PERFORMANCE SCREENING RESULTS FOR BARBREN-713 DERIVED LINES

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Introduction

The germplasm line BARBREN-713 was publicly released through a combined effort of Texas A&M and USDA-ARS in search for a high level of genetic resistance to reniform nematode (RN). Two genes associated with resistance were present in the line, named *Ren*^{barb2} and *Ren*^{barb3} (Gutie ´rrez et al., 2011).

Methods

A breeding program at Auburn University took advantage of the release and developed population 148 by crossing BARBREN-713 with elite breeding line AU3202. 100 F_2 plants were genotyped at the *Ren*^{barb2} locus using closely linked SSR marker BNL3279. $F_{2:3}$ lines were then derived from those plants. There was not enough time to overcome difficulties associated with genotyping *Ren*^{barb3}, so further experiments were conducted on *Ren*^{barb2} only.

Forty lines from population 148 were chosen, 20 of which were homozygous positive at *Ren*^{barb2} locus (res group) and 20 were homozygous negative (sus group). $F_{2:5}$ seeds from these lines, along with seeds of SG747 (commercial cultivar susceptible to RN), LONREN 21-4 (germplasm line highly resistant to RN), AU3202 (susceptible parent), BARBREN-713 (resistant parent), and E103-123 (line derived from LONREN with exceptional fiber strength), were included in the greenhouse and microplot trials, and field study.

Previously established protocols for inoculation and nematode population development (Weaver et al., 2007) were used for the greenhouse and microplot trials. Two fields at Tennessee Valley Research and Extension Center (TVREC) of Auburn University were used in the field study. One was RN free, and the other was infested with RN. A random complete block design was used for the experiments, and each field was divided into 5 blocks, each with 45 lines randomized and planted as single row plots.

Nematode egg production (count per gram of root) data were gathered for all three tests. A 25-boll sample were taken and ginned. Bolls were also harvested for each plot in the field separately to determine seed cotton yield. Lint yield was calculated from multiplying seed cotton yield with turnout-ratio obtained from ginning. Due to time constraints, fiber quality data was not available at the time of the conference. All data was analyzed and plotted with the R package version 3.1.2. General linear model was constructed and analyzed with the ANOVA test.

Results

With regard to nematode egg count per gram of root, all three tests consistently showed that the res group had significantly lower nematode reproduction than the sus group ($p<0.001$). On average, the res group egg count was as low with only 30% of the egg count of the sus group. This was reflected in the field performance comparison of the two groups (Figure 1), as the res group yielded 1074 kg/ha lint on average in the RN infested field, and was 22% higher than the mean of the sus group. On the other hand, the res group lagged behind the sus group in the non-nematode infested field. The res group produced 1394 kg/ha lint on average in the absence of reniform nematode, and the sus group produced 1553 kg/ha lint on average. There was a 10% difference.

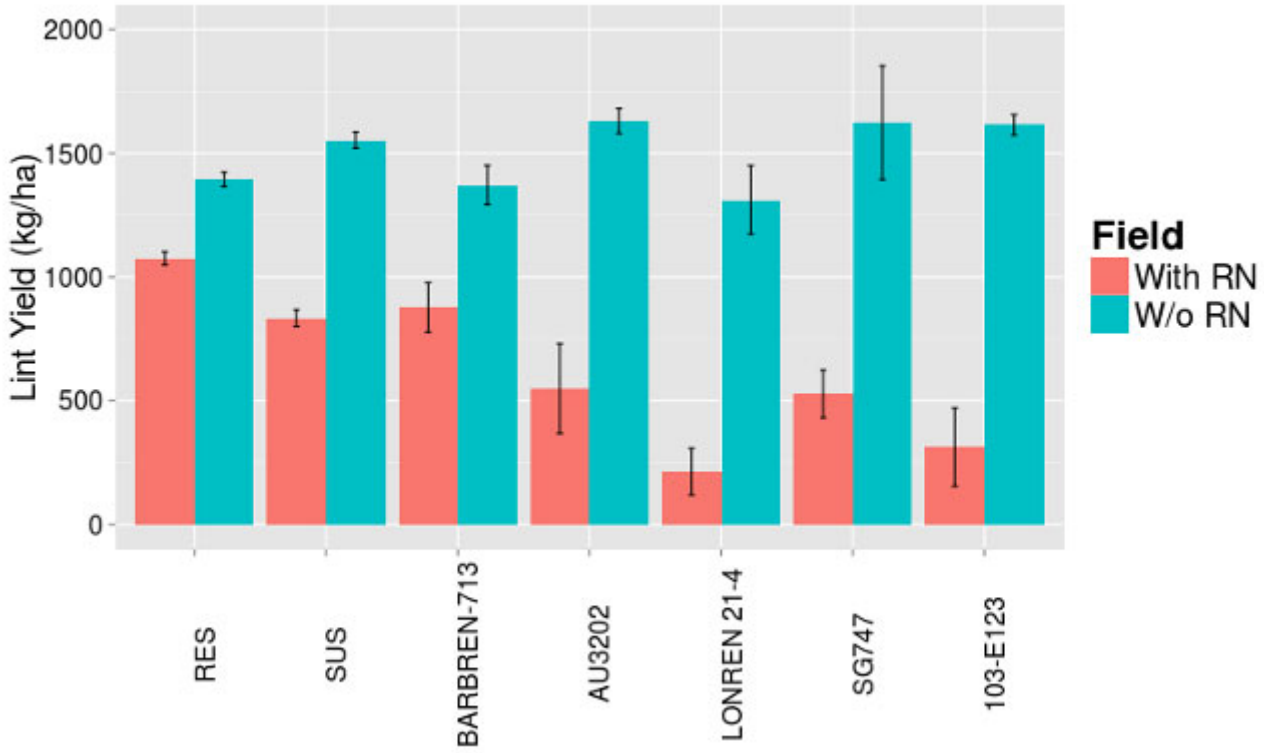

Figure 1. Lint yield of res group, sus group and controls in both RN infested and no RN field.

Thus, we conclude that the QTL *Ren*^{barb2} does contribute significant resistance to reniform nematode, with the associated resistance leading to less yield loss under high nematode stress. However, *Ren*^{barb2} might introduce a small yield drag in optimal conditions compared to lines without the QTL.

References

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