial activity of chitosan against *Burkholderia cenocepacia*. *Asia J Chem*, 25: 891-894. (IF=0.266)

92.Zhou Q, Qiu H, Shan CL, Li B*, IBRAHIM M, XIE GL, Wang YL, Sun GC (2013). Antibacterial Activity of Chitosan against the Asian Pear Pathogenic Bacterium *Bacillus pumilus*. *Asia J Chem*, 25: 4337-4339. (IF=0.266)

93.Zhang H, Huang L, Li X, Ouyang Z, Yu Y, Li D, Song F (2013). Overexpression of a rice long-chain base kinase gene *OsLCBK1* in tobacco improves oxidative stress tolerance. *Plant Biotechnol*, 30(1): 9-16. (IF=0.935)

2012年发表

1.Huang XH, Kurata N, Wei XH, Wang ZX, Wang AH, Zhao Q, Zhao Y, Liu KY, Lu HY, Li WJ, Guo YL, Lu YQ, Zhou CC, Fan DL, Weng QJ, Zhu CR, Huang T, Zhang L, Wang YC, Feng L, Furuumi H, Kubo T, Miyabayashi T, Yuan XP, Xu Q, Dong GJ, Zhan QL, Li CY, Fujiyama A, Toyoda A, Lu TT, Feng Q, Qian Q, Li JY & Han B^{1*}(2012). A map of rice genome variation reveals the origin of cultivated rice. *Nature*, doi: 10.1038/nature11532. (IF=38.597)

2. Wang S, Wu K, Yuan Q, Liu X, Liu Z, Lin X, Zeng R, Zhu H, Dong G, Qian Q, Zhang G, Fu XD* (2012). Control of grain size, shape and quality by *OsSPL16* in rice. *Nature Genetics*, 44(8):950-954.(参与) (IF=35.209)

3.Huang XH, Zhao Y, Wei XH, Li CY, Wang AH, Zhao Q, Li WJ, Guo YL, Deng LW, Zhu CR, Fan DL, Lu YQ, Weng QJ, Liu KY, Zhou TY, Jing YF, Si LZ, Dong GJ, Huang T, Lu TT, Feng Q, Qian Q, Li JY & Han B*(2012). Genome-wide association study of flowering time and grain yield traits in a world-wide collection of rice germplasm. *Nature Genetics*,44(1): 32-39. (IF=35.209)

4.Xiao YT, Wang Q, Erb M, Turlings TCJ, Ge LQ, Hu LF, Li JC, Han X, Zhang TF, Lu J, Zhang GR, Lou YG* (2012) Specific herbivore-induced volatiles defend plants and determine insect community composition in the field. *Ecology Letters*,15:1130-1139. (IF=17.949)

5.Ye RQ, Wang W, Iki T, Liu C, Wu Y, Ishikawa M, Zhou XP, Qi YJ* (2012). Cytoplasmic Assembly and Selective Nuclear Import of Arabidopsis ARGONAUTE4/siRNA Complexes. *Molecular Cell*, 46(6): 859-870. (IF=15.28)

- 6.Liu XH, Gao HM, Xu F, Lu JP, Devenish RJ, Lin FC* (2012). Autophagy Vitalizes the Pathogenicity of Pathogenic Fungi. *Autophagy*, 8(10):1415-1425. (**IF=12.042**)
- 7.Xu C,Wang Y,Yu Y,Duan J, Liao Z, Xiong G, Meng X, LiuG, Qian Q*, Li J* (2012). Degradation of MONOCULM 1 by APC/C(TAD1) regulates rice tillering. *Nat Commun*, Mar20;3:750.doi: 10.1038/ncomms1743. (**IF=10.015**)
- 8.Sun CH, Fang J, Zhao TL, Xu B, Zhang FT, Liu LC, Tang JY, Zhang GF, Deng XJ, Chen F, Qian Q, Cao XF, Chu CC* (2012). The Histone Methyltransferase SDG724 Mediates H3K36me2/3 Deposition at MADS50 and RFT1 and Promotes Flowering in Rice. *Plant Cell*, 24(8): 3235–3247. (**参与**) (**IF=9.251**)
- 9.Tong H, Liu L, Jin Y, Du L, Yin Y, Qian Q, Zhu L, Chu C*(2012). DWARF AND LOW-TILLERING Acts as a Direct Downstream Target of a GSK3/SHAGGY-Like Kinase to Mediate Brassinosteroid Responses in Rice. *Plant Cell*, 24(6):2562-2577. (**参与**) (**IF=9.251**)
- 10.Xin ZJ, Yu ZN, Erb M, Turlings TCJ, Wang BH, Qi JF, Liu SN, and Lou YG* (2012). The broad leaf herbicide 2,4-dichlorophenoxyacetic acidturns rice into a living trap for a major insect pest and a parasitic wasp. *New Phytologist*, 194(2),498-510. (**IF=6.736**)
- 11.Wang Y, Bai XF, Yan CH, Gui YJ, Wei XH, Zhu QH, Guo LB*, Fan LJ* (2012). Genomic dissection of small RNAs in wild rice (*Oryza rufipogon*):lessons for rice domestication. *New Phytologist*, 196(3):914-25. (**IF=6.736**)
- 12.Sun JT†, Qian QT†, Ma DR†, Xu ZJ, Liu D, Du HB and Chen WF* (2012). Introgression and selection shaping the genome and adaptive loci of weedy rice in northern China. *New Phytologist*, doi: 10.1111/nph.12012. (**IF=6.736**)
- 13.Zhang Q, Li Jj, Zhang Wj, Yan SN, Wang R, Zhao JF, Li YJ, Qi ZG, Sun ZX, Zhu ZG* (2012). The putative auxin efflux carrier OsPIN3t is involved in the drought stress response and drought tolerance. *Plant J*, 72:805–816. (**参与**) (**IF=6.582**)
- 14.Su N, Hu ML, Wu DX, Wu FQ, Fei GL, Lan Y, Chen XL, Shu XL, Zhang X, Guo XP, Cheng ZJ, Lei CL, Qi CK, Jiang L, Wang HY, Wan JM* (2012). Disruption of a rice pentatricopeptide repeat protein causes a seedling-specific albino phenotype and its utilization to enhance seed purity in hybrid rice production. *Plant Physiology*, 159: 227–238. (**IF=6.555**)
- 15.Xiang JJ†, Zhang GH†, Qian Q, Xue HW* (2012). *Semi-rolled leaf1* encodes a putative glycosyl phosphatidylinositol-anchored protein and modulates rice leaf rolling by regulating the formation of bulliform cells. *Plant Physiology*, 159(4):1488-1500. (**参与**) (**IF=6.555**)
- 16.Zhang T, Luan JB, Qi JF, Li M, Huang CJ, Zhou XP*, Liu SS* (2012). Begomovirus-white fly mutualism is achieved through repression of plant defenses by a virus pathogenicity factor. *Molecular Ecology*,

21(5):1294-304. (IF=6.275)

- 17.Wang J, Hu J, Qian Q, Xue HW*(2012). LC2 and OsVIL2 Promote Rice Flowering by Photoperiod-Induced Epigenetic Silencing of OsLF. *Mol Plant*, doi:10.1093/mp/ss096. (参与) (IF=6.126)
- 18.Ying JZ, Shan JX, Gao JP, Zhu MZ, Shi M, Lin HX* (2012).Identification of quantitative trait Loci for lipid metabolism in rice seeds. *Mol Plant*, 5:865-875. (IF=6.126)
- 19.Huang J, Wu SF, Li XH, Adamo SA, Ye GY* (2012). The characterization of a concentration-sensitive alpha-adrenergic-like octopamine receptor found on insect immune cells and its possible role in mediating stress hormone effects on immune function. *Brain Behav Immun*, 26:942-950. (IF=5.612)
- 20.Shen CJ†, Wang SK†, Zhang SN, Xu YX, Qian Q, Qi YH*, Jiang DA (2012). OsARF16, a transcription factor, is required for auxin and phosphate starvation response in rice (*Oryza sativa* L.). *Plant Cell and Environment*, Aug 23. doi: 10.1111/pce.12001. (参与) (IF=5.135)
- 21.Wang HM, Zhou L, Fu YP, Cheung MY, Wong FL, Phang TH, Sun ZX, Lam HM (2012). Expression of an apoplast-localized BURP-domain protein fromsoybean (GmRD22)enhances tolerance towards abiotic stress. *Plant Cell and Environment*, 35, 1932-1947. (参与) (IF=5.135)
- 22.Hao C, Stout MJ, Qian Q, Chen F*(2012). Genetic,molecular and genomic basis of rice defense against insects. *Critical Reviews in Plant Sciences*, 31(1):74–91. (参与) (IF=4.356)
- 23.Zhang HJ, Zhai J, Mo JB, Li DY, Song FM*(2012).Overexpression of a rice sphingosine-1-phosphate lyase gene OsSPL1 in transgenic tobacco reduces salt and oxidative stress tolerance. *Journal of Integrative Plant Biology*, 54(9): 652–662. (IF=3.75)
- 24.Jia LM, Yan WG, Zhu CS, Agrama HA, Jackson A, Yeater K, Li XB, Huang BH, Hu BL, McClung A, Wu DX* (2012). Allelic analysis of sheath blight resistance with association mapping in rice. *PLoS One*, 7(3):e32703. doi:10. 1371/journal.pone.0032703. (IF=3.73)
- 25.Li XB, Yan WG, Agrama H, Jia LM, Jackson A, Moldenhauer K, Yeater K, McClung A, Wu DX* (2012). Unraveling the complex trait of harvest index with association mapping in rice (*Oryza sativa* L.). *PLoS One*, 7(1): e29350. doi:10.1371/journal.pone.0029350. (IF=3.73)
- 26.Liu C, Li J, Gao J, Shen Z, Lu B-R, C. Lin* (2012). A Built-In Mechanism to Mitigate the Spread of Insect-Resistance and Herbicide-Tolerance Transgenes into Weedy Rice Populations. *PLoS One*, e31625.doi:10. 1371/journal. pone.0031625. (IF=3.73)
- 27.Zhang ZH, Wang K, Guo L, Zhu YJ, Fan YY, Cheng SH*, Zhuang JY* (2012). Pleiotropism of the photoperiod-insensitive allele of *Hd1* on heading date, plant height and yield traits in rice. *PLoS One*, DOI:10.1371/ journal.pone. 0052538. (IF=3.73)

