



Soybean PI 494182: A New Source of More Durable Resistance to Nematode Populations

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INTRODUCTION

Soybean cyst nematode (SCN; *Heterodera glycines* Ichinohe) is the most pervasive pest of soybean (*Glycine max* (L.) Merr.) in the United States and worldwide. In 2012, SCN reduced yields in the U.S. by an estimated \$1 billion. These losses have been contained at a stable level with the use of resistant cultivars but, over time, genetically heterogeneous nematode populations will continue to evolve and adapt to deployed resistance alleles. Currently, SCN resistance genes among cultivars in the U.S. are derived predominantly from PI 88788 or 'Peking'; both are black-seeded soybean lines originating from China. New resistance sources are desired to develop cultivars with more durable resistance. In this research, we have made crosses with PI 494182, a recent yellow-seeded introduction from Japan with resistance to HG Types 0 and 2.5.7. In a cluster analysis, PI 494182 was found to be genetically dissimilar from PI 88788 and Peking (Chen et al., 2006), indicating it could be a new genetic source for resistance. Progenies from four crosses are in development, with several selections undergoing yield testing in 2017.

MATERIALS & METHODS

- The following lines were crossed with PI 494182 in Isabela, Puerto Rico in 2010:
 1. '5002T' (Pantalone et al., 2004),
 2. 'Prohio' (Mian et al., 2008),
 3. LG05-2870-3-1 [(Sel.) from cross H2885 x LG00-6313; R. Nelson, personal communication, 2007].
- F₃ populations from the 5002T x PI 494182 and Prohio x PI 494182 were planted to the field in Jackson, TN in 2012.
- F₄ populations were screened with simple sequence repeat (SSR) marker Satt309, associated with SCN resistance gene *rhg1* on chromosome 18, beginning in 2013.
- Greenhouse bioassays for SCN resistance were conducted on selected F₇ and F₈ lines.
- The F₃ LG05-2870-3-1 (Sel.) x PI 494182 population was put in cold storage, and planted to the field in Jackson in 2016. This population is currently F₄, and has not undergone any selection for resistance.
- A population from a cross of 'Sylla' x PI 494182 were previously developed as part of a mapping study (Ebrahimi et al., 2005; Wang et al., 2006).



Figure 1. New resistance source PI 494182 growing in Isabela, PR in 2011.

