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Mapping QTL associated with resistance to bacterial pustule, bud blight, and soybean mosaic virus in soybean

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Objectives

The objective of this study was to use simple sequence repeat (SSR) markers to map genes associated with soybean resistance to bacterial pustule (*Xanthomonas campestris* pv.*glycine*; BP), bud blight (genus *Nepovirus*; BB), and soybean mosaic virus (genus *Potyvirus*; SMV).

Materials and Methods

1. Material

A total of 240 F_6-derived lines from a cross of Benning x PI 416937

2. Methods:

DNA from each of the 240 lines and the two parents was extracted from the first trifoliate leaves using the modified CTAB procedure. PCR reaction was performed in a dual 384-well or a 96-well GeneAmp PCR System 9700. Data were collected on 240 polymorphic SSR markers spanning the soybean genome. Separation of the sample was on a 4.8 % polyacrylamide gel using ABI PRISM 377 DNA Sequencer, followed by fragment analysis with GeneScan and scoring with Genotyper software.

Results and Discussion

A marker on linkage group (LG) D2 was associated with BP resistance (R^2 = 39%), and a marker on LG F was associated with resistance to BB (R^2 = 41%) and SMV (R^2 = 19%). These markers reside in the same genomic regions previously found to be associated with resistance to these diseases in the original mapping populations. The QTL for BP and BB inherited their resistance alleles from Benning, while the resistance allele for SMV was from PI 416937. Multiple regression analysis and interval mapping confirmed genetic attributes and genomic locations of the QTL for BP, BB, and SMV, which had LOD=26, 27, and 11, respectively. The confirmation of these QTL should facilitate selection for resistance to these diseases.

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