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Evolution, history and genomics of tomato fruit size and shape

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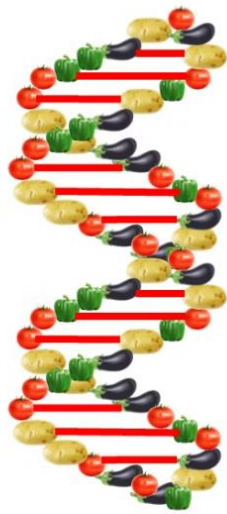
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SOL2023
XVIII International
Solanaceae
Genome
Conference

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 Strömvik 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 Strömvik

SOL2023 co-chairs

Presentations

Evolution, history and genomics of tomato fruit size and shape

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Within the EU-funded G2P-SOL initiative, a diverse set of 15,504 accessions of tomato and its wild relatives, derived from 7 worldwide genebanks, were genotyped, featuring >150 K variants from 5 K loci. Additionally, fruit size and shape were determined by analyzing the available historical genebank data and photographs. This dataset was utilized to uncover the evolutionary trajectories of each genomic region, and to conduct a genome-wide association study (GWAS)..

Evolutionary patterns were discerned by calculating allelic frequencies across various groups, including *S. pimpinellifolium* (SP), wild and domesticated *S. lycopersicum* var. *cerasiforme*, Spanish vintage, Italian and American early improved materials, as well as modern improved varieties.

While most loci in the genome follow a straightforward pattern—exhibiting an allele nearing fixation in cultivated varieties, distinct from the SP allele—most QTLs encompassing known fruit size and shape genes diverged from this simple pattern. Instead, the results revealed more intricate evolutionary histories, highlighting distinctions between loci selected in Spain, Italy, or within more contemporary cultivars.