



# COOL SEASON FOOD LEGUME CROP DATABASE RESOURCES

## A resource for pea, lentil, faba bean and chickpea genetics, genomics, and breeding

Jodi L. Humann<sup>1</sup>, Sook Jung<sup>1</sup>, Chun-Huai Cheng<sup>1</sup>, Taein Lee<sup>1</sup>, Ping Zheng<sup>1</sup>, Morgan Frank<sup>1</sup>, Deah McGaughey<sup>1</sup>,  
Kristin Scott<sup>1</sup>, Katheryn Buble<sup>1</sup>, Jing Yu<sup>1</sup>, Heidi Hough<sup>1</sup>, Marwa Sanad<sup>1</sup>, Clare Coyne<sup>2</sup>, Rebecca McGee<sup>2</sup>, Dorrie Main<sup>1</sup>

<sup>1</sup>Washington State University, Pullman, WA; <sup>2</sup>USDA-ARS, Pullman, WA  
Contact info: jhumann@wsu.edu, dorrie@wsu.edu

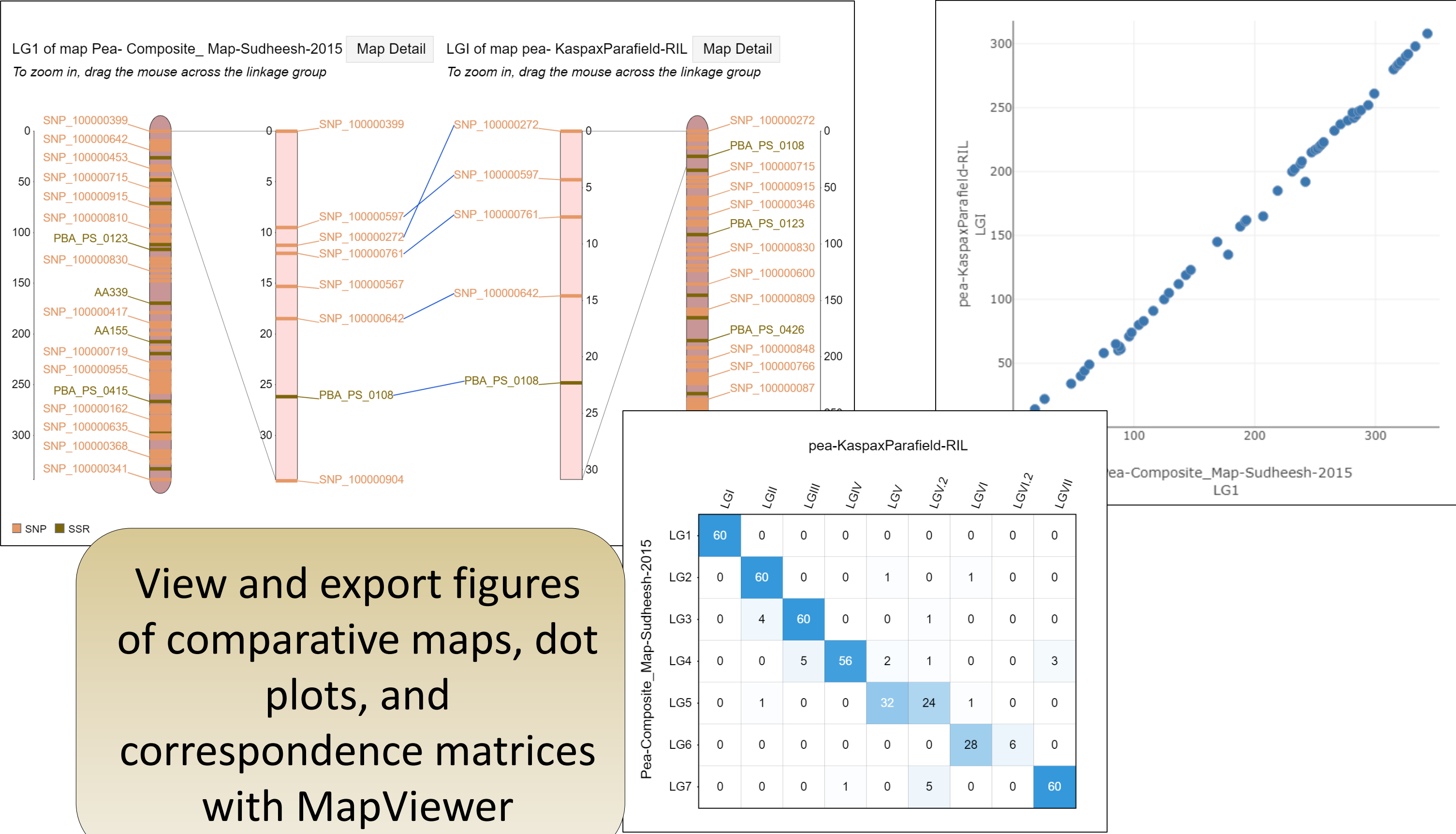
[www.coolseasonfoodlegume.org](http://www.coolseasonfoodlegume.org)

