MOLECULAR STUDIES OF BETA-CAROTENE CONTENT FROM MULTIPLE SOURCES IN CASSAVA

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The objective of this study was to identify simple sequence repeat (SSR) markers associated with beta carotene content in cassava through the bulked segregant analysis (BSA) of F_1 and S_1 families segregating for beta-carotene content. Three families, namely GM708, GM 734, and CM 9816 were selected for further study. In addition, eleven S_1 families, obtained from self-pollinating high, medium, and low genotypes from the three selected F_1 families, were also chosen for validation of associations between SSR markers and high carotenoids and/or β-carotene content. The bulks and parents were evaluated with 140 SSR markers that have earlier been selected from the genetic map of cassava to cover the entire cassava genome at a marker density of one marker every 10-20cM. To identify association between molecular markers associated with total carotenoids (TCC) or β-carotene (TBC) contents after the BSA, a correlation and simple regression analysis was conducted, considering the marker genotypic classes as independent variable and content of total carotenes as dependent variable. Markers that explain large amounts of phenotypic variation for total carotenes were evaluated in the S_1 families for further marker validations. Frequency distribution of TCC in the three families tends to follow normal distribution, suggesting that several genes control TCC. Markers polymorphic were evaluated in the individuals of the bulks and those that showed consistency with results from analysis of the bulks were analyzed in all progenies. Single marker analysis, by simple regression, of association between the polymorphic markers and total carotene content revealed a number of major quantitative trait loci (QTL) controlled beta-carotene content in cassava. The QTLs explained up to 26% of phenotypic variation. Five QTLs were identified on linkage group D for all of the 3 families, suggesting major QTLs that go across different sources of enhanced beta-carotene content reside on this linkage group. Families GM708 and CM9816 also had QTLs on linkage group G. Six other QTLs were unique amongst the 3 families. Single marker analysis, by simple regression, of association between the polymorphic markers and total carotene content in families S_1 confirmed the existence of major quantitative trait loci (QTL) controlled beta-carotene content in cassava. The QTLs explained up to 32% of phenotypic variation.

Keywords: *Manihot esculenta*, plant breeding, molecular markers.