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GRAMENE News

Gramene News

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For an example of how a researcher has used the Gramene Database in their research, see Joshua C. Johnson, Rudi Appels, Mrinal Bhave. (2006). The PDI genes of wheat and their syntenic relationship to the esp2 locus of rice. Functional & Integrative Genomics, 6(2), 104-21.

For information on the "Rice: Research to Production" course last May, see: www.ricehapmap.org/courses.aspx

Gramene Receives NSF PGRP Award

Gramene, the only platform for plant research that enables both forward and reverse genetics, has been awarded funding resources through the NSF Plant Genome Research Resource award, Award #0703908 . This abstract is shown here:

The Gramene database (http://www.gramene.org) is an online resource, jointly supported by NSF and the US Department of Agriculture's Agricultural Research Service. It integrates the genomic, genetic and phenotypic information in rice, maize and other cereals, thereby giving scientists and other end-users easy access to this integrated information. This project will provide for the enhancement of Gramene by incorporating biological pathway and genetic diversity information from maize, rice, wheat, sorghum, and other cereals into the resource. Comparative genomics tools will be developed, thereby allowing researchers to use knowledge gained in one plant species to identify and characterize functionally significant genes and other elements in the genomes of other species. Scientists can use the resource to make advances in our fundamental understanding of the plant processes of economic importance such as hybrid vigor, grain development, seed dormancy, drought tolerance, and resistance to diseases. In addition, the tools developed will allow for the estimation of the breeding value of individual genetic variants, thereby providing breeders with the ability to select the ideal combinations of seed stocks to create varieties that have desirable traits such as robustness, the ability to grow in marginal environments, or have high potential as a source for biofuels and other materials of high economic value.

Information resources developed, and being developed, through genomics efforts are key elements to advance our fundamental knowledge base for a future bio-based economy and to address the expected need for feeding an expanding world population. Many of the information resources are still underutilized because of the fragmentation of the datasets and the absence of tools to make meaningful connections among them. To fully unlock the potential of plant genome data, the diverse datasets must be integrated so that information is shared both within and between species. It is one of the goals of Gramene to provide that integration. Another goal of the project is to deliver the integrated dataset into the hands of plant geneticists, molecular biologists, evolutionary biologists and breeders by providing compelling, intuitive, user interfaces. Lastly, the project will reach out to students, the public, and to underrepresented minorities via a series of online tutorials and on-site workshops that involves a novel, and cost-effective, public/private partnership.

All the information resources generated by Gramene will be available to scientists, breeders, and members of the general public free of charge and without intellectual property restrictions.

PI: Lincoln Stein (Cold Spring Harbor Laboratory)
CoPIs: Doreen Ware (Cold Spring Harbor Laboratory), Susan McCouch, Edward Buckler, and Pankaj Jaiswal (Cornell University; subawardee)

Gramene Release 26

Have you visited Gramene's web-accessible database recently? If not, you may be in for a few surprises!

The Gramene website layout was reformatted back in January, and now the majority of the Gramene datasets (modules) have a consistent interface to aid in the integration of all the data sets. Rather than having module sub-menus, the Genes, Markers, QTL, Proteins, Ontologies, Diversity and Publications present a new layout with collapsible and expandable sections (*see Figure 1*). When opening the information page for an item in any of these categories, the general information will be displayed and remain open at the top of the page. Below this general information will be sections for links to other datasets (with the number of links identified for each section) and will vary depending upon the module you are in. Each section can be expanded or collapsed by clicking on the section title. Categories with no correspondences will be greyed out. On these pages, the "Map Positions" offers a "CMap Preview" option. Click on this option to get a preview of the map in CMap, or click on "View Comparative Map" to go to the actual map.

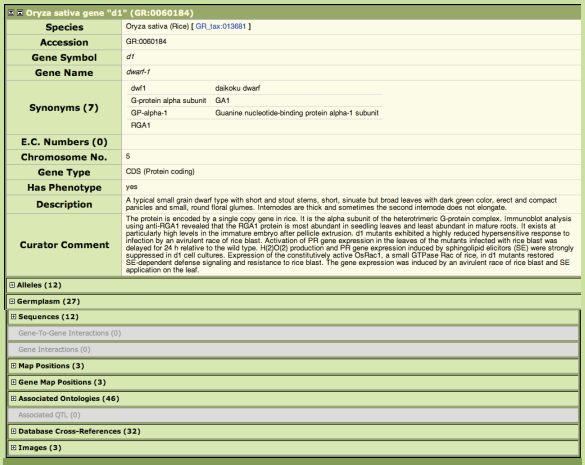


Figure 1

The help documentation has also been put into this consistent interface with expandable/collapsible sections. You may view it at http://www.gramene.org/db/help (*see Figure 2*).

