

# SoyBase, the USDA-ARS Soybean Genetics and Genomics Database

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# Selected Examples of Recent Additions to SoyBase

- **GRIN Data Explorer**
- **Gene Expression Explorer**
- **Cultivar and Experimental Line pedigrees**
- **Data downloads**

# GRIN Data Explorer

SoyBase Home Help & Tutorials Genetic Map Genome Browser Expression Mutants Projects Tools Community Site Map

**Data Explorer**

In collaboration with the USDA Germplasm Resources Informatics System, we facilitate searches of the GRIN Descriptor Data (data currently available for 10,000 accessions). Loci for the GRIN soybean germplasm collection were provided by the USDA and the University of Illinois.

To use the tool, use the checkboxes select the trait(s) of interest. The traits chosen will be used on the next page.

**Production**

- Yield

**Root**

- Root Fluorescence

**Growth**

- Stem Termination Type
- Height

**Stress**

- High Temperature
- Chlorosis Score
- Salt Reaction

**User Submitted**

- E1 (imputed from haplotype)
- E2 (imputed from haplotype)
- E3 (imputed from haplotype)

**Phenology**

- Flowering
- Maturity Date
- Twining Date
- Maturity Group

**Insect**

- Defoliation
- Leaf Hopper Injury
- Mexican Bean Beetle Damage
- Beet Armyworm
- Soybean Looper
- Velvetbean Caterpillar
- Corn Ear Worm
- Soybean Aphid Resistance

**Nematode**

- Reniform Nematode
- Cyst Nematode Race 1
- Cyst Nematode Race 2
- Cyst Nematode Race 3
- Cyst Nematode Race 4
- Cyst Nematode Race 5
- Cyst Nematode Race 14
- Cyst Nematode

**Chemical**

- Arginine
- Cysteine
- Iodine Number
- Isoleucine
- Leucine
- Linoleic
- Linolenic
- Lysine
- Methionine
- Oil
- Oleic
- Other Fatty Acid Composition
- Palmitic
- Petiole Ureide
- Human Allergen P34
- Protein
- Stachyose
- Stearic
- Sucrose
- Threonine
- Tryptophan
- Valine

**Morphology**

- Lower Leaflet Area
- Upper Leaflet Length
- Pod Length
- Late Shattering Score
- Early Shattering Score
- Mottling Score
- Flower Color
- Seed Shape Of G. Soja
- Hilum Color
- Leaflet Shape Of Glycine soja
- Leaflet Size Of Glycine soja
- Other Leaf Traits
- Other Plant Traits
- Other Seed Traits
- Pod Color
- Pubescence Color
- Pubescence Density

**Search all of SoyBase**

- Compare Genetic Map Order & Sequence Map Order
- BLAST
- Soybean Ontology
- Soybean Metabolic Pathways
- Soybean Pedigrees
- Northern Uniform Trials Experimental Results
- GRIN Soybean Data Explorer
- Gene Annotation Lookup
- Affymetrix Soybean GeneChip1
- GO Term Enrichment Tool
- Convert Gene Model Names

**Phytophthora Rot Races**

- Southern Stem Canker
- Bacterial Pustule
- Brown Stem Rot
- Frogeye C-32 Isolate
- Frogeye Race 2
- Frogeye Race 11
- Frogeye, Unspecified Race
- Phytophthora Rot Race 1
- Phytophthora Rot Race 2
- Phytophthora Rot Race 3
- Phytophthora Rot Race 4
- Phytophthora Rot Race 5
- Phytophthora Rot Race 6
- Phytophthora Rot Race 7
- Phytophthora Rot Race 8
- Phytophthora Rot Race 9
- Phytophthora Rot Race 10
- Phytophthora Rot Race 12
- Phytophthora Rot Race 17
- Phytophthora Rot Race 20
- Phytophthora Rot Race 25
- Phytophthora Rot Race 30
- Phytophthora Rot Race 30T
- Phytophthora Rot Race 31
- Phytophthora Rot Race 33
- Phytophthora Rot Race 38
- Phytophthora Rot
- Pythium Ultimum
- Soybean Mosaic Virus
- Soybean Mosaic Virus Strain G1
- Soybean Mosaic Virus Strain G2
- Soybean Mosaic Virus Strain G3
- Soybean Mosaic Virus Strain G4
- Soybean Mosaic Virus Strain G5
- Soybean Mosaic Virus Strain G6
- Soybean Mosaic Virus Strain G7
- Bean Pod Mottle Virus
- Peanut Mottle Virus
- Soybean Rust Mixed

E3

15896 records possible.

