

# 赵团结

## 个人信息:

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## 受教育作经历:

1992 年安徽农学院获农学学士学位; 1995 年南京农业大学作物遗传育种专业毕业, 获农学硕士学位, 2006 年获农学博士学位。

## 研究方向:

从事作物遗传育种和生物统计学教学科研工作, 侧重大豆优异基因资源发掘与分子育种研究。

## 承担课题情况:

1. 大豆种质对细菌性斑疹病不同菌株抗性的遗传解析, 国家自然科学基金面上项目, 2019-2022, 项目主持
2. 长江下游鲜食大豆化肥农药减施关键技术集成研究及示范, 国家重点研发计划任务, 2018-2020, 任务主持
3. 南方抗除草剂转基因大豆新品种培育, 国家转基因专项, 2016-2020, 子课题主持
4. 野生大豆 PI342618B 高耐淹性的形态生理机制与 QTL/基因体系研究, 国家自然科学基金面上项目, 2016-2019, 项目主持
5. 大豆曲茎重叠基因的克隆、调控网络及育种潜力研究, 国家自然科学基金面上项目, 2013-2016, 项目主持
6. 高产优质抗逆大豆分子育种与品种创制, 863 计划 课题, 2012-2015, 课题主持
7. 大豆重要功能基因的单元型效应和互作分析, 973 计划 课题, 2010-2014, 课题主持

## 主要研究进展:

育成大豆新品种 8 个, 创制大豆优异种质和遗传材料共 2000 余份; 发掘一批控制大豆产量及相关性状 (株型、雄性不育)、品质 (蛋白质、油脂含量等)、耐逆性 (耐涝、抗细菌性病害等) 的重要基因/QTL。发表论文 200 余篇 (SCI 收录 70 余篇), 参编专著和教材 4 本, 获发明专利 4 项, 获教育部高校自然科学二等奖和科技进步二等奖各 1 项、省部级三等奖 2 项。

## 近 5 年发表的主要论文:

1. Liu Meifeng, Wang Yaqi, Nie Zhixing, Gai Junyi, Bhat Javaid Akhter, Kong Jiejie, Zhao Tuanjie\*. Double mutation of two homologous genes YL1 and YL2 results in a leaf, yellowing phenotype in soybean [*Glycine max* (L.) Merr]. *Plant Molecular Biology*, 2020 DOI:10.1007/s11103-020-01008-9
2. Yang Chengfeng, Huang Yanzhong, Lv Wenhuan, Zhang Yingying, Bhat Javaid Akhter, Kong