- 28.Xu Y, Huang LZ, Fu S, Wu JX*, Zhou XP*(2012). Population Diversity of Rice Stripe Virus-Derived siRNAs in Three Different Hosts and RNAi-Based Antiviral Immunity in *Laodelphgax striatellus*. *PLoS One*, 7(9):e46238. (IF=3.73)
- 29.Tian JC, Chen Y, Li ZL, Li K, Chen M, Peng YF, Hu C, Shelton AM, Ye GY*(2012). Transgenic *Cry1Ab* rice does not impact ecological fitness and predation of a generalist spider. *PLoS One*, 7:e35164. (IF=3.73)
- 30.Guo JY, Dong SZ, Yang XL, Cheng L, Wan FH, Liu SS, ZhouXP, Ye GY*(2012). Enhanced vitellogenesis in a white fly via feeding on abegomovirus-infected plant. *PLoS One*, 7:e43567. (IF=3.73)
- 31.Ibrahim M, Shi Y, Qiu H, Jabeen A, Li LP, Liu H, Li B*,Kube M, Xie GL, Wang Y, Sun GC (2012). Differential expression of in vivo and in vitro protein profile of outer membrane of *Acidovorax avenae* subsp. *Avenae*. *PLoS One*, 7(11) : e49657. (IF=3.73)
- 32.Shao T, Qian Q, Tang D, Chen J, Li M, Cheng Z, Luo Q*(2012). A novel gene *IBF1* is required for the inhibition of brown pigment deposition in rice hull furrows. *Theor Appl Genet*, 125(2):381-90. (参与) (IF=3.658)
- 33.Shao GN, Wei XJ, Chen ML, Tang SQ, Luo J, Jiao GA, Xie LH,Hu PS*(2012). Allelic variation for a candidate gene for GS7, responsible for grain shape in rice. *Theor Appl Genet*, 125(6), 1303-1312. (IF=3.658)
- 34.Hong L, Qian Q, Tang D, Wang K, Li M, Cheng Z*(2012). A mutation in the rice chalcone isomerase gene causes the golden hull and internode 1 phenotype. *Planta*, 236(1):141-51. (参与) (IF=3.347)
- 35.Tan YY, Fu HW, Zhao HJ, Lu S, Fu JJ, Li YF, Cui HR, ShuQY*(2012). Functional molecular markers and high resolution melting curve analysis of low phytic acid mutations for marker-assisted selection in rice. *Molecular Breeding*, DOI10.1007/S11032-012-9809-5. (IF=3.251)
- 36.Wang L, Fang Q, Zhu J, Wang F, Rean Akhtar Z, Ye G*(2012). Molecular cloning and functional study of calreticulin from a lepidopter anpest, *Pieris rapae*. *Dev Comp Immunol*, 38:55-65. (IF=3.238)
- 37.Wu SF, Yao Y, Huang J, Ye GY*(2012). Characterization of a beta-adrenergic-like octopamine receptor from the rice stem borer (*Chilosuppressalis*). *J Exp Biol*, 215:2646-2652. (IF=3.236)
- 38.Wang Y, Fan HW, Huang HJ, Xue J, Wu WJ, Bao YY, Xu HJ,Zhu ZR, Cheng JA, Zhang CX*(2012). Chitin synthase 1 gene and its two alternative splicing variants from two sap-suckinginsects, *Nilaparvata lugens* and *Laodelphax striatellus* (Hemiptera:Delphacidae). Insect Biochemistry and Molecular Biology, 42(9) 637-646. (IF=3.234)
- 39.Liu H, Qiu H, Zhao WJ, Cui ZQ, Ibrahim M, Jin GL, Li B, Zhu B, Xie GL* (2012). Genome Sequence of the Rice-Pathogenic Bacterium *Pseudomonassyringae* pv.*panici* LMG 2367. *J Bacteriology*, 194 (20)

:5693-5694. (**IF=3.194**)

- 40.Li B, Shi Y, Ibrahim M, Liu H, Shan CL, Wang YL, Kube M, Xie GL* (2012). Genome Sequence of the Rice-Pathogen *Dickeya zeae* strain ZJU1202. *J Bacteriology*, 194(16):4452-4453. (**IF=3.194**)
- 41.Zhu B, Liu H, Tian WX, Fan XY, Li B, Zhou XP, Jin GL, Xie GL* (2012). Genome Sequence of *Stenotrophomonas maltophilia* RR-10, Isolated as an Endophyte from Rice Root. *J Bacteriology*, 194(5):1280-1281. (**IF=3.194**)
- 42.Xie GL*, Cui ZQ, Tao ZY, Hui Qiu, He Liu, MuhammadIbrahim, Bo Zhu (2012). Genome Sequence of the Rice-Pathogen *Pseudomonas fuscovaginae* CB98818. *J Bacteriology*, 194(19): 5479-5780. (**IF=3.194**)
- 43.Ye WJ, Ye ST, Liu J, Chang SP, Chen MY, Zhu B, Guo LB*, An QL (2012). Genome Sequence of a Pathogenic *Herbaspirillum seropedicae* Strain Os34 Isolated from Rice Roots *J. Bacteriol*, 194(24) doi:10.1128/JB.01934-12. (**IF=3.194**)
- 44.Liu J, Zhou Q, Ibrahim M, Liu H, Jin GL, Zhu B and Xie GL*(2012). Genome Sequence of the Biocontrol Agent *Microbacterium barkeri* Strain 2011-R4. *J. Bacteriol*, 194(23): DOI: 10.1128/JB.01468-12. (**IF=3.194**)
- 45.Yao M, Zhang TQ, Zhou T, Zhou YJ, Zhou XP*, Tao XR*(2012). Repetitive prime-and-realign mechanism converts short capped RNA leaders into longer ones that may be more suitable for elongation during Ricestripe virus transcription initiation. *Journal of General Virology*, 93(1) : 194-202. (**IF=3.127**)
- 46.Wang YL, Zhou Q, Li B*, Liu BP, Wu GX, Ibrahim M, Xie GL* (2012). Differentiation in MALDI-TOF MS and FTIR spectrabetween two closely related species *Acidovorax oryzae* and *Acidovorax citrulli*. *BMC Microbiology*, 12: 182. (**IF=3.104**)
- 47.Bao YY, Wang Y, Wu WJ, Zhao D, Xue J, Zhang BQ, Shen ZC, Zhang CX* (2012). De novo intestine-specific transcriptome of the brown planthopper *Nilaparvata lugens* revealed potential functions in digestion, detoxification and immune response. *Genomics*, 99(4):256-264. (**IF=3.01**)
- 48.Xue DW, Jiang H, Hu J, Zhang XQ, Guo LB, Zeng DL, Dong GJ,Sun GC, Qian Q* (2012). Characterization of physiological response andidentification of associated genes under heat stress in rice seedlings. *Plant Physiology and Biochemistry*, 61,46-53. (**IF=2.775**)
- 49.Chen Y, Tian JC, Wang W, Fang Q, Akhtar ZR, Peng YF, Cui H, Guo YY, Song QS, Ye GY* (2012). Bt rice expressing Cry1Ab does not stimulate an outbreak of its non-target herbivore, *Nilaparvata lugens*. *Transgenic Res*, 21:279-291. (**IF=2.609**)
- 50.Wu SF, Huang J, Ye GY* (2013). Molecular cloning and pharmacological characterisation of a tyramine receptor from the rice stemborer, *Chilo suppressalis* (Walker). *Pest Manag Sci*, 69,126-134. (**IF=2.594**)

- 51.Zhou WW, Li XW, Quan YH, Cheng J, Zhang CX, Gurr G, ZhuZR* (2012). Identification and expression profiles of nine glutathione S-transferase genes from the important rice phloem sap-sucker and virus vector Laodelphax striatellus(Fallén) (Hemiptera: Delphacidae). *Pest Manag Sci*, 68:1296-1305. (IF=2.594)
- 52.Li B*, Liu BP, Changlin S, Ibrahim M, Lou YH, Wang YL, Xie GL (2012). Antibacterial activity of two chitosan solutions and their effect on rice bacterial leaf blight and leaf streak. *Pest Manag Sci*, DOI 10.1002/ps.3399. (IF=2.594)
- 53.Li SJ, Yan S, Wang AH, Zou GH, Huang XH, Han B, Qian Q*, TaoYZ* (2012). Identification of QTLs associated with tissue culture response through sequencing-based genotyping of RILs derived from 93-11 × Nipponbare in rice (*Oryza sativa*). *Plant Cell Rep*, DOI10.1007/s00299-012-1345-6. (IF=2.509)
- 54.Chen ML, Luo J, Shao GN, Wei XJ, Tang SQ, Sheng ZH, SongJ, Hu PS* (2012). Fine mapping of a major QTL for flag leaf width in rice, *qFLW4*, which might be caused by alternative splicing of *NAL1* rice. *Plant Cell Rep*, 31(5),863-872. (IF=2.509)
- 55.Wang QZ, Fu HW, Huang JZ, Zhao HJ, Li YF, Zhang B, ShuQY* (2012). Generation and characterization of bentazon susceptible mutants of commercial male sterile lines and evaluation of their utility in hybrid rice production. *FIELD CROP RES*, 137:12–18. (IF=2.474)
- 56.Wang YL, Li LP, Li B*, Wu GX, Tang QM, Ibrahim M, Li HY, XieGL, Sun GC (2012). Action of Chitosan Against *Xanthomonas* Pathogenic Bacteria isolated from *Euphorbia pulcherrima*. *Molecules*, 17:7028-7041. (IF=2.428)
- 57.Wu WJ, Wang Y, Huang HJ, Bao YY*, Zhang CX* (2012). Ecdysone receptor controls wing morphogenesis and melanization during rice planthopper metamorphosis. *Journal of Insect Physiology*, 58(3):420–426. (IF=2.379)
- 58.Li BL, Chen W, Liu L, Zhang XC, Bao YY, Cheng JA, Zhu ZR*, Zhang CX* (2012). Molecular characterization of two acetylcholinesterase genes from the brown planthopper, *Nilaparvata lugens* (Hemiptera: Delphacidae). *Pesticide Biochemistry and Physiology*, 102,198–203. (IF=2.111)
- 59.Frank T, Reichardt B, Shu QY, Engel KH* (2012). Metabolite profiling of colored rice (*Oryza sativa* L.) grains. *Journal of Cereal Science*, 55(2):112-119. (参与) (IF=2.088)
- 60.Du J†, Zeng D†, Wang B, Qian Q, Zheng S, Ling HQ (2012). Environment effects on mineral accumulation in rice grains and identification of ecological specific QTLs. *Environ Geochem Health*. (参与) (IF=2.076)
- 61.Ying JZ, Gao GP, Shan JX, Zhu MZ, Shi M, Lin HX* (2012). Dissecting the genetic basis of extremely large grain shape in rice cultivar 'JZ1560'. *J Genet Genomics*, 39:325-333. (IF=2.076)

- 62.Zhang JP, Duan GF, Zhu K, Zhou YJ and Yu LQ* (2012). Screening and Identification of Insertion Mutants from Bipolaris eleusines by Mutagenesis Based on Restriction Enzyme-Mediated Integration. *FEMS microbiology letters*, 330(2) : 90-97. (**IF=2.049**)
- 63.Zulfiqar A, Zhang J, Cui X, Qian Y, Zhou X, Xie Y* (2012). A new begomovirus associated with alpha- and betasatellite molecules isolated from Vernonia cinerea in China. *Archives of Virology*, 157(1):189-191. (**IF=2.03**)
- 64.Liu H, Tian WX, Li B, Wu GX, Ibrahim M, Tao ZY, Wang YL, XieGL* (2012). Antifungal effect and mechanism of chitosan solution against rice sheath blight pathogen Rhizoctonia solani. *Biotechnol Lett*, DOI10.1007/s10529-012-1035-z. (**IF=1.853**)
- 65.E ZG, Ge L, Wang L* (2012). Molecular mechanism of adventitious root formation in rice. *Plant Growth Regulation*, 68(3): 325-331. (**IF=1.67**)
- 66.Liu H, Zhu B, Xie GL*, Li B (2012). Characterization of *pilP*, a gene required for twitching motility, pathogenicity, and biofilm formation of Acidovorax avenae subsp.avenae RS-1. *Eur J Plant Pathol*, 134:551-560. (**IF=1.61**)
- 67.Fu BX, Bellis GA, Hong J, Wang JR, Wu Q, Tang QY, Cheng JA, Zhu ZR* (2012). Morphology, Distribution and Abundance of Antennal Sensilla of Male and Female Macropterous and Brachypterous Small Brown Planthopper, Laodelphax striatellus (Fallén) (Hemiptera: Delphacidae). *MICROSCOPY RESEARCH AND TECHNIQUE*, 75(11):1492-1512. (**IF=1.593**)
- 68.Wang H, Li K, Zhu JY, Fang Q, Ye GY* (2012). Cloning and expression pattern of heat shock protein genes from the endoparasitoid wasp, Pteromalus puparum in response to environmental stresses. *Arch Insect Biochem Physiol*, 79:247-263. (**IF=1.515**)
- 69.Liu S, Zhang YR, Zhou WW, Liang QM, Yuan X, Cheng J, Zhu ZR, Gong ZJ (2012). IDENTIFICATION AND CHARACTERIZATION OF TWO SENSORY NEURONMEMBRANE PROTEINS FROM Cnaphalocrocis medinalis (LEPIDOPTERA: PYRALIDAE). *Arch Insect Biochem Physiol*, DOI:10.1002/arch.21069. (**IF=1.515**)
- 70.Zhang Q, Zhang W, Lin CY, Xu XL, Shen ZC* (2012). Expression of an Acidothermus cellulolyticus endoglucanase in transgenic rice seeds. *Protein Expression and Purification*, 82:279–283. (**IF=1.429**)
- 71.Zhu B, Zhou Q, Xie GL*, Zhang GQ, Zhang XW, Wang YL, SunGC, Li B (2012). Inter kingdom Gene Transfer May Contribute to the Evolution of Phytopathogenicity in Botrytis Cinerea. *Evolutionary Bioinformatics*, 8:105-117. (**IF=1.326**)
- 72.Chen ML, Wei XJ, Shao GN, Tang SQ, Luo J, Hu PS* (2012). Fragrance of the rice grain achieved via artificial micro RNA-induced down-regulation of OsBADH2. *Plant Breeding*, 131(5): 584-590. (**IF=1.175**)

