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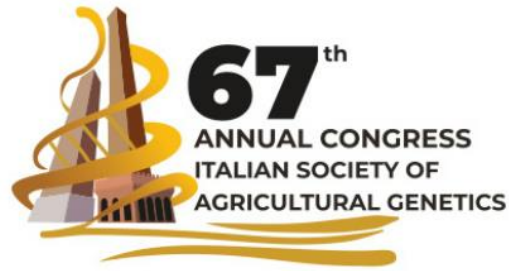
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Bologna, 10-13 September 2024

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# Graph pangenome of eggplant and (its) allied species

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Recent advances in sequencing technologies and the reduction of their costs have accelerated the assembly of plant genomes. However single reference genomes do not fully capture the species diversity, leading to the development of the pangenome concept. A pangenome encompasses all DNA sequences available for a species or larger taxa, including single nucleotide polymorphisms (SNPs) and small/large structural variants (SVs).

To better characterize these variations, the development of graph-based pangenomes have emerged. They store sequence and SV information in nodes and paths, thereby expanding the linear reference genome's coordinate system to more effectively capture genetic diversity.

In this study, Oxford Nanopore long reads from 40 accessions, including 33 accessions of *Solanum melongena* among which the reference line '67/3', as well as 7 accessions of the allied species *S. insanum* and *S. incanum* were assembled using NextDenovo. The resulting assemblies were polished with Medaka and chromosome-scale assemblies were generated for six *S. melongena* and two accessions each of *S. insanum* and *S. incanum*, by incorporating chromosome conformation capture (Hi-C) data. The chromosomes of the other 30 accessions were reconstructed using RagTag, based on the reference line '67/3' sequence. A combination of Helixer (Deep Neural Networks *ab initio* gene prediction) and Braker-3 (both *ab initio* and evidence-based gene prediction) was applied to annotate each genome, resulting in a gene set ranging from 30,886 to 33,449, with a BUSCO completeness from 95.3 to 97.2%.

The obtained assemblies were used to build up two different graph-based pangenomes. The first one, which includes the 40 accessions, was built using the PanGenome Graph Builder (PGGB) pipeline. The second one, comprising only the 33 *S. melongena* accessions, was obtained with Minigraph-Cactus pangenome pipeline. The latter was then used for genotyping 311 *S. melongena* accessions from the EU G2P-SOL project core collection, which were sequenced with Illumina short read sequencing. Overall, 4,532 high-quality SVs were identified.

The accession panel was phenotyped, among others, for resistance to fungal wilts at two sites: Montanaso Lombardo (Italy), and Antalya (Türkiye), and associations between phenotype and genotype were identified using BLINK model within GAPIT R package, on multi-environment data. Here, we report the genome-wide association (GWA) results for resistance to *Fusarium oxysporum* f. sp. *melongenae* and *Verticillium dahliae*.

Our results highlight that the graph pangenome provides an efficient model for representing and analyzing multiple genomes and their variations. This offers a comprehensive resource for eggplant breeding programs and enhances the understanding of eggplant genetic architecture of traits, particularly in relation to fungal wilt resistance.

**Keywords:** *Solanum melongena*, *Solanum insanum*, *Solanum incanum*, graph pangenome, structural variations, GWAS

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