Cool Season Food Legume Crop Database Resources

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North American Pulse Improvement Association Biannual Meeting
November 4-6, 2015
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CSFL Crops Data Search Tools General Login Search

Cool Season Food Legume Crop Database Resources

Genomic, Genetic and Breeding Resources for Pea, Lentil, Chickpea and Faba Bean Crop Improvement

News and Events

- Redesigned CSFL launched November 2, 2015
- NAPIA Meeting, Niagra Falls, Canada, November 5-6, 2015
- CSFL to be presented at PAG XXIV, January 9-13, 2016
- 2nd International Legume Society Conference, Oct 12-14, 2016

more...

Crops Quick Start

lentil

pea

chickpea

faba bean

Tools Quick Start

genomics

- View Genomes
- Find Sequences
- Search Transcripts
- BLAST Sequences

genetics

- Browse Maps
- Search Markers
- Find QTLs
- Compare Maps

breeding

- Manage Breeding
- Manage Data
- Analyze Data
- Decision Tool

general

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- Presentations
- Work in Progress
- Contact Us

USA Dry Pea & Lentil Council | Northern Pulse Growers Association | NRSP10 Crop Database Resources | USDA ARS Agricultural Research Service | Washington State University

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Pea
Lentil
Chickpea
Faba Bean

Data

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CMap
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Cicer arietinum

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- Transcripts

Tools
- Batch BLAST
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- Downloads
- KEGG
- PathwayCyc

Overview

Genus	*Cicer*
Species	*arietinum*
Common Name	chickpea
Abbreviation	*C. arietinum*
Ploidy	Diploid
Chromosome Number	2n=16
Genome Size	~740 Mbp
Available Markers	31,069
Available Maps	40
Available QTLs	505
Available MTLs	19
Available Traits	47
Available Genomes	2

Search Transcripts

Search by Name

Species Any

Name contains

Search by Assembly

Analysis

Any
C. arietinum CSFL RefTrans V1
Cicer arietinum unigene v1
Lens culinaris unigene v1

Search by Putative Function

GO Term contains

BLAST Description contains resistance

KEGG Description contains

INTERPRO Description contains

Submit Reset

439 records were returned

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#	Name	Organism	Length	Type	GO Term	BLAST	KEGG	INTERPRO
1	c.arietinum_csfl_reftransV1_0000062	Cicer arietinum	4404	contig	ADP binding. protein binding. signal transduction	sp|Q40392|TMVRN_NICGU TMV resistance protein N OS=Nicotiana glutinosa GN=N PE=1 SV=1. tr|V5UP77|V5UP77_CICAR TIR-NBS-LRR disease resistance protein OS=Cicer arietinum PE=4 SV=1		ADP binding. ATP BINDING PROTEIN-RELATED. Cytoplasmic domain. DISEASERSIST. L domain-like. LEUCINE-RICH REPEAT-CONTAINING PROTEIN. Leu-rich_rpt_Cys-con_subtyp. Leu-rich_rpt_typical-subtyp. LRR_CC. LRR_TYP. NB-ARC. Non cytoplasmic domain. P-loop containing nucleoside triphosphate hydrolases. P-loop_NTPase. protein binding. signal transduction. TIR. TIR_dom. Toll/Interleukin receptor TIR domain. Transmembrane region
2	c.arietinum_csfl_reftransV1_0000208	Cicer arietinum	292	contig	membrane	sp|Q7PC84|AB39G_ARATH ABC transporter G family member 39 OS=Arabidopsis thaliana GN=ABCG39 PE=3 SV=1. tr|G7L5Z3|G7L5Z3_MEDTR Drug resistance transporter-like ABC domain protein OS=Medicago truncatula		ABC2_membrane. ABC_2_trans. ABC TRANSPORTER G FAMILY MEMBER 29-RELATED. ATP-BINDING CASSETTE TRANSPORTER. Cytoplasmic domain. membrane. Non

c.arietinum_csfl_reftransV1_0000062

- Overview
- Analyses
- Annotated Terms
- Homology
- InterPro
- Sequences

Overview

Name	c.arietinum_csfl_reftransV1_0000062
Unique Name	c.arietinum_csfl_reftransV1_0000062
Type	contig
Organism	*Cicer arietinum* (chickpea)
Sequence length	4404

c.arietinum_csfl_reftransV1_0000062

- Overview
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Analyses

This contig is derived from or has results from the following analyses

Analysis Name	Date Performed
C. arietinum CSFL RefTrans V1	2015-10-19
Homology Analysis:Cicer arietinum CSFL RefTrans V1 vs TrEMBL	2015-10-26
Homology Analysis for Cicer arietinum CSFL RefTrans V1 vs SwissProt	2015-10-26
InterProScan analysis for C. arietinum CSFL RefTrans V1	2015-10-29