Next →

Select All

Reset Form

# GRIN Data Explorer

## Data Explorer

← Back one step.

This page provides two tools for searching the germplasm phenotype data. One returns a list of germplasm accessions based on the phenotype data for the trait(s) previously selected. The other accepts a list of germplasm accessions and returns a table of phenotype data for the selected trait(s).

### Identify Germplasm Based on Phenotype Data

Trait	Valid Range	
Flowering	609–929	>= 609 and <= 929
Maturity Date	135–1214	>= 135 and <= 1214
E1 (imputed from haplotype)		= e1-as
E2 (imputed from haplotype)		= e2
E3 (imputed from haplotype)		= e3
Maturity Group		= IV

Submit

- II
- III
- IV
- I
- VI
- O
- V
- VII
- VIII
- X
- IX
- 00

### Retrieve Phenotype Data from a Germplasm List

PI603421A  
PI507259  
PI407946-2  
PI90576-1  
PI80837  
PI89012-1  
PI189940  
PI60296  
PI71463  
PI479714

#### Fetching Values For

E1 (imputed from haplotype)  
E2 (imputed from haplotype)  
E3 (imputed from haplotype)  
Flowering  
Maturity Date  
Maturity Group

[Click to Load Example List](#)

Submit

← OR →

# Gene Expression Explorer

SoyBase Home Help & Tutorials Genetic Map Genome Browser Expression Mutants Projects Tools Community Site Map

**Gene Expression Explorer** RNA SEQ Atlas  
Severin et al.  
NCBI GEO expression data at SoyBase

← Go Back One Step Proceed to the Next Step →

Selecting by Experiment [Click here to Select by Tissue](#)

Use this page to select gene expression samples for display in the SoyBase genome browser grouped by experiment. An alternative selection page with the samples grouped by tissue is available [here](#).

This page shows the gene expression data at SoyBase organized by Experiment. Use the check box to choose one or more Experiments for further analysis, then click on the 'Proceed to the Next Step' button at the top right of the page.

To facilitate searching, gene expression projects at SoyBase have been classified as either [Descriptive](#) or [Comparative](#).

**Descriptive** - gene expression for untreated tissues or structures, for example a RNA-seq experiment using seed coats or a chip hybridization experiment with RNA from roots

**Comparative** - gene expression in the same tissue or structure under different biotic or abiotic treatments, at different developmental stages, or in different cultivars

- Biotic
  - Phakopsora pachyrhizi
  - Bradyrhizobium japonicum
  - Phytophthora sojae
  - Soybean aphid
  - Mycorrhization
- Abiotic
  - Day length
  - Iron deficiency
  - Alkaline stress
  - Aluminum
  - Constant light
  - Temperature
  - Salinity
- Transgenic
  - RNAi
- Treatment
  - Effect of bud removal on leaflet

The Experiment title is a link to an expanded summary of the experiment.  
The link within the square brackets, eg. [GeneChip], will open the experiment's page at GEO.

**Descriptive**

- Transgenic** and conventional cultivar comparison [GeneChip]
- Early maturation-stage **seed** compartments [GeneChip]
- Globular-stage **seed** compartments [GeneChip]
- Heart-stage **seed** compartments [GeneChip]
- Cotyledon stage **seed** compartments [GeneChip]

# Gene Expression Explorer

## Gene Expression Explorer

[← Go Back One Step](#)

Selecting by Tissue

[Click here to Select by Experiment](#)

[Proceed to the Next Step →](#)

Use this page to select gene expression samples for display in the SoyBase genome browser grouped by tissue. An alternative selection page with the samples grouped by experiment is available [here](#).

This page shows the gene expression data at SoyBase organized by Tissue. Use the check box to choose one or more Tissues for further analysis. Then click on the 'Proceed to the Next Step' button at the top right of the page.

