

PRELIMINARY DATA ON THE DE NOVO GENOME OF CITRUS RELATIVE SPECIES, EREMOCITRUS GLAUCA AND MURRAYA SPP., AS RESISTANCE/TOLERANCE SOURCES TO HUANGLONGBING

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Huanglongbing (HLB) is the most destructive citrus disease worldwide, which is causing billions of dollars in annual production losses. To date, despite extensive research efforts, no cure, no management tools to treat HLB-positive trees or to prevent new infections are available. Citrus trees severely HLB-infected produce small and irregularly shaped fruits with a thick green peel and fruit color inversion, yellow from the peduncular end, and the stylar end remaining green (hence the common name 'greening'). These symptoms make the fruits unmarketable. Moreover, leaf and fruit drop is a common characteristic also exasperated by drought conditions. HLB is caused by *Candidatus Liberibacter* (*Ca. L.*), an unculturable alpha-proteobacterium, transmitted by two psyllid vectors, *Diaphorina citri* and *Trioza erytreae*. Three species of *Ca. L.* (*Ca. L. asiaticus*, *Ca. L. africanus*, *Ca. L. americanus*) have been associated with HLB and *Ca. L. asiaticus* (CLAs) is the most virulent and extensively distributed worldwide. Unfortunately, all commercial citrus species are susceptible to CLAs infection; HLB tolerance has been observed in some rootstocks hybrids, while some *Citrus* relatives of Australian origin (e.g. *Microcitrus australiasica*, *Eremocitrus glauca*) were described as full-resistant. In addition, among *Citrus* relatives *Murraya paniculata* is a transient host for *D. citri*, but resistant to CLAs, as well as *Berberis koenigi*. Less clear is the behavior on *Murraya ovatifoliolata*. Although sexual compatibility with *Citrus* is restricted to some true citrus species, graft compatibility is widely reported also for *Citrus* on *Clausena* and on *M. paniculata*, even though studies to evaluate the incoming incompatibility under field conditions are ongoing.

In the preHLB project, a European Consortium is working to study short, medium and long term strategies to prevent the income of HLB in Europe. Here we present a preliminary de novo genome of *E. glauca*, *M. paniculata* and *M. ovatifoliolata* produced using a combination of a long-reads (Oxford Nanopore) and short-reads (Illumina) technology. A genome of around 340 Mb has been produced for *E. glauca* and *M. ovatifoliolata*, while of around 220 Mb for *M. paniculata*. A pool of RNAs extracted from shoots, cortex, rind, flesh, flowers, and other part of flowers has been sequenced to support the gene prediction and functional annotation procedures. Moreover, the Hi-C scaffolding is ongoing, with the aim to reconstruct the pseudomolecules.

The availability of these genomes and the identification of resistance sources will be strategic for breeding programs, also taking advantage of the use of the recently developed biotechnological approaches.

Cisgenesis and genome editing could overcome the graft incompatibility of Citrus on its relatives.