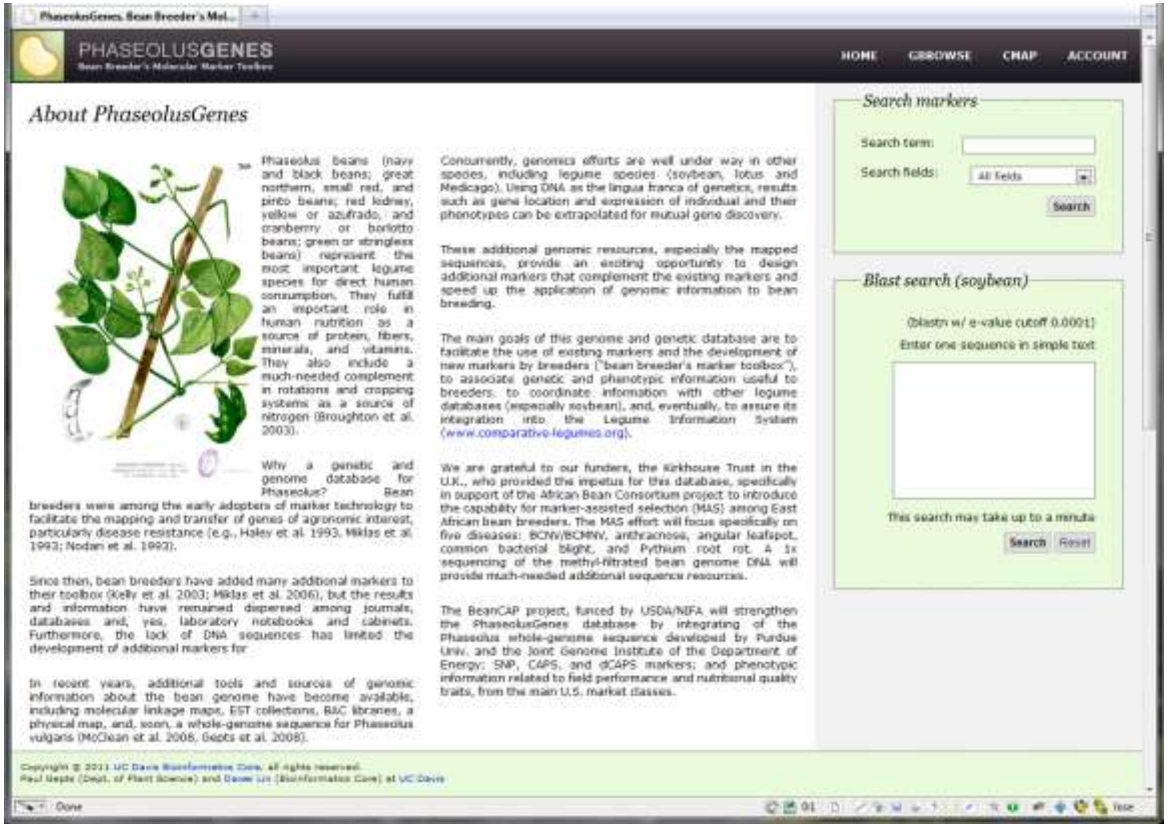

About PhaseolusGenes

Phaseolus beans (navy and black beans; great northern, small red, and pinto beans; red kidney, yellow or azufrado, and cranberry or borlotto beans; green or stringless beans) represent the most important legume species for direct human consumption. They fulfill an important role in human nutrition as a source of protein, fibers, minerals, and vitamins. They also include a much-needed complement in rotations and cropping systems as a source of nitrogen (Broughton et al. 2003).

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In recent years, additional tools and sources of genomic information about the bean genome have become available, including molecular linkage maps, EST collections, BAC libraries, a physical map, and, soon, a whole-genome sequence for Phaseolus vulgaris (McClean et al. 2008, Gepts et al. 2008).

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Search markers

Search term:

Search fields: All Fields

Blast search (soybean)

(blastn w/ e-value cutoff 0.0001)

Enter one sequence in simple text

This search may take up to a minute

Paul Gepts (Dept. of Plant Science) and Dawei Lin (Bioinformatics Core) at UC Davis

Contribution of UC Davis to the BeanCAP

Further Development of PhaseolusGenes,
Bean Breeder's Marker Toolbox

United States Department of Agriculture
National Institute of Food and Agriculture

Contributors

- Dawei Lin
- Jose Boveda
- Monica Britton
- Joe Fass
- Nikhil Joshi
- Zhi-Wei Lu
- Shelby Repinski
- Adriana Navarro Gómez
- Paul Gepts

Outline

- Introduction: Paul
- Database structure: Dawei
- Microsatellite marker integration: Paul
- QTL survey: Adriana
- Conclusion: Paul

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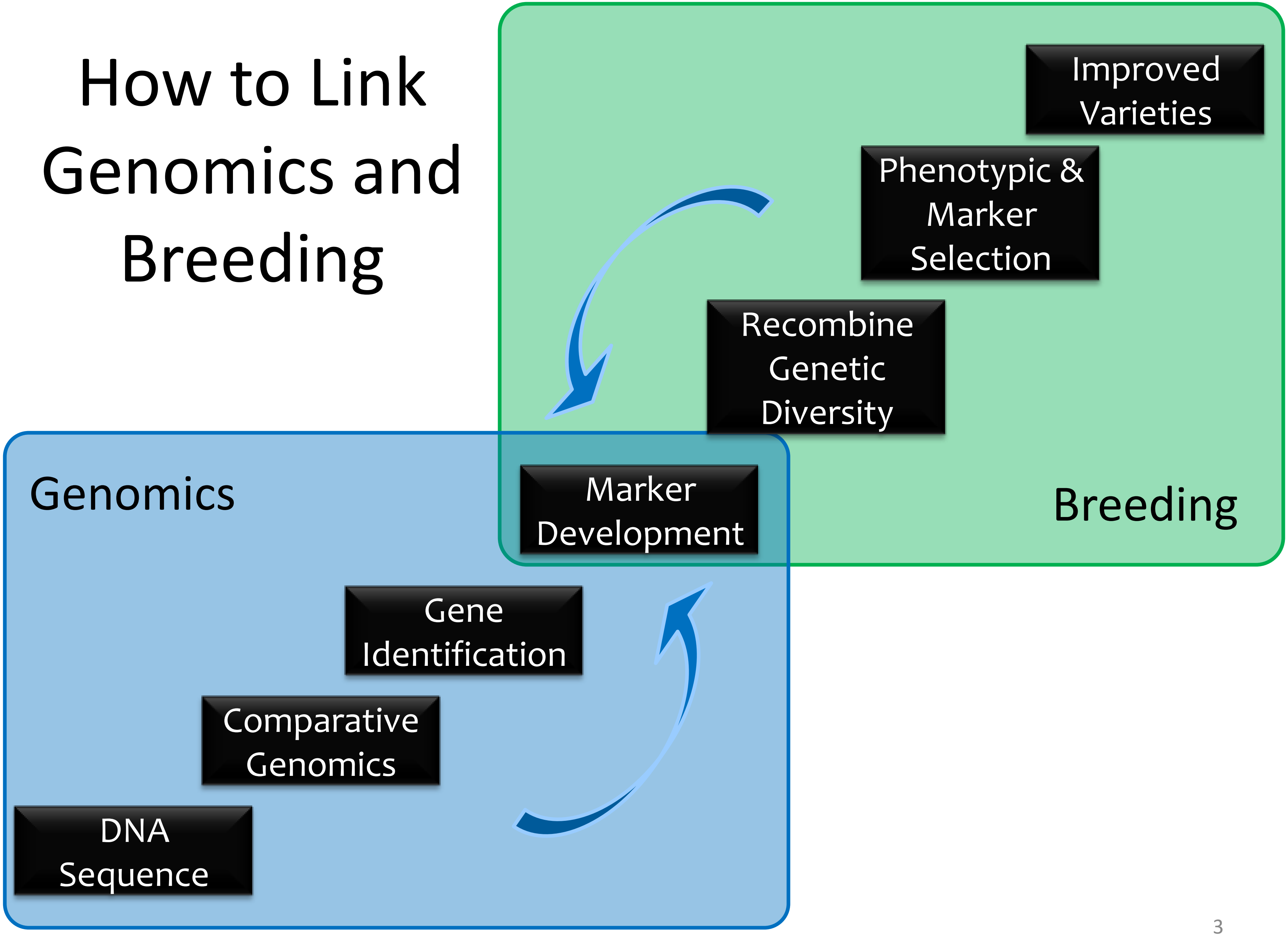
BEAN CAP

How to Link Genomics and Breeding



Genomics

DNA Sequence

Comparative Genomics

Gene Identification

Marker Development

Breeding

Recombine Genetic Diversity

Phenotypic & Marker Selection

Improved Varieties

Antecedents (I)

- Bean researchers have actively developed markers since early 1990s:
  - currently 76 SCAR markers;
  - 80-90% of released bean varieties in last decade have a MAS component
  - main limiting factor: absence of sequence
- Information about markers is dispersed
- African Bean Consortium project: early version of database; limited by its objectives:
  - Introduce MAS
  - 5 major diseases

Markers in *Phaseolus*

Marker Type	Examples	Number
SCAR markers	ALS, ANT, BCM, BCT BGYM, CBB, HB, Rust, WM, FW, Apion, Seed or Floral Pigmentation/pattern	76
Genes of putative agronomic interest	P metabolism, polyphenolics, flowering time, …	38
RAPD	Rust	1
STSs	RFLP, Leg, g	633
SSRs	BM, GATS, PvBR, BMd, BMc, SSR-IAC, PV, FJ, …	795
	Total	~ 1540

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Antecedents (II)

- New types of data:
  - ESTs
  - Genome survey sequence
  - Whole-genome sequence
  - SNP
  - Comparative genomics: soybean WGS, Arabidopsis
- Rapid addition of new information

Dawei Lin:
Director, Bioinformatics Core, Genome Center, UC Davis

United States Department of Agriculture
National Institute of Food and Agriculture