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**Comparative** - gene expression in the same tissue or structure under different biotic or abiotic treatments, at different developmental stages, or in different cultivars

### Leaflet

#### Descriptive

- Leaflet
- Leaflet Palisade Mesophyll Parenchyma
- Leaflet Paraveinal Mesophyll

#### Comparative

- Leaflet
- Leaflet (RNAi Stunted)
- Leaflet (RNAi Varigated)

### Embryo

#### Descriptive

- Embryo
- Embryo Axis Epidermis
- Embryo Axis Root Apical Meristem
- Embryo Axis Shoot Apical Meristem
- Embryo Axis Vascular Bundle
- Embryo Endothelium
- Embryo Epidermis
- Embryo Parenchyma
- Embryo Plumule

### Seed

#### Descriptive

- Seed
- Seed Coat
- Seed Coat Aleurone Layer
- Seed Coat Hilum
- Seed Coat Hourglass
- Seed Coat Inner Integument
- Seed Coat Outer Integument
- Seed Coat Palisade
- Seed Coat Parenchyma
- Seed Cotyledon Abaxial Epidermis
- Seed Cotyledon Abaxial Parenchyma
- Seed Cotyledon Adaxial Epidermis
- Seed Cotyledon Vascular Bundle
- Seed Endosperm
- Seed Suspensor

### Hypocotyl

#### Comparative

- Hypocotyl
- Hypocotyl Root

### Shoot

#### Comparative

- Shoot
- Shoot Apical Meristem

#### Descriptive

- Shoot Apical Meristem

### Multiple Tissues

#### Descriptive

- Root, Stem, Leaflet



# Gene Expression Explorer

## Experiment Sample Selection

← Go Back  
One Step

Proceed to the  
Next Step →

This page shows all of the samples with gene expression data organized by Experiment. When an Experiment was chosen previously all of the samples are pre-selected for further analysis. When a Tissue was chosen, all of the samples for each Experiment that studied that tissue are shown with only the selected Tissue pre-selected. Use the check boxes to **add** or **delete** samples to generate the final list for further analysis. When your selections are complete click on the 'Proceed to the Next Step' button at the top right of the page.

### Table of Contents

- Fungal pathogen *Phakopsora pachyrhizi* effect on leaves: time course
- Lipo-chitoooligosaccharide effect on first trifoliolate leaf
- Leaf response to fungal pathogen *Phakopsora pachyrhizi*
- Analysis of iron deficiency in soybean leaf tissue
- Alterations in soybean gene expression profile after foliar application of lipo-chitoooligosaccharide (lco) from *Bradyrhizobium japonicum* under sub-optimal temperature
- The effects of bud removal on soybean leaf gene expression.
- Comparative physiology and transcriptional networks underlying the heat shock response in *Populus trichocarpa*, *Arabidopsis thaliana* and *Glycine max*
- GmMPK4 is a negative regulator of SA-mediated defense response
- Molecular characterization of the incompatible and compatible interaction of soybean rust disease in RPP3-containing PI462312 line
- Molecular characterization of the RPP4 resistance response
- Transcript profiling of soybean msh1 RNAi transgenic lines
- Response of RPP4-silenced plants to soybean rust

### Fungal pathogen *Phakopsora pachyrhizi* effect on leaves: time course

ID:		Tissue(s)	Cultivar	Treatment
GDS3230	Analysis of leaves up to 48 hours post-inoculation with <i>Phakopsora pachyrhizi</i> isolates, Hawaii 94-1 (HW94-1) and Taiwan 72-1 (TW72-1). HW94-1 produces a resistant reaction in the host, TW72-1 a susceptible reaction. Results provide insight into the molecular basis of resistance to a fungal pathogen.	<input checked="" type="checkbox"/> leaflet	Komata	mock inoculated; time 0
<b>Group:</b> biotic: <i>Phakopsora pachyrhizi</i>		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 6 hours post infection
<b>Platform:</b> GPL4592		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 6 hours post infection
<b>Type:</b> Expression_GeneChip		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 12 hours post infection
<b>Class:</b> comparative		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 12 hours post infection
		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 48 hours post infection
		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 48 hours post infection
		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 24 hours post infection
		<input checked="" type="checkbox"/> leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 24 hours post infection

