Identification of putative QTL that underlie yield in interspecific soybean crosses. (C01-diers131651-Poster)

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Abstract:

Glycine soja, the wild progenitor of soybean, is a potential source of useful genetic variation in soybean improvement. The objective of our study was to map quantitative trait loci (QTL) from G. soja that could improve the crop. The mapping was done with a set of five populations of BC2F4-derived lines developed using a G. max cultivar as a recurrent parent and a G. soja PI as the donor parent. The populations were evaluated in field tests in two locations and years for yield and other agronomic traits and seed composition. The populations were analyzed with simple sequence repeat markers and QTL were mapped through composite interval mapping using a 5% experimentwise error rate. There was significant genetic variability in the population for all measured traits. Across the populations, we mapped five QTL controlling seed yield, six controlling plant height, and protein and oil content, four controlling date of maturity, and one controlling lodging. The QTL alleles for increased yield were from the soybean parent and the allele for greater lodging was from the G. soja parent. The positive QTL alleles for the remaining traits came from both the soybean and G. soja parent.

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