New Sources of Resistance to *Phytophthora sojae* in the Soybean Plant Introductions

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ABSTRACT

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Single dominant *Rps* genes have been highly effective in managing *Phytophthora sojae*. However, numerous physiological races of *P. sojae* have developed in response to deploying single gene resistance. New sources of resistance with potentially novel *Rps* genes are needed. A selection of accessions (PI273483 to PI427107) from the United States Department of Agriculture Soybean Germplasm collection were evaluated for resistance to *P. sojae* using the hypocotyl inoculation technique for *Rps* genes and the layer test for partial resistance. Of the 1,015 accessions tested, 159 accessions were susceptible to races 7 (vir 1a, 2, 3a, 3c, 4, 5, 6, 7), 17 (1b, 1d, 2, 3a, 3b, 3c, 4, 5, 6, 7), and 25 (1a, 1b, 1c, 1k, 7). However, 162 accessions were resistant to these three races and 32 accessions were resistant to an additional five races chosen specifically to elicit a susceptible interaction with two and three *Rps* gene combinations. In addition, 55.5% of the 887 accessions tested had high levels of partial resistance or tolerance (scores ≤ 4.0) to *P. sojae*. The majority of the accessions that were resistant to all of the races tested and those that had very high levels of partial resistance originated in the Republic of Korea. These results indicate that this region is an area with many sources of resistance to *P. sojae* for both specific *Rps* genes and partial resistance.

Additional keywords: partial resistance, *Phytophthora* root rot, *Phytophthora* stem rot

Phytophthora sojae is the major pathogen of soybeans in Ohio and contributes to losses in several production regions in the United States and the world (13,26). Under saturated soil conditions, *P. sojae* produces motile zoospores which locate and infect soybean plants throughout the growing season. *Phytophthora* seed rot and damping off are early-season diseases, whereas *Phytophthora* stem rot occurs at mid- to late season.

Host resistance has been an effective tactic for managing *Phytophthora* damping off and stem rot (16). Single *Rps* genes which interact with *P. sojae* in a gene-for-gene system (6) have been utilized extensively. In contrast, partial resistance (formerly described as tolerance [25], general resistance, and rate reducing resistance [20]) has been used to a limited extent. Soybeans with partial resistance to *P. sojae* develop root rot following infections but

damage is limited in comparison with susceptible cultivars.

Single resistance genes have provided a somewhat durable disease management strategy. Cultivars with single *Rps* genes were first deployed in Ohio during the 1960s. Thirteen *Rps* genes have been identified, of which eight (*Rps1a*, *Rps1b*, *Rps1c*, *Rps1k*, *Rps2*, *Rps3a*, *Rps6*, and *Rps7*) have been used in commercial soybean cultivars. Following deployment of each single *Rps* gene, races of *P. sojae* were subsequently identified that had a susceptible interaction with the *Rps* gene. Single *Rps* genes have been effective for 8 to 15 years, depending on inoculum density and environmental conditions (16). *Phytophthora* root rot was identified in fields in which cultivars with the single gene *Rps1k* were grown as early as 1990 in Ohio (18). Races of *P. sojae* that elicit a susceptible interaction with *Rps1k* have also been isolated from soil in Indiana (1) and plants in Iowa (28) during 1993 and 1991, respectively. In addition, races of *P. sojae* with virulence pathotypes for *Rps* genes that have never been deployed have also been identified (1,18,21).

As the complexity of the virulence pathotypes of *P. sojae* continues to increase and the number of designated races increases in soybean production fields, finding additional sources of partial resistance and incorporation of this resistance into commercial cultivars will be essential to manage this disease effectively. There is

evidence that partial resistance is a highly heritable, quantitative trait (4,25). St. Martin et al. (19) reported that partial resistance (tolerance) does not negatively impact yield potential of soybean cultivars. In addition, differences in yield among cultivars planted in *P. sojae*-infested soil could be attributed to the degree of partial (rate-reducing) resistance present in the cultivar (22).

