

CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research

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What's new in CGD?

New Training Videos

- [Finding a marker associated with a trait](#) (2:30 mins)
- [Downloading markers from a map region](#) (2:12 mins)

New Data and Functionality

- 19 new genomes – 12 citrus, 7 from related genera
- 4 expression datasets and 1 GWAS dataset
- Additional permission levels added to BIMS

New data added in first quarter of 2024

So far, 2024 has been mostly about new genome data. The genes and mRNAs from the genomes are available to search in the database and the genomes are available in the BLAST, JBrowse, CitrusCyc, and Synteny Viewer tools. There are also some new expression datasets which are available in the Expression Heatmap tool and new GWAS data that is searchable within the database.

New citrus genomes

- [C. australasica CRC3672](#)
- [C. australasica cv. AZM](#)
- [C. glauca CRC3463](#)
- [C. hongheensis cv. HH](#)
- [C. inodora CRC3784](#)
- [C. ichangensis cv. ZGYCC](#)
- [C. limon cv. Xiangshui](#)
- [C. linwuensis cv. LW](#)
- [C. mangshanensis cv. MSYG](#)
- [C. maxima cv. HZY-T](#)
- [C. maxima cv. XGF](#)
- [C. sinensis cv. Gannanzao](#)

New genomes of related genera

- [Aegle marmelos cv. AEG](#)
- [Atalantia buxifolia cv. HKC \(v2.0\)](#)
- [Citropsis gilletiana cv. CGI](#)
- [Clausena lansium cv. HP](#)
- [Luvunga scandens cv. SYT](#)
- [Murraya paniculata \(Kunming\)](#)
- [Murraya paniculata cv. JLX](#)

New GWAS data

- Shen et al. [Elucidation of the melitidin biosynthesis pathway in pummelo.](#)

New expression data

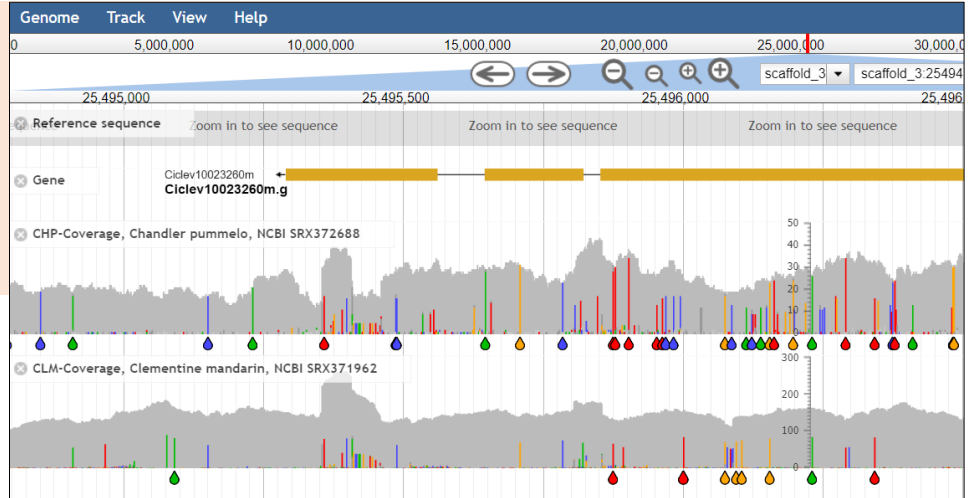
- Zheng et al. [Evolution-guided multiomics provide insights into the strengthening of bioactive flavone biosynthesis in medicinal pummelo.](#)
- Wang et al. [Function and molecular mechanism analysis of CaLasSDE460 effector involved in the pathogenesis of "Candidatus Liberibacter asiaticus" in citrus.](#)
- Huang et al. [Transcriptomic and targeted metabolome analyses revealed the regulatory mechanisms of the synthesis of bioactive compounds in Citrus grandis 'tomentosa'.](#)
- Neupane et al. [Poor shoot and leaf growth in Huanglongbing-affected sweet orange is associated with increased investment in defenses.](#)

CGD genome tools

Here is a brief reminder of what tools are available for genomes on CGD and what they do.

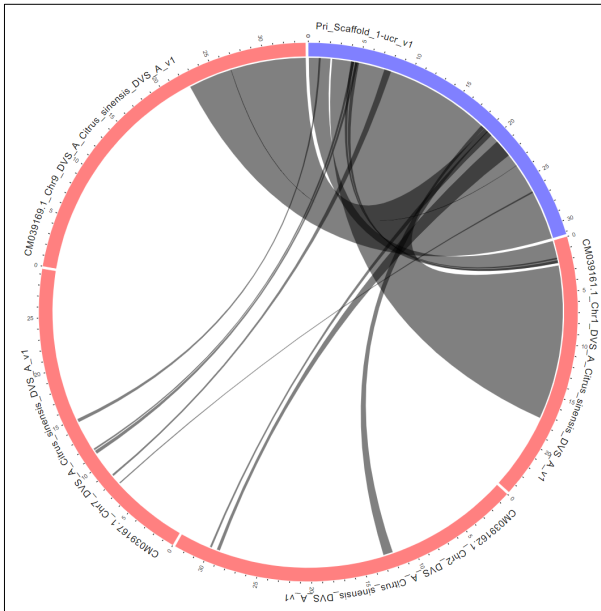
JBrowse

- Used to view the genome assembly and gene and mRNA annotations
- Links back to CGD info on gene/mRNA and aligned features



BLAST+

- Used to query a sequence against the genome assembly, transcripts, or protein sequences
- Results can be viewed online and/or downloaded



Synteny Viewer

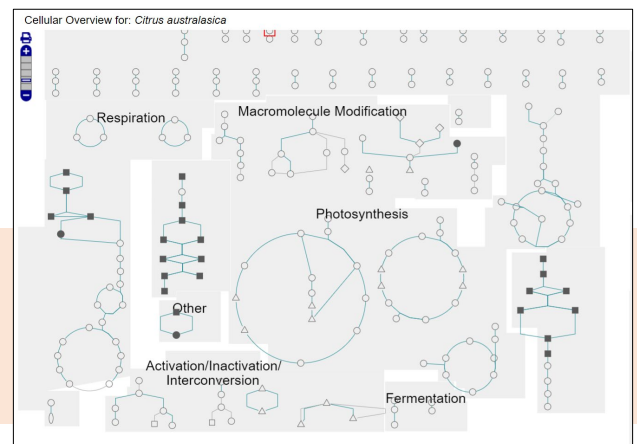
- Displays syntenic blocks between two genomes
- Links to more details about each gene and data used to populate [Ortholog/Paralog Search](#)

Gene and Transcript Search

- Search for genes and transcripts by name, genome, position
- Also search by functional annotation terms
- Customize what data is displayed/downloaded

CitrusCyc

- Displays metabolic and biochemical pathways of genome
- Users can overlay -omics data



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