



Mapping of AFLP loci linked to tolerance to cowpea golden mosaic virus

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ABSTRACT. AFLP markers combined with the bulk segregant analysis methodology was used for the identification of molecular markers associated with the cowpea golden mosaic virus (CGMV) resistance gene in 286 F₂ cowpea plants derived from the cross IT97K-499-35 x Canapu T16. Segregation data in the F₂ population demonstrated that tolerance to CGMV is controlled by a single dominant gene. Among the 196 combinations of AFLP primers tested, which generated approximately 3800 amplicons, three markers linked to the CGMV resistance gene were identified: E.AAC/M.CCC₅₁₅ at 4.3 cM, E.AGG/M.CTT₂₈₀ at 14.2 cM and E.AAA/M.CAG₃₅₂ at 16.8 cM, with 50.4, 24.4, and 28.7 LOD scores, respectively; the former two markers flank the CGMV loci. These markers could be used for the development of 'sequence characterized amplified region' type markers or for greater saturation of this region, to increase the precision of assisted selection for the development of cowpea strains tolerant to CGMV.

Key words: *Vigna unguiculata*; Bulk segregant analysis; Genetic mapping