Bioinformatics in Marker Discovery

- Genomics
  - – Genome Browsing
  - – Comparative Genomics
  - – Large Scale Functional Predictions
- Curated Functional Information
- Genetic Mapping

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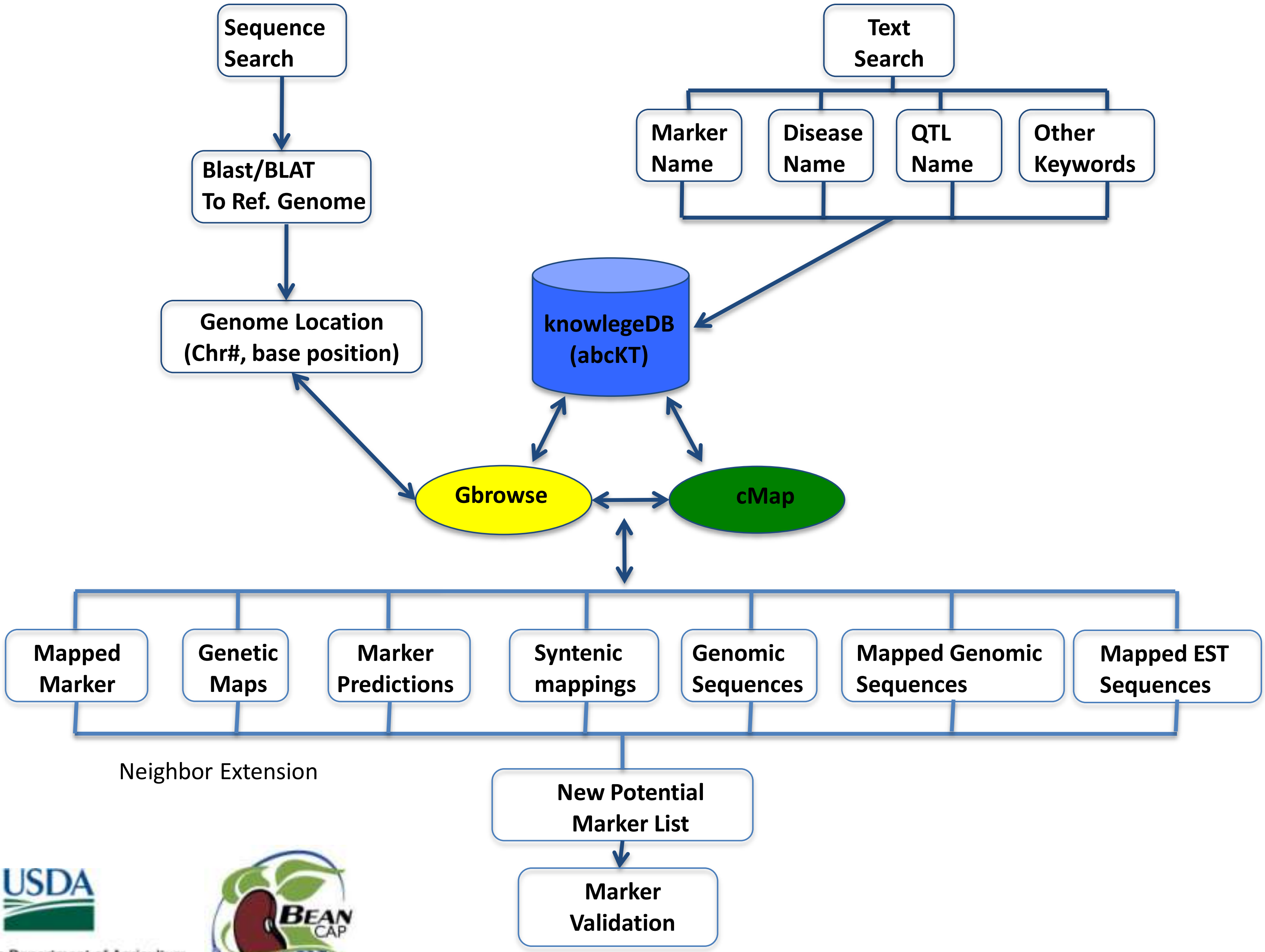

Sequence Search

Blast/BLAT To Ref. Genome

Genome Location (Chr#, base position)

Text Search

Marker Name

Disease Name

QTL Name

Other Keywords

knowlegeDB (abcKT)

Gbrowse

cMap

Mapped Marker

Genetic Maps

Marker Predictions

Syntenic mappings

Genomic Sequences

Mapped Genomic Sequences

Mapped EST Sequences

Neighbor Extension

New Potential Marker List

Marker Validation

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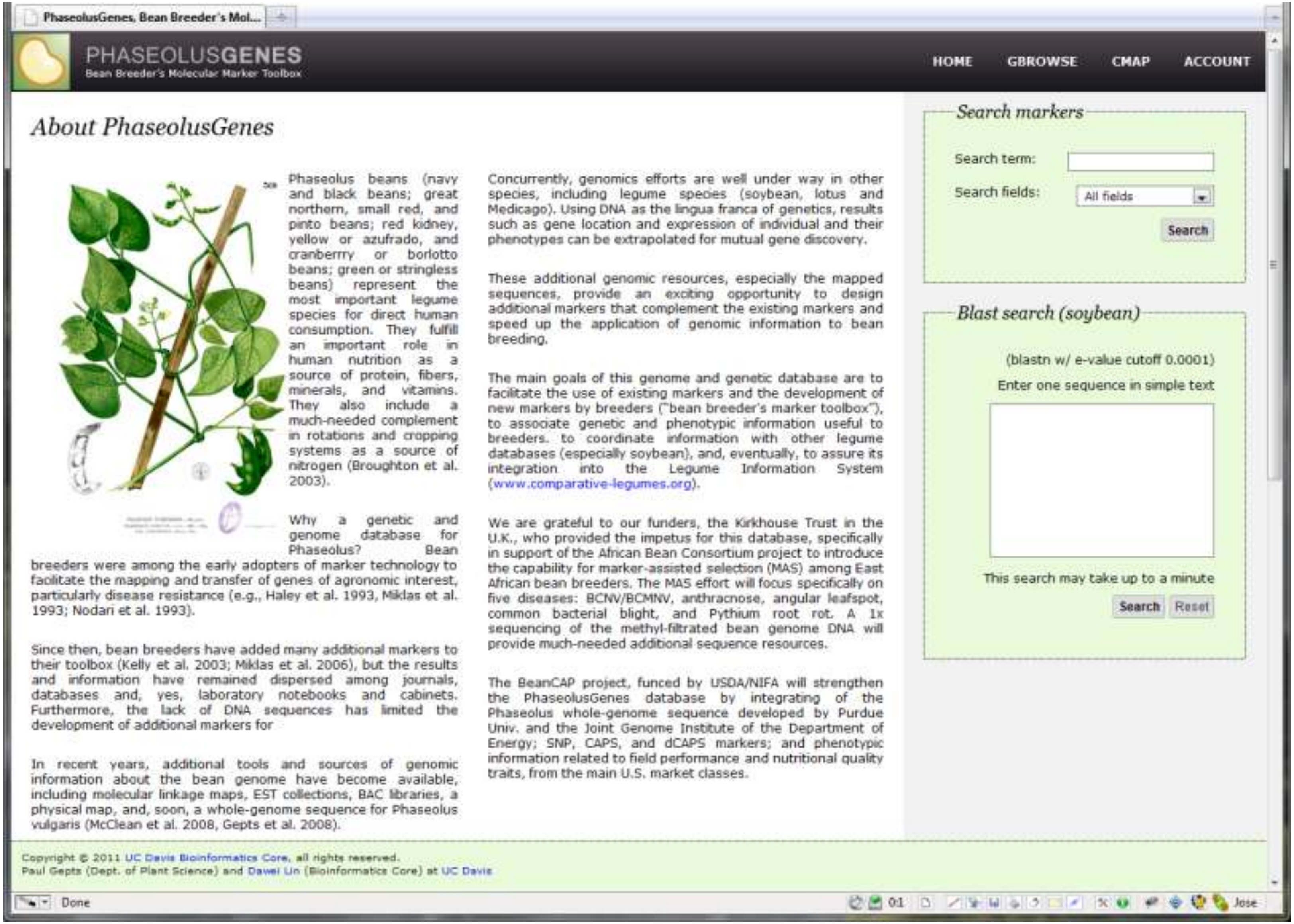

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Search markers

Search term:

Search fields: All fields

Blast search (soybean)

(blastn w/ e-value cutoff 0.0001)

Enter one sequence in simple text

This search may take up to a minute

Paul Gepts (Dept. of Plant Science) and Dawei Lin (Bioinformatics Core) at UC Davis

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Best A thaliana hit: At5g136301;Annotation (inheri...