- 73.Ji ZJ, Wang XG, Zeng YX, Ma LH, Li XM, Liu BX and Yang CD*(2012). Comparison of physiological and yield traits between purple- and white-pericarp rice using SLs. *Breeding Science*, 62:71-77. (IF=1.04)
- 74.Ojaghian MR, Cui ZQ, Xie GL*, Li B, Zhang JZ (2012).Brassica green manure rotation crops reduce potato stem rot caused by Sclerotinia sclerotiorum. *Australasian Plant pathol*, 41(4), 347-349. (IF=1.021)
- 75.Hu Q, Jiang T, Xue CY, Zhou XP* (2012). Characterization and complete nucleotide sequence of two isolates of tomato mosaic virus. *Journalof Phytopathology*, 160(3):115-119. (IF=1)
- 76.Tang P, Belokobylskij SA, van Achterberg C, Chen XX* (2012). Halycaea Cameron, 1903 (Hymenoptera: Braconidae, Doryctinae) from Chinawith a key to world species. *Zootaxa*, 3218: 18–30. (IF=0.974)
- 77.Tang P, Wu Q, Belokobylskij SA, Chen XX* (2012). The rare genus Leptospathius Szépligeti (Hymenoptera, Braconidae, Doryctinae) from China, with description of a new species. *Zootaxa*,3219: 62–66. (IF=0.974)
- 78.Belokobylskij SA, Tang P, He JH, Chen XX* (2012). The genus Doryctes Haliday, 1836 (Hymenoptera: Braconidae, Doryctinae) in China. *Zootaxa*,3226: 46–60. (IF=0.974)
- 79.Yan CJ, van Achterberg C, Chen XX* (2012). The genusTaphaeus Wesmael, 1835 (Hymenoptera: Braconidae: Helconinae) from China with description of a new species. *Zootaxa*, 3519: 85–88. (IF=0.974)
- 80.Tang P, Liu Z, Chen XX* (2012). The genus Biroia Szépligeti, 1900 (Hymenoptera, Braconidae, Agathidinae) in China, with description of two new species. *Zootaxa*, 3519: 69–76. (IF=0.974)
- 81.Ojaghian MR, Xie GL*, Zhang JZ, Li B (2012). In vitro biofumigation of Brassica tissues against potato stem rot caused by Sclerotinias clerotiorum. *Plant Pathol J*, 28(2) : 185-190. (IF=0.667)

2011年发表

- 1.Chen M, Shelton A*, Ye GY* (2011). Insect-resistantgenetically modified rice in China:from research to commercialization. *Annu Rev Entomol*, 56:81-101. (IF=12.18)
- 2.Zhang BC, Liu XL, Qian Q, Liu LF, Dong GJ, Xiong GY, Zeng DL, Zhou YH* (2011).Golgi nucleotide sugar transporter modulates cell wall biosynthesis and plant growth in rice. *PNAS*, 108(12): 5110-5115. (IF=9.771)
- 3.Li W, Zhong S, Li G, Li Q, Mao B, Deng Y, Zhang H, Zeng L,Song F, He ZH* (2011). Rice RING protein OsBBI1 with E3 ligase activity confersbroad-spectrum resistance against *Magnaporthe oryzae* by modifying the cell wall defence. *Cell Research*, 21(5):835-848. (IF=9.417)
- 4.Li J, Jiang JF, Qian Q, Xu YY, Zhang C,Xiao J, Du C, Luo W, Zou GX, Chen ML, Huang YQ, Feng YQ, Cheng ZK, Yuan M, ChongK* (2011). Mutation of Rice BC12/GDD1, Which Encodes a Kinesin-Like

- Protein That Binds to a GA Biosynthesis Gene Promoter, Leads to Dwarfism with Impaired Cell Elongation. *Plant Cell*, 23:628–640. (IF=9.396)
- 5.Wang W, Ye RQ, Xin Y, Fang XF, Li CL, Zhou XP, Qi YJ* (2011). An Importin β Protein Negatively Regulates MicroRNA Activity in Arabidopsis. *Plant Cell*, on line:October 2011 tpc.111.091058. (IF=9.396)
- 6.Zhang ZH, Chen H, Huang XH, Xia R, Zhao QZ, Lai JB, Teng KL,Li Y, Liang LM, Du QS, ZhouXP, Guo HS, Xie Q* (2011). BSCTVC2 attenuates the degradation of SAMDC1 to suppress DNA methylation-mediated gene silencing. *Plant Cell*, 23: 273-288. (IF=9.396)
- 7.Yang XL, Xie Y, Raja P, Wolf JN, Li SZ, Shen QT, Bisaro DM*, Zhou XP* (2011). Suppression of Methylation-Mediated Transcriptional Gene Silencing by β C1-SAHH Protein Interaction during Geminivirus-Betasatellite Infection. *PLoS Pathogens*, 7(10):e1002329. (IF=9.079)
- 8.Yan X, Li Y, Yue XF, Wang CC, Que YW, Kong DD, Ma ZH, Talbot NJ, Wang ZY* (2011). Two novel transcriptional regulators are essential for infection-related morphogenesis and pathogenicity of the rice blast fungus *Magnaporthe oryzae*. *PLoS Pathogens*, 7(12):e1002385. (IF=9.079)
- 9.Lu J, Ju HP, Zhou GX, Zhu CS, Erb M, Wang XP, Wang P, Lou YG* (2011). An EAR-motif-containing ERF Transcription Factor Regulates Herbivore-Induced Signaling, Defense and Resistance in Rice. *Plant Journal*, 68(4): 583-596. (IF=6.948)
- 10.Yan YS, Zhang YM, Yang K, SunZX, Fu YP, Chen XY,Fang RX* (2011). Small RNAs from MITE-derived stem-loop precursors regulate abscisic acid signalingand abiotic stress responses in rice. *Plant Journal*, 65(5):820-828. (IF=6.948)
- 11.Xu F, Liu XH, Zhuang FL, Zhu J, Lin FC* (2011). Analyzing autophagy in *Magnaporthe oryzae*. *Autophagy*,7(5): 525-530. (IF=6.643)
- 12.Shen QT, Liu Z, Song FM, Xie Q,Linda HB, Zhou XP* (2011). Tomato SISnRK1 protein interacts with and phosphorylates β C1, a pathogenesis protein encoded by a geminivirusbetasatellite. *Plant Physiology*,157(3): 1394-1406. (IF=6.451)
- 13.Qi JF, Zhou GX, Yang LJ, Erb M, Lu YH, Sun XL, Cheng JA, LouYG* (2011).The Chloroplast-Localized PhospholipasesD α 4and α 5 Regulate Herbivore-Induced Direct and Indirect Defenses in Rice. *Plant Physiology*, 157: 1987-1999. (IF=6.451)
- 14.hu BF, Si L, Wang Z, Zhou Y, Zhu J, Shangguan Y, Lu D, Fan D, Li C, Lin H, Qian, Q, SangT, Zhou B, Minobe Y, Han B* (2011). Genetic control of a transition from black to straw-white seed hull in ricedomestication. *Plant Physiology*,155(3): 1301-1311. (IF=6.451)
- 15.Luan WJ*, Liu YQ, Zhang FX, Song YL, Wang ZY, Peng YK, Sun ZX (2011). *OsCD1* encodes aputative member of the cellulose synthase-like D sub-family and is essential for rice plant architecture and growth. *Plant Biotechnology Journal*, 9(4):513-524. (IF=4.886)

- 16.Xiong J*, Fu GF, Yang YJ, Zhu C,Tao LX* (2011). Tungstate: is it really a specific nitrate reductase inhibitor in plant nitric oxide research? *Journal of Experimental Botany*, DOI:10.1093/jxb/err268. (IF=4.818)
- 17.Yang XL, Wang Y, Guo W, Xie Y, Xie Q, Fan LJ, Zhou XP* (2011). Characterization of small interfering RNAs derived from the geminivirus/betasatellite complex using deep sequencing. *PLoS One*,6(2): e16928. (IF=4.411)
- 18.Fang Q, Wang F, Gatehouse JA, GatehouseAMR, Chen XX, Hu C, Ye GY* (2011). Venom of Parasitoid, Pteromalus puparum, Suppresses Host, Pieris rapae,Immune Promotion by Decreasing Host C-Type Lectin Gene Expression. *PLoS One*, 6(10) :e26888. (IF=4.411)
- 19.Xu WY,Yang RD, Li MN, Xing Z, Yang WQ,Chen G, Guo H, Gong XJ, Du Z, Zhang ZH, Hu XM, Wang D, Qian Q, Wang T, Z SH,Xue YB* (2011). Transcriptome phase distribution analysis reveals diurnal regulated biological processes and key pathways in rice flag leaves and seedling leaves. *PLoS one*, 6(3): e17613. (IF=4.411)
- 20.Yan YS, Chen XY, Yang K, Sun ZX, Fu YP, Zhang YM, Fang RX* (2011). Overexpression of an F-box Protein Gene Reduces Abiotic Stress Tolerance and Promotes Root Growth in Rice. *Molecular Plant*, 4(1): 190-197. (参与) (IF=4.296)
- 21.Zhang YM, Yan YS, Wang LN, Yang K, Xiao N, Liu YF, Fu YP, Sun ZX, Fang RX, Chen XY* (2011). A Novel Rice Gene, NRR Responds to Macronutrient Deficiency and Regulates Root Growth. *Molecular Plant*, doi:10. 1093/mp/ssr066. (参与) (IF=4.296)
- 22.Zhu B, Lou MM, Xie GL, Zhang GQ, Zhou XP, Li B*, Jin GL* (2011). Horizontal gene transfer in silk worm, *Bombyx mori*. *BMC Genomics*,12:248. (IF=4.206)
- 23.Yu P, Wang CH, Xu Q, Feng Y, Yuan XP, Yu HY, Wang YP, Tang SX, Wei XH* (2011). Detection of copy number variations in rice using array-based comparative genomic hybridization. *BMC Genomics*, 12: 372.(IF=4.206)
- 24.Zhu L, Hu J, Zhu KM, Fang YX, Gao ZY, He YH, Zhang GH, Guo LB, Zeng DL, Dong GJ, Yan MX, Liu J, Qian Q*(2011). Identification and characterization of *SHORTENED UPPERMOSTINTERNODE 1*, a gene negatively regulating uppermost internode elongation in rice. *Plant Mol Biol*, 77: 475–487. (IF=4.149)
- 25.Zhou L, Cheung MY, Li MW, Fu YP, Sun ZX, Sun SM, Lam HM* (2011). Rice Hypersensitive Induced Reaction Protein 1 (*OsHIR1*) associates with plasma membrane and triggers hypersensitive cell death. *BMC Plant Biology*, 10:290. (参与) (IF=4.085)
- 26.Ruan SL*, Ma HS*, Wang SH, Fu YP, Xin Y, Liu WZ, Wang F, Tong JX, Wang SZ, Chen HZ (2011). Proteomic identification of OsCYP2, a rice cyclophilin that confers salt tolerance in rice (*Oryza sativa L.*) seedlings when overexpressed. *BMC plant Biology*, 11:34. (参与) (IF=4.085)

