Search for new genes conferring resistance to SMV in soybean

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Abstact: 【Objective】 The objective of this research was to search unique soybean germplasm for breeding programs. 【Method】 The study was based on screening 254 genotypes collected from 26 countries with six SMV strains. 【Result】 The results demonstrated that 158 genotypes were susceptible to SMV and 95 genotypes showed resistance to some strains of SMV. Only seven germplasm, Kaigen's kingenzu (PI 88486), PI 62202 and PI 407733 from China, Ito San (PI 189920) from France, PI 84549 from South Korea, and Shirome choutan (PI 417329) and Tousan 101(PI 507439) from Japan, showed resistance to all tested SMV strains. 14 genotypes showed resistance or early-seedling-stage resistance to six strains and presumed carry *Rsv*4 allele, 50 genotypes exhibited similar reaction patterns with known alleles to six strains of SMV, two genotypes at *Rsv*1, 22 at *Rsv*1-*k*, 16 at *Rsv*1-*y*, one at *Rsv*1-*t*, and 10 at *Rsv*3. 25 genotypes showed distinct reaction patterns to six strains of SMV and presumably carry new alleles at the *Rsv*1, *Rsv*3, or *Rsv*4 locus. Research is underway to confirm the new resistance alleles via genetic study and molecular approach. 【Conclusion】 The new identified genotypes resistant to SMV will be used as parents in the soybean breeding programs for resistance to SMV.

Key words: *Soybean mosaic virus* (SMV); resistance; germplasm; *Glycine max* Merr. L.

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大豆花叶病(SMV)新抗性基因的初步鉴定

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[摘 要] 【目的】鉴定出携带特异抗性基因的种质。【方法】利用美国的 6 个 SMV 株系(G1～G3, G5～G7)对来自 26 个国家和地区的 254 份大豆种质进行人工接种鉴定。【结果】158 份材料感所有病毒株系; 95 份材料抗某些病毒株系; 只有 7 份种质兼抗所有 6 个鉴定株系: 中国种质 3 份('Kaigen's kingenzu' PI 88486, PI 62202 和 PI 407733), 法国种质 1 份('Ito San' PI 189920), 韩国种质 1 份(PI 84549), 日本种质 2 份('Shirome choutan' PI 417329 和'Tousan 101' PI 507439)。14 份材料对 6 个株系表现抗病或幼苗早期抗病, 推测可能携带 *Rsv*4 基因; 50 份材料对 6 个株系的反应型与已报道的抗性等位基因

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类似,推测其中携带 *Rsv*1 抗性基因材料 2 份,*Rsv*1-*k* 22 份,*Rsv*1-*y* 16 份,*Rsv*1-*t* 1 份,*Rsv*3 10 份。25 份材料对 6 个 SMV 株系表现型特殊,可能携带 *Rsv*1,*Rsv*3,或 *Rsv*4 位点新的等位基因。【结论】这些新的抗源可以用于 SMV 抗病育种的亲本。

[关键词] 大豆花叶病;抗病性;种质资源;大豆育种

Soybean mosaic virus (SMV) is one of the most prevalent and destructive viral pathogens in soybean-producing regions of the world [1], causing significant yield loss and quality deterioration. Wrather et al[2] estimated that SMV and bud blight accounted for 1 377.2 thousand metric tons yield reduction in the top ten soybean-producing countries during 1998. SMV has been listed as the most important disease in China since 1994. In Brazil, epidemic of SMV has caused lower yields or discarded mottled seeds [3]. Furthermore, necrosis caused by SMV is a concerned problem for causing serious yield losses in a large production area in Korean[4].

Soybean mosaic virus is an RNA-based pathogen and easily evolved due to the selection pressure overtime imposed by host cultivars as well as by aphid and seed transmission, or changes of environment conditions[5]. Selection pressure of host resistance is a main force to promote SMV evolvement. In South Korea, a severe necrotic strain, SMV-N, was found in some of the SMV resistant cultivars just within a short time after soybean cultivars resistant to SMV were developed[4]. During 1980s, G5H was the most prevalent strain[6]. With the utilization of resistant soybean cultivars, the relative incidence of G5H decreased gradually[7]. In the 1990s, another severe isolate emerged, and designated as SMV-G7H with the similar biological properties of SMV-G7[8]. During 1999—2000, SMV-G7H was reported as a predominant strain in Suweon, Korea[4]. Recently, more virulent strains have been reported in Korea[6,8]. In China, new isolates of SMV were reported continuously, the number of SMV strains in China have increased from eight (Sc1-8) to seventeen (Sc1-17)[9-11].