Plant breeders favor single gene resistance due to ease of incorporation. Therefore, new sources of resistance need to be identified in order to maintain single *Rps* genes as a viable tool. Various strategies have been used to screen soybeans for possible new *Rps* genes and gene combinations. Lohnes et al. (11) inoculated soybean plant introductions (PIs) from eastern China with four different isolates which represented *P. sojae* races 1, 7, 17, and 25. These races had corresponding virulence pathotypes for all of the 13 identified single *Rps* genes and many gene combinations. Kyle et al. (9) screened a collection of soybean PIs with 10 different races of *P. sojae*, many of which had very similar virulence pathotypes.

In order to identify new sources of resistance and subsequently novel *Rps* genes, we used a strategy in which three isolates were chosen which had virulence pathotypes encompassing each of the *Rps* genes and many combinations similar to Lohnes et al. (11) for the preliminary screening. For those accessions which were resistant to these three isolates of *P. sojae*, additional isolates were then selected with virulence pathotypes for specific two- and three-gene combinations which, if present, would have a susceptible interaction. The purpose of this study was to identify new sources of *Rps* and partial resistance to *P. sojae* in the United States Department of Agriculture (USDA) Soybean Germplasm collection.

MATERIALS AND METHODS

Plant introductions. The soybean germplasm examined in this study included PI accession numbers PI273483 to PI 427107, in maturity groups 000 to IV, from the USDA Soybean Germplasm Collection in Urbana, IL. Laviolette and Athrow previously evaluated many of the accessions in this collection for resistance to frogeye leafspot race 2 and *P. sojae* races 1, 2, 3, and 4 (12). Some lines also were evaluated for reaction to *P. sojae* races 5, 6, 7, 8, and

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9 (12). The 1,015 accessions selected for the current study were resistant or not tested in Laviolette and Athow's previous evaluation. In the sample, 69 and 22% of the accessions originated in South Korea and Japan, respectively; whereas only 7% of the accessions originated in China. In addition, one to four accessions originated from each of the following countries: France, Germany, Hungary, Poland, Romania, Russia, Sweden, Taiwan, and Yugoslavia.

Detection of sources of *Rps* genes. The isolates that were used in inoculations and their virulence pathotype are listed in Table 1. All of the isolates originated in Ohio. Races 7, 17, and 25 collectively have susceptible interactions with all of the designated *Rps* genes and many *Rps* gene combinations. Additional isolates were then selected which elicit a susceptible interaction with specific 2-*Rps* gene combinations (Table 2). For example, *P. sojae* race 31 has a susceptible interaction with an *Rps* gene combination of *Rps1k* and *Rps6*, but races 7, 17, or 25 have a resistant reaction. The race designations for *P. sojae* are based on the susceptible reaction of 8 of the 13 differentials *Rps1a*, *Rps1b*, *Rps1c*, *Rps1d*, *Rps1k*, *Rps3a*, *Rps6*, and *Rps7* (1,18,28). We used the combination of race-isolate code for 30-T to indicate that there is a difference in the pathotype among two isolates which are designated *P. sojae* race 30 (Table 1).

The hypocotyl inoculation technique (17) was used to evaluate the accessions for *Rps* genes. Inoculum was prepared by growing *P. sojae* for approximately 7 days on lima bean soft agar (12 g of agar per

liter). Colonized areas of the plate were removed and placed in a hypodermic syringe, then mixed to make a slurry by forcing the mycelium and agar through the syringe two times. In all, 8 to 10 seeds of each accession were planted in vermiculite in the greenhouse. After 7 to 10 days, an incision was made in the hypocotyl and approximately 0.2 to 0.4 ml of a mycelium agar slurry was placed in the wound. The plants were covered overnight with plastic to prevent the agar from drying out. Seedlings were evaluated for resistant (hypersensitive) and susceptible reactions 4 to 6 days after inoculations. Inoculations of accessions that were resistance to *P. sojae* races 7, 17, and 25 were repeated five times. Accessions that were inoculated with *P. sojae* races 31, 30-T, 30, 33, and 38 were evaluated a minimum of three times with each race.

