Pathogenic variation of soybean rust in South America

Soybean [*Glycine max* (L.) Merrill] is an economically important crop and is a valuable source of oil and protein worldwide as well as of food products traditional to the Orient. South American countries are the largest soybean producers in the world, with production centered in Brazil, Argentina, and Paraguay. Soybean rust, caused by *Phakopsora pachyrhizi* Sydow & P. Sydow, is one of the most destructive and economically important diseases of soybean. Understanding the pathogenicity of indigenous fungal populations is useful for identifying resistant plant genotypes and targeting effective cultivars against certain populations. The objective of this study was to investigate pathogenicity of *P. pachyrhizi* infecting soybean in the 3 South American countries in 2007–2010, and to compare the rust pathogenicity geographically and temporally.

Soybean rust samples were collected in Argentina, Brazil, and Paraguay in the 3 cropping seasons of 2007/2008, 2008/2009, and 2009/2010. For comparative analysis of soybean rust pathogenicity between South America and Japan, rust samples were collected in Japan in 2007 and 2008. A total of 16 soybean genotypes including cultivars and lines (Table 1) were selected as a differential set to test soybean rust populations from South American countries. Nine differentials were reported to carry *Rpp* (resistance to *P. pachyrhizi*) genes (Table 1): *Rpp1* in Plant Introduction (PI) 200492, PI 368039, PI 587880A, and PI 587886; *Rpp2* in PI 230970 and PI 417125; *Rpp3* in PI 462312; *Rpp4* in PI 459025; and *Rpp5* in Shiranui. Sixteen soybean differentials were grown at 24°C with a 14 h photoperiod under rust-free conditions in a growth chamber and inoculated with *P. pachyrhizi* urediniospore suspension using a paintbrush or a glass atomizer. Two weeks after inoculation, lesion appearance [presence (+) or absence (−) of lesions] and sporulation level (SL) on the differential set were determined macroscopically. SL was rated using a 0–3 scale: 0, none; 1, little; 2, moderate; 3, abundant (Fig. 1). A few soybean leaves for each differential were detached from the inoculated plants, and the number of uredinia per lesion (NoU) formed on the abaxial side of the leaves were counted under a stereomicroscope. The NoU was calculated from 30 lesions per genotype. Data for the 3 parameters, (i) presence (+) or absence (−) of lesions, (ii) SL, and (iii) NoU, were collected for all rust populations and converted into infection types caused by the rust populations (Table 2). Infection types without lesions (immune) and with lesions showing SL 0 or 1 and NoU <1.5 were classified as resistant (R) indicated in red, whereas those with lesions showing SL 2 or 3 and NoU ≥1.5 were classified as susceptible (S) indicated in blue. When lesions with SL 2 or 3 and NoU <1.5 or SL 0 or 1 and NoU ≥1.5 were observed, the infection types were classified as intermediate (IM) indicated in yellow.

Fifty-nine rust samples from Argentina, Brazil, and Paraguay in 3 cropping seasons of 2007–2010 were evaluated for pathogenicity using 16 soybean differentials (Table 3). In the South American populations analyzed, only 2 pairs of populations yielded identical pathogenicity profiles in the 16 differentials: BE4-2 and PA5-3 from Brazil and Paraguay, respectively, and PC1-1 and PA9-1 from Paraguay, indicating substantial pathogenic variation in the rust populations. Each of the rust samples with identical pathogenicity profiles was collected from different locations, suggesting no association between pathogenicity and geographical origins of the samples. Comparative analysis of 59 South American and 5 Japanese samples revealed that pathogenic differences were not only detected within South America but also distinct between the *P. pachyrhizi* populations from South America and Japan. In addition, pathogenic differences were observed among South American *P. pachyrhizi* populations with the same geographical origin but different temporal origins. Thus, yearly changes in rust pathogenicity were detected during the sampling period. The differentials containing resistance genes *Rpp1*, *Rpp2*, *Rpp3*, and *Rpp4*, except for PI 587880A, displayed resistant reaction to only 1.8%–14%, 24%–28%, 22%, and 36% of South American *P. pachyrhizi* populations, respectively. In contrast, PI 587880A (*Rpp1*), Shiranui (*Rpp5*), and 3 *Rpp*-unknown differentials, PI 587855, PI 587905, and PI 594767A showed resistant reaction to 78%–96% of all populations. This study demonstrated pathogenic diversity of *P. pachyrhizi* populations in South America and that the known *Rpp* genes other than *Rpp1* in PI 587880A and

Rpp5 have been less effective against recent pathogen populations in the countries studied.

