

GRAMENE: A Resource For Comparative Genomics in Plants

Charles Chen^{1*}, Vindhya Amarasinghe⁴, Edward Buckler^{1,2,3}, Terry Casstevens², Genevieve DeClerck¹, Palitha Dharmawardhana⁴, Pankaj Jaiwal⁴, AS Karthikeyan¹, Marcela Monaco⁵, Susan McCouch¹, Will Spooner⁵, Joshua Stein⁵, Jim Thomason², Sharon Wei⁵, Ken Youens-Clark², Jon Zhang¹ and Doreen Ware⁵

¹ Department of Plant Breeding and Genetics, Cornell University, Ithaca, New York 14853, USA

² Institute For Genomic Diversity, Cornell University, Ithaca, New York 14853, USA

³ Robert W. Holley Center for Agriculture and Health, United States Department of Agriculture - Agriculture Research Service, Ithaca, New York 14853, USA

⁴ Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331, USA

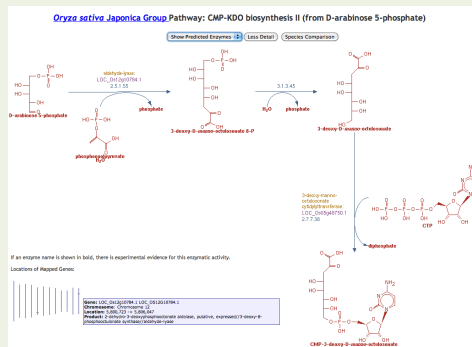
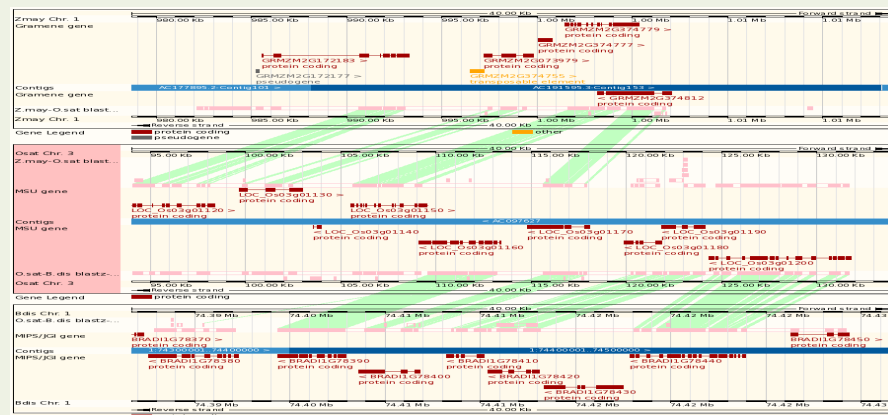
⁵ Cold Spring Harbor Laboratory, Cold Spring Harbor, New York 11724, USA

*Email: cc859@cornell.edu

Gramene (www.gramene.org) is a curated data resource that integrates genomic knowledge in sequences, genes, proteins and pathways and genetic diversity data and germplasm information. Equipped with phylogeny-based ortholog assignments and topological dating of gene duplication nodes, we provide functional annotation based on homologous relationship of genes that also allow us to develop species-specific bio-pathway databases like RiceCyc.

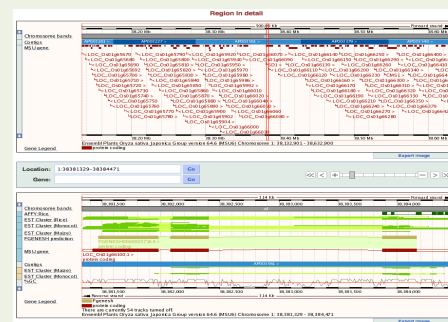
Gramene Genetic Diversity is specially designed to facilitate genome-wide association research that seeks the links between phenotypic and genetic variation within broad panel of germplasms. To encourage further use of our high-resolution diversity data, Gramene Genetic Diversity also provides web-launch statistical package, TASSEL, and other visualization and data mining tools.

Whole Genome Alignment: rice genome displayed in a multi-specie viewer



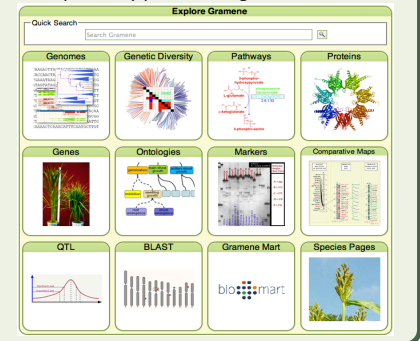
Metabolic Pathways: Gramene Pathway module annotates bio-pathway information for 11 plant genomes, including rice, maize, sorghum and Arabidopsis

Genome Browser for 15 species: Rice, both domesticated and wild ones, maize, sorghum, Brachypodium and Arabidopsis thaliana and A. lyrata..

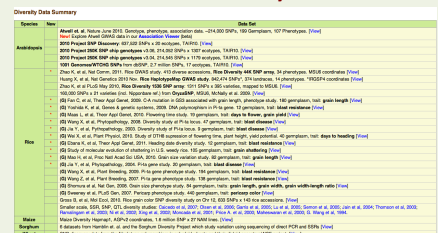


GRAMENE Home Page:

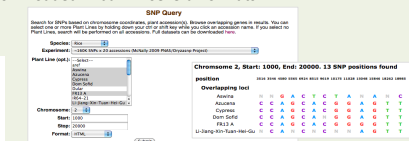
Multiple entry points into genomic data



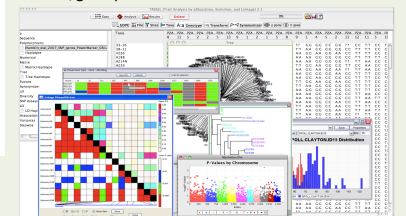
GRAMENE Genetic Diversity



Diversity data and data download Gramene Diversity specializes in large-scale SNP/indel based association studies with billions of allele calls. All diversity data can be downloaded in bulk in several formats



SNP Query returns subsets of allele calls for full or sub-sets of germplasm based on genome coordinates or QTL/gene positions



TASSEL 4.0 is a JAVA software package for evaluating trait associations, evolutionary patterns and linkage disequilibrium analyses



Flapjack is a stand-alone JAVA tool for genotype and phenotype visualization

Comparative Map (CMap): rice maps are jointed with over 200 genetic, QTL, physical and sequence maps from 32 species