### Lipo-chitoooligosaccharide effect on first trifoliolate leaf

ID:		Tissue(s)	Cultivar	Treatment
GDS3231	Analysis of first trifoliolate leaf from cv. OAC Bayfield plants treated with <i>Bradyrhizobium japonicum</i> lipo-chitoooligosaccharide (LCO, Nod factor). Foliar application of LCO can induce changes in hormone level and enzymatic activity. Results provide insight into the	<input checked="" type="checkbox"/> leaflet	Bayfield	normal control: water; 48 hour
<b>Group:</b> biotic: <i>Bradyrhizobium</i>		<input checked="" type="checkbox"/> leaflet	Bayfield	lipo-chitoooligosaccharide (NOD factor) induced; 48hour

# Gene Expression Explorer

## Experiment Explorer

[← Go Back One Step](#)

[Add Another Experiment or Tissue](#)

[Clear This Basket and Start Over](#)

[View in Genome Browser →](#)

This page shows a summary of the samples selected for further analysis.

To proceed to the graphical display click on the 'View on GBrowse' button at the top right of the page.

To return to the Experiment or Tissue picker page click 'Add Another Experiment or Tissue' to add more samples.

This 'shopping cart' is cumulative.

### Transgenic and conventional cultivar comparison

Tissue	Cultivar	Treatment
leaflet	2601R	unfurled first trifoliolate
leaflet	Bayfield	unfurled first trifoliolate
leaflet	Mandarin	unfurled first trifoliolate
leaflet	PS46R	unfurled first trifoliolate
leaflet	S03W4	unfurled first trifoliolate

### Fungal pathogen *Phakopsora pachyrhizi* effect on leaves: time course

Tissue	Cultivar	Treatment
leaflet	Komata	mock inoculated; time 0
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 6 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 6 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 12 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 12 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 48 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 48 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 24 hours post infection
leaflet	Komata	<i>Phakopsora pachyrhizi</i> infected; 24 hours post infection

### Lipo-chitooligosaccharide effect on first trifoliolate leaf

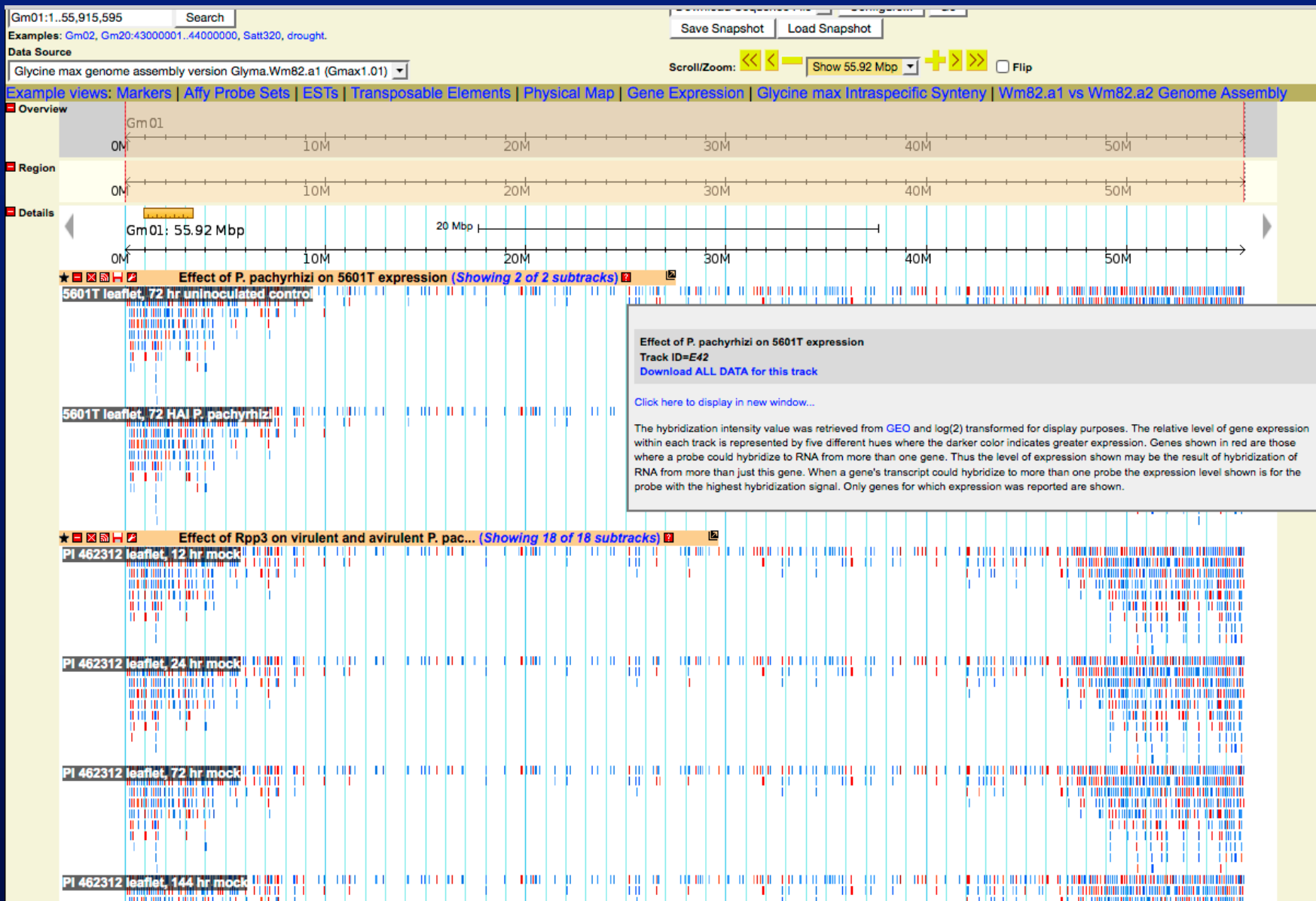
Tissue	Cultivar	Treatment
leaflet	Bayfield	normal control: water; 48 hour
leaflet	Bayfield	lipo-chitooligosaccharide (NOD factor) induced; 48hour

