Resistance

Resistance to Soybean Mosaic Virus in Soybeans

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ABSTRACT

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Soybean line SS74185 (PI 486.355), which was collected in Korea, was resistant to all previously known seven (G1-G7) strains of soybean mosaic virus (SMV) and to an unclassified SMV isolate, C14. Soybean line Suweon 97 (PI 483.084) previously identified as resistant to the seven strains was susceptible to isolate C14. PI 96983 was susceptible to strain G7 but was resistant to strains G1-G6 and isolate C14. Isolate C14 caused necrotic symptoms in susceptible soybeans and its pathogenicity was shown to be different from the seven strains previously described. The F₂ plants from crosses of the susceptible cultivars Williams 79 and Franklin with PI 483.084 segregated in a 3 resistant: 1 susceptible ratio when inoculated with strains G2 or G7. The F₂ plants from cross PI 96983 × PI 483.084 inoculated with G7 also segregated in a 3 resistant:1 susceptible ratio indicating that resistance in PI 483.084 to these two SMV strains was conferred by a single dominant gene. The F_2 progenies of a cross (PI 483.084 × PI 486.355) that were inoculated with isolate C14 segregated in a 3 resistant:1 susceptible ratio indicating that resistance in PI 486.355 was conferred by a single dominant gene. The F₂ plants derived from all the possible crosses involving three resistant lines segregated in a 15 resistant:1 susceptible ratio when inoculated with SMV strains G2, G7, or isolate C14 as expected for dominant genes segregating independently. These results indicated that resistance in each of the three lines P196983, P1483.084, and P1486.355 was conferred by a different dominant gene. P196983 carries a dominant gene Rsv that conditions resistance to strains SMV-1 (G2) and SMV-1-B (G3). Genes in P1483.084 and P1486.355 cannot be assigned until further tests are performed to determine which of the genes are different from a newly identified gene Rsv₂ that confers resistance to all seven strains in soybean cultivar Raiden (P1360.844). P1360.844 plants inoculated with isolate C14 developed a severe necrotic symptom similar to the reaction of P1483.084, indicating that resistance in P1483.084 to all seven SMV strains was probably conditioned by the same gene, Rsv₂, and that the resistance gene in P1486.355 was different from gene Rsv₂.

Additional key words: genetics, Glycine max.

Soybean mosaic virus (SMV) is one of the most prevalent viral diseases of soybeans, *Glycine max* (L.) Merr., in the world. Yield reductions of up to 35% have been observed in SMV-susceptible soybeans when compared to closely related SMV-resistant lines similarly exposed to indigenous inoculum in the field (11).

Pathogenic variation among SMV isolates and various types of soybean reactions have been reported (4,10). Some SMV isolates obtained from seeds of soybean germ plasm collections were classified into seven strains (G1-G7) based on the reactions of eight soybean differentials (2). Mosaic, necrotic, or symptomless reactions have been observed in soybean cultivars inoculated with SMV.

Various sources of SMV resistance have been identified in soybeans (2,3). Most sources were resistant to some, but not all seven, strains of the SMV. Resistance to some SMV strains that produce mosaic symptoms was shown to be conditioned by a single dominant gene (5,6,11), whereas resistance to a severe isolate, SMV-N (which produces necrotic symptoms on susceptible soybeans) was shown to be conditioned by a single recessive gene (7). Recently, a soybean line, Suweon 97 (PI 483.084), obtained from the Crop Experiment Station, Suweon, Korea, was identified as resistant to all previously known seven SMV strains (8). Additional sources of resistance to all seven SMV strains were found from several other soybean lines collected in Korea (3). The soybean line OX670, a selection from a cross involving resistant cultivar Raiden (PI 360.844), was also shown to be resistant to all seven strains (1). Resistance in OX670 to strains G7 and G7A was conditioned by a dominant gene Rsv2 (1). Resistance to strains SMV-1 and SMV-1-B in PI 96983 was conditioned by a dominant

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gene Rsv (5). Strain SMV-1 was similar to G2 and SMV-1-B was similar to G3 (3).