Detection of partial resistance. Once a *P. sojae* isolate was identified that had a susceptible interaction with an accession, that isolate was then chosen to evaluate partial resistance. *P. sojae* races 7, 17, 25, 30, and 31 were used to evaluate for partial resistance with the inoculum layer test (17) in 14 separate screenings. Each inoculum layer test was arranged in a randomized complete block design with three replications which included five soybean cultivars with known resistance response. For example, the controls for *P. sojae* race 25 were: Chapman (*Rps-3a*, resistant), Conrad (high partial resistance), Resnik (moderate partial resistance), Williams (moderately susceptible), and Sloan (susceptible). Standard soybean cvs. Sloan and Conrad were included with each test so that comparisons could be made with all of the accessions evaluated with the different *P. sojae* races. The inoculum consisted of 2-week-old *P. sojae* cultures grown on dilute lima bean agar (extract from 50 g of ground lima beans in 1 liter) in glass petri plates. The *P. sojae*-colonized agar was removed intact from the petri plate and placed 5 cm below the seed (12 soybean seeds per pot) in coarse vermiculite in 1.2-liter polystyrene containers with bottom drainage. The pots were watered to run-through twice daily. Seedling roots were inoculated with *P. sojae* as they grew through the agar layer. Three weeks after planting, the root mass was removed from the pot, the vermiculite shaken off, and the plants scored on the

following scale: 1 = no root rot; 2 = up to 10% root mass rotted; 3 = up to 25% of root mass rotted; 4 = 50% of root mass rotted; 5 = all roots rotted, up to 20% seedlings killed; 6 = up to 50% seedlings killed; 7 = up to 75% of plants killed; 8 = up to 90% seedlings killed; 9 = all plants killed. In order to compare the results from multiple tests as well as isolates with different levels of aggressiveness, the partial resistance rating of three replications were adjusted for the results from the standard check cultivars, Sloan and Conrad, as follows: the means of the partial resistance rating for the standard cultivars were all adjusted by adding or subtracting 0.5 to 1.5 to equal the scores for Conrad (3.5) and susceptible cv. Sloan (6.0). The scores of the controls were analyzed with the PROC GLM procedure in SAS (SAS Institute, Cary, NC) for the effects of test and test by cultivar interaction. The corrected means for all of the accession data was then pooled and analyzed with PROC GLM using SAS (SAS Institute).

RESULTS

Sources of *Rps* genes. Of the 1,015 soybean PIs evaluated for new sources of *Rps* genes in this study, 159, or approximately 16%, were susceptible to all three races (7, 17, and 25) of *P. sojae*, indicating that they either had *Rps7* or there were no *Rps* genes present. In contrast, 162, or 16%, were resistant to all three races. Of these 162, 32 were resistant to an additional five races of *P. sojae* (Table 3). These additional races (30-T, 30, 31, 33, and 38) have a susceptible interaction with many 2-*Rps* gene combinations (Table 2). These five isolates of *P. sojae* do not have a susceptible interaction with four 3-*Rps* gene combinations: *Rps1c*, *Rps3a*, *Rps4*; *Rps1c*, *Rps3b*, *Rps4*; *Rps1c*, *Rps2*, *Rps3a*; and *Rps1c*, *Rps2*, *Rps3b* (Table 3). Therefore, the 130 of the 162 soybean PIs that had a susceptible interaction with these five additional isolates potentially have more than one *Rps* gene. The possibility also exists that an unidentified *Rps* gene could have a susceptible interaction with these additional races with a previously unidentified virulence pathotype.

Sources of partial resistance. In all, 49 accessions had a mean root rot rating ≤ 3.0 and 438 had ratings from 3.1 to 4.0, indicating very high levels of partial resistance

Table 1. Differential reaction and race designations of isolates of *Phytophthora sojae* used to detect new sources or resistance in soybean plant introductions (PI 273483–427107)

Race ^a	Virulence pathotype ^b
7	1a, 2, 3a, 3c, 4, 5, 6, 7
17	1b, 1d, 2, 3a, 3b, 3c, 4, 5, 6, 7
25	1a, 1b, 1c, 1k, 7
31	1b, 1c, 1k, 2, 3c, 4, 5, 6, 7
30-T	1a, 1b, 1k, 2, 3a, 3c, 4, 5, 6, 7
30	1a, 1b, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7
33	1a, 1b, 1c, 1d, 1k, 3b, 5, 7
38	1a, 1b, 1c, 1d, 1k, 3a, 3b, 3c, 5, 6, 7

^a Isolates of *P. sojae* are listed as the race designation. T is used to separate two isolates which would be designated race 30 based on the reaction of the isolate on differentials *Rps1a*, *Rps1b*, *Rps1c*, *Rps1d*, *Rps1k*, *Rps3a*, *Rps6*, and *Rps7*.

