Gramene: A Resource For Comparative Genomics in Plants

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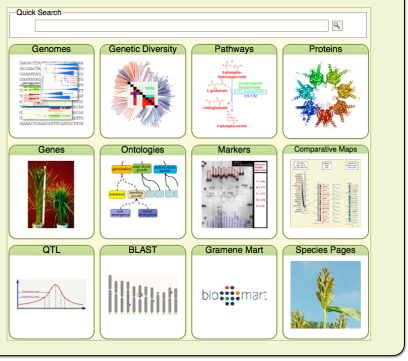
Gramene is used by plant biologists to conduct basic and applied research in genomics. Its power comes from the integration of functional, genetic & comparative information.

Gramene Provides Multiple Entry Points into Genomic Data

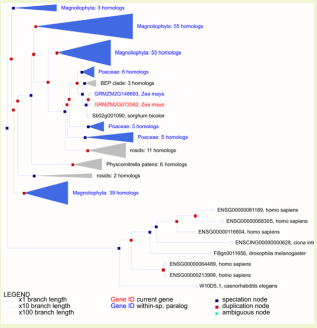


Genome Browsers for 15 Species

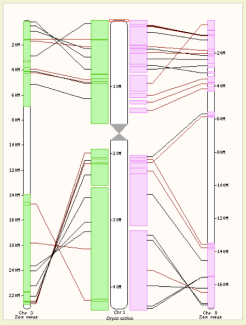
Maize, sorghum, domesticated and wild rice, *Brachypodium* and *Physcomitrella*. Eudicots *Arabidopsis thaliana*, *A. lyrata*, soybean, poplar, and grape. Algae, moss and spikemoss.

Phylogenomics

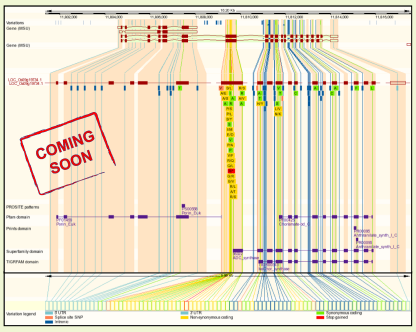
Ensembl Compara GeneTrees



Automated ortholog and paralog calls made by reconciliation of gene trees with species tree. Orthologs used to detect synteny between genomes.

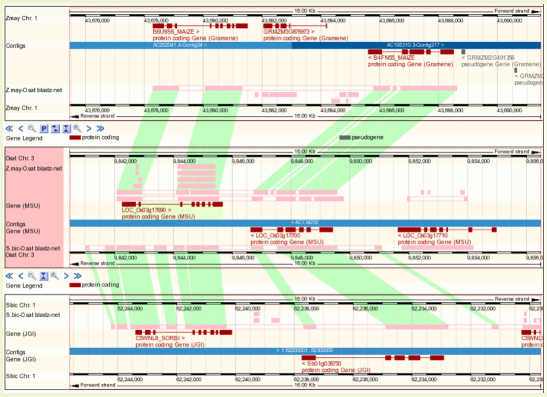


SNP Diversity Displayed in the Context of Functional Domains



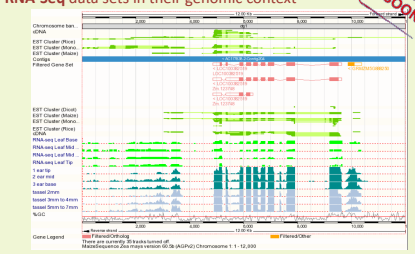
Species	Status	Data Set
Arabidopsis	New	Atwell et. al, Nature June 2010. Genotype, phenotype, association data. ~214,000 SNPs, 199 Germplasm, 107 Phenotypes. [View]
	Unchanged	2010 Project SNP Discovery: 637,522 SNPs x 20 ecotypes, TAIR9. [View]
		2010 Project 250K SNP chip genotypes v3.04, 214,000 SNPs x 1179 ecotypes, TAIR9. [View]
		1001 Genomes/WTCHG SNPs from dbSNP, 2.7 million SNPs, 17 ecotypes, TAIR9. [View]
Rice	New	Zhao et. al PLoS May 2010, "1536 Assay": 1311 SNPs x 395 varieties, mapped to MSU6. [View]
		Gross B, et. al, Mol Ecol. Aug 2010 Rice grain color SNP diversity study, 633 SNPs x 143 rice accessions. [View]
		Sweeney et al, 2007, Pericarp color phenotype study (Rc gene) with 440 germplasm accessions. [View]
	Unchanged	160,000 SNPs x 21 varieties (incl. Nipponbare ref.) from OryzaSNP, MSU6, McNally et al. 2009. [View]
		Smaller scale, SSR, SNP, QTL diversity studies: Caicedo et al. 2007; Olsen et al. 2006; Garris et al. 2005; Lu et al. 2005; Semon et al. 2005; Jain et al. 2004; Thomson et al. 2003; Ramalingam et al. 2003; Ni et al. 2002; Xing et al. 2002; Moncada et al. 2001; Price A. et al. 2000; Maheswaran et al. 2000; G. Wang et al. 1994.
Maize	New	Maize Diversity Hapmap1, AGPv2 coordinates, 1.6 million SNP x 27 NAM lines. [View]
Sorghum	Unchanged	8 datasets from Hamblin et. al. and the Sorghum Diversity Project which study variation using sequencing of direct PCR and SSRs [View]
Wheat	Unchanged	SNP discovery data from the 'Haplotype polymorphism in polyploid wheats and their diploid ancestors' NSF project. [View]

Whole Genome Alignments Displayed in Multi-species View



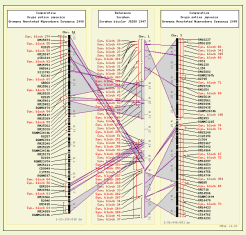
More Upcoming Maize Features

RNA-Seq data sets in their genomic context

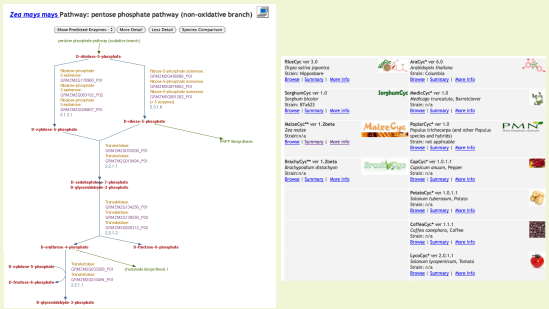


Credits: Image by courtesy of maizesequence.org; RNA-Seq data from Tom Brutnell (Cornell University) and Andrea Eveland (CSHL).

Comparative Map Viewer (CMap): Maize maps will join over 200 genetic, QTL, physical, & sequence maps from 32 species.



Metabolic Pathways Annotated for 10 Plant Genomes



Selected Publications

Youens-Clark K, et al. (2010) Gramene database in 2010: updates and extensions. *Nucleic Acids Research*, 39 (suppl 1): D1085-D1094.
Jaiswal P, et al. (2006) Gramene: a bird's eye view of cereal genomes. *Nucleic Acids Research*.
Yamazaki Y, et al. (2005) *Plant Cell Physiol* 46: 63-68.
Ware D, et al. (2002) Gramene: a resource for comparative grass genomics. *Nucleic Research*, 30, 103-105.
Ware DH, et al. (2002) Gramene, a tool for grass genomics. *Plant Physiol* 130: 1606-1613.
Jaiswal P, et al. (2002) Gramene: development and integration of trait and gene ontologies for rice. *Comparative and Functional Genomics* 3: 132-136.

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