The classification system of SMV isolates was first established by Cho and Goodman[12-13], based on the reactions of eight differentials, including Clark, Rampage, Davis, York, Kwanggyo, Marshall, Ogden, and Buffalo. Ninety-eight isolates were grouped to seven strains, designated G1 through G7 based on its virulence. G1, the least virulent strain, only infected susceptible cultivars (Clark and Rampage); G2 showed similar reaction pattern as G1 except necrosis on Marshall; for G3, Ogden was added to the necrotic group besides Marshall; G4 could break the resistance (necrosis) in York and Davis which were resistant to G1 to G3; G5 caused mosaic in York and Davis and necrosis Kwanggyo; G6 had similar pattern as G5 but caused necrosis in Marshall; and G7 was the most virulent strain that infected all cultivars tested and caused necrosis in Kwanggyo, Marshall, Ogden, and Buffalo and mosaic symptoms in Davis and York. In this system, necrosis in cultivars Marshall, Ogden, and Kwanggyo always exhibit local lesion on uninoculated leaves and stem-tip necrosis and presumably conditioned by SMV resistance gene. This classification system has been recently updated by Chen and Choi[1].

Three independent resistance loci, *Rsv*1, *Rsv*3, and *Rsv*4, have been identified and each locus may have single or multiple alleles. Nine alleles at the *Rsv*1 locus have been reported, i.e. *Rsv*1, *Rsv*1-*t*, *Rsv*1-*y*, *Rsv*1-*m*, *Rsv*1-*k*, *Rsv*1-*s*, *Rsv*1-*h*, *Rsv*1-*r*, *Rsv*1-*n* in PI 96983, Ogden, York, Marshall, Kwanggyo, LR1, Suweon 97, Raiden, and PI 507389 respectively[14-23]. Most *Rsv*1 alleles condition necrosis to single or multiple SMV strains[17]. However, plants carrying *Rsv*1-*y* exhibit resistance to low-numbered strains and susceptibility to high-numbered strains[14], but plants containing *Rsv*1-*n* just show necrosis to G1, G2, G5 and G6, but susceptibility to G3, G4 and G7[22].

The *Rsv*3 locus in L29 derived from 'Hardee' confers a susceptible reaction to less virulent stains (G1 to G4), but resistant reaction to more virulent strains (G5 to G7) [16]. The *Rsv*4 locus was identified in a breeding line V94-5152 derived from 'Essex' × PI 486355 that showed resistance to all seven SMV strains[15]. An allele at *Rsv*4 in PI 88788 conferred early-seedling-stage resistance and

delayed discolored lesions[24].

To date, most of germplasm that have been identified as resistant to SMV possess a dominant gene at *Rsv*1, *Rsv*3, or *Rsv*4 [25]. However, some cultivars were reported to carry two genes, including *Rsv*1 + *Rsv*3 in OX670 [26], 'Hourei' and 'Tousan 140'[27], 'Zao 18'[28], and 'J05'[29]; *Rsv*1 + *Rsv*4 in PI 486355[18, 21], and *Rsv*3 + *Rsv*4 in 'Columbia'[30]. However, no germplasm has been found to carry all three SMV resistance genes.

The development of resistant cultivars is the most effective and economical strategy against the epidemic of SMV. Appearances of new resistance-breaking SMV isolates in China and Korea[8,10,11] indicate that searching for diversified resistant germplasm is still necessary for controlling the new SMV variants. The objective of this research was to search for new resistant genotypes based on phenotypic reactions to six SMV strains, which can be used in soybean breeding for SMV resistance and avoiding genetic uniformity and vulnerability.

1 Materials and methods

Two hundred and fifty-four diverse soybean germplasms originated from 26 countries were provided by Dr. Randy Nelson, curator of the USDA Soybean Germplasm Collection USDA-ARS, at the University of Illinois. Plants of each soybean genotype were grown in 15 cm-diameter plastic pots with three replications in the greenhouse with temperature controlled at (25±3) ℃ and a 14 h photoperiod. Approximately, eight plants of one pot per genotype were kept uninoculated as a control. Eight plants in another pot of each genotype were inoculated with each SMV strain at the unifoliolate leaf stage. Inoculated plants were monitored for symptom expression for 4 wk after inoculation. The reaction of each genotype to SMV was classified as resistant (R, symptomless), early resistant (ER, resistant at the early seedling stage, then transitory chlorotic island or rings appeared on trifoliate leaves), necrotic (N, systemic necrosis), or susceptible (S, mosaic).

