Resistance genes analogs (RGAs) co-locclize with reistance gene/QTL(s) loci in common bean (Phaseolus vulgaris L.). (C01-budak230640-Poster)

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Abstract:

Resistance gene containing nucleotide binding site (NBS)-leucine rich repeats (LRR) are the most prevalent types of resistance (R) genes in plants. The objective of this study was to develop R-gene specific, PCR based markers for common bean (Phaseolus vulgaris L). A unique and simple method was used to identify and confirm R-gene specific markers without the use of cloning and sequencing. Twenty degenerate primers were designed from the most common peptide sequences of kinase-1a and hydrophobic domains (HD). Known NBS-LRR type R genes and EST databases were used to determine the most common peptide sequences conserved among R genes for the two domains. Sixty-six of the 100 primer combinations tested in a common bean recombinant inbred line (RIL) population, BAT93 x Jalo EEP558, yielded polymorphisms from which 32 RGA markers were mapped. They mapped on all but the B4 linkage group, with a strong tendency for clustering. Nineteen of the 32 RGA markers had sizes larger than 500 bp, which indicates that these are functional genes. The remaining 13 markers are probably incomplete sequences not related to avirulence as the sizes were less than 500 bp. All 32 markers mapped close to the known R genes on B11, and to QTLs for R on B2, B6, B8, B10, and B11.

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