ACTA AGRONOMICA SINICA
Volume 38, Issue 2, February 2012
Online English edition of the Chinese language journal

Available online at www.sciencedirect.com
ScienceDirect

Cite this article as: Acta Agron Sin, 2012, 38(2): 202–209.

RESEARCH PAPER

Inheritance of Resistance 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], and **ZHI Hai-Jian**[1,*]

[1] National Key Laboratory for Crop Genetics and Germplasm Enhancement/ Soybean Research Institute, Nanjing Agricultural University/ National Center for Soybean Improvement, Nanjing 210095, China

[2] Crop Research Institute, Anhui Academy of Agricultural Sciences/ Key Laboratory of Crop Quality Improvement of Anhui Province, Hefei 230031, China

Abstract: The objective of this study was to understand the genetic and allelomorphic relationships among different soybean (*Glycine max* L. Merr.) cultivars with resistance to *Soybean mosaic virus* (SMV). Twelve resistant (R) soybean cultivars were crossed with a susceptible (S) cultivar (Nannong 1138-2, NY30, NY185, 86-4, or 8101) to determine the inheritance of resistance to SMV strain SC4 or SC8, which were predominant in the Huang-Huai-Hai Rivers Region and Yangtze Valley in China. The R parents were also crossed with each other for allelic analysis of resistance genes from different sources. The results indicated that Ji LD42, Xudou 1, and Yuejin 4 and Qihuang 1, Zhongzuo 229, and NY58 carried a dominant resistance gene for SMV strains SC4 and SC8, respectively, whereas Kefeng 1, PI 96983, Jinda 74, Fendou 56, Dabaima, and Qihuang 22 carried single dominant resistance gene for both SC4 and SC8. The allelism test of the resistance genes to SC4 showed that the resistance genes between Dabaima and Fendou 56, Kefeng 1, and Qihuang 1, between Ji LD42 and Fendou 56, and between Jinda 74 and Zhongzuo 229 were not at the same loci. The study of resistance of F_2 plants and $F_{2:3}$ families to SC8 indicated that the single dominant resistance genes in Jinda 74 and Fendou 56 shared a common locus or two closely loci. The resistance genes between Qihuang 1 and Kefeng 1 and between Dabaima and Fendou 56 were not at the same locus for SC8. These results are useful to understand the genetic and allelomorphic relationships among various sources of resistance.

Keywords: soybean; *Soybean mosaic virus* (SMV); inheritance of resistance; allelism

Soybean mosaic disease, caused by *Soybean mosaic virus* (SMV), is one of the most broadly distributed viral diseases worldwide in soybean (*Glycine max* L. Merr.). The disease causes severe yield loss and degraded seed quality. The utilization of resistant varieties is the most economical and environmentally safe approach to control this disease; however, the success or failure of breeding resistant varieties depends on the realization of the inherited mechanisms of resistance to SMV strains.

Genetic resistance to SMV has been identified in different soybean cultivars from various countries or regions. Researchers have hypothesized a single dominant gene, a single recessive gene, 2 pairs of complementary dominant genes, or 2 pairs of complementary recessive genes corresponding to the resistance [1–6]. Such discrepancies may result from differences in the definition of resistance and susceptibility, for example, necrotic plants are defined as 'susceptible' in some studies but as 'resistant' in other studies [4, 7].

To date, 3 independent and dominant loci, *Rsv1*, *Rsv3*, and *Rsv4*, conferring resistance to SMV strains, have been identified in the germplasm from the United States for disease control. Nine *Rsv1* resistance alleles have been defined in cultivars or lines York, Mashall, Kwanggyo, Ogden, PI 96983, Raiden, Suweon 97, LR1, and PI 507389 [1, 2, 8, 9]. *Rsv3* alleles have been described in different soybean cultivars, including Columbia, Hardee, and Harosoy [10, 11], and *Rsv4* alleles have been described in PI 88788 and V94-5152 [12, 13]. Furthermore, various soybean cultivars resistant to SMV revealed

---

Received: 22 July 2011; Accepted: 17 October 2011.

