GESIIQUA

Project title: Genotype-EnvironmentS Interaction for Improving QUAlity and stability of carrot crop

Acronym: GESIIQUA

Project duration: 36 months – Start date: 01/12/2017 End date: 30/11/2020

Key-words: carotenoid, genetics, biosynthesis pathway,

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Financial support from « Objectif Végétal »: 115 800 € (PhD grant from University of Angers and Running costs 25 000 € from Région Pays de la Loire)

Summary:

Context – There is an increasing society concern about nutritional and organoleptic quality of fruits and vegetables. However, this trait is only poorly integrated in breeding programs, contrary to yield and disease resistance, due to the quality complexity both on genetic determinism and growing conditions effect points of view. Carrot is consumed worldwide and is the second most consumed vegetable in France. This economic importance combined with its role as an essential dietary source of provitamin A and society and breeders demands make carrot a model species for root crops to study the determinants of product quality elaboration. The main nutritional quality attribute of carrot is the carotenoid content, along with other compounds such as fibers, sugars, vitamins and minerals.

Goals –The genetic determinism of carotenoids has been studied recently, with mainly the involvement of carotenoid biosynthesis genes. However there are two main limitations: the approach targeting the biosynthesis pathway explains only partially the genetic determinism and the modulation of genetic factors by the environment is largely unknown. Some genotypes are more stable than others in this regard. The objective of the project is to identify the determinants of carotenoid content in carrot by evaluating the impact of environmental factors and the genotype X environment (GxE) effect, along with a non-targeted approach and, more globally, to understand the bases of genotype adaptability for nutritional traits which has not been studied so far.

Methodology - A panel of carrot material representative of the species diversity and varietal evolution will be studied in about 10 characterized environments over two years in the framework of the collaborative project CaroQual. The harvested lots will be characterized by the PhD for carotenoid (secondary metabolite) and sugar (primary metabolite as a comparison) contents. The weight of environmental factors will be evaluated by multiple regression analysis and GxE interaction effect by various analysis methods. Selected contrasted lots for GxE interaction and carotenoid content levels will be analyzed through a transcriptomic chip to identify the biosynthesis pathways and genes involved in differences of carotenoid accumulation and corresponding adaptability.