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Introduction

- Over 80% of the United States gene pool originates from less than a dozen soybean introductions, implying that the genetic base is too narrow for sustained yield advances in commercial soybean [*Glycine max* (L.) Merr.] (Gizlice et al., 1993).
- Exotic germplasm, such as the wild progenitor of soybean, *Glycine soja* [Sieb. & Zucc.], may be an excellent source of agronomic genes and genetic variability (Lee et al., 2008) and might have yield genes that could increase the yield of cultivated varieties (Delheimer, 2012; Li et al., 2008).
- Hybrid vigor could be a signal to detect yield alleles in wild soybean. Measuring the performance of F₂ bulk populations created from *max-soja* derived lines crossed back to the original *G. max* parent (the only new alleles contributed to the F₂ hybrids from *G. soja*) could be a method to detect yield genes from wild soybean (Burton and Brownie, 2006).
- Objectives:** Examine heterosis in F₂ bulks derived from breeding lines which are themselves developed from a cross between *Glycine max* and *Glycine soja*; assess whether heterosis indicates the existence of yield genes from wild soybean; and ascertain the possibility of predicting heterosis using genetic markers.

Materials and Methods

Selection of *G. max* x *G. soja* Parental Stock



- Dr. Jacob Delheimer and Dr. Thomas Carter (USDA-ARS) at NCSU developed upright breeding lines from a single cross between *G. max* 'N7103' and *G. soja* PI 366122 using mega population sizes and intense selection.
- 19 maturity group VII breeding lines from that study were chosen for the present work. Lines were selected based on seed yield and resistance to bacterial pustule.
- Percent *G. soja* alleles in these *G. max* x *G. soja* breeding lines ranged from 17 to 40%, based on 558 single nucleotide polymorphism (SNP) markers.

Development of F₂ Hybrids

19 *max* x *soja*-derived breeding lines, F_{4:7} x N7103 plants

19 F₁ combinations

19 F₂ bulks

- Crosses made between 19 N7103 x *G. soja* breeding lines and N7103 (original *G. max* parent) in Clayton, North Carolina, summer 2011
- Total of 798 F₁ seeds, 42 F₁ seeds from each cross, planted in Puerto Rico winter nursery, winter 2011-2012
- Yield trials in North Carolina and Georgia (4 locations with 3 replications per location), summer 2012

