CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research

Issue 10 | January 2024

What's new in CGD?

Outreach

- <u>How to view correspondences between</u> genomes and genetic maps (2:47 mins)
- Presentations in Citrus Workshop and NRSP10 Database Workshop at PAG

New Data and Functionality

- 261 genetic markers, 1 genetic map, 52 QTL, and 252 GWAS added in last quarter
- Image management added to BIMS breeders can now load images into BIMS

Recap of data added in 2023

Below is information about the data we added in 2023. A huge 'Thank You' to the citrus community for contributing this data!

New genomes

- C. sinensis
 - Valencia v2.0
 - Valencia v1.0 phased, <u>DVS-A</u> and <u>DVS-B</u>
 - <u>DHSO v3.0</u>
 - Newhall v1.0
- <u>C. limon cv. Eureka v1.0</u>
- <u>C. australis v1.0</u>
- <u>C. maxima</u> Cupi Majiayou v1.0
- <u>P. trifoliata acc. ZK8 v1.0</u>
- <u>F. hindsii S3y-45v2.0</u>

New expression datasets

- Aligned to C. sinensis DHSO genome
 - <u>Amino acid biosynthesis in C. sinensis cv. Newhall on</u> <u>different rootstock</u>
 - <u>Flavonoid biosynthesis in *C. sinensis* cv. Newhall on different rootstock</u>
 - <u>C. sinensis cv. Newhall flavonoid biosynthesis under</u> <u>magnesium stress</u>
- Aligned to *C. maxima* cv. Wanbaiyou
 - Male-sterile somatic cybrid and fertile mesophyll parent
 - High versus low citric acid pummelo cultivars

New markers, genetic maps, GWAS and/or QTL added from these manuscripts:

- Montalt et al. 2023. <u>Genotyping by Sequencing for SNP-Based Linkage Analysis and the Development of KASPar</u> Markers for Male Sterility and Polyembryony in Citrus.
- Kumar et al. 2023. <u>Construction of a high-density genetic linkage map to define the locus conferring seedlessness</u> from Mukaku Kishu mandarin.
- Ferrer et al. 2023. Inheritance and Quantitative Trait Loci Mapping of Aromatic Compounds from Clementine (Citrus × clementina Hort. ex Tan.) and Sweet Orange (C. × sinensis (L.) Osb.) Fruit Essential Oils.
- Asins et al. 2023. <u>Combining Genetic and Transcriptomic Approaches to Identify Transporter-Coding Genes as Likely</u> <u>Responsible for a Repeatable Salt Tolerance QTL in Citrus</u>.
- Gao et al. 2023. Citrus genomic resources unravel putative genetic determinants of Huanglongbing pathogenicity.
- Mattia et al. 2022. Genome-Wide Association Study of Healthful Flavonoids among Diverse Mandarin Accessions.
- Matsumoto et al. 2022. <u>QTL mapping of polymethoxyflavone (PMF) accumulation in citrus</u>.
- Yang et al. 2022. <u>QTL analysis reveals the effect of CER1-1 and CER1-3 to reduce fruit water loss by increasing cuticular wax alkanes in citrus fruit</u>.
- Zheng et al. 2018. <u>SLAF-based construction of a high-density genetic map and its application in QTL mapping of carotenoids content in citrus fruit</u>.

CGD by the Numbers

The database has seen growth in the number of users, citations, and data over the years. Let's look at the numbers! First, let's look at usage. The number of users has grown and the number of times they visit the site (Session) and the number of pages they view (Pageviews) each visit is growing.

	Con usage by fear										
	Year	Sessions	Pageviews	Users	Countries						
	2023	17,464	142,119	9,618	137						
	2022	26,195	186,500	16,381	166						
	2021	21,329	145,698	11,933	152						
	2020	14,912	100,889	9,004	128						
	2019	16,500	103,066	10,450	135						
	2018	11,660	70,770	6,635	131						
	2017	10,211	76,653	5,410	127						
	2016	6,392	23,943	4,414	121						
	2015	6,463	22,737	4,460	123						
	2014	6,099	21,060	4,126	115						
	2013	6,459	25,312	3,901	119						
	2012	8,678	34,475	5,244	125						
	2011	3,944	15,296	2,306	101						

Last, let's look at the amount of data that has been added over the last 4 years. The amount of genetic data (markers, maps, QTL) has grown steadily. This year we started adding GWAS data. We are adding data as it is published and feature newly curated data in the News section of the homepage.

Genome data has also steadily grown. At least 20 more genomes will be added to CGD in 2024. Be on the look out for the new additions!

The number of manuscripts that cite CGD has also grown over the years and will continue to grow as more data, analyses, and tools are added. Primary citations refer to manuscripts that cite CGD directly. Secondary citations are the number of times the primary citations were cited. We would like to thank our users for citing CGD!

CGD Peer-Reviewed Citations by Year

Year	Primary Citations	Secondary Citations		
2011	4	135		
2012	7	496		
2013	16	952		
2014	10	755		
2015	11	361		
2016	24	1,058		
2017	12	353		
2018	8	300		
2019	16	647		
2020	23	478		
2021	51	694		
2022	23	121		
2023	19	30		
Total	224	6,380		

Total CGD Data by Year

Year	Genomes	Genes	mRNA	Maps	Markers	QTL	GWAS
2023	32	698,961	1,162,365	92	66,214	776	397
2022	24	366,169	649,803	85	60,407	673	NA
2021	24	337,336	649,803	85	60,407	673	NA
2020	22	239,770	527,520	81	52,555	662	NA

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Funded by: USDA-SAES NRSP10, USDA-NIFA SCRI, USDA-NIFA ECDRE, NSF PGRP, and WSU

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