RESULTS

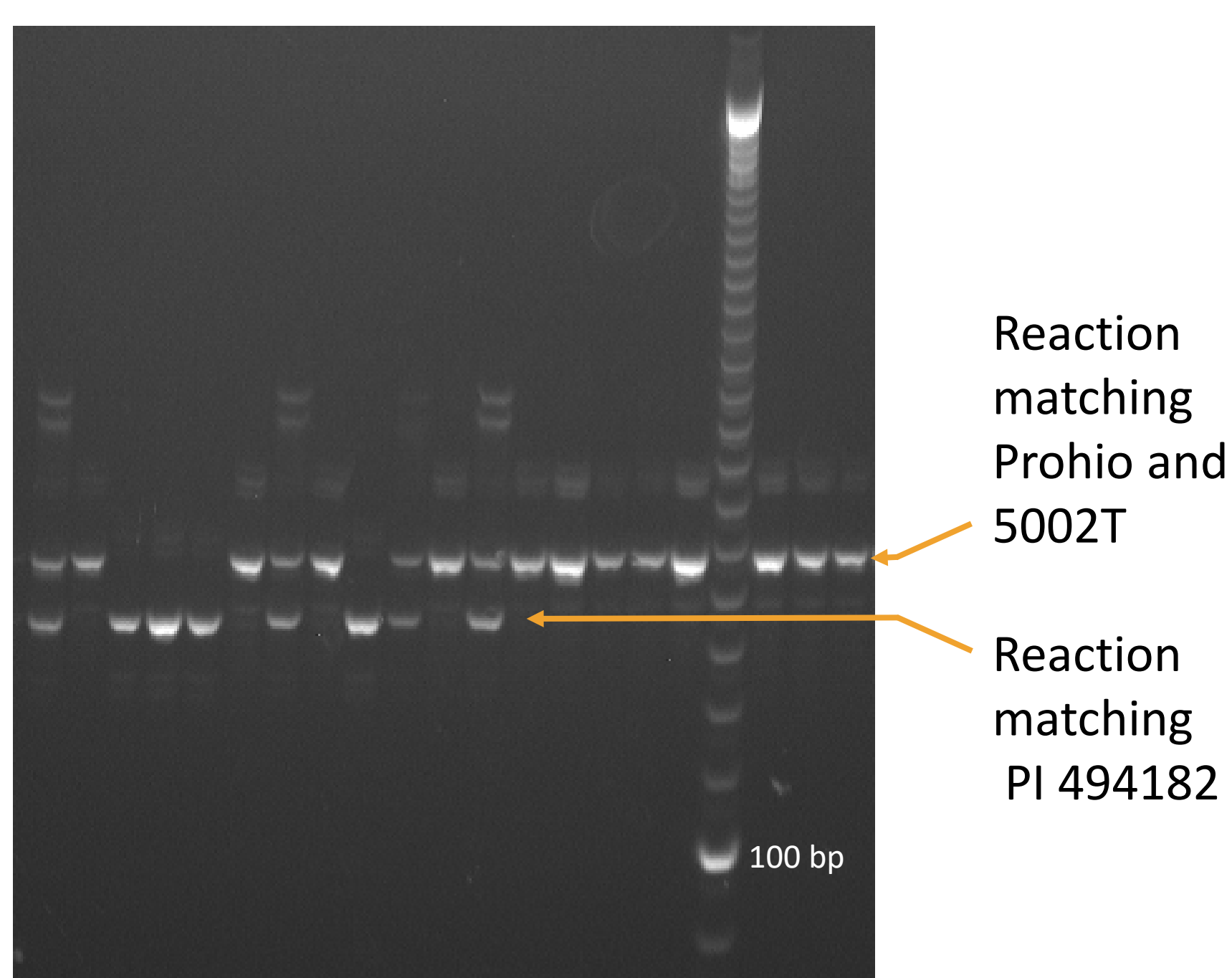


Figure 2. Initial screening with simple sequence repeat (SSR) marker Satt309 was performed on the 5002T x PI 494182 and Prohio x PI 494182 progenies in 2013. In this acrylamide gel photo, F_{2,4} lines are evaluated for their reaction. Lines that were homozygous or heterozygous for the PI 494182 allele at this locus were selected and advanced.



Figure 3. An F₁₇ selection of Sylla x PI 494182 (left) beside an F₈ selection of Prohio x PI 494182 (right) in Milan, TN in July 2017.



Figure 4. Numerous 4-bean pods are seen on this F₈ selection of Prohio x PI 494182 growing in Jackson, TN. This characteristic was observed among several lines at both the Jackson and Milan test sites in 2017.



Figure 5a. Dr. Prakash Arelli with one of the F₈ 5002T x PI 494182 lines in Milan in 2017. **Figure 5b.** The same line at maturity.



Figure 6. Lines in development range from early maturity group (MG) III to mid MG IV.