Gene type: marker | Gbrowse mappings (2): link link

REFERENCE ID	112
GENE (PHENOTYPE)	Best A thaliana hit: At5g136301;Annotation (inherited from A thaliana) : cobalamin biosynthesis protein;Jalo EEP558 GenBank accession : DX823979;BAT93 GenBank accession : DX823442;Forward primer : GAAGGCATTGATCGTTGAACTTCATAGC;Reverse primer : TATTTGTTCACAGGGGTTGGAGTT;BAT93 result : larger;Jalo EEP558 result : smaller;Polymorphic populations : A55/G122;Source : Genomic; feature_aliases : Pv-2490;
MARKER	g2490
SEQUENCE	TCGTGAGATTGAGAAGAGACTAACCAACACAGTGGGATGGAGTGCAACTTCAGGCCAAGT TGACAACTGGGTGTACGAAGAAGCCAACACTACATTCATTCTAGATGAGAAAATGCTGTA CAAGCTCATGAACACTAATCCAAACTCCTTCAGGAAGCTGGTGCAGACTTTCTTGGAAGC CAATGGACGTGGTTACTGGGAAACTTCAGAAGACAATATTGAGAAGCTCAAGCAGTTGTA TTCGGAGGTGGAAGACAAAATTGAAGGCATTGATCGTTGAACTTCATAGCTACTATTGAG AAGACTATACAACAGTGAAGAAGAAGAAAAACACTTTTCTAATGTGATTTTGTTTACTTT
GENBANK CODE	DX823442
FORWARD PRIMER	GAAGGCATTGATCGTTGAACTTCATAGC
REVERSE PRIMER	TATTTGTTCACAGGGGTTGGAGTT
LINKAGE GROUP	1
REFERENCE	P. McClean, pers. comm.
HYPERLINK	[u'http://lis.comparative-legumes.org/cgi-bin/cmap/viewer?mapMenu=&featureMenu=& amp;corrMenu=&displayMenu=&advancedMenu=&ref_species_acc=Pv& amp;ref_map_set_acc=PvMcCleanNDSU2007&sub=Show+Selected+Set%27s+Maps& amp;prev_ref_species_acc=Pv&prev_ref_map_set_acc=0&highlight=&pixel_height=& amp;image_type=png&data_source=cmap_preview,']

Search Markers

Search term:

Search fields: All fields

Results

1. Best A thaliana hit AT23434
2. Best A thaliana hit AT23432
3. (None)
4. Pfe-1: halo blight (HB) resist

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Paul Gepts (Dept. of Plant Science) and Daniel Lin (Bioinformatics Core) at UC Davis

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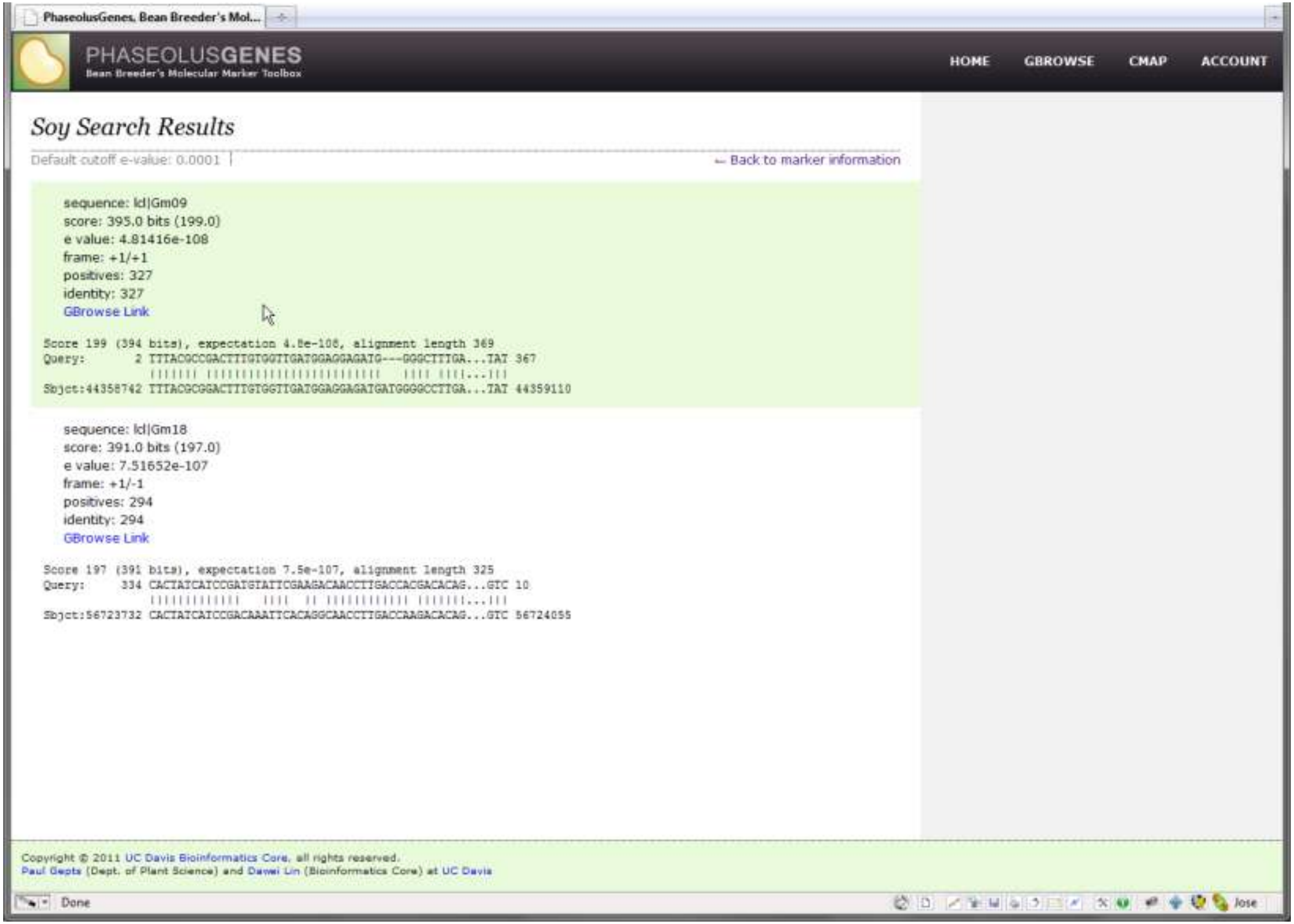

Soy Search Results

Default cutoff e-value: 0.0001

← Back to marker information

sequence: lcl|Gm09
score: 395.0 bits (199.0)
e value: 4.81416e-108
frame: +1/+1
positives: 327
identity: 327
GBrowse Link

```
Score 199 (394 bits), expectation 4.8e-108, alignment length 369
Query:       2 TTTACGCCGACTTTGTGGTTGATGGAGGAGATG---GGGCTTTGA...TAT 367
               ||||||| |||||||||||||||||||||||||   |||| ||||...|||
Sbjct:44358742 TTTACGCGGACTTTGTGGTTGATGGAGGAGATGATGGGGCCTTGA...TAT 44359110
```

sequence: lcl|Gm18
score: 391.0 bits (197.0)
e value: 7.51652e-107
frame: +1/-1
positives: 294
identity: 294
GBrowse Link

```
Score 197 (391 bits), expectation 7.5e-107, alignment length 325
Query:     334 CACTATCATCCGATGTATTCGAAGACAACCTTGACCACGACACAG...GTC 10
               |||||||||||||   ||||  || |||||||||||| |||||||...|||
Sbjct:56723732 CACTATCATCCGACAAATTCACAGGCAACCTTGACCAAGACACAG...GTC 56724055
```

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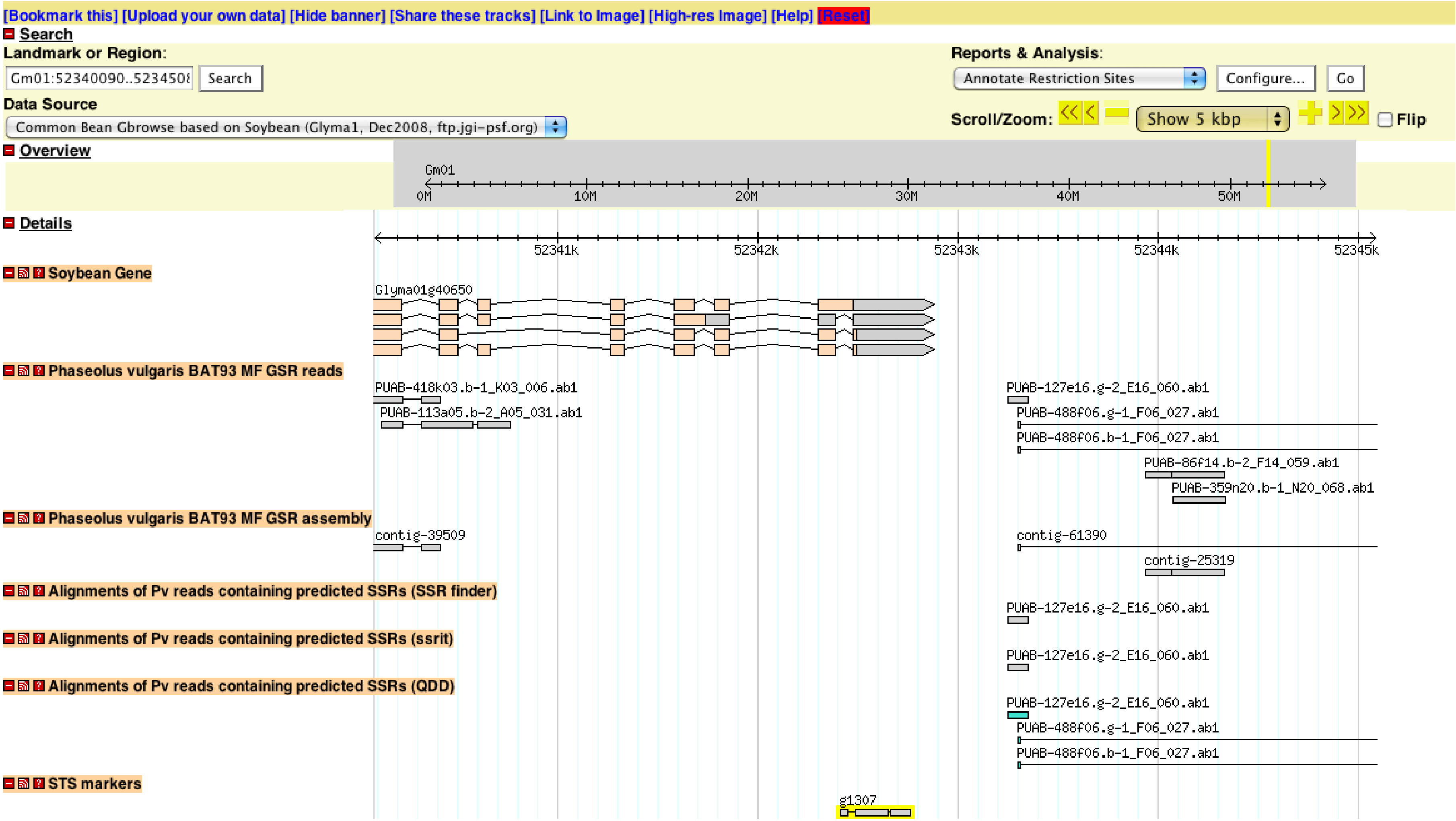