- 27.Fang Q, Wang L, Zhu YK, Stanley DW, Chen XX, Hu C, Ye GY* (2011). Pteromalus puparum venom impairs host cellular immune responses by decreasing expression of its scavenger receptor gene. *Insect Biochem Molec*, 41(11): 852-862. (IF=4.018)
- 28.Yang XL, Guo W, Ma XY, An QL, Zhou XP*(2011). Molecular characterization of a distinct tomato-infecting begomovirus in China and functional analyses of its associated betasatellite. *A ppiled and Environmental Microbiology*, 77(9):3092-3101. (IF=3.778)
- 29.Zhu B, Zhang GQ, Lou MM, Tian WX, Li B, Zhou XP, Wang GF, He L, Xie GL*, Jin GL* (2011). Genome sequence of the *Enterobacter mori* type strain, LMG 25706, a pathogenic bacterium of *Morus alba* L. *J Bacteriol*, 193(14): 3670-3671. (IF=3.726)
- 30.Xie GL, Zhu B, Zhang GQ, Liu H, Lou MM, Tian WX, Li B, Zhou XP, Jin GL* (2011). Genome sequence of the rice pathogenic bacterium *Acidovorax avenae* subsp. *avenae* RS-1. *J Bacteriol*, 193(18): 5013-5014. (IF=3.726)
- 31.Ye Hongxia, Zhang Xiao-Qi, Broughton Sue, Westcott Sharon, Wu Dianxing*, Lance Reg, Li Chengdao (2011). A nonsense mutation in a putative sulphate transporter gene results in low phytic acid in barley. *Funct Integr Genomics*, 11: 103-110. (IF=3.397)
- 32.Yan X, Ma WB, Li Y, Wang H, Que YW, Ma ZH, Talbot NJ, Wang ZY* (2011). Asterol 14 α -demethylase is required for conidiation, virulence and formulating sensitivity to sterol demethylation inhibitors by the rice blast fungus *Magnaporthe oryzae*. *Fungal Genet Biol*, 48(2): 144-153. (IF=3.333)
- 33.Cheng XF, Wang XQ, Wu JX, Zhou XP* (2011). β C1 encoded by tomato yellow leaf curl China virus betasatellite forms multimeric complex *in vitro* and *in vivo*. *Virology*, 409(2):156-162. (IF=3.305)
- 34.Su Y, Rao YC, Hu SK, Yang YL, Gao ZY, Zhang GH, Liu J, Hu J, Yan MX, Dong GJ, Zhu L, Guo LB, Qian Q*, Zeng DL* (2011). Map-based cloning proves qGC-6, a major QTL for gel consistency of japonica/indica cross, responds by Waxy in rice (*Oryza sativa* L.). *Theor Appl Genet*. 123(5): 859-867. (IF=3.264)
- 35.Wang L, Wang AH, Huang XH, Zhao Q, Dong GJ, Qian Q, Sang T, Han B* (2011) . Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombinant inbred lines. *Theor Appl Genet*, 122(2): 327-340. (参与) (IF=3.264)
- 36.Deng MJ, Bian HW, Xie YK, Kim YH, Wang WZ, Lin EP, Zeng ZH, Guo F, Pan JW, Han N, Wang JH, Qian Q, Zhu MY* (2011). Bcl-2 suppresses hydrogen peroxide-induced programmed cell death via OsVPE2 and OsVPE3, but not via OsVPE1 and OsVPE4, in rice. *FEBS J*, 278(24):4797-4810. (参与) (IF=3.129)
- 37.Li XB, Yan WG, Agrama HH, Jia LM, Shen XH, Jackson A, Moldenhauer K, Yeater K, McClung A, Wu DX* (2011). Mapping QTLs for improving grain yield using the USDA rice mini-core collection. *Planta*, 234: 347-367. (IF=3.098)

- 38.Zhou GX, Wang X, Yan F, Wang X, Li R, Cheng JA, Lou YG* (2011). Genome-wide transcriptional changes and defense-related chemical profiling of rice in response to infestation by the rice striped stem borer *Chilo suppressalis*. *Physiologia Plantarum*, 143: 21-40. (IF=3.067)
- 39.Li K, Tian J, Wang Q, Chen Q, Chen M, Wang H, Zhou Y, Peng Y, Xiao J, Ye GY* (2011). Application of a novel method PCR-ligase detection reaction for tracking predator-prey trophic links in insect-resistant GM rice ecosystem. *Ecotoxicology*, 20(8):2090-2100. (IF=3.051)
- 40.Liu CK, Ye LF, Lang GJ, Zhang CX, Hong J*, Zhou XP* (2011). The VP37 protein of Broad bean wilt virus 2 induce stubule-like structures in both plant and insect cells. *Virus Research*, 155(1): 42-47. (IF=2.905)
- 41.Zhu B, Lou MM, Xie GL* (2011). Characterization and inference of Gene Gain/Loss Along *Burkholderia* Evolutionary History. *Evolutionary Bioinformatics*, 7:191-200. (IF=2.684)
- 42.Chen Y, Tian JC, Wang W, Fang Q, AkhtarZR, Peng YF, Cui H, Guo YY, Song QS, Ye GY* (2011). Bt rice expressing Cry1Ab does not stimulate an outbreak of its non-target herbivore, *Nilaparvata lugens*. *Transgenic Res.* (IF=2.569)
- 43.Shang HL, Xie Y, Zhou XP, Qian YJ, Wu JX* (2011). Monoclonal antibody-based serological methods for detection of Cucumber green mottle mosaic virus. *Virology Journal*, 8: 228. (IF=2.546)
- 44.Li G, Nasar V, Yang Y, Li W, Liu B, Sun L, Li D, Song FM* (2011). Arabidopsis poly(ADP-ribose) glycohydrolase 1 is required for drought, osmotic and oxidative stress responses. *Plant Science*, 180: 283-291. (IF=2.481)
- 45.Zhou XP* (2011). Plant defense and geminivirus counter-defense. *Phytopathology*, 101(6S): S207-S207. (IF=2.428)
- 46.Liu XH, Yang J, He RL, Lu JP, Zhang CL, Lu SL, Lin FC* (2011). An autophagy gene, *TrATG5*, affects conidiospore differentiation in *Trichoderma reesei*. *Res Microbiol*, 162(8): 756-763. (IF=2.405)
- 47.Lou MM, Zhu B, Jin GL, Xie GL* (2011). Specific and sensitive detection of *Enterobacter morus* using reliable RT-PCR reaction. *Plant Disease*, 95(9): 1070-1074. (IF=2.387)
- 48.Basnayake BM, Li D, Zhang H, Li G, Virk N, Song FM* (2011). Arabidopsis DAL1 and DAL2, two RING finger proteins homologous to *Drosophila DIAP1*, are involved in regulation of programmed cell death. *Plant Cell Reports*, 30(1): 37-48. (IF=2.279)
- 49.Yao FX, Huang JL, Cui KH, Nie LX, Xiang J, Liu XJ, Wu W, Chen MX, Peng SB* (2011). Agronomic performance of high-yielding rice variety grown under alternate wetting and drying irrigation. *Field crops research*, 126:16-22. (参与) (IF=2.232)
- 50.Wu JX*, Meng CM, Shang HL, Rong S, Zhang C, Hong J, Zhou XP (2011). Monoclonal antibody-based triple antibody sandwich-enzyme-linked immunosorbent assay and immunocapture

reversetranscription-polymerase chain reaction for *Odontoglossum ringspot virus* detection. *Journal of Virological Methods*, 171(1): 40-45. (IF=2.139)

51.Gao J, Zhang Y, Zhu Q, Lin C, Xu X, Shen ZC* (2011). Transgenic rice expression a fusion protein of Cry1Ab and Cry9Aa confersresistance to a broad spectrum of Lepidopteran pests. *Crop Science*, 51:2535-2543. (IF=2.02)

52.Jia LM, Yan WG*, Agrama HA, Yeater K, Li XB, Hu BL,Moldenhauer K, McClung A, Wu DX. Searching for Germplasm Resistant to Sheath Blightfrom the USDA Rice Core Collection. *Crop Science*, 51: 1507-1517. (IF=2.02)

53.Haden VR*, Xiang J, Peng SB,Bouman BAM, Visperas R, Ketterings QM, Hobbs P, Duxbury JM(2011). Relative effects of ammonia and nitrite on the germination and earlygrowth of aerobic rice. *J Plant Nutr Soil Sci*, 174(2): 292–300. (参与) (IF=1.969)

54.Liu XH, Zhuang FL, Lu JP, Lin FC* (2011). Identification and molecular cloning *Moplaa* gene, a homologue of *Homo sapiensPLAA*, in *Magnaporthe oryzae*. *Microbiol Res*, 167: 8-13. (IF=1.958)

55.HadenVR*, Xiang J, Peng S, Ketterings QM, Hobbs P, Duxbury JM (2011). Ammonia toxicity in aerobic rice: use of soil properties to predictammonia volatilization following urea application and the adverse effects ongermination. *European Journal of Soil Science*, 62(4): 551–559. (参与)(IF=1.932)

56.Zhu B, Lou MM, Xie GL*, Wang GF, Zhou Q,Wang F (2011). *Enterobacter mori* sp.nov., a novel *Enterobacter* speciesassociated with bacterial wilt on *Morusalba* L. *International Journal of Systematic and Evolutionary Microbiology*,61(11): 2769-2774. (IF=1.93)

57.LouMM, Zhu B, Ibrahim M, Li B, Xie GL*, Wang YL, L HY. Sun GC (2011). Antibacterialactivity and mechanism of action of chitosan solutions against apricot fruitrot pathogen *Burkholderia seminalis*. *Carbohydrate Research*, 346 (11): 1294-1301. (IF=1.898)

58.Ibrahim M, WangF, Lou MM, Xie GL* (2011),Li B, Zhu B, Zhang GQ, Liu H, Wareth A (2011). Copper as an antibacterial agent for human pathogenic multidrug resistantBurkholderia cepacia complex bacteria. *Journal of Bioscience and Bioengineering*, 112(6): 570-576. (IF=1.707)

59.Huang QN, Shi YF, Yang Y, Feng BH, Wei YL, Chen J, BaraoidanM, Leung H, Wu JL* (2011). Characterization and geneticanalysis of a light- and temperature-sensitive spotted-leaf mutant in rice(*Oryza sativa* L.). *J Integr Plant Biol*, 53(8): 671-681. (IF=1.603)

60.G ZY, Zeng DL, Cheng FM, Tian ZX, Guo LB,Su Y, Yan MX, Jiang H, Dong GJ, Huang YC, Han B, Li JY, Qian Q*(2011).ALK,the Key Gene for Gelatinization Temperature, is a Modifier Gene for GelConsistency in Rice. *J Integr Plant Biol*,53(9): 756-765. (IF=1.603)

61.Zhang XQ, Zhang GP, Guo LB, Wang HZ,Zeng DL, Dong GJ, Qian Q*, Xue DW* (2011). Identification of quantitative traitloci for Cd and Zn concentrations of brown rice grown in Cd-polluted soils.

