

GENOME WIDE ASSOCIATION ANALYSIS OF AGRONOMICALLY RELEVANT TRAITS IN AN EGGPLANT CORE COLLECTION REPRESENTATIVE OF THE WORLDWIDE GENETIC VARIATION

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Eggplant (*Solanum melongena* L.) represents the third most important crop within the *Solanaceae* family after tomato and potato, with a global production of 57 Mt in 2020 (FAOSTAT).

In the frame of the EU G2P-SOL project (<http://www.g2p-sol.eu>), a core collection including 322 *S. melongena* accessions, as well as members of wild species belonging to its primary, secondary, and tertiary gene pools was established. This core collection is representative of the genetic diversity of over 3,600 accessions maintained in major European and International repositories.

The core collection was phenotyped for 46 plant and fruit related traits at three sites: Montanaso Lombardo (Italy), Valencia (Spain) and Antalya (Turkey). Furthermore, the core collection was resequenced at 20X, resulting in >51M high quality SNPs over the whole genome.

After quality filters, a genome-wide association (GWA) study was performed

on 309 *S. melongena* accessions for mapping genes/QTLs controlling all the analysed phenotypic traits, using >1.2M SNPs and the BLUP values of each accession for each trait as well as a multi-environment approach. Three multilocus mixed models (MLMM, FarmCPU and BLINK, available within GAPIT R package) were applied to compare their strength and power of association detection. Overall, a set of 1,126 QTLs, ranging from 1 to 41 QTL for each trait, was identified using the three multilocus models. Candidate genes are being investigated to identify a list of candidate loci associated with the traits in study as well as to provide new insights into their genetic architecture.