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Silvina Maria Stewart
Iowa State University

Alison E. Robertson
Iowa State University, alisonr@iastate.edu

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Pathotype Structure of *Phytophthora sojae* with Cultivar Rotation in Soybeans

Abstract

Phytophthora sojae is an oomycete that causes *Phytophthora* stem and root rot (PRR) of soybeans. The disease has traditionally been managed primarily by incorporating single gene resistance into commercial cultivars. Fourteen known resistant genes (Rps) confer resistance to *P. sojae*. However, the pathogen has the ability to develop new pathotypes (originally called races) that overcome these Rps genes and thus they become ineffective. This is known as pathotype (or race) shift. Durability of Rps resistance in the field has been estimated in 8-15 years. Alternatively, PRR can be managed using partial resistance (tolerance), which is a polygenic resistance that reduces disease and is effective against all pathotypes of the pathogen. It is considered more durable since it does not impose selection pressure on the pathogen.

Keywords

RFR A1068, Plant Pathology and Microbiology

Disciplines

Agricultural Science | Agriculture | Plant Pathology

Pathotype Structure of *Phytophthora sojae* with Cultivar Rotation in Soybeans

RFR-A1068

Silvina Stewart, graduate student
Alison Robertson, assistant professor
Department of Plant Pathology

Introduction

Phytophthora sojae is an oomycete that causes Phytophthora stem and root rot (PRR) of soybeans. The disease has traditionally been managed primarily by incorporating single gene resistance into commercial cultivars. Fourteen known resistant genes (*Rps*) confer resistance to *P. sojae*. However, the pathogen has the ability to develop new pathotypes (originally called races) that overcome these *Rps* genes and thus they become ineffective. This is known as pathotype (or race) shift. Durability of *Rps* resistance in the field has been estimated in 8-15 years. Alternatively, PRR can be managed using partial resistance (tolerance), which is a polygenic resistance that reduces disease and is effective against all pathotypes of the pathogen. It is considered more durable since it does not impose selection pressure on the pathogen.

Changes in the pathotype structure of *P. sojae* have been attributed to overuse of soybean cultivars with a specific *Rps* resistant gene, which results in selection for a resistant pathotype. This hypothesis has not been tested.

It has been proposed that rotating cultivars that differ in single gene resistance or, rotating cultivars with single gene resistance with cultivars with high partial resistance might reduce selection pressure on the pathogen and thus extend the durability of a resistance gene. This approach has been studied with the tobacco shank pathogen, *Phytophthora*

nicotianae. Rotation of single gene resistance and cultivars with high level of partial resistance resulted in a reduction in disease incidence and also minimized race shifts of the pathogen.

The objective of this experiment was to determine if cultivar rotation could be used to effectively reduce the incidence of PRR as well as minimize pathotype shift within the pathogen.

Materials and Methods

A soybean cultivar rotation was conducted using microplots at Kanawha. The experiment consisted of six treatments arranged in a complete randomized block design with four repetitions, in a four-year rotation (Table 1). Cultivars (cv.) with different levels of resistance were used; a susceptible cv. with no *rps*, a cv. with high partial resistance, a cv. with *Rps1k*, a cv. with *Rps1c*, and a cv. *Rps3a*.

The site was *P. sojae* free and therefore it was artificially inoculated in year one with *P. sojae* race 1 (virulent on *Rps 7*). Soil samples from each microplot were collected twice during each growing season, two weeks after sowing and just prior to harvest. Isolates of *P. sojae* were recovered from each soil sample and pathotyped using a standard set of soybean lines that each contain a specific *Rps* gene.

Results and Discussion

Out of the 124 isolates recovered throughout the four years of experiment, 45 percent of them were race 1. The remaining isolates (55%) were virulent on at least one additional *Rps* gene, with a maximum of four new virulent genes in an isolate (Figure 1). New

pathotypes were recovered as early as the second sampling date (harvest of year 1).

Our research showed *P. sojae* has the potential to shift pathotype or evolve new pathotypes very quickly. We were unable, however, to demonstrate that pathotype shift was a function of cultivar rotation. Thus, overuse of an *Rps* gene is not the primary

reason for changes in pathotype structure of *P. sojae*.

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Table 1. Four-year soybean-cultivar rotation.

Year	Rotation treatment					
	1	2	3	4	5	6
2007	Susceptible	Susceptible	Rps1k	Rps1k	Partial R	Rps1k
2008	Susceptible	Rps1k	Partial R	Rps1c	Partial R	Rps1k
2009	Susceptible	Susceptible	Partial R	Rps3a	Partial R	Rps1k
2010	Susceptible	Rps1k	Rps1k	Rps1k	Partial R	Rps1k

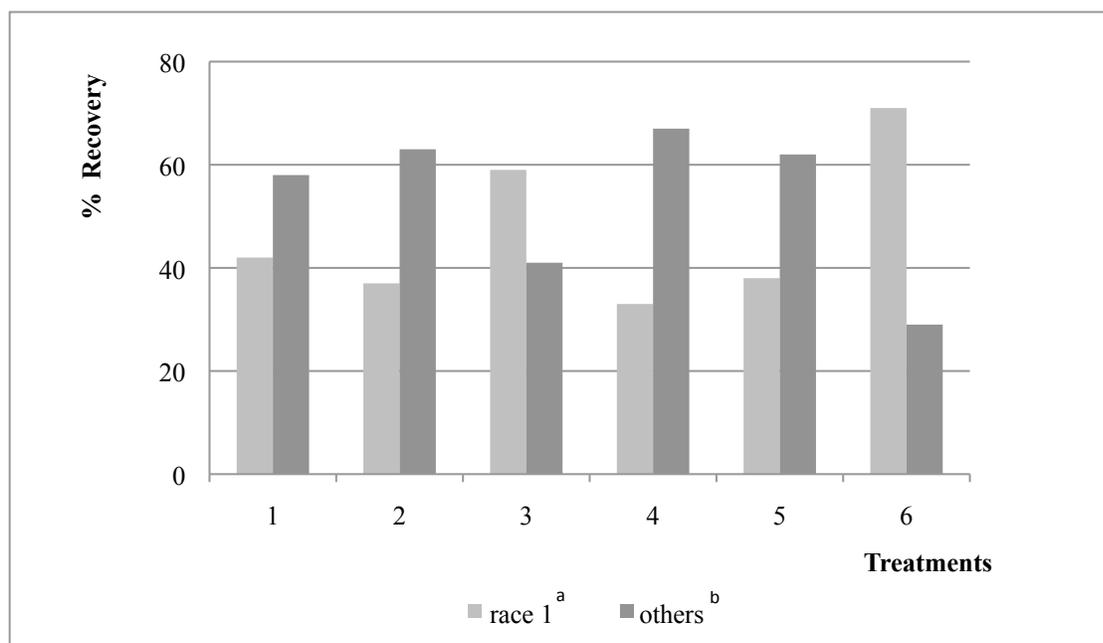


Figure 1. Percent race/pathotype recovery of *P. sojae* from soybean cultivar rotation treatments, 2007-2010.

^aRace 1 = virulent formula (7).

^bOthers include virulence formulas (1d), (1d,7), (1a,7), (2,7), (3b,7), (1c,7), (1d,2,7), (1a,1c,7), (1k,2,7), (1d,1k,7), (1b,2,3b,7), (1a,1c,2,7), (1b,1c,1k,7), (1a,1c,1d,7), and (1a,1c,1d,3b,7).