### Abstract

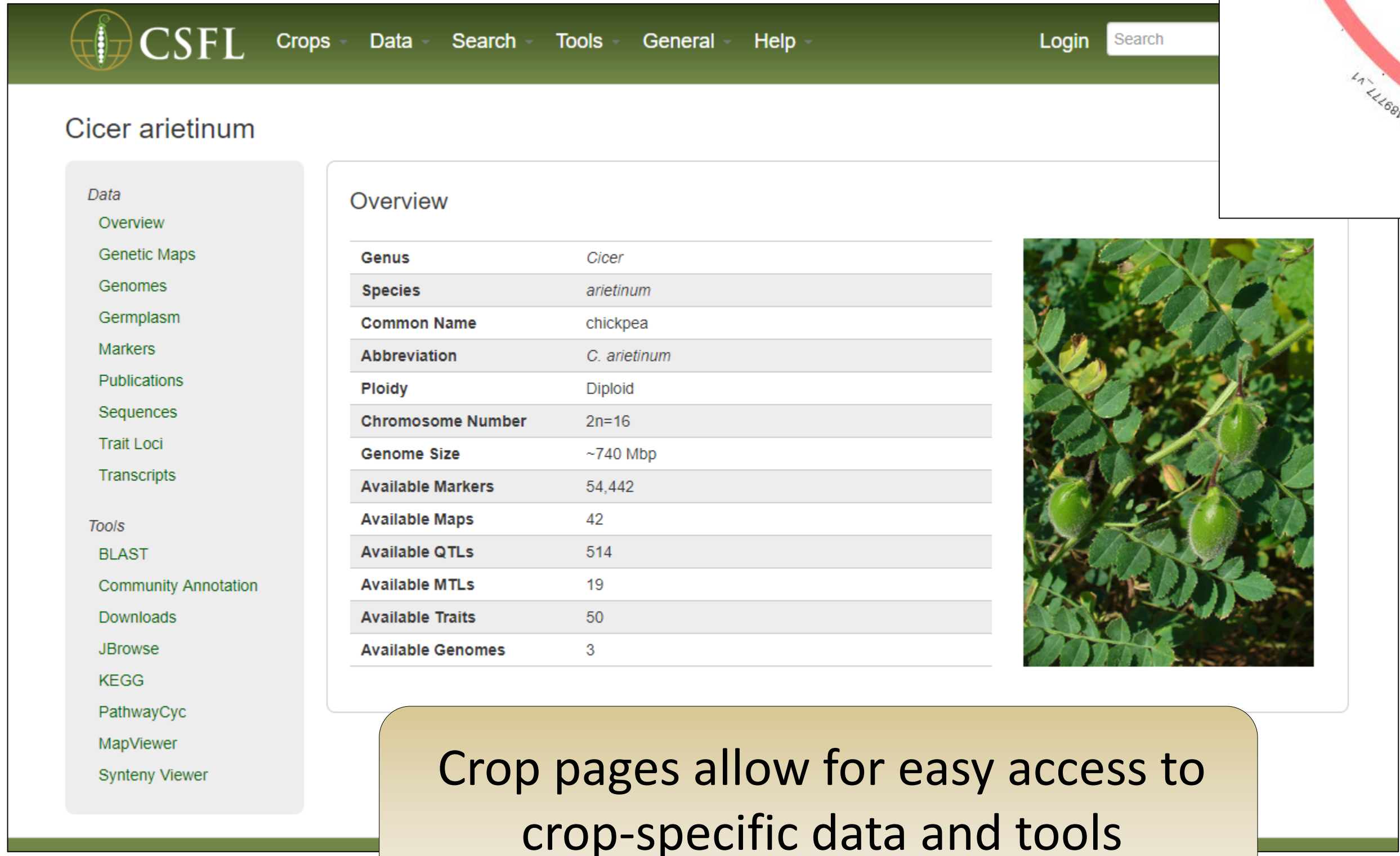
The Cool Season Food Legume Genome database (CSFL) is a curated and integrated database resource for genomics, genetics, and breeding research of chickpea, lentil, pea, and faba bean. CSFL currently contains three annotated genome sequences for Cicer sp.; annotated reference transcriptomes analyzed from published RNA-seq and EST data for all four crops; 167 genetic maps; 137,268 markers; 2,952 QTL; 2,429 germplasm; metabolic pathways for the Cicer sp. genomes; and synteny data for the Cicer sp. genomes with links to genes, mRNA, orthologs and function. Tools include the genome browser JBrowse, Synteny Viewer, MapViewer, PathwayCyc, BLAST+, and the Breeding Information Management System (BIMS), an online system to manage and analyze private breeding data. BIMS works with Field Book, an Android app used to efficiently collect the field data. Public cool season legume phenotype data from the USDA-GRIN database is available to explore with BIMS by all CSFL users. Genes and transcripts, maps, markers, germplasm, QTL, sequences and publications can be queried through the search interfaces on CSFL with results available to download. CSFL is built using the Tripal database platform supported by USDA NRSP10, the USA Dry Pea and Lentil Council, Northern Pulse Growers Association, USDA-ARS and Washington State University.

