

GENOMIC AND TRANSCRIPTOMIC PROFILING OF EGGPLANT'S FRUITS PEEL DIFFERING IN ANTHOCYANINS CONTENT

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Within the Solanaceae family, eggplant (*Solanum melongena* L.) is the second most important berry-producing crop after tomato. Eggplants are known for being highly variable in fruit shape, size and color, ranging from white to green or dark violet due to the presence and concentration of anthocyanin and chlorophyll in the peel. Black- purple fruits gain more economic relevance due to their high anthocyanin content.

In field, a genotype bearing green fruits was identified as a natural mutant of the dark violet-fruited eggplant variety "Black Beauty" (BB). Morphological data confirmed that BB and the green-fruited mutant ("Green Beauty", GB) are identical, except for berry's peel color and calyx prickliness.

To understand the molecular bases of the differences in peel color between BB and GB, genomic and transcriptomic studies have been conducted. The results of a whole genome re-sequencing of the two varieties were filtered for homozygous variants of single nucleotide polymorphism and structural variations and highlighted a mutation of a histone-lysine N-methyltransferase H3 lysine-9, SU(var)3-9 homolog 5 (SUVH5). Recently in poplar, the involvement of the H3K9 methylation/demethylation mechanism in the control of genes responsible for anthocyanin biosynthesis has been highlighted, and the histone demethylase JMJ25 was found to specifically regulate the repressor of anthocyanin pathway *PtrMYB182*; thus we focused our attention on investigating *SUVH5*. A CRISPR/Cas9-mediated knockout of *SUVH5* has been performed on BB in order to assess the role of the mutated gene and its putative involvement in the regulation of the anthocyanin

biosynthetic pathway. An edited T0 plant carrying a heterozygous mutation resembling the spontaneous one has been obtained and the phenotypic characterization will be settled on T1 plants.

Moreover, a RNA-seq analysis of BB and GB at three stages of fruit development (newly formed fruit still surrounded by sepals, developed fruit partially out of sepals and commercial stage fruit) has been conducted. As expected, the majority of differential expressed genes between BB and GB are the structural ones involved in anthocyanin production. Particularly, part of the early genes (CHS, CHI, and F3H) and all the late genes (DFR, ANS and UFGT) were found downregulated or absent in GB. Data analysis is currently focusing on transcription factors belonging to the MBW complex (e.g. MYB, bHLH, WD40) playing a key role in anthocyanin biosynthesis regulation.