

## GENOME-WIDE ASSOCIATION STUDY FOR AGRONOMICALLY RELEVANT TRAITS AND FRUIT QUALITY-RELATED METABOLITES IN A WORLDWIDE EGGPLANT CORE COLLECTION

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Eggplant (*Solanum melongena* L.,  $2n=2x=24$ ) belongs to the *Solanaceae* family and is cultivated worldwide, with Italy being the leading European producer. It represents the most important solanaceous berry-producing crop after tomato, with an estimated global production of 59 Mt (FAOSTAT 2023). In addition to containing a variety of vitamins and minerals, eggplant fruits boast high amounts of antioxidants such as phenolics, anthocyanins and chlorogenic acid, acting as cellular free radical scavengers.

In the frame of the EU G2P-SOL project (<http://www.g2p-sol.eu>), a core collection of 321 accessions was selected within more than 3,600 samples of *S. melongena* as well as members of wild species belonging to its primary to tertiary gene pools, from worldwide genebanks. The core collection was phenotyped for 46 agronomic traits at three sites: Montanaso Lombardo (Italy), Valencia (Spain) and Antalya (Türkiye).

Fruits of trials carried out in Italy and Spain were harvested at the commercial ripening stage. Fruit peel and flesh were sampled separately,

and 80 and 82 semi-polar metabolites were identified and quantified by LC-PDA-HRMS (Q-Exactive™), respectively. The core collection was also re-sequenced at 20X, resulting in >51M SNPs and >1.9M structural variations (SVs). A *k-mers* presence/absence table was also constructed.

After quality filtering, >1.2M SNPs, >71k SVs and >4M *k-mers* were employed to perform a genome-wide association study (GWAS) based on 309 accessions. Both agronomic and metabolic traits were considered by applying a multi-environment approach and three multi-locus mixed models (MLMM, FarmCPU and BLINK).

For each trait class, hundreds of quantitative trait loci (QTLs) were identified and the majority of them were consistent for SNP-, SV- and *k-mer*-based GWAS.

Accessions showing contrasting phenotypes were also analysed with the goal to detect selective sweeps (SSs) for agronomic and metabolic traits putatively involved in selection signatures.

Candidate genes located in QTL regions and SSs are under investigation to provide a valuable resource for clarifying the genetic architecture of eggplant traits and the genomic events underlying eggplant domestication.

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