Citrus Genome Database resources for HLB and *Citrus* genomics, genetics, and breeding research

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Abstract: The Citrus Genome Database (CGD, www.citrusgenomedb.org) is a resource for HLB and citrus researchers and citrus breeding programs. CGD has tools for citrus and *Ca.* Liberibacter genomics research such as the JBrowse genome browser, a BLAST tool to search genome sequences, and a genome synteny viewer to compare analyzed genomes. Currently, CGD has genomes of six different *Citrus* species and the complete genomes of *Ca.* Liberibacter asiaticus, americanus, africanus, and solanacearum, as well as the complete genome of *Liberibacter crescens*. CitrusCyc, which is a tool to explore the metabolic maps of the JGI produced *C. clementina* and *C. sinensis* genomes, is also available. CGD has a functionally annotated reference transcriptome (RefTrans) generated from the assembly of published RNA-Seq and EST datasets from *C. sinensis*. For citrus, genetic marker, genetic map, and QTL data, current with published papers, is viewable and searchable in the database. Genetic maps can be viewed and compared using MapViewer, allowing export of map images, dot plots, and correspondence matrices for use in presentations and publications. For citrus breeding programs, CGD has the Breeding Information Management System (BIMS) which is an online system to manage and analyze private breeding data. BIMS works with the Android app called Field Book, which is used to collect the field data. Public citrus phenotype data from the USDA-GRIN database is available to explore with BIMS by all users. CGD is being developed based on user feedback and needs from the scientific community to ensure it provides integrated data and tools that enable citrus discovery and crop improvement. CGD is supported by USDA-NRSP10, NSF-PGRP, USDA-SCRI and US Land Grant Universities.

Non-technical summary: The Citrus Genome Database (CGD, www.citrusgenomedb.org) is an integrated community resource for citrus genetics, genomics, and breeding research. The database has tools for citrus breeding management as well as tools for basic and applied research of the host and HLB pathogen.