### Leaf response to fungal pathogen *Phakopsora pachyrhizi*

Tissue	Cultivar	Treatment
leaflet	5601T	normal control
leaflet	5601T	Asian soybean rust infected



# Gene Expression Explorer





# Cultivar Pedigrees at SoyBase

## Record for Cultivar Bragg

Cultivar	Synonyms	Maternal Parent X Paternal Parent	Comment	Google Search (New Window)
Bragg	F58-3786 PI 548660	Jackson X D49-2491		<a href="#">Scour Google For This Line</a>

## Records Containing Bragg

Cultivar	Synonyms	Maternal Parent X Paternal Parent	Comment
4-74-6-3		Forrest (2) X [ Govan x ( Bragg x PI 229358 ) ]	Insect resistant selection
Braxton	F71-1180 PI 548659	F59-1505 X ( Bragg (3) x D69-7965 )	PVP 8000075
Coker 338	Co68-38 PI 556515 Co338	Hampton 266 X Bragg	Coker's Pedigreed Seed Co.
Coker 485	Co80-764 Co485	Centennial X [ ( Hampton 266 x Bragg ) x Hutton ]	
Coker 488	Co73-410 PI 556537 Co488	Hampton 266 X Bragg	
Coker 68-38	Co68-38	Hampton 266 X Bragg	
Coker 68-41	Co68-41	Hampton 266 X Bragg	
Coker 69-119	Co69-119	Hampton 266 X Bragg	
Coker 71-211	Co71-211	Hampton 266 X Bragg	
Coker 72-286	Co72-286	Hampton 266 X Bragg	
Coker 73-410	Coker 488 PI 556537	Hampton 266 X Bragg	PVP 7800035
Coker 73-473	Co73-473	Hampton 266 X Bragg	
Coker 80-764	Coker 485 Co80-764	Centennial X [ ( Hampton 266 x Bragg ) x Hutton ]	
D66-8556		Bragg X Semmes	
D66-8666	Govan PI 548979	Bragg X Semmes	
D67-10507		Dyer X Bragg	SCN race 3 resistant selection
D68-127		Dyer X Bragg	
D68-128	PI 548655 Forrest	Dyer X Bragg	PVP 7300058
D68-18		Dyer X Bragg	
D68-180		Dyer X Bragg	Resistant to CN race 3
D68-201		Dyer X Bragg	
D68-216		Dyer X Bragg	later maturing, CN race 3 resistant selection
D68-78		Dyer X Bragg	
D69-262		Bragg (2) X D69-7965	

# Cultivar Pedigrees at SoyBase

Google

Bragg OR F58-3786 OR PI 548660 soybean

All News Shopping Images Maps More Settings Tools

About 32 results (0.64 seconds)

