Evaluation of Soybean Germplasm for Soybean Rust (*Phakopsora pachyrhizi*) Resistance in Ha Noi, Vietnam

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ABSTRACT

Soybean rust (*Phakopsora pachyrhizi* Syd.), a fungal pathogen causing significant yield losses in many soybean production areas of the world, was reported in the continental U.S. in November 2004. The US commercial soybean cultivars are all presumably susceptible to the rust fungus. Evaluation of the USDA soybean germplasm collection, as well as other germplasm, for resistance to the disease is needed to develop soybean rust resistant cultivars. The objective of this study was to evaluate soybean accessions from the U.S. and Vietnam for resistance to the disease at Vietnam Agriculture Science Institute (VASI). Fifty seven soybean entries from the US that had been previously evaluated under containment at Fort Detrick, MD, and local checks were blocked by maturity and grown in the field in 1-m plots with three replications. Plants were inoculated with $5x10^4$ spores/ml twice at the V6 and R1 growth stages. From R2 through R6 stages, disease severity was assessed on five plants at three canopy positions (upper, middle, lower) on each plant, using a 0-3 severity scale, where 0 = no symptoms and 3 = heavy number of pustules (>500). Area under disease progress curve (AUDPC) was computed for statistical analysis using SAS with linear models. An additional evaluation was also conducted in a net house using similar inoculation technique and disease severity assessment. Several U.S. soybean plant introductions (PIs) had soybean rust assessments similar to the local resistant check in both net house and field evaluations. These PIs and local cultivars may serve as resistant sources for developing lines with soybean rust resistance.

MATERIALS AND METHODS

Field evaluation

***Plant materials and Experimental design*:**

Fifty seven U.S. soybean plant introductions (PIs) and varieties were selected from an evaluation under containment at Fort Detrick, MD, and grouped by maturity. Local susceptible and resistant checks were included in each maturity group. The experiment was conducted from February to August 2005 at the Vietnam Agriculture Science Institute (VASI), Ha Noi, Vietnam. The experimental design was randomized complete block with three replicates. Each entry was grown in 1-m plots with spacing between and within rows of 60 and 10 cm, respectively.

Field plot at VASI

Disease rating

Inoculation method:

A local susceptible soybean cultivar was grown in border rows as a source of inoculum. Additionally, plants were inoculated twice at growth stages V6 and R1 with a spore suspension ($5x10^4$ spores/ml) of a local unpurified isolate of the fungus. Prior to inoculation, the plots were thoroughly irrigated and covered with plastic sheets to maintain humidity for 12–16 h. The following morning, humidity inside was checked prior to removing the plastic sheets.

Incubation with plastic sheets

Infected leaves

Disease assessment and Statistical analysis:

Disease severity was assessed at different times from growth stages R2 to R6 on five plants at three canopy positions: lower, middle, and upper (Fig. 1) on each plant, using a 0-3 severity scale (Table 1). Area under disease progress curve (AUDPC) of each entry was computed for statistical analysis using the GLM procedure of SAS 9.1 (SAS Institute, Cary NY).

Figure 1. Canopy positions

Table 1. A 0-3 scale was employed for disease rating

Scale	Disease severity
0	no symptoms
1	light number of lesions (1-100)
2	moderate number of lesions (101-500)
3	heavy number of lesions (>500)

Net house evaluation

Soybean accessions were also evaluated as seedlings in a net house at VASI from January to May, 2005. Plants were inoculated at growth stages V2 and V4 with a spore suspension as previously described for the field study. Disease severity of each leaf at each node was assessed at three time points using a 0-3 rating scale as described. AUDPC was computed for statistical analysis.

Seedlings in a net house

Infected leaves

RESULTS AND DISCUSSION

Table 2. Area under disease progress curve and lesion type (T = Tan, RB = red brown, and M = mixed) of maturity group III-IV soybean accessions tested at two sites.