The objectives of this study were to determine the inheritance of resistance to SMV in two soybean lines, PI 483.084 and SS74185 (PI 486.355), and to identify the genes conditioning their resistance.

MATERIALS AND METHODS

Soybean lines PI 483.084, PI 486.355, and PI 96983 and soybean cultivars Williams 79 and Franklin were used as parents in the following crosses: Williams 79 × PI 483.084, Franklin × PI 483.084, $PI96983 \times PI483.084$, $PI96983 \times PI486.355$, and $PI483.084 \times PI$ 486.355. PI 483.084 and PI 486.355 are soybean germ plasm collections from Korea and are resistant to SMV strains G1-G7. PI 96983 is resistant to strains G1-G6 and susceptible to strain G7. Williams 79 and Franklin are susceptible to all seven strains. Williams 79 is in maturity group (MG) III, is resistant to Phytophthora root rot, and is widely grown in the midwestern United States. Franklin is in MG IV, is resistant to the soybean cyst nematode and is recommended for fields in which cyst nematode is a problem. Crosses were made in the greenhouse and field at Urbana, IL, during 1979 and 1980. Parents and progenies of the F₁ and F₂ generations of five crosses were grown in the greenhouse in 15-cm-diameter clay pots filled with a sterilized mixture of clay loam and sand (2:1, v/v). Each pot contained two to three plants. Number of plants for each generation of the crosses varied from six to 11 F₁ plants, 115 to 165 F₂ plants, and 10 plants for each of the

The seven SMV strains G1-G7 (obtained from E. K. Cho and R. M. Goodman, Department of Plant Pathology, University of Illinois) and an unclassified isolate C14 (obtained from Z. Xu and R. M. Goodman) were maintained on Williams 79 plants in the greenhouse. Soybean leaves were infected with each of the strains and isolate C14. The infected leaves were freeze-dried in small vials which were sealed and placed in test tubes containing calcium sulfate (CaSO₄). Sealed tubes were stored at -5 C. Freshly harvested leaves of Williams 79 plants that showed mosaic

symptoms 3-4 wk after inoculation were homogenized with a chilled mortar and pestle in three to five volumes (milliliters per gram) of 0.01 sodium phosphate buffer (pH 7.0) to produce inoculum. The homogenate was strained through several layers of cheesecloth. A small amount of 600-mesh Carborundum was added to the inoculum. Inoculations were made by gently rubbing primary leaves of the plants at the two- to three-internode growth stage with cotton-tipped applicators that had been dipped in the inoculum.

All five parents were inoculated with each of the seven SMV strains and isolate C14. Parents and progenies of the F1 and F2 generations from the crosses of Williams 79, Franklin, and PI 96983 with PI 483.084 were inoculated separately with SMV strains G2 and G7. Parents and F₁ and F₂ plants from the cross PI 483.084 × PI 486.355 were inoculated separately with strain G7 and isolate C14. Parents and F_1 and F_2 plants from the cross PI 96983 \times PI 486.355 were inoculated with isolate C14. G2 is the most common SMV strain that causes mosaic symptoms. G7 and isolate C14 are severe strains of SMV that cause necrotic symptoms on susceptible soybeans. Plants were classified resistant if a symptomless reaction occurred, and susceptible if mosaic or necrotic symptoms occurred. Symptomless plants of the resistant parents were assayed for SMV by indexing on leaves of bean (Phaseolus vulgaris) cultivar Top Crop (9). Infected soybean leaves from the susceptible parents were used as the control in Top Crop assay. The chi-square (X²) test was used to determine the goodness of fit of observed F₂ segregations to the expected ratios, 3:1 and 15:1, for single- and two-dominantgene segregations, respectively.

TABLE 1. Reaction of selected soybean cultivars and lines to strains of soybean mosaic virus (SMV)

Soybean cultiva	SMV strains							
and lines	G1	G2	G3	G4	G5	G6	G7	C14 ^a
Williams 79	S(M) ^b	S(M)						
Franklin	S(M)	S(M)	S(M)	S(M)	S(M)	S(M)	S(M)	S(M)
PI 96983	R	R	R	R	R	R	S(N)	R
PI483.084	R	R	R	R	R	R	R	S(N)
PI 486.355	R	R	R	R	R	R	R	R

^a An unclassified SMV isolate.

