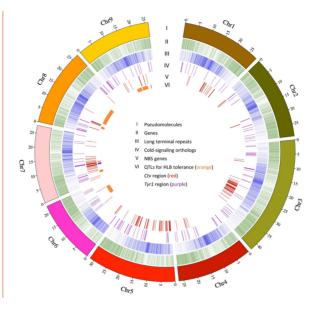# Citrus Genome Sequencing to Support Modern Genetic Improvement in the Fight Against HLB

Overview of the trifoliate orange genome assembly showing 9 basic chromosomes, the locations of all genes, and highlighting genes contained in the genome that are responsible for cold-hardiness, general disease resistance, and specific resistance to CTV and citrus nematodes, and regions conferring strong tolerance to HLB.

Researchers: Fred G. Gmitter, Jr., Dan Rokhsar, Guohong Albert Wu, Zhanao Deng

Contact: Fred G. Gmittter, Jr. **fgmitter@ufl.edu**

UF/IFAS CREC

The most desirable, durable solution to the challenge of HLB is to develop trees that can resist or are even immune to *C*Las, 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, whether by traditional breeding or modern genetic manipulations, will be greatly benefitted by having the highest quality genome sequence assemblies possible, as a resource tool. We currently are developing new citrus genome assemblies for the many important citrus cultivars including 'Valencia' orange, 'Ruby Red' grapefruit, 'Clementine' mandarin, 'Eureka' lemon, and 'LB8-9' Sugar Belle®; other useful genetic resources are also included on our list. We are using the most advanced sequencing system and genome assembly platforms, so we can produce assemblies on a chromosome scale, with as nearly complete and accurate sequence as possible. We have already used our platform for the HLB-resistant trifoliate orange, and the quality of our assembly is the highest of any citrus genome assembly to date. Once completed, these high-quality genome assemblies will tremendously improve the efficiency and effectiveness of CRISPR editing projects, as well as substantially support future genome-based breeding efforts.