


ABSTRACTS BOOK

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mya), and a positive correlation is observed between numbers of retrotransposons and chromosomal translocation rates. Species-specific tandem amplification of R genes provides a basis for the differential pathogen sensitivity of Solanaceae, and the absence of a glycoalkaloid gene cluster on chromosome 12 provides a basis for the absence of these secondary metabolites in pepper. Overexpression of TAGL1 in tomato and eggplant results in similar developmental phenotypes (sepal expansion), but in different biochemical ones (lycopene vs flavonol accumulation). Solanaceae genomes contain 10 to 15% of syntenic paralogs (ohnologs), generated by the four paleopolyploid events that occurred before the radiation of seed plants, angiosperms, eudicots and Asterid II plants. These ohnologs are enriched in transcription factor genes in *Solanum*, but not *Capsicum*, providing a possible explanation for the huge morphological differentiation in the former genus. The regulatory module comprising transcriptional regulators controlling fruit ripening is populated with ohnologous pairs dating back to the angiosperm paleopolyploidy event or even before, suggesting that the basic network controlling fruit ripening in Solanaceae was present in the common angiosperm ancestor.

RESEQUENCING OF SEVEN EGGPLANT (*SOLANUM MELONGENA*) AND ONE WILD RELATIVE (*S. INCANUM*) ACCESSIONS FOR GENETIC DIVERSITY EVALUATION AND USE IN BREEDING

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Common eggplant (*Solanum melongena* L., $2n = 2x = 24$) lagged behind in genomic sequencing compared to other major crops, despite its economic importance. Here we report the results of the resequencing of seven common eggplants from different areas of Europe and Asia and one accession of the eggplant wild relative *S. incanum* collected in Israel. The eight accessions displayed a high phenotypic diversity in traits with agronomical interests such as color (black, purple, purple striped, green and white), shape (elongated, ovoid, flattened), size, prickliness, as well as phenolics content and tolerance to abiotic stresses. The genomes were reconstructed at a chromosomal scale using a mapping approach (20X) and interrogated for variants (around 15M) and variant effects on genes. The variants of each chromosome and genotype were also plotted and compared to search genomics regions with the same variants distribution, as well as missed regions in the reference genome. The genomes were also functionally and structurally annotated based on comparison with public databases. Undoubtedly, *S. incanum* was the most genetically distinct among the accessions, presented the lowest number of mapped reads (95% vs nearly 100% of the others) and the highest number of variants compared to the reference genome (11.7M, 7.6 to 10.6 fold more than the other genotypes). This preliminary study was a starting point to better understand the unexplored genetic diversity in the eggplant gene pool from the genomic point of view and how to use it for broadening the narrow genetic base using a wild relative.

HIGH QUALITY GENOME OF THE HIGHLY HOMEOLOGOUS ALLOTETRAPLOID *COFFEA ARABICA* L.

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