Evaluation of partial resistance to *Phytophthora sojae* in a diverse collection of soybean cultivars, breeding lines, and plant introductions

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Introduction

o   *Phytophthora sojae* is an oomycete pathogen of soybean (*Glycine max*) causing ~$300 M in crop losses annually in the US.[1]

o   Management of *P. sojae* is through race-specific and/or quantitative (partial) resistance.

o   Race-specific resistance (conferred by *Rps*-genes) exhibits a gene-for-gene relationship with the pathogen (**Fig. 1**).

o   In contrast, partial resistance is quantitatively inherited (**Fig. 2**) & generally controlled by many genes of small effect.

o   Due to the diversity & rapid evolution of *P. sojae* populations, partial resistance is theoretically more durable than race-specific resistance.

o   South Korea has been proposed as the origin of the soybean-*P. sojae* pathosystem. Thus, soybean lines from S. Korea may posses high levels of resistance[2].

FIGURE 1: Example of gene-for-gene resistance.

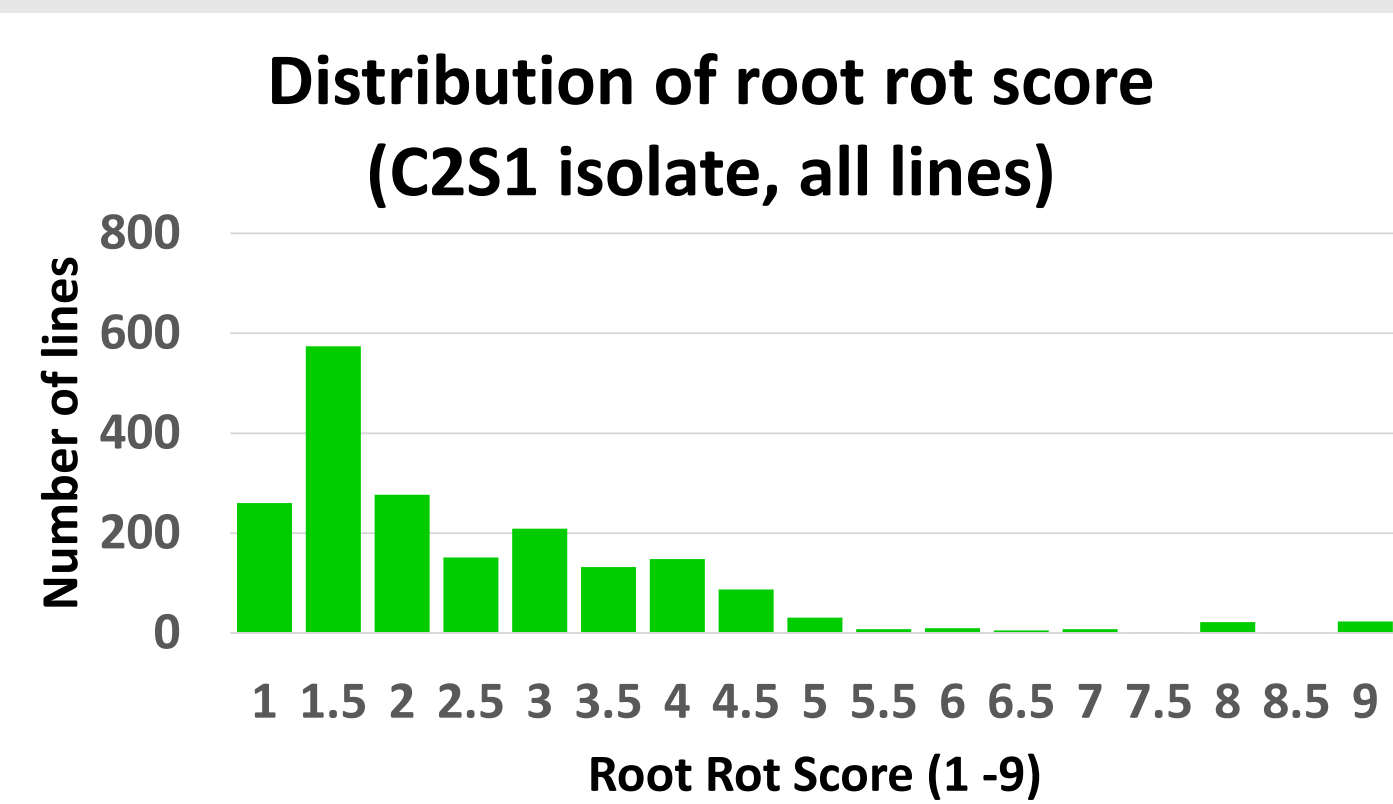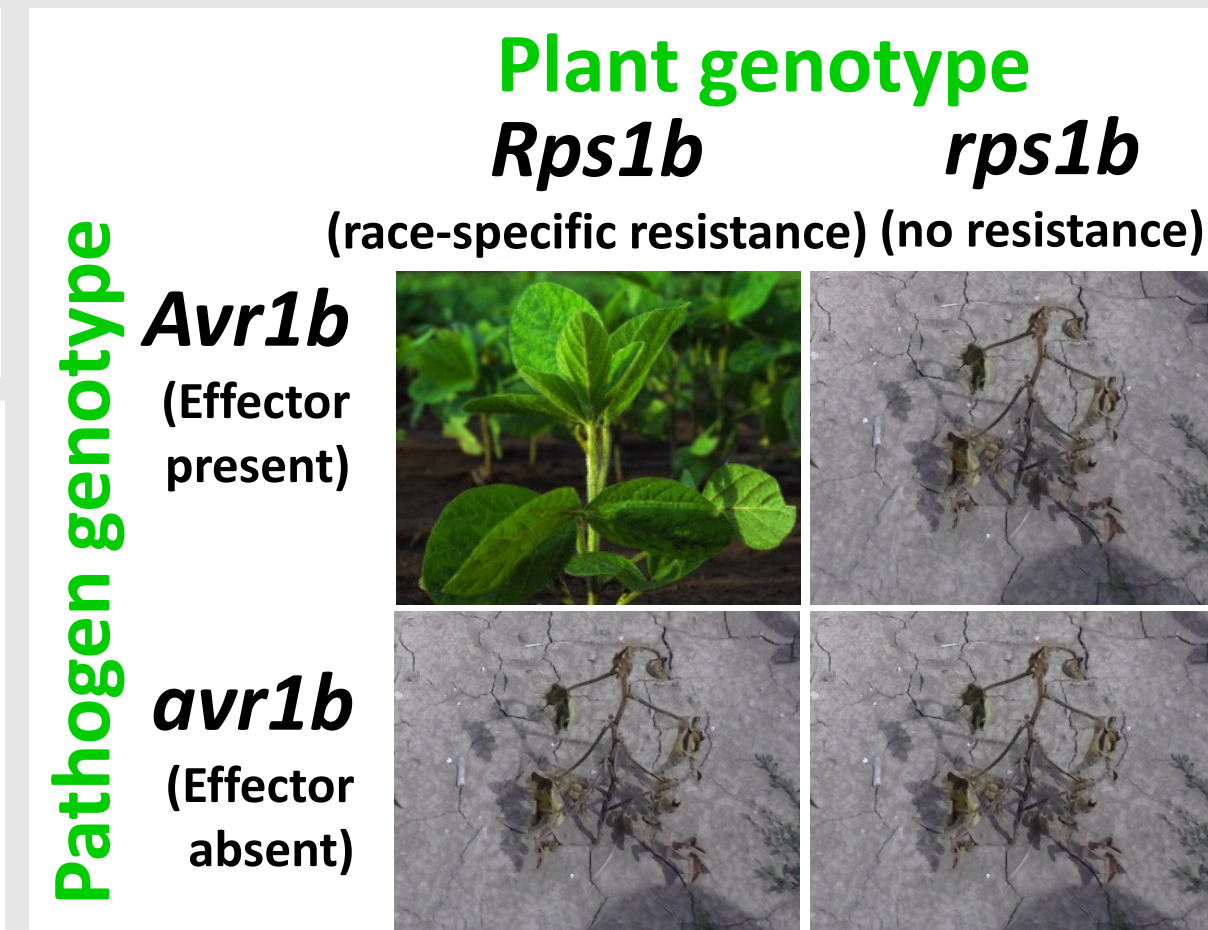Resistance occurs only when *Rps* and *Avr* alleles are present in plant & pathogen

FIGURE 2: Partial resistance exhibits a quantitative distribution

Distribution of root rot score (C2S1 isolate, all lines)

Objectives

Evaluate partial resistance to *Phytophthora sojae* in three populations:
   1. 293 breeding lines and cultivars from the OSU breeding program.
   2. 91 historically popular North American cultivars
   3. 1,392 Plant Introductions from South Korea

Materials and Methods

1. Screen to select virulent & aggressive *Phytophthora sojae* isolates

a. Hypocotyl test   b. Tray test [3]