***Euphytica*, 180: 173-179. (IF=1.597)**

- 62.Liang YS, Zhan XD, Gao ZQ, LinZC, Yang ZL, Zhang YX, Shen XH, Cao LY*, Cheng SH* (2011). Mapping of QTLs associated with important agronomic traits using three populations derived from a super hybrid rice Xieyou9308. ***Euphytica***, DOI 10.1007/s10681-011-0456-4. (IF=1.597)
- 63.Shen B, Yu WD, Zhu YJ, Fan YY, Zhuang JY* (2011). Fine mapping of a major quantitative trait locus, *qFLL6.2*, controlling flag leaf length and yield traits in rice (*Oryza sativa L.*). ***Euphytica***, DOI:10.1007/s10681-011-0539-2. (IF=1.597)
- 64.Kang GJ, Gong ZJ, Cheng JA, Mao CG, Zhu ZR* (2011). Cloning and expression analysis of a G-protein α subunit—G α 0 in the rice water weevil *Iissorhoptrus oryzophilus*Kuschel. ***Archives of Insect Biochemistry and Physiology***, 76(1): 43-45. (IF=1.564)
- 65.Liu ZR, Gao YL, Luo J, Lai FX, LiYH, Fu Q*, Peng YF (2011). Evaluating the non-rice host plant species of *Sesamia inferens* (Lepidoptera: Noctuidae) as natural refuges: resistance management of Bt rice. ***Environ Entomol***, 40(3): 749-754. (IF=1.534)
- 66.Xiong J*, Zhang L, Fu GF, Yang YJ, Zhu C, Tao LX* (2011). Drought-induced proline accumulation is uninvolved with increased nitric oxide, which alleviates drought stress by decreasing transpiration in rice. ***Journal of Plant Research***, DOI:10.1007/s10265-011-0417. (IF=1.512)
- 67.Lou MM, Fang Y, Zhang GQ, Xie GL*, Zhu B, Ibrahim M (2011). Diversity of *Burkholderia cepacia* Complex from the Moso Bamboo (*Phyllostachys edulis*) Rhizosphere Soil. ***Curr Microbiol***, 62: 650-658. (IF=1.51)
- 68.Chen J, Shi YF, Liu WZ, ChaiRY, Fu YP, Zhuang JY, Wu JL* (2011). A Pid3 allele from rice cultivar Gumei2 confers resistance to *Magnaporthe oryzae*. ***J Genet Genomics***, 38 : 209-216. (IF=1.494)
- 69.Dong SZ, Ma Y, HouY, Yu XP, Ye GY* (2011). Development of an ELISA for evaluating the reproductive status of female brown planthopper, *Nilaparvata lugens*, by measuring vitellogenin and vitellin levels. ***Entomologia Experimentalis EtApplicata***, 139(2): 103-110. (IF=1.404)
- 70.Zhang H, Hu H, Zhang XB, Zhu LF, Zheng KF*, Jin QY*, Zeng FP (2011). Estimation of rice neck blasts severity using spectral reflectance based on BP-neural network. ***Acta Physiol Plant***, 33: 2461–2466. (IF=1.344)
- 71.Shen B, Yu WD, Du JH, Fan YY, Wu JR, Zhuang JY* (2011). Validation and dissection of quantitative trait loci for leaf traits in interval RM4923-RM402 on the short arm of rice chromosome 6. ***J Genet***, 90(1): 39-44. (IF=1.338)
- 72.Fang Y, Xie GL*, Lou MM, Li B, Ibrahim M (2011). Diversity Analysis of *Burkholderia cepacia* Complex in the Water Bodies of West Lake, Hangzhou, China. ***The Journal of Microbiology***, 49(2): 309-314. (IF=1.266)

- 73.Li B*, Liu BP, Yu RR, Lou MM, Wang YL, Xie GL*, Li HY, Sun GC (2011). Phenotypic and molecular characterization of rhizobacterium Burkholderia sp. strain R456 antagonistic to Rhizoctonia solani, sheath blight of rice. *World J Microbiology and Biotechnology*, 27(10):2305-2313. (IF=1.214)
- 74.Huang J, Wu SF, Ye GY* (2011). Molecular characterization of a prolinetransporter from Chilo suppressalis. *Insect Science*, 18(5):495-502. (IF=1.129)
- 75.Wang X, Hu LC, Zhou GX, Cheng JA, Lou YG* (2011). Salicylic acid and ethylene signaling pathways are involved in the production of the ricetrypsin proteinase inhibitors induced by the leaf folder *Cnaphalocrocis medinalis* (Guenée). *Chinese Science Bulletin*, 56(22): 2351-2358. (IF=1.087)
- 76.Li B, Ravnskov S, Xie GL*, Larsen J(2011).Differential effects of organic compounds on cucumber damping-off and biocontrol activity of antagonisticbacteria. *J Plant pathology*, 93(1): 43-50. (IF=1.054)
- 77.Huang CJ, Zhang T, Li FF, Zhang XY, Zhou XP* (2011). Development and application of an efficient andvirus-induced gene silencing system in *Nicotianatabacum* using geminivirus alphasatellite molecule. *Journal of Zhejiang University-Science B*,12(2):83-92. (IF=1.027)
- 78.Zhu JY, Fang Q, Ye GY*, Hu C (2011). Proteome changes in the plasma of Pierisrapae parasitized by the endoparasitoid wasp Pteromalus puparum. *Journal of Zhejiang University-Science B*,12(2): 93-102. (IF=1.027)
- 79.Guo JY*, Dong SZ, Ye GY, Li K, Zhu JY, Fang Q, Hu C (2011). Oosorption in theendoparasitoid, Pteromalus puparum. *J Insect Sci*, 11(90):1-11. (IF=1.014)
- 80.Xie L, Zhang JZ, Meng CM, Hong J*, Zhou XP* (2011). Maize lethal necrosis disease in Yunnan, Chinawas caused by mix-infection of *Maize chlorotic mottle virus* and a potyvirus. *Journal of Phytopathology*, 159(3): 191-193. (IF=0.937)
- 81.Channinun Pornsuriya, KasemSoytong, SupattarPoeaim, Somdej Kanokmedhakul, PrimmalaKhumkomkhet, Fu-ChengLin, Hong Kai Wang& Kevin Hyde (2011). Chaetomium siamense sp.nov., a soilisolate from Thailand, produces a new chaetoviridin, G. *Mycotaxon*, 115(9): 19-27. (参与) (IF=0.752)
- 82.Li B , Liu BP , Yu RR , Tao ZY , Wang YL , Xie GL* (2011). Bacterial brown stripeof rice in soil-less culture system caused 3 by *Acidovorax avenae* subsp. *avenae* in China. *J Gen Plant Pathol*, 77(1):64-67. (IF=0.687)
- 83.Zhang JP, Duan GF, Zhou YJ, Yu LQ*(2011). Fungal phytotoxins for weed control. *Allelopathy Journal*, 27(1): 1-13. (IF=0.635)
- 84.Li B*, Yu RR,Liu BP, Tang QM, Zhang GQ, Wang YL, Xie GL* (2011). Characterization andcomparison of *Serratia marcescens* isolated from edible cactus and from silkworm for virulence potentialand chitosan susceptibility. *Brazilian Journal of Microbiology*, 42(1): 96-104. (IF=0.632)

- 85.Li B, Yu RR, Tang QM, Chen XL, Wu ZY, Wang YL*, Xie GL, Li HY, Sun GC* (2011). Carbon adaptation influence the antagonistic ability of *Pseudomonas aeruginosa* against *Fusarium oxysporum* f. sp. melonis. *Afr J Biotech*, 10(65):14348-14354. (**IF=0.573**)
- 86.Li B, Yu RR, Tang QM, Ting S, Chen XL, Zhu B, Wang YL*, Xie GL, Sun GC (2011). Biofilm formation ability of *Paenibacillus polymyxa* and *Paenibacillus macerans* and their inhibitory effect against tomato bacterial wilt. *Afr J Micro Res*, 5(25): 4260-4266. (**IF=0.528**)
- 87.Ibrahim M, Wang F, Xie GL* (2011). Prevelence of potential pathogenicity and molecular characterizations of Burkholderiaceae complex (BCC) among isolates from bamboo rhizosphere in China. *Res J chem Env*, 15(2): 1003-1011. (**IF=0.292**)
- 88.Deng XX, Zhang XQ, Song XJ, Lai KK, Guo LB, Xin YY, Wang HZ, Xue DW* (2011). Response of transgenic rice at germination traits under salt and alkali stress. *African Journal of Agricultural Research*, 6(18): 4335-4339. (**IF=0.263**)

2010年发表

- 1.Jiao YQ, Wang YH, Xue DW, Wang J, Yan MX, Liu GF, Dong GJ, Zeng DL, Lu ZF, Zhu XD, Qian Q*, Li JY* (2010). Regulation of OsSPL14 by OsmiR156 define ideal plant architecture in rice. *Nature Genetics*, 42(6):541-544. (**IF2009=34.28**)
- 2.Huang XH, Wei XH, Sang T, Zhao Q, Feng Q, Zhao Y, Li CY, Zhu CR, Lu TT, Zhang ZW, Li M, Fan DL, Guo YL, Wang AH, Wang L, Deng LW, Li WJ, Lu YQ, Weng QJ, Liu KY, Huang T, Zhou TY, Jing YF, Li W, Lin Z, Buckler ES, Qian Q, Zhang QF, Li JY, Han B* (2010). Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature Genetics*. 42(11): 961-967. (**IF2009=34.28**)
- 3.Wei TY, Zhang CW, Hong J, Xiong RY, Kasschau K, Zhou XP, James C, Wang AM*.() Formation of complexes at plasmodesmata for potyvirus intercellular movement is mediated by the viral protein P3N-PIPO. *PLoS Pathogens*, 6(6): e1000962. (**IF2009=8.978**)
- 4.Zhao SQ, Hu J, Guo LB, Qian Q*, Xue HW* (2010). Rice leaf inclination2, a VIN3-like protein, regulates leaf angle through modulating cell division of the collar. *Cell Research*, 20(8):935-947. (**IF2009=8.15**)
- 5.Zhang M, Zhang BC, Qian Q, Yu YC, Li R, Zhang JW, Liu XL, Zeng DL, Li JY, Zhou YH* (2010). Brittle Culm12, a dual-targeting kinesin-4 protein, controls cell-cycle progression and wall properties in rice. *Plant J*, 63(2): 312-328. (**IF2009=6.95**)
- 6.Xiong GY, Li R, Qian Q, Song XQ, Liu XL, Yu YC, Zeng DL, Wan JM, Li JY, Zhou YH* (2010). The rice dynamin-related protein DRP2B mediates membrane trafficking, and thereby plays a critical role in secondary cell wall cellulose biosynthesis. *Plant J*, 64(1): 56-70. (**IF2009=6.95**)