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

Landmark or Region: Gm01:52340090..523450 Search

Data Source: Common Bean Gbrowse based on Soybean (Glyma1, Dec2008, ftp.jgi-psf.org)

Reports & Analysis: Annotate Restriction Sites Configure... Go

Scroll/Zoom: Show 5 kbp ☐ Flip

Overview

Details

Soybean Gene

Phaseolus vulgaris BAT93 MF GSR reads

Phaseolus vulgaris BAT93 MF GSR assembly

Alignments of Pv reads containing predicted SSRs (SSR finder)

Alignments of Pv reads containing predicted SSRs (ssrit)

Alignments of Pv reads containing predicted SSRs (QDD)

STS markers

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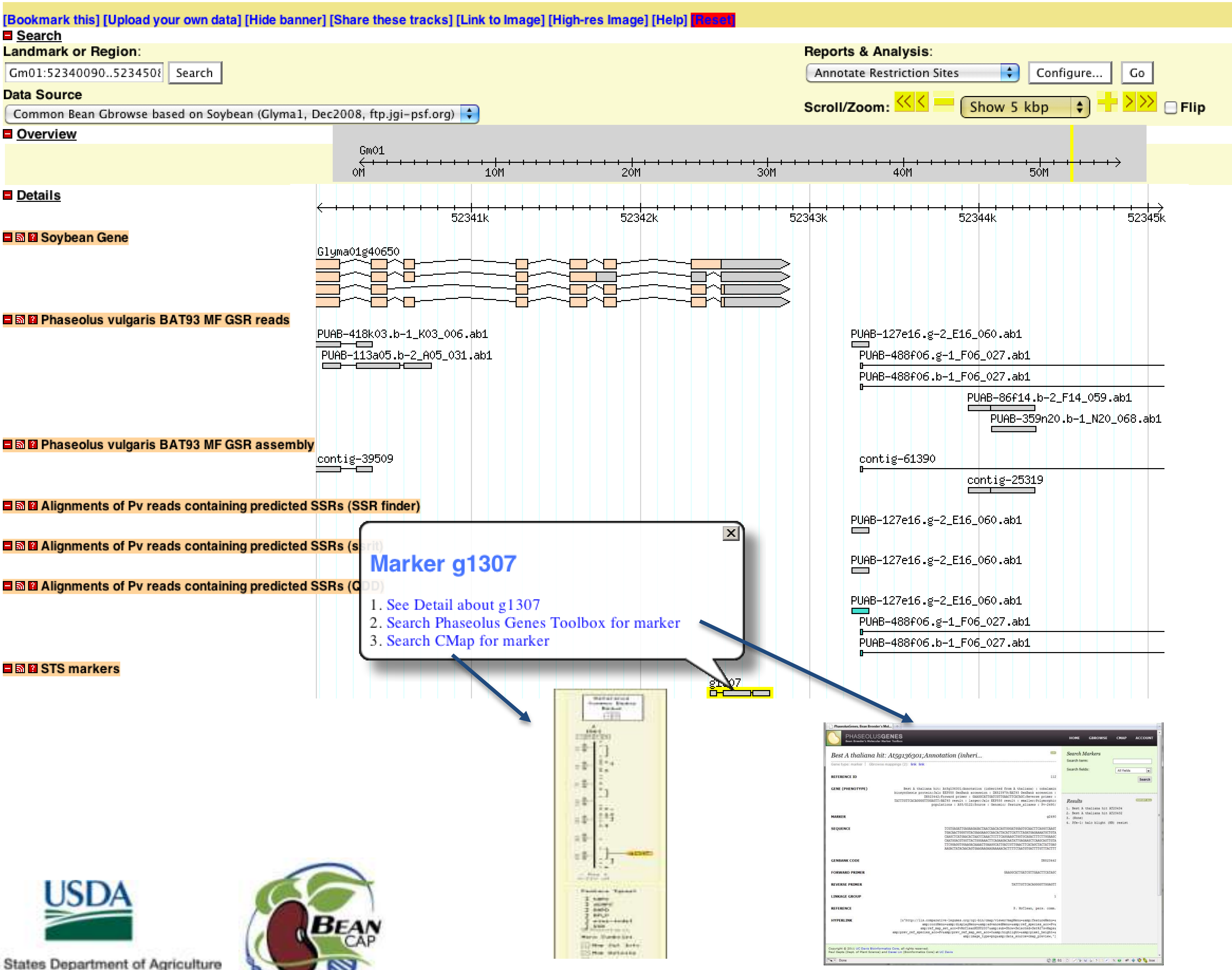

[Bookmark this] [Upload your own data] [Hide banner] [Share these tracks] [Link to Image] [High-res Image] [Help] [Reset]

Search

Landmark or Region: Gm01:52340090..523450[8] Search

Reports & Analysis: Annotate Restriction Sites · Configure... · Go

Data Source: Common Bean Gbrowse based on Soybean (Glyma1, Dec2008, ftp.jgi-psf.org)

Scroll/Zoom: Show 5 kbp ☐ Flip

Overview

Details

Soybean Gene: Glyma01g40650

Phaseolus vulgaris BAT93 MF GSR reads: PUAB-418k03.b-1_K03_006.ab1, PUAB-113a05.b-2_A05_031.ab1, PUAB-127e16.g-2_E16_060.ab1, PUAB-488f06.g-1_F06_027.ab1, PUAB-488f06.b-1_F06_027.ab1, PUAB-86f14.b-2_F14_059.ab1, PUAB-359n20.b-1_N20_068.ab1

Phaseolus vulgaris BAT93 MF GSR assembly: contig-39509, contig-61390, contig-25319

Alignments of Pv reads containing predicted SSRs (SSR finder): PUAB-127e16.g-2_E16_060.ab1

Alignments of Pv reads containing predicted SSRs (s…rit): PUAB-127e16.g-2_E16_060.ab1

Alignments of Pv reads containing predicted SSRs (Q…DD): PUAB-127e16.g-2_E16_060.ab1, PUAB-488f06.g-1_F06_027.ab1, PUAB-488f06.b-1_F06_027.ab1

STS markers: g1307

Marker g1307

1. See Detail about g1307
2. Search Phaseolus Genes Toolbox for marker
3. Search CMap for marker

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SSR Motif Discovery

1. Genome survey sequence (funded by the ABC project)

- 1x methyl-filtrated DNA of breeding line BAT93
  - Good quality reads: 414,923
  - Average length: 635 bp
  - Total sequence: 263.5 Mbp (~ 44% of genome)
  - Probable or possible cytoplasmic sequences: 31,985
  - Hits to *Phaseolus*: 51% (note: *Phaseolus* BLAST database: all available markers, BES, all nucleotide/EST sequences in NCBI (E-value cutoff: E-10)

SSR Motif Discovery (II)

2. SSR detection *in silico*:

- Three programs:
  - SSRFinder (Sanchez-Villeda et al. 2003, http://maizemap.org/bioinformatics/SSRFINDER/SSR_Finder_Download.html)
  - SSRIT (Temnykh et al. 2001, http://www.gramene.org/db/markers/ssrtool)
  - QDD (Meglécz et al. 2010, http://gsite.univ-provence.fr/gsite/Local/egee/dir/meglecz/QDD.html)

- Common set of parameters:
  - Repeat lengths: 2 to 6
  - Minimum number of repeats: 4
  - No multiples of repeats

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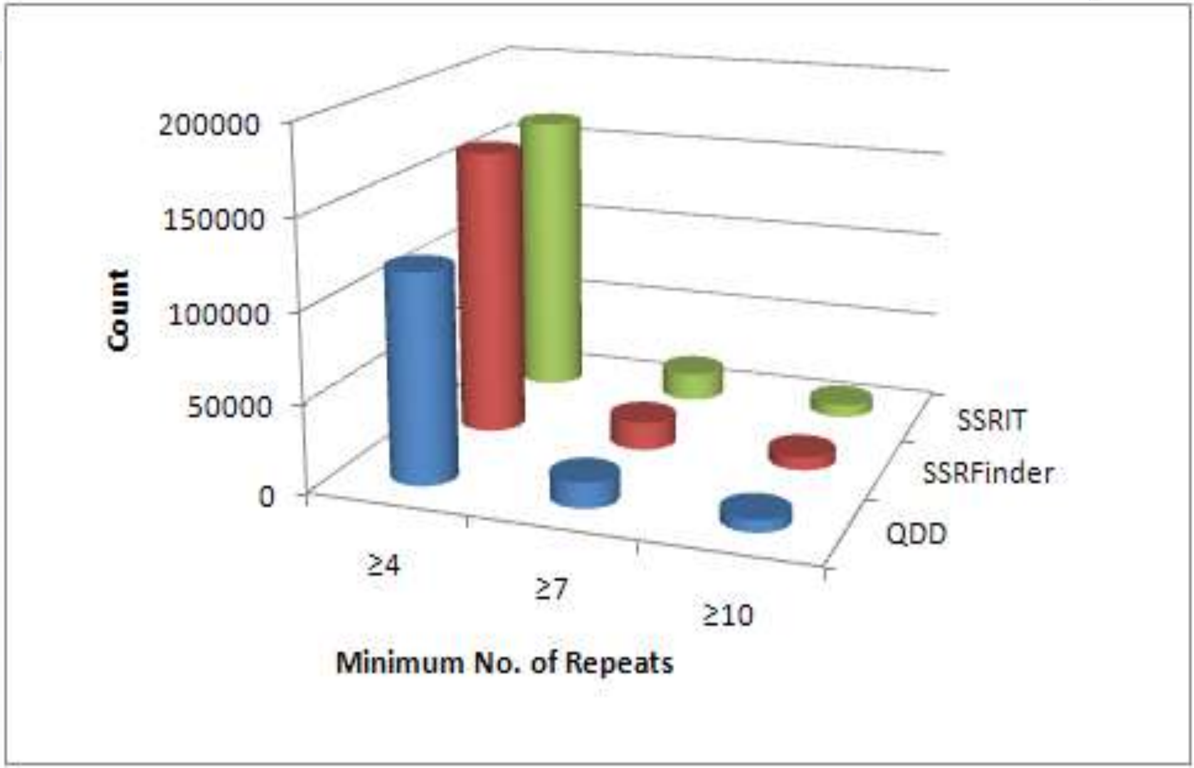
SSR Motif Discovery (III)