- Jiejie, Xing Han, Zhao Jinming\*, Zhao Tuanjie\*. GmNAC8 acts as a positive regulator in soybean drought stress. *Plant Science*, 2020, 293: 110442.
3. Fei Yun-Yan, Bhat Javaid Akhter, Gai Jun-Yi, Zhao Tuan-Jie\*. Global Transcriptome profiling of enterobacter strain nrs-1 in response, to hydrogen peroxide stress treatment. *Applied Biochemistry and Biotechnology*, 2020, DOI:10.1007/s12010-020-03313-x
  4. Karikari Benjamin, Bhat Javaid A, Denwar Nicholas N, Zhao Tuanjie\*. Exploring the genetic base of the soybean germplasm from Africa America and Asia as well as mining of beneficial allele for flowering and seed weight. *3 BIOTECH*, 2020, 10:195.
  5. Sharmin Ripa Akter, Bhuiyan Mashiur Rahman, Lv Wenhuan, Yu Zheping, Chang Fangguo, Kong Jiejie, Bhat Javaid Akhter\*, Zhao Tuanjie\*. RNA-Seq based transcriptomic analysis revealed genes associated with seed-flooding tolerance in wild soybean (*Glycine soja* Sieb. & Zucc.). *Environmental and Experimental Botany*, 2020, 171: 103906.
  6. Hina Aiman, Cao Yongce, Song Shiyu, Li Shuguang, Sharmin Ripa Akter, Elattar Mahmoud A., Bhat Javaid Akhter\*, Zhao Tuanjie\*. High-resolution mapping in two RIL populations refines major "QTL Hotspot" regions for seed size and shape in soybean (*Glycine max* L.). *International Journal of Molecular Sciences*, 2020, 21:1040.
  7. 曹永策, 李曙光, 张新草, 孔杰杰, 赵团结\*. 夏大豆重组自交系群体遗传图谱构建及开花期 QTL 分析. *中国农业科学*, 2020, 53(4): 683-694.
  8. Liu Meifeng, Wang Yaqi, Gai Junyi, Bhat Javaid Akhter, Li Yawei, Kong Jiejie, Zhao Tuanjie\*. Genetic Analysis and gene mapping for a short-petiole mutant in soybean (*Glycine max* (L.) Merr.). *Agronomy*, 2019, 9:709.
  9. Yu Zheping, Chang Fangguo, Lv Wenhuan, Sharmin Ripa Akter, Wang Zili, Kong Jiejie, Bhat Javaid Akhter, Zhao Tuanjie\*. Identification of QTN and candidate gene for seed-flooding tolerance in, soybean [*Glycine max* (L.) Merr.] using genome-wide association study (GWAS). *Genes*, 2019,10: 957.
  10. Al Amin G. M., Kong Keke, Sharmin Ripa Akter, Kong Jiejie, Bhat Javaid Akhter\*, Zhao Tuanjie\*. Characterization and rapid gene-mapping of leaf lesion mimic phenotype of spl-1 mutant in soybean (*Glycine max* (L.) Merr.). *International Journal of Molecular Sciences*, 2019, 20(9): 2193.
  11. Karikari Benjamin, Li Shuguang, Bhat Javaid Akhter, Cao Yongce, Kong Jiejie, Yang Jiayin, Gai Junyi\*, Zhao Tuanjie\*. Genome-wide detection of major and epistatic effect QTLs for seed protein and oil content in soybean under multiple environments using high-density Bin map. *International Journal of Molecular Sciences*, 2019, 20(4): 979.
  12. Li Shuguang, Xu Haifeng, Yang Jiayin\*, Zhao Tuanjie\*. Dissecting the genetic architecture of seed protein and oil content in soybean from the Yangtze and Huaihe River Valleys using multi-locus genome-wide association studies. *International Journal of Molecular Sciences*, 2019, 20(12): 3041.
  13. Wang Ruikai, Liu Li, Kong Jiejie, Xu Zhiyong, Bhat Javaid Akhter, Zhao Tuanjie\*. QTL architecture of vine growth habit and gibberellin oxidase gene diversity in wild soybean (*Glycine soja*). *Scientific Reports*, 2019, 9: 7393.
  14. Zhang Xi, Hina Aiman, Song Shiyu, Kong Jiejie, Bhat Javaid Akhter\*, Zhao Tuanjie\*. Whole-genome mapping identified novel QTL hotspots regions for seed storability in soybean (*Glycine max* L.). *BMC Genomics*, 2019, 20: 499.
  15. Cao Yongce, Li Shuguang, Chen Guoliang, Wang Yanfeng, Bhat Javaid Akhter, Karikari

