

# CITRUS GENOME DATABASE



Resources for citrus genomics, genetics, breeding and disease research

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## What is CGD?

CGD is a centralized database containing genomics, genetics, and breeding data and analysis tools for citrus research. Genome sequences are available to view and search and there is also information about genetic maps, molecular markers, and QTL. If you are a breeder who needs to manage private breeding program data, access to the Breeding Information Management System (BIMS) can be requested. Visit us at [www.citrusgenomedb.org](http://www.citrusgenomedb.org) to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available.

## Tools and data for genetics research

There are multiple tools on CGD to enable genetics research. Data searches and MapViewer allow researchers to easily access, view, and download data. Let's look at what data is available and how you can search and view that data.

### What genetics data is in CGD?

CGD enters genetic marker, map, and quantitative trait loci data from peer-reviewed publications. Here is a list of data types and numbers to give you an idea of the database size:

- 60,407 genetics markers
- 86 genetic maps
- 673 QTL for 153 agronomic traits
- 23,070 phenotypic measurements for 38 trait descriptors

## Marker and QTL Searches

All searches can be accessed via the 'Search' menu in the website header. The [Marker Search](#) interface has a variety of options to create a very broad or specific search. The Marker Search allows you to search using the marker name, type, mapped in/developed in species, genetic map location, and if the marker is associated with a trait. The results of the search are displayed in a table with hyperlinks to more detailed information about the marker or to view the corresponding genetic map. The results table can also be downloaded and viewed in Excel.

The [QTL Search](#) also has a variety of search options. QTL can be searched by the species, trait name, published symbol, and the QTL label that has been assigned by CGD. CGD curates the entered QTL and standardizes the trait names between datasets to make it easier to find traits for the same phenotype. You can also search the [CGD trait abbreviations](#) and find a list of QTL associated with that trait.

## MegaSearch

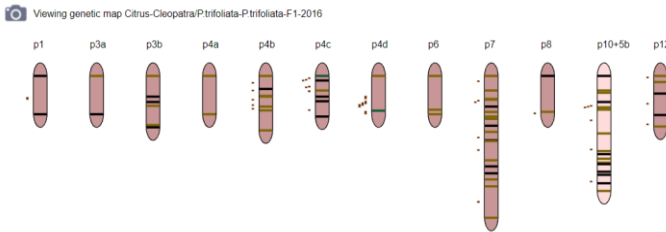
You can also use [MegaSearch](#) to search the marker, map, or QTL data types. There are some different search options available in MegaSearch as well as more control over the output file. You can select which fields are displayed on the results table and select a preferred file format (CSV or TSV) for data download.

For example, when searching QTL data with MegaSearch, you can also restrict the search to a certain population or parent, by colocalizing and neighboring markers, statistic values, or citation.

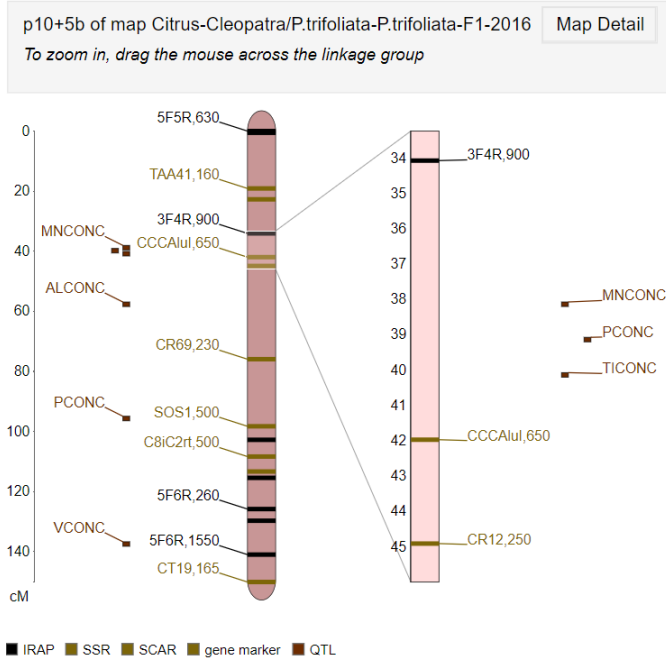
# MapViewer

CGD uses the MapViewer tool to display genetic maps. MapViewer provides a dynamic map viewing experience with customized views and the ability to easily export figures for presentations.

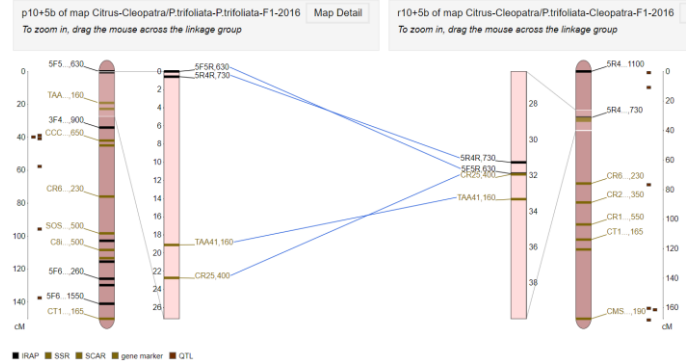
[MapViewer](#) can be accessed via the 'Tools' menu or through the Map Overview pages where an overview graphic of all linkage groups is displayed.



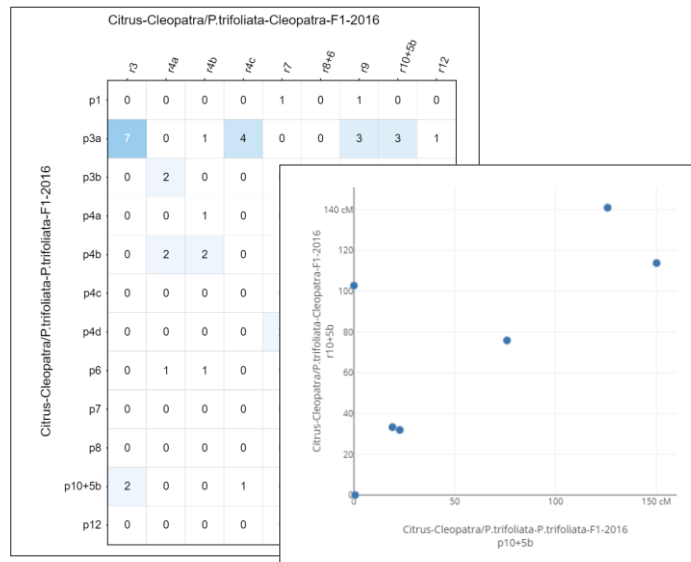
The horizontal lines represent markers and the squares to the side of the linkage groups indicate QTL. To see a closer view, click on a linkage group.



The detailed view has an overview of the whole linkage group on the left with a closer view on the right. The view on the right can be adjusted by dragging and resizing the box on the overview diagram. Clicking on the marker and QTL names will open more details about those features. You can also change which marker types are displayed, the color of the markers, and ruler and position label settings for the displayed linkage group. There is also an option to display a comparison map.



Corresponding markers are indicated with connecting blue lines and the view can be adjusted on each linkage group separately. For comparison maps, the correspondence matrix and dot plot can also be viewed.



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