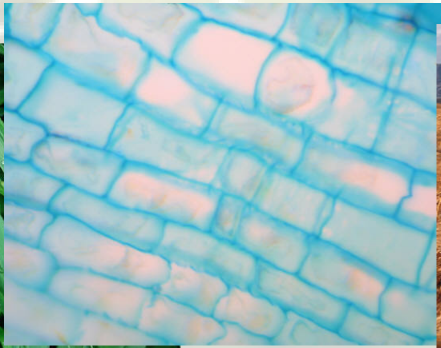
Welcome to the Quantitative Trait Loci (QTL) Tutorial

This tutorial will describe how to navigate the section of Gramene that provides information on Quantitative Trait Loci (QTL). QTL are a statistical creation that identifies a particular region of the genome as containing a gene (or genes) that is associated with the trait being assayed or measured.



Tutorial Help

The hand icon indicates a link that allows you to go to the same page in your web browser.

If you are viewing this tutorial with Adobe Acrobat Reader, click the "bookmarks" on the left hand side of the Reader for easier navigation.

Action Options are noted in this type of font.

Notes or comments use this style font.

Trait Categories in Trait Ontology

Traits at Gramene are identified by Trait Ontology (TO), and are categorized according to:

Abiotic stress: Traits related to stresses from abiotic environment, e.g., water, light, temperature, or chemical.

Anatomy: Traits directly measuring plant parts such as root, stem or leaf.

Biochemical: Biochemical and physiological traits, e.g., enzyme activity.

Biotic stress: Traits related to stresses from pests and pathogens.

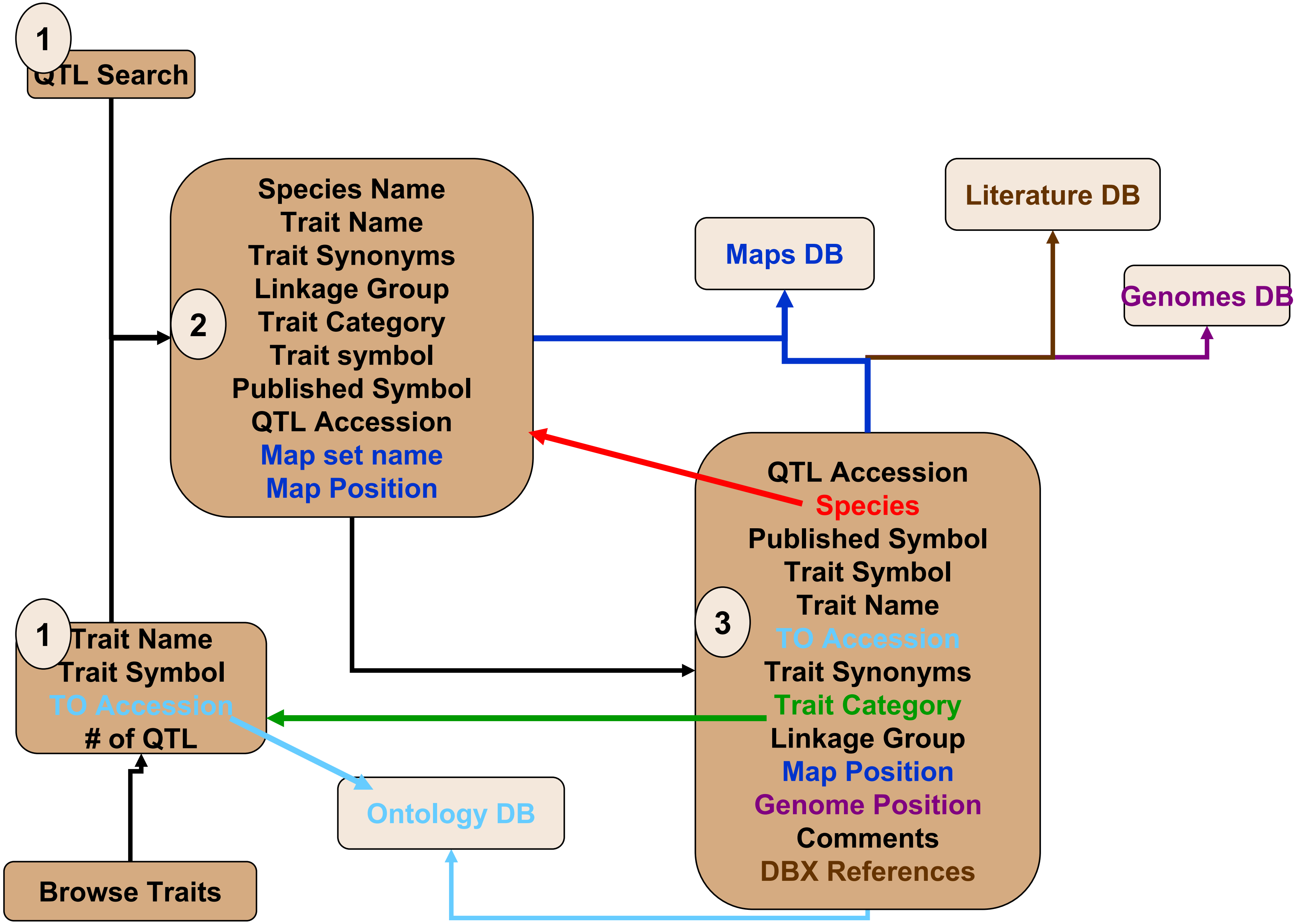
Development: Traits related to plant and plant part development. Also includes maturity related traits.

Quality: Traits of economic importance that may affect product quality.

Sterility or fertility: Traits related to male and female flower sterility or fertility, including incompatibility.

Vigor: Traits related to growth and dormancy.

Yield: Traits contributing directly to yield based on economic value.



1 QTL Search

2
Species Name
Trait Name
Trait Synonyms
Linkage Group
Trait Category
Trait symbol
Published Symbol
QTL Accession
Map set name
Map Position

Maps DB

Literature DB

Genomes DB

3
QTL Accession
Species
Published Symbol
Trait Symbol
Trait Name
TO Accession
Trait Synonyms
Trait Category
Linkage Group
Map Position
Genome Position
Comments
DBX References

1
Trait Name
Trait Symbol
TO Accession
# of QTL

Ontology DB

Browse Traits

Gramene Home Page

Click here to open QTL Home Page

Quick Search

Have Questions...?

- Gramene now has **tutorials** for every module.
- Ask questions through Feedback or Email

Gramene Tips:

The SSR Marker Search is listed under the Marker database.

All Tips

Quick Start

nced genomes for Rice, Maize & Arabidopsis; Look for rice/maize h with GrameneMart; Search for sequence alignment with tology.

Site or Browse by Gene Ontology using GO Slim.

physical m , and Compar ent

MOLECULAR MARKERS: Use the S ; or search by marker type or species,

TRAITS: Search the Genes or QTL database for important phenotype-releated loci such as Rice Genes, Rice QTL, Maize QTL. Don't forget to explore traits in Ontologies.

