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Marker-assisted backcrossing for introgression of SMV resistance genes into soybean cultivars

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Objectives

The most effective and reliable method to control *Soybean mosaic virus* (SMV) disease is the utilization of resistant genes, *Rsv1*, *Rsv3* and *Rsv4*. In order to maximize the gene effects to SMV, pyramiding multiple resistance genes into a cultivar is a good method. The objectives of this study were to construct near-isogenic lines containing SMV resistance gene(s) using marker-assisted introgression of resistance genes, *Rsv1*, *Rsv3* and *Rsv4*.

Materials and Methods

1. Materials

- * Donor lines: PI96983 (*Rsv1*), L29 (*Rsv3*), V94-5152 (*Rsv4*)
- * Recurrent lines: Hwangkeumkong, Taekwangkong, Sowonkong

2. Methods

- * Breeding, Marker-assisted selection

Results and Discussion

One line for *Rsv1*, five lines for *Rsv3*, and seven lines for *Rsv4* were successfully developed as near-isogenic lines. Based on co-dominant molecular marker data from BC₁F₁ to BC₄F₁ generation, modified two-step approaches were applied efficiently in the aspect of reducing gene-drag and fast recovery of recurrent parent genome: simultaneous use of foreground and background selection markers on carrier chromosome at BC₁F₁ or BC₂F₁ generation.

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