



454 Life Sciences, University of Florida, and DOE JGI Sequence Sweet Orange Genome, Publish Annotated Assembly to Public Database

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BRANFORD, Conn.--([EON: Enhanced Online News](#))--Researchers from the International Citrus Genomics Consortium announced this weekend at the Plant and Animal Genome (PAG) XIX conference in San Diego, California the availability of the sequence assembly and annotation of the first citrus genomes, the sweet orange (*Citrus sinensis*) and the Clementine mandarin (*Citrus clementina*). The sweet orange genome was sequenced and analyzed in joint collaboration between the University of Florida, DOE Joint Genome Institute, the Georgia Institute of Technology and [454 Life Sciences](#), a Roche Company, using the high-throughput [GS FLX System](#). Funded in part by the Florida Citrus Production Research Advisory Council, a citrus grower industry organization, the project is expected to assist geneticists and breeders improve these important fruit crops. The assembled and annotated genomes have been added to the publicly available database Phytosome.net, a project of the DOE JGI and the Center for Integrative Genomes.

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Grown in more than 100 nations worldwide, the sweet orange is one of the most economically significant and widely grown fruit crops in the world. In the United States alone, the citrus industry is worth \$20 billion annually. The citrus industry is under attack by several, highly contagious plant pathogens, particularly citrus greening, or Huanglongbing, which debilitate the trees and threaten the future viability of citrus

production in Florida, as well as many other growing regions worldwide. This threat has stimulated very significant investment of grower dollars in research to seek solutions.

“The immediate availability of these annotated assemblies will enable breeders to mine the database for genes associated with key agricultural traits, such as disease-resistance, temperature tolerance, fruit quality, and yield,” explained Fred Gmitter, Chair of the International Citrus Genomics Consortium and a citrus geneticist and breeder at the University of Florida. “In addition, they will enable research to understand the interaction of the host plant with the pathogen to develop disease mitigation strategies.”

In order to assess the quality of the assembly and refine genome annotation, the researchers also used [454 Sequencing Systems](#) to analyze 16 transcriptome samples isolated from sweet orange seedlings which were subject to different environmental stressors, such as infection by pathogens and temperature extremes. “The resulting *de novo* transcriptome assembly proved to be extremely useful for gene prediction, allowing accurate reconstruction of full-length gene models and alternative spliced transcripts,” said Gmitter. “Mapping the transcript sequence reads from the different conditions to the draft genome assembly will be critical for inferring the pattern of gene expression in sweet orange in response to these different stressors, which were selected due to their relevance to plant breeders seeking to address industry needs.”

The sweet orange joins the growing list of plant genomes sequenced using next-generation 454 Sequencing Systems. Throughout just the last year, international research teams announced the draft sequences of the apple, cassava, soybean, wheat, wild strawberry, and cacao genomes, representing some of the most economically important crops for global food supply.

For more information on 454 Sequencing Systems, visit www.454.com.

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