

# Accessing Gramene

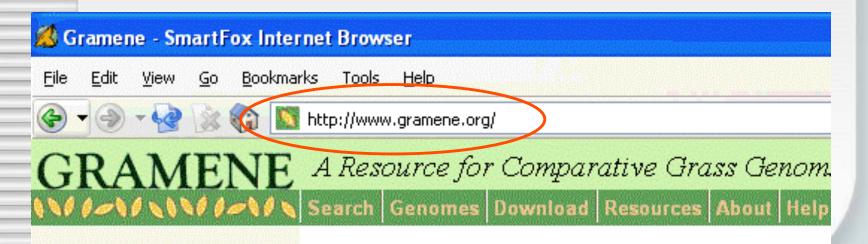
To access Gramene, open your internet browser (such as Netscape, IE, or Safari).

(If some website features don't work correctly, try using a different browser. We recommend a Mozilla based browser.)

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# Option 1 -

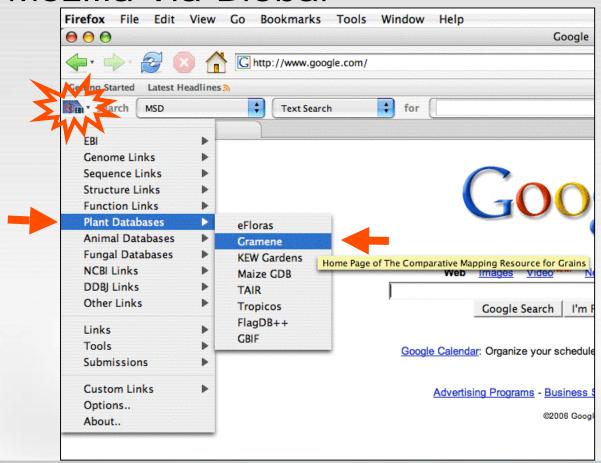
In the address bar type
 "www.gramene.org" and press
 "Enter" to open the Gramene Home
 Page.



### Get Biobar at

http://biobar.mozdev.org/

# Option 2: Access Gramene on Mozilla via Biobar



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Date and Release # of current version of database. (Only on home page)

# Home Page

Quick search –
general search of
multiple modules plus
website pages

GR

NE Home

Genomes Species Download Resources About He

Find anything

Feedback

A Resource Comparative Grass enomics

#### Release # 26

September 2007

#### News

- October 15-17, 2007 5th International Sypposium of Rice Functional Symics in Tsukuba, Japan
- Sept 2007, V 26
  release notes.
- Gramene July/August
  Newsletter

#### Have Questions...?

- NEW Quick Search Help
- Tutorials See what you can do and how to do it.
- Ask questions through-Feedback or Email.
- See FAQ.

Outreach Calendar Presentation Materials

#### Quick Start

■GENOMES: Browse assembled genomes for Oryza Sativa, Oryza rufipogon, Marice/maize synteny; Narrow your search with GrameneMart; Search for sequence by Gene Ontology.

### Gramene Calendar

■PROTEINS: Search by PFam or ProSite or Browse by Gene Ontology using GC

Wheat, Barley, Oats, Sorghum, and other grass maps of different types and species. View map

**News** about the current release and the grass genomic community is listed here

s (RFLPs, Sequence ESTs, etc.), DNA Probes (Primers, Overgos, etc.), Genomic ESTs, etc.). Search by species such as Sorghum, by ecies and the sequence Repeat

Quick Start helps get you directly to where you want to go fast.

ice Genes, Rig

eat gern sms.

BIOCHEMICAL PATHWAYS: Search for ALL the rice pathways on starch piosynthesis or get an metabolic network. Compare rice and Arabidopsis pathway datasets.

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

SPECIES PAGES projection information, picture Hordeum. Avena. Setaria.

Gramene **Help** and **Tips** give advice on using the site. Click "All Tips" for more pointers.

Triticum

### Visit with us at

- Sypt 21-22Agricultural Ontology Service (AOS)
   Workshop
- Jan 12-16, 2008 PAG XVI

### Gramene Tip:

All visualizations in the CMap views (mapsets, maps, features, and correspondences) are enerated from the Markers Module.

