

# Soybean Reaction to Races 1 and 2 of *Heterodera glycines*

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## ABSTRACT

Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is a serious pest of soybean [*Glycine max* (L.) Merr.] in the USA and worldwide. A current classification system has designated 16 different races of SCN populations. In the Southern USA, SCN Races 1 and 2 are becoming more prevalent. It is important to identify soybean accessions with resistance to these races. The objective of this study was to bioassay 32 soybean plant introductions (PIs) for resistance to SCN Races 1 and 2 together with standard host differentials and a susceptible control. The bioassays were performed for each of the two races during 1997 to 1998 in thermoregulated water baths in the greenhouse. The results indicated that 25 PIs had resistance to Race 1 and 24 PIs had resistance to Race 2. PIs which were resistant to Race 1 and either moderately resistant or moderately susceptible to Race 2 included PIs 468915, 494182, 507354, 507422, and 509100. PIs 467327, 468903, and 507471 were resistant to Race 2 and additionally were either moderately susceptible or moderately resistant to Race 1. Soybean PIs that were yellow seeded and had various levels of resistance to both races included PIs 494182, 507354, 507422, and 507471. These are the most desirable sources for development of soybean cultivars with resistance to SCN Races 1 and 2. These soybean lines are being fingerprinted by means of microsatellites to identify unique types to allow broadening the diversity of resistance gene introgression.

SOYBEAN CYST NEMATODE is the most widespread pest of soybean in the USA and worldwide. First reported in North Carolina (Winstead et al., 1955), SCN has since spread throughout most of the soybean production states. In 1997, SCN reduced soybean yields in USA by an estimated 596 000 Mg (J. A. Wrather, 1998, personal communication). After field infestation with SCN, the number of nematodes may be reduced by carefully managing crop rotation, but they are never completely eradicated. The most efficient way to control SCN is to plant resistant soybean cultivars in rotation with non-host crops.

Soybean resistance to SCN was initially identified by Ross and Brim (1957) and included Peking, PI90763, PI209332, and PI84751. Soybean germplasm continued to be introduced mainly from China, and today 118 resistant sources are identified in the USA (Rao-Arelli et al., 1997). The current classification system for SCN populations has designated 16 different races on the basis of their ability to parasitize a set of soybean host differentials (Riggs and Schmitt, 1988). The SCN population originally identified from North Carolina was later categorized as Race 1 (Golden et al., 1970).

Several accessions from soybean germplasm collec-

tions were evaluated for resistance to Races 3, 5, and 14 with 118 found to have resistance to one or more races (Anand et al., 1985; Young, 1990, 1995; Nelson et al., 1994). More recently, soybean cultivars in the Southern USA with resistance to Races 3 and 14 are threatened by the widespread occurrence of Race 2 (J.G. Shannon, 1997, personal communication). We have evaluated 86 of the 118 resistant accessions to SCN Races 1 and 2 and nine were determined to have resistance to both races (Rao-Arelli et al., 1997). The objective of this research was to bioassay the remaining 32 accessions from the original 118 for reaction to SCN Races 1 and 2.

## MATERIALS AND METHODS

Collection and culturing methods of two near-homogeneous races of SCN used in this research have been reported (Rao-Arelli et al., 1997). We have developed and used similar near-homogeneous races of SCN in previous genetic studies for stable reactions (Rao-Arelli et al., 1989). Briefly, a SCN field population of Race 1 was obtained from Cape Girardeau County, Missouri, and was cultured on the roots of susceptible 'Hutcheson' (Buss et al., 1988), adopting limited inbreeding for more than 24 generations. This population was categorized as Race 1 according to the classification system of Riggs and Schmitt (1988), and was maintained on the roots of Hutcheson.

A Race 2 population was collected from soybean fields in Beaufort County, North Carolina. This was cultured with limited inbreeding and maintained on roots of 'Pickett-71' (Hartwig et al., 1971) for 31 generations before it was used as inoculum in this bioassay.