LITERATURE: Search the literature for your friends and topics of interest.

SUBMISSION: Submit a Rice Gene or Ontology Term to Gramene.

Gramene is a curated, open-source, web-accessible data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

Featured News

- Gramene Release 20 for March 2006. See the release notes.
- Gramene News Archive
- RTWG Gramene workshop materials are available.
- Rice News Worldwide from IRRI

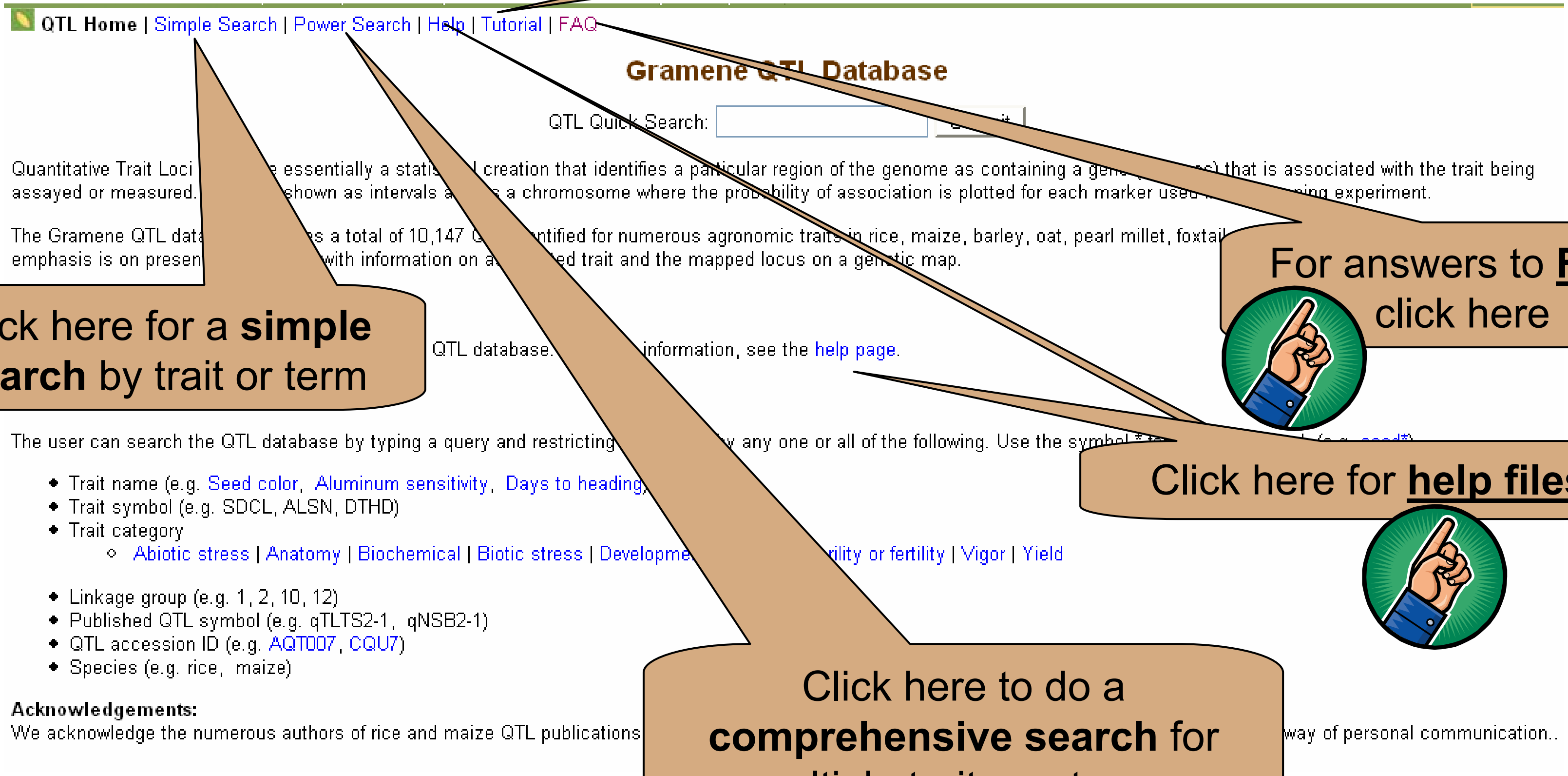
Visit with us at

- 48th Maize Genetics Conference, March 9-12, 2006, Asilomar, Pacific Grove, CA

Gramene Calendar

Last modified: Thu Mar 2 15:54:55 2006

QTL Home Page



QTL Home | Simple Search | Power Search | Help | Tutorial | FAQ

Gramene QTL Database

QTL Quick Search:

Quantitative Trait Loci … e essentially a statis… l creation that identifies a particular region of the genome as containing a gene … that is associated with the trait being assayed or measured. … shown as intervals a… a chromosome where the probability of association is plotted for each marker used … ping experiment.

The Gramene QTL data… s a total of 10,147 Q… ntified for numerous agronomic traits in rice, maize, barley, oat, pearl millet, foxtail … emphasis is on presen… with information on a… ed trait and the mapped locus on a genetic map.

… QTL database. … information, see the help page.

The user can search the QTL database by typing a query and restricting … y any one or all of the following. Use the symbol * …

- Trait name (e.g. Seed color, Aluminum sensitivity, Days to heading…
- Trait symbol (e.g. SDCL, ALSN, DTHD)
- Trait category
  - Abiotic stress | Anatomy | Biochemical | Biotic stress | Developme… …ility or fertility | Vigor | Yield
- Linkage group (e.g. 1, 2, 10, 12)
- Published QTL symbol (e.g. qTLTS2-1, qNSB2-1)
- QTL accession ID (e.g. AQT007, CQU7)
- Species (e.g. rice, maize)

Acknowledgements:
We acknowledge the numerous authors of rice and maize QTL publications … way of personal communication..