The genome web server was upgraded to Ensembl release 46 , and there is a new genome browser for *Oryza sativa ssp. indica*. New gene tracks include a Gramene evidence-based gene track (37,176 genes); a RAP (The Rice Annotation Project, http://rapdb.dna.affrc.go.jp) gene track (29,132 genes); and the Consensus gene track: (14,842 genes). The OMAP sets have been remapped, and, new Poaceae EST/mRNA/GSS DNA sequences were downloaded from NCBI GenBank to the Gramene Markers database, and then mapped to the*Oryza sativa* TIGR v5 assembly using BLAT. The succesfully mapped sequences can be viewed as DNA aligned features in the contigview.

Figure 2

New markers of note are 2,243 maize eSSRs from the Maize Genome Sequencing Project.

Data in the Maps Module is built out of the mappings in the Markers Module. Updates in the latter module are encorporated here. Of note is the new sequence map for indica, and, as noted in the "Genomes" section above, the OMAP sets have all been updated.

Most of the rice genes with the first character of the gene symbol from "A" to "Z" in our database now have ontology associations to TO, GO and PO. Additionally, 3,385 new genes records were downloaded from GrainGenes.

One recent improvement is that all QTL have been described and annotated by multiple ontologies. In addition to the Trait Ontology (TO) and Plant Ontology (PO) terms used in previous releases, Environment Ontology (EO) terms have been added this build to describe environmental conditions under which a particular QTL has been identified. These terms have been annotated by creating a default mapping based on the expertly identified TO and EO associations.

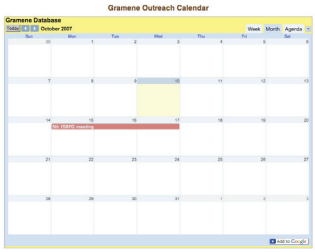
Another recent important improvement in this release is the provision of QTL-associated molecular marker info. We currently provide two types of associated markers for a particular QTL: Co-localized markers are the markers co-localized or overlapping with a QTL region on the original QTL map; and neighboring markers are those not overlapped but closely adjacent to a QTL region. The associated marker info is crucial for QTL fine mapping, map-based positional cloning, and marker-assisted selection (MAS) for plant breeding.

We are pleased to announce the addition of five new species to the Gramene pathway tools (RiceCyc) module. These are *Capsicum anuum, Coffea canephora, Medicago truncatula, Solanum lycopersicum* and *Solanum tuberosum*. RiceCyc now allows you to draw comparisons among the data sets from eight species.

Six pathways were added, two pathways deleted, and five pathways modified during this round of curation.

Upcoming Outreach:

Gramene will offer a database presentation at the **2008 PAG** in January. This workshop is currently planned for Tuesday afternoon, January 15. In addition to the workshop, we will have a poster, and you can visit us, along with several other plant databases, in our booth.



New: Gramene now uses Google Calendars to record Gramene outreach. The calendar can be found on the web at http://www.gramene.org/outreach/calendar.html

Community Calendar

2007

Oct. 9-14. 4th International Rice Blast Conference. Vaya Huatian International Hotel, Changsha, Hunan, China
Oct. 15-17. 5th International Symposium for Rice Functional Genomics. Tsukuba, Japan
Oct 22-24 ACPFG Genomics Symposium - The Genomics of Drought. Adelaide, SA
Oct 24-25 7th Annual RiceTec Hybrid Rice Conference; Little Rock, AR, USA
Nov 4-8. Crop Sciences International Meeting (ASA-CSSA-SSSA). New Orleans, LA, USA
Nov 5-9. 11th International Symposium on Pre-harvest Sprouting in Cereals. Mendoza, Argentina
Dec 2-4. 2007 National Fusarium Head Blight Forum. Kansas City, Missouri USA

2008

January 6-11. 8th Annual Long-Oligonucleotide Microarray Workshops. Tucson, AZ
January 12-16. PAG-XVI. San Dieg April 13-18. 5th International Crop Science Congress, Jeju, Korea o, CA, USA
Feb 18-21. RTWG Meeting. San Diego, CA, USA
April 5-10. 10th International Barley Genetics Symposium (IBGS). Alexandria, Egypt
April 13-18. 5th International Crop Science Congress, Jeju, Korea
August 11-15. Monocots IV, Copenhagen, Denmark.
August 20-23. 4th Int'l Symposium on Rhizoctonia; Berlin, Germany
August 24 –27. Ag. Biotech. Int'l Conf.. Cork, Ireland.
August 24-29. 11th International Wheat Genetics Symposium. Brisbane, Australia

Gramene FAQ

Contact Gramene through the "Feedback" link at the top of any page to ask questions. Here are some recent questions that have been answered.

***Q:* I want to search markers linked to a specific disease. Is this possible?**

A: *Markers are associated with sequences or other mapped features, such as QTL - you cannot associate a marker with a trait. However, QTL are associated with traits, and markers can be associated with QTL. Therefore, I suggest going to the QTL database and searching your trait (by name of disease) and finding a QTL on the chromosome you are researching. Follow the QTL information to its mappings, and using the comparative map viewer (CMAP) you can pull up maps that have correspondences, and look for the markers on your QTL or associated maps.*

Q: Why are the location and sequences in the Gramene database different from the data provided by the McCouch Lab and available at http://www.gramene.org/microsat/50_ssr.html?