- 7.Liu TB, LiuXH, Lu JP, Zhang L, Min H, Lin FC*. (2010) The cysteine protease MoAtg4interacts with MoAtg8 and is required for differentiation and pathogenesis inMagnaporthe oryzae. *Autophagy*, 6(1): 74-85 (IF₂₀₀₉=6.829)
- 8.Yang Q, GongZJ, Zhou Y, Yuan JQ, Cheng JA, Tian L, Li S, Lin XD, Xu RJ, Zhu ZR*, Mao CG. (2010)Role of Drosophila alkaline ceramidase (Dacer) in Drosophila development andlongevity. *Cellular and Molecular Life Sciences*, 67: 1477-1490 (IF₂₀₀₉=6.09)
- 9.Luan WJ*, Liu YQ, Zhang FX, Song YL,Wang ZY, Peng YK, Sun ZX (2010). OsCD1 encodes a putative member of thecellulose synthase-like D sub-family and is essential for rice plant architecture and growth. *Plant Biotechnol J*, doi:10.1111/j.1467-7652.2010.00570.x. (IF₂₀₀₉=4.73)
- 10.Li Y, Yan X, Wang H, Liang S, Ma WB, Fang MY,Nicholas JT, Wang ZY. (2010) MoRic8 Is a Novel Component of G-Protein Signaling During PlantInfection by the Rice Blast Fungus Magnaporthe oryzae. *Mol Plant MicrobeInteract*, 23(3): 317-331. (IF₂₀₀₉=4.407)
- 11.Li Y, Liang S, Yan X, Wang H, Li DB, Soanes DM, Talbot NJ, Wang ZH, WangZY. (2010) Characterization of MoLDB1 Required for Vegetative Growth,Infection-Related Morphogenesis, and Pathogenicity in the Rice Blast Fungus Magnapor the oryzae. *Mol Plant Microbe Interac*, 23(10): 1260-1274 (IF₂₀₀₉=4.407)
- 12.Teng K, Chen H, Lai J, Zhang Z, Fang Y, Xia R, Zhou XP, Guo H, Xie Q*. (2010)Involvement of C4 protein of beet severe curly top virus (family geminiviridae)in virus movement. *PLoS One* , 5(6): e11280. (IF₂₀₀₉=4.351)
- 13.Hu J, Zhu L, Zeng DL,Gao ZY, Guo LB, Fang YX, Zhang GH, Dong GJ, Yan MX, Liu J, Qian Q* (2010).Identification and characterization of NARROW AND ROLLED LEAF 1, a novel gene regulating leaf morphology and plantarchitecture in rice. *Plant Mol Biol*, 73(3): 283-292. (IF₂₀₀₉=3.98)
- 14.Fang Q, WangL, Zhu JY, Li YM, Song QS, StanleyDW, Akhtar ZR, Ye GY*. (2010) Expression of immune-response genes inlepidopteran host are suppressed by venom from an endoparasitoid, Pteromaluspuparum. *BMC Genomics*, 11: 484 (IF₂₀₀₉=3.759)
- 15.TianCH, Gao B, Fang Q, Ye GY, Zhu SY*. (2010) Antimicrobial peptide-like genes inNasonia vitripennis: a genomic perspective. *BMC Genomics*, 11: 187 (IF₂₀₀₉=3.759)
- 16.YuanZL, Zhang CL*, Lin FC*, Kubicek CP. (2010) Identity, diversity and molecularphylogeny of the endophytic mycobiota in rare wild rice roots (*Oryza granulata*)from a nature reserve in Yunnan, China.*Applied and Environmental Microbiology*, 76(5): 1642-1652 (IF₂₀₀₉=3.686)
- 17.Wu C, Fu YP, Hu G C, Si HM,Cheng SH* , Liu WZ* (2010). Isolation andcharacterization of a rice mutant with narrow and rolled leaves. *Planta*,232(2): 313-324. (IF₂₀₀₉=3.372)

- 18.Guo YS, Huang CJ, Xie Y, Song FM, Zhou XP*. (2010) A novel tomatoglutaredoxin gene SIGRX1 positively regulates plant responses to oxidative,drought and salt stresses. *Planta*, 232(6): 1499-1509 (IF₂₀₀₉=3.372)
- 19.WangL, Wang AH, Huang XH, Zhao Q, Dong GJ, Qian Q, Sang T, Han B* (2010). Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombinant inbred lines. *Theor Appl Gene*, DOI10.1007/s00122-010-1449-8. (IF₂₀₀₉=3.36)
- 20.Xiong J, Fu GF , Tao LX* ,Zhu C* (2010). Roles of nitric oxide in alleviating heavy metal toxicity in plants. *Archives of Biochemistry and Biophysics*, 497: 13-20. (IF₂₀₀₉=3.05)
- 21.Yan X, Ma WB, Li Y, Wang H, Que YW, Ma ZH, Talbot NJ, Wang ZY*. (2010) A sterol 14 α -demethylase is required for conidiation, virulence and for mediating sensitivity to sterol demethylation inhibitors by the rice blast fungus Magnaporthe oryzae. *Fungal Genet Biol.*, doi:10.1016/j.fgb.2010.09.005 (IF₂₀₀₉=2.961)
- 22.Yuan ZL, Zhang CL, Lin FC*. (2010) Role of diverse non-systemic fungal endophytes in plant performance and response to stress: progress and approaches. *Journal of Plant Growth Regulation*, 29(1): 116-126 (IF₂₀₀₉=2.438)
- 23.Xie Y, Wu PJ, Liu P, Gong HR, Zhou XP*. (2010) Characterization of alphasatellites associated with monopartite begomovirus/betasatellite complexes in Yunan, China. *Virology Journal*, 7: 178. (IF₂₀₀₉=2.435)
- 24.Bao YY, Li BL, Liu ZB, Xue J, Zhu ZR, Cheng JA, Zhang CX*. (2010) Triazophos up-regulated gene expression in the female brown planthopper, Nilaparvata lugens. *J Insect Physiology*, 56(9): 1087-1094 (IF₂₀₀₉=2.235)
- 25.Wu J, Zhang J, Zhou XP (2010). AV2 protein encoded by Tomato yellow leaf curl Chinavirus is a RNA silencing suppressor. *Phytopathology*, 100:S139. (IF₂₀₀₉=2.22)
- 26.Huang C*, ZhouXP (2010). Development and use of an efficient and temperature-insensitive virus induced gene silencing system in *Nicotiana tabacum*. *Phytopathology*, 100: S52. (IF₂₀₀₉=2.22)
- 27.YuanZL, Lin FC, Zhang CL*, Kubicek CP. (2010) A new species of Harpophora(Magnaportheaceae) recovered from healthy wild rice (*Oryza granulata*) roots, representing a novel member of beneficial dark septate endophyte. *FEMS Microbiology Letters*, 307(1): 94-101 (IF₂₀₀₉=2.199)
- 28.Huai Y, Yu SH, Xie GL*, Wang F, Su T, Li B. (2010) Grain Discoloration of Rice Caused by *Pantoea ananatis* (synonym *Erwinia uredovora*) in China. *Plant Disease*, 94: 482 (IF₂₀₀₉=2.121)
- 29.Zhang X, Li D, Zhang H, Wang X, Zheng Z, Song FM*. (2010) Molecular characterization of rice OsBIANK1, encoding a plasma membrane-anchored ankyrin repeat protein, and its inducible expression

in defense responses. ***Molecular Biology Reports***, 37(2): 653-660 (IF₂₀₀₉=2.038)

30.WangGF, Xie GL*, Zhu B, Huang JS, Liu B, Praphat K, Benyon L, Duan YP. (2010) Identification and characterization of the Enterobacter complex causing mulberry (*Morus alba*) wilt disease in China. ***Eur J Plant Pathol.***, 126: 65-478 (IF₂₀₀₉=1.931)

31.Dong SZ, Ye GY*, Guo JY, Yu XP, Hu C. (2010) Oogenesis and programmed cell death of nurse cells in the endoparasitoid, *Pteromalus puparum*. *Microscopy Research and Technique*, 73(7): 673-680 (IF₂₀₀₉=1.85)

32.Gao YL, Hu Y, Fu Q*, Zhang J, Oppert B, Lai FX, Peng YF, Zhang ZT. (2010) Screen of *Bacillus thuringiensis* toxins for transgenic rice to control *Sesamia inferens* and *Chilo suppressalis*. ***Journal of Invertebrate Pathology***, 105(1): 11-15 (IF₂₀₀₉=1.807)

33.Shen XJ, Ye GY*, Cheng XY, Yu CY, Altosaar I, Hu C. (2010) Characterization of an abaecin-like antimicrobial peptide identified from a *Pteromalus puparum* cDNA clone. ***Journal of Invertebrate Pathology***, 105(1): 24-29 (IF₂₀₀₉=1.807)

34.Shen XY, Ye GY*, Cheng XY, Yu CY, Yao HW, Hu C. (2010) Novel antimicrobial peptides identified from an endoparasitic wasp cDNA library. *Journal of Peptide Science*, 16(1): 58-64 (IF₂₀₀₉=1.807)

35.Liu XH, Lu JP, Dong B, Lin FC*. (2010) Disruption of MoCMK1, encoding a putative calcium/calmodulin-dependent kinase, in *Magnaporthe oryzae*. ***Microbiological Research***, 165(5): 402-410 (IF₂₀₀₉=1.771)

36.Li J, Zhou XP*. (2010) Molecular characterization and experimental host-range of two begomoviruses infecting *Clerodendrum cyrtophyllum* in China. ***Virus Genes***, 41(2):250-259 (IF₂₀₀₉=1.705)

37.Lin CY, Nie P, Lu W, Zhang Q, Li J, Shen ZC*. (2010) A selectively terminable transgenic rice line expressing human lactoferrin. ***Protein Expr Purif***, 74(1): 60-64 (IF₂₀₀₉=1.563)

38.Zhu JY, Fang Q, Wang L, Hu C, Ye GY*. (2010). Proteomic analysis of the venom from the endoparasitoid wasp *Pteromalus puparum* (Hymenoptera: Pteromalidae). ***Archives of Insect Biochemistry and Physiology***, 75(1): 28-44 (IF₂₀₀₉=1.381)

39.Wang WX, Zhu TH, Lai FX, Fu Q*. (2010) Event-specific detection of transgenic rice Kefeng No.6 by characterization of the transgene flanking sequence. ***European Food Research Technology***, DOI:10.1007/s00217-010-1389-1. (IF₂₀₀₉=1.37)

40.Chen Y, Tian JC, Shen ZC, Peng YF, Hu C, Guo YY, Ye GY*. (2010) Transgenic Rice Plants Expressing a Fused Protein of Cry1Ab/Vip3H Has Resistance to Rice Stem Borers Under Laboratory and Field Conditions. ***Journal of Economic Entomology***, 103(4): 1444-1453 (IF₂₀₀₉=1.296)

- 41.AkhtarZR, Tian JC, Chen Y, Fang Q, Hu C, Chen M, Peng YF, Ye GY*. (2010) Impacts of six Bt rice lines on non-target rice feeding Thrips, *Stenchaetothrips biformis*(Thysanoptera:Thripidae) under laboratory and field conditions. *Environmental Entomology*, 39(2): 715-726 (IF₂₀₀₉=1.154)
- 42.Tian JC, Liu ZC, Chen M, Chen Y, Chen XX, Peng YF, Hu C, Ye GY*. (2010) Laboratory and Field Assessments of Prey-Mediated Effects of Transgenic Bt Rice on Ummeliatain secticeps (Araneida: Linyphiidae). *Environmental Entomology*, 39(4):1369-1377 (IF₂₀₀₉=1.154)
- 43.Fang Y, Lou MM, Li B, Xie GL*, Wang F, Zhang LX, Luo YC. (2010) Characterization of *Burkholderia cepacia* complex from cystic fibrosis patients in China and their chitosansusceptibility. *World J Microbiol Biotechnol*, 26: 443-450 (IF₂₀₀₉=1.082)
- 44.Zhu JY, Ye GY*, Fang Q, Hu C. (2010) Alkalinephosphatase from venom of the endoparasitoid wasp, *Pteromalus puparum*. *Journal of Insect Science*. 14 :1-15. (IF₂₀₀₉=1.069)
- 45.Zhang H, Ma XY, Qian YJ, Zhou XP*. (2010) Molecular characterization and pathogenicity of Papaya leaf curl China virus infecting tomato in China. *Journal of Zhejiang University-Science B*, 11(2): 109-114 (IF₂₀₀₉=1.041)
- 46.Feng Y, Cao LY, Wu WM, Sheng XH, Zhan XD, Zhai RR, Wang RC, Chen DB, Cheng SH*(2010). Mapping QTLs for nitrogen-deficiency tolerance at seeding stage in rice(*Oryza sativa* L.). *Plant Breeding*, 129(6): 652-656. (IF₂₀₀₉=1.03)
- 47.Cao LY, Wu JL, Fan YY, Cheng SH*, Zhuang JY*(2010). QTL analysis for heading date and yield traits using recombinant inbred lines of indica rice grown in different cropping seasons. *Plant Breeding*, 129(6):676-682. (IF₂₀₀₉=1.03)
- 48.Shao GN, Tang A, Tang SQ, Luo J, Jiao GA, Wu JL, Hu PS*(2010). A new deletion mutation of fragrant gene and the development of three molecular markers for fragrance in rice. *Plant Breeding*, doi:10.1111/j.1439-0523.2009.01764.x. (IF₂₀₀₉=1.03)
- 49.Xu Q, Yuan XP, Yu HY, Wang YP, Tang SX, Wei XH * (2010). Mapping quantitative trait loci for sheath blight resistance in rice using double haploid population. *Plant Breeding*, doi:10.1111/j.1439-0523.2010.01806.x. (IF₂₀₀₉=1.03)
- 50.Soad AE, Xie GL*, Li B, Su T, Larsen J*. (2010) Effects of Paenibacillus strains and chitosan on plant growth promotion and control of ralstonia wilt in tomato. *Journal of Plant Pathology*, 92: 595-602 (IF₂₀₀₉=0.974)
- 51.Gong JY, Wu JR, Wang K, Fan YY, Zhuang JY* (2010). Fine mapping of qHUS6.1, a quantitative trait locus for silicon content in rice (*Oryza sativa* L.). *Chinese Sci Bull*, 55(29): 3283-3287. (IF₂₀₀₉=0.90)