Analysis of Heterosis & SNP Markers

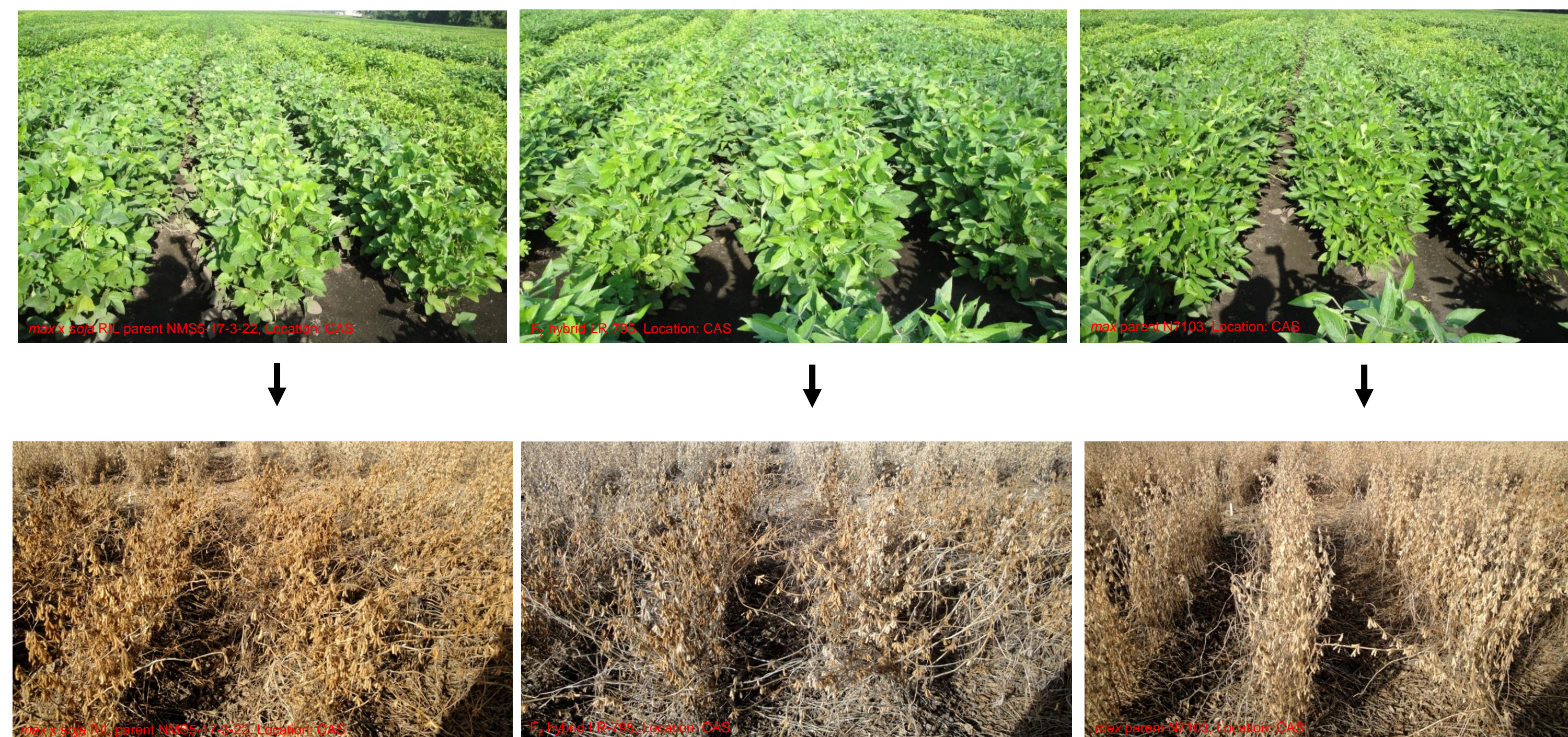
- LSMEANS were obtained for seed yield.
- Mid-parent heterosis was calculated by comparing each F₂ bulk population's mean yield with the respective mid-parent yield across all locations.
- Stepwise regression analysis was used to identify genomic regions across all 558 SNP markers that might influence mid-parent heterosis and seed yield.

Results

2012 Yield Trials

- Each parental line was planted in a subplot next to its respective F₂ progeny in a three or four row standard yield plot.
- A nested split-plot field design was used at all locations.