^b Pathotype indicates to which *Rps* genes in the host the *P. sojae* isolates have a susceptible interaction. *P. sojae* races were determined on the following differentials: Williams (universal suspect); Harlon (*Rps1a*), Harsoy 13XX (*Rps1b*), Williams 79 (*Rps1c*); PI103091 (*Rps1d*); Williams 82 (*Rps1k*); L76-1988 (*Rps2*); L83-570 (*Rps3*); PRX 146-36 (*Rps3b*); PRX 145-48 (*Rps3c*); L85-2352 (*Rps4*); L85-3059 (*Rps5*); Harsoy 62XX (*Rps6*) and Harsoy (*Rps7*).

Table 2. Selected 2 *Rps*-gene combinations that are susceptible to specific *Phytophthora sojae* races

Race	Selected susceptible <i>Rps</i> gene combinations
7	1a,2; 1a,3a; 1a,3c; 1a,4; 1a,5; 1a,6; 1a,7; 2,3a; 2,3c; 2,4; 2,5; 2,6; 2,7; 3a,4; 3a,5; 3a,6; 3a,7; 3c,4; 3c,5; 3c,6; 3c,7; 4,5; 4,6; 4,7; 5,6; 5,7; 6,7
17	1b,2; 1b,3a; 1b,3c; 1b, 4; 1b,5; 1b,6; 1b,7; 2,3b; 3b,4; 3b,5; 3b,6; 3b,7
25	1c,7; 1k,7
31	1c,2; 1c,3c; 1c,4; 1c,5; 1c,6; 1k,2; 1k,3c; 1k,4; 1k, 5; 1k,6
30	1k,3a
30T	1a,3b; 1k,3b
33	1c,3b
38	1c,3a

in the 877 soybean PIs that were inoculated with a race of *P. sojae* that had a susceptible hypocotyl interaction (Fig. 1, Table 4). The levels of partial resistance were equal to or better than the standard cv. Conrad, which has a partial resistance score of 3.5 with most isolates. The standard cultivars which were included in each inoculum layer test were significantly different from each other ($P = 0.001$) and both the greenhouse tests and greenhouse test by cultivar interaction was not significant ($P > 0.05$). The accessions were highly significantly different ($P < 0.001$) for the partial resistance rating. The least significant difference between the accessions was 1.3. Partial resistance scores from the inoculum layer test of 3.0 to 4.0 will have limited yield losses in the field under moderate *Phytophthora* disease pressure (A. E. Dorance and S. K. St. Martin, unpublished data).

All but 4 of the 32 soybean PIs that were resistant to all of the races that were used

Fig. 1. Greenhouse evaluations for partial resistance of 887 plant introductions (accessions 273.483–427.107). Scores are the mean of three replications of the inoculum layer test. In order to compare the results from multiple tests as well as isolates with different levels of aggressiveness, the means of three replications were adjusted for the standard check cultivars which were also evaluated with each experiment: high levels of partial resistance, Conrad (score 3.5); moderate levels of partial resistance, Resnik (score 4.5) and Edison (score 5.5); and susceptible cultivar Sloan (score 6.0).

Table 3. Soybean plant introductions, accessions 273483–427107, with resistance to *Phytophthora sojae* races following inoculations with each race separately using the hypocotyl inoculation method in the greenhouse^a