A: *The positions of the SSRs in Gramene are based on the current rice pseudomolecules, as assemblies from TIGR. We re-run the pipeline that positions these SSRs on the rice genome (based on e-PCR with the primer pairs) with every build of Gramene. Thus, as the assemblies of the rice pseudomolecules are updated in Gramene, the bp positions of the SSRs change, reflecting their current positions on the latest assembly of the pseudomolecules. In addition, you will find that the positions of the SSRs published in 2005 were based on the 2005 assembly of the rice pseudomolecule by the IRGSP. That assembly differs from the TIGR pseudomolecules, even though the underlying sequence information is the same.*

Opportunities

Please check with each organization to confirm due dates, as they are prone to change.

- The Third International Joint Conferences on Computer, Information, and Systems Sciences, and Engineering (CISSE 2007). Abstracts due: **10/22/07**
- *RTWG Meeting* Title-Summary due: **11/1/07**, Abstracts due: **12/1/07**
- *Monocots IV*. Abstracts for oral contributions and posters due **5/31/08.**
- The Agricultural Biotechnology International Conference (ABIC) is accepting proposals to host ABIC 2011, scheduled to be held in Europe. Proposal deadline: **3/14/08**
- Looking for a job, or have one to post? Visit the Jobs Postings webpage from GrainGenes.

Volume 53 of the Annual Wheat Newsletter has been published and is now available on-line at: http://wheat.pw.usda.gov/ggpages/awn/53/

GRAMENE

A GENOMIC RESOURCE FOR CEREALS

BLAST
Genome Browser
CMap
Genetic Diversity
Genes & Alleles
Maps and CMap
QTL
Ontologies
Pathways
Literature
Proteins
Markers
GrameneMart

Gramene is a curated, open-source, web-accessible free 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.

email gramene@gramene.org

For updates on releases and other information, join Gramene's mailing list or view the mailing list archive.

www.gramene.org

RTWG Conference Highlights

Conference Website
http://www.plantsciences.ucdavis.edu/rtwg/index.htm

Titles and Summaries Due
Nov. 1, 2007

Abstracts Due
December 1, 2007

Award Nominations Due
December 1, 2007

Presentation Submission to Panel Chairs Due
February 1, 2008

Conference Registration (Last Day for early, on-line registration)
January 15, 2008

Dates
Feb. 18 - 21, 2008

Location
San Diego, CA, USA

For world-wide rice news, check out IRRI's news page at http://ricenews.irri.org/

Recommended Reading

The PDI genes of wheat and their syntenic relationship to the esp2 locus of rice. Joshua C. Johnson, Rudi Appels, Mrinal Bhave. *Functional & Integrative Genomics* 2006 6(2), 104-21. PMID: 16187074

Annual Wheat Newsletter: Contents: Sahram Mohammady-D. Physiological characters associated with water-stress tolerance under pre anthesis water-stress conditions in wheat; N.F. Veesar et al., Influence of water stress imposed at different stages on growth and yield attributes in bread wheat genotypes (Triticum aestivum L.); Nobuyuki Mizuno et al., Production of reactive oxygen species under low temperature condition in seedling leaves of common wheat.

Genome Halving with an Outgroup. Chunfang Zheng, Qian Zhu and David Sankoff. Evolutionary Bioinformatics. 2006 (2): 319–326

The molecular analysis of the shade avoidance syndrome in the grasses has begun. Kebrom TH, Brutnell TP. J Exp Bot. 2007 Oct 5; [Epub ahead of print] PMID: 17921475

Patterns of selection and tissue-specific expression among maize domestication and crop improvement loci. Hufford KM, Canaran P, Ware DH, McMullen MD, Gaut BS. Plant Physiol. 2007 Jul;144(3):1642-53. PMID: 17496114

Genome-wide patterns of nucleotide polymorphism in domesticated rice. Caicedo AL, Williamson SH, Hernandez RD, Boyko A, Fledel-Alon A, York TL, Polato NR, Olsen KM, Nielsen R, McCouch SR, Bustamante CD, Purugganan MD. PLoS Genet. 2007 Sep 7;3(9):1745-56. PMID: 17907810

Gramene Staff

Lincoln Stein, PI
Susan McCouch, Co-PI
Doreen Ware, Co-PI
Pankaj Jaiswal, Co-PI, Curator
Ed Buckler, Co-PI
Chengzhi Liang, Coordinator
Junjian Ni, Curator
Immanuel Yap, Curator
Dean Ravenscroft, Curator
Chih-Wei Tung, Curator
Ken Youens-Clark, Developer
Shulamit Avraham, Developer
Liya Ren, Developer
William Spooner, Developer
Payan Canaran, Developer
Sharon Wei, Developer
Terry Casstevens, Developer
Jim Thomason, Developer
Claire Hebbard, Outreach

To submit items for this newsletter, contact the editor at: cer17@cornell.edu