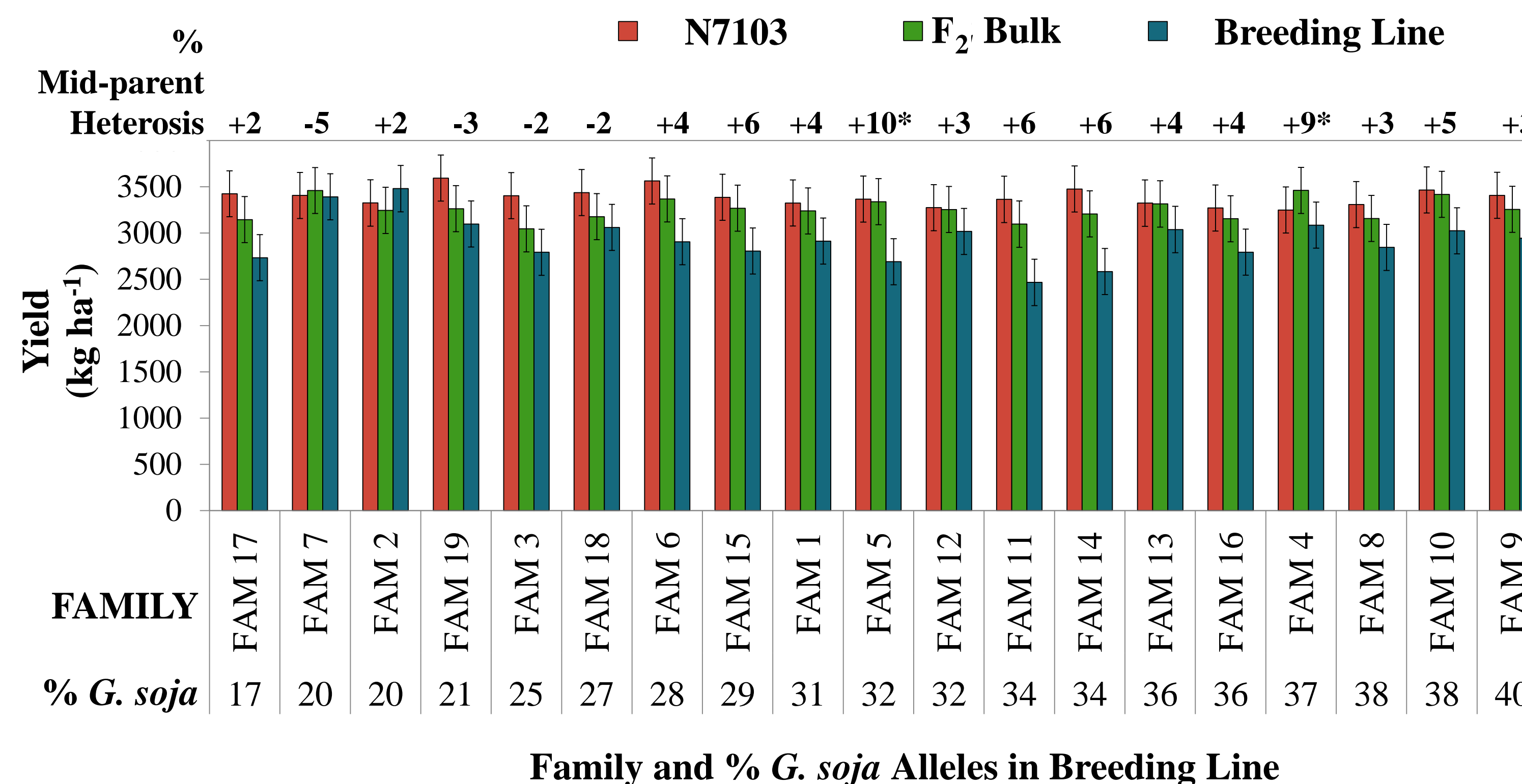
G. max x *G. soja* parent F₂ bulk N7103 parent



- Seed yield mid-parent heterosis ranged from -2% to +10%. The mean percent mid-parent heterosis was +3%.
- Significant mid-parent heterosis was observed in two families (Family 5 & 4; Figure 1).

Figure 1.) Mean seed yield of parents and F₂ hybrids. Percent mid-parent heterosis across all hybrids in 2012, in replicated tests averaged across locations.