Click here for this **tutorial**

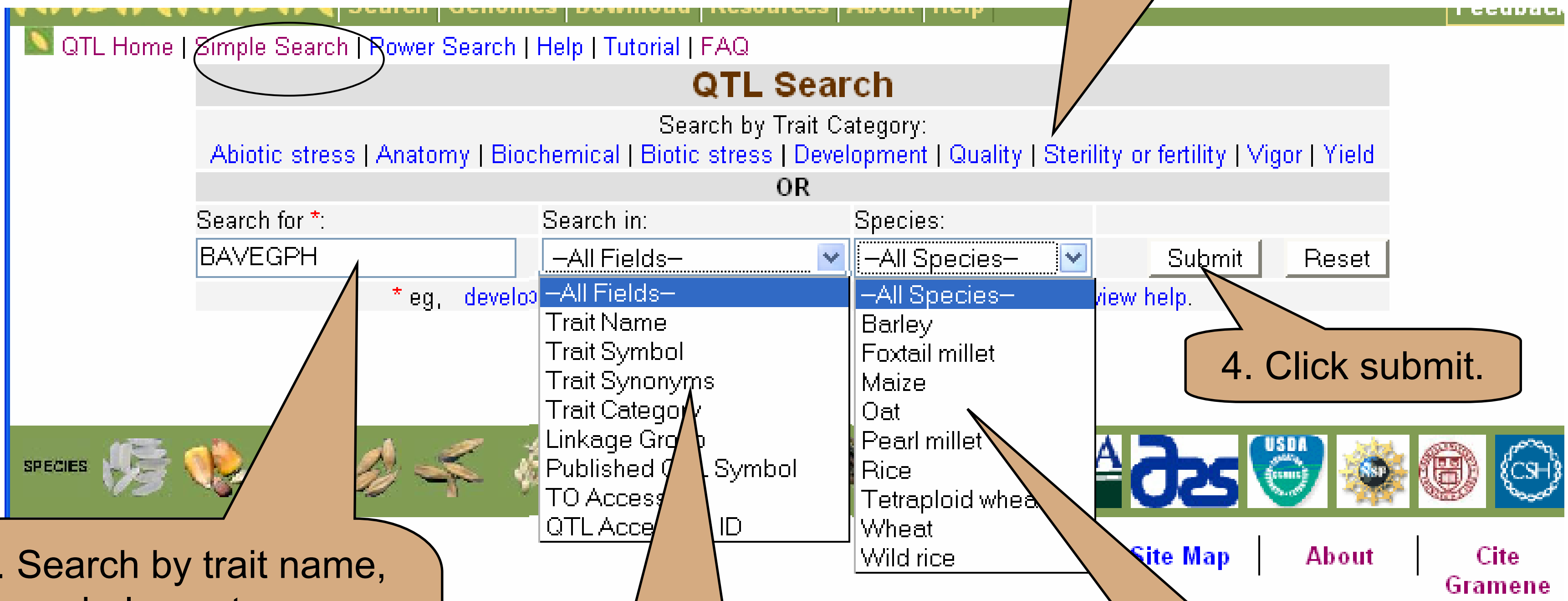
For answers to **FAQ,** click here

Click here for a **simple search** by trait or term

Click here for **help files**

Click here to do a **comprehensive search** for multiple traits or terms

1. Simple Search: by Trait



QTL Home | Simple Search | Power Search | Help | Tutorial | FAQ

QTL Search

Search by Trait Category:

Abiotic stress | Anatomy | Biochemical | Biotic stress | Development | Quality | Sterility or fertility | Vigor | Yield

OR

Search for *: BAVEGPH

Search in: –All Fields–

Species: –All Species–

Submit Reset

* eg, develo

iew help.

Click a trait to **browse QTL** in that trait category

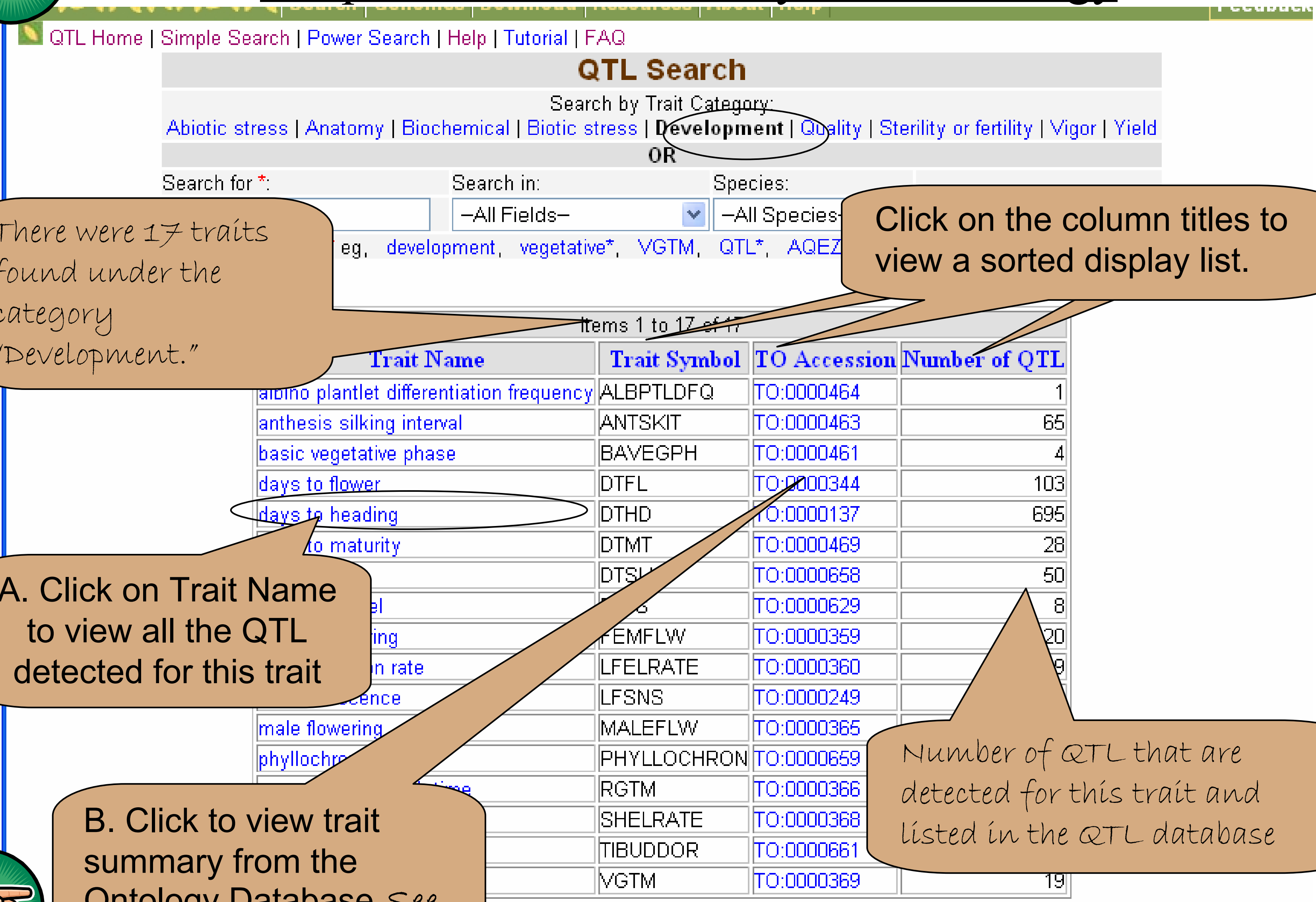
1. Search by trait name, symbol or category, chromosome #, QTL symbol or accession ID. Wildcard searches include the * (i.e. seed*)