Net house					Field			
No.	Accession	AUDPC		Type	Accession	AUDPC		Type
1	PI243524	263.9	a	T	Williams 82	129.5	a	T
2	Rend	262.0	a	M	PI385942	127.0	ab	RB
3	Williams 82	247.7	ab	T	PI548178	126.3	ab	T
4	PI547875	244.1	ab	T	PI508269	124.6	abc	T
5	DT12	228.8	bc	T	PI567565	116.8	abcd	RB
6	PI092560	227.2	bc	T	PI083881	116.2	abcde	T
7	PI385942	225.6	bc	T	PI594250	114.4	abcdef	T
8	PI547878	224.0	bc	T	PI091730	114.4	abcdef	T
9	PI091730	222.5	bc	T	PI243524	114.0	bcdefg	T
10	PI407730	217.5	c	T	PI068494	113.7	bcdefg	T
11	PI594250	217.0	c	T	PI437323	110.9	cdefgh	RB
12	PI083881	215.9	c	M	PI547875	110.3	cdefghi	T
13	PI508269	215.2	c	T	PI547878	107.9	defghi	T
14	PI068494	209.6	c	T	PI092560	105.4	defghij	T
15	PI088452	207.0	c	T	Pana	104.9	defghij	T
16	Ina	178.5	d	T	PI407730	103.3	defghij	T
17	PI567565	176.0	d	T	PI088452	102.9	defghij	T
18	Pana	172.8	d	T	Vang HG	99.2	fghij	RB
19	PI437323	170.7	de	RB	Rend	99.0	ghij	T
20	PI549017	160.6	de	T	PI549017	97.3	hij	RB
21	PI561287A	158.0	de	T	GC84058-5	95.4	ij	RB
22	PI548178	146.8	e	T	PI561287A	95.3	ij	T
23	DT2000	85.3	f	RB	DT2000	94.8	j	RB
	LSD0.5	*25.5*			*LSD0.5*	*15.2*		

Table 3. Area under disease progress curve and lesion type (T = Tan, RB = red brown, and M = mixed) of maturity group V-VII soybean accessions tested at two sites.

Net house					Field			
No.	Accession	AUDPC		Type	Accession	AUDPC		Type
1	Lee 74	258.5	a	T	PI424456	192.9	a	RB
2	PI594172A	241.1	ab	T	PI200492	190.2	ab	T
3	PI424456	230.3	abc	M	PI417088	181.3	abc	RB
4	Essex	229.5	abcd	T	PI628859	172.6	abcd	T
5	DT12	228.8	abcd	T	PI398998	170.3	abcd	RB
6	PI561381	227.3	abcde	T	PI561381	167.6	abcde	T
7	PI417088	226.8	bcde	RB	PI165914	166.3	abcdef	T
8	PI459025B	222.1	bcdef	RB	PI459025F	166.2	abcdef	T
9	PI548484	207.7	cdefg	T	Essex	164.3	abcdefg	T
10	Bragg	199.3	cdefgh	T	Lee74	162.6	bcdefg	T
11	PI518759	199.1	defgh	T	PI594172A	160.5	cdefg	T
12	PI085089	196.4	efghi	T	Bragg	159.9	cdefgh	T
13	PI459025F	195.4	fghi	T	PI459025B	157.7	cdefgh	RB
14	PI548463	192.5	fghi	T	PI548484	154.0	cdefgh	T
15	PI165914	186.1	ghi	T	PI085089	148.0	defgh	T
16	PI208437	176.3	hij	M	PI548463	147.2	defgh	T
17	PI319525	176.2	hij	RB	PI561287B	145.3	defgh	T
18	PI561287B	169.0	hij	T	PI518759	143.5	defgh	T
19	PI200492	167.7	ij	M	PI319525	140.4	efgh	T
20	PI398998	154.7	jk	RB	PI429329	138.1	fgh	T
21	PI230970	153.7	jk	RB	PI230970	136.5	gh	RB
22	PI628859	147.8	jk	T	PI427241	135.7	gh	T
23	PI427241	131.2	jk	T	PI208437	130.7	h	RB
24	PI429329	128.4	jk	T	DT2000	94.8	i	RB
25	DT2000	85.3	l	RB	*LSD0.5*	*29.3*		
	LSD0.5	*31.1*						

Table 4. Area under disease progress curve and lesion type (T = Tan, RB = red brown, and M = mixed) of maturity group VIII-IX soybean accessions tested at two sites.

