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Genetics underlying flavonoid variation in pepper fruit.

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10 Oral presentation

TITLE: GENETICS UNDERLYING FLAVONOID VARIATION IN PEPPER FRUIT

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Abstract: Pepper fruit (*Capsicum* spp.) is a good source of specialized nutritional metabolites such as flavonoids, which play an important role in both plant physiology and ecology as well as human nutrition. The regulation of flavonoid biosynthesis has been extensively studied in *Arabidopsis*, tomato and petunia, but is only partially explored in pepper. In this study, a QTL on chromosome 5 of pepper was found to be highly associated with quantitative variation in flavonoids in an F_2 population and later verified in NILs developed from a cross between *C. annuum* accessions Long Sweet and AC2212. A transcription factor highly homologous to the master regulator of the flavonoid pathway in tomato – SIMYB12 – was identified as a candidate gene underlying the effect of the locus. VIGS of CaMYB12-like in the high-flavonoid accession cv. Long Sweet led to a significant decrease in the expression of flavonoid pathway genes and drastic decrease of flavonoid levels in silenced fruits. Overexpression of CaMYB12-like in the SIMYB12-deficient tomato *y* mutant led to a partial complementation of its low flavonoid phenotype. In a parallel study ripe fruit of a core collection of about 400 *C. annuum* accessions was developed and fruit metabolomics was carried out in the G2P-SOL project. A GWAS analysis revealed the most significant association for flavonoid variation

precisely in the CaMYB12-like locus, which suggests the general key role of this gene as a master regulator of flavonoid content in *C. annuum* and makes it a straightforward target for classical breeding. Introgression of the CaMYB12-like allele into two cultivated varieties confirmed the potential of CaMYB12-like to breed for high flavonoid content in different pepper backgrounds.

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