- Benjamin, Kong Jiejie, Gai Junyi\*, Zhao Tuanjie\*. Deciphering the genetic architecture of plant height in soybean using two RIL populations sharing a common M8206 parent. *Plants*, 2019, 8:373.
16. Karikari Benjamin, Chen Shixuan, Xiao Yuntao, Chang Fangguo, Zhou Yilan, Kong Jiejie, Bhat Javaid Akhter\*, Zhao Tuanjie\*. Utilization of interspecific high-density genetic map of ril population, for the QTL detection and candidate gene mining for 100-seed weight in soybean. *Frontiers in Plant Science*, 2019, 10:1001.
  17. Zhang, Xi; Xu, Mengge; Hina, Aiman; Kong, Jiejie; Gai, Junyi; He, Xiaohong; Zhao, Tuanjie. Seed storability of summer-planting soybeans under natural and artificial aging conditions. *Legume Research*, 2019, 42(2): 250-259.
  18. Fei Yun-Yan, Bhat Javaid Akhter, Zhang Ying-Ying, Al Amin G. M., Gai Jun-Yi, Zhao Tuan-Jie\*. Complex gene response of herbicide-resistant *Enterobacter* strain NRS-1 under different glyphosate stresses. *3 BIOTECH*, 2018, 8(10):422.
  19. Chang Fangguo, Guo Chengyu, Sun Fengluan, Zhang Jishun, Wang Zili, Kong Jiejie, He Qingyuan, Sharmin Ripa A., Zhao Tuanjie\*. Genome-wide association studies for dynamic plant height and number of nodes on the main stem in summer sowing soybeans. *Frontiers in Plant Science*, 2018, 9: 1184.
  20. Niu Jingping, Guo Na, Zhang Zhang, Wang Zili, Huang Jianli, Zhao Jinming, Chang Fangguo, Wang Haitang, Zhao Tuanjie\*, Xing Han\*. Genome-wide SNP-based association mapping of resistance to *Phytophthora sojae* in soybean (*Glycine max* (L.) Merr.). *Euphytica*, 2018, 214(10): UNSP 187.
  21. 张雅娟, 曹永策, 李曙光, 常芳国, 孔杰杰, 盖钧镒, 赵团结\*. 夏大豆重组自交系群体 NJRIMN 开花期和株高 QTL 定位. *大豆科学*, 2018, 37(06):860-865
  22. 简朴, 王亚琪, 李亚蔚, 孔杰杰, 赵团结\*. 大豆波状卷叶新种质 NWL1 特性鉴定与基因定位. *大豆科学*, 2018, 37(5):690-696
  23. 滕康开, 曹永策, 李曙光, 孔杰杰, 邢静\*, 赵团结\*. 夏大豆重组自交系群体籽粒蛋白质含量 QTL 定位. *分子植物育种*, 2018, 16(18):5987-5993
  24. 金尚昆, 朱玉萍, 缪依琳, 孔可可, 孔杰杰, 赵团结\*. 黄淮海地区新育成大豆品系 SSR 标记多样性分析. *大豆科学*, 2018, 37(2):173-178
  25. 孔可可, 许孟歌, 刘美凤, 孔杰杰, 盖钧镒, 赵团结\*. 大豆芽黄新突变体 vl-1 的光合特性与基因定位. *核农学报*, 2018, 32(5):840-847
  26. 滕康开, 郭呈宇, 张吉顺, 孔杰杰\*, 赵团结\*. 江淮地区夏大豆新品系 SSR 和 PAV 分子标记多样性分析. *分子植物育种*, 2018, 16(15):4971-4981
  27. Cao Yongce, Li Shuguang, He Xiaohong, Chang Fangguo, Kong Jiejie, Gai Junyi\*, Zhao Tuanjie\*. Mapping QTLs for plant height and flowering time in a Chinese summer planting soybean RIL population. *Euphytica*, 2017, 213(2): UNSP 39.
  28. Cao Yongce, Li Shuguang, Wang Zili, Chang Fangguo, Kong Jiejie, Gai Junyi\*, Zhao Tuanjie\*. Identification of major quantitative trait loci for seed oil content in soybeans by combining linkage and genome-wide association mapping. *Frontiers in Plant Science*, 2017, 8: 1222.
  29. Li Shuguang, Cao Yongce, He Jianbo, Zhao Tuanjie\*, Gai Junyi\*. Detecting the QTL-allele system conferring flowering date in a nested association mapping population of soybean using a novel procedure. *Theoretical and Applied Genetics*, 2017, 130(11): 2297-2314.
  30. Niu Jingping, Guo Na, Sun Jutao, Li Lihong, Cao Yongce, Li Shuguang, Huang Jianli, Zhao Jinming, Zhao Tuanjie\*, Xing Han\*. Fine Mapping of a resistance gene RpsHN that controls