Net house					Field			
No.	Accession	AUDPC		Type	Accession	AUDPC		Type
1	DT12	228.8	a	T	PI462312	137.6	a	T
2	PI462312	202.2	ab	M	PI594538A	128.9	ab	RB
3	PI417317	194.3	bc	T	PI240667A	115.9	abc	T
4	Cook	179.5	bcd	T	PI417089A	112.3	abc	T
5	PI206258	173.7	cde	T	Jupiter-R	112.0	abc	T
6	PI164885	153.0	def	T	Cook	94.9	bcd	T
7	PI189402	145.5	efg	T	PI189402	93.7	bcd	T
8	PI423972	142.7	fg	RB	PI206258	91.1	cd	T
9	Jupiter-R	135.6	fgh	T	PI164885	82.3	cd	T
10	PI417089A	131.9	fgh	T	PI417317	79.9	cd	T
11	PI240667A	130.2	fgh	T	Cao Bang	78.7	cd	RB
12	PI434973A	118.7	gh	T	DT2000	74.3	d	RB
13	PI340898A	109.1	hi	T	PI423972	65.3	d	RB
14	DT2000	85.3	ij	RB	*LSD0.5*	*37.4*		
15	PI594538A	79.5	j	M				
	LSD0.5	*28.2*						

Previously identified single genes for rust resistance have been reported to be susceptible to certain isolates of *P. pachyrhizi* (Hartman et al., 2004). Thus, partial resistance, indicated by low rust severity and/or fewer lesions, may be an efficient approach for developing durable resistance (Hartman et al., 2005). Initial evaluation of U.S. soybean germplasm has identified potential sources of resistance (Miles et al., 2005). These lines require further field evaluation to identify those with high levels of partial resistance.

In this study, 57 soybean accessions were grouped by maturity and blocked with local checks in both net house and field evaluations. Statistical analysis of AUDPC within each maturity group are presented in Tables 2 (MG III-IV), 3 (MG V-VII), and 4 (MG VIII-IX). Overall, rust severity in the net house evaluation was much greater than under field conditions. It seems that the controlled conditions in the net house facilitated disease development.

Within each maturity group, disease severity had a wide range and significantly differed among soybean accessions. Among PIs, some had lower levels of disease in both evaluations and some were not significantly different from DT2000, a local resistant check. These included PI561287A, PI549017 (Table 2); and PI230970, PI427241, and PI429329 (Table 3); and PI594538A in the net house but not in the field (Table 4).

Several public soybean varieties were also evaluated, and none was as resistant as the check cultivar. In addition to DT2000, which originated from a breeding line at the Asian Vegetable Research and Development Center (Shanmugasundaram et al., 2004) and had low rust severity in the field trials (Kawuki et al., 2003), two other local cultivars, Vang Ha Giang and Cao Bang also showed less rust severity when tested in the field (Table 2 & 4) and may serve as potential sources of resistance to *P. pachyrhizi*.

Considering reaction types, both tan and red brown types were observed in the net house and field tests, but mixed reaction were only observed in the net house. There was no correlation between reaction types and rust severity and no consistency between the two evaluations for reaction types. Reactions of PI549017 and PI561287A were tan type in the net house, but their AUDPC values were low in both tests.

In summary, several plant introductions and Vietnamese soybean cultivars, including the check DT2000, consistently showed low levels of soybean rust severity when tested in the net house and field conditions at Vietnam Agriculture Science Institute. Additional tests are in progress to confirm these results, along with further genetic characterization of resistance.

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