TABLE 2. Segregation for resistance to soybean mosaic virus (SMV) strains G2 and G7 and an isolate C14 in the F_2 generations of crosses of susceptible and resistant soybeans

	Numbe	r of plants	Chi-square 3:1 ratio		
Cross	Resistanta	Susceptible	Value	Probability	
G2 inoculation					
Williams 79 ×					
PI 483.084	98	27	0.771	0.38	
Franklin×					
PI 483.084	92	34	0.265	0.61	
Total	190	61	0.065	0.80	
G7 inoculation					
Williams 79 ×					
PI 483.084	97	29	0.265	0.61	
Franklin×					
PI 483.084	89	26	0.351	0.55	
PI 96983 ×					
PI 483.084	127	38	0.341	0.56	
Total	313	93	0.949	0.33	
Pooled	503	154	0.853	0.36	
Heterogeneity			1.140	0.89	
C14 inoculation					
PI 483.084 ×					
PI 486.355	121	37	0.211	0.65	

^aResistant = no symptoms and susceptible = mosaic or necrotic symptoms.

RESULTS AND DISCUSSION

Reactions of five parental lines to each of the seven SMV strains and isolate C14 are given in Table 1. The reactions of PI 483.084 and PI 96983 to each of the seven SMV strains have been reported (3,8). The development of necrotic symptoms on PI 483.084 and the lack of symptom development on PI 96983 and PI 486.355 plants inoculated with isolate C14 indicated that the pathogenicity of isolate C14 differed from that of any of the seven SMV strains previously described (2). These results suggest that more than seven SMV strains exist, and therefore PI 483.084 and PI 486.355 should be added to the set of eight soybean differentials (2) to more completely evaluate viral variability.

No local lesions developed on Top Crop bean leaves when inoculated with inoculum prepared from symptomless plants of the resistant soybeans that were inoculated with SMV. Inoculum prepared from SMV-infected plants of the susceptible soybeans produced local lesions within 48 hr after inoculations on Top Crop. The Top Crop bean leaf assay has been reported (2,3,9) to be sufficiently sensitive to be used for determining the relative infectivity to, and the concentration of, SMV in soybeans.

In the genetic study, all F₁ plants from the three crosses of Williams 79, Franklin, and PI 96983 with PI 483.084, were resistant to strains G2 and G7. Reactions of the F₂ progenies from the crosses Williams $79 \times PI$ 483.084 and Franklin \times PI 483.084 to strains G2 and G7 and reactions of F2 progenies of PI 96983 × PI 483.084 to strain G7 segregated 3 resistant:1 susceptible ratios (Table 2). The X² values for testing goodness of fit to an expected ratio of 3:1 within each cross, and the heterogeneity X² value for testing the goodness of fit to the homogeneity between the F₂ populations were acceptable, P > 0.1. These results indicated that the resistance in PI 483.084 to strains G2 and G7 was conferred by a single dominant gene. PI 96983 was resistant to SMV strains G1 through G6 but was susceptible to G7, whereas, PI 483.084 was resistant to all seven strains (Table 1). The F₂ plants from cross PI 96983 × PI 483.084 fit a 15 resistant:1 susceptible ratio when inoculated with strain G2. These results indicated that there were two dominant genes for SMV resistance segregating independently (Table 3). All F_1 plants from cross PI 483.084 \times PI 486.355 were resistant to isolate C14. The reaction of 158 F₂ plants to isolate C14 fit a 3 resistant: I susceptible ratio which indicated that resistance in PI 486.355 was conditioned by a single dominant gene (Table 2). The F₂ progenies from this cross segregated 15 resistant:1 susceptible when inoculated with strain G7 which indicated that dominant gene for resistance in PI 483.084 and PI 486.355 were two different genes (Table 3). Reactions of the F2 progeny from cross PI 96983 × PI 486.355 to isolate C14 also fit a 15 resistant: 1 susceptible ratio as expected for two dominant genes segregating independently (Table 3).