<i>P. sojae</i> races	MG ^b	Source ^c	Resistant accessions ^d						
7, 17, 25	I	Japan	416757						
	III	Japan	417137	416918 ^{NT}					
	III	S. Korea	399077	424540					
	IV	Japan	360845	378682A	378682B	378682C	416983 ^{NT}	417005 ^{NT}	
	IV	S. Korea	340037	340046	398276	398299	398306	398495	398540
			399006	407817	407869A	407959A	408016B	408068B	408074A
			408074B	423827A	423837A	424171B	424569B		
7, 17, 25, 30	IV	S. Korea	273483C						
7, 17, 25, 31	IV	S. Korea	408004-1	408020A					
7, 17, 25, 30T	III	Japan	393537	423885					
	IV	Japan	393540	417412	423910				
	IV	S. Korea	398298	398680	399022	407778A	408319A	424348C	424549B
7,17,25,30T,33	IV	S. Korea	407781B						
7,17,25,30,31	IV	S. Korea	408108						
7,17,25,30T,31	IV	S. Korea	398996	407781A	408169A	424406A	424249C	424409	424414
7,17,25,30,30T,31	III	S. Korea	399008	399080	424358				
	IV	S. Korea	398249	398371	398565	398674	398764	398773	398774
			398775	398790	398791	398880	398940	398944	398946
			399015	407772B	407812	407847	407934	407960B	408017
			408020C	408062	408111	408124A	408124C	408125C	408132
			408196B	408224B	408260B	408288	423741	423850	424135
			424238	424342B	424430	424450	424477	424479	424509
			424525	424529	424549A	424555B	424559	424615	
7,17,25,30,30T,33	IV	S. Korea	398223	424355					
7,17,25,30,31,33	IV	Japan	274421						
7,17,25,30,31,33,38	IV	S. Korea	340035						
7,17,25,30,30T,33,38	III	Japan	393538						
	IV	S. Korea	423858						
7,17,25,30T,31,33,38	II	Japan	423871						
7,17,25,30,30T,31,33	III	S. Korea	398275	424159A					
	IV	S. Korea	398664	398959	399004	399017	407806A	407823	407900
			408210	408287	408319B	424237A	424320	424413	424499A
			424499C	424531					
7,17,25,30,30T,31,33,38	III	Japan	274456	417229					
	III	S. Korea	398295	398643	398693	398694	398697	407974B	424247A
	IV	Japan	416840						
	IV	Russia	404159						
	IV	S. Korea	273483D	398440	398666	399036	399073	399079	407861C
			407985	408015	408029	408097	408137A	408211B	408225A
			408319C	424169A	424234B	424247B	424354	424487B	424533

^a Each accession was evaluated with each race separately. Eight seedlings were inoculated with a mycelium slurry from a 7-day-old culture of *P. sojae* in the hypocotyl with a syringe. After 5 days, reactions were recorded as resistant or susceptible. Inoculations were repeated three times for each race.

^b MG = maturity group as designated in Nelson et al. (12). Note: both MG IV and late IVs as designated (12) are combined in this table.

^c Seed source = source of the actual seeds that were submitted to the USDA Soybean Germplasm collection at Urbana, IL.

^d NT = not tested for any additional races due to lack of seed.

Table 4. Soybean plant introductions, accessions 273483–427107, with high levels of partial resistance (scores 2.5 to 3.9) to *Phytophthora sojae* as determined by the inoculum layer test in greenhouse evaluations^a

