

EREMOCITRUS GLAUCA, A GENETIC SOURCE TO FIGHT AGAINST HUANGLONGBING, A HIGHLY DESTRUCTIVE CITRUS DISEASE

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Huanglongbing (HLB) is a devastating citrus disease associated with the unculturable and phloem-limited *Candidatus Liberibacter* (CL) spp, mainly *Ca. L. asiaticus* (CLas). CLas is naturally transmitted by the psyllids, of which *Diaphorina citri* is the most efficient vector. At the beginning of 2022 *D. citri* was detected in Israel. Therefore, a possible arrival of HLB in Southern Europe, where most of citrus cultivation is concentrated, is increasingly fearing. All commercial citrus are susceptible to CLas infection, allowing bacterial multiplication and showing symptoms which severely impact the citrus production. Resistance in species belonging to *Eremocitrus* and *Microcitrus* genera, as well as in some hybrids among them and hybrids with *Citrus*, were reported after applying an aggressively challenge-inoculate system.

The genomes of many Citrus genotypes, such as sweet orange, mandarin, lemon, have been released in the last 10 years. The first aim of our work consisted in genome sequencing of *E. glauca*, an essential approach to support the genotyping of *E. glauca* hybrids populations. Using sequenced coupling short (Illumina) and long reads (Oxford Nanopore) technologies we obtained a 270 Mb large genome, each were assembled in 9 pseudomolecules. Gene structural prediction and functional annotation using the Gene Ontology (GO) terms were processed sequencing the RNA pooled of leaves, cortex, peel, petals, flowers (petals except) tissues. Structurally, point, short and large variants were identified by comparing *E. glauca* genome with those of other Citrus related genera.

The second aim consisted in the identification of genes putatively responsible for the resistance of *E. glauca*. Therefore a RNAseq analysis was carried out on four plants of *E. glauca* grafted on 'Rangpur' lime rootstock after two years of inoculation by grafting sweet orange CLas+ budwoods; these data were compared with those of three CLas- plants also propagated onto the 'Rangpur' lime rootstock and grafted with Las-negative budwoods from healthy sweet orange plants. A total of 2,045 differential expressed genes (DEGs) were found ($p_{adj} < 0.01$, \log_2FC greater than $|1|$), 1,184 down- and 861 up-regulated. Preliminary data showed a high number of DEGs involved in the response to pathogens, some of them were up-regulated, others, such as the pathogenesis-related gene 1, proposed to be involved in the immunity to HLB, were down-regulated. The validation through qRT-PCR of some DEGs is in progress, as well as the GO enrichment analysis, an approach aimed to functionally clusterize DEGs. These preliminary data need to be deeply analyzed and integrated with the genome, which availability is an essential prerequisite for genotyping and further functional studies; they concur to identify resistance and susceptible genes to be used in new biotechnological approaches, so to introduce precisely the resistance trait in susceptible varieties, reducing the long times requested by sexual crossings.