Six SMV strains used in this study, G1 to G7 except G4 (unavailable), were kindly provided by Dr. Sue Tolin of Virginia Polytechnic Institute and State University. Each SMV strain was maintained separately by mechanical inoculation in susceptible soybean cultivar Essex or Lee 68 in the greenhouse. Infected leaves with each SMV stain were also stored in a freezer (−80 ℃) as back-up inoculum source. SMV strain identity was confirmed by inoculation on a set of differential soybean genotypes[12,20,22,24,27], including Essex /Lee68, PI 96983, Suweon 97, York, Kwanggyo, Raiden, Ogden, Marshall, PI 507389, L29, V94-5152, obtained from Dr. Glenn Buss of Virginia Polytechnic Institute and State University. Mechanical inoculation procedure was referred to Chen et al. [17]. Virus inoculum was prepared by grinding systemically infected leaves from the strain-maintaining plants with a mortar and pestle in 0.05 mol/L potassium phosphate buffer at an approximate dilution of 1 ∶ 10 (w/v) with pH 7.2. Inoculations were performed by rubbing the inoculum onto both unifoliolate leaves predusted with carborundum. Reaction patterns to the six SMV strains were compared with that of known alleles, new allele was assumed if a different reaction pattern was observed.

2 Results and discussion

2.1 Confirmation of the pathogen identity of SMV strains

Two hundred fifty-four soybean genotypes were screened along with a group of 11 differential genotypes for their reactions to SMV strains G1, G2, G3, G5, G6, and G7. The reactions of 11 differential soybean genotypes (Table 1) to the six SMV strains were in perfect agreement with previous reports[12-13,16-17,19-22,24,27,31]. These results demonstrated the allele diversity in soybean germplasm and confirmed the pathogen identity of the SMV strains used in this study. The unique reaction pattern of each differential soybean genotype with specific alleles to a set of six SMV strains allows for differentiation of any soybean germplasm in question based on phenotypic responses to the SMV strain groups, and new alleles with a differ-

ent SMV reaction pattern can be identified. While genotypes under testing can be classified into specific alleles by comparison with the differential set, the limitation of this differential system is that genotypes with *Rsv*1-*h* or multiple resistance genes (*Rsv*1+3, *Rsv*1+4, *Rsv*3+4, and *Rsv*1+3+4) can not be differentiated according to their phenotypic reactions to SMV because they are all resistant to all six strains. In such cases, molecular markers designed from the candidate genes are effective in identification of specific genes. Nowadays, only *Rsv*1 candidate gene 3*gG*2 can be detected using this strategy[32]. Non-3*gG*2 at *Rsv*1, as well as at the *Rsv*3 and *Rsv*4 locus, no molecular markers were available to detect the absence of resistance gene directly, although several markers closely linked to *Rsv*3 and *Rsv*4 have been reported [33-36]. Thus, allelism test is still necessary to identify new allele or gene conditioning resistance to SMV. Anyway, gene presumption based on the reaction pattern to a set of SMV strains will give a clue and focus on the unique genotypes that may contain new resistance allele or gene for SMV.

Table 1 Reactions of differential soybean genotypes to seven *Soybean mosaic virus* (SMV) strains identified in the U. S.

Genotype	Reaction to SMV strain							Gene
	G1	G2	G3	G4	G5	G6	G7	
Essex, Lee68	S	S	S	S	S	S	S	*rsv*
PI 96983	R	R	R	R	R	R	N	*Rsv*1
Suweon 97	R	R	R	R	R	R	R	*Rsv*1-*h*
York	R	R	R	N	S	S	S	*Rsv*1-*y*
Raiden	R	R	R	R	N	N	R	*Rsv*1-*r*
Kwanggyo	R	R	R	R	N	N	N	*Rsv*1-*k*
Ogden	R	R	N	R	R	R	N	*Rsv*1-*t*
Marshall	R	N	N	R	R	N	N	*Rsv*1-*m*
PI 507389	N	N	S	S	N	N	S	*Rsv*1-*n*
L29	S	S	S	S	R	R	R	*Rsv*3
V94-5152	R	R	R	R	R	R	R	*Rsv*4

Note: R. resistant (symptomless); N. necrotic (systemic necrosis); S. susceptible (mosaic).