C. arietinum CSFL RefTrans V1

Overview

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Overview

Analysis Name	C. arietinum CSFL RefTrans V1
Method	reftrans (1.0)
Source	c.arietinum_csfl_reftransV1
Date performed	2015-10-19
Materials & Methods	CSFL Chickpea RefTrans combines published RNA-Seq and EST data sets to create a reference transcriptome (RefTrans) for chickpea and provides putative gene function identified by homology to known proteins. In C.arietinum_RefTrans_V1, 462 million RNA-Seq reads from publicly available peer-reviewed chickpea RNA-Seq data sets (Garg et al, 2011, Singh et al, 2013, Garg et al, 2011), and 44,618 ESTs, were downloaded from the NCBI Short Read Archive database (SRP003236, SRP017394, SRP006039) and the NCBI dbEST database, respectively. These RNA-Seq data sets include 396 million single-end reads and 66 million paired-end reads generated from Illumina and 454 platforms. The RNA-Seq sequences were subjected to quality control using the NGS QC Toolkit (V2.3.3, default parameters, Patel and Jain, 2012) and custom Perl scripts. The remaining 405 million RNA-Seq reads were assembled de novo with Trinity (v2.0.6, Grabherr et al, 2011) using default assembly parameters and a minimum coding length of 200 bases. Quality control of the ESTs included vector sequence screening (UniVec_Core, ftp://ftp.ncbi.nih.gov/pub/UniVec/) using cross_match (Gordon et al, 1998), removal of tRNA/rRNA/snRNA sequences identified using tblastx (Altschul et al, 1990), and Poly-A tail trimmimg. The filtered ESTs were assembled using the CAP3 program (P -90, Huan and Madan, 1999). Bowtie (v 0.12.7) (Langmead et al, 2009) was applied to multi-map the RNA-Seq reads and ESTs back to the assembled contigs and singlets. The contigs and singlets were hierarchically clustered into genes using Corset (v1.0.4) (Davidson and Oshlack, 2014) with default parameters. The longest isoform was selected to represent each Corset cluster, creating a RefTrans V1 for chickpea of 50,864 sequences. The RefTrans were functionally characterized by pairwise comparison using the BLASTX algorithm against the Swiss-Prot (UniProtKB/Swiss-Prot Release 2015_10) and TrEMBL (UniProtKB/TrEMBL Release 2015_10) (Boeckmann et al, 2003) protein databases. Information on the top 25 matches with an expect (E) value of ≤ 1E-06 were recorded and stored in the database. The transcriptome and annotation (GO Terms, match description, InterPro domains) are available for searching and downloading.

c.arietinum_csfl_reftransV1_0000062

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Homology

The following BLAST results are available for this feature:

- BLAST of c.arietinum_csfl_reftransV1_0000062 vs. TrEMBL
- BLAST of c.arietinum_csfl_reftransV1_0000062 vs. SwissProt

BLAST of c.arietinum_csfl_reftransV1_0000062 vs. TrEMBL
Analysis Date: 2015-10-26 (Homology Analysis:Cicer arietinum CSFL RefTrans V1 vs TrEMBL)
Total hits: 25

Match Name	E-value	Identity	Description
V5UP77_CICAR	0.000000e+0	100.00	TIR-NBS-LRR disease resistance protein OS=Cicer ar...
G7LDU5_MEDTR	0.000000e+0	78.21	Disease resistance protein (TIR-NBS-LRR class), pu...
G7LDU6_MEDTR	0.000000e+0	76.97	Disease resistance protein (TIR-NBS-LRR class), pu...
K7L9P5_SOYBN	0.000000e+0	67.13	Uncharacterized protein OS=Glycine max PE=4 SV=1
K7L9P4_SOYBN	0.000000e+0	67.08	Uncharacterized protein OS=Glycine max PE=4 SV=1
V7C932_PHAVU	0.000000e+0	67.37	Uncharacterized protein OS=Phaseolus vulgaris GN=P...
F6HPI4_VITVI	0.000000e+0	54.88	Putative uncharacterized protein OS=Vitis vinifera...
A5AIN4_VITVI	0.000000e+0	53.15	Putative uncharacterized protein OS=Vitis vinifera...
A0A067GVJ1_CITSI	0.000000e+0	56.25	Uncharacterized protein OS=Citrus sinensis GN=CISI...
A0A061E7D8_THECC	0.000000e+0	56.18	Tir-nbs-lrr resistance protein, putative isoform 1...

1 2 3 next › last »

Search QTLs

Search QTLs and/or MTLs (Mendelian Trait Loci) by any combination of species, trait category, trait name, publish

Type

Any
MTL
QTL

Species

Any
Cicer arietinum
Cicer sp.
Pisum sativum

Trait Category

Any
anatomy and morphology trait
biochemical trait
growth and development trait

Trait Name contains ▾ seed yield (e.g. seed yield, pod number)

Published Symbol contains ▾ (e.g. QBrp.ncl-1.1)

QTL/MTL Label contains ▾ (e.g. qBPL.JG62xVijay.LG1.III)

Submit Reset

51 records were returned

#	Type	Label	Trait Name	Published Symbol	Map
1	QTL	qSYLD.Wt10245xWt11238-F4.LGI	seed yield	2yd-1	
2	QTL	qSYLD.Wt10245xWt11238-F4.LGII	seed yield	2yd-2	
3	QTL	qSYLD.Wt10245xWt11238-F4.LGIII	seed yield	2yd-3	
4	QTL	qSYLD.Wt10245xWt11238-F4.LGIII.2	seed yield	2yd-4	
5	QTL	qSYLD.Wt11238xWt3557.LGVb.B	seed yield	Q1-YIELD-B	pea-Wt11238xWt3557-F5
6	QTL	qSYLD.Wt11238xWt3557.LGVb	seed yield	Q1-YIELD	pea-Wt11238xWt3557-F5
7	QTL	qSYLD.Wt10245xWt11238.LGII	seed yield	Q2-YIELD	pea-Wt10245xWt11238-F5
8	QTL	qSYLD.PrimoxOSU442-15.LGIII.YLD99	seed yield	yld3.1	pea-PrimoxOSU442-15-F2
9	QTL	qSYLD.PrimoxOSU442-15.LGIV.YLD03	seed yield	yld4.2	pea-PrimoxOSU442-15-F2
10	QTL	qSYLD.PrimoxOSU442-15.LGVII.YLD03	seed yield	yld7.2	pea-PrimoxOSU442-15-F2
11	QTL	qSYPLOT.PrimoxOSU442-15.LGVII.YLD98	seed yield per plot	yld7.1	pea-PrimoxOSU442-15-F2
12	QTL	qSYLD.PrimoxOSU442-15.LGVII.YLD99	seed yield	yld7.2	pea-PrimoxOSU442-15-F2
13	QTL	qSYLD.Wt10245xWt11238-F2.LGIII	seed yield	1yd-1	
14	QTL	qSYLD.Wt10245xWt11238-F2.LGIV	seed yield	1yd-2	
15	QTL	qSYLD.Wt10245xWt11238-F2.LGVII	seed yield	1yd-3	
16	QTL	qSYLD.Wt10245xWt11238-F4.LGIII.3	seed yield	2yd-5	
17	QTL	qSYLD.Wt10245xWt11238-F4.LGVI	seed yield	2yd-6	
18	QTL	qSDYD.CarnevalxMP1401.LGII.E_2000	seed yield	GY.LGII.gccc3.E_2000	
19	QTL	qSDYD.CarnevalxMP1401.LGII.M_2000	seed yield	GY.LGII.gccc3.M_2000	
20	QTL	qSDYD.CarnevalxMP1401.LGVI.F_2000	seed yield	GY.LGVI.gcta2.F_2000	