SCN Resistant Lines Confirmed by Greenhouse Bioassay

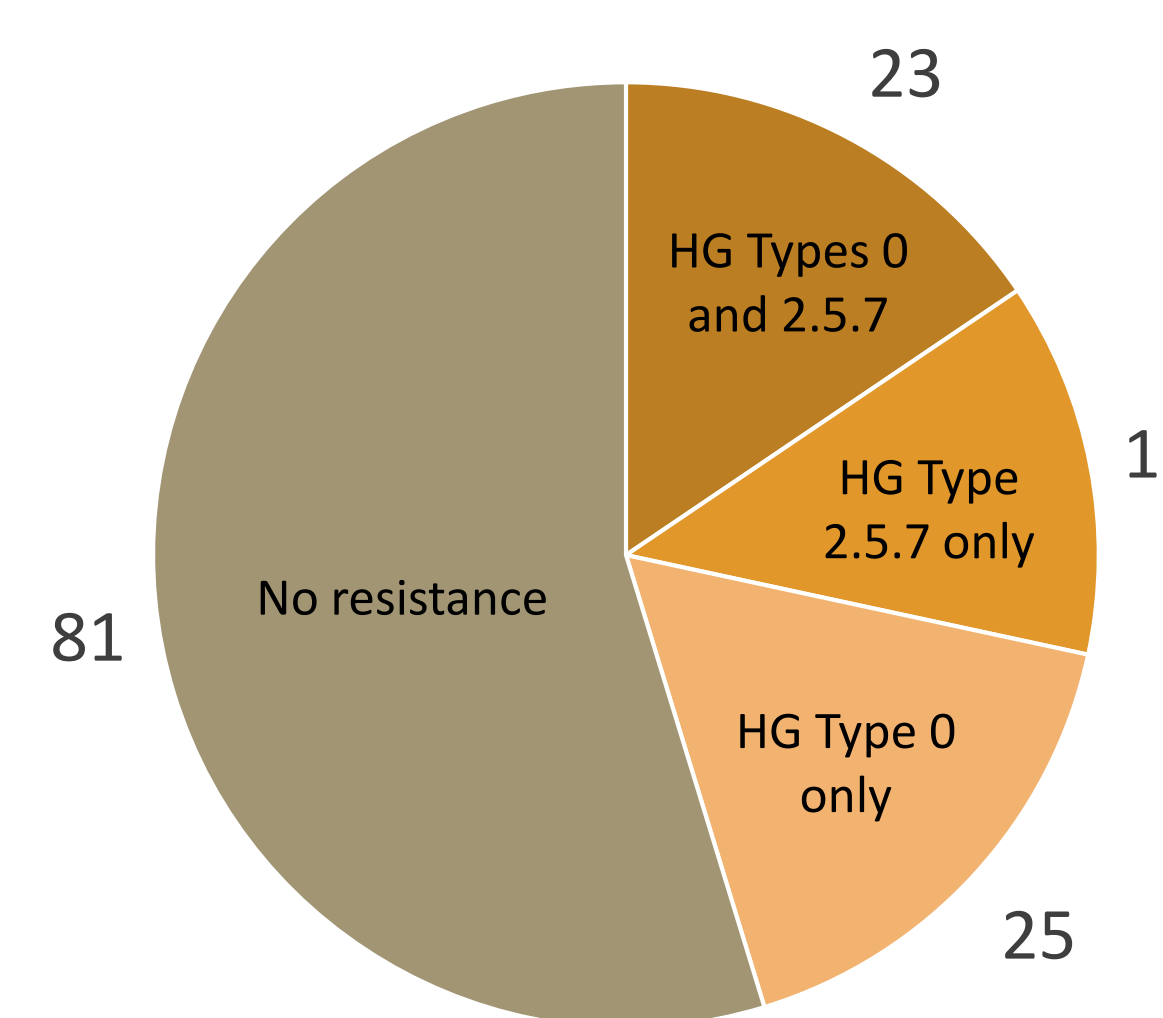


Figure 7. Of 148 unique lines screened in the greenhouse for HG Types 0 and 2.5.7, 67 (45%) have resistance or moderate resistance to one or both populations. The screened lines come from crosses of PI 494182 to: 5002T, Prohio, and Sylla.



Figure 8. Shattering has been a challenge in developing lines from crosses with PI 494182.