**SoyBase - Uniform Soybean Tests Parentage Information**  
<https://www.soybase.org/uniformtrial/index.php?page=lines&filter=Bragg> ▾  
The **soybean** parentage information in this database was partially gleaned from the Uniform **Soybean** Tests for the Southern and Northern regions as well as ... If a strain was named its PI number was also included as a synonym. ... PI 548660

**Genetic separation of southern and northern soybean breeding ...**  
<link.springer.com/article/10.1007/s11032-016-0611-7>  
by G Wolfgang - 2017 - Related articles  
Jan 11, 2017 - Genetic separation of southern and northern **soybean** breeding programs in North America and their associated allelic variation at four maturity ...

**[PDF] PI 548659-continued origin: United States, origin institute: Florida Agr ...**  
[www.ars-grin.gov/npgs/pi\\_books/scans/200pt1/pi200pt1\\_336.pdf](http://www.ars-grin.gov/npgs/pi_books/scans/200pt1/pi200pt1_336.pdf) ▾  
PI 548660. Glycine max (L.) Merr. FABACEAE Soybean. Donated by: Hartwig, Edgar E., USDA-ARS Delta Branch Experiment. Station, P.O. Box 197, Stoneville, ...

**Resistance to Soybean - Publication : USDA ARS**  
<https://www.ars.usda.gov/research/publications/publication/?seqNo115=230001>  
by L Hesler - 2009 - Cited by 2 - Related articles  
Nov 17, 2009 - Title: Resistance to **Soybean** Aphid Among **Soybean** Lines, ... Kosamame (PI 171451, test II), Bhart (PI 165989, test III), and **Bragg** (PI 548660, ...

(M2) SOYBEAN: Glycine max L. (Merrill) RESISTANCE TO SOYBEAN

# Data Downloads

## Download Data

### Table of Contents

#### Download Data

##### SoyBase Data

##### *Genetic Map*

- Download genetic map coordinates for selected features
- Download sequences for genetic loci

##### *Genome Sequence*

- Download sequences from SoyBase BLAST target databases
- Glyma 1.1 to Glyma2.0 Correspondence Lookup
- Download genome sequence coordinates for selected features
- Download genome sequence coordinates for selected features by chromosome
- Download a list of names and sequence coordinates for gene models or markers in a chromosomal region
- Download genome or predicted protein sequence for gene calls
- Download annotations for selected gene calls
- Download gene model flanking sequence
- Download gene model 3' and 5' UTR sequences
- Download SoySNP50K Data

#### External Data Sources

# Options for the Future of SoyBase

- Business as usual
- Increased community involvement



# 1024 QTL for 104 Traits Added in 2016

Asian Soybean Rust	Leaflet weight, specific	SCN	Seed set, 2 or 3 per pod
Branching	Lodging	SDS	Seed set, 2 per pod
Chlorophyll fluorescence TRo/ABS	mqCanopy wilt	Seed coat hardness	Seed set, 3 per pod
Chlorosis, leaflet UV-B induced	mqPlant height	Seed conglycinin, beta	Seed set, 4 per pod
cqSeed oil	mqSeed Oil	Seed Cys	Seed thickness
cqSeed protein	Node number	Seed daidzein	Seed Thr
cqSeed weight	Nodule number	Seed genistein	Seed tocopherol, alpha
First flower	Nodule size	Seed glycinin	Seed tocopherol, delta
Flower color	Petiole color, UV-B induced	Seed glycinin plus beta-conglycinin	Seed tocopherol, gamma
Foxglove aphid, primary damage, choice	Phomopsis seed decay	Seed glycinin to beta-conglycinin ratio	Seed tocopherol, total
Foxglove aphid, primary damage, no choice	Phytoph	Seed glycitein	Seed total isoflavone
Foxglove aphid, total damage, choice	Plant damage, UV-B induced	Seed hardness	Seed viability
Foxglove aphid, total damage, no choice	Plant height	Seed height	Seed weight
Hypocotyl length	Plant P	Seed isoflavone	Seed weight per plant
Internode length	Pod maturity	Seed length	Seed width
Japanese beetle resistance	Pod number	Seed length to height ratio	Seed width to thickness ratio
Leaf Damage, ozone, 2nd trifoliolate leaf	R/V photo-thermal sensitivity	Seed length to thickness ratio	Seed winter hardness
Leaf Damage, ozone, 3rd trifoliolate leaf	Reproductive period	Seed length to width ratio	Seed yield
Leaf Damage, ozone, 3rd-5th trifoliolate leaves	Reproductive period photo-thermal sensitivity	Seed length to width ratio	Shoot length
Leaf Damage, ozone, 4th trifoliolate leaf	Reproductive to vegetative period ratio	Seed Lys	Shoot weight
Leaf Damage, ozone, 5th trifoliolate leaf	Root density, lateral	Seed Met	Shoot weight, dry
Leaf Damage, ozone, 6th trifoliolate leaf	Root length, primary	Seed Met plus Cys	Soybean mosaic virus
Leaflet area	Root nodule weight, dry	Seed number	Stem length, main
Leaflet chlorophyll	Root to Shoot weight ratio	Seed oil	Stem weight, dry
Leaflet shape 10-1	Root volume	Seed protein	Total growth duration
Leaflet shape, UV-B induced	Root weight, dry	Seed set, 1 per pod	Vegetative period