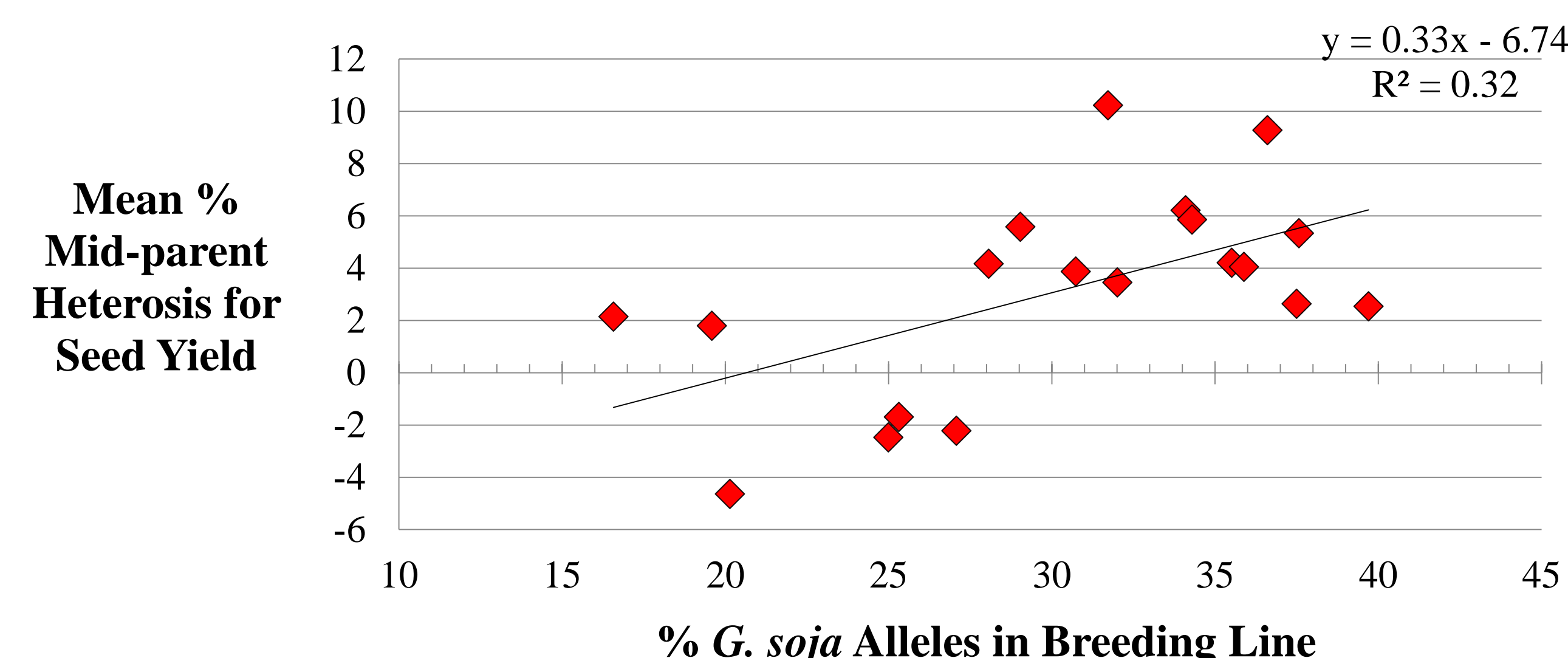
* P-value ≤ 0.05



More *G. soja* Alleles, More Heterosis

- The percent *G. soja* alleles from each parental breeding line could be used as a predictor of percent heterosis in theory. This study shows a moderate and significant correlation ($r = 0.57$) between the percent of *G. soja* alleles and percent heterosis (Figure 2).