* Corresponding author. E-mail: zhj@njau.edu.cn

Chinese edition available online at http://www.chinacrops.org/zwxb/

DOI: 10.1016/S1875-2780(11)60100-4

additional and non-allelic resistance loci in China [5, 6, 14–20].

The purpose of this study was to identify the inheritance and test the allelic relationships of resistance genes to the predominant and widespread SMV strains, SC4 and SC8, in the Huang-Huai-Hai Rivers Region and Yangtze Valley in China. These results are useful to understand the genetic and allelomorphic relationships of resistance genes from various soybean germplasm resources and to make full use of the available germplasm in soybean resistance breeding programs.

1 Materials and methods

1.1 Plant materials and SMV strains

Twelve soybean resistant (R) cultivars, Dabaima, Ji LD42, Fendou 56, Kefeng 1, NY58, Xudou 1, Jinda 74, PI 96983, Qihuang 22, Yuejin 4, Zhongzuo 229, and Qihuang 1, were crossed with a susceptible (S) cultivar, Nannong 1138-2, NY30, NY185, 86-4, or 8101, respectively. The R parents were also crossed with each other. The F_1, F_2, and $F_{2:3}$ families derived from the R × S cross were used to determine the inheritance of resistance to SMV strains SC4 or SC8, together with their parents. The progenies derived from the R × R cross were used to test the allelic relationship of resistance genes. The SC4 and SC8 isolated by Wang et al. [21] are currently prevailing strains of SMV in the Huang-Huai-Hai Rivers Region and the Yangtze Valley in China. All the soybean cultivars and SMV strains were provided by the National Center for Soybean Improvement of Nanjing Agricultural University, Nanjing, China.

1.2 Identification of SMV resistance

Seeds of the F_1, F_2, and $F_{2:3}$ families and their corresponding parents were grown in pots in an aphid-free net-room in 2009 and 2010 growing seasons. The unifoliolate leaves were inoculated with the inoculum by gently rubbing the newly unfolded primary leaves at the V1 stage. Disease symptom was classified as either asymptomatic, necrotic or mosaic. Asymptomatic and necrotic plants were classified as resistant reaction and mosaic plants as susceptible reaction [6]. The ratio of segregation between resistance and susceptibility was statistically tested by Chi-square analysis.

2 Results

2.1 Inheritance of resistance to SMV strain SC4 in soybean

2.1.1 Genetic analysis of resistance to SC4 In the reciprocal crosses between Dabaima and Nannong 1138-2, when inoculated with SMV strain SC4, all of the F_1 individuals and 797 and 130 F_2 plants showed resistance, whereas 250 and 44 F_2 plants were susceptible (Table 1). In the $F_{2:3}$ families of reciprocal crosses, 26 and 16 lines were resistant, 22 and 14 lines were susceptible, and 50 and 27 lines were segregating. The results of Chi-square test confirmed the Mendelian segregating ratio of 3R:1S in both F_2 populations and a segregating ratio of 3R:2 segregating:1S in the $F_{2:3}$ families. Therefore, resistant parent, Dabaima, was inferred to carry a single dominant resistance gene without cytoplasmic effect.

Table 1 Reactions to SMV strain SC4 in F_1, F_2,and $F_{2:3}$ generations derived from resistant (R) × susceptible (S) crosses in soybean

Cross or parent	No. of plants or lines				χ^2	P
	Total	Resistant	Segregating	Susceptible		
Dabaima (P_1)	30	30				
F_1	10	10				
F_2	1047	797		250	0.70 (3:1)	0.40
$F_{2:3}$	98	26	50	22	0.37 (1:2:1)	0.83
Nannong 1138-2 (P_2)	31			31		
Nannong 1138-2 (P_1)	21			21		
F_1	10	10				
F_2	174	130		44	0.01 (3:1)	0.93
$F_{2:3}$	57	16	27	14	0.30 (1:2:1)	0.86
Dabaima (P_2)	27	27				
Ji LD42 (P_1)	32	32				
F_1	6	6				
F_2	394	298		96	0.08 (3:1)	0.77
$F_{2:3}$	114	32	57	25	0.85 (1:2:1)	0.65
Nannong 1138-2 (P_2)	33			33		

(*To be continued*)