Result 1:

- There is a large number of SSRs: >150,000; comparable between SSRFinder and SSRIT, 1/3 less in QDD
- Sharp drop-off after filtering for repeat number



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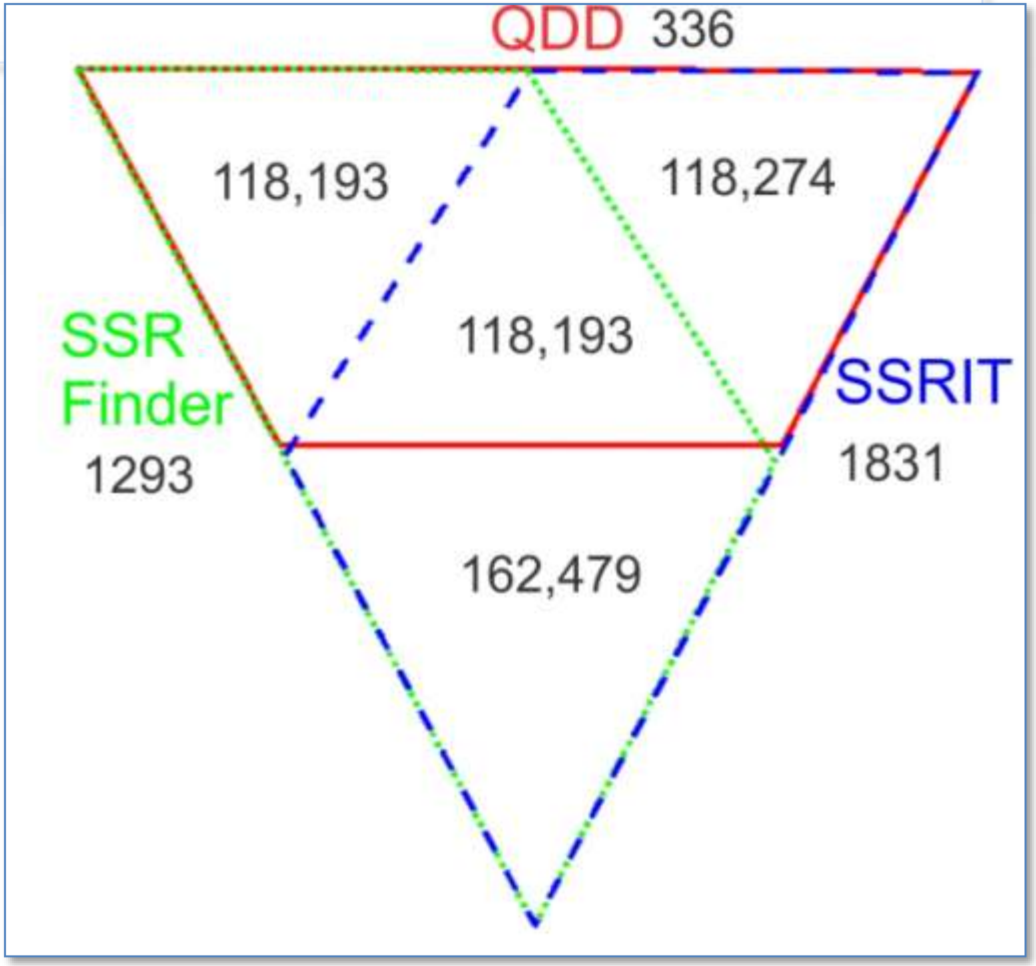
SSR Motif Discovery (IV)

Result 2:

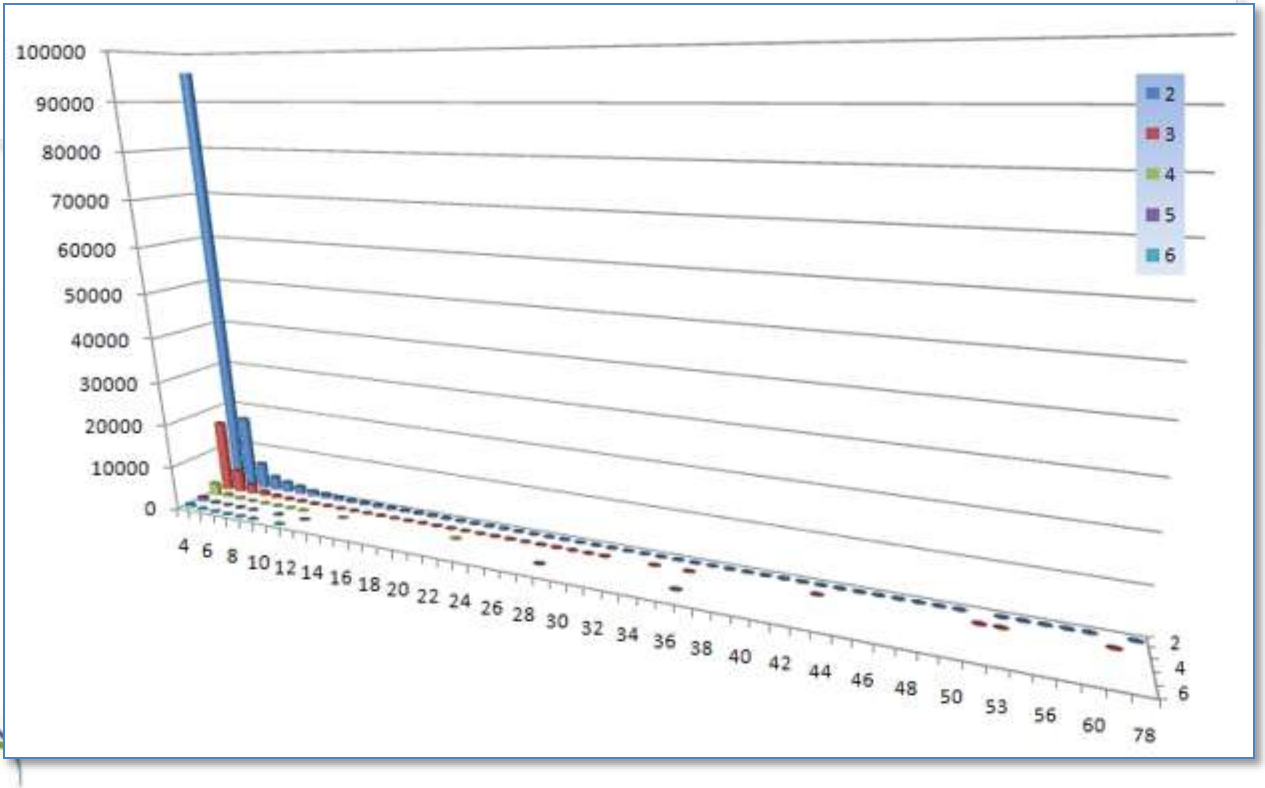
There is a large overlap among programs, with few unique SSRs identified by individual programs



SSR Motif Discovery (V)

Result 3:

The majority of SSRs are di-nucleotides, with few repeats; the polymorphism levels of the different classes remains to be determined.



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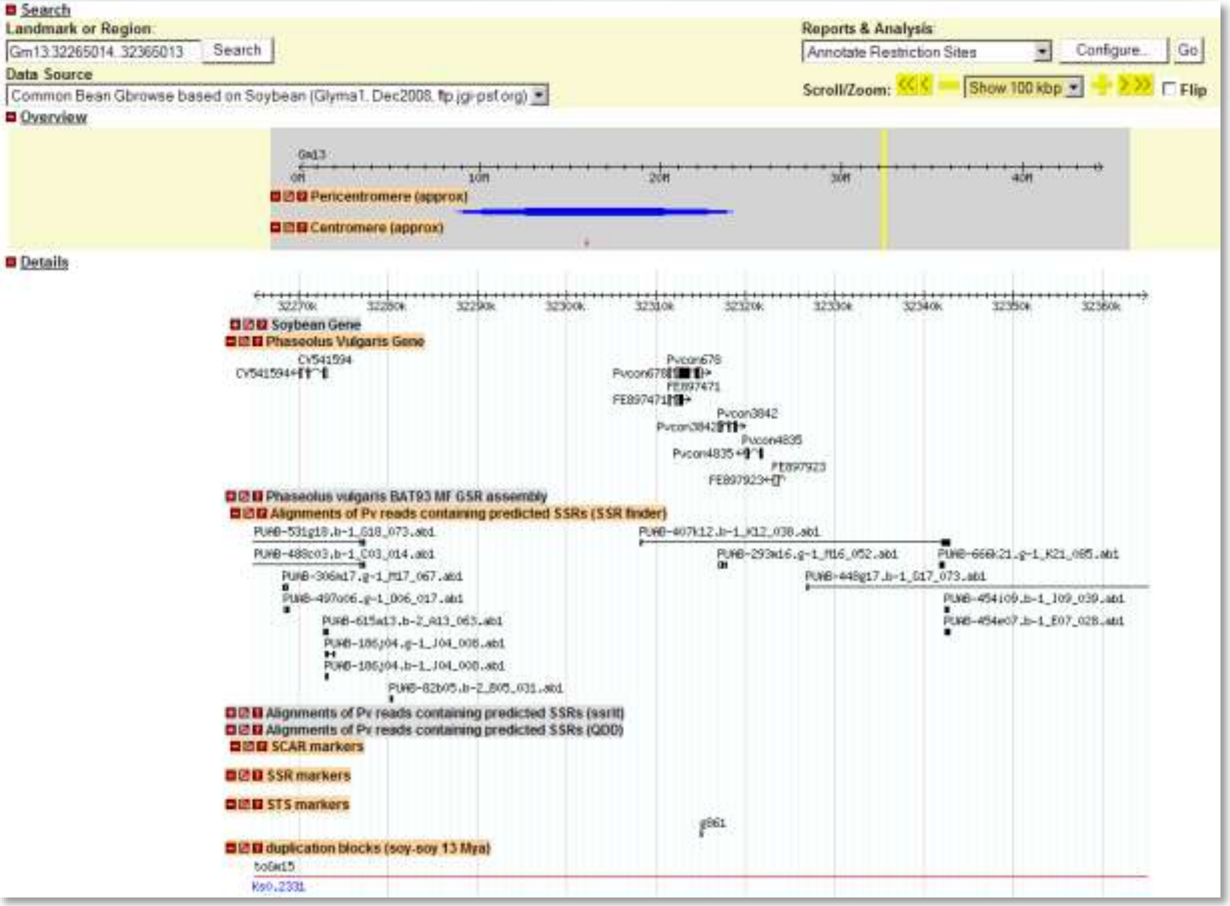
SSR Motif Discovery (VI)