2. Conduct layer test[4] on 1,776 lines from three populations (see objectives).

Non-inoculated   Inoculated

3. Collect data: Root rot score, plant height, root & shoot weight.

Root Rot Score 1.5
Root Rot Score 9
Root Rot Score 4
Root Rot Score 3.5

4. Extract genotypic Best Linear Unbiased Predictors (BLUP) values.

Group 1 (both reps with isolate C2S1):
Y= Class+ Genotype(Class)+ Rep+ Block(Rep)+ error

Group 2 (1st rep C2S1 & 2nd rep with HenryS.1) :
Y= Class+ Genotype(Class)+Isolate+ Block(Isolate)+Isolate*Genotype(Class)+ error
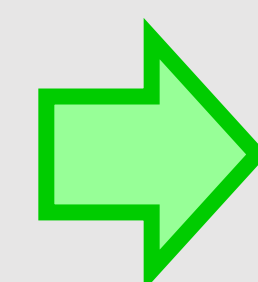
References

[1] Wrather, J., and Koenning, S., 2006. Estimates of disease effects on soybean yields in the United States 2003-2005. J Nematol. 38:173-180.
[2] Dorrance, A.E. and Schmitthenner, A.F. 2000. New sources of resistance to *Phytophthora sojae* in the soybean plant introductions. Plant Disease 84:1303-1308.
[3] Wang, H., St.Martin, S.K., and Dorrance, A.E. 2012. Comparison of phenotypic methods and yield contributions of quantitative trait loci for partial resistance to *Phytophthora sojae* in soybean. Crop Sci. 52:609-622
[4] Dorrance, A., Berry, S., Anderson, T., and Meharg, C., 2008. Isolation, storage, pathotype characterization, and evaluation of resistance for *Phytophthora sojae* in soybean. Plant Health. Prog.doi.10.1094/PHP-2008-0118-01-DG.

Acknowledgements

Results

Root rot score is quantitatively distributed & skewed right. **Fig. 2** shows the excess of lines with root rot scores < 2 for inoculation with isolate C2S1 in the first set of inoculations. This indicates possible race-specific resistance to C2S1. Lines with low root rot scores were labeled as "Group 2" and inoculated with a different isolate in the second set of inoculations.

TABLE 1: Pearson's correlation between BLUP values.

	Root Rot Score	Plant Height	Root Weight	Shoot Weight
Root Rot Score		<0.0001 (1) <0.0001 (2)	<0.0001 (1) <0.0001 (2)	<0.0001 (1) <0.0001 (2)
Plant Height	-0.26 (1) -0.42 (2)		<0.0001 (1) <0.0001 (2)	<0.0001 (1) <0.0001 (2)
Root Weight	-0.46 (1) -0.55 (2)	0.50 (1) 0.50 (2)		<0.0001 (1) <0.0001 (2)
Shoot Weight	-0.21 (1) -0.43 (2)	0.33 (1) 0.46 (2)	0.67 (1) 0.71 (2)	

Lower left: correlation coefficient. *Upper right*: significance of correlation (*p*-value).

The four traits are all significantly correlated with each other in **group 1** & **group 2**.

TABLE 2: Genetic variance of each trait.

	INOCULATED				NON-INOCULATED			
	Group 1 (C2S1 isolate)		Group2 (C2S1 & Henry isolates)		Group 1 (C2S1 isolate)		Group2 (C2S1 & Henry isolates)	
	H²*	Sig. of Genetic Variance (*p*-value)	H²	Sig. of Genetic Variance (*p*-value)	H²*	Sig. of Genetic Variance (*p*-value)	H²	Sig. of Genetic Variance (*p*-value)
Root Rot Score	0.23	<0.0001	0.52	<0.0001	0.27	<0.0001	0.2	0.0024
Plant Height	0.64	<0.0001	0.3	<0.0001	0.71	<0.0001	0.59	<0.0001
Root Weight	0.46	0.0047	0.35	<0.0001	0.63	<0.0001	0.53	<0.0001
Shoot Weight	0.56	<0.0001	0.5	<0.0001	0.66	<0.0001	0.6	<0.0001

Traits have moderate heritability & significant genetic variance for both inoculated and non-inoculated treatments. *H^2 = broad sense heritability =genetic variance/ [(genetic variance + (var(error)/Number of Reps)]

FIGURE 3: Box-plot of root rot score BLUP values for each population.

