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Genetics underlying flavonoid variation in pepper fruit

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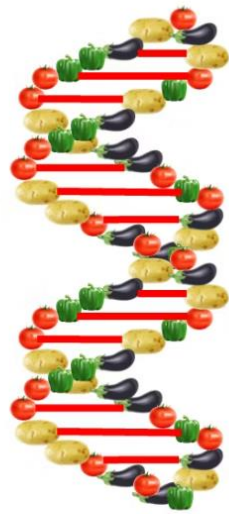
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SOL2023
XVIII International
Solanaceae
Genome
Conference

Montreal, Canada
Oct. 14-18, 2023

📅 October 14-18, 2023

SOL2023

Welcome to SOL2023, the XVIII International Solanaceae Genome Conference to be held Oct. 14-18, 2023 in Montréal, Québec, Canada at Le Sheraton Hotel, 1201 Boulevard René-Lévesque O, Montréal, QC, Canada H3B 2L7.

The International Solanaceae Genome Conferences brings together researchers working on the Solanaceae family of plants at sites around the world annually. In 2023 the meeting is organized by Dr. Helen Tai of Agriculture and Agri-Food Canada and Dr. Martina Strömviik of McGill University. SOL2023 covers 'omics (genomics, transcriptomics, proteomics, metabolomics, phenomics, epigenomics), biotechnology, bioinformatics, systematics, stress physiology, plant development, genetics, breeding and more topics focused on the Solanaceae plant family. Presentations in oral and poster sessions are anticipated to cover cutting-edge and advanced research on the Solanaceae family.

We look forward to hosting you in the beautiful autumn season in Montréal.

Please check back for more information on accommodations and program details for the conference.

Helen Tai and Martina Strömviik

SOL2023 co-chairs

Presentations

Genetics underlying flavonoid variation in pepper fruit

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Pepper fruit (*Capsicum* spp.) is a good source of specialized nutritional metabolites such as flavonoids. 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 F₂ 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 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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