## Getting Data into SoyBase

Adding the 1024 QTL took over 10 person months, primarily due to the idiosyncratic way papers are written. Often the only place in the paper that the map positions of the QTL are given is a figure. We then must analyze the figure to determine the coordinates of the QTL ends and in addition often convert the genetic positions reported in the paper to the coordinate system used at SoyBase.

For comparison, the Gene Expression Explorer I described took about 2 person months to develop and populate while the GRIN Data Explorer took about 1 month.

# Options for the Future of SoyBase

- Business as usual
- Increased community involvement
  - Talk to us early when initiating a project  
grant proposal data management plan  
nomenclature and data format
  - Direct data submission to SoyBase

# Direct Data Submission

SoyBase Home Help & Tutorials Genetic Map Genome Browser Expression Data Browser

- Genetic Map Tutorials
- Sequence Map Tutorials
- Database Searching Tutorials
- Growth & Development Tutorials
- Soybean Disease Tutorials
- Soybean Pest Tutorials
- Methods & Protocols Tutorials
- [How to submit your data to SoyBase](#)
- [How to Cite SoyBase](#)
- Site Map
- Contact Us

Update Emails

Advanced Search →

## Data Submission Templates and Instructions

These templates are under active development. Please return here to get the latest versions

### Data Types

Bi-allelic QTL Data

[Excel spreadsheet for data entry](#)

Genome Wide Association QTL Data

Coming Soon

Gene Data

[Excel spreadsheet for data entry](#)

Re-sequencing Data (SNPs, CNV, etc.)

[Contact us for instructions](#)

Expression or Transcriptomic Data (RNA-seq, GeneChip, custom chips, etc.)

[Contact us for instructions](#)

### Other Data Types

In addition to the more established data types above, we recognize that the soybean research community will sometimes generate novel data that would be appropriate for inclusion in SoyBase. Because these data will be, by definition, different from what is already present in SoyBase, the underlying database infrastructure and web displays to accommodate them will need to be developed. To facilitate this effort it would be very helpful to consult with us early in the project so that we can efficiently plan how SoyBase staff effort will be allocated. These early discussions will ensure that optimal decisions can be made about nomenclature, data file formats, etc. so there will be a minimal delay in making your data available to the community.

# Contact SoyBase



## SoyBase and the Soybean Breeder's Toolbox

Integrating Genetics and Molecular Biology for Soybean Researchers

[SoyBase Home](#) [Help & Tutorials](#) [Genetic Map](#) [Genome Browser](#) [Expression](#) [Mutants](#) [Projects](#) [Tools](#) [Community](#) [Site Map](#)

### Contact Us/User Feedback

Contact Us/User Feedback Form

All Fields Required

From:

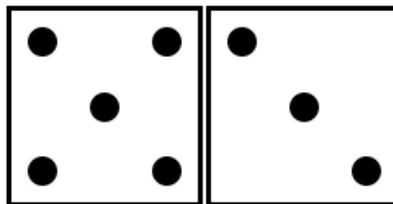
Email Address:

Subject Line:

Message:

All fields required

What did you get?



What did you get?

# Questions?

We value your opinion!!

Please take our quick six question survey using the link on the SoyBase home page or at <https://www.soybase.org/survey/>