2.2 Soybean germplasm susceptible to four SMV strains

One hundred fifty-eight of 254 screened soybean genotypes were susceptible to four SMV strains G1, G3, G6, and G7 (Table 2) and presumed absence of SMV resistance gene. More than half of collected germplasm showed susceptibility to SMV. Among them, 31 genotypes are originated from China, 28 from Japan, 25 from South Korea, and 29 from the United States.

Table 2 Evaluation of 158 soybean germplasm originated from 26 countries that are susceptible to four strains of *Soybean mosaic virus* (SMV) [a]

Genotype	Origin
Blaen Small, PI 438341	Algeria (2/5)[b]
Bicolor	Angola (1/1)
Dunfield	Belgium (1/1)
Harman	Canada (1/2)
Canli, Dasili, Fyn sen baj pi, Haouben, Huaixuan No. 1, Jin Dou 33, Liuyuexian, Nagaobaao, Nguu Mao Hong, PI 68609, PI 69507, PI 70013, PI 79797, PI 79832, PI 89074, PI 91153, PI 92659, PI 92651, PI 92713, PI 158765, PI 253665, PI 407749, PI 407752, PI 407758, PI 407763, PI 578368, PI 603395, PI 603497, Pin din kuaw, Trung quoc mat den, Xing ning da li huang	China (31/56)
Erectus, Japonica, PI 105579, Vert d'Agen, Washington 37563	France (5/8)
Gurijiscaja, Gurijskaja 0565, PI 404160, Saksaj 02	Georgia (4/6)
Kleverhof 527	Germany (1/1)
PI 346306, PI 346309, PI 578486	India (3/8)
Asahi rokojugo, Bansei hikarikuro, Cha Mame, Daruma niju, Eda Mame Uase Chaurame, Ibaragi mame 7, Ichou, Kanenari No. 1, Kantou 11, Kinako daizu, Kinoshita mame, Kouto 40, Kurohira, Mamyo 50-2, Mochi mame, Okuro Maru Daizu, O Tsubu Aojiro Daizu, PI 64747, PI 378682, PI 506528, PI 507016, PI 507530, Shikou Obbikuri Daizu, Shiro tsurunoko, Taihaku, Takaoka zairai, Tsura no tamago 5, Wase asajiro, Wase midori oosodefuri	Japan (28/44)

续表 2　**Continued Table** 2

Genotype	Origin
An-byon-tae, Illini, KAERI-GNT 173-1, KAERI-GNT 180-1, KAERI-GNT 330-16-1, KAERI-GNT 390-11, Kandokon, KAS 200-40, KAS 530-1, KAS 549-9, KAS 571-11, KAS 632-25, KAS 635-2-1, KAS 643-2, Kum-kang-so-ryu, PI 85424, PI 85658, PI 96118, PI 96169, PI 97038, PI 438310, PI 458111, PI 458123, Rokukon, Zomukon	Korea, South (25/33)
CNS 657, PI 283331	Moroco (2/3)
PI 471931, PI 471942	Nepal (2/3)
Red China x Clark	Pakistan (1/1)
PI 104708	Poland (1/1)
PI 92463, PI 437338, Ussurijscaja	Russian Federation(3/5)
PI 170895	South Africa (1/2)
PI 417567, Pingtung Pearl, Taichung Green, Taichung Green Bean	Taiwan, China (4/9)
Mammoth Yellow, PI 170380, PI 171652, PI 172902	Turkey (4/4)
5002T, AG 4403, Bavender Special A, Essex, Feyette, Hartwig, Hollybrook, Kahala, (Kahala), Kaikoo, Kailua, Kim, Luthy, Mokapu summer, Narrow, L72-1404, L81-4274, L76-2023, L88-8226, L82-2020, L82-2024, Mansoy, Mingo, Pella 86, PI 548262, S97-1688, UA 4805, Vintin 81, Walters	United States (29/33)
PI 235346	Uruguay (1/5)
Den bac ha, Den cao bang, Song boi, Tung nghia 2, Tuqui Xanh b, Xanh ha bac	Vietnam (6/6)

Note: a. Eight plants of each genotype screened with SMV strain G1, G3, G6, and G7; b. x/y, x, number of susceptible genotypes; y, total number from each country.