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Table 1. Soybean differential genotypes used for the evaluation

Differential		Resistance gene [a]	Origin
1	PI 200492	*Rpp1*	Japan
2	PI 368039	*Rpp1*	Taiwan
3	PI 230970	*Rpp2*	Japan
4	PI 417125	*Rpp2*	Japan
5	PI 462312	*Rpp3*	India
6	PI 459025	*Rpp4*	China
7	Shiranui	*Rpp5*	Japan
8	PI 416764	ND	Japan
9	PI 587855	ND	China
10	PI 587880A	*Rpp1*	China
11	PI 587886	*Rpp1*	China
12	PI 587905	ND	China
13	PI 594767A	ND	China
14	BRS 154	ND	Brazil
15	TK5	ND	Taiwan
16	Wayne	ND	USA

[a] *Rpp1*–*Rpp5* have been mapped to different loci.
ND: not determined.

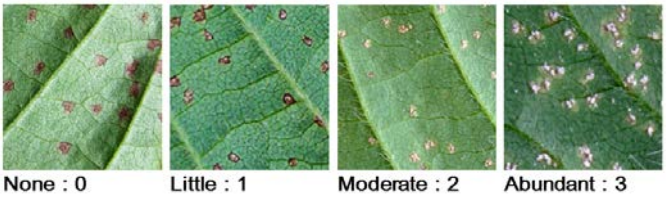

Fig. 1. Assessment of fungal sporulation on *Phakopsora pachyrhizi*-inoculated soybean leaves.

Table 2. Classification of infection types produced by soybean rust

Lesion	Sporulation level	No. of uredinia [a]	Infection type
Absence	-	-	Resistant
Presence	0 or 1	<1.5	Resistant
Presence	2 or 3	<1.5	Intermediate
Presence	0 or 1	1.5 or more	Intermediate
Presence	2 or 3	1.5 or more	Susceptible

[a] No. of uredinia per lesion was calculated from 30 lesions per differential

Table 3. Infection types of *Phakopsora pachyrhizi* samples from South America collected in 2007–2010 on the 16 differentials [a]

Sample [b]		Differential 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Argentina	AP1-1																
	AP1-3																
	AP2-2																
	AP2-3																
	AP3-3																
	AP4-3																
	AP5-3																
	AE6-2																
	AE6-3																
	AE7-1																
	AE7-3																
	AE8-1																
	AW9-3																
	AW10-3																
	AW11-3																
	AW12-2																
Brazil	BS1-1																
	BS1-2																
	BS1-3																
	BS2-1																
	BS2-2																
	BS2-3																
	BS3-1																
	BRP-1																
	BRP-2																
	BE4-2																
	BC5-1(1)																
	BC5-1(2)																
	BC5-3																
	BC6-1																
	BC7-1																
	BC8-3																
Brazil	BC9-1																
	BC10-1																
	BC11-1																
	BC11-2																
	BC11-3																
	BN12-1																
	BN12-2																
	BN12-3																
Paraguay	PC1-1																
	PC2-1																
	PC3-3																
	PA4-3																
	PA5-3																
	PA6-1																
	PA6-2																
	PA7-3																
	PA8-2																
	PA9-1																
	PI10-1																
	PI11-3																
	PI12-2																
	PI13-1																
	PI13-2																
	PI14-3																
	PI15-1																
	PI15-2																
	PI15-3																
Japan	JRP																
	T1-2																
	N1-1																
	E1-4																
	N2-1																

[a] Infection types were classified according to Table 2. The column with grey indicates that infection type was not determined because of preparation failure.

[b] AP: Pampa region; AE: Northeast region; AW: Northwest region; BS: South region; BE: Southeast region; BC: Central-West region; BN: North region; PC: Canindeyú prefecture; PA: Alto Paraná prefecture; PI: Itapúa prefecture. The following numbers represent sampling locations in each country (1–12, 1–12, and 1–15) and sampling season (1: 2007/08 ; 2: 2008/09 ; 3: 2009/10). Samples with the same location number were derived from the same location. Samples derived from the same location were indicated in yellow in each location. BRP-1, BRP-2, and BS3-1 were collected from the same location and season.