Molecular Marker Mapping of Genes Controlling Isoflavone Levels in Soybean Seed. (C07-rajcan151516-Oral)

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Abstract:

Soybean isoflavones have been shown to reduce risks of several major diseases in humans. Conversely, in some studies they have also been associated with negative effects on babies. Breeding soybeans for high or low levels of isoflavones is difficult because of strong influence by the environment and the high cost of isoflavone analyses. The objective of this study is to develop molecular markers as a cost-effective breeding strategy for developing high and low isoflavone soybean varieties. A total of 196 F4 recombinant inbred lines (RIL) from the biparental cross RCAT Angora x AC756 were grown in 2000 at two locations (Harrow and Ridgetown, Ontario). Four-gram samples of seed from each F5 RIL were analyzed for daidzein, genistein and glycitein content. Distribution patterns for the three isoflavones suggested that the traits were quantitative with possibly several major genes involved. Approximately 70 polymorphic SSR markers are currently being used to screen the RIL population. Linkage maps will be used to develop molecular markers tightly linked to quantitative trait loci (QTL) associated with isoflavone levels in soybean seeds, which can be used in marker-assisted selection.

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