MG ^b		Soybean plant introduction accession number					
000	379563						
00	361078	417564	423707	417512A	417512B		
0	407707	416845	417095	417187	423864	423954	
I	407705	416878	416915	417012	417210	417244	417453
	416805	416910	416946	417143	417227	417296	
II	291327	416875	417142	417173	417274	423933	427105B
	404196 A	417020	417154	417246	417315	423941	427106
	407661	417062	417160	417255	417459	423951	
III	339995	398755	408048A	416916	417303	424366	
	340017	398806	408048B	416918	417354	424444A	
	342438	398814	408052 A	416988	423747A	424568	
	360841	398841	408138C	416991	423814A	424569A	
	393537	399077	408255A	416993	423818		
	398227	404169B	408312A	417015	423885		
	398230	404188B	416753	417032	423896		
	398297	407850	416823	417152	423946		
	398395	407907A	416856	417161	423948B		
	398494	407922	416868B	417177	424134		
	398710	407926B	416889	417178	424143		
	398737	407933	416896	417192	424155A		
IV	274212	398857	407827	408114	417001	424234A	
	339864A	398887	407833A	408135B	417003	424249D	
	339868D	398970	407845A	408140A	417004	424264	
	398191	399001	407848	408140B	417092	424285A	
	398198	399016	407862	408169D	417176	424285C	
	398242	399027	407877A	408201B	417200	424305	
	398243	399051	407877B	408211A	417202	424349B	
	398244	399119	407892A	408224A	417245	424349C	
	398272	404183	407908	408236	417279	424389	
	398276	404185	407914A	408258	417283	424397	
	398298	404197	407959A	408265B	417298	424405C	
	398306	407658A	407960A	408269A	417336	424429	
	398317	407658C	407981A	408269B	417368	424444B	
	398321	407727	408016B	408272B	417424	424504B	
	398359	407770	408819B	408275	417479	424511	
	398386	407772A	408050B	408280	417488	424512	
	398495	407773B	408055A	408281A	420338	424528	
	398640	407778 A	408057	408295A	423893	424535A	
	398656	407786A	408068 A	408318A	423977	424546A	
	398741	407788B	408076A	416769C	423979	424549 B	
	398765	407795B	408079A	416914	424152	424569 B	
	398772	407805C	408090	416963	424154A	424604	
	398804	407805D	408092A	416965	424155B	424608A	
	398805	407806B	408095A	416968	424159C		
	398815	407817	408095B	416984	424160		
	398820	407818A	408105A	416987	424219A		
	398847	407821A	408105B	416997			
L-IV	274205	399006	407913A	408212B	423842	424352	
	339981	399018	407913B	408222C	423877	424400	
	340034	399019	407914D	408227	423902	424412	
	340037	399020	407917	408272C	423975	424426	
	342004	399022	407918B	408289	423983	424458	
	361103	399023	407924	408300	424164A	424495	
	379560	399028	407927B	408307C	424168A	424499D	
	398282	406708	407928	408335B	424168B	424521A	
	398299	407776	407959B	416801	424169B	424527	
	398303	407778C	407975A	416839	424171A	424536	
	398355	407818B	408816A	416958	424214A	424544	
	398375	407820	408019C	416959	424214C	424566	
	398389	407863	408068B	417412	424221B	424572	
	398464	407867B	408074B	423789	424255C	424582	
	398631	407869A	408076B	423791	424257B	424583	
	398717	407869B	408124D	423792	424276	424592	
	398843	407872 C	408166A	423811	424278B	424607	
	398919	407873	408169B	423827A	424293	424608B	
	398985	407892C	408173	423833A	424294B	424612	
	398987	407895	408186B	423836	424344		
	398988	407906	408197A	423837 A	424348 C		

^a Accessions were rated on the following scale: 1 = no root rot; 2 = up to 10% of root mass rotted; 3 = up to 25% of root mass rotted; 4 = 50% of root mass rotted; 5 = all roots rotted, up to 20% of seedlings killed; 6 = up to 50% of seedlings killed; 7 = up to 75% of plants killed; 8 = up to 90% of seedlings killed; 9 = all plants killed.

^b MG = maturity group.

in this study were collected in South Korea. In addition, 67.6% of the lines with high levels of partial resistance were also collected from South Korea. Previous efforts to evaluate germ plasm has focused on soybean production regions in People's Republic of China.

DISCUSSION

In order to detect new sources of resistance to *P. sojae* with potentially novel *Rps* genes, we used a strategy of inoculating soybean germ plasm with isolates with specific pathotypes that would provide a susceptible reaction with all of the known *Rps* genes, as well as 2-*Rps* and many 3-*Rps* gene combinations. This follows Flor's (6) hypothesis that resistance genes may be identified based on the susceptible or resistance response following inoculations with races of a pathogen with known virulence pathotypes. Lohnes et al. (11) screened a collection of PIs with only four races of *P. sojae*. Although these isolates, *P. sojae* races 1, 7, 17, and 25, have a susceptible interaction with all of the *Rps* genes that have been identified to date, there are many 2-*Rps* gene combinations (Table 2) that would have a resistant interaction when inoculated with these isolates. Athow et al. (3) reported two *Rps* genes in each of five accessions in their study, three of which were also evaluated in this study. Rennie et al. (14) identified two *Rps* genes in Japanese cultivars. Soybean breeders could potentially begin to incorporate these "new sources" of resistance into U.S. germ plasm when, in fact, the resistance is a 2-*Rps* gene combination for which races of *P. sojae* already exist that have susceptible interactions. Ultimately, once a source of resistance is identified, inheritance studies will be necessary to identify if it is an additional allele at a known locus or a new locus altogether, as well as the number of genes involved, to verify if the source contains a truly "novel gene".

