QTL ANALYSES REVEAL CLUSTERED LOCI FOR ACCUMULATION OF MAJOR CAROTENES AND LYCOPENE LOCI IN CARROT ROOTS

Santos, CAF¹; Simon, PW² ¹Embrapa Semi-Arido, Caixa Postal 23. 56300-000. Petrolina, PE. ²USDA-ARS and Department of Horticulture, 1575 Linden Drive, University of Wisconsin, Madison, WI 53706 casantos@cpatsa.embrapa.br Palavras-chave: Related enzymes, linked pathway genes

QTLs associated with carotenoid pathway products, including lycopene and the provitamin A carotenes, ?- and ?-carotene, were investigated in two unrelated F₂ carrot populations: orange cultivated B493 x white wild QAL (Population 1) and orange cultivated Brasilia x dark orange cultivated HCM (Population 2). The mapping populations of 160 and 180 individuals, respectively, were analyzed with single marker and interval mapping statistical approaches, considering coupling linkage maps for each parent. Single markers were selected for further analysis based on the Wilcoxon sum-rank nonparametric test. Interval mapping performed with Population 2 detected four, eight, three, one and five putative QTLs associated with accumulation of ?-carotene, a-carotene, ß-carotene, lycopene and phytoene, respectively. Among these, major QTLs explained 13.0%, 10.2%, 13.0%, 7.2% and 10.2% of total phenotypic variation. In Population 1 single marker analysis identified loci explaining up to 13.8%, 6.8%, 19.3%, 5.7%, and 17.5% of total phenotypic variation for these same respective carotenoids. Overall analysis demonstrated clustering of these QTLs associated with the carotenoid pathway: AFLP loci AACCAT178-Q and AAGCAG233-Q, in the linkage group five, explained 17.8%, 22.8% and 23.5% of total phenotypic variation of ?-carotene, phytoene and ?-carotene in Population 1. Two major clusters of QTLs, with LOD scores greater than 1.8, mapped to intervals not greater than 2 cM for ?-carotene ?-carotene, ?-carotene and lycopene in linkage group three, and ?-carotene and phytoene in linkage group nine which explained 3.7% to 13.0% of each carotenoid product. Thus, these results suggested clusters of related-pathway loci as an evolutionary mechanism since the closely linked "pathway mates" are not easily separated due to recombination events.