Thirty-two soybean accessions (PI458175B through PI532444B) with known reaction to SCN Races 3, 5, and 14 were bioassayed in this research. These were in Maturity Groups 0 to VII, and were collected from China, Japan, and South Korea. These accessions plus the four standard host differentials ('Peking', PI90763, PI88788, and Pickett-71), and Hutcheson, a susceptible control, were included in each bioassay. Seeds of PI lines used in this research were obtained from R. L. Nelson, Curator, USDA-ARS, National Soybean Research Laboratory, Urbana, IL.

Bioassays were performed individually for each of the two SCN races in the greenhouse during 1997 to 1998 as described previously (Rao-Arelli et al., 1997). Ten seedlings were included for each of the 32 accessions, susceptible control, and host differentials. Each seedling represented a single replication within a genotype, and the test was completely randomized. In brief, the techniques involved growing plants in 200- by 25-mm plastic micropots filled with steam-pasteurized Brosely fine sandy soil (loamy, mixed thermic Arenic Hapludalf). Approximately 20 of these micropots were placed in a polypropylene container (20-cm diam), and maintained at 27 °C in a thermoregulated water bath. Two seeds were planted in each micropot and were thinned to a single seedling per pot after germination. The seedlings were grown for 4 to 5 d prior to their inoculation with SCN eggs. Each seedling was inoculated with 1200 ± 25 eggs in 5 mL of suspension (distilled water) with an automatic pipetter (Rao-Arelli et al., 1991).

Approximately 30 d after inoculation, plant roots were indi-

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**Table 1.** Maturity group, seed coat color, and mean female index for 32 soybean accessions, standard host differentials, and a susceptible control bioassayed with isolates of SCN Races 1 and 2.

ID accession	Maturity group	Seed coat color	SCN race 1		SCN race 2	
			FI†%	Reaction rating	FI†%	Reaction rating
PI458175B	IV	Yellow	94	S	72	S
PI458199	IV	Black	69	S	22	MR
PI458519A	II	Black	35	MS	25	MR
PI458520	II	Green	56	MS	36	MS
PI461509	I	Brown	37	MS	19	MR
PI464912	IV	Green	93	S	107	S
PI464915B	II	Black	37	MS	24	MR
PI467310	II	Yellow	74	S	54	MS
PI467312	II	Green	60	MS	26	MR
PI 467327	II	Green	54	MS	1	R
PI467332	II	Green	35	MS	32	MS
PI468903	II	Black	22	MR	2	R
PI468915	II	Black	1	R	18	MR
PI475810	II	Yellow	36	MS	48	MS
PI490769	III	Black	37	MS	22	MR
PI494182	0	Yellow	1	R	20	MR
PI495017C	IV	Green	46	MS	30	MR
PI506862	IV	Yellow	72	S	25	MR
PI507354	I	Yellow	1	R	22	MR
PI507422	VI	Yellow	8	R	49	MS
PI507423	VI	Yellow	17	MR	72	S
PI507443	IV	Yellow	13	MR	76	S
PI507470	VI	Yellow	1	R	83	S
PI507471	III	Yellow	17	MR	3	R
PI507475	V	Yellow	2	R	76	S
PI507476	VI	Yellow	25	MR	36	MS
PI509095	VII	Yellow	12	MR	77	S
PI509100	VII	Green	4	R	37	MS
PI518772	V	Yellow	65	S	90	S
PI532434	II	Black	42	MS	17	MR
PI53444A	I	Brown	67	S	15	MR
PI532444B	II	Brown	41	MS	14	MR
<b>Standard host differentials</b>						
Peking	IV	Black	1	R	48	MS
PI90763	IV	Black	1	R	0	R
PI88788	III	Black	76	S	61	S
Pickett-71	VI	Yellow	2	R	107	S
<b>Susceptible Control</b>						
Hutcheson	V	Yellow	137‡	S	136‡	S
LSD (P ≤ 0.05)			6		3	

† Female index is the number of white, yellow, and brownish colored SCN females occurring on a soybean plant 30 d after inoculation, expressed as the percentage of mean number of females on Hutcheson: mean of three tests. Reaction ratings indicated by FI values include: resistant (R) ≤ 0 to 9, moderately resistant (MR) ≤ 10 to 30, moderately susceptible (MS) ≤ 31 to 60, and susceptible (S) ≤ 60.

