What is PCD?

PCD is a centralized database containing genomics, genetics, and breeding data and analysis tools for pulse crops. Annotated 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.pulsedb.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. Short monthly how-to videos are available from the site.
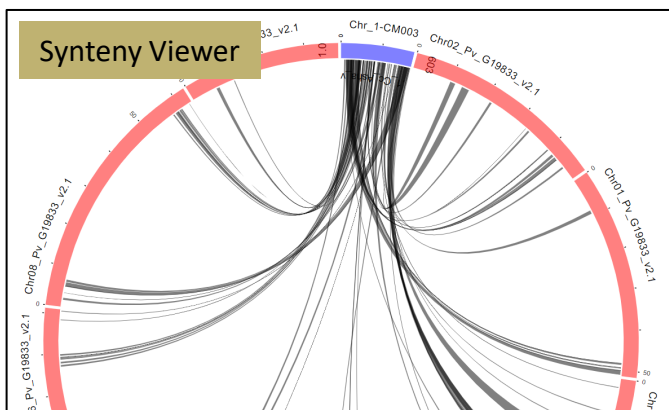
More PCD training and tools

Thanks to a new award from the USDA-SCRI, PCD and the other MainLab specialty crop databases will continue to grow to provide the tools, data, and training that breeders and researchers need. You can read more about the award here: Enabling Genomics-Assisted Specialty Crop Breeding and Research Through Advanced Database Resources.
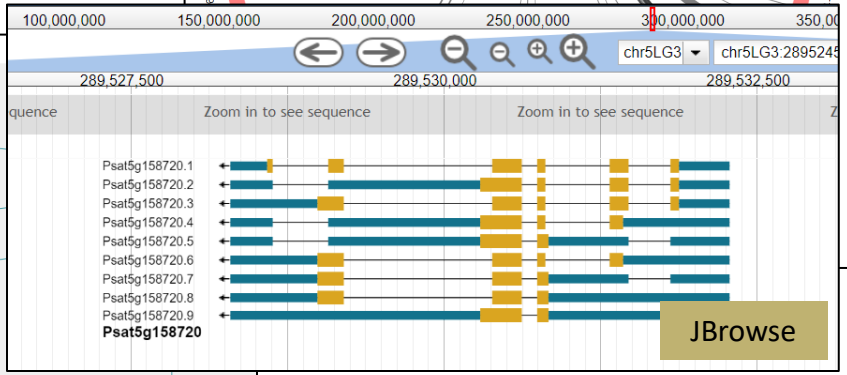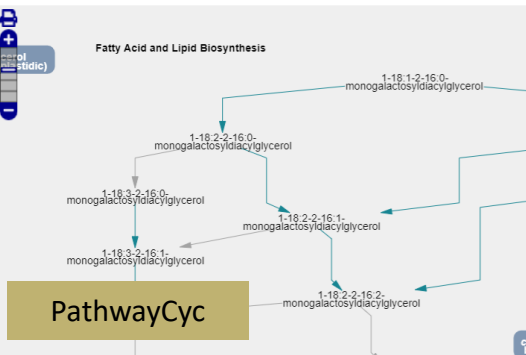
The continued funding will provide new tools and resources for big data, data management, and staff for in-person training with PCD users. We will be announcing all the new developments via the PCD mailing list, so please subscribe if you have not done so already.

Genomic resources on PCD

There are genomes from ten different crops on PCD. These genomes are available to view in JBrowse, sequences can be searched in BLAST, and the mRNA and gene annotations are available to search in the database via MegaSearch. These genomes are also available in PathwayCyc and Synteny Viewer. More genomes will be added soon, so keep watch for those.

Synteny Viewer

JBrowse

PathwayCyc

Ortholog/Paralog MegaSearch

We have made a new MegaSearch for the data that is stored during the Synteny Viewer analysis. Now you can search that data without going through the Synteny Viewer.

The new Ortholog/Paralog Search interface is simple to use. First select the primary genome and chromosome/scaffold of interest. Or provide a single gene/transcript ID or a file of them.

Once parameters are set, you can preview the number of results by clicking "Refresh Count". And then you can configure what data will be returned and available for download.

When viewing the results on the website, there are green hyperlinks that open details about the associated transcripts including the annotated terms, homology to SwissProt, InterPro results, and mRNA and protein sequences.

Tripal MegaSearch

Tripal MegaSearch is a tool for downloading biological data. (Current limit per download: 1,000,000 records. 200,000 FASTA sequences.)
Video tutorial: 2020 presentation | 2021 tutorial (Gene/Transcript) | 2022 tutorial (QTL)

Select a data type to start building your own query and download data in bulk:

Data Type [Ortholog/Paralog ▾]   [Reset]

1,250 Ortholog/Paralog. *Note: actual rows in downloaded file depend on the selected fields.*

Query

Field	
Genome	Phaseolus vulgaris G19833 genome v2.1 ▾
Chromosome/Scaffold	Chr01 ▾
Start	> ▾
Stop	< ▾
Gene/Transcript Name	contains ▾
	Choose File No file chosen
Compare to	Cicer reticulatum L. PI489777 genome v1 Lupinus angustifolius L. Tanjil genome v1.0 Phaseolus vulgaris G19833 genome v2.1 Pisum sativum Cameor genome v1a Vigna angularis Jingnong 6 genome v1.1
Chromosome/Scaffold	Any ▾

[Clear] [Refresh Count]

Genome 1

Gene/transcript name

Genome 2

Options to view and download data

Downloadable Fields

[View] [CSV] [TSV]

☑ All Fields
☑ Genome1
☑ Chromosome1
☑ Location1
☑ Ortholog1
☑ Genome2
☑ Chromosome2
☑ Location2
☑ Ortholog2
☑ Associated Gene

1252 records were returned

#		Genome1	Chromosome1	Location1	Ortholog1	Genome2	Chromosome2	Location2	Ortholog2
1	☐	Phaseolus vulgaris G19833 genome v2.1	Chr01	Chr01:10013523..10014819	Phvul.001G073800.1	Pisum sativum Cameor genome v1a	chr5LG3	chr5LG3:40608058..40609707	Psat5g02160
2	☐	Phaseolus vulgaris G19833 genome v2.1	Chr01	Chr01:10013523..10014819	Phvul.001G073800.1	Pisum sativum Cameor genome v1a	chr6LG2	chr6LG2:30967195..30968373	Psat6g03784

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