



PULSE CROP DATABASE

Genomic, Genetic, and Breeding Resources
for Pulse Crop Improvement

The Pulse Crop Database: A resource for pulse crop research and improvement

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www.pulsedb.org

Abstract

The Pulse Crop Database (PCD, www.pulsedb.org), is an online resource that focuses on providing access to curated and integrated data and tools to enable pulse crop research, translation, and improvement. PCD includes publicly available genomics, genetics and breeding data including genomes, genes, transcripts, genetic maps, markers, QTL, germplasm, phenotype data, and publications with integrated tools to easily access, view, filter and download the data. Genetic maps can be viewed and compared using the MapViewer tool and marker information easily viewed and searched. Genomes can be viewed using the JBrowse, Synteny Viewer, and PathwayCyc tools; genome sequences searched using BLAST; and the gene and mRNA information viewed and searched within the database. For breeders, PCD hosts the Breeding Information Management System (BIMS) which allows for management of breeding programs via private user accounts while also enabling access to publicly available pulse phenotype data downloaded from the GRIN database.

Data in CSFL

Crop	Markers	Maps	QTL	Genomes
Pea	175156	71	1405	1
Cowpea	159091	21	444	1
Pigeon Pea	151970	12	55	1
Faba Bean	138239	33	338	
Chickpea	100025	98	1587	3
Lentil	84198	43	372	
Common Bean	43048	33	811	1
Lupin	19195	11	70	1
Adzuki Bean	7771			1
Bambara Bean	4288	4	105	

PCD Crops Data Search Tools General Help

Easy-to-use homepage

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News and Events

- Map (10), MTL (1), QTL (50) and marker (1886) data from 12 publications added for bean, lentil, pea, lupin and Vigna (9/2021)
- Map (3), marker (130516), QTL (47), trait (5) data from 9 publications added for chickpea, common bean, cowpea, faba bean and Vigna (8/2021)

Crops Quick Start

Tools Quick Start

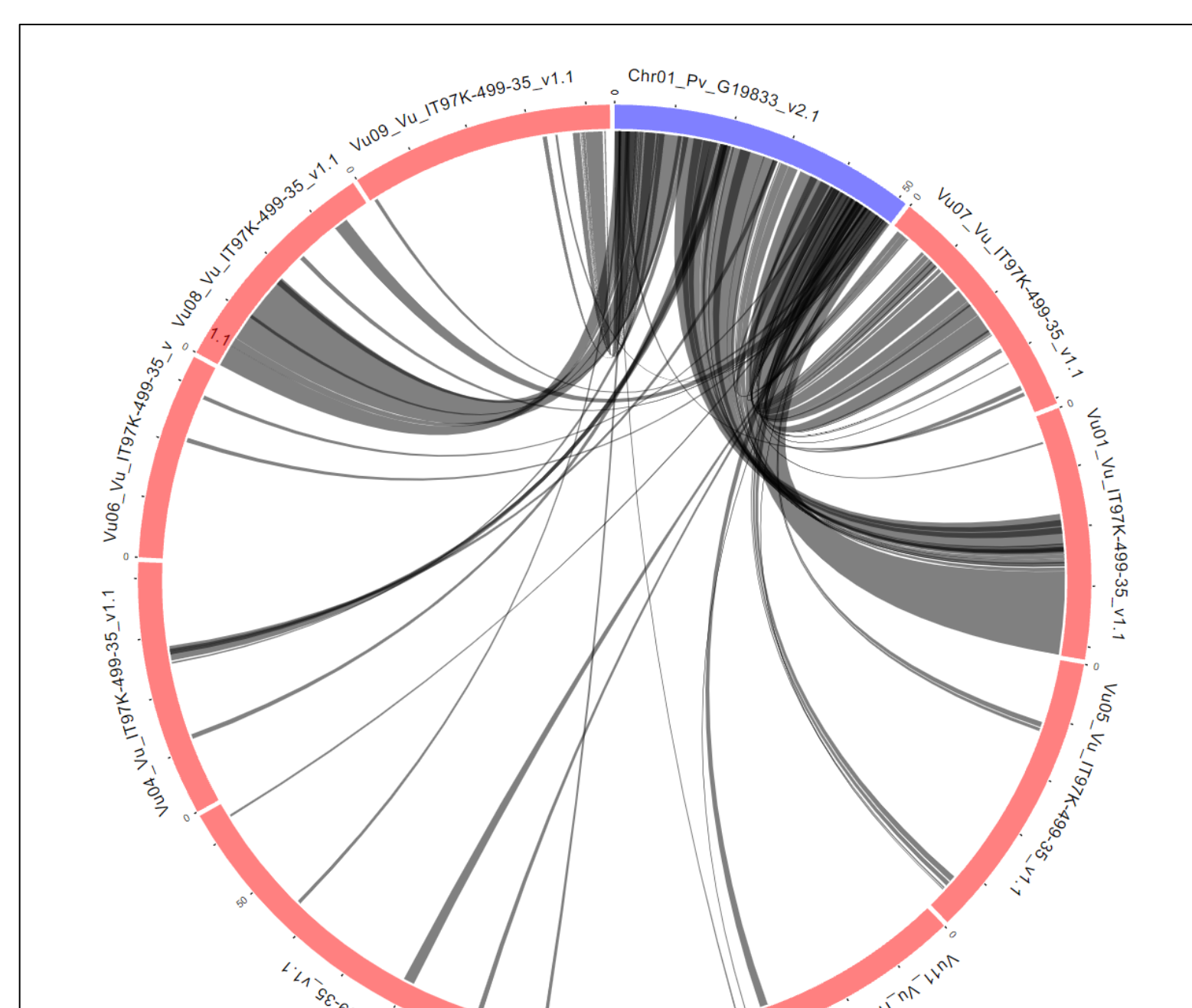
Genomics
View Genomes
Find Sequences
Search Genes
BLAST Sequences

