What’s new in CGD?

**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

**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.

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).
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.

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