

The Gramene Genetic Diversity Module: a resource for genotype-phenotype association analysis in grass species

With the deluge of data coming from high-throughput sequencing and array-based genotyping platforms, there is increasing interest in associating molecular genetic variation with physiological and phenotypic variation. Not only does the high volume of information generated for diverse species strengthen our understandings of the genetic mechanisms that underlay natural variation, it also poses significant challenges in terms of data post-processing, data storage and visualization, and the computationally intensive area of data analysis.

Gramene (<http://www.gramene.org>, Figure 1) is a comprehensive resource of comparative and functional genomics for a number of plant species, with a focus on grasses. The database hosts annotated genomes of 15 plant species, including *Oryza* species, *Zea mays*, *Sorghum bicolor*, *Brachypodium distachyon*, *Arabidopsis thaliana* and *lyrata*, *Vitis vinifera*, and *Populus trichocarpa*

Evolutionary context and inference of orthologs and paralogs are browsable in phylogenetic trees built from multiple alignments of protein sequences in fifteen species, including five non-plant models. Whole genome alignments and synteny maps promote interspecies comparisons over conserved regions. Seamless integration of these data with searching and visualization tools (CMap, <http://www.gramene.org/cmap/>, Youens-Clark *et al.*, 2009) allows a powerful discovery platform using both forward and reverse genetics approaches.

Gramene's Genetic Diversity module (<http://www.gramene.org/diversity>) is specifically designed to handle associations from genotypic and phenotypic data and to facilitate data integration and analyses. It uses the Genomic Diversity and Phenotype Data Model (GDPDM; <http://maizegenetics.net/gdpdm>; GNU LGPL) to store RFLP, SSR and SNP allele data, information about QTL, passport data for wild and cultivated germplasms from rice, maize, wheat, and *Arabidopsis*, and quantitative phenotypic data for some of these accessions. With live database connectivity, large datasets of SNP variation can be

queried by defining a genomic position of interest on a sequenced genome, with the Gramene SNP Query tool (http://www.gramene.org/diversity/snp_query, GNU GPL); and, trait associations, patterns of linkage disequilibrium and diversity can be evaluated using a Java Web Start enabled version of TASSEL (<http://www.gramene.org/diversity/tools.html>; GNU GPL, Bradbury *et al.*, 2007).

Of increasing importance for the Diversity module is the effort to leverage data generated in rice, maize, and *Arabidopsis* to allow users to integrate information from these model genomes to better understand the functional significance and evolutionary history of genes controlling plant morphology, development and response to the environment. Gramene scientists are developing tools and statistical techniques that allow users to build hypotheses about phenotype-genotype relationships in the plant kingdom based on the advantages and compensating for the disadvantages of each experimental system. The Gramene database is updated twice a year, with the most recent release (Build #31) completed in May 2010

References

- Bradbury, P. J., Z. Zhang, D. E. Kroon, T. M. Casstevens, Y. Ramdoss, and E. S. Buclker. 2007. TASSEL, software for association mapping of complex traits in diverse samples. *Bioinformatics* 23: 2633-2635.
- Youens-Clark, K., B. Faga, I. V. Yap, L. Stein and D. Ware. 2009. CMap 1.01. *Bioinformatics* 25: 3040-2042.

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Release #31
 May 2010
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- Plant Genome Resources Booth at Plant Biology 2010
 Gramene is please to contribute to the Plant Genome Resources exhibition booth at the upcoming Plant...
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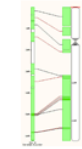
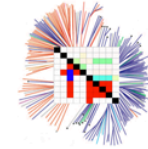
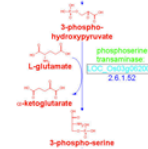
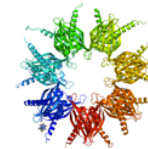

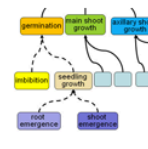

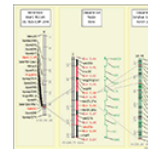
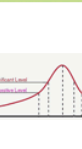
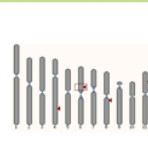

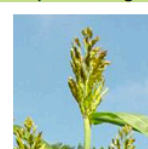
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Gramene is a curated, open-source, data resource for comparative genome analysis in

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Figure 1. Home page of www.gramene.org- a database of comparative plant genomics resources