- 52.Zhu B, Wang GF, Xie GL*, Zhou Q, Zhao M, Kawicha P, Li B, Tian WX. (2010) Enterobacterspp.: A new evidence causing bacterial wilt on mulberry. *Science China*, 53: 292-300 (IF₂₀₀₉=0.83)
- 53.ShaoGN, Tang SQ, Luo J, Jiao GA, Wei XJ, Tang A, Wu JL, Zhuang JY, Hu PS* (2010) Mapping of qGL7-2, a grain length QTL onchromosome 7 of rice. *J Genet Genomics*, 37: 523-531. (IF₂₀₀₉=0.82)
- 54.RaoYC, Dong GJ, Zeng DL*, Hu J, Zeng LJ, Gao ZY, Zhang GH, Guo LB, Qian Q* (2010).Genetic analysis of leaffolder resistance in rice. *J Genet Genomics*, 37(5):325-331. (IF₂₀₀₉=0.82)
- 55.SunFL, Zhang WP, Xiong GS, Yan MX, Qian Q, Li JY, Wang YH* (2010). Identificationand functional analysis of the MOC1 interacting protein 1. *J Genet Genomics*, 37(1):69-77. (IF₂₀₀₉=0.82)
- 56.HongLL, Qian Q, Zhu KM, Tang D, Huang ZJ, Gao L, Li M, Gu MH, Cheng ZK* (2010). ELErestrains empty glumes from developing into lemmas. *J Genet Genomics*, 37(2):101-115. (IF₂₀₀₉=0.82)
- 57.Li B, Liu BP,Su T, Fang Y, Xie GL*, Wang GF, Wang YL, Sun GC*. (2010) Effect of ChitosanSolution on the Inhibition of Pseudomonas fluorescens Causing Bacterial HeadRot of Broccoli. *Plant Pathol. J*, 26: 189-193 (IF₂₀₀₉=0.744)
- 58.Li B, Fang Y,Zhang GQ, Yu RR, Lou MM, Xie GL*, Wang YL, Sun GC*. (2010) MolecularCharacterization of Burkholderia cepacia Complex Isolates Causing BacterialFruit Rot of Apricot. *Plant Pathol. J*, 26: 223-230 (IF₂₀₀₉=0.744)
- 59.Cheng JL, ZhouY, Zhao JH, Zhang CL, Lin FC*. (2010) Synthesis and antifungal activity oftrichodermin derivatives. *Chinese chemical letters*, 21(9):1037-1040 (IF₂₀₀₉=0.643)
- 60.Li B*, Su T,Chen XL, Liu BP, Zhu B, Fang Y, Qiu W, Xie GL*. (2010) Effect of chitosansolution on the bacterial septicemia disease of Bombyx mori (Lepidoptera:Bombycidae) caused by Serratia marcescens. *Appl Entomol Zool*, 5: 145-152 (IF₂₀₀₉=0.616)

2009年发表

- 1.Huang XZ, Qian Q, Liu ZB, Sun HY, He SY, Luo D, Xia GM, Chu CC, Li JY, Fu XD* (2009). Natural variation at the *DEP1* locus enhances grain yield in rice.*Nature Genetics*, 41:494-497. (IF₂₀₀₉=34.28)
- 2.HuangXH, Feng Q, Qian Q,Zhao Q, Wang L, Wang AH, Guan JP, Fan DL, Weng QJ, Huang T, Dong GJ, Sang T, HanB* (2009). High-throughput genotyping by whole-genome resequencing. *Genome Research*, 19: 1068-1076. (IF₂₀₀₉=11.34)
- 3.TianZX, Qian Q, Liu QQ, Yan MX, Liu XF, Yan CJ, Liu GF, Gao ZY, Tang SZ, Zeng DL,Wang YH, Yu JM*, Gu MH*, Li JY* (2009). Allelic diversities in rice starchbiosynthesis lead to a diverse array of rice eating and cooking qualities. *PNAS*. 22: 21760-21765. (IF₂₀₀₉=9.43)

- 4.Zhang GH,Xu Q, Zhu XD, Qian Q, XueHW*(2009). **SHALLOT-LIKE1** is a KANADI transcription factor that modulates rice leaf rolling by regulating leaf abaxial cell development. *Plant Cell*, 21: 719-735. (IF₂₀₀₉=9.29)
- 5.Yu YC, Tang T, Qian Q, Wang YH, YanMX, Zeng DL, Han B, Wu CI*, Shi SH*, Li JY* (2008). Independent losses offunction in a polyphenol oxidase in rice differentiation in grain discolorationbetween subspecies and the role of positive selection. *Plant Cell*, 20:2946-2959. (IF₂₀₀₉=9.29)
- 6.LinH, Wang RX, Qian Q, Yan MX,Meng XB, Fu ZM, Yan CY, Jiang B, Su Z, Li JY, Wang YH* (2009). DWARF27, an iron-containing protein requiredfor the biosynthesis of strigolactones, regulates rice tiller bud outgrowth. *Plant Cell*, 21: 1512-1525. (IF₂₀₀₉=9.29)
- 7.Zhou Y, Li S,Qian Q, Zeng D, Zhang M, Guo L, Liu X,Zhang B, Deng L, Liu X, Luo G, Wang X, Li J* (2009). BC10, a DUF266-containing and golgi-located type II membraneprotein, is required for cell-wall biosynthesis in rice (*Oryzasativa L.*). *Plant Journal*, 57(3): 446-462. (IF₂₀₀₉=6.95)
- 8.LiS,Qian Q, Fu Z, Zeng D,Meng X, Kyozuka J, Maekawa M, Zhu X, Zhang J, Li J, Wang Y* (2009). Short panicle1 encodes a putative PTRfamily transporter and determines rice panicle size. *Plant Journal*, 58(4): 592-605. (IF₂₀₀₉=6.95)
- 9.TongH, Jin Y, Liu W, Li F, Fang J, Yin Y, Qian Q, Zhu L, Chu C* (2009). DWARFAND LOW-TILLERING, a new member of the GRAS family, plays positive roles inbrassinosteroid signaling in rice. *Plant Journal*, 58(5): 803-816. (IF₂₀₀₉=6.95)
- 10.YuanZ, Gao S, Xue DW, Luo D, Li LT, Ding SY, Yao X, Wilson ZA, Qian Q, Zhang DB* (2009).RETARDED PALEA1 controls palea development and floral zygomorphy in rice. *Plant Physiol*, 149(1): 235-244. (IF₂₀₀₉=6.24)
- 11.LuanWJ, Chen HZ, Fu YP, Si HM, Peng W, Song SS, Liu WZ, Hu GC, Sun ZX*, Xie DX*,Sun CQ* (2009). The effect of the crosstalk between photoperiod and temperatureon heading-date in rice. *PLoS One*, 4(6): e5891. (IF₂₀₀₉=4.35)
- 12.Gao ZY, Qian Q*, Liu XH, Yan MX, Feng Q, Dong GJ, Liu J, Han B* (2009). Dwarf 88, a novel putative esterase geneaffecting architecture of rice plant. *Plant Mol Biol*, 71: 265-276. (IF₂₀₀₉=3.98)
- 13.Zhang BC, Deng LW, Qian Q, Xiong GY, Zeng DL, Li R, Guo LB,Li JY, Zhou YH* (2009). A missense mutation in the transmembrane domain of CESAsignificantly affects protein abundance in the plasma membrane and results in abnormal cellwall biosynthesis in rice. *Plant Mol Biol*, 71: 509-524. (IF₂₀₀₉=3.98)
- 14.Guo LB, Kong ZS, Qian Q, Liu B* (2009). Evaluating the microtubulecytoskeleton and its interacting proteins in monocots by mining the ricegenome. *Ann of Botany*, 103: 387-402. (IF₂₀₀₉=3.51)

- 15.LiuWZ*, Wu C, Fu YP, Hu GC, Si HM, Zhu L, Luan WJ, He ZQ, Sun ZX (2009). Identification and characterization of *HTD2*: a novel gene negatively regulating tiller bud outgrowth in rice. *Planta*, 230(4): 649-658. (IF₂₀₀₉=3.37)
- 16.Xiong J, An Ly, Lu H, Zhu C* (2009). Exogenous nitric oxide enhances cadmium tolerance of rice by increasing pectin and hemicellulose contents in root cell wall. *Planta*, 230(4): 755-765. (IF₂₀₀₉=3.37)
- 17.HuWH, Hu GC, Han B* (2009). Genome-wide survey and expression profiling of heat shock proteins and heat shock factors revealed overlapped and stress specific response under abiotic stresses in rice. *Plant Science*, 176: 583-590. (IF₂₀₀₉=2.05)
- 18.WanFJ, Zeng B, Sun ZX, Zhu C* (2009). Relationship between proline and Hg²⁺-induced oxidative stress in a tolerant rice mutant. *Arch Environ Contam Toxicol*, 56(4): 723-731. (IF₂₀₀₉=1.74)
- 19.Guo LB, Ma LL, Jiang H, Zeng DL, Hu J, Wu LW, Gao ZY, Zhang GH, Qian Q* (2009). Genetic analysis and fine mapping of two genes for grain shape and weight in rice. *Journal of Integrative Plant Biology*, 51(1): 45-51. (IF₂₀₀₉=1.40)
- 20.Zeng DL, Hu J, Dong GJ, Liu J, Qian Q* (2009). Quantitative trait loci mapping of flag-leaf ligule length in rice and alignment with *ZmLG1* gene. *Journal of Integrative Plant Biology*, 51(4): 360-366. (IF₂₀₀₉=1.40)
- 21.Ma LY, Bao JS, Guo LB, Zeng DL, Li XM, Ji ZJ, Xia YW, Yang CD*, Qian Q* (2009). Quantitative trait loci for panicle layer uniformity identified in doubled haploid lines of rice in two environments. *Journal of Integrative Plant Biology*, 51(9): 818-824. (IF₂₀₀₉=1.40)
- 22.Gao ZY, Liu XH, Guo LB, Liu J, Dong GJ, Hu J, Han B, Qian Q* (2009). Identification of a novel tillering dwarf mutant and fine mapping of the *TDDL*(T) gene in rice (*Oryza sativa*L.). *Chinese Science Bulletin*, 54(12): 2062-2068. (IF₂₀₀₉=0.90)
- 23.Ma YM, Liu L, Zhu CG, Sun CH, Xu B, Fang J, Tang JY, Luo AD, Cao SY, Li GP, Qian Q, Xue YB, Chu CC* (2009). Molecular analysis of rice plants harboring a multi-functional T-DNA tagging system. *J Genet Genomics*, 36(5): 267-276. (IF₂₀₀₉=0.82)
- 24.Ma LY, Yang CD, Zeng DL, Cai J, Li XM, Ji ZJ, Xia YW, Qian Q*, Bao JS* (2009). Mapping QTLs for heading synchrony in a doubled haploid population of rice in two environments. *J Genet Genomics*, 36(5): 297-304. (IF₂₀₀₉=0.82)
- 25.Wei XH*, Yuan XP, Yu HY, Wang YP, Xu Q, Tang SX. (2009). Temporal changes in SSR allelic diversity of major rice cultivars in China. *J Genet Genomics*, 36(6): 363-370. (IF₂₀₀₉=0.82)