Result 4:

The sequence reads containing SSRs have been mapped onto the soybean whole-genome sequence displayed in PhaseolusGenes



Landmark or Region: Gm13:32265014..32365013

Data Source: Common Bean Gbrowse based on Soybean (Glyma1, Dec2008, ftp.jgi-psf.org)

Reports & Analysis: Annotate Restriction Sites

Scroll/Zoom: Show 100 kbp ☐ Flip

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Adriana Navarro Gómez

United States Department of Agriculture
National Institute of Food and Agriculture

QTLs-Literature review

2500 papers (abstracts and whole papers) read:

- Bean Improvement Cooperative (BIC)
- Google Scholar
- ISI Web of Knowledge
- Crop Science (https://www.crops.org/publications/cs)
- Journal of the American Society for Horticultural Science (http://journal.ashspublications.org/)
- Other Journal’s web sites

> 45 papers used
From 1993 to 2011

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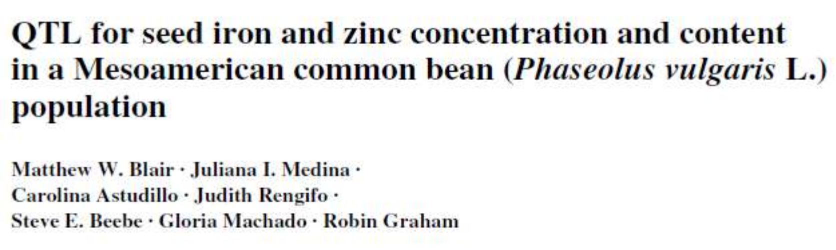
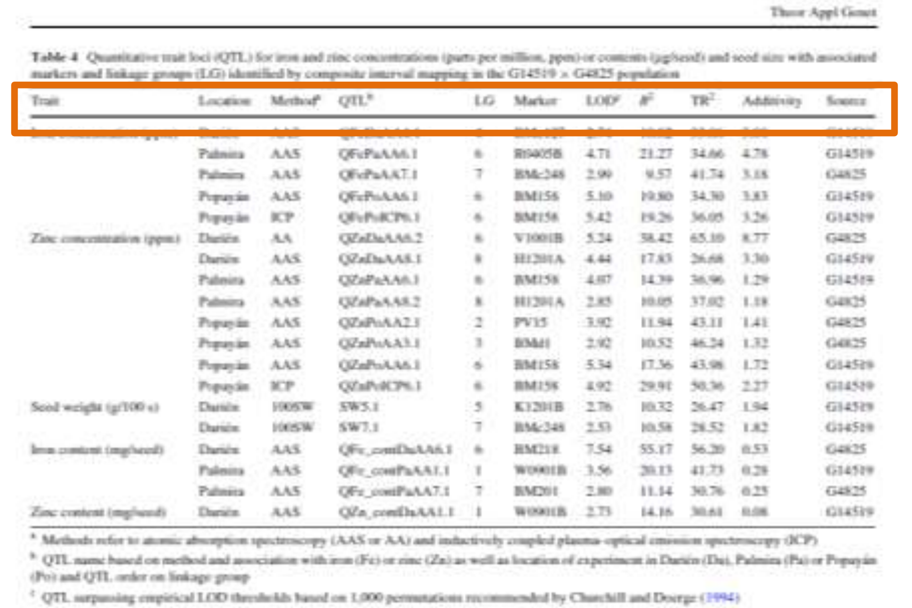
Example 1



QTL for seed iron and zinc concentration and content in a Mesoamerican common bean (*Phaseolus vulgaris* L.) population

Matthew W. Blair · Juliana I. Medina ·
Carolina Astudillo · Judith Rengifo ·
Steve E. Beebe · Gloria Machado · Robin Graham



Theor Appl Genet

Table 4 Quantitative trait loci (QTL) for iron and zinc concentrations (parts per million, ppm) or contents (µg/seed) and seed size with associated markers and linkage groups (LG) identified by composite interval mapping in the G14519 × G4825 population

Trait	Location	Method[a]	QTL[b]	LG	Marker	LOD[c]	R^2	TR^2	Additivity	Source
Iron concentration (ppm)	Darién	AAS	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
	Palmira	AAS	QFePaAA6.1	6	BI9405B	4.71	21.27	34.66	4.78	G14519
	Palmira	AAS	QFePaAA7.1	7	BMc248	2.99	9.57	41.74	3.18	G4825
	Popayán	AAS	QFePoAA6.1	6	BM156	5.10	19.80	34.30	3.83	G14519
	Popayán	ICP	QFePoICP6.1	6	BM158	5.42	19.26	36.05	3.26	G14519
Zinc concentration (ppm)	Darién	AA	QZnDaAA6.2	6	V1001B	5.24	38.42	65.10	8.77	G4825
	Darién	AAS	QZnDaAA8.1	8	H1201A	4.44	17.83	26.68	3.30	G14519
	Palmira	AAS	QZnPaAA6.1	6	BM158	4.07	14.39	36.96	1.29	G14519
	Palmira	AAS	QZnPaAA8.2	8	H1201A	2.85	10.05	37.02	1.18	G4825
	Popayán	AAS	QZnPoAA2.1	2	PV15	3.92	11.94	43.11	1.41	G4825
	Popayán	AAS	QZnPoAA3.1	3	BMd1	2.92	10.52	46.24	1.32	G4825
	Popayán	AAS	QZnPoAA6.1	6	BM158	5.34	17.36	43.98	1.72	G14519
	Popayán	ICP	QZnPoICP6.1	6	BM158	4.92	29.91	50.36	2.27	G14519
Seed weight (g/100 s)	Darién	100SW	SW5.1	5	K1201B	2.76	10.32	26.47	1.94	G14519
	Darién	100SW	SW7.1	7	BMc248	2.53	10.58	28.52	1.82	G14519
Iron content (mg/seed)	Darién	AAS	QFe_contDaAA6.1	6	BM218	7.54	55.17	56.20	0.53	G4825
	Palmira	AAS	QFe_contPaAA1.1	1	W0901B	3.56	20.13	41.73	0.28	G14519
	Palmira	AAS	QFe_contPaAA7.1	7	BM201	2.80	11.14	30.76	0.25	G4825
Zinc content (mg/seed)	Darién	AAS	QZn_contDaAA1.1	1	W0901B	2.73	14.16	30.61	0.08	G14519

[a] Methods refer to atomic absorption spectroscopy (AAS or AA) and inductively coupled plasma-optical emission spectroscopy (ICP)

[b] QTL name based on method and association with iron (Fe) or zinc (Zn) as well as location of experiment in Darién (Da), Palmira (Pa) or Popayán (Po) and QTL order on linkage group

[c] QTL surpassing empirical LOD thresholds based on 1,000 permutations recommended by Churchill and Doerge (1994)

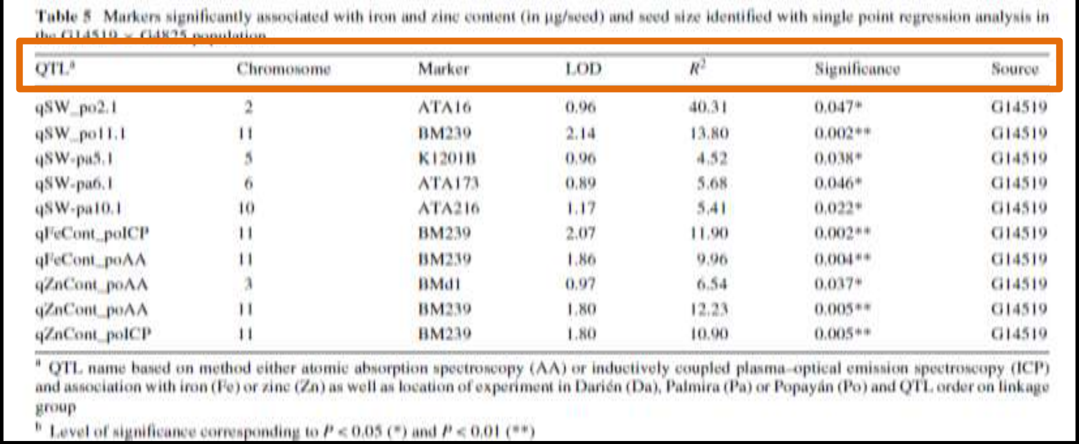


Table 5 Markers significantly associated with iron and zinc content (in µg/seed) and seed size identified with single point regression analysis in the G14519 × G4825 population

