

Mapping of QTLs for Seed Quality Traits in an Interspecific Soybean Population. (C07-rajcan161349-Oral)

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Abstract:

Seed quality traits of soybean (*Glycine max* (L.) Merr.) can be modified for industrial and food markets using the natural genetic diversity found in wild soybean (*Glycine soja* Sieb. et Zucc.). The objective of this study was to identify molecular markers for seed quality traits that could be used to alter the protein, oil and linolenic acid levels in soybean breeding programs. An interspecific population of 286 F₂ plants was grown in Woodstock, ON, and analyzed for seed protein, oil and fatty acid content. Quantitative trait loci (QTL) were localized on a genetic linkage map that was constructed using 150 simple sequence repeat (SSR) markers. A major QTL for protein was confirmed on linkage group (LG) I and accounted for 18.3 % of the observed phenotypic variance. An additional QTL that explained 10.1 % of the protein variance was localized on LG L. To our knowledge, the latter QTL represents a new protein locus from *G. soja*. A single QTL for oil on LG I explained 20.4 % of the observed variance. Two major QTLs for linolenic acid were identified on LG C2 and accounted for 15.7 % and 27.6 % of the variance, respectively. The QTLs will be confirmed on seeds advanced to the F₄ generation using single seed descent.

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