Number of branches per plant

- QTL Overview
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QTL Overview

QTL Label	qBPL.JG62xVijay.LG2.P
Published Symbol	QBrp.ncl-2.1
Trait Name	Number of branches per plant
Trait Alias	N/A
Trait Study	Chickpea-agronomic_yield_trait-Kadoo-2011
Population	JG62_x_Vijay-RIL
Female Parent	JG62
Male Parent	Vijay
Colocalizing Marker	TA47
Neighboring Marker	N/A
LOD	3.20
Additivity Dominance Ratio	N/A
R2	0.11
Comments	N/A

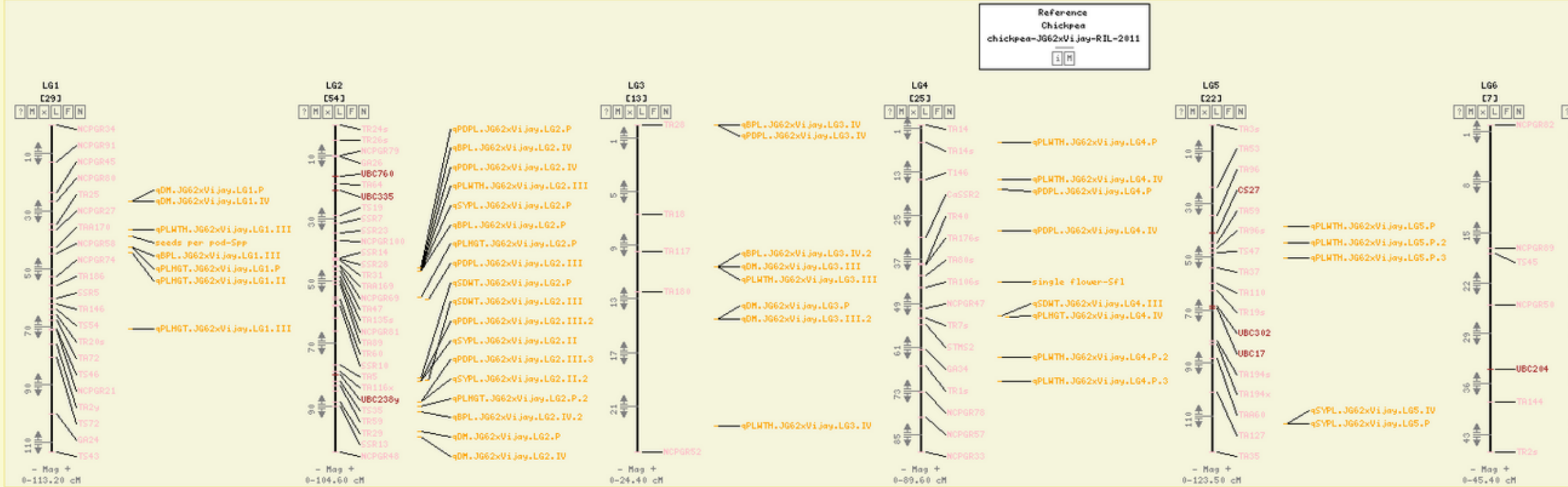
chickpea-JG62xVijay-RIL-2011

- Map Overview
- Map Loci
- Cross References
- Publications
- Contact

Map Overview

Name	chickpea-JG62xVijay-RIL-2011 [View in CMap]
Species	Cicer arietinum
Map type	genetic
Population type	RIL
Map unit	cM
Maternal parent	JG62
Paternal parent	Vijay
Population size	197
Number of loci	112
Number of linkage groups	8
Publication	[view all]
Contact	Naredra Kadoo

