Genomes & Diversity

Gramene currently hosts 67 complete reference genomes. In collaboration