2.3　Soybean germplasm resistant to six SMV strains

Twenty-one of 254 screened soybean genotypes showed resistance to six SMV strains G1 through G7 except G4 (Table 3). 14 of 21 resistant genotypes showed early seedling stage resistance and delayed susceptible symptoms with discolored islands in upper leaves to one or more strains. These genotypes presumed carrying an allele at *Rsv*4 are the unique breeding sources for SMV resistance because *Rsv*4 has conferred as suppression of virus invasion of the plants in both short and long distance movement[24] and benefit the yield for restriction of virus development in the soybean field. Seven genotypes, Kaigen's kingenzu (PI 88486), PI 62202 and PI 407733 from China, Ito San (PI 189920) from France, PI 84549 from South Korea, and Shirome choutan (PI 417329) and Tousan 101(PI 507439) from Japan, showed resistance to six SMV strains and presumely contain *Rsv*1-*h* or bigenic combinations, *Rsv*1+3, *Rsv*1+4, *or Rsv*3+4, which need to confirmed by allelism test.

Table 3　**Identification of** 21 **diverse soybean germplasm from** 26 **countries that are resistant to six strains of *Soybean mosaic virus* (SMV)**[a]

Genotype	Origin	Reaction to SMV strain[b]						Expected resistance genes
		G1	G2	G3	G5	G6	G7	
A. K. (Harrow)	Canada	ER	ER	ER	R	ER	ER	Rsv4(new)
Hubert 33	Algeria	ER	R	ER	R	R	R	
PI 438357	Bulgaria							
Bergerac	France							
Wilson	United States	R	R	ER	R	ER	R	
PI 548433(Virginia)		R	R	R	R	ER	ER	
SAO 196-C	Algeria	ER	R	R	R	R	R	
Kuro masshokutou (Kou 205)	China							
Sjao-tsin-do	Russian Federation							
PI 437482								
Pekin kuro daizu,	China	R	R	ER	R	R	R	
PI 89772								
PI 157435	Korea, South							
Dun cuan	China	R	R	ER	ER	R/N	R	
Kaigen's Kingenzu, PI 62202, PI 407733	China	R	R	R	R	R	R	*Rsv*1-*h* *Rsv*1+3 *Rsv*1+4 *Rsv*3+4
Ito San	France							
PI 84594	Korea, South							
Shirome choutan, Tousan 101	Japan							

Note: a. Eight plants of each genotype Screened with six SMV strains; b. R, resistant (symptomless); ER, resistant at the early seedling

stage of soybean, discolored islands later; N, systemic necrosis.

2.4 Soybean germplasm shown similar reaction patterns with known alleles to six SMV strains

Fifty of 254 screened soybean genotypes exhibited similar reaction patterns with known alleles *Rsv*1, *Rsv*1-*k*, *Rsv*1-*y*, *Rsv*1-*t*, and *Rsv*3 to six SMV strains (Table 4). Among them, two genotypes, Epps and L80-5227 from the U. S. showed similar reaction pattern as PI 96983 (*Rsv*1) and pedigree analysis indicated that their resistance gene *Rsv*1 is derived from PI 96983. 22 genotypes showed resistance to G1 through G3 and susceptibility to G5 to G7 with the same reaction pattern as Kwanggyo and presumed carry *Rsv*1-*k*. 16 of 50 genotypes showed similar reaction pattern as York and presumably carry *Rsv*1-*y* allele. PI 471938 from Nepal may carry *Rsv*1-*t* for the same reaction pattern as Ogden. Ten genotypes were identified resistant to high-numbered strains G5 — G7 and susceptible to low-numbered strains G1 through G3, and presumably carry the same allele as *Rsv*3 in L29. It is clear that the widely distributed resistance alleles at the *Rsv*1 locus are *Rsv*1-*k* and *Rsv*1-*y*.

Table 4 Identification of fifty diverse soybean germplasm exhibiting similar reaction Patterns with known alleles to six strains of *Soybean mosaic virus* (SMV)

Genotype	Origin	Reaction to SMV strain[b]						Expected resistance gene
		G1	G2	G3	G5	G6	G7	
Epps, L80-5227	United States	R	R	R	R	R	N	*Rsv*1
PI 264555 Shou outou Mocinabe 7	Argentina China Georgia	R	R	R	N	N	N	*Rsv*1-*k*
Akit ani, Kantou 9, Kantou 63, Kou kei 74, Kawangagare (Iwate), Shiro higo, Tousan 52, Tousan kei B62, Yatsufusa	Japan							
Pulaska Zolta Wczesna	Poland							
Fengshan lu tsao shen, Sundar No. 1, Lu tsao shen, Mao 205, Yao tou	Taiwan, China							
Mukden, PI 235339, PI 235344, Seneca (Cornell)	Uruguay							
PI 89061, (Ping ding huang) Aze daizu, (Rokugatsu daizu)	China Japan	R	R	R	S	S	S	*Rsv*1-*y*
KAERI-GNT 330-3,								
KAERI-GNT 340-1,								
KAS 643-8, PI 82210	Korea, South							
GL 2678B/96	Korea, North							
Mocinave 7	Russian Federation							
Dorman, Okute Mame, PI 417582, Toano, V01-1702, York	United States							
PI 471938	Nepal	R	R	N	R	R	N	*Rsv*1-*t*
Paoting Graine jaune Unie Enoki	China France Japan	S	S	S	R	R	R	*Rsv*3
PI 323555, PI 323556, VIR 5532, PLSO-63, PLSO-70	India							
OCB-81	Tailand							

