

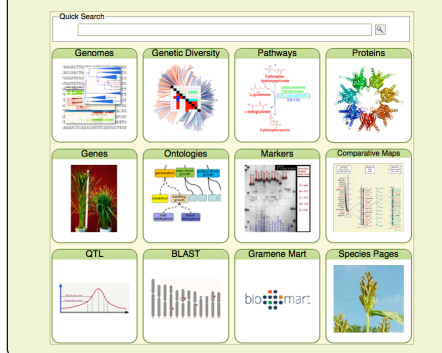
Gramene: A Resource For Comparative Genomics in Plants

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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



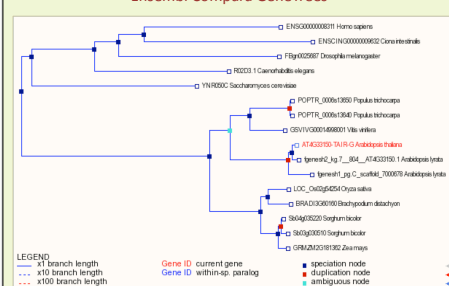
Genome Browsers for 15 Species

Grasses, domesticated and wild rice, maize, sorghum, *Brachypodium* and *Physcomitrella*. Eudicots *Arabidopsis thaliana*, *A. lyrata*, poplar, and grape.

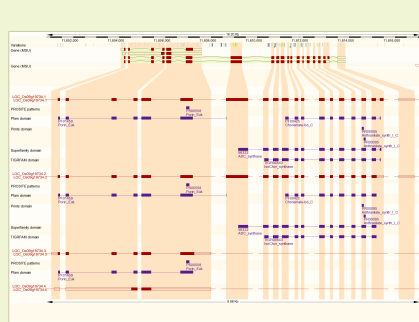


Phylogenomics

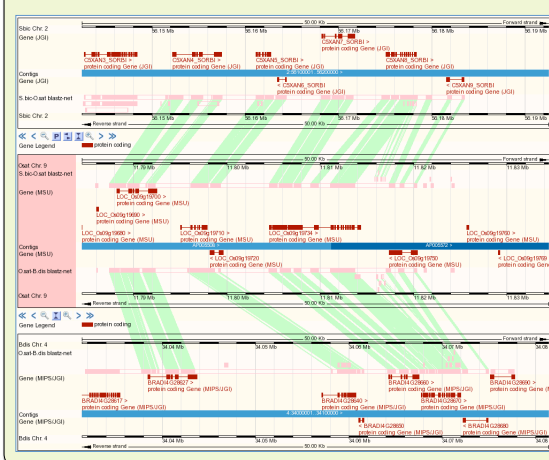
Ensembl Compara GeneTrees



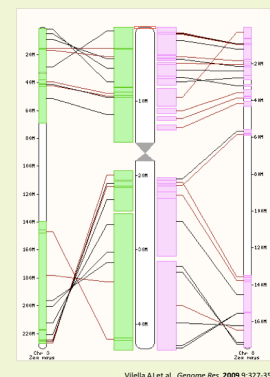
SNP Diversity Displayed in the Context of Functional Domains



Whole Genome Alignments Displayed in Multi-species View

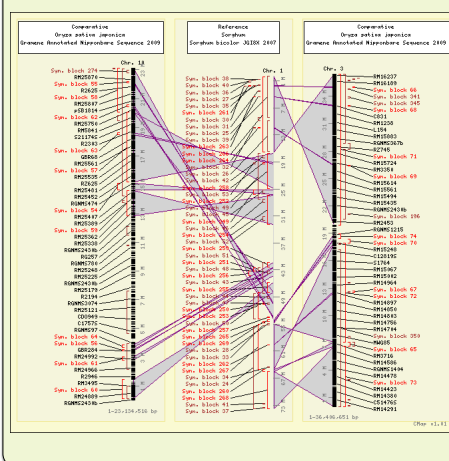


Automated ortholog and paralog calls made by reconciliation of gene trees with species tree. Orthologs used to detect synteny between genomes.

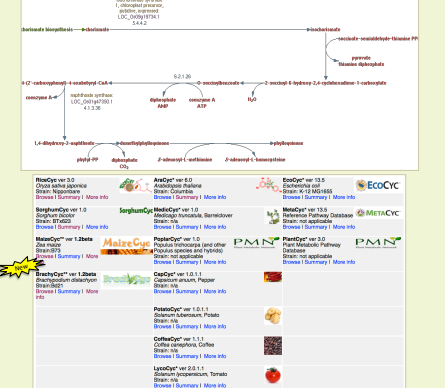


Comparative Map Viewer (CMap)

View correspondences between over 200 genetic, QTL, physical, & sequence maps from 30 species



Metabolic Pathways Annotated for 10 Plant Genomes



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*, 34 (suppl 2): D63-D68.
Ware D, et al. (2002) Gramene: a resource for comparative grass genomics. *Nucleic Acids 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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