



Carotenoid biosynthesis genes provide evidence of geographical subdivision and extensive linkage disequilibrium in the carrot

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According to the history of the cultivated carrot, root colour can be considered as a structural factor of carrot germplasm. Therefore, molecular variations of carotenoid biosynthesis genes, these being involved in colour traits, represent a good putative source of polymorphism related to diversity structure. Seven candidate genes involved in the carotenoid biosynthesis pathway have been analysed from a sample of 48 individual plants, each one from a different cultivar of carrot (*Daucus carota* L. ssp. *sativus*). The cultivars were chosen to represent a large diversity and a wide range of root colour. A high single nucleotide polymorphism (SNP) frequency of 1 SNP per 22 bp (mean π sil = 0.020) was found on average within these genes. The analysis of genetic structure from carotenoid biosynthesis gene sequences and 17 putatively neutral microsatellites showed moderate genetic differentiation between cultivars originating from the West and the East ($F_{ST} = 0.072$), this being consistent with breeding history, but not previously evidenced by molecular tools. Surprisingly, carotenoid biosynthesis genes did not exhibit decay of LD (mean $r^2 = 0.635$) within the 700–1,000 bp analysed, even though a fast decay level of LD is expected in outcrossing species. The high level of intralocus LD found for carotenoid biosynthesis genes implies that candidate-gene association mapping for carrot root colour should be useful to validate gene function, but may be unable to identify precisely the causative variations involved in trait determinism. Finally this study affords the first molecular evidence of a genetic structure in cultivated carrot germplasm related to phylogeography.

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Liens

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- [2] <http://okina.univ-angers.fr/geoffriau/publications>
- [3] [http://okina.univ-angers.fr/publications?f\[author\]=21228](http://okina.univ-angers.fr/publications?f[author]=21228)
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