Confirmation of Quantitative Trait Loci (QTL) controlling Hybrid Seed Yield in Multiple Backgrounds of Spring Canola. (C07-quijada161201-Poster)

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Abstract:

After QTL discovery researchers are then faced with the arduous task of QTL confirmation. Here, we describe a novel approach to confirm two hybrid seed yield QTL that were identified in an Inbred Backcross Line (IBL) population developed to study the effect of winter germplasm introgression into spring canola. The QTL were located in linkage groups N3 and N14. The alleles from the donor parent contributed positively to seed yield in each QTL. In order to confirm these QTL, one IBL segregating for markers flanking these two genomic regions was selfed and crossed to three spring canola lines with different genetic backgrounds. Doubled haploid (DH) lines from each F1 were developed by microspore culture. The DH lines of each population were genotyped with markers flanking the QTL. Based on their genotypes they were grouped into four classes. For each population fifteen lines of each class were bulked (3 bulks of 5 lines) and crossed to two testers. Bulked hybrid seeds of each class were planted in a randomized block design with a split-split plot array and 12 replicates in one location. This refined experiment allowed us to confirm the QTL located in linkage group N3.

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