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 to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available.

Updates to Genetic Data Resources

There have been a few improvements to the search interfaces for genetic data and MapViewer over the last few months.

Improved Map Search – Previously the map search was more of a filtering interface with only genus and species as the option, but now that we are using a MegaSearch interface users have numerous options on how to configure the search. Organism is still an option and the following have been added: map name, mapping population name, maternal parent name, paternal parent name, QTL labels, QTL traits, publication citation, and number of map LG and loci.

Map Search Interface

Data Type	Map ▾	Reset

85 Map. *Note: actual rows in downloaded file depend on the selected fields.*

Query

Organism
- Any
- Citrus clementina
- Citrus grandis
- Citrus reshni

Clear | Refresh Count

Map Name
Any

Mapping population

Population	contains ▾	
Maternal Parent	contains ▾	
Paternal Parent	contains ▾	

QTL

Publication

Size

Expandable option fields

Downloadable Fields

View | CSV | TSV

- ☑ All Fields
- ☑ Map Name
- ☑ Description
- ☑ Unit Type
- ☑ Organism
- ☑ Population
- ☑ Maternal Parent
- ☑ Paternal Parent
- ☑ Number of LG
- ☑ Number of Loci
- ☑ Number of QTL
- ☑ Publication

Select what is viewed/downloaded

Improved MapViewer Features

We have made it easier to download corresponding marker information and compare maps. From the 'Tools' menu, select 'MapViewer'. And then click on the 'View Correspondence Matrix and browse correspondences between genetic maps'. Two sets of pull-down menus appear, and you can select maps that have correspondences.

Once you click submit, a Correspondence Matrix appears with numbers that correspond to the number of corresponding markers between linkage groups. Clicking on the number opens the maps of the linkage groups so you can view them and download information on the corresponding markers and view a dot plot graph.

MapViewer Quick Start

MapViewer is a graphical tool for viewing and comparing genetic maps. It includes dynamically scrollable maps, correspondence matrices, dot plots, links to details about map features, and exporting functionality. It was developed by the MainLab at Washington State University and is available for download for use in other Tripal databases.

Select a map and start using MapViewer

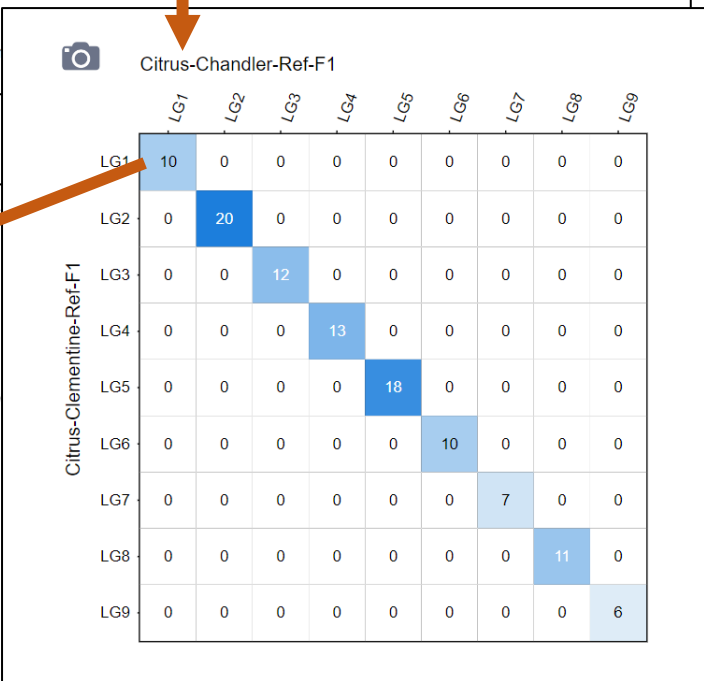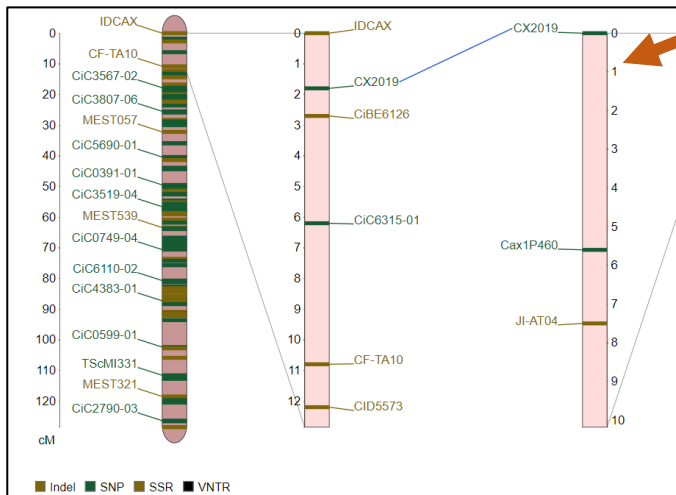View the Correspondence Matrix and browse correspondences between genetic maps

When the Submit button is clicked, a new correspondence matrix page will appear to allow browsing correspondence between two genetic maps or between all genetic maps in a species and one genetic map.

Species [Citrus clementina ▼] **Map** [Citrus-Clementine-Ref-F1 ▼]

Compare To

Species [Citrus grandis ▼] **Map** [Citrus-Chandler-Ref-F1 ▼] [Submit]

View the Correspondence Matrix and browse correspondences between whole genom...

Citrus-Chandler-Ref-F1

Citrus-Clementine-Ref-F1

	LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8	LG9
LG1	10	0	0	0	0	0	0	0	0
LG2	0	20	0	0	0	0	0	0	0
LG3	0	0	12	0	0	0	0	0	0
LG4	0	0	0	13	0	0	0	0	0
LG5	0	0	0	0	18	0	0	0	0
LG6	0	0	0	0	0	10	0	0	0
LG7	0	0	0	0	0	0	7	0	0
LG8	0	0	0	0	0	0	0	11	0
LG9	0	0	0	0	0	0	0	0	6

IDCAX, CF-TA10, CiC3567-02, CiC3807-06, MEST057, CiC5690-01, CiC0391-01, CiC3519-04, MEST539, CiC0749-04, CiC6110-02, CiC4383-01, CiC0599-01, TScMI331, MEST321, CiC2790-03

IDCAX, CX2019, CiBE6126, CiC6315-01, CF-TA10, CID5573

CX2019, Cax1P460, JI-AT04

Indel SNP SSR VNTR

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