2. Limit search by term field. Default searches all fields.

3. Limit search by species if desired.

4. Click submit.

Simple Search: Browse by Trait Ontology



QTL Home | Simple Search | Power Search | Help | Tutorial | FAQ

QTL Search

Search by Trait Category:

Abiotic stress | Anatomy | Biochemical | Biotic stress | **Development** | Quality | Sterility or fertility | Vigor | Yield

OR

Search for *: | Search in: –All Fields– | Species: –All Species–

eg, development, vegetative*, VGTM, QTL*, AQEZ

Items 1 to 17 of 17

Trait Name	Trait Symbol	TO Accession	Number of QTL
albino plantlet differentiation frequency	ALBPTLDFQ	TO:0000464	1
anthesis silking interval	ANTSKIT	TO:0000463	65
basic vegetative phase	BAVEGPH	TO:0000461	4
days to flower	DTFL	TO:0000344	103
days to heading	DTHD	TO:0000137	695
to maturity	DTMT	TO:0000469	28
	DTS	TO:0000658	50
el	S	TO:0000629	8
ing	FEMFLW	TO:0000359	20
n rate	LFELRATE	TO:0000360	9
ence	LFSNS	TO:0000249	
male flowering	MALEFLW	TO:0000365	
phyllochr	PHYLLOCHRON	TO:0000659	
ime	RGTM	TO:0000366	
	SHELRATE	TO:0000368	
	TIBUDDOR	TO:0000661	
	VGTM	TO:0000369	19

There were 17 traits found under the category "Development."

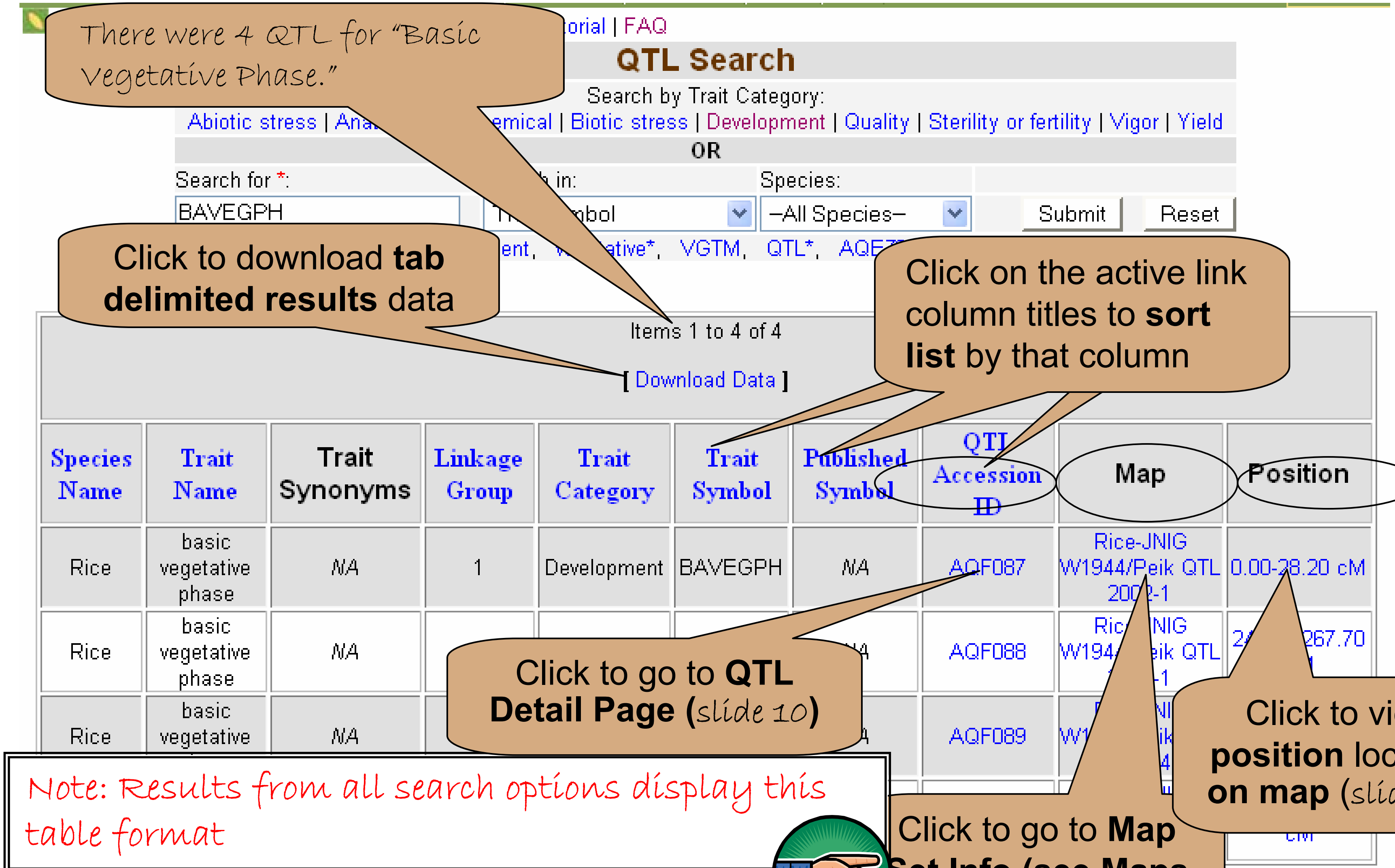
Click on the column titles to view a sorted display list.

A. Click on Trait Name to view all the QTL detected for this trait

Number of QTL that are detected for this trait and listed in the QTL database

B. Click to view trait summary from the Ontology Database See Ontology Tutorial

Results for simple search



orial | FAQ

QTL Search

Search by Trait Category:

Abiotic stress | Ana emical | Biotic stress | Development | Quality | Sterility or fertility | Vigor | Yield

OR

Search for *: | h in: | Species:

BAVEGPH | T mbol | –All Species– | Submit | Reset

ent, ative*, VGTM, QTL*, AQE

Items 1 to 4 of 4

[Download Data]

Species Name	Trait Name	Trait Synonyms	Linkage Group	Trait Category	Trait Symbol	Published Symbol	QTL Accession ID	Map	Position
Rice	basic vegetative phase	NA	1	Development	BAVEGPH	NA	AQF087	Rice-JNIG W1944/Peik QTL 2002-1	0.00-28.20 cM
Rice	basic vegetative phase	NA				A	AQF088	Ric NIG W194 eik QTL -1	2 267.70
Rice	basic vegetative	NA				A	AQF089	W1 ik 4	

There were 4 QTL for "Basic Vegetative Phase."

