**Viewing Expression Data**

You can now explore gene or mRNA expression levels on PCD 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).

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**What’s new in PCD?**

**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 Workshops**
- BIC & NAPIA Breeding Tools Workshop featuring Breeding Information Management System, Nov. 5, 2-5 PM
- NRSP10 Database Workshop at PAG featuring Pulse Crop Database, Jan. 14, 1:30-3:40 PM

**Tool Improvements**
- Expression Heatmap Tool added to view RNA-seq expression datasets, data also displayed on gene/mRNA pages

**New Data**
- 12,457 genetic markers, 7 genetic maps, 82 QTL, and 187 GWAS added in last quarter
- 5 expression datasets (chickpea, pea, lentil, bean)
- Differentially methylated region track in mung bean genome JBrowse

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**PCD Newsletter | www.pulsedb.org**
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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