2017 Yield Testing

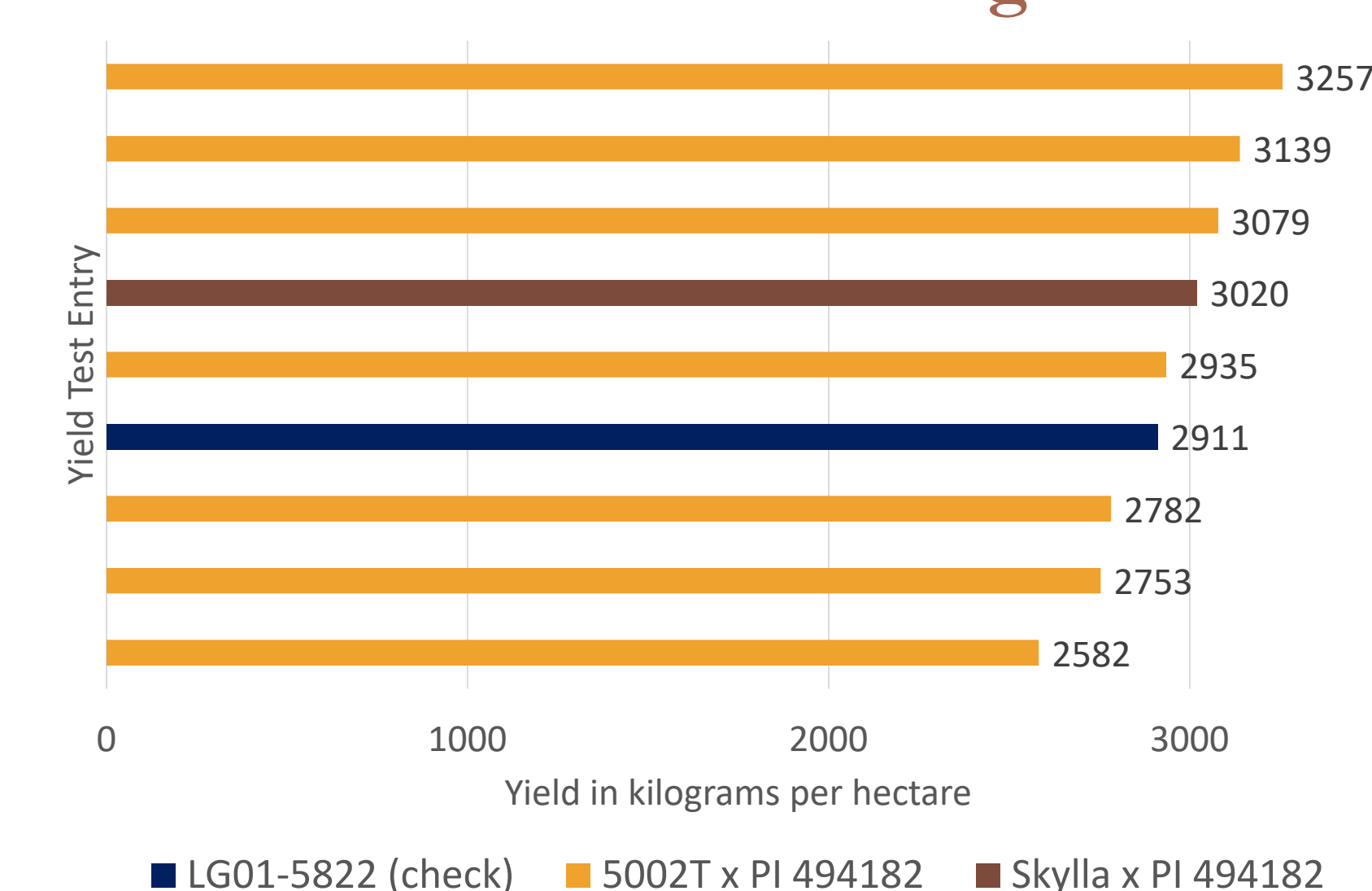


Figure 9. Of the top 9 yielding entries tested in Milan in 2017, 7 were from the cross of 5002T x PI 494182.



Figure 10. Seed of some of the 5002T x PI 494182 lines in development.

DISCUSSION

Selections continue to be made to identify resistant lines with desirable agronomic traits. Although the Sylla x PI 494182 population is the most advanced, resistant lines continue to segregate for agronomic traits. In 2017 yield testing, lines from the 5002T x PI 494182 population stand out as having the best combination of resistance and agronomic traits. Selections continue to be made and advanced among all four populations. Development of desirable agronomic lines from this source will offer an alternate genetic source of resistance for areas where nematode populations have already overcome the resistance of PI 88788 and Peking.

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