Click to download **tab delimited results** data

Click on the active link column titles to **sort list** by that column

Click to go to **QTL Detail Page** (slide 10)

Click to go to **Map Set Info (see <u>Maps tutorial</u>)**

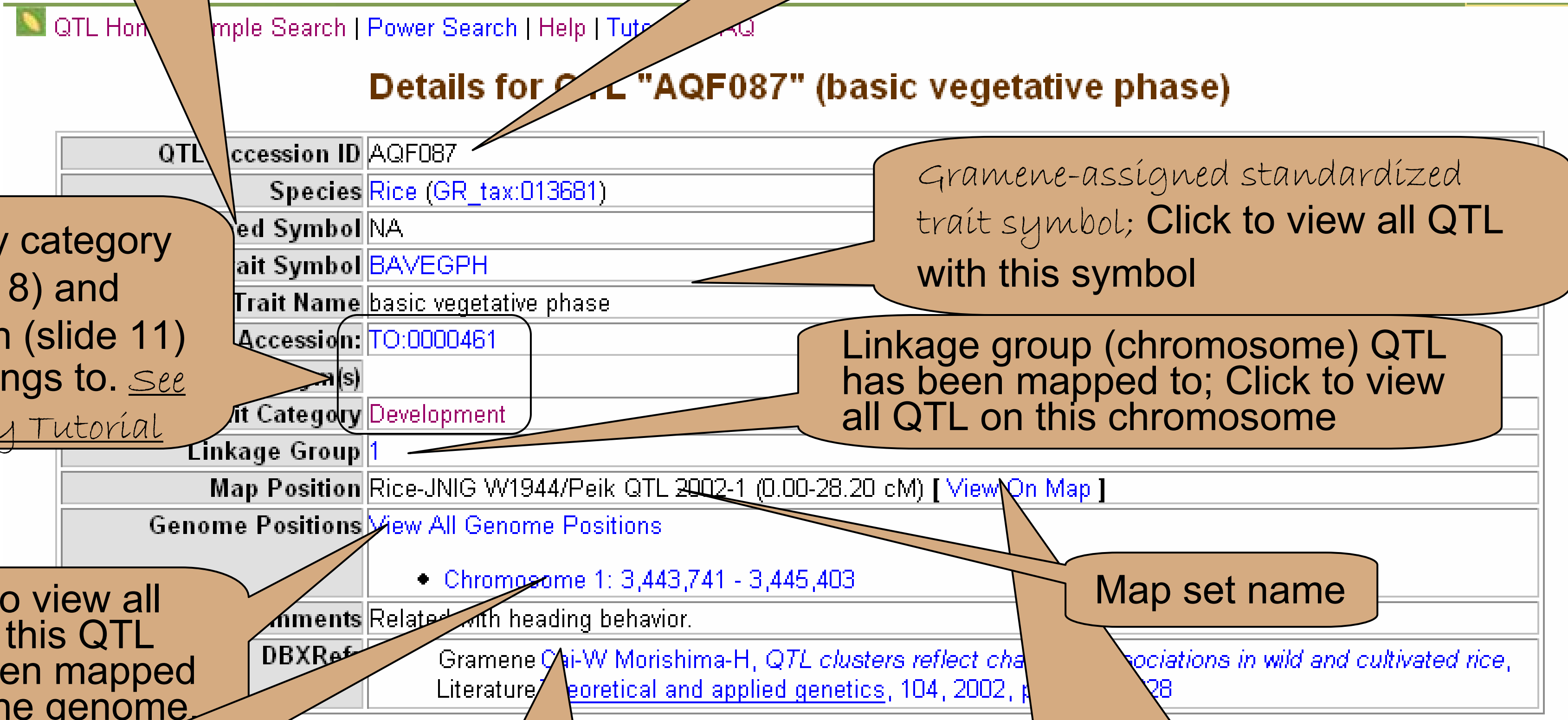
Click to view **position** location **on map** (slide 12)

Note: Results from all search options display this table format

QTL Detail

QTL symbol as assigned in the publication cited

Gramene-assigned QTL accession ID



QTL Hon | mple Search | Power Search | Help | Tut | AQ

Details for "AQF087" (basic vegetative phase)

QTL ccession ID	AQF087
Species	Rice (GR_tax:013681)
ed Symbol	NA
ait Symbol	BAVEGPH
Trait Name	basic vegetative phase
Accession:	TO:0000461
n(s)	
it Category	Development
Linkage Group	1
Map Position	Rice-JNIG W1944/Peik QTL 2002-1 (0.00-28.20 cM) [View On Map]
Genome Positions	View All Genome Positions • Chromosome 1: 3,443,741 - 3,445,403
mments	Related with heading behavior.
DBXRef	Gramene Literature Cai-W Morishima-H, *QTL clusters reflect cha ociations in wild and cultivated rice*, eoretical and applied genetics, 104, 2002, p 28

Gramene-assigned standardized trait symbol; Click to view all QTL with this symbol

Ontology category (slide 8) and accession (slide 11) QTL belongs to. See Ontology Tutorial

Linkage group (chromosome) QTL has been mapped to; Click to view all QTL on this chromosome

Map set name

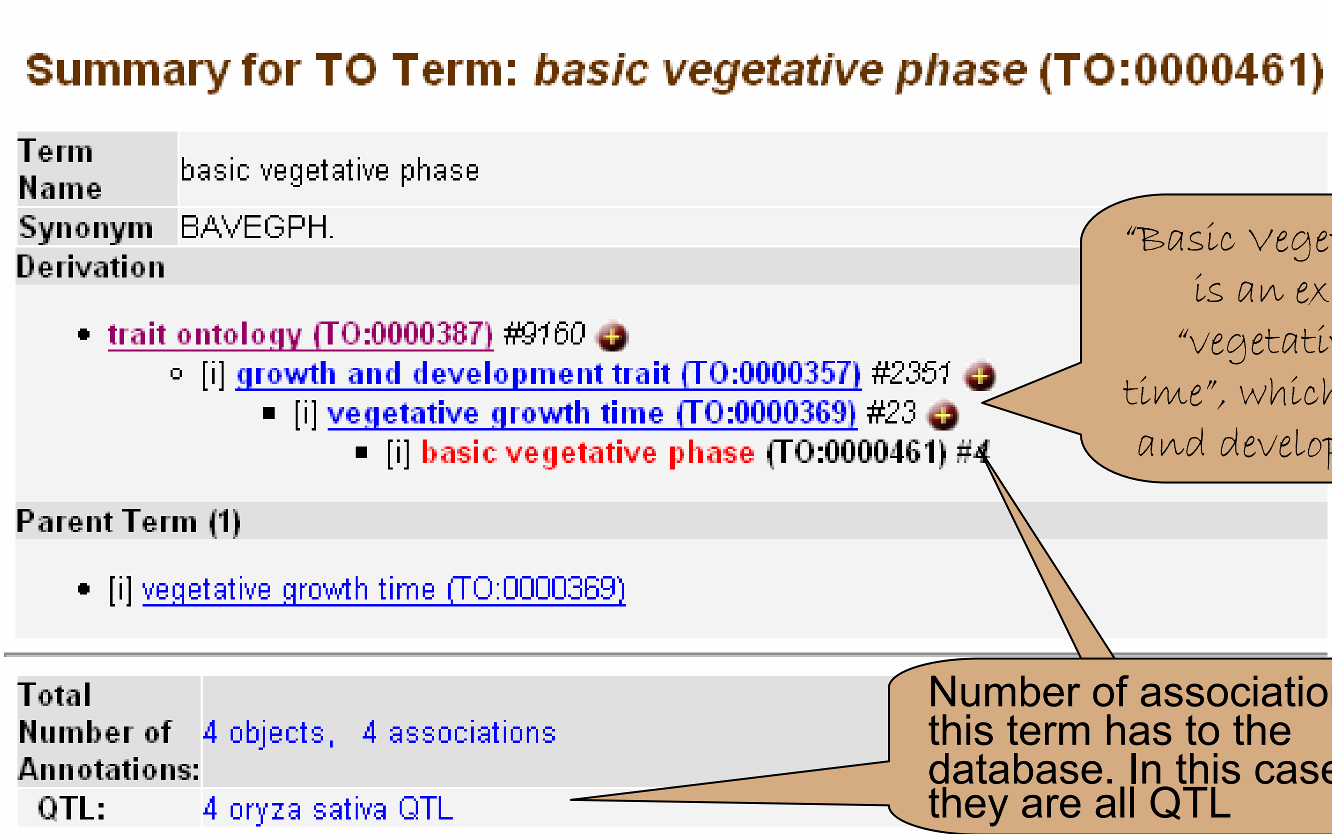
Click to view all places this QTL has been mapped to on the genome