• Browse All Tips

Gramene is a curated, opensource, data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of crossspecies homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and physical mapping, interpretation of biochemical

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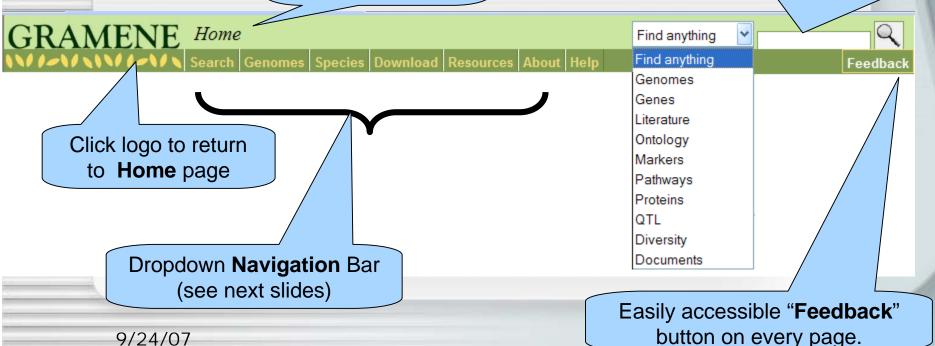
# Page Navigation

www.gramene.org

(If some website features don't work correctly, try using a different browser)