CMap


Reference
Chickpea
chickpea-JG62xVijay-RIL-2011
LG1
[29]
qDM.JG62xVijay.LG1.P
qDM.JG62xVijay.LG1.IV
qPLWTH.JG62xVijay.LG1.III
seeds per pod-Spp
qBPL.JG62xVijay.LG1.III
qPLHGT.JG62xVijay.LG1.P
qPLHGT.JG62xVijay.LG1.II
qPLHGT.JG62xVijay.LG1.III
- Mag +
0-113.20 cM
LG2
[54]
UBC760
UBC335
UBC238y
qPDPL.JG62xVijay.LG2.P
qBPL.JG62xVijay.LG2.IV
qPDPL.JG62xVijay.LG2.IV
qPLWTH.JG62xVijay.LG2.III
qSYPL.JG62xVijay.LG2.P
qBPL.JG62xVijay.LG2.P
qPLHGT.JG62xVijay.LG2.P
qPDPL.JG62xVijay.LG2.III
qSDWT.JG62xVijay.LG2.P
qSDWT.JG62xVijay.LG2.III
qPDPL.JG62xVijay.LG2.III.2
qSYPL.JG62xVijay.LG2.II
qPDPL.JG62xVijay.LG2.III.3
qSYPL.JG62xVijay.LG2.II.2
qPLHGT.JG62xVijay.LG2.P.2
qBPL.JG62xVijay.LG2.IV.2
qDM.JG62xVijay.LG2.P
qDM.JG62xVijay.LG2.IV
- Mag +
0-104.60 cM
LG3
[13]
qBPL.JG62xVijay.LG3.IV
qPDPL.JG62xVijay.LG3.IV
qBPL.JG62xVijay.LG3.IV.2
qDM.JG62xVijay.LG3.III
qPLWTH.JG62xVijay.LG3.III
qDM.JG62xVijay.LG3.P
qDM.JG62xVijay.LG3.III.2
qPLWTH.JG62xVijay.LG3.IV
- Mag +
0-24.40 cM
LG4
[25]
qPLWTH.JG62xVijay.LG4.P
qPLWTH.JG62xVijay.LG4.IV
qPDPL.JG62xVijay.LG4.P
qPDPL.JG62xVijay.LG4.IV
single flower-Sfl
qSDWT.JG62xVijay.LG4.III
qPLHGT.JG62xVijay.LG4.IV
qPLWTH.JG62xVijay.LG4.P.2
qPLWTH.JG62xVijay.LG4.P.3
- Mag +
0-89.60 cM
LG5
[22]
CS27
UBC302
UBC17
qPLWTH.JG62xVijay.LG5.P
qPLWTH.JG62xVijay.LG5.P.2
qPLWTH.JG62xVijay.LG5.P.3
qSYPL.JG62xVijay.LG5.IV
qSYPL.JG62xVijay.LG5.P
- Mag +
0-123.50 cM
LG6
[7]
UBC204
- Mag +
0-45.40 cM
Feature Types:
ISSR
RAPD
STMS
MTL
QTL
Menu Symbols:
Map Set Info
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Matrix View
Limit to One Map
Delete Map Set
Delete Map
Flip Map

Search Markers

Search by Name

Marker Name contains

File Upload Choose File No file chosen Provide marker names in a file. Separate each name

Restrict by Features

Marker Type Any

Marker Developed from Species Any

Marker Mapped in Species Any

Restrict by Location

Map Any

Linkage Group Any **between** **and** **cM**

Submit Reset

1187 records were returned

Download Table

#	Name	Alias	Type	Species	Map	Linkage Group	Start	Stop
1	AD57	AD57_280; PSAD57	SSR	Pisum sativum	pea-ShawneexBohatyr-RIL	pea-ShawneexBohatyr-RIL.LGIIIb.3	0	
2	AD175	AD175_405; PSMPSAD175; AD175-405; PSAD175	SSR	Pisum sativum	pea-OrbxCDCStriker-RIL	pea-OrbxCDCStriker-RIL.LGV	43.1	
3	AB104	AB104-242; AB104_1; AB104_2; AB104_242	SSR	Pisum sativum	pea-ShawneexBohatyr-RIL	pea-ShawneexBohatyr-RIL.LGIIIa.3	36.8	
4	AD61	AD61_138	SSR	Pisum sativum	pea-microsatComposite-2005	pea-microsatComposite-2005.LGIV	165.8	
5	AA153	AA153_253; AA153-370	SSR	Pisum sativum	pea-ShawneexBohatyr-RIL	pea-ShawneexBohatyr-RIL.LGIIa.3	89.2	
6	AD144	PSMPSAD144; AD144-250	SSR	Pisum sativum	pea-OrbxCDCStriker-RIL	pea-OrbxCDCStriker-RIL.LGII-2	12.9	
7	AD180	AD180_190; AD180c; AD180b; AD180-133; AD180-161; AD180-190; PSMPSAD180; AD180_60; AD180_161	SSR	Pisum sativum	pea-ShawneexBohatyr-F7-RIL	pea-ShawneexBohatyr-F7-RIL.LGIII	27	
8	AD147	PSMPSAD147; PSAD147	SSR	Pisum sativum	pea-TeresexChampagne-RIL	pea-TeresexChampagne-RIL.LGI.2	70.6	
9	PSIAA6D		SSR	Pisum sativum	pea-JI296xDP-F2:6-RIL	pea-JI296xDP-F2:6-RIL.LG7	210	

TA194

Marker Overview
Map Positions
Publications
Relationships
Synonyms

Marker Overview

Name	TA194
Alias	TA194s TA194x
Genbank ID	N/A
Type	STMS
Probe	N/A
Species	Cicer arietinum
Germplasm	ILC3279
Source Sequence	N/A
Source Type	N/A
Repeat Motif	(TTA)21
PCR Condition	N/A
Primer 1	TA194.Forward primer: TTTTTGGCTTATTAGACTGACTT
Primer 2	TA194.Reverse primer: TTGCCATAAAATACAAAATCC
Product Length	132
Max Length	N/A
Restriction Enzyme	N/A

Search Sequences

Search for sequences by entering names in the field below. Alternatively, you may upload a file of names. You may also filt
source. To select multiple options click while holding the "ctrl" key. The results can be downloaded in FASTA or CSV tabula

Species

Any
Cicer arietinum
Lens culinaris
Pisum sativum

Type

Any
contig
EST
mRNA

Source

Any
C. arietinum CDC Frontier Whole Genome v1.0 Assembly and Annotation
C. arietinum CSFL RefTrans V1
Cicer arietinum unigene v1

Name contains

File Upload Choose File No file chosen Provide sequence names in a file. Separate each name by a new line.