Click to view QTL on genome browser. (see genomes tutorial)

Click to view literature for citations (See Literature Tutorial)

Click to view position on Map (see Map Tutorial) (see slide 12)

Trait Ontology (TO) Accession



Summary for TO Term: *basic vegetative phase* (TO:0000461)

Term Name	basic vegetative phase
Synonym	BAVEGPH.

Derivation

- trait ontology (TO:0000387) #9160 ⊕
    - [i] growth and development trait (TO:0000357) #2351 ⊕
        - [i] vegetative growth time (TO:0000369) #23 ⊕
            - [i] basic vegetative phase (TO:0000461) #4

Parent Term (1)

- [i] vegetative growth time (TO:0000369)

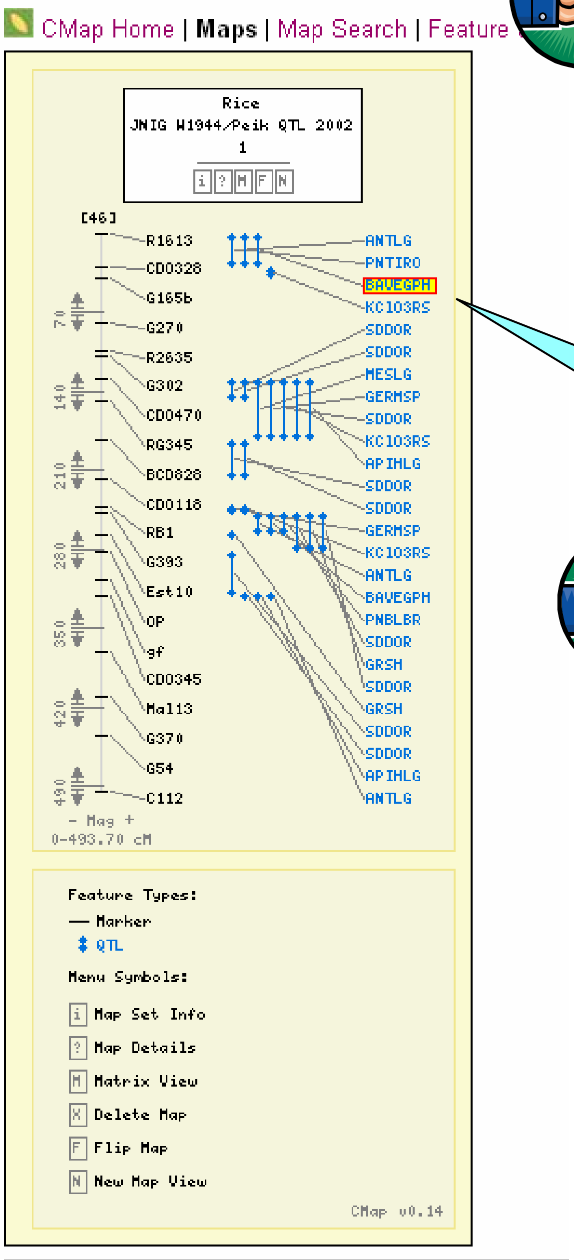
Total Number of Annotations:	4 objects, 4 associations
QTL:	4 oryza sativa QTL

"Basic vegetative phase" is an example of "vegetative growth time", which is a growth and development trait.

Number of associations this term has to the database. In this case, they are all QTL

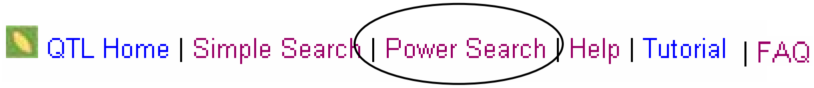
See Ontology Tutorial for more information on ontology

Map Position



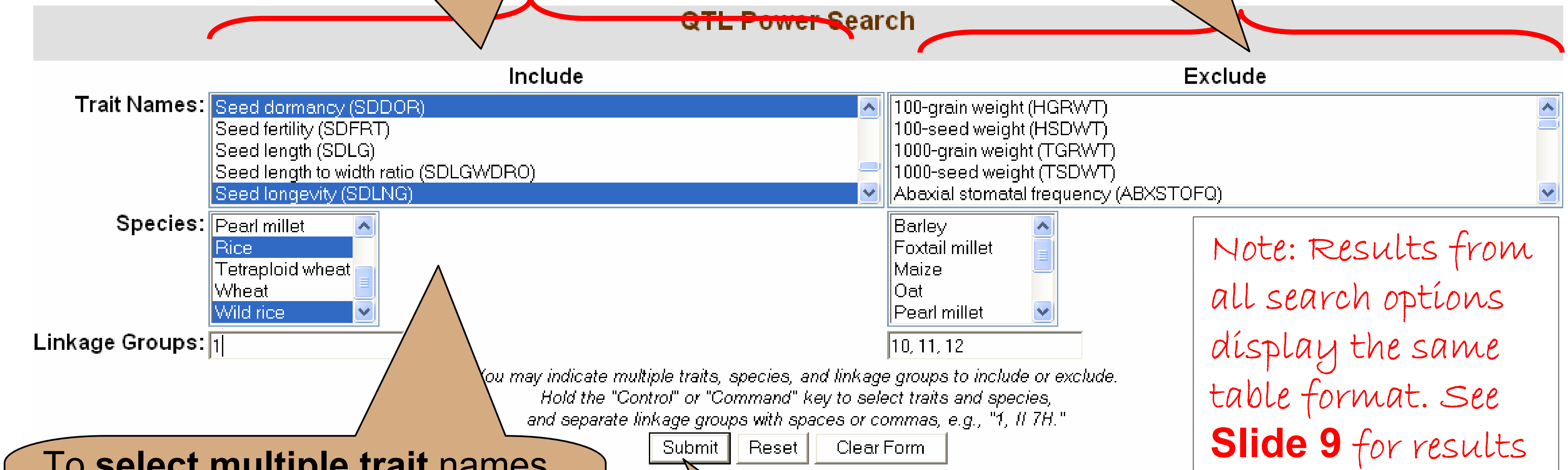
QTL map shows QTL trait symbols as features. Click on any feature to view more information about that feature. See Maps tutorial for more information.

