

Title Mapping wound-response genes involved in post-harvest physiological deterioration (PPD) of cassava (*Manihot esculenta* Crantz)

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Abstract

The genome locations of the wound-response genes that were expressed during the post-harvest physiological deterioration (PPD) of cassava, such as phenylalanine ammonia lyase, β -1,3 glucanase, hydroxyl proline rich glycoprotein, catalase, 1-aminocyclopropane 1-carboxylate, cysteine protease inhibitor, aspartic protease, a partial cDNA for serine/threonine protein kinase and peroxidase, have been identified on the framework molecular genetic map of cassava. Also, molecular markers linked to putative quantitative trait loci (QTLs) influencing PPD of cassava were mapped using an F_1 mapping population derived from elite parental lines (TMS 30572 \times cm 2177-2). A molecular linkage map previously constructed based on the segregation of 240 RFLP, 100 RAPD, 85 microsatellite and five isoenzyme markers on 144 F_1 individuals was used for the QTL mapping. A set of 10 molecular markers with a significant association with putative QTLs for PPD were identified based on probability values < 0.005 in order to minimize the detection of false positives. Based on single-marker regression, eight putative QTLs located on the linkage groups G, P, L, U, and X of the female-derived framework map were found to explain between 5–12% of the phenotypic variance of the PPD. In the male-derived framework map, two putative QTLs on linkage groups C and L explained 13% and 11% of this variance, respectively. This study thus identified the major genome regions of cassava related to physiological post-harvest deterioration, thereby providing tools for the identification of gene(s) controlling this trait.