- Phytophthora sojae using recombinant inbred lines and secondary populations. *Frontiers in Plant Science*, 2017, 8: 538.
31. Zhao Jing, Chen Lei, Zhao Tuanjie\*, Gai Junyi\*. *Chicken Toes-Like Leaf and Petalody Flower (CTP)* is a novel regulator that controls leaf and flower development in soybean. *Journal of Experimental Botany*, 2017, 68(20): 5565-5581.
  32. 王应党, 许孟歌, 张雅娟, 翁焯阳, 李晓勇, 孔杰杰, 赵团结\*, 何小红\*. 江淮大豆育种种质苗期耐旱性鉴定. *大豆科学*, 2017, 36(5):669-678
  33. 孔可可, 许孟歌, 王亚琪, 孔杰杰, Al-Amin G M, 赵团结\*. 大豆黄绿叶突变体 NJ9903-5 性状表现与基因定位研究. *大豆科学*, 2017, 36(4):494-501
  34. 王亚琪, 简朴, 费云燕, 孔杰杰, 赵团结\*. 大豆 2 个种皮不完整突变体的形态特点与遗传分析. *核农学报*, 2017, 31(4):621-626
  35. Li Lihong, Guo Na, Niu Jingping, Wang Zili, Cui Xiaoxia, Sun Jutao, Zhao Tuanjie\*, Xing Han\*. Loci and candidate gene identification for resistance to *Phytophthora sojae* via association analysis in soybean [*Glycine max* (L.) Merr.]. *Molecular Genetics and Genomics*, 2016, 291(3): 1095-1103.
  36. Wang Wubin, Li Xuliang, Chen Shixuan, Song Shiyu, Gai Junyi\*, Zhao Tuanjie\*. Using presence/absence variation markers to identify the QTL/allele system that confers the small seed trait in wild soybean (*Glycine soja* Sieb. & Zucc.). *Euphytica*, 2016, 208(1): 101-111.
  37. Wang Wubin, Liu Meifeng, Wang Yufeng, Li Xuliang, Cheng Shixuan, Shu Liping, Yu Zheping, Kong Jiejie, Zhao Tuanjie\*, Gai Junyi\*. Characterizing two inter-specific bin maps for the exploration of the QTLs/genes that confer three soybean evolutionary traits. *Frontiers in Plant Science*, 2016, 7:1248.
  38. Wang Yaqi, Chen Wei, Zhang Ye, Liu Meifeng, Kong Jiejie, Yu Zheping, Jaffer Ali M., Gai Junyi\*, Zhao Tuanjie\*. Identification of two duplicated loci controlling a disease-like rugose leaf phenotype in soybean. *Crop Science*, 2016, 56(4): 1611-1618.
  39. 费云燕, 盖钧镒, 赵团结\*. 突变肠杆菌株 NRS-1 中 5 个草甘膦逆境应答基因的克隆与功能研究. *微生物学通报*, 2016, 43(8):1690-1698
  40. 程伟, 许媛, 王自力, 孔杰杰, 高学文, 盖钧镒, 赵团结\*. 江淮大豆育种种质对细菌性斑点病 S1 菌株的抗性鉴定. *大豆科学*, 2016, 35(1):100-105
  41. 王自力, 张吉顺, 郭呈宇, 孙峰峦, 李忠洋, 孔杰杰, 盖钧镒\*, 赵团结\*. 大豆 3 个核心亲本及其衍生品系基于 PAV 分子标记的亲缘关系研究. *大豆科学*, 2016, 35(1):1-10
  42. He Qingyuan, Yang Hongyan, Xiang Shihua, Tian Dong, Wang Wubin, Zhao Tuanjie\*, Gai Junyi\*. Fine mapping of the genetic locus L1 conferring black pods using a chromosome segment substitution line population of soybean. *Plant Breeding*, 2015, 134(4): 437-445.
  43. Zhang YingHu, Liu MeiFeng, He JianBo, Wang YuFeng, Xing GuangNan, Li Yan, Yang ShouPing, Zhao TuanJie\*, Gai JunYi\*. Marker-assisted breeding for transgressive seed protein content in, soybean [*Glycine max* (L.) Merr.] *Theoretical and Applied Genetics*, 2015, 128(6): 1061-1072.
  44. Zhang Yinghu, He Jianbo, Wang Yufeng, Xing Guangnan, Zhao Jinming, Li Yan, Yang Shouping, Palmer R. G., Zhao Tuanjie\*, Gai Junyi\*. Establishment of a 100-seed weight quantitative trait locus-allele matrix of the germplasm population for optimal recombination design in soybean breeding programmes. *Journal of Experimental Botany*, 2015, 66(20): 6311-6325.
  45. 王自力, 郭呈宇, 张吉顺, 孙峰峦, 李忠洋, 何小红, 孔杰杰, 盖钧镒\*, 赵团结\*. 江淮

地区大豆籽粒高蛋白含量新品系的发掘与遗传关系分析. 中国油料作物学报, 2015, 37(6):780-788

46. 刘莉, 邢光南, 栗旭亮, 许志永, 孔杰杰, 盖钧镒\*, 赵团结\*. 野生大豆 PI342618B 蔓生性 QTL 定位研究. 大豆科学, 2015, 34(6):933-937
47. 许媛, 程伟, 伍辉军, 郑蕾琦, 赵团结\*, 高学文\*. 大豆细菌性斑疹病的病原鉴定及大豆新种质抗性评价. 大豆科学, 2015, 34(03):463-469
48. 高初蕾, 乔峰, 安怡昕, 赵团结\*, 孔杰杰\*. 商业化转基因大豆育种研发进展与展望. 分子植物育种, 2015, 13(06):1396-1406