



## Use of carrot genetic resources to understand root carotenoid content: preliminary steps to an association mapping study

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Auteur	Jourdan, Matthieu [1], Soufflet-Freslon, Vanessa [2], Clotault, Jérémy [3], Briard, Mathilde [4], Peltier, Didier [5], Geoffriau, Emmanuel [6]
Pays	France
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Mots-clés	association mapping [7], carotenoid isomerase gene. [8], Carrot [9], linkage disequilibrium [10], population structure [11]
Résumé en anglais	Association mapping becomes one of the major genetic methods used to understand genetic control of complex traits. This method allows the use of natural populations with high resolution thanks to ancestral recombinations. Resolution is given by linkage disequilibrium (LD) extend. But false positives can be detected when phenotypic traits are correlated with underlying population stratification at non causal loci. Knowledge of population structure is then a preliminary step for association mapping studies. Here the population structure was investigated in cultivated carrot and the LD extend in the carotenoid isomerase gene, a key gene in the carotenoid biosynthesis pathway. An unexpected high LD for outcrossing species was found in this gene. Population stratification analysis confirmed the differentiation of the carrot germplasm in two clusters. The first one comprised European and American accessions, the second one Asian accessions. These are preliminary steps to perform association mapping studies to understand root carotenoid content in cultivated carrot.
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