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IDENTIFICATION OF GENES OF THE CAROTENOID METABOLIC PATHWAY IN *TRITICUM TURGIDUM* BY SNP MARKERS

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Carotenoids are isoprenoid pigments present in wheat endosperm that determine the yellow flour color and confer healthy benefits to end-products as precursor of vitamin-A. Despite the carotenoid content and composition have been an increasing focus in food crops, the genes of the carotenoid metabolic pathway are not well characterized in *Triticum turgidum*. The grain color quantitative trait loci (QTLs) have been studied and located on chromosomes 1B, 2A, 3B, 4A, 4B, 5A, 6A, 7A and 7B. The association of QTLs with genes involved in carotenoid pathway has been reported only for phytoene synthase (PSY), lycopene ε -cyclase (ε -LCY), and carotenoid β -hydroxylase (HYD) enzymes.

In the present study, a list of gene sequences associated with carotenoid biosynthesis was generated using information publically available in *Arabidopsis*, as model genome species. All genes were BLAST analyzed (e-value threshold \leq E-10 and identity percentage higher than 80%) using homology prediction in NCBI EST wheat and *Brachypodium* genome database. The selected sequences were then used as queries for BLASTn search against 81,587 wheat SNP markers sequences (~100 bp) and 102 SNP markers matching with 24 carotenoid biosynthetic genes were identified. The selected SNPs were characterized for map position and single amino acid change on enzyme functionality.

A tetraploid wheat collection, including durum cultivars, landraces and wild accessions was genotyped by Illumina 90K SNP assay. The natural genetic diversity of the tetraploid wheat collection for carotenoid composition was explored evaluating the association of all the subset SNP markers with the phenotypic trait. The statistical analysis revealed 16 SNPs (matching with 8 carotenoid genes) highly associated to the trait.

These results provide information on the existing variability in *Triticum turgidum* on pigment content and generate genetic resources useful for breeding purposes toward the increment of grain carotenoid concentration.