Location Any **between** **and**

Submit Reset

File Upload Choose File No file chosen Provide sequence names in a file. Separate each name by a new line.

Location Any ▼ between and

Submit Reset

68622 records were returned

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#	Name	Uniquename	Type	Organism	Source	Location
1	Ps_singlet_mira-and-tgicl-ass_franssen_3249	Ps_singlet_mira-and-tgicl-ass_franssen_3249	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
2	Ps_singlet_mira-and-tgicl-ass_franssen_8516	Ps_singlet_mira-and-tgicl-ass_franssen_8516	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
3	Ps_singlet_mira-and-tgicl-ass_franssen_4718	Ps_singlet_mira-and-tgicl-ass_franssen_4718	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
4	Ps_contig_mira-and-tgicl-ass_franssen_42043	Ps_contig_mira-and-tgicl-ass_franssen_42043	contig	Pisum sativum	Franssen 2011 P. sativum unigene	
5	Ps_singlet_mira-and-tgicl-ass_franssen_26159	Ps_singlet_mira-and-tgicl-ass_franssen_26159	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
6	Ps_contig_mira-and-tgicl-ass_franssen_27762	Ps_contig_mira-and-tgicl-ass_franssen_27762	contig	Pisum sativum	Franssen 2011 P. sativum unigene	
7	Ps_singlet_mira-and-tgicl-ass_franssen_12600	Ps_singlet_mira-and-tgicl-ass_franssen_12600	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
8	Ps_contig_mira-and-tgicl-ass_franssen_37507	Ps_contig_mira-and-tgicl-ass_franssen_37507	contig	Pisum sativum	Franssen 2011 P. sativum unigene	
9	Ps_contig_mira-and-tgicl-ass_franssen_40898	Ps_contig_mira-and-tgicl-ass_franssen_40898	contig	Pisum sativum	Franssen 2011 P. sativum unigene	
10	Ps_singlet_mira-and-tgicl-ass_franssen_8024	Ps_singlet_mira-and-tgicl-ass_franssen_8024	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
11	Ps_singlet_mira-and-tgicl-ass_franssen_9186	Ps_singlet_mira-and-tgicl-ass_franssen_9186	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
12	Ps_singlet_mira-and-tgicl-ass_franssen_5116	Ps_singlet_mira-and-tgicl-ass_franssen_5116	EST	Pisum sativum	Franssen 2011 P. sativum unigene	
13	Ps_contig_mira-and-tgicl-ass_franssen_6576	Ps_contig_mira-and-tgicl-ass_franssen_6576	contig	Pisum sativum	Franssen 2011 P. sativum unigene	
14	Ps_singlet_mira-and-tgicl-ass_franssen_2062	Ps_singlet_mira-and-tgicl-ass_franssen_2062	EST	Pisum	Franssen 2011 P. sativum unigene	

Search Publications

To search for publications enter keywords in the text boxes below. You can limit your search by selecting the field in the dropdown box. Click the add and remove buttons to add additional fields for searching.

Authors ▼ coyne

AND ▼ Any Field ▼ Add Remove

Years ▼ from 2014 to 2015

Search Reset

Found 4 Results

	Year	Publication
1.	2015	Association mapping of agronomic and quality traits in USDA pea single-plant collection Cheng P, Holdsworth W, Ma Y, Coyne CJ, Mazourek M, Grusak MA, Fuchs S, McGee RJ. Association mapping of agronomic and quality traits in USDA pea single-plant collection. Molecular breeding. 2015; 35(2):277.
2.	2015	Identification of QTL controlling high levels of partial resistance to Fusarium solani f. sp. pisi in pea Coyne CJ, Pilet-Nayel ML, McGee RJ, Porter LD, Smykal P, Grunwald NJ. Identification of QTL controlling high levels of partial resistance to Fusarium solani f. sp. pisi in pea. Plant Breeding. 2015.
3.	2014	Geographical Gradient of the eIF4E Alleles Conferring Resistance to Potyviruses in Pea (Pisum) Germplasm Konečná E, Safářová D, Navrátil M, Hanáček P, Coyne C, Flavell A, Vishnyakova M, Ambrose M, Redden R, Smýkal P. Geographical Gradient of the eIF4E Alleles Conferring Resistance to Potyviruses in Pea (Pisum) Germplasm. PloS one. 2014; 9(3):e90394.
4.	2014	Target region amplification polymorphism (TRAP) for assessing genetic diversity and marker-trait associations in chickpea (Cicer arietinum L.) germplasm Kumar Y, Kwon SJ, Coyne CJ, Hu J, Grusak MA, Kisha TJ, McGee RJ, Sarker A. Target region amplification polymorphism (TRAP) for assessing genetic diversity and marker-trait associations in chickpea (Cicer arietinum L.) germplasm. Genetic resources and crop evolution. 2014; 61(5):965-977.

Association mapping of agronomic and quality traits in USDA pea single-plant collection

Overview
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Overview

Title	Association mapping of agronomic and quality traits in USDA pea single-plant collection
Authors	Cheng P, Holdsworth W, Ma Y, Coyne CJ, Mazourek M, Grusak MA, Fuchs S, McGee RJ
Type	Journal Article
Journal Name	Molecular breeding
Volume	35
Issue	2
Year	2015
Page(s)	277
Citation	Cheng P, Holdsworth W, Ma Y, Coyne CJ, Mazourek M, Grusak MA, Fuchs S, McGee RJ. Association mapping of agronomic and quality traits in USDA pea single-plant collection. Molecular breeding. 2015; 35(2):277.

