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Application of comparative genomics in development of molecular markers tightly linked to the virus resistance gene *Rsv4* in soybean

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Objectives

The *Rsv4* gene confers resistance to all the known strain groups of SMV in soybean [*Glycine max* (L.) Merr.]. The objective of this study was to construct a fine genetic map near *Rsv4*.

Materials and Methods

1. Materials

* An F₂ population of V94-5252 x Sowon

2. Methods

* Sequences of *Rsv4*-linked markers derived from expressed sequence tags (ESTs) showed high similarity with gene sequences of a transformation-competent artificial chromosome (TAC) clone of the model legume *Lotus japonicus*. This information was integrated with a comparative genomics approach, utilizing *Lotus* genome sequence information.

Results and Discussion

A marker developed from one of soybean homologous ESTs of *Lotus* genes within a TAC was mapped to the other side of the *Rsv4* gene. The results suggested that the *Rsv4* soybean chromosomal region is microsyntenic with the *Lotus* chromosomal region. The identification of the microsyntenic region facilitated the development of additional 3 markers. Several other markers developed in this study were mapped to putative homoeologous or duplicated chromosomal regions in soybean. This targeted comparative mapping serves to provide a foundation for marker-assisted selection and cloning of the *Rsv4* gene.

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