Sources of resistance to host-specific plant pathogens are often found in regions of the greatest differentiation within the host species (10,24). In theory, both host and pathogen have putatively coevolved in these regions over long periods of time and this protracted association leads to diversity. Previous efforts to identify new sources of resistance in soybeans have focused primarily on accessions collected in the People's Republic of China (9,11). A high percentage of the soybean accessions in eastern China, specifically in the provinces of Anhui, Hubei, Jiangsu, and Sichuan, have been identified as having resistance to a number of *P. sojae* races (9,11). It was proposed that the diversity of resistance was due to the favorable environmental conditions for *P. sojae* that exist in these regions due to the significant amounts of rainfall: 2,000 mm in Anhui and Jiangsu (5,9,11).

The majority of the accessions (28 out of 32) that were resistant to all of the races of *P. sojae* tested in this study were collected from South Korea, including Chongju, Chonju, Ch'unch'on, Kwangju, Masan, Seoul, Taegu, and Taejon (12). In addition, 68% of accessions that were evaluated had very high levels of partial resistance, a trait that is thought to be controlled by several genes. Environmental conditions which would favor *P. sojae* also exist in this region because average rainfall is nearly 1,250 mm per year in South Korea and is concentrated from April through September (23). In Athow and Laviolette's (12) previous screening of this collection (PI273483 to PI 427107), approximately 29% of the accessions from South Korea were resistant to more than one race of *P. sojae*. This is comparable with earlier results reported for accessions from eastern China (11). These results suggest that South Korea may be another region to explore for additional sources of *Rps* genes as well as partial resistance to *P. sojae*.

P. sojae was only recently identified as a soybean pathogen in China: during 1989 in the Heilongjiang and Jilin provinces and Beijing City in Northern China (27) and during 1996 in the Chungnam province of Korea (8). Although resistance to *P. sojae* has been identified in these regions, a significant proportion of the accessions are also susceptible to *P. sojae* race 1 (vir 7) (11). The soybean accessions screened in this and other studies (9,11) have been land races, originating from farmers' garden plots. It is conceivable that garden cultivation is not favorable for the development of *Phytophthora* root rot, potentially due to good disease management practices (improved drainage, rotations, high organic matter). If *P. sojae* is present in these soils, it may be present at very low levels, or antagonists may also be present in the soil. It is possible that the *Rps* genes identified in these accessions were indirectly selected because of linkage to a favorable trait, and have been maintained in the germ plasm for several millennia. Examining the wild soybean for resistance and the genetic diversity of *P. sojae* within these regions will ultimately lead to a greater understanding of where these two species coevolved. Determining the region where these two species coevolved should help to focus screening efforts on the region where potentially more sources of novel *Rps* genes and genes which impart partial resistance may exist.

Based on the susceptible response to inoculations with of *P. sojae* isolates with specific virulence pathotypes, many accessions tested must have more than one *Rps* gene. The presence of multiple *Rps* genes within germ plasm poses a risk of falsely attributing resistance to a novel source when, in fact, a combination of known *Rps* genes are present. Therefore, the selection of which isolates to screen for new sources

of resistance becomes critical. Many races of *P. sojae* have been identified in the past 10 years (1,2,7,15,18,28). Fortunately, we now have the ability to identify races with specific virulence pathotypes to screen for single *Rps* genes and *Rps* gene combinations. All of the *P. sojae* isolates that we chose for this study were complex, in that they had a susceptible interaction with five or more of the single *Rps* gene differentials. Using this screening technique should expedite evaluation and confirmation of novel *Rps* genes. Ultimately, if novel sources of *Rps* genes do become limited, then the South Korean germ plasm will serve as an excellent source of high levels of partial resistance for management of *P. sojae*.

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