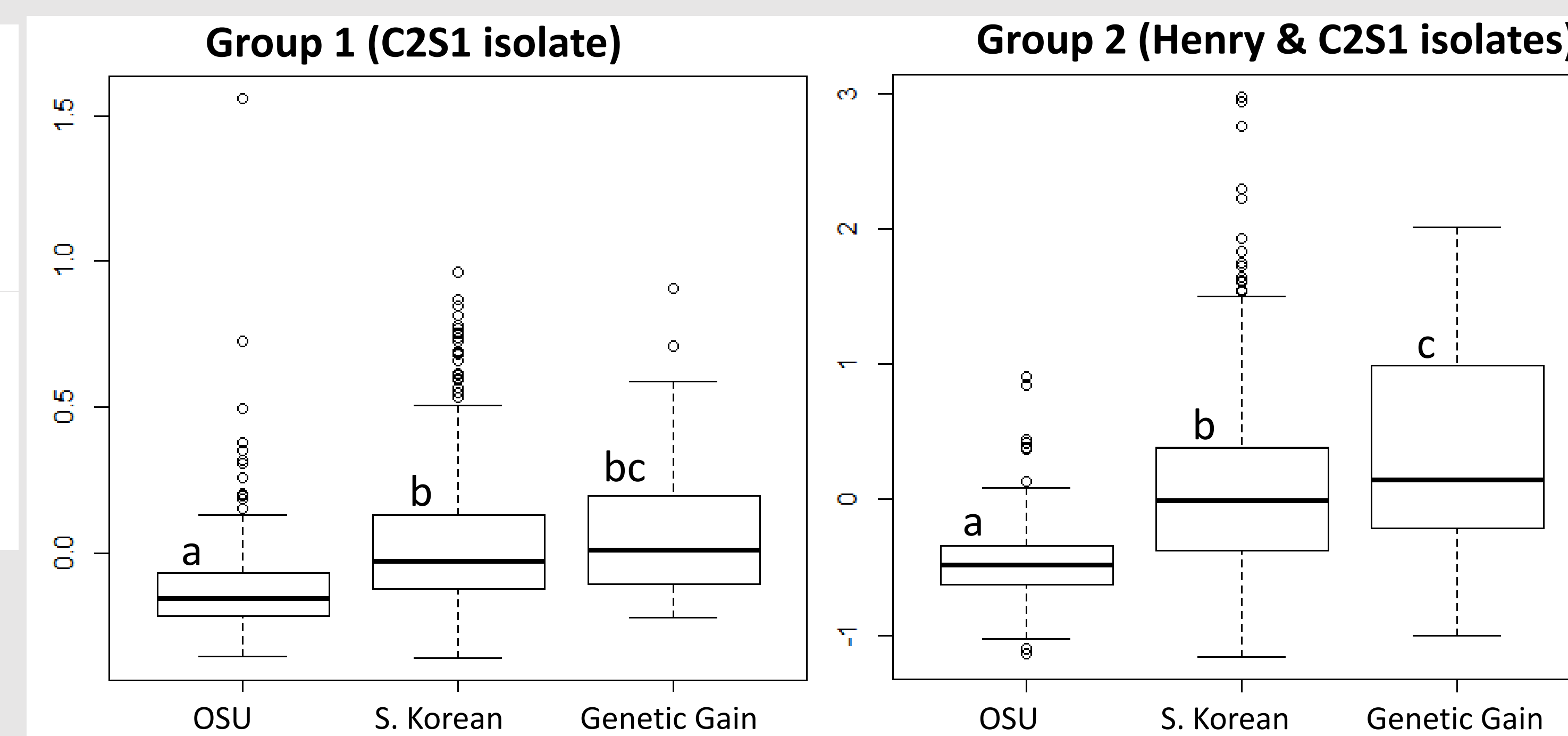OSU breeding lines have the lowest root rot scores (most resistant).

Group 1 (C2S1 isolate)   Group 2 (Henry & C2S1 isolates)

TABLE 3: Extreme resistant and susceptible soybean lines.

Group 1 (C2S1 isolate)				Group 2 (C2S1 & Henry isolates)			
Rank(of 1,044)*	Line	Root Rot Score	Population	Rank (of 736)	Line	Root Rot Score	Population
1	M09-W148	1.5	OSU	1	M10-W232	1.5	OSU
2	PI 424309 A	1.5	S. Korean	2	M11-W208	1.5	OSU
3	M11-M055	1.5	OSU	3	M11-W116	2	OSU
1042	PI 398867	9	S. Korean	734	PI 398310	9	S. Korean
1043	PI 398859	9	S. Korean	735	PI 424372	9	S. Korean
1044	M11-W118	9	OSU	736	PI 398604	9	S. Korean

High levels of resistance are found mainly in the OSU population with some in the South Korean population.

*Based on root rot score BLUP values

Conclusions & Future Work

o   High levels of partial resistance exist in OSU & South Korean germplasm.

o   Significant genetic variation and moderate levels of heritability indicate selection for improved resistance is feasible.

o   Phenotypic & genotypic data will be combined for association mapping and studies on genomic selection.