QTL[a]	Chromosome	Marker	LOD	R^2	Significance	Source
qSW_po2.1	2	ATA16	0.96	40.31	0.047*	G14519
qSW_po11.1	11	BM239	2.14	13.80	0.002**	G14519
qSW-pa5.1	5	K1201B	0.96	4.52	0.038*	G14519
qSW-pa6.1	6	ATA173	0.89	5.68	0.046*	G14519
qSW-pa10.1	10	ATA216	1.17	5.41	0.022*	G14519
qFeCont_poICP	11	BM239	2.07	11.90	0.002**	G14519
qFeCont_poAA	11	BM239	1.86	9.96	0.004**	G14519
qZnCont_poAA	3	BMd1	0.97	6.54	0.037*	G14519
qZnCont_poAA	11	BM239	1.80	12.23	0.005**	G14519
qZnCont_poICP	11	BM239	1.80	10.90	0.005**	G14519

[a] QTL name based on method either atomic absorption spectroscopy (AA) or inductively coupled plasma–optical emission spectroscopy (ICP) and association with iron (Fe) or zinc (Zn) as well as location of experiment in Darién (Da), Palmira (Pa) or Popayán (Po) and QTL order on linkage group

[b] Level of significance corresponding to $P < 0.05$ (*) and $P < 0.01$ (**)

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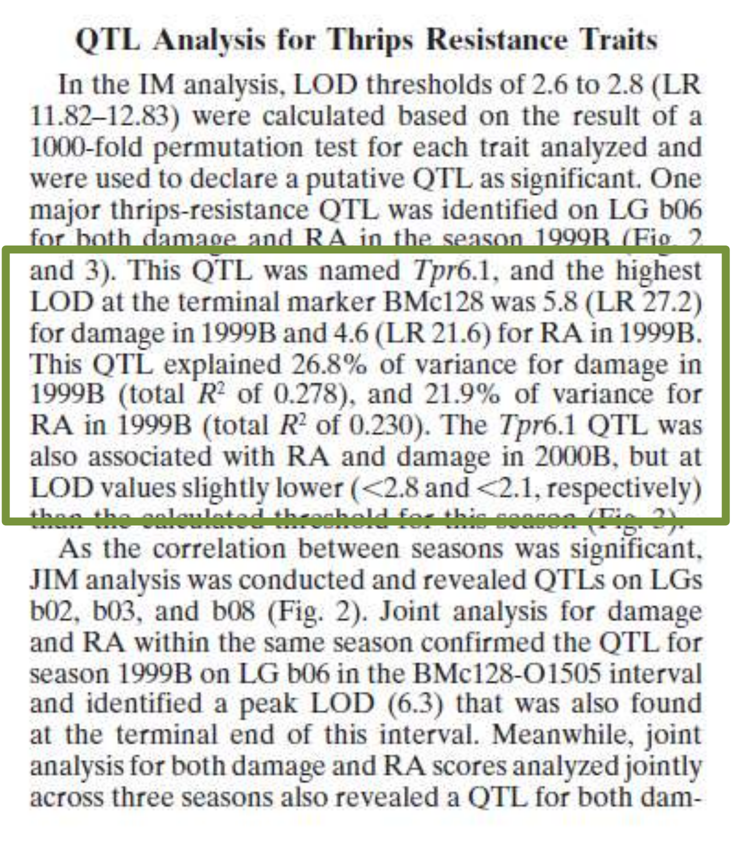
Example 2

QTL Mapping of Resistance to *Thrips palmi* Karny in Common Bean

A. Frei, M. W. Blair,* C. Cardona, S. E. Beebe, H. Gu, and S. Dorn



QTL Analysis for Thrips Resistance Traits

In the IM analysis, LOD thresholds of 2.6 to 2.8 (LR 11.82–12.83) were calculated based on the result of a 1000-fold permutation test for each trait analyzed and were used to declare a putative QTL as significant. One major thrips-resistance QTL was identified on LG b06 for both damage and RA in the season 1999B (Fig. 2 and 3). This QTL was named *Tpr*6.1, and the highest LOD at the terminal marker BMc128 was 5.8 (LR 27.2) for damage in 1999B and 4.6 (LR 21.6) for RA in 1999B. This QTL explained 26.8% of variance for damage in 1999B (total R^2 of 0.278), and 21.9% of variance for RA in 1999B (total R^2 of 0.230). The *Tpr*6.1 QTL was also associated with RA and damage in 2000B, but at LOD values slightly lower (<2.8 and <2.1, respectively) than the calculated threshold for this season (Fig. 3).

As the correlation between seasons was significant, JIM analysis was conducted and revealed QTLs on LGs b02, b03, and b08 (Fig. 2). Joint analysis for damage and RA within the same season confirmed the QTL for season 1999B on LG b06 in the BMc128-O1505 interval and identified a peak LOD (6.3) that was also found at the terminal end of this interval. Meanwhile, joint analysis for both damage and RA scores analyzed jointly across three seasons also revealed a QTL for both dam-

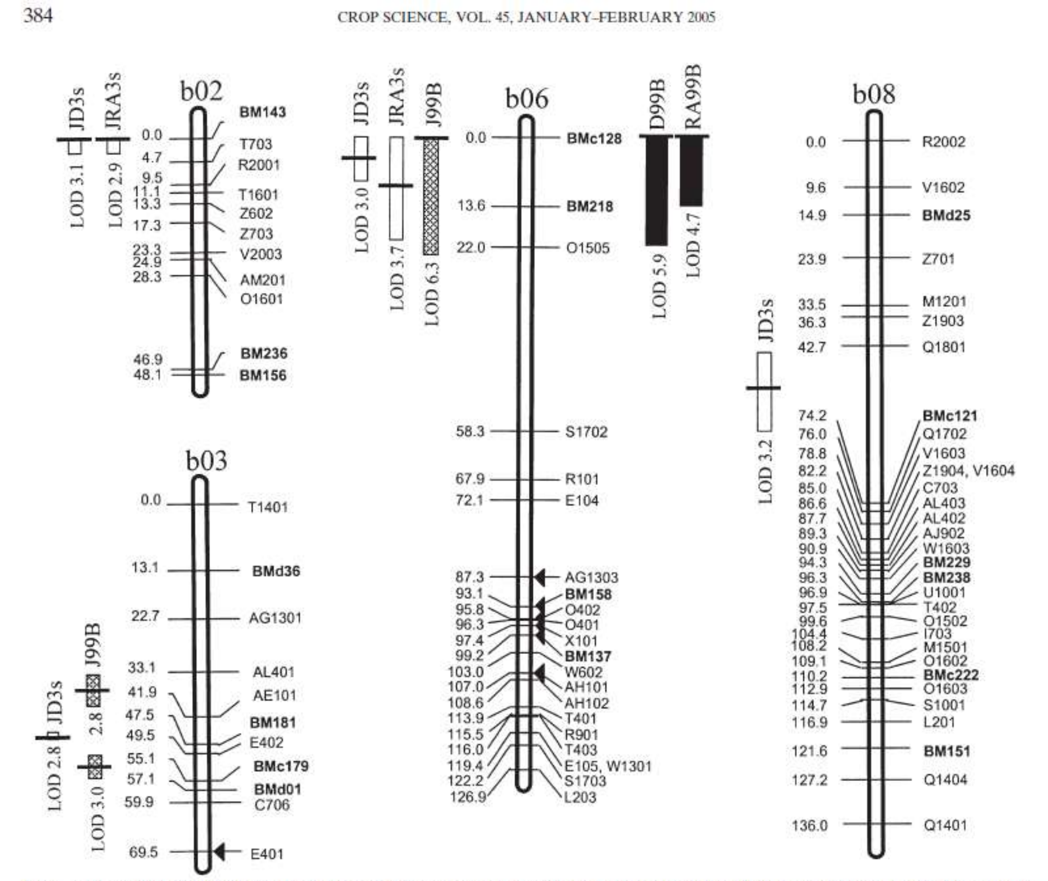


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Fig. 2. Genetic linkage map for the BAT 881 × G 21212 population, showing linkage groups that contained significant QTLs for *Thrips palmi* resistance. The QTLs were identified by single interval mapping (black boxes, D99B = damage 1999B, RA99B = reproductive adaptation 1999B), by joint interval mapping for resistance traits within the same season (gray boxes, J99B = joint for damage and RA in 1999B) and by joint interval mapping for each resistance trait across three seasons (white boxes, JD3s = joint for damage across three seasons, JRA3s =

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QTL-survey

Information on QTLs was collected for addition to PhaseolusGenes (Table 1) from > 45 papers.

Table 1. QTL information collected

Trait	Female, male parent	R^2	Markers, Flanking markers
Year	QTL	LOD	Source of allele
Location	Population size, type	P value	Type of analysis
Literature source	URL		Trait ontology