Abstract

Association mapping is an efficient approach for the identification of the molecular basis of agronomic traits in crop plants. For this purpose in pea (Pisum sativum L.), we genotyped and phenotyped individual lines of the single-plant-derived core collection of the USDA pea collection including accessions from 330 landraces and cultivars of Pisum sativum subsp. sativum var. sativum, 28 P. sativum subsp. elatius var. elatius, 16 P. sativum subsp. sativum var. arvense, four P. sativum subsp. elatius var. pumilio, three P. abyssinicum, two P. fulvum, and one P. sativum subsp. transcaucasicum. These 384 accessions were collected or donated from a total of 64 countries. The accessions were genotyped with 256 informative SNPs using a primer extension chemistry and matrix-assisted laser desorption/ionization (MALDI–TOF) mass spectrometry assay. Genetic structure analysis showed that the collection was structured into two main groups, corresponding roughly to the cultivated types/landraces and the more primitive form species and subspecies, with some intermediates. Linkage disequilibrium of pairwise loci and population structure of the collection were analyzed, and an association analysis between SNP genotypes and 25 valuable traits such as disease resistance, seed type/color, flower color, seed low molecular weight carbohydrate concentration, and seed mineral nutrient concentration was performed using a mixed linear model. A total of 71 marker–trait associations were detected as significant with 1–34 markers per trait based on the false discovery rate (FDR < 0.05). This study demonstrates the potential of using association mapping to identify markers for pea breeding.

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Molecular Breeding
February 2015, 35:75

First online: 08 February 2015

Association mapping of agronomic and quality traits in USDA pea single-plant collection

Peng Cheng, William Holdsworth, Yu Ma, Clarice J. Coyne, Michael Mazourek, Michael A. Grusak, Sam Fuchs, Rebecca J. McGee

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Cicer arietinum

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- Transcripts

Tools
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- BLAST
- CMap
- Community Annotation
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- KEGG
- PathwayCyc

Overview

Genus	*Cicer*
Species	*arietinum*
Common Name	chickpea
Abbreviation	*C. arietinum*
Ploidy	Diploid
Chromosome Number	2n=16
Genome Size	~740 Mbp
Available Markers	31,069
Available Maps	40
Available QTLs	505
Available MTLs	19
Available Traits	47
Available Genomes	2

Cicer arietinum ICC 4958 genome v2.0

Overview

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Overview

Analysis Name	Cicer arietinum ICC 4958 genome v2.0
Method	whole genome and paired-end sequencing (454/Roche and Illuminia HiSeq1000). NEWBLER v2.6 and SOAP de novo gap closure v1.1
Source	Cultivar ICC4958, desi type chickpea
Date performed	2015-08-11

Publication

Parween et al. 2015. An advanced draft genome assembly of a *desi* type chickpea (*Cicer arietinum* L.). Scientific Reports 5:12806

About the Assembly (from Parween et al.):

Total size (base)	510,879,539
Number of scaffolds	38,513
Minimum scaffold length(bp)	1000
Maximum scaffold length(bp)	54,992,815
Average scaffold length(bp)	13,265
N50 length(bp)	39,901,017
N50 index	6
GC content (%)	27.95

Cicer arietinum ICC 4958 genome v2.0

Overview

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***C. arietinum* ICC 4958, Desi Type, Genome Assembly v2.0 Files:**

- Chromosomes and scaffolds [Fasta Format]
- CDS [Fasta Format]
- Peptides [Fasta Format]
- Gene Models [GFF3 Format]

Cicer arietinum

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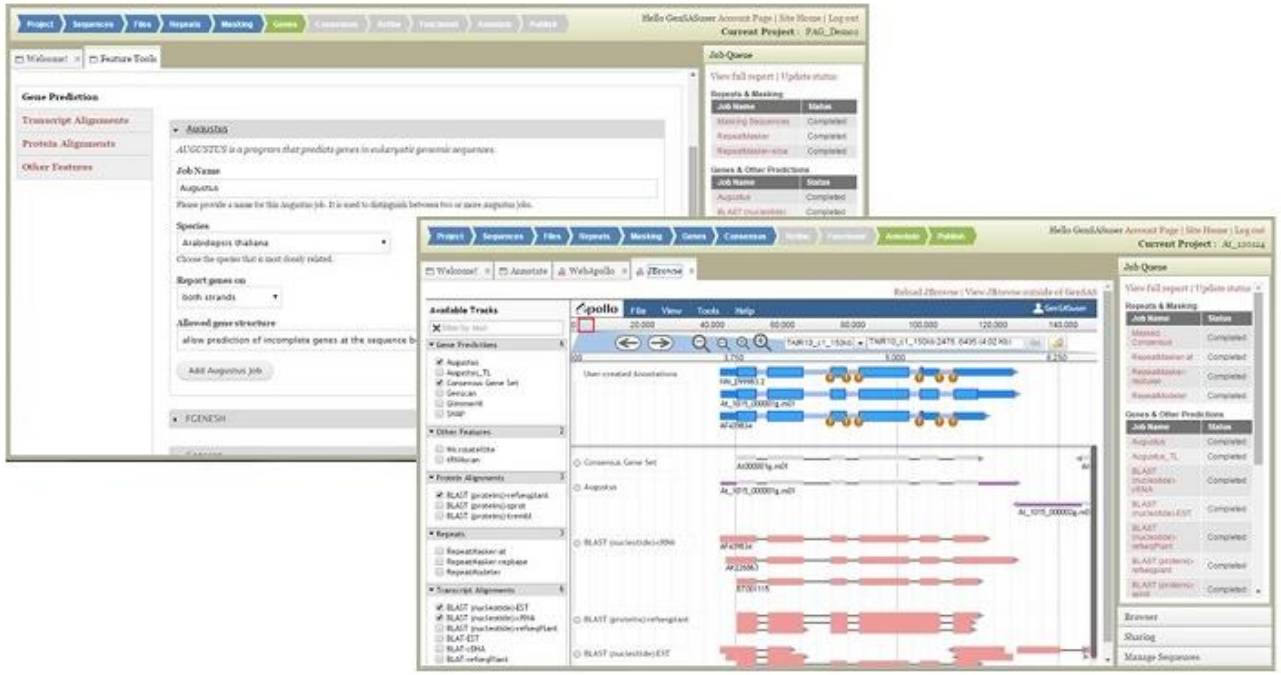
Available MTLs	19
Available Traits	47
Available Genomes	2