Note: a. Eight plants of each genotype Screened with six SMV strains; b. R, resistant (symptomless); N, systemic necrosis; S, susceptible (mosaic).

2.5 Soybean germplasm with distinct reaction to six SMV strains

Twenty-five of 254 soybean genotypes showed distinct reaction to six SMV strains as compared to known differential genotypes and presumed some variance at resistance gene locus happened (Table

5). 16 of 25 screened genotypes showed resistance to most of SMV strains and necrosis to some strains which is the character of alleles at *Rsv*1[17]. Five genotypes showed a tendency of resistance (necrosis) to low-numbered strains (G1－G3) and susceptibility to high-numbered strains (G5－G6) and presumed new allele as *Rsv*1-*y*. And three genotypes showed the tendency of susceptibility to low-numbered strains (G1 － G3) and resistance (necrosis) to high-numbered strains (G5－G6) and presumed new alleles at *Rsv*3. Shin 2 from Japan has lost the resistance to some strains but still keep the resistance to G7 and partial resistance to G1 and G3, which may carry an allele at *Rsv*4.

Table 5　Identification of 25 diverse soybean germplasm shown distinct reaction pattern to six strains of *Soybean mosaic virus* (SMV) as compared to all known differential genotypes [a]

Genotype	Origin	Reaction to SMV strain[b]						Expected resistance gene
		G1	G2	G3	G5	G6	G7	
PI 170896	outh Africa	R	R	R	R	S	R	*Rsv*1-*new*
PI 407765	SChina	R	R	S	R	R	R	
Bukalasa 2,	Uganda	R	S	R	S	S	R	
Okatsu mame	Japan	R	S	S	R	S	R	
PI 97253	Korea	R	S	S	R	R	S	
Shang tsai	China	R/N	N	R	R	R	R	
E dou no. 2		R/N	N	R/N	R	R	R	
Krasnoarmejshaja		R/N	N		R	R	R	
Tailunyuan		R/N	N	R/N	R	R	R	
Sherwood	U. S. A.	R/N	N	N	R	R	R	
Tun czou	China	R/N	N?	R	R	S	R	
Dyn haj hun mao czy		N/R	N	S	R	R/N	S	
PI 90402		N	N	R/N	R	R	R	
Kakira 13	Uganda	N	N	R	ER	R	R	
CNS-65F	Morocco	R/N	N	R	R	R	S	
Tun san si he czao	China	R	N?	S	R	S	S	
Tekkyou seitou	China	N/R	N	S	R	S	S	*Rsv*1-*y* (*new*)
Tochikubo	Japan	R	N	R	S	N	S	
KAS 530-5	Korea	R	S	R		S	S	
(Casa Grande),	Peru	R	N	R	S	S	S	
(Gun li huang),	China	S	R	S	R	R/N	R	
PI 91346	China	S	S	S	R	R	S	*Rsv*3-*new*
Tej send a baj pi	Georgia	S/R	S	S/R	R	R	R/N	
Kolhida 4,		S/R	S	S	S	S	N	
Shin 2	Japan	R/ ER	S	ER	S	S	R	*Rsv*4(*new*)

Note: a. Eight plants of each genotype Screened with six SMV strains; b. R, resistant (symptomless); ER, resistant at the early seedling stage of soybean, discolored islands later; N, systemic necrosis; S, susceptible (mosaic).

3　Conclusion

Two hundred fifty-four germplasm originated from 26 countries were screened with six SMV strains in this study. 158 genotypes were susceptible to SMV. Only seven genotypes showed resistance to all screening strains. Fourteen genotypes showed resistance or early seedling stage resistance to SMV strains. *Rsv*1 is widely distribution resistance alleles and focus on *Rsv*1-*k* and *Rsv*1-*y*. More variability at different resistance gene loci was observed. The new identified gene sources can be used in the soybean breeding program for resistance to soybean mosaic virus.

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