



Evaluations of soybean germplasm accessions and F₅ recombinant inbred lines for resistance to *Phakopsora pachyrhizi*

Pratibha Srivastava¹, David R. Walker², Sheeja George¹, Jim J. Marois¹ and David L. Wright¹

¹University of Florida, North Florida Research and Education Center, Quincy, FL 32351

²USDA-ARS Soybean/Maize Germplasm, Pathology and Genetics Research Unit, Urbana IL 61801



ABSTRACT

One of the most important constraints to soybean production in some parts of the world is soybean rust, caused by *Phakopsora pachyrhizi*. The lack of high yielding cultivars with high levels of resistance to the pathogen has prompted a search for novel sources of resistance. Twenty-six soybean germplasm accessions were evaluated for resistance in the greenhouse. Disease severity was determined 2 weeks after inoculation with a greenhouse population of the fungus from Quincy, Florida. Significant differences in disease severity were observed among the 26 accessions tested. Accessions PI417089B (MG IX), PI459025B (*Rpp4*; MG VIII) and PI612157 (MG VIII) were found to have more than 50% disease severity, whereas PI567104B, PI605773, PI615437, PI605773 and PI567090 showed greater resistance to a 2008 *P. pachyrhizi* isolate from Quincy, FL. In a related study, Soybean lines from two F₅ Recombinant Inbred Line (RIL) populations were also rated for resistance to natural rust infection in the field in 2008 in Quincy. F_{5,6} progenies from subsets of susceptible and resistant lines from each population were selected for evaluation in the greenhouse to compare their responses to those observed in the field. Significant differences in rust severity between the field and greenhouse were observed among lines from the two F₅ derived RIL populations. Discrepancies between the field and greenhouse ratings may be indicative of a difference in the genetic composition of the *P. pachyrhizi* populations or in differences between the reactions of seedlings and adult plants.

MATERIALS & METHODS

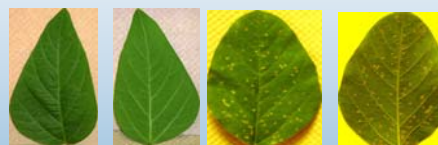
This experiment was conducted at the North Florida Research and Education Center (NFREC) at Quincy, FL in 2008 and 2009. The objective of this study was to compare reactions of soybean lines to soybean rust to identify potential lines with resistance. In separate experiment twenty-six soybean germplasm accessions were evaluated for resistance in the greenhouse. Population (Pop) 14-1 was derived from USDA breeding line LG00-3372 (MG III) x PI 467046A (MG VIII), and Pop. 16-1 was from LG00-3372 x PI 567104B (IX). In the greenhouse assays, 'Benning' (VIII), 'Pritchard' (VIII) and 'Williams 82' (III) and subsets of RILs from Pop 14-1 and Pop 16-1 were inoculated with urediniospores and were assessed for disease after 2 wk (Table 1) Five plants of each family were evaluated with two replications in 2008 and 2009.

F₅-derived recombinant inbred lines (RILs) from two populations to soybean rust (SBR); caused by *Phakopsora pachyrhizi* in the greenhouse and in the field. Seedlings were rated for SBR reactions in the greenhouse, whereas adult plants were evaluated in the field (Figure 1).

Disease severity was rated as relative portion of leaf surface with SBR lesions using a 1 to 5 scale in which 1 = no lesions and 5 = high density of lesions. In the field, the PIs and RILs were rated by examining 10 leaves from each family grown in two replications. The hypothesis is that relative disease levels on seedlings in the greenhouse can be used to predict the resistance of adult plants in the field.

Reactions	Population							
	GH (2008-2009)		Field (2008-2009)		GH & Field (2008-2008)		GH & Field (2009-2009)	
	14-1	16-1	14-1	16-1	14-1	16-1	14-1	16-1
	14-1	16-1	14-1	16-1	14-1	16-1	14-1	16-1
Resistant	82%	91%	72%	84%	62%	81%	100%	100%
Susceptible	5%	0	28%	16%	38%	19%	0	0
Moderate	13%	9%	0	0	0	0	0	0

Table 1 Percentages of reactions for 14-1 & 16-1 assays in greenhouse and field in 2008 and 2009 planting



16-1 Resistant

16-1 Susceptible



14-1 Resistant

14-1 Susceptible

Fig. 1. Field and greenhouse assays, and examples of resistant and challenged greenhouse leaves from Pop 16-1 and Pop14-1, showing adaxial (upper) and abaxial (lower) surfaces. SBR lesions are clearly visible two weeks after inoculation.

Reaction 2008	Population 2009											
	GH						Field					
	14-1			16-1			14-1			16-1		
	R	S	M	R	S	M	R	S	M	R	S	M
Resistant	40%	6%	9%	57%	0	4%	38%	0	4%	42%	6%	11%
Susceptible	17%	0	6%	13%	0	0	11%	19%	28%	17%	14%	6%
Moderate	23%	0	0	22%	0	4%	0	0	0	3%	3%	0

Table 2 Comparison of percentages of F₅ plants and F₆ reaction classes in 2008 in greenhouse and field with reaction in 2009 planting

RESULTS AND DISCUSSION

• In RIL Pop 14-1, 82% of the F_{5,6} families from F₅ plants that were resistant in the field in 2008 were resistant in the 2008 greenhouse assay; 72% were resistant in the field in 2009, and all of the F_{5,6} lines from both populations that were resistant in the 2009 greenhouse assay were also resistant in the field that year (Table 1).

• In a comparison of disease ratings on single Pop 14-1 F₅ plants grown in the field and GH in 2008, and ratings on their F_{5,6} progenies tested for resistance in 2009. There was a 40% correspondence for resistance in the 2009 greenhouse assays, and 38% correspondence in the 2009 field in Pop 16-1, and there was 57% correspondence for resistance in the 2009 greenhouse assays and 42% for plants grown in the field in 2009 (Table 2).

• Significant differences in disease severity were observed among the 26 accessions. PI417089B (MG IX), PI459025B (*Rpp4*; MG VIII) and PI612157 (MG VIII) were found to have more than 50% disease severity, whereas PI567104B, PI605773, PI615437, PI605773 and PI567090 showed greater resistance to a 2008 *P. pachyrhizi* isolate from Quincy, FL.

• The lack of complete correspondence between resistance ratings for F₅ plants and their F_{5,6} progenies could have resulted from: (1) disease escape or erroneous ratings for some susceptible F₅ plants; (2) segregation of a major dominant resistance gene that was heterozygous in some F₅ plants; (3) differences in resistance due to the physiological age of plants in the greenhouse seedling assays compared to evaluations of adult plant resistance in the field; or (4) race shifts in the local *P. pachyrhizi* population between 2008 and 2009. Changes in the local population were clearly possible, but major changes in the short time period would have been unlikely.

ACKNOWLEDGEMENT

The authors wish to acknowledge the University of Florida, the USDA-ARS, the United Soybean Board and the North Central Soybean Research Program for funding this research.