**Title** identifies the page being viewed.

**Quick search**, optionally select a specific database to search, enter a term to search for, and click on "search."



Click "Species" or seed images to link to species pages

### Footer

**Collaborators** and **funding sources** are linked along the bottom





About

Cite

Gramene

Site Map

Last modified: Thu Aug 17 18:56:28 2006

Provides an **overview** of everything on the site

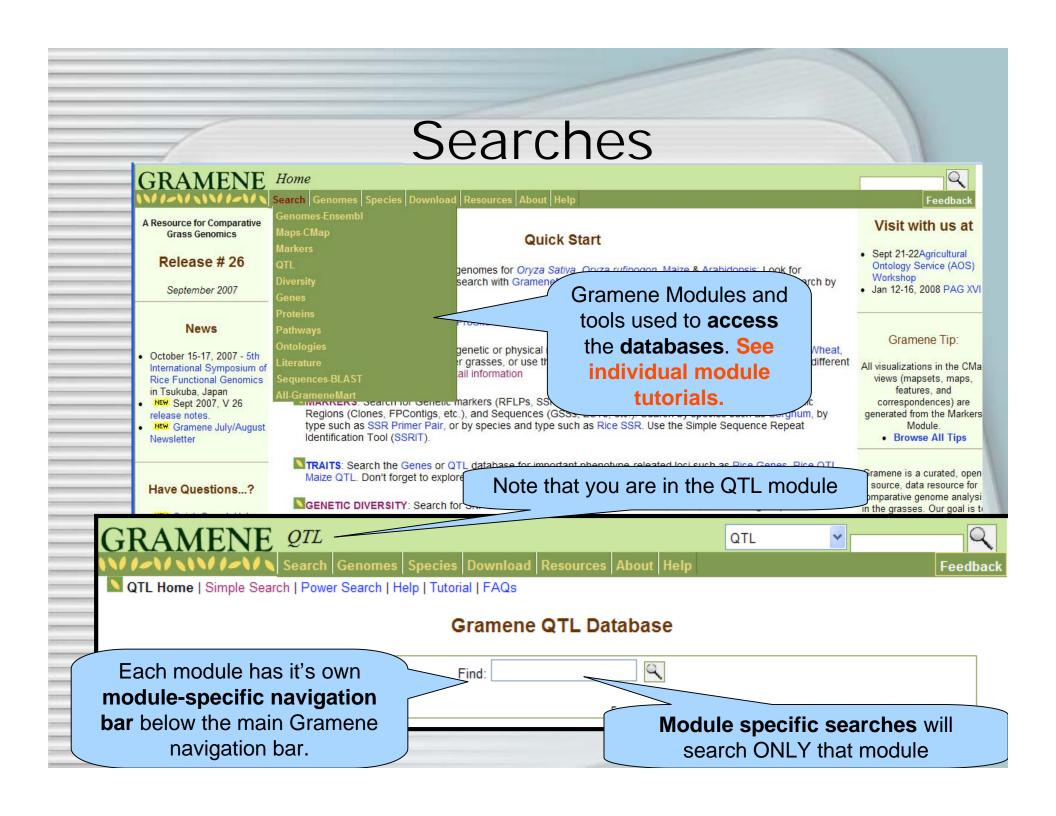
Gramene purpose, history and people

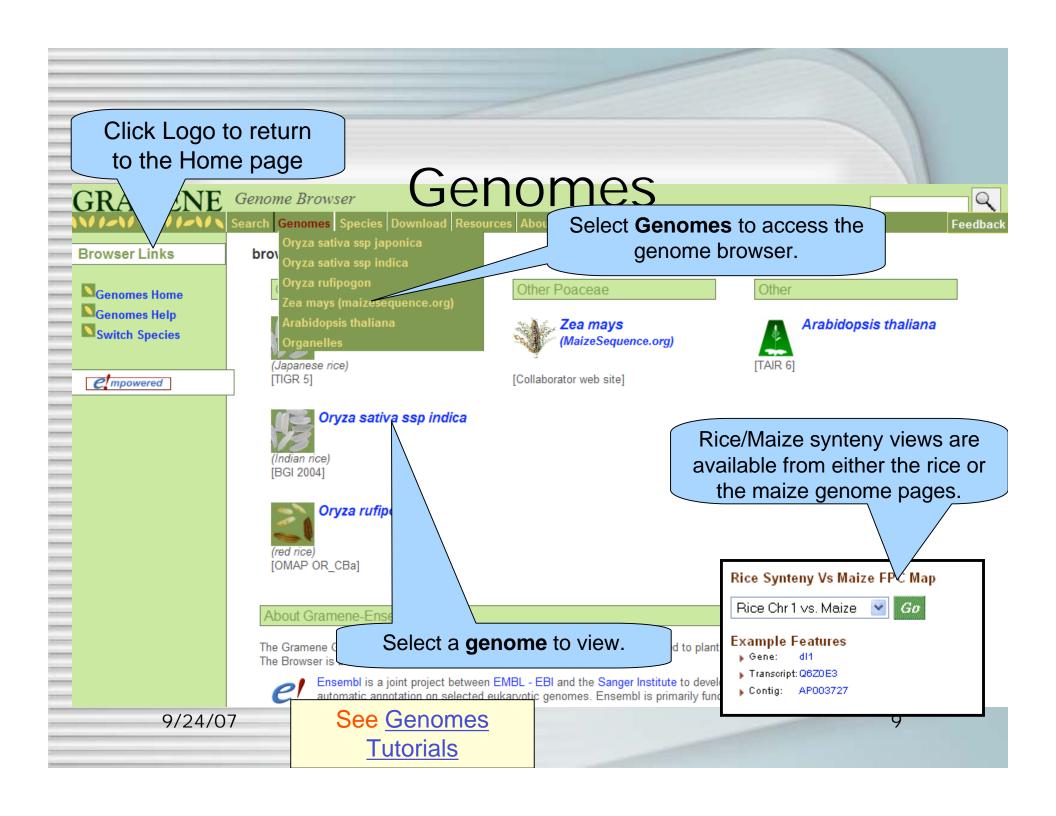
Home

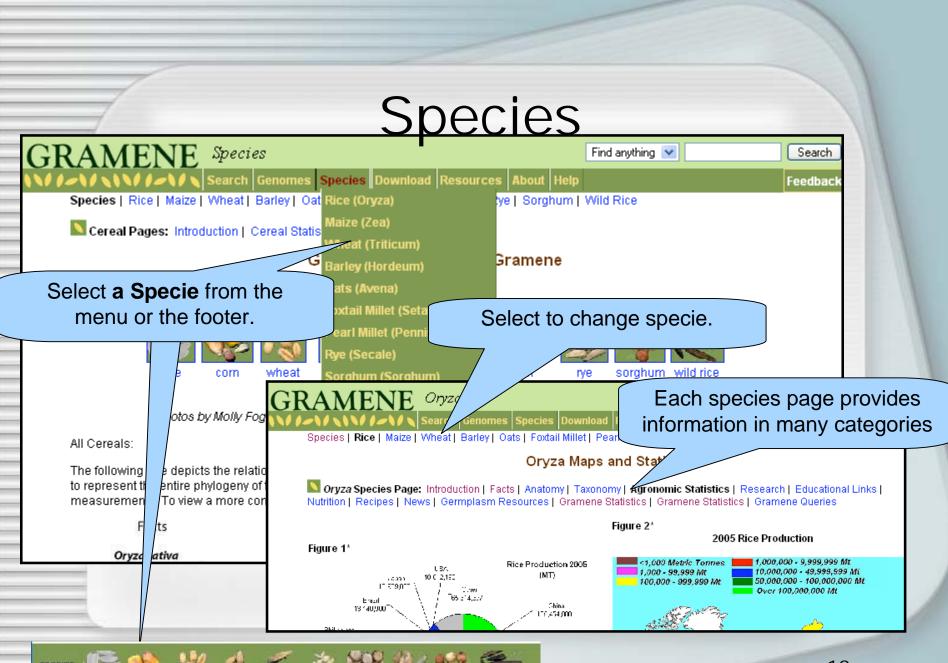
Information about citing Gramene

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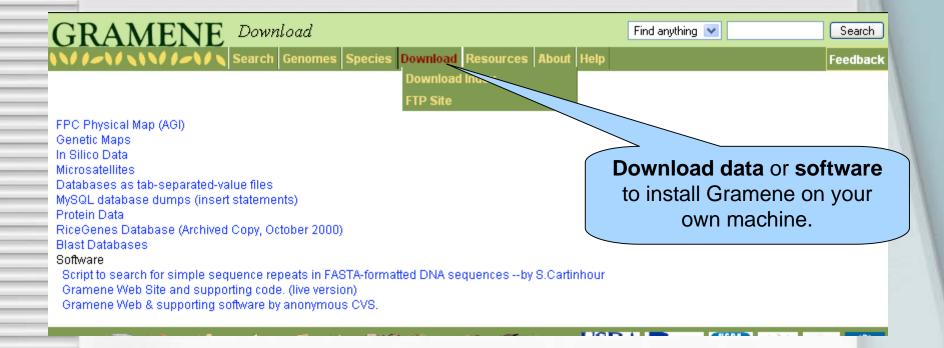
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### Downloads



### Resources

Definitions of terms, abbreviations and acronyms used. Links to other on-line glossaries

Cerear <del>Cenome Sequencing Enous</del>

Cereal Genomic Databases

**Functional Genomics** 

Genomic Research and Education

Tools for Nucleotide and Protein Sequence Analyses

Provides links to other websites of interest

omy orm Submit a Term graphy

Plant Bree Newsletters

Germplasm Res virces Pathology Agriculture
Other (non-cei Ontole

**Submit** a gene or ontology term to the database

### Complete Rice (Oryza sp.) Sequ

- IRGSP sequences
- · TIGR pseudomolecule

### Links page of **genetic newsletters** for cereals

### **Cereal Genome Sequencing Efforts**

#### Rice

• International Rice Genome Sequencing Project (IRGSP) - The International Rice Genome Sequencing Project (IRGSP), a consortium of publicly funded laboratories, was established in 1997 to obtain a high quality, map-based sequence of the rice genome using the cultivar Nipponbare of Oryza sativa ssp. japonica. It is currently comprised of ten members: Japan, the United States of America, China, Taiwan, Korea, India, Thailand, France, Brazil, and the United Kingdom. The IRGSP adopts the clone-by-clone shotgun sequencing strategy so that each sequenced clone can be associated with a specific position on the genetic map and adheres to the policy of immediate release of the sequence data to the public domain. In December 2004, the IRGSP completed the sequencing of the rice genome. The high-quality and map-based sequence of the entire genome is now available in public databases.