### Data in CSFL

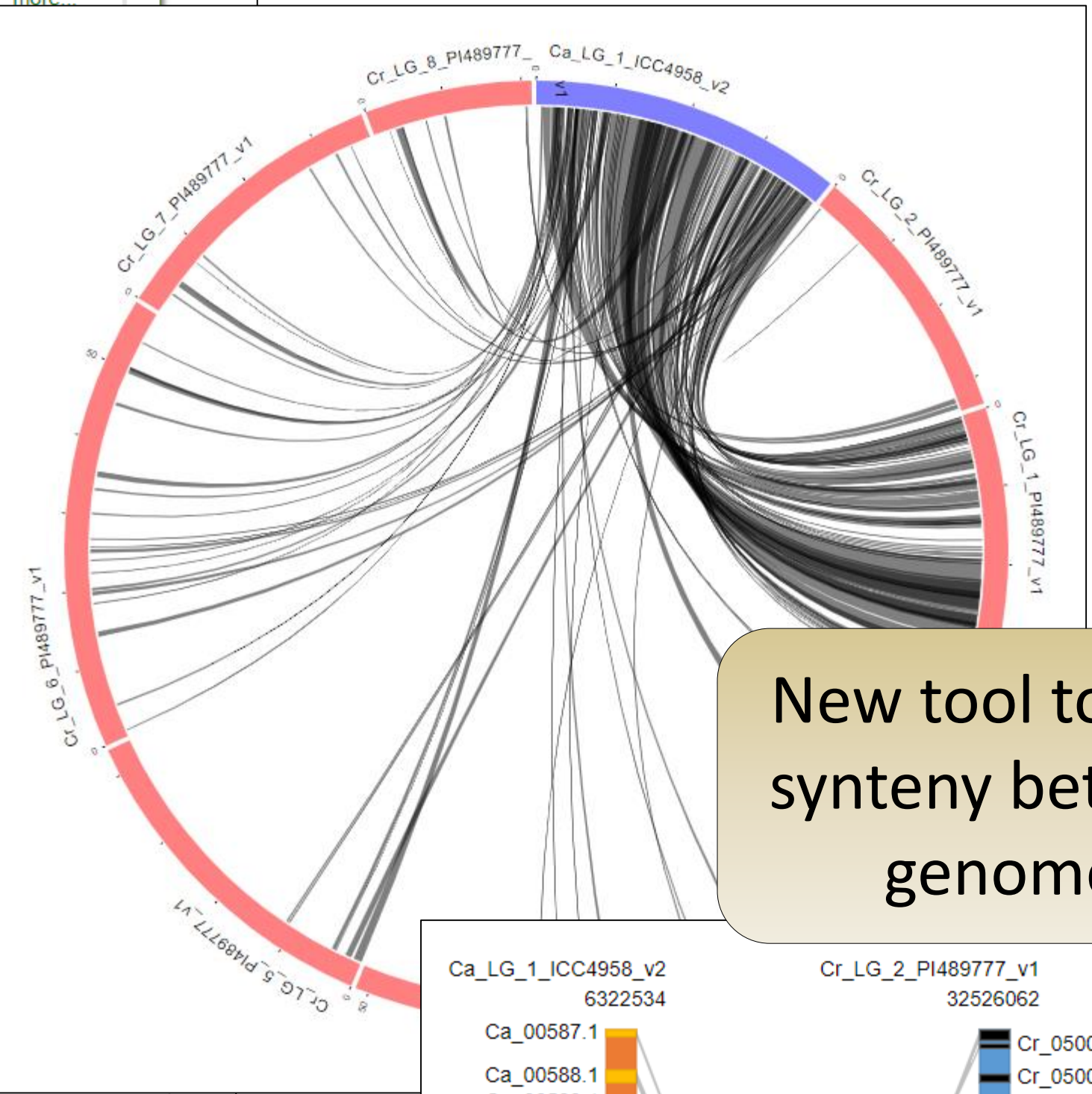
Available Resources	Pea	Lentil	Chickpea	Faba Bean
Markers	11,455	63,474	58,898	3,441
Genetic Maps	45	32	69	21
QTLs	1,320	257	1,104	271
RefTrans v2 Transcripts	63,990	33,613	56,176	37,378
Genomes	0	0	3	0



