# CITRUS GENOME DATABASE

Resources for citrus genomics, genetics, breeding and disease research

## What's new in CGD?

### Outreach

- [How to go from a trait to a GWAS to a gene and to an ortholog](#) (2:52 mins)
- [How to use the Expression Heatmap Tool](#) (2:23 mins)

### Upcoming PAG Database Workshop

- [NRSP10 Database Workshop](#) featuring Citrus Genome Database, Jan. 14, 1:30-3:40 PM.

### New Data

- 3,297 genetic markers, 2 genetic maps, 20 QTL, and 145 GWAS added in last quarter
- *C. sinensis* cv. Newhall genome added to database, JBrowse, BLAST, Synteny Viewer
- 5 new expression datasets (orange, pummelo)
- Differentially methylated region track in *C. sinensis* cv. Valencia JBrowse

## Viewing Expression Data

You can now explore more gene or mRNA expression levels on CGD using the Expression Heatmap Tool. This tool displays expression levels of genes or mRNA from published manuscripts. Access the tool via the "Expression Heatmap" link in the Tools menu. You then are taken to an overview page with a few different sections. First note the table of Expression Datasets that are available with links to more information about the study and the genome the data is aligned to. You can create the heatmap by adding gene/mRNA names to the text box or by selecting the organism and then selecting features from the box or searching for a gene/mRNA name. Then click "Display Expression Heatmap" (also see video linked above).



Choose organism and select from list that populates below

Enter gene or mRNA names here

Links to dataset and genome details

# Heatmap and Gene/mRNA and Biosample Pages

There are links to details about the gene/mRNA and the sequenced samples along the axes of the heatmap. You can also adjust what is displayed on the heatmap and download the data.

## Heatmap Results

**Select an analysis to display**
Expression: C. sinensis cv. Newhall flavonoid biosynthesis under magnesium stress

**Select a property to sort**
sample_name

Adjust how the data is displayed

Expression: C. sinensis cv. Newhall flavonoid biosynthesis under magnesium stress Expression

Cs_ont_1g000580_Citrus_sinensis_DHSO_v3.0
Cs_ont_1g000530_Citrus_sinensis_DHSO_v3.0
Cs_ont_1g000510_Citrus_sinensis_DHSO_v3.0

MS3-3 MS3-2 MS3-1 MS2-3 MS2-2 MS2-1 MS1-3 MS1-2 MS1-1 MD3-3 MD3-2 MD3-1 MD2-3 MD2-2 MD2-1 MD1-3 MD1-2 MD1-1

200
100

## Expression

**Available Analyses**

- Expression: Amino acid biosynthesis in C. sinensis cv. Newhall on different
- Expression: Flavonoid biosynthesis in C. sinensis cv. Newhall on different
- Expression: C. sinensis cv. Newhall flavonoid biosynthesis under magnesi

**Select an Expression Analysis**

Expression: Amino acid biosynthesis in C. sinensis cv. Newhall on different roots

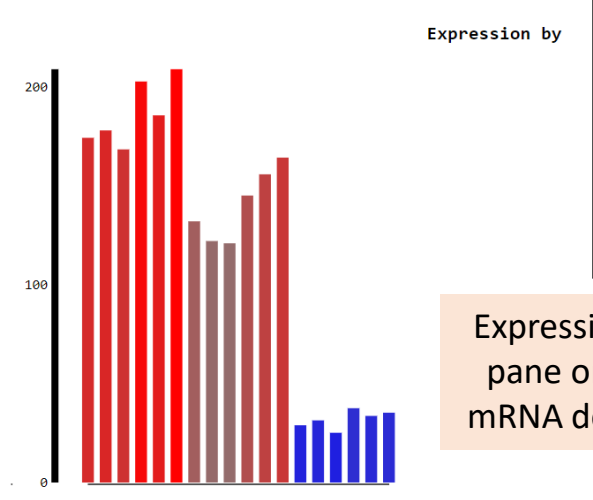**Select a property to group and sort biological samples** sample_name

**Select a property to color biological samples** Expression value

Hover the mouse over a column in the graph to view more information about that groups along the x-axis. You can also click and drag to move the legend.

Only Non-Zero Values | Reset

Expression by

Expression Details pane on gene or mRNA details page

## Biosample Overview

| | |
|---|---|
| **Name** | MD3-3 |
| **Organism** | Citrus sinensis (Sweet orange) |
| **Analysis** | Expression: C. sinensis cv. Newhall flavonoid biosynthesis unde |
| **Collection Date** | n/a |
| **Location** | China: Leibo County, Liangshan Prefecture, Sichuan Province |
| **Tissue** | peel |
| **Description** | Leaf yellowing from magnesium deficiency |
| **Sample name** | MD3-3 |
| **Isolate** | 18 |
| **Age** | Thirteen-year-old trees |
| **Biosample accession** | SAMN33285737 |
| **Sra accession** | SRS16794900 |
| **Biomaterial provider** | Qin Li |
| **Dev stage** | fruit maturity period, November |
| **Contact** | Qin Li |

Details about samples that were sequenced

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