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首页 | 期刊介绍 | 编委会 | 投稿指南 | 期刊订阅 | 下载中心 | 留 言 板 | 联系我们 English

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大豆花叶病毒(SMV)株系SC4和SC8的抗性遗传分析

王大刚[1,2]，马莹[1]，刘宁[1]，郑桂杰[1]，杨中路[1]，杨永庆[1]，智海剑[1,*]*

1南京农业大学大豆研究所 / 国家大豆改良中心 / 作物遗传与种质创新国家重点实验室，江苏南京210095；2安徽省农业科学院作物研究所 / 安徽省农作物品质改良重点实验室, 安徽合肥230031

Inheritance of Resistances to Soybean Mosaic Virus Strains SC4 and SC8 in Soybean

WANG Da-Gang[1,2],MA Ying[1],LIU Ning[1],ZHENG Gui-Jie[1],YANG Zhong-Lu[1],YANG Yong-Qing[1],ZHI Hai-Jian[1,*]*

1 National Key Laboratory for Crop Genetics and Germplasm Enhancement / Soybean Research Institute of Nanjing Agriculture University / National Center for Soybean Improvement, Nanjing 210095, China; 2 Crop Institute of Anhui Academy of Agricultural Sciences / Key Laboratory of Crop Quality Improvement of Anhui Province, Hefei 230031, China

摘要 参考文献 相关文章

摘要 选用我国黄淮和长江流域大豆产区发生频繁的SMV株系SC4和SC8，利用大豆抗病材料和感病材料配制抗感和抗抗杂交组合，研究抗病材料对SC4和SC8株系的遗传方式以及不同大豆材料对SMV抗性基因位点间的等位性关系。结果表明, 接种SC4株系后，由冀LD42、徐豆1号、跃进4号、科丰1号、PI96983、晋大74、汾豆56、大白麻和齐黄22为抗源配制的9个抗感组合的F_1均表现抗病，经卡方测验, F_2抗感分离比例3∶1，$F_{2:3}$家系分离比例为1(抗)∶2(分离)∶1(感)，表明这些抗源均有1对基因控制对SC4株系的抗性，且抗病表现为显性；5个抗抗组合的F_1均表现抗病，F_2群体分离比例15(抗)∶1(感)，表明大白麻与汾豆56、科丰1号和齐黄1号携带抗SC4的基因是不等位的，冀LD42与汾豆56，晋大74与中作229是不等位的。接种SC8株系后，用齐黄1号、中作229、NY58、科丰1号、PI96983、晋大74、汾豆56、大白麻和齐黄22为抗源配制的抗感组合杂交后代分离符合1对基因的分离比例且F_1均表现抗病，说明这些品种对SC8株系的抗性也均由1对显性基因控制。抗抗组合晋大74×汾豆56接种SC8株系后的F_2群体全部表现抗病，$F_{2:3}$家系没有抗感分离，表明抗病品种晋大74与汾豆56携带的抗病基因是等位的；齐黄1号×科丰1号、大白麻×汾豆56的F_2群体分离比例15(抗)∶1(感)，表明抗病亲本齐黄1号与科丰1号、大白麻与汾豆56携带抗SC8的基因是不等位的，而且独立遗传。

关键词： 大豆 大豆花叶病毒 抗性遗传 等位性

Abstract: Soybean mosaic virus (SMV) disease is one of the most destructive viral diseases worldwide, resulting in significant yield losses and seed-quality deterioration in soybean [*Glycine max* (L.) Merr.]. Utilization of resistant varieties is the most economical and environmentally safe approach to controlling this disease. The SMV strains SC4 and SC8 were predominant and widespreading in Huang-Huai-Hai and Yangtze valley in China. Twelve soybean resistant (R) cultivars were crossed respectively with susceptible (S) cultivars (Nannong1138-2, NY30, NY185, 86-4 or 8101) to determine resistance to SC4 or SC8. Resistant parent was also crossed with each other to identify whether resistant genes from different cultivars are at the same or at different loci by the test of allelic relationships of the resistance genes. The experiments were performed under greenhouse/net-house conditions. The F_2 populations and $F_{2:3}$ lines derived from all the possible crosses (R×S) exhibited a segregation pattern of 3R:1S and 1R:2segregating:1S ratio respectively when inoculated with the SMV strains SC4 and (or) SC8. The results indicated that Ji LD42, Xudou 1, Yuejin 4 and Qihuang 1, Zhongzuo 229, NY 58 carried a dominant resistant gene for SMV strains SC4 and SC8 respectively; Kefeng 1, PI96983, Jinda74, Fendou 56, Dabaima, and Qihuang 22 carried single dominant resistant gene for both SC4 and SC8. The test of the allelism of the resistance genes to SC4 showed that the F_2 populations from R×R crosses exhibited a segregation pattern of 15R:1S. The results suggested that the resistance genes between Dabaima and Fendou56, Kefeng 1, Qihuang 1; between Ji LD42 and Fendou56; and between Jinda74 and Zhongzuo229 were not at the same locus. Resistance reactions of F_2 and $F_{2:3}$ families to SC8 indicated that single dominant resistant gene in Jinda74 and Fendou56 was at a same locus or closely linked two loci. The resistance genes between Qihuang 1 and Kefeng 1 and between Dabaima and Fendou56 were not at same locus for SC8. These results are useful to understand the genetic and allelomorphic relationship among various sources of resistance and make the better use of available germplasm in soybean resistance breeding programs.

Keywords: Soybean Soybean mosaic virus Inheritance of resistance Allelism

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Corresponding Authors: 智海剑, E-mail: zhj@njau.edu.cn, Tel: 025-84396463

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