GenSAS v4.0

Home | Use GenSAS | Available Tools | Help

Welcome to GenSAS

The Genome Sequence Annotation Server (GenSAS) is an online tool that provides a pipeline for whole genome structural annotation. Users can upload genome sequences and select from a variety of tools for repeat masking, prediction of gene models and other structural features. GenSAS integrates with JBrowse and Web Apollo to provide visualization and editing. Please see our video tutorial under the "Help" tab. Full support for functional annotation is coming soon!



What's Coming!

Look for these improvements soon!

User login

Username *

Password *

- Create new account
- Request new password

Log in

GenSAS tools

Repeat Finding
RepeatMasker
RepeatModeler

Other
Getorf
SSR finder
tRNAScan

Refine Gene Model
PASA

Result viewer
JBrowse

Gene Prediction
Augustus
Genscan
GlimmerM
SNAP
Glimmer3

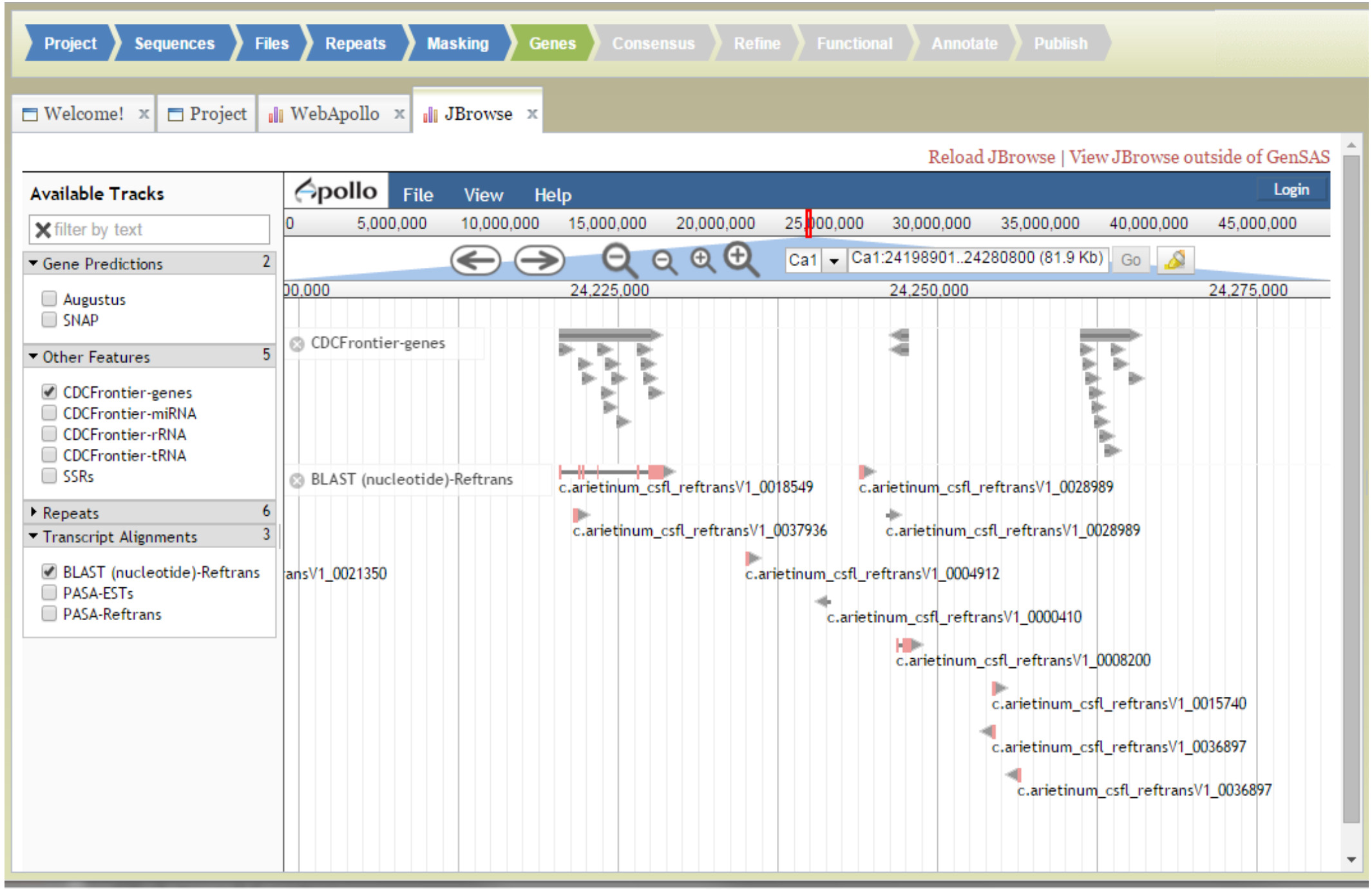
Functional
BLAST
InterProScan
Pfam
SignalP
TargetP