2008年发表

- 1.Wang ET, Wang JJ, Zhu XD, Hao W, Wang L, Li Q, Zhang LX, He W, Lu BR, Lin HX, Ma H, Zhang GQ, He ZH* (2008). Control of rice grainfilling and yield by a gene with a potential signature of domestication. *Nature Genetics*, 40: 1370-1374. (IF2008=30.30)
- 2.Fang J, Chai CL, Qian Q , Li CL, Tang JY, Sun L, Huang ZJ, Guo XL, Sun CH , Liu M,Zhang Y, Lu QT, Wang YQ , Lu CM, Han B, Chen F, Cheng ZK, Chu CC* (2008).Mutations of genes in synthesis of the carotenoid precursors of ABA lead to pre-harvestsprouting and photo-oxidation in rice. *Plant Journal*, 54 (2): 177-189. (IF2008=6.50)
- 3.Li HG, Xue DW, Gao ZY, Yan MX, Xu WY, Xing Z, Huang DN*, Qian Q*, Xue YB* (2008).A putative lipase gene *EXTRA GLUME1*regulates both empty glume fate and spikelet development in rice. *Plant Journal*, 57(4): 593-605. (IF2008=6.50)
- 4.Qi J, Qian Q, Bu QY, Li SY, Chen Q, Sun JQ, Liang WX, Zhou YH, Chu CC, Li XG, Ren FG, Palme K, Zhao BR, Chen JF, Chen MS, Li CY* (2008).Mutation of the rice *Narrow leaf1*gene, which encodes a novel protein, affects vein patterning and polar auxintransport. *Plant Physiol*, 147: 1947-1959. (IF2008=6.11)
- 5.Yao KM, Hu N, Chen WL, Li RZ, Yuan QH,Wang F, Qian Q, Jia SR* (2008).. Establishment of a rice transgene flow modelfor predicting maximum distances of gene flow in southern China. *New Phytologist*, 180: 217-228. (IF2008=5.18)
- 6.Cheng MY, Zeng NY, Tong SW, Francisca Li WY, Xue Y, Zhao KJ, Wang CL, Zhang Q, Fu YP,Sun ZX, Sun Samuel SM , Lam HM* (2008). Constitutive expression of a rice GTPase activating protein induces defense responses. *New Phytologist*, 179: 530-545. (IF2008=5.18)
- 7.Peng ZY, Zhang HY, Liu TT, Dzikiewicz KM, Li SG, Wang XF, Hu GC, Zhu ZG, Wei XH, Zhu QH, Sun ZX, Ge S, Ma LG, Li L*, Deng XW* (2008). Characterization of the genomeexpression trends in the heading-stage panicle of six rice lineages. *Genomics*, on line. (IF2008=3.08)
- 8.Luan WJ, He CK, Hu GC, Dey M, Fu YP, Si HM, Zhu L, Liu WZ, Duan F, Zhang H, Liu WY,Zhuo RY, Garg A, Wu R*, Sun ZX* (2008). An efficient field screening procedurefor identifying transposants for constructing an Ac/Ds-based insertional-mutant library of rice. *Genome*, 51(1): 41-49. (IF2008=1.71)
- 9.Dai WM, Zhang KQ, Wu JR, Wang L, Duan BW, Zheng KL, Cai R, Zhuang JY* (2008).Validating a segment on the short arm of chromosome 6 responsible for geneticvariation in the hull silicon content and yield traits of rice. *Euphytica*,160: 317-324. (IF2008=1.40)

- 10.LiuBM, Wu YJ*, Fu XD, Qian Q (2008). Characterizations and molecular mapping of novel dominant semi-dwarf gene *sdd(t)* in rice (*Oryza sativa*). *Plant Breeding*, 127: 125-130. (IF₂₀₀₈=1.28)
- 11.GuoLB, Ma LL, Jiang H, Zeng DL, Hu J, Wu LW, Gao ZY, Zhang GH, Qian Q* (2008). Genetic analysis and fine mapping of two genes for grain shape and weight in rice. *Journal of Integrative Plant Biology*, 50(12): 1645-1651. (IF₂₀₀₈=0.86)
- 12.MaLY, Ji ZJ, Bao JS, Zhu XD, Li XM, Zhuang JY, Yang CD, Xia YW*. Response of rice genotypes carrying different dwarf genes to *Fusarium moniliforme* and Gibberellic acid. *Plant Production Science*, 11(1): 134-138. (IF₂₀₀₈=0.76)
- 13.JiangL, Guo LB*, Jiang H, Zeng DL, Hu J, Wu LW, Gao ZY, Qian Q* (2008). Genetical analysis and fine-mapping of a dwarfing withered leaf-tip mutation in rice. *J Genet Genomics*, 35: 715-721. (IF₂₀₀₈=0.36)

2007年发表

- 1.DingY, Wang X, Su L, Zhai JX, Cao SY, Zhang DF, Liu CY, Bi YP, Qian Q, Cheng ZK, ChuCC*, Cao XF (2007). SDG714, a Histone, H3K9 Methytransferase, is involved in Tos17 DNA methylation and transposition in rice. *Plant Cell*, 19: 9-22. (IF₂₀₀₇=9.65)
- 2.Ji XM, Van den Ende W, Schroeven L, Clerens S, Geuten K, Cheng SH, Bennett J* (2007). The rice genome encodes two vacuolar invertases with fructan exohydrolase activity but lacks the related fructan biosynthesis genes of the Pooideae. *New Phytologist*, 173(1): 50-62. (IF₂₀₀₇=5.35)
- 3.ZhangJ, Zhu YG*, Zeng DL, Cheng WD, Qian Q, Duan GL (2007). Mapping quantitative trait loci associated with arsenic accumulation in rice (*Oryza sativa*). *New Phytologist*, 177(2): 350-355. (IF₂₀₀₇=5.35)
- 4.LiPJ, Wang YH, Qian Q, Fu ZM, Wang M, Zeng DL, Li BH, Wang XJ, Li JY* (2007). LAZY1 controls rice shoot gravitropism through regulating polar auxin transport. *Cell Research*, 17: 402-410. (IF₂₀₀₇=4.22)
- 5.LiuXH, Lu TT, Yu SL, Li Y, Huang YC, Huang T, Zhang L, Zhu JJ, Zhao Q, Fan DL, MuJ, Shangguan YY, Feng Q, Guan JP, Ying K, Zhang Y, Lin ZX, Sun ZX, Qian Q, Lu YP, Han B* (2007). A collection of 10,096 indica rice full-length cDNAs reveals highly expressed sequence divergence between *Oryza sativa* indica and japonica subspecies. *Plant Mol Biol*, 65: 403-415. (IF₂₀₀₇=3.85)
- 6.ZengDL, Yan MX, Wang YH, Liu XF, Qian Q, Li JY* (2007). Du1, encoding a novel Prp1 Protein, regulates starch biosynthesis through affecting the splicing of Wxb Pre-mRNAs in rice (*Oryza sativa* L.). *Plant Mol Biol*, 65: 501-509. (IF₂₀₀₇=3.85)

- 7.Yuan QH, Shi L, Wang F, Cao B, Qian Q, Lei XM, Liao YL, Liu WG, Cheng L, Jia SR*(2007). Investigation of rice transgene flow in compass sectors by using malesterile line as a pollen detector. *Theor Appl Genet*, 115: 549-560. (IF₂₀₀₇=3.14)
- 8.LiuWzhen, Fu YP, Hu GC, Si HM, Zhu L, Wu C, Sun ZX* (2007). Identification and fine mapping of a thermo-sensitive chlorophyll deficient mutant in rice (*Oryza sativa* L.). *Planta*, 226: 785-795. (IF₂₀₀₇=3.06)
- 9.XiaZH, Jiang GH, Qian Q, Li AL, Cheng ZK, Zhu LH, Mao L*. Zhai WX* (2007). A paracentric inversion suppresses genetic recombination at the *FON3* locus with breakpoints corresponding to sequence gaps on rice chromosome 11L. *Mol Genet Genomics*, 277(3): 263-272. (IF₂₀₀₇=2.98)
- 10.ChengSH*, Zhuang JY, Fan YY, Du JH, Cao LY (2007). Progress in research and development on hybrid rice, a super-domesticate in China. *Annals of Botany*, 100: 959-966. (IF₂₀₀₇=2.94)
- 11.WangDK, Pei KM, Fu YP, Sun ZX, Li SJ, Liu HQ, Tang K, Han B*, Tao YZ* (2007). Genome-wide analysis of the auxin response factors (ARF) gene family in rice (*Oryza sativa*). *Gene*, 394 (1): 13-24. (IF₂₀₀₇=2.87)
- 12.CuiJJ, Fan SC, Shao T, Huang ZJ, Zeng DL, Tang D, Li M, Qian Q*, Cheng ZK* (2007). Characterization and fine mapping of the *ibf* mutant in rice. *Journal of Integrative Plant Biology*, 49(5): 678-685. (IF₂₀₀₇=2.01)
- 13.Liu M, Zhu J, Sun ZX*, Xu T (2007). Possible suppression of exogenous b-1,3-glucanase gene *gluc78* on rice transformation and growth. *Plant Science*, 172: 888-896. (IF₂₀₀₇=1.80)
- 14.ZhuoRY*, Qiao GR, Sun ZX (2007). Transgene expression in Chinese sweetgum driven by the salt induced expressed promoter. *Plant Cell Tiss Organ Cult*, 88: 101-107. (IF₂₀₀₇=1.07)
- 15.Ouyang YN, Zeng FR, Zhuang JY, Yu SM, Zhu LF, Jin QY*, Zhang GP* (2007). Genetic analysis of genotype x iron nutrition interaction on coleoptile elongation rate in rice (*Oryza sativa* L.). *Euphytica*, 156(3): 311-318. (IF₂₀₀₇=1.05)
- 16.Chen J, Zhu C*, Lin D, Sun ZX (2007). The effects of Cd on lipid peroxidation, hydrogen peroxide content and antioxidant enzyme activities in Cd-sensitive. *Canadian J Plant Sci*, 87(1): 49-57. (IF₂₀₀₇=0.72)
- 17.ChengSH*, Cao LY, Zhuang JY, Chen SG, Zhan XD, Fan YY, Zhu DF, Min SK (2007). Super Hybrid Rice Breeding in China: Achievements and Prospects. *Journal of Integrative Plant Biology*, 49 (6): 805-810. (IF₂₀₀₇=0.67)

- 18.JiangH, Guo LB, Qian Q* (2007). Recent Progress on Rice Genetics in China. *Journal of integrative Plant Biology*, 49(6): 776-790. (IF₂₀₀₇=0.67)
- 19.ZhaoCY, Qian Q*, Wang HZ, Huang DN (2007). Co-transformation of gene expressioncassettes via particle bombardment to generate safe transgenic plant withoutany unwanted DNA. *In Vitro Cell Dev Biol Plant*, 43: 328-334. (IF₂₀₀₇=0.55)

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