Genetics
Browse Maps
Search Markers
Find QTLs
Compare Maps

Breeding
Manage Breeding
Search Descriptors
Search Traits
Field Book

USDA Dry Pea & Lentil Council Northern Pulse Growers Association NRSPIO USDA Agricultural Research Service WASHINGTON STATE UNIVERSITY

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View synteny between genomes in addition to BLAST, JBrowse, and PathwayCyc tools

Pea Crop Pea-GRIN Program

About BIMS Help Archive Manage Breeding Data Import Search Search Accession

Choose property

Properties

Name Format Seed hundred weight numeric

Data 6663 [634]

Max: 53.00 [317]

Min: 1.00

Mean: 18.33

STD: 6.39

Maximum 53.00

Please specify the maximum value of the trait.

Minimum 1.00

Traits

Root length

Root surface area

Root to shoot ratio

Root volume

Rust AUDPC

Rust leaf area

Seed boron concentration

Seed calcium

Seed carbon

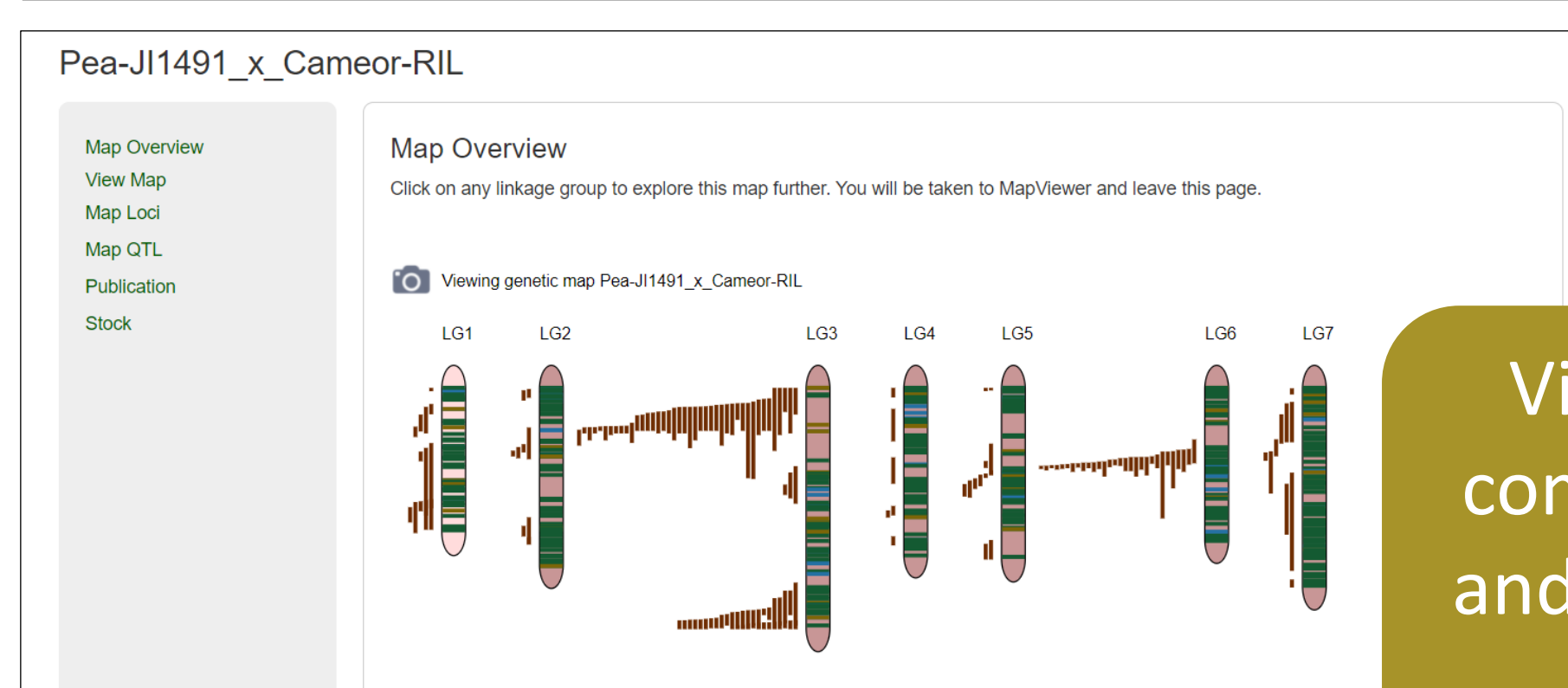
Seed nitrogen

Seed phosphorus

Please choose a property

Field Book Management Data Analysis Breeding Decision Tools

Breeding Information Management System (BIMS) available for private breeding program management
USDA-GRIN phenotype data available to explore using BIMS



View and export figures of comparative maps, dot plots, and correspondence matrices with MapViewer

Gene A	Gene B	e-value
Phv01.001510400.2	Vigna01g104300.1	2e-40
