

Genetic Analysis of Phytophthora Rot Resistance in the Soybean PI 567.496

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Introduction

Phytophthora root rot, caused by *Phytophthora sojae*, has been a very harmful disease in soybeans for many years. Recent crop loss estimates have ranked Phytophthora root rot as the second or third most destructive disease for soybeans ([Doupnik, 1993](#)). Resistance to Phytophthora in soybeans is controlled by thirteen dominant genes. There are fifty-three known races of the pathogen ([Ryley et al., 1998](#)). The pathogen may attack plants in all stages of growth with disease development favored by poorly drained soils and cool wet weather ([Moots, et al., 1988](#)).

After re-evaluating [PI 567.496](#), we found it to be resistant to races 1, 3, 4, 5, 13, and 25 and susceptible to races 7, 12, 17, and 20 of *Phytophthora sojae*, and was predicted to carry a single gene, either the [Rps3a](#) gene or possibly a new gene, based on previous genetic analysis ([Kyle and Nickell, 1998](#)). This resistance pattern is the same as that of *Rps3a*. The objective of this study was to determine the genetic control of resistance to race 25 of *Phytophthora sojae* in PI 567.496.

Materials and Methods

In the summer of 1996, crosses were made between four different isolines of the cultivar '[Harosoy](#)' and PI 567.496 at the Crop Sciences Research and Education Center in Urbana, IL. These crosses included: LNX96062 (Harosoy 15xx ([Rps1k](#)) x PI 567.496), LNX 96063 (Harosoy 32xx ([Rps3a](#)) x PI 567.496), LNX 96064 (Harosoy 62xx ([Rps6](#)) x PI 567.496), and LNX 96065 (Harosoy ([Rps7](#)) x PI 567.496). The F₁ plants were grown in 1997 to produce F₂ seed. During the winter of 1998, 50 F₂ seeds from each cross were planted in the greenhouse for evaluation of their reaction to race 25 of *P. sojae*. Plants were inoculated by the

hypocotyl inoculation method with zoospores ([Moots, et al., 1983](#)). Parental lines were included in the experiment to check their reaction to race 25 of *P. sojae*. Four days after inoculation, the number of alive and dead plants were counted for each F₂ population. The data were analyzed using chi-square goodness of fit test to expected ratios.

Results and Discussion

After inoculation with race 25 of *P. sojae*, Harosoy 62xx, Harosoy 32xx and PI 567.496 were resistant, while Harosoy 15xx and Harosoy were susceptible ([Table 1](#)). The cross of Harosoy with PI 567.496 appeared to segregate approximately 3 resistant to 1 susceptible suggesting segregation of one gene for resistance ([Table 1](#)), which agrees with [Kyle and Nickell \(1998\)](#). In crosses with known alleles for resistance to *P. sojae*, Harosoy 15xx (*Rps1k*) x PI 567.496 segregated 3 R:1 S ($p= 0.274$), again suggesting that the PI has a single gene for resistance to race 25. All progeny from the cross of Harosoy 32xx (*Rps3a*) with PI 567.496 were resistant suggesting the gene in PI 567.496 is allelic to the *Rps3a* gene. The segregation of progeny from the cross of Harosoy 62xx (*Rps6*) with PI 567.496 should segregate 15 R:1 S when inoculated with race 25 of *P. sojae*. However, this population appeared to segregate 3 R:1 S ([Table 1](#)). This ratio could be explained if the wrong pollen source, perhaps Harosoy or Harosoy 15XX, were used in this cross instead of Harosoy 62XX. The results of this study suggest that PI 567.496 carries the *Rps3a* gene for resistance to *P. sojae*.

References

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Table 1. Response of F₂ populations and parents to race 25 of *P. sojae*.

Population or Parent	Res.*	Susc.**	Theoretical Ratio	Chi-Square	Chi-Square Prob.
LNX 96062	32	15	3:1	1.20	0.274
Harosoy 15xx (Rps1k)	All				
LNX 96063	29	0	All R	-	-
Harosoy 32xx (Rps3a)	All				
LNX 96064	35	11	3:1 15:1	0.01 27.4	0.93 0.00
Harosoy 62xx (Rps6)	All				
LNX 96065	26	19	3:1	7.12	0.01
Harosoy		All			
PI 567.496	All				

*Observed number of resistant plants.

**Observed number of susceptible plants.
