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Carotenoid Gene Nucleotide Diversity Reflects Carrot History and Selection

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Carotenoid content is an important quality attribute for carrot, with a high variation exhibited in this species and along the history of cultivated carrot. The purpose of our work was to study the nucleotide diversity of carotenoid biosynthesis genes. A sample of 48 genotypes, representing a wide carrot diversity, was studied for the sequence polymorphism of seven genes chosen for their position in the carotenoid pathway (*IPI*, *PDS*, *CRTISO*, *LCYB1*, *LCYE*, *CHXE* and *ZEP*). Compared to other species, a quite high single nucleotide (SNP) frequency was found for these genes (1/22 bp on average; 1/11 to 1/38 bp range). The haplotype diversity ranged from 0.523 to 0.851, with 9 to 15 haplotypes per gene. However, this high diversity was mainly due to silent or synonymous sites. The nucleotide diversity was shown to be structured by cultivar geographical origin, reflecting the species history, but also stressing out the consequence of this result when studying carotenoid genetics using association approaches. A second important factor was shown to be the gene position in the carotenoid pathway. When looking for signatures of selection, *CRTISO*, *LCB1* and *LCYE* genes, located in a central position in the pathway, displayed a pattern consistent with a diversifying selection. However, the impact of selection varies depending on the root color group. Upstream genes, such as *PDS*, displayed a negative selection pattern, and may have been subjected to high constraints due to their overall importance for the subsequent pathway. Besides better understanding the functioning of this important pathway, our results provide valuable information for the identification of critical genes for carotenoid genetic studies, and about carrot evolutionary genetics and root color history.