‡ Actual mean number of females found on Hutcheson soybean, not a Female index.

vidually washed with a strong jet of water to dislodge white females and cysts. These were counted under a stereomicroscope, and female index (FI) was calculated for the number of females developing on each line in each replication (Golden et al., 1970). Bioassays were repeated three times for each race.

Data for three tests for each race were combined for ANOVA of female indices by the Statistical Analysis System Software (SAS, 1991) and means were separated with Fisher's LSD based on a significant *F* test. Ratings of resistant (IP ≤ 0–9%), moderately resistant (IP ≤ 10–30%), moderately susceptible (IP ≤ 31–60%), and susceptible (IP ≤ 60%) used to classify the reaction of accessions were based on Schmitt and Shannon (1992).

## RESULTS AND DISCUSSION

We identified 25 accessions with various levels of resistance to SCN Race 1 in our bioassays (Table 1).

These included seven resistant, six moderately resistant, and 12 moderately susceptible soybean accessions. For Race 2, 24 soybean accessions were found with various levels of resistance reactions. These included three resistant, 14 moderately resistant, and seven moderately susceptible accessions (Table 1).

We also identified several soybean PI lines with various levels of resistance to both SCN Races 1 and 2. PI lines which were resistant to Race 1, and either resistant, moderately resistant or moderately susceptible to Race 2 included PIs 468915, 494182, 507354, 507422, and 509100. PIs 467327, 468903, and 507471 were resistant to Race 2 and each was either moderately susceptible or moderately resistant to Race 1. Soybean PIs that were yellow seeded, a trait that is commercially most valuable, and having various levels of resistance to both Races of SCN included PIs 494182, 507354, 507422, and 507471.

PI 494182 was resistant to SCN Races 3, 5, and 14 (Young, 1995) and additionally found to be resistant to Race 1 and moderately resistant to Race 2 (Table 1). PI 467312 that was previously reported to be resistant to SCN Races 3, 5, and 14 (Young, 1995) was found to be moderately susceptible to Race 1 and moderately resistant to Race 2 (Table 1). PI 507354 was resistant to SCN Races 3 and 5 (Young, 1995) and resistant to Race 1 and moderately resistant to Race 2 (Table 1).

The soybean germplasm collection is a valuable reservoir of genes for continued genetic improvement of soybean. It is also an invaluable gene pool resource for pest resistance and genetic studies. We are currently determining the genetic diversity for these soybean lines using microsatellites. Unique types that are not closely related to Peking, PI88788, and PI437654 will be identified and used for developing soybean cultivars with durable resistance to SCN.

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## Effectiveness of Different Sources of Stem Rust Resistance in Barley

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### ABSTRACT

Stem rust (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. & Henn.) pathotype QCCJ is a potential threat to barley (*Hordeum vulgare* L.) production in North America. A field test was conducted for 3 yr to evaluate the effectiveness of several new sources of stem rust resistance to reduce losses. A randomized complete block design was used, with a split-plot arrangement of treated (propiconazole fungicide) and untreated plots. Nine lines used in the test were classed as resistant (R), moderately resistant (MR), moderately susceptible (MS), and susceptible (S). The yield losses in each group were: R—Q21861 (12%), QSM-041 (12%), BM8923-46 (12%); MR—'Diamond' (21%), SB90585 (26%); MS—'Robust' (30%), 'Bonanza' (33%), 'Harrington' (37%); S—'Klages' (53%). There were highly significant effects on 1000-kernel weight, test weight, and percentage kernel plumpness for all entries. The losses in kernel weight ranged from 7% (Q21861) to 43% (Klages), in test weight from 3% (Q21861) to 26% (Klages), and kernel plumpness from 5% (Q21861) to 95% (Klages). There were no significant effects of rust infection on plant height and days to heading. Effects on lodging were variable, and reduced days to maturity was highly significant for all entries. Lines with combinations of genes *Rpg1/rpg4* (Q21861, Q/SM-041) and *Rpg1/Rpg3* (BM8923-46) provided the highest levels of protection, with a somewhat lesser level provided by *Rpg1/RpgU* (Diamond). Combinations of these genes should provide effective stem rust resistance in barley breeding.

