

Citrus Genome Sequencing to Support Modern Genetic Improvement in the Fight Against Huanglongbing

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UF/IFAS CREC

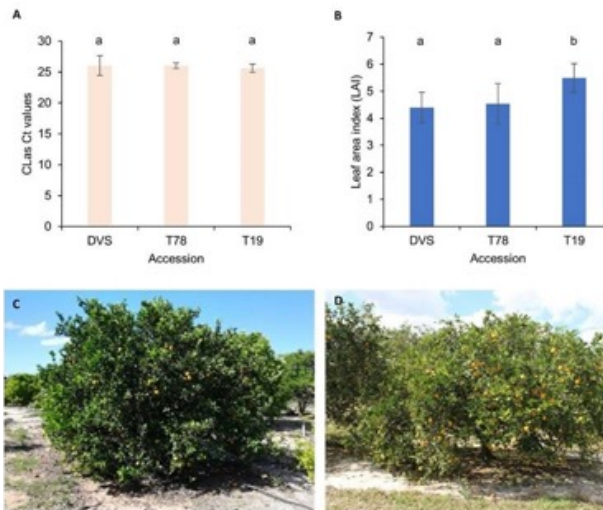


Image A shows that qPCR in the mutant and the sensitive trees are the same, but image B shows increased leaf area index (LAI, a surrogate for tree health) in the mutant. Image C shows an HLB-tolerant Valencia orange mutant and image D shows a normal HLB-affected 'Valencia' tree.

Take Home Message:

- Genome sequencing projects are proceeding using the most advanced technologies to produce the most accurate and complete genome assemblies.
- High-quality genome sequence assemblies support CRISPR gene editing as well as conventional genome-based breeding approaches.
- High-quality genome assemblies are very valuable tools that are revealing molecular mechanisms that underlie HLB-tolerance and resistance.

Effort Statement: A high-quality genome of 'Valencia' orange was used to decipher resistance mechanisms in a tolerant mutant. New highly tolerant rootstock mutants are being sequenced, to learn how they have evolved greater HLB tolerance. Sequencing is being used to study

HLB resistance in a unique breeding population.

Summary: The most desirable, durable solution to the challenge of huanglongbing (HLB) is to develop trees that can resist or are even immune to CLAs, the bacterium that causes the disease. There are several pathways to accomplish the goals of resistance breeding, but none are simple, straightforward, or fast. Breeders are making crosses and evaluating thousands of new individuals in the hope of improving resistance to HLB. Several laboratories are using new technologies such as CRISPR to edit genes or regions of citrus genomes in such a way that new, non-GMO plants can be created with robust and durable resistance to the disease. All such efforts, traditional breeding or modern genetic manipulations, will benefit by having the highest quality genome sequence assemblies as a resource. We use the

most advanced sequencing system and genome assembly platforms, so we can produce assemblies with as nearly complete and accurate sequence information as possible. We have developed new, high-quality genome assemblies for many important citrus cultivars including 'Valencia' orange, that have been used to understand mechanisms of HLB tolerance in a 'Valencia' mutant, for example. Projects are underway to produce genome assemblies of tolerant, possibly resistant, new rootstock mutants we have selected. Genome sequencing also is being used to investigate what appears to be HLB-resistance in a unique citrus family developed by the UF/IFAS CREC breeding program. As more genomes are completed, these high-quality assemblies will tremendously improve the efficiency and effectiveness of CRISPR editing projects, as well as substantially support future genome-based breeding efforts.

Funding:



National Institute of Food and Agriculture
U.S. DEPARTMENT OF AGRICULTURE



Citrus Research and Development Foundation, Inc