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

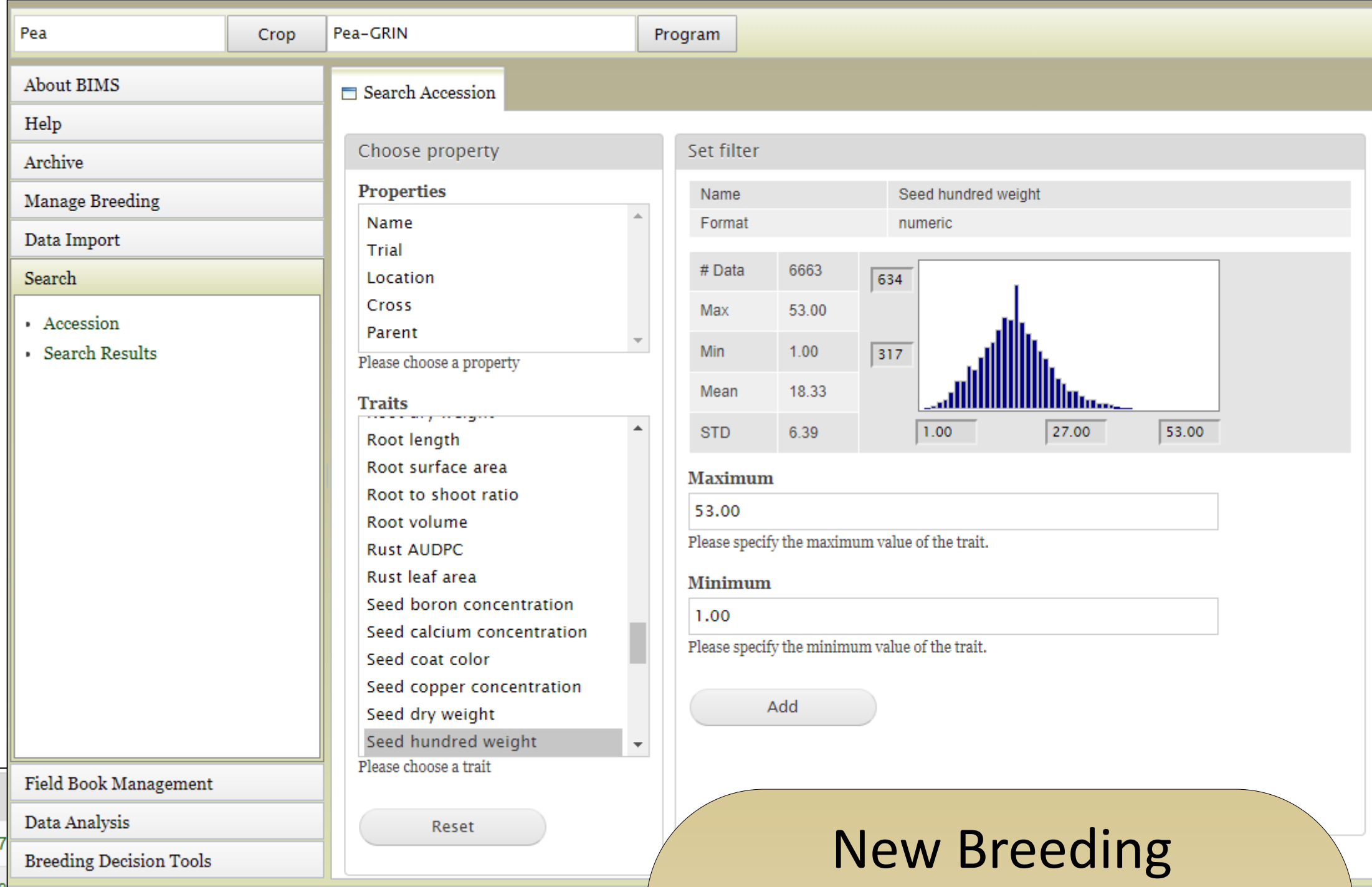


Crop pages allow for easy access to  
crop-specific data and tools



New tool to view  
synteny between  
genomes

Gene A	Gene B
Ca_00587.1	Cr_05000.1
Ca_00588.1	Cr_05002.1
Ca_00589.1	Cr_05005.1
Ca_00590.1	Cr_05006.1
Ca_00591.1	Cr_05009.1
Ca_00592.1	Cr_05011.1
Ca_00593.1	Cr_05014.1
Ca_00594.1	Cr_05016.1
Ca_00595.1	Cr_05018.1
Ca_00596.1	Cr_05021.1
Ca_00597.1	Cr_05025.1
Ca_00598.1	Cr_05027.1
Ca_00599.1	Cr_05032.1
Ca_00600.1	Cr_05034.1
Ca_00601.1	Cr_05036.1
Ca_00602.1	Cr_05038.1
Ca_00603.1	Cr_05040.1
Ca_00604.1	Cr_05044.1
Ca_00605.1	Cr_05046.1
Ca_00606.1	Cr_05048.1
Ca_00607.1	Cr_05050.1
Ca_00608.1	Cr_05051.1
Ca_00609.1	Cr_05055.1
Ca_00610.1	Cr_05056.1



New Breeding  
Information Management  
System (BIMS) available  
for private breeding  
program management.  
USDA-GRIN phenotype  
data for pea, lentil, faba  
bean, and chickpea also  
available to explore using  
BIMS

Funding provided by

Thanks to

