

GENOMIC INSIGHTS INTO THE DOMESTICATION AND SELECTION OF KEY AGRONOMIC TRAITS IN EGGPLANT FOLLOWING IMPROVED GENOME ASSEMBLY AND PAN-GENOME ANALYSIS

BARCHI L.*, RABANUS-WALLACE M. T.**, PROHENS J.***, TOPPINO L.****, PADMARASU S.**, PORTIS E.*, ROTINO G. L.****, STEIN N.**, LANTERI S.*, GIULIANO G.*****

*) DISAFA - Plant genetics - University of Turin, 10095 Grugliasco (TO), Italy

**) Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Seeland, Germany,

***) COMAV, Universitat Politècnica de València, 46022 Valencia, Spain

****) CREA Research Centre for Genomics and Bioinformatics, Via Paullese 28, 26836 Montanaso Lombardo (LO), Italy

*****) ENEA, Casaccia Res Ctr, Via Anguillarese 301, 00123 Rome, Italy

Solanum melongena, whole genome resequencing, pan-genome, domestication, selective sweeps

Solanum melongena L., also known as brinjal eggplant or aubergine ($2n = 2x = 24$), is the second most important solanaceous crop grown for its fruit after tomato, being its worldwide production over 55M tons (FAO, 2019). A novel, highly contiguous genome assembly of the eggplant line '67/3' was developed by Hi-C retrofitting of a previously released short read and optical mapping-based assembly. Not-anchored sequences were hugely reduced to ~51 Mb, and both the anchored genes (96.4% of the total) and the sizes of the 12 chromosomes were comparable to the one of a recently published chromosome-level assembly.

An eggplant pan-genome was obtained, based on the re-sequencing data of 23 accessions of *S. melongena* representative of the worldwide phenotypic and genetic diversity as well as geographic origin, plus one accession of the eggplant wild progenitor *S. insanum* and one of the closely related species *S. incanum*. The pan-genome includes ~51.5 additional megabases and 816 additional genes with respect to the reference genome. A pan-plastome was

also obtained which showed limited genetic variation.

Selective sweeps associated with the selection of key agronomic traits were identified, of which 53, related to fruit color, prickliness and fruit shape, represent genomic signatures which have led to the present-day *S. melongena* cultivars from its wild ancestor. Selective sweeps revealed candidate genes among which a *MYBL1* repressor and a *CHALCONE ISOMERASE* (for fruit color), homologs of Arabidopsis *GLABRA 1* and *GLABROUS INFLORESCENCE STEMS 2* (for prickliness) and orthologs of tomato *FW2.2*, *OVATE*, *LC/WUSCHEL*, *SUPPRESSOR OF OVATE (SOV)* and *CELL SIZE REGULATOR* (for fruit size/shape). Our results provide insights for understanding the genomic events underlying the domestication and selection of this important vegetable species.