3. Power Search



To construct a comprehensive query, select **criteria to include** in your search

To construct a comprehensive query, select **criteria to exclude** in your search



QTL Power Search

	Include	Exclude
Trait Names:	Seed dormancy (SDDOR) Seed fertility (SDFRT) Seed length (SDLG) Seed length to width ratio (SDLGWDRO) Seed longevity (SDLNG)	100-grain weight (HGRWT) 100-seed weight (HSDWT) 1000-grain weight (TGRWT) 1000-seed weight (TSDWT) Abaxial stomatal frequency (ABXSTOFQ)
Species:	Pearl millet Rice Tetraploid wheat Wheat Wild rice	Barley Foxtail millet Maize Oat Pearl millet
Linkage Groups:	1	10, 11, 12

You may indicate multiple traits, species, and linkage groups to include or exclude. Hold the "Control" or "Command" key to select traits and species, and separate linkage groups with spaces or commas, e.g., "1, II 7H."

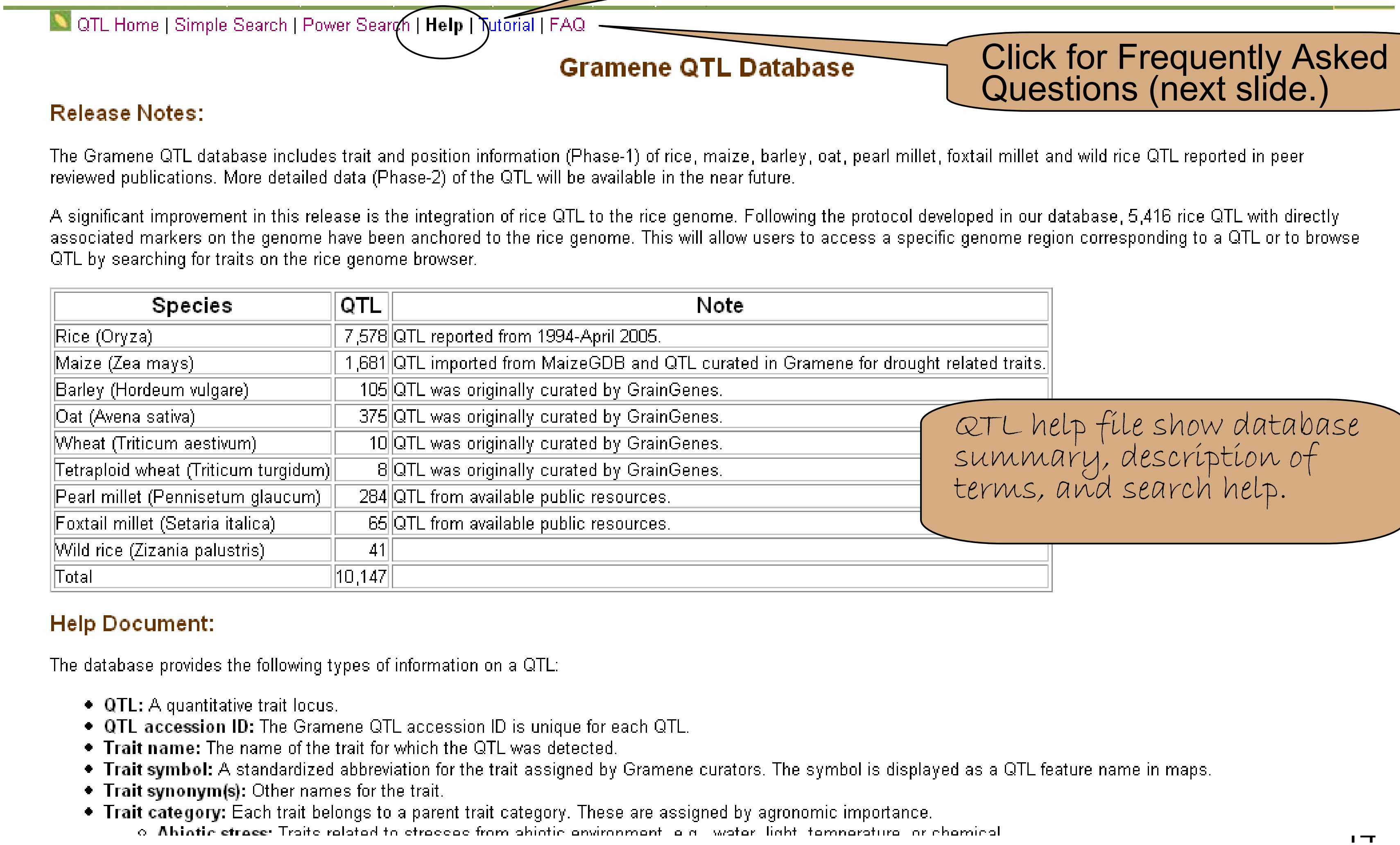
To **select multiple trait** names or species, hold "Control" (or "Command" on Mac) key while selecting multiple traits.

Click to submit

Note: Results from all search options display the same table format. See **Slide 9** for results navigation.

QTL Help

Tutorial link offers three tutorial formats – PowerPoint, PDF or HTML.



QTL Home | Simple Search | Power Search | **Help** | Tutorial | FAQ

Click for Frequently Asked Questions (next slide.)

Gramene QTL Database

Release Notes:

The Gramene QTL database includes trait and position information (Phase-1) of rice, maize, barley, oat, pearl millet, foxtail millet and wild rice QTL reported in peer reviewed publications. More detailed data (Phase-2) of the QTL will be available in the near future.

A significant improvement in this release is the integration of rice QTL to the rice genome. Following the protocol developed in our database, 5,416 rice QTL with directly associated markers on the genome have been anchored to the rice genome. This will allow users to access a specific genome region corresponding to a QTL or to browse QTL by searching for traits on the rice genome browser.