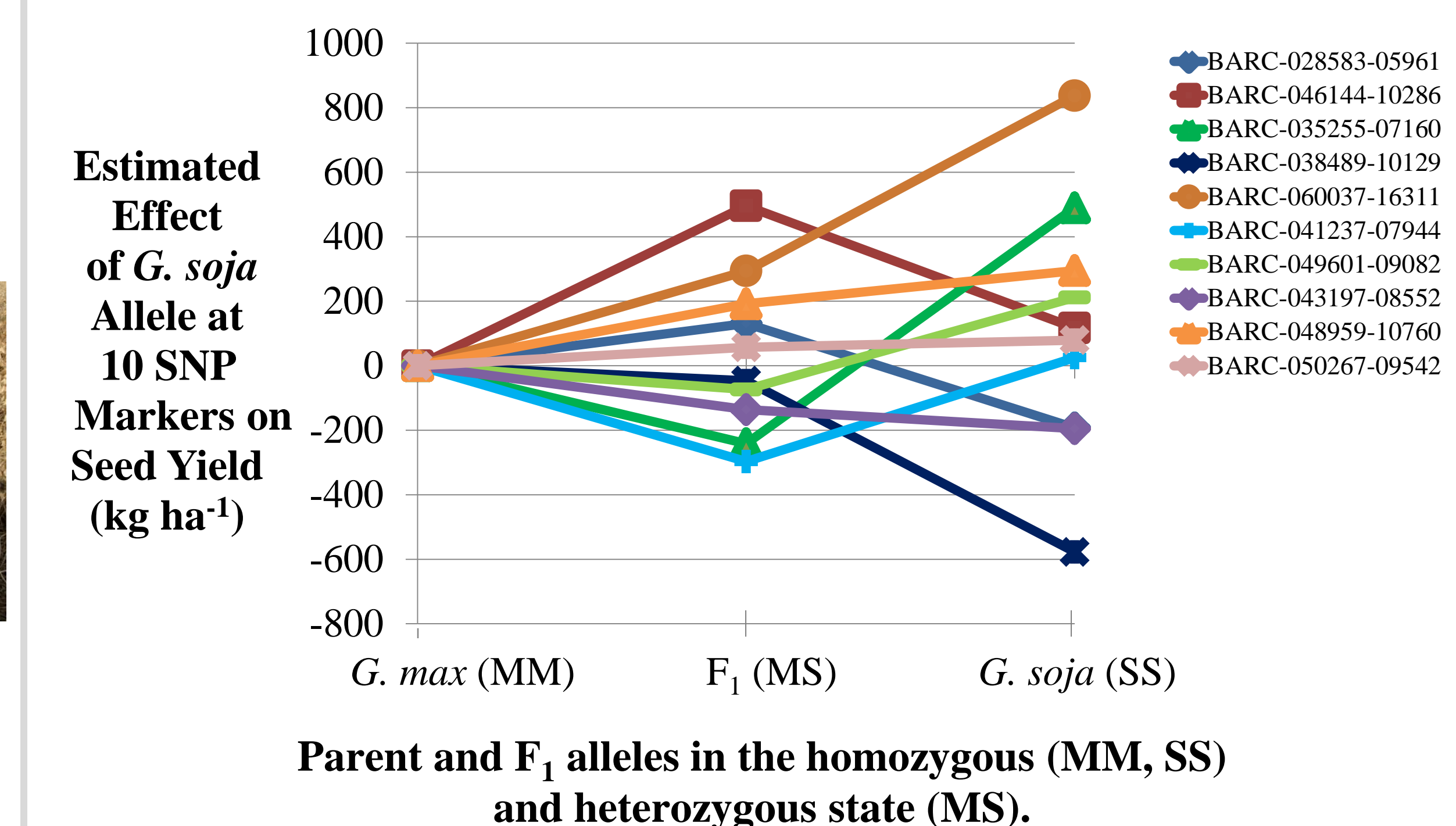
Figure 2.) Mean % mid-parent heterosis of each F₂ bulk vs. % *G. soja* alleles in breeding lines across all locations.



G. soja Gene Action

- 15 SNP markers from the *G. soja* parent were found to significantly affect mid-parent heterosis and seed yield.
- The *G. soja* alleles showed positive and negative impact on mid-parent heterosis and on seed yield in the hybrid progeny and inbred lines (Figure 3).

Figure 3.) 10 of 15 SNP markers identified from *G. soja* to significantly affect seed yield and estimated effects in parent and F₁ progeny.



Conclusions & Agricultural Impact

- The yield trials suggest hybrid vigor exists. This evidence of heterosis supports the hypothesis that yield genes might exist from *G. soja*.
- Mid-parent heterosis and the positive gene action from *G. soja* could indicate that dominance from unique *G. soja* alleles is causing the increased yield in the F₂. This dominance could be fixed in inbred line development and result in higher yielding inbred cultivars.
- Positive heterotic effects modeled from the *G. soja* alleles suggest that not all *G. soja* effects are masked by *G. max* alleles in hybrid progeny. These positive SNP effects further support the hypothesis that yield genes might exist from *G. soja*.
- We suggest that soybean breeders may want to use the results from this study to direct further research in incorporating new yield genes from wild soybean into their breeding programs.
- In the future, researchers and farmers could produce soybeans that are higher yielding and more genetically diverse than present soybean cultivars.

Acknowledgements

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