IRGSP Members:

9/24/07 Rice Genome Program (RGP). Japan RGP is a joint project of the National Institute of Agrobiological Sciences (NIAS)

### **About**



As an information resource to data sets available within the public sector, which will facilitate researchers' ability to understand the rice genome and leverage the rice genomic sequence for identifying and understanding corresponding genes, pathways and phenotypes in other crop grasses. This is achieved by building automated and curated relationships between rice and other cereals for both sequence and biology. The automated and curated relationships are queried and displayed using controlled vocabularies and web-based displays. The controlled vocabularies (Ontologies), currently being utilized include Gene ontology, Plant ontology, Trait ontology, Environment ontology and Gramene Taxonomy ontology. The web-based displays for phenotypes include the Genes and Quantitative Trait Loci (QTL) modules. Sequence based relationships are displayed in the Genomes module using the genome browser adapted from Ensembl, in the Maps module using the comparative map viewer (CMap) from GMOD, and in the Proteins module displays. BLAST is used to search for similar sequences. Literature supporting all the above data is organized in the Literature database.

The technological core of Gramene is the MySQL database management system. We have developed a rational schema to represent the various biological entities of Gramene, and a middleware layer to dynamically translate this information into Web pages.

### **Funding**

Gramene project is supported by an IFAFS grant from the USDA Cooperative State Research and Education Service (CSREES), PGI grant from the National Science Foundation, and was previously supported by a Cooperative Agreement through the USDA Agricultural Research Service.

#### Name

The name Gramene is a play on the name of the Grameen Bank which specializes in small loans to the poor (mostly women) in emerging

# Help

