

LOCAL SYSTEMS BIOLOGY AND ANALYSIS OF TRANSCRIPTIONAL-METABOLIC NETWORKS IN FRUITS OF TOMATO (*SOLANUM LYCOPERSICON* L.) CAROTENOID MUTANTS REVEAL NOVEL FINDINGS IN THE REGULATION OF FRUIT CAROTENOGENESIS

FRUSCIANTE S., GIULIANO G., DIRETTO G.

Agenzia Nazionale per le Nuove Tecnologie, l'Energia e lo Sviluppo Economico Sostenibile (ENEA), Casaccia Research Center, 00123 Roma (Italy)

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Carotenoids represent one of the larger and more important class of natural compounds, playing essential roles in human nutrition on the basis, for many of them, of strong antioxidant activities. In plants, they have fundamental functions as photosynthetic pigments in leaves, hormone precursors, and secondary metabolite pigments in flowers and fruits. Tomato has been extensively investigated as model system for carotenoid pathway due to the extensive genetic variation affecting carotenoid composition during fruit ripening; anyhow, most of them have been, so far, characterized merely by through the identification of the source of the gained or lost activity. Here, we report an extensive investigation, both at the biochemical (LC-DAD-APCI-MS) and molecular (Real-Time PCR) levels, of a collection comprising the mutants “apricot” (*at*, loss-of-function of the chromoplast-specific isopentenyl diphosphate isomerase (*Ipi*)), “yellow flesh” (*r*, loss-of-function of the chromoplast-specific phytoene synthase gene (*Psy1*)), “tangerine” (*t*, loss-of-function of carotenoid isomerase gene (*CrtISO*)), “Delta” (*Del*, gain of function of the chromoplast-specific lycopene β -cyclase (*CrtL-e*)), “Beta” (*B*, gain of function of the chromoplast-specific lycopene β -cyclase (*CYC-b*)) and “white-flower” (*wf*, loss-of-function of the chromoplast-specific β -carotene hydroxylase gene (*CrtR-b2*)) throughout four different stages of fruit development.

A great extent of large alterations are observed, at late fruit stages, in the profiles of both carotenoids and other classes of isoprenoids and, more interestingly and unexpectedly, in the overall expression pattern of the endogenous genes, independently by the distance from the mutated enzymatic step. A powerful correlation networks approach has been used in order to reveal and predict regulatory relationships between metabolites, transcripts, and metabolite-transcripts so providing a better understanding of the mechanisms regulating fruit carotenogenesis in tomato. Furthermore, a powerful approach of untargeted non-polar metabolomics, has been, finally, carried out to identify a large set of differentially accumulated metabolites in each mutant so to deduce novel metabolic cross-talks within tomato fruit metabolome.

REFERENCES

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