THE NORTH CENTRAL GREAT PLAINS of the USA and the eastern prairie region of Canada are important barley-growing regions under risk of crop loss due to stem rust. Before the introduction in North America of barley cultivars with gene *Rpg1* for stem rust resistance, yield losses to natural epidemics of stem rust were as high as 12 to 15% in the north-central USA (Roelfs, 1978) and in Canada (McDonald, 1970). Extensive losses to naturally occurring stem rust were reported in susceptible cultivars in Australia in 1982 and 1983 (Dill-Macky et al., 1990). Although *P. g. tritici* occurs on barley in many parts of the world, there is little other data on estimated losses in barley due to this disease.

Gene *Rpg1* has provided effective resistance to stem rust since the introduction of barley cultivars with this gene in 1938, and it has remained as a principal source of resistance (Steffenson, 1992). Other genes for stem

rust resistance known in barley are *Rpg2* from 'Hietpas-5' (Patterson, 1951), *Rpg3* from PI 382313 (Jedel et al., 1989), *rpg4* from Q21861/PI 584766 (Jin et al., 1994), *RpgU* occurring in several barley cultivars (Fox and Harder, 1995), and a second recessive gene in Q21861 (Jin et al., 1994; Fox and Harder, 1995). Factors modifying resistance to stem rust were observed in the cross OAC 21/'Chevron' (Lejeune, 1946) and in the crosses Minn. 615/'Kindred' and Minn. 615/'Montcalm' (Miller and Lambert, 1955). The expression of *Rpg1* varies to some extent with genetic background (Steffenson, 1992). The effectiveness of the *Rpg1* resistance appears to be enhanced by the presence of gene *Rpg3* (Jedel et al., 1989). Experience with *P. g. tritici* in inoculated field nurseries has shown a wide range of reactions to stem rust by various barley lines and cultivars (D.E. Harder, 1990-1998, unpublished data), further indicating interactions of genes for resistance with a number of other genetic factors to confer variable resistance levels.

In 1988 a new pathotype of *P. g. tritici* was first observed (Martens et al., 1989) that showed higher levels of virulence to barley cultivars with *Rpg1*. This pathotype was designated as QCC according to the original nomenclature of Roelfs and Martens (1988) and subsequently identified as QCCJ to differentiate it from other isolates of QCC that are avirulent to *Rpg1* (Fox et al., 1995). In Manitoba field nurseries inoculated with QCCJ, various barley lines or cultivars, with or without *Rpg1*, have shown very high levels of infection, typically 80 to 90%, with susceptible-type reactions (D.E. Harder, 1994-1998, unpublished data). Late-sown barley fields in Manitoba's Red River Valley have shown up to 65% infection levels (Harder, 1997). A general epidemic of stem rust in barley involving QCCJ has yet to occur, although the observations suggest that a potential for an epidemic exists. Western Canadian breeding programs are actively incorporating stem rust resistance into breeding lines. The known genes for resistance other than *Rpg1* confer varying intermediate levels of resistance to QCCJ (Liu and Harder, 1996). The level of protection from QCCJ under field conditions afforded by alternative resistance sources is not documented. The objective of this study was to determine the effectiveness of various sources of stem rust resistance in barley to prevent yield and quality losses.

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**Abbreviations:** AAFC, Agriculture & Agri-Food Canada; kw, 1000-kernel weight; MR, moderately resistant; MS, moderately susceptible; PGR, Plant Gene Resources of Canada; plump, percentage kernel plumpness; R, resistant; S, susceptible; tw, test weight.