Transcript Alignment
BLAST
BLAT
PASA

Protein Alignment
BLAST

Gene Model Consensus
Evidence Modeler

Annotation Editor
Web Apollo


Project
Sequences
Files
Repeats
Masking
Genes
Consensus
Refine
Functional
Annotate
Publish
Welcome!
Project
WebApollo
JBrowse
Reload JBrowse | View JBrowse outside of GenSAS
Available Tracks
filter by text
Gene Predictions 2
Augustus
SNAP
Other Features 5
CDCFrontier-genes
CDCFrontier-miRNA
CDCFrontier-rRNA
CDCFrontier-tRNA
SSRs
Repeats 6
Transcript Alignments 3
BLAST (nucleotide)-Reftrans
PASA-ESTs
PASA-Reftrans
Apollo
File
View
Help
Login
0
5,000,000
10,000,000
15,000,000
20,000,000
25,000,000
30,000,000
35,000,000
40,000,000
45,000,000
Ca1
Ca1:24198901..24280800 (81.9 Kb)
Go
00,000
24,225,000
24,250,000
24,275,000
CDCFrontier-genes
BLAST (nucleotide)-Reftrans
c.arietinum_csfl_reftransV1_0018549
c.arietinum_csfl_reftransV1_0028989
c.arietinum_csfl_reftransV1_0037936
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https://www.coolseasonfoodlegume.org/data_submission

Bookmarks wsu email YouTube Google facebook Intranet Mainlab CottonGen GDR GNews Twinkle Amazon weather Gene | Cottongen Other book

Data Submission

Please contact us to arrange transfer of data to the Cool Season Food Legume Genome database from accepted peer reviewed work. Below are Excel template files for genetic map, QTL, genotype and phenotype data. We recommend you contact us before filling in the template so that we can work closely with you to ensure this process is expediated easily and quickly. If you have other data types such as transcriptome data or genome data, please contact us and we will work with you to get the data accessible in the database..

- Diversity data template
- Map (genetic) data template (for quick display in CMap, use CMap template)
- Map (QTL) data template
- Breeding data templates

USA Dry Pea & Lentil Council
Northern Pulse Growers Association
NRSP10 Crop Database Resources
USDA ARS Agricultural Research Service
Washington State University

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NRSP_Databases.pptx
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Publication Datasets

This page provides links to the original author datasets referred to in publication text.

Cheng P, Holdworth W, Ma Y, Coyne CJ, Mazourek M, Grusak MA, Fuchs S, McGee, RJ. 2015. Association mapping for agronomic and quality traits in USDA Pea Single-Plant collection. Molecular Breeding 35(2):75. DOI 10.1007/s11032-015-0277-6

- Excel file of SNP data from Cheng et al.

Arun-Chinnappa KS, McCurdy DW. 2015. De novo assembly of a genome-wide transcriptome map of Vicia faba (L.) for transfer cell research. Frontiers in Plant Science. 6:217. doi:10.3389/fpls.2015.00217

- Fasta file of transcriptome contigs from Arun-Chinnappa and McCurdy

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Work in Progress

- Addition of marker (11 pubs), map (6 pubs) and QTL (11 pubs) data for lentil
- Generation of ChickpeaCyc for desi type genome (ICC 4958)
- Continued addition of newly published marker, map, and QTL data for chickpea, pea, and faba bean
- Creation of Reference Transcriptome (RefTrans) for pea, lentil, faba bean
- Integrated GenSAS instance for CSFL community annotation projects
- Further improvements of website for increased usability
- Addition of breeding and phenotype data and development of a breeding management system
- Preparation of short tutorial videos to train users
- Manuscript in preparation

Breeding Management System Outline

As part of our NRSP10 Project we are developing a Breeding Management System for Tripal databases. In the text below we describe our goals and an outline of the functionality. Please let us know if you have any questions and/or suggestions.

Vision:

To provide individual breeders with a secure and comprehensive online breeding management system which will allow them to store, manage and analyze their private data, fully integrated with publicly available genomic, genetic and breeding data. The BMS will support the use of Field Book App, an Android App for collecting phenotype data in the field.

Components of BMS (Shown in navigation bar format)**:**

Manage Breeding

- Breeding program
- Manage lists (generate lists to download data and/or to use in other tools of BMS such as creating trials/crosses or generating Field Book input file)
- Location
- Trial
- Cross

Data import

- Germplasm
- Trait descriptors
- Phenotyping data
- Genotyping data

Breeding Management System Outline Cont.

Search/Download

- Search Germplasm
  - by name (limit by program, trial and location)
  - by phenotype
  - by genotype
  - by parentage
- Compare Germplasm
- Search Dataset
- Search Marker
- Search QTL

Field Book App Management

- Download files for Field Book App
- Load Field Book output

Data Analysis Tools

- Statistical analysis for the dataset

Breeding Decision Tools

- Cross Assist (Tool to choose the most efficient parents to produce progeny with certain traits)
- Seedling Select (Tool to determine the cost efficiency of marker-assisted breeding)

Acknowledged with Thanks

- Funding Sources

USA Dry Pea & Lentil Council | Northern Pulse Growers Association | NRSP10 Crop Database Resources | USDA ARS Agricultural Research Service | Washington State University

- The Tripal and Bioinformatics community
- The Legume Community