CITRUS GENOME DATABASE



Resources for Citrus Genomics, Genetics, Breeding and Disease Research

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www.citrusgenomedb.org

Liberibacter Resources

Complete genome sequences for Ca. Liberibacter asiaticus, africanus,

Bacterial genomes loaded into the JBrowse genome viewer along

Bacterial genome, CDS, and protein sequences searchable in BLAST

Genes and sequences are searchable with downloadable results in

BLAST Results - 5772 Candidatus Liberibacter asiaticus str. psy62, complete genome Blast Hi

JBrowse and

BLAST for Citrus

genomes too

Login

The Citrus Research Community

The AgBioData Community

The Bioinformatics Community

Thanks to

WP_012778351.1 WP_015453069.1 WP.

BLAST results have link-out to genome sequence in JBrowse or

americanus, solanacearum, and Liberibacter crescens in CGD

with gene, CDS, tRNA and mRNA features

CDS/Protein entry in CGD

LAST Command executed: blastn -max_target_seqs -evalue 0.001 -word_size 11 -gapopen 5 -gapextend 2 -penalty -2 -reward 1 -culling_limit 0

Species - Data - Search - Tools - General - Help -

Search

Powered by Tripal

X filter tracks

■ BLAST Result

table or FASTA format

The image above shows the relationship between query and target for this particular

Non-Technical Summary

The Citrus Genome Database (CGD) is being developed as an one-stop 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, pathogen, and vector.

Abstract

The Citrus Genome Database (CGD) is being developed as a one-stop, integrated and curated resource for citrus genetics, genomics, breeding and disease research. In this presentation we highlight CGD features that provide the citrus community with data and tools to help Huanglongbing (HLB) research. The database has been redesigned and features a streamlined user interface that allows for quick access to data and tools. It contains curated citrus genetic marker, map, and QTL data, genome data for clementine and sweet orange, as well as annotated reference transcriptomes (RefTrans) generated by analysis of published RNA-Seq and EST datasets. The database also has the most up-todate version of CitrusCyc v3.0 which includes metabolic maps for the C. clementing and C. sinensis genomes. Tools such as BLAST for searches against the genome sequences and annotations, JBrowse for viewing genomes, and CMap/MapViewer for viewing and comparing genetic map data are also available on CGD. The Breeding Information Management System (BIMS) V1.0 is currently being implemented in CGD. It enables breeders to upload, manage and analyze their breeding program data within their private, secure account, while also providing access to the public data and tools. In addition to citrus data, the genomes of the Candidatus *Liberibacter'* species and the psyllid vector are available in JBrowse and the sequence data is searchable with the BLAST tool. As a community resource, CGD is being developed based on user feedback to provide the data and tools that will enable research and crop improvement.

MapViewer

Funding

provided by

News and Events CITRUS GENOME DATABASE See the CGD poster at IRCHLB V New Citrus Genome Database interface debuts Orl-1 of map Citrus-Orlando-CO-F1 CitrusCyc v3.0 now available To zoom in, drag the mouse across the linkage group Click on any linkage group to explore this map further. You will be taken to MapViewer and leave this page. Citrus Genome Database activities at PAG 2017 Resources for citrus genomics, genetics, breeding and disease research Viewing genetic map Citrus-Orlando-CO-F1 SRAP Em12Me6c-New MapViewer **Species Quick Start Tools Quick Start** allows for easy **HLB links** Genomics Genetics Breeding viewing of map View Genomes View Genomes Browse Maps Manage Breeding SRAP_Em2ME3c— BLAST Sequences Find Sequences Search Marker Manage Data regions with SRAP Em4ME5b~ Search Genes Find QTLs Analyze Data Decision Tool clementina trifoliata Find Sequences Compare Maps reticulata sinensis SSR_TGG02.170draggable zoom CitrusCyc to SSR CAC33.200-ISSR_(TAA)8csettings and user view pathways in OP_A17.2100-New homepage design NIFA Specialty Crop SSR_TAA41.145-Supported by USDA NIFA National Research Support Project 10 (2014-2019), N defined feature C. sinensis and C. for easier access to data Copyright © 2011-2017 | Developed by the Main B colors Cellular Over clementina and tools Species genomes Marker color Search and download ▼ Show ▼ Submit Marker visibility information in tables for maps, markers, QTLs, genes, Species - Data - Search - Tools - General - Help -Login Search Search Sequences transcripts Citrus sinensis source. To select multiple options click while holding the "ctrl" key. The results can be downloaded Search sequence information Email us with problems and suggestions Data Overview Search Gene and Transcripts and download in excel and Overview Any Genetic Maps Citrus Genus Any Search genes and transcripts by species, dataset, genome location Genomes **FASTA** formats Species sinensis term, or InterPro term. | Short video tutorial | Text tutorial | Email Germplasn Common Name Sweet Orange mRNA Species information easily Markers Abbreviation C. sinensis Species Any ▼ Publications Dataset 🚱 Ploidy Genbank Dataset @ Sequences accessed using Species 2n=2x=18 Chromosome Number NCBI (**Genbank Genes** Trait Loci Predicted NCBI gene and mRNA sequences Genome Size Predicted Genes Transcripts Quick Start Available Markers 443 Ca. L. africanus PTSAPSY genome Any ▼ Available Maps Genome Location contains Available QTLs BLAST Species pages allow for Available MTLs Choose File No file chosen Gene/Transcript Name contains 🔻 File Upload Choose Fil Available Traits easy access to species-(eg. polygalacturonase, resistance, EC:1.4.1.3, cell cycle, ATP binding, zinc finger) contains ▼ Available Genomes Reset Search

specific data and tools

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