Phv01.00152000.1	NA	NA
NA	Vigna01g104600.1	NA
Phv01.00152000.1	Vigna01g104600.1	0
Phv01.001520700.1	NA	NA
Phv01.001520800.2	NA	NA
Phv01.001520900.1	Vigna01g104700.1	NA
Phv01.001520900.1	Vigna01g104800.1	NA
Phv01.001520900.1	Vigna01g104900.1	4e-42
Phv01.001521000.2	NA	NA
Phv01.001521000.2	Vigna01g105000.3	NA
Phv01.001521000.2	Vigna01g105000.5	NA
Phv01.001521100.1	Vigna01g105200.1	3e-164
Phv01.001521300.1	NA	NA
Phv01.001521400.2	NA	NA

Mailing List

- <https://www.pulsedb.org/ mailing list>
- Newsletters, How-to Tips, Webinars

Contact Form

- <https://www.pulsedb.org/ pulsedb contact>
- Questions or suggestions

Data Type: QTL

5,423 QTLs. Note: actual rows in downloaded

Query

Type: Any

Organization: Any

Trait Category: Any

Trait Name: contains

Name: Published Symbol: contains QTL Label: contains

Population: contains

Maternal Parent: contains

Genetic location: Map: Any Linkage Group: Any Start: > Stop: >

Downloadable Fields

All Fields View CSV TSV

QTL Name

Trait Name

Organization

Type

Published Symbol

LOD

R2

Category

Map

Linkage Group

Start

Stop

Colocalizing Marker

Neighboring Marker

Population

Maternal Parent

Paternal Parent

Citation

New MegaSearch tool adds more options to search and download data from the database

Funding provided by



WASHINGTON STATE UNIVERSITY



Agricultural Research Service



Thanks to