These results demonstrated that resistance to SMV in the three soybean lines, PI 96983, PI 483.084, and PI 486.355, was conditioned by three independent genes that were completely dominant over the susceptibility alleles in cultivars Williams 79 and Franklin. Resistance to strains SMV-1 (G2) and SMV-1-B (G3) in

TABLE 3. Segregation for resistance to soybean mosaic virus (SMV) strains G2 and G7 and an isolate C14 in the F_2 generations of crosses of two resistant soybeans

	Numbe	r of plants	Chi-square 15:1 ratio		
Cross	Resistanta	Susceptible	Value	Probability	
G2 inoculation					
PI 96983 ×					
PI 483.084	112	5	0.780	0.38	
G7 inoculation					
PI 483.084 \times					
PI 486.355	93	4	0.748	0.39	
C14 inoculation					
PI 96983 ×					
PI 486.355	90	5	0.167	0.68	

^a Resistant = no symptoms and susceptible = mosaic or necrotic symptoms.

 $^{{}^}bR$ = resistant (no symptom) and S = susceptible with mosaic (M) or necrotic (N) symptoms; based on reactions of 10 soybean plants from each entry to each SMV strain.

PI 96983 was reported to be conditioned by a dominant gene Rsv (5). Resistance to all seven SMV strains transferred from PI 360.844 to the soybean line OX670 was shown to be conditioned by a dominant gene Rsv_2 (1). From this study, it was not possible to determine if the genes conditioning SMV resistance in PI 483.084 and PI 486.355 were different from Rsv_2 ; however, when PI 360.844 plants were inoculated with isolate C14, all 20 inoculated plants developed severe necrotic symptoms similar to the reaction of PI 483.084. Therefore, resistance in PI 483.084 and PI 360.844 was probably conditioned by the same gene, Rsv_2 , since reactions of PI 483.084 and PI 360.844 to all the seven SMV strains and isolate C14 were similar. Since the dominant gene in PI 486.355 differs from the gene in PI 483.084, it probably was at a third locus. Further study is needed to compare these genes by evaluating reactions of the F_2 and testcross progeny plants to SMV strains.

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Resistance

Resistance to Watermelon Mosaic Virus II Multiplication in Cucumis melo

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ABSTRACT

Moyer, J. W., Kennedy, G. G., and Romanow, L. R. 1985. Resistance to watermelon mosaic virus II multiplication in *Cucumis melo*. Phytopathology 75: 201-205.

The objective of this study was to compare watermelon mosaic virus II (WMV II) multiplication in susceptible genotypes of *Cucumis melo* and in plants of breeding line 91213. WMV II multiplication was measured weekly at three leaf positions by using the ELISA and a local lesion assay to monitor the accumulation of viral antigen and infectious virus, respectively. WMV II multiplication in comparable tissues and following comparable

incubation was significantly lower in 91213 than in the other genotypes. There was no evidence for the presence of inhibitors in 91213 that would interfere with either assay. The difference in WMV II multiplication in 91213 and two other genotypes was also observed under field conditions. This form of resistance may have significantly reduced spread in these field trials.

WMV II is responsible for serious losses each year in *Cucumis melo* L. and *Cucurbita pepo* L. Control of this disease has relied heavily on oil sprays, reflective mulches, and avoidance. A source of WMV II resistance similar to the high levels of resistance available for WMV I (15,16) has not been identified for these cucurbit species (10). Other forms of resistance (for example, Lecoq et al [8] describe a form of resistance that suppresses the transmission efficiency of cucumber mosaic virus by an aphid) may be available.

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infected plants of breeding line 91213 of *C. melo* which were associated with low levels of WMV II acquisition. These studies were initiated to analyze the forms of quantitative resistance to WMV II.

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We detected abnormally low levels of WMV II antigen in

The specific objectives of this research were to compare WMV II multiplication in the susceptible or normal genotypes to that in 91213 and then to determine if this form of resistance would influence the interplant movement of WMV II in the field.

MATERIALS AND METHODS

Host and virus. A single WMV II isolate was used throughout this study. This isolate was obtained from a commercial field of yellow crook-neck summer squash (C. pepo) grown in North Carolina. The homogeneity of the isolate was ensured by repeated