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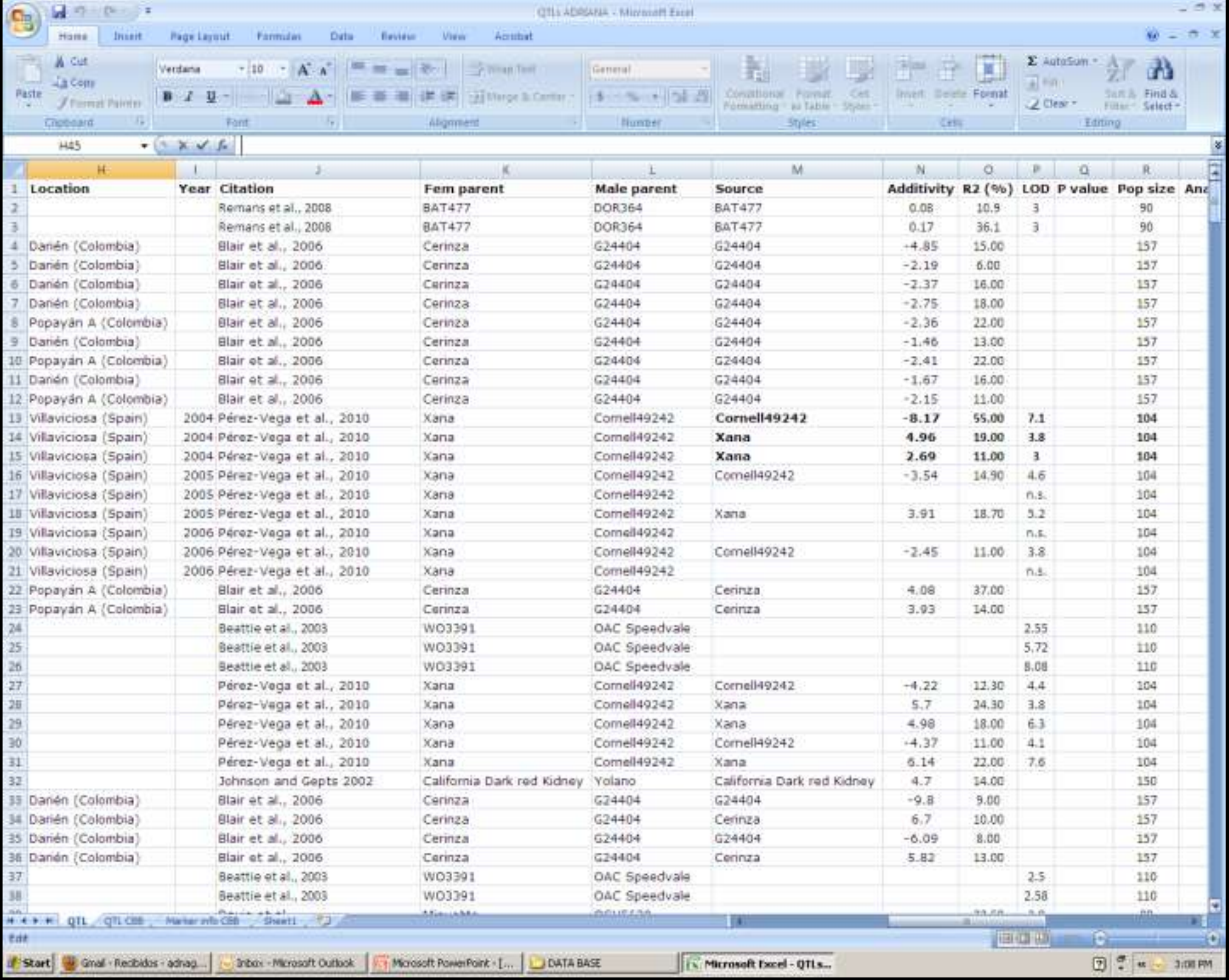
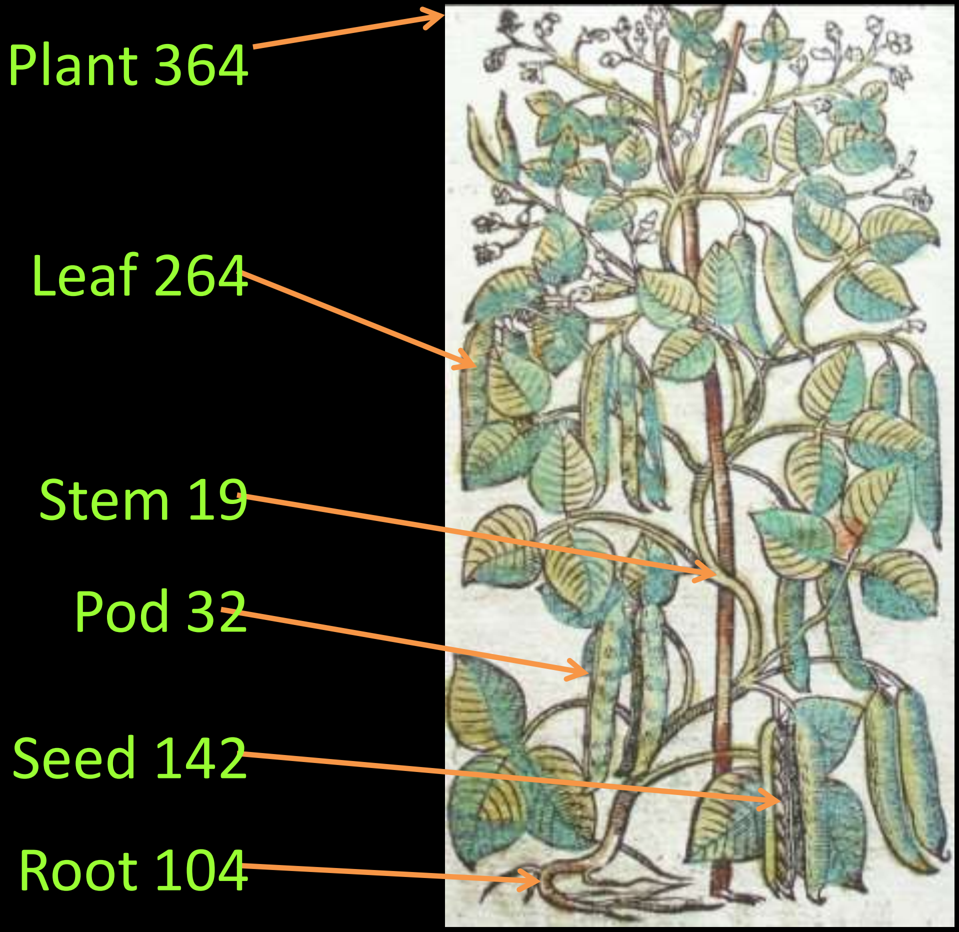
More Information Associated with Each QTL than with Major Genes or Markers →Adjust Structure of Database



Location	Year	Citation	Fem parent	Male parent	Source	Additivity	R2 (%)	LOD	P value	Pop size	Ana
		Remans et al., 2008	BAT477	DOR364	BAT477	0.08	10.9	3		90	
		Remans et al., 2008	BAT477	DOR364	BAT477	0.17	36.1	3		90	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-4.85	15.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.19	6.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.37	16.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.75	18.00			157	
Popayán A (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.36	22.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-1.46	13.00			157	
Popayán A (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.41	22.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-1.67	16.00			157	
Popayán A (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-2.15	11.00			157	
Villaviciosa (Spain)	2004	Pérez-Vega et al., 2010	Xana	Cornell49242	**Cornell49242**	**-8.17**	**55.00**	**7.1**		**104**	
Villaviciosa (Spain)	2004	Pérez-Vega et al., 2010	Xana	Cornell49242	**Xana**	**4.96**	**19.00**	**3.8**		**104**	
Villaviciosa (Spain)	2004	Pérez-Vega et al., 2010	Xana	Cornell49242	**Xana**	**2.69**	**11.00**	**3**		**104**	
Villaviciosa (Spain)	2005	Pérez-Vega et al., 2010	Xana	Cornell49242	Cornell49242	-3.54	14.90	4.6		104	
Villaviciosa (Spain)	2005	Pérez-Vega et al., 2010	Xana	Cornell49242				n.s.		104	
Villaviciosa (Spain)	2005	Pérez-Vega et al., 2010	Xana	Cornell49242	Xana	3.91	18.70	5.2		104	
Villaviciosa (Spain)	2006	Pérez-Vega et al., 2010	Xana	Cornell49242				n.s.		104	
Villaviciosa (Spain)	2006	Pérez-Vega et al., 2010	Xana	Cornell49242	Cornell49242	-2.45	11.00	3.8		104	
Villaviciosa (Spain)	2006	Pérez-Vega et al., 2010	Xana	Cornell49242				n.s.		104	
Popayán A (Colombia)		Blair et al., 2006	Cerinza	G24404	Cerinza	4.08	37.00			157	
Popayán A (Colombia)		Blair et al., 2006	Cerinza	G24404	Cerinza	3.93	14.00			157	
		Beattie et al., 2003	WO3391	OAC Speedvale				2.55		110	
		Beattie et al., 2003	WO3391	OAC Speedvale				5.72		110	
		Beattie et al., 2003	WO3391	OAC Speedvale				8.08		110	
		Pérez-Vega et al., 2010	Xana	Cornell49242	Cornell49242	-4.22	12.30	4.4		104	
		Pérez-Vega et al., 2010	Xana	Cornell49242	Xana	5.7	24.30	3.8		104	
		Pérez-Vega et al., 2010	Xana	Cornell49242	Xana	4.98	18.00	6.3		104	
		Pérez-Vega et al., 2010	Xana	Cornell49242	Cornell49242	-4.37	11.00	4.1		104	
		Pérez-Vega et al., 2010	Xana	Cornell49242	Xana	6.14	22.00	7.6		104	
		Johnson and Gepts 2002	California Dark red Kidney	Yolano	California Dark red Kidney	4.7	14.00			150	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-9.8	9.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	Cerinza	6.7	10.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	G24404	-6.09	8.00			157	
Darién (Colombia)		Blair et al., 2006	Cerinza	G24404	Cerinza	5.82	13.00			157	
		Beattie et al., 2003	WO3391	OAC Speedvale				2.5		110	
		Beattie et al., 2003	WO3391	OAC Speedvale				2.58		110	

QTL-survey

925 QTLs (trait x population x environment) have been reported.
They concerned all major organs (roots, stem, leaves, pods, and seeds)



Plant 364

Leaf 264

Stem 19

Pod 32

Seed 142

Root 104

Matthioli 1572

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QTL-survey

And agronomically important trait categories: development and performance, biotic and abiotic stresses, nutritional composition

Trait category	QTL number
Abiotic stress T	98
Biotic stress R	521
Composition	66
Development/performance	240
Total	925

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Average Genetic Parameters for QTLs

33 populations; average pop. size: 100; 28 QTLs per population

	R^2 (%)	LOD	P value
Average (925 QTLs)	17.2	5.0	0.03

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What is Next for QTLs?

- Integrate the information into PhaseolusGenes
  - Searchable table
  - Links with:
    - Gbrowse (for markers)
    - Cmap
- Downloadable table with all QTL information

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What is Next for PhaseolusGenes?

- QTL information
- Complete mapping information in BJ (and other populations)
- Add other markers:
  - – SNPs: Hyten et al. 2010, BeanCAP, etc.
  - – COS markers
  - – BAC ends
- Integration of whole-genome sequences
- Trait ontogenies

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