Species	QTL	Note
Rice (Oryza)	7,578	QTL reported from 1994-April 2005.
Maize (Zea mays)	1,681	QTL imported from MaizeGDB and QTL curated in Gramene for drought related traits.
Barley (Hordeum vulgare)	105	QTL was originally curated by GrainGenes.
Oat (Avena sativa)	375	QTL was originally curated by GrainGenes.
Wheat (Triticum aestivum)	10	QTL was originally curated by GrainGenes.
Tetraploid wheat (Triticum turgidum)	8	QTL was originally curated by GrainGenes.
Pearl millet (Pennisetum glaucum)	284	QTL from available public resources.
Foxtail millet (Setaria italica)	65	QTL from available public resources.
Wild rice (Zizania palustris)	41	
Total	10,147	

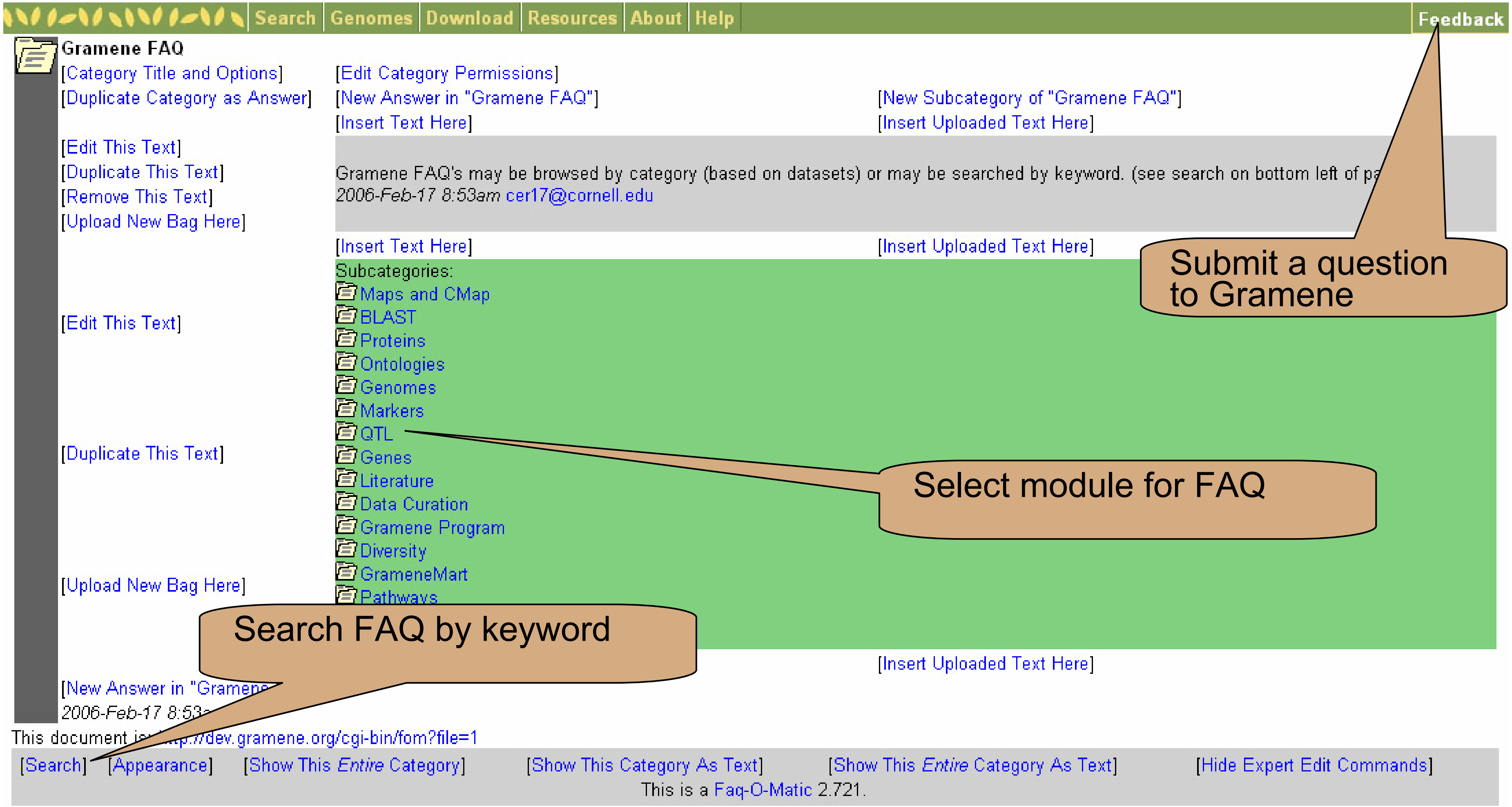
QTL help file show database summary, description of terms, and search help.

Help Document:

The database provides the following types of information on a QTL:

- **QTL:** A quantitative trait locus.
- **QTL accession ID:** The Gramene QTL accession ID is unique for each QTL.
- **Trait name:** The name of the trait for which the QTL was detected.
- **Trait symbol:** A standardized abbreviation for the trait assigned by Gramene curators. The symbol is displayed as a QTL feature name in maps.
- **Trait synonym(s):** Other names for the trait.
- **Trait category:** Each trait belongs to a parent trait category. These are assigned by agronomic importance.
  - **Abiotic stress:** Traits related to stresses from abiotic environment, e.g., water, light, temperature, or chemical

FAQ



Gramene FAQ

[Category Title and Options] [Edit Category Permissions]
[Duplicate Category as Answer] [New Answer in "Gramene FAQ"] [New Subcategory of "Gramene FAQ"]
[Insert Text Here] [Insert Uploaded Text Here]

[Edit This Text]
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[Remove This Text]
[Upload New Bag Here]

Gramene FAQ's may be browsed by category (based on datasets) or may be searched by keyword. (see search on bottom left of pa
2006-Feb-17 8:53am cer17@cornell.edu

[Insert Text Here] [Insert Uploaded Text Here]

Subcategories:
- Maps and CMap
- BLAST
- Proteins
- Ontologies
- Genomes
- Markers
- QTL
- Genes
- Literature
- Data Curation
- Gramene Program
- Diversity
- GrameneMart
- Pathways

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[New Answer in "Gramene
2006-Feb-17 8:53

This document i tp://dev.gramene.org/cgi-bin/fom?file=1

[Search] [Appearance] [Show This *Entire* Category] [Show This Category As Text] [Show This *Entire* Category As Text] [Hide Expert Edit Commands]
This is a Faq-O-Matic 2.721.

Submit a question to Gramene

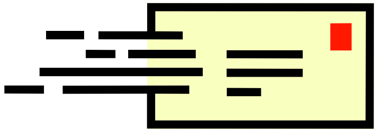
Select module for FAQ

Search FAQ by keyword

Contact Gramene

Use the feedback button, located at the top of every page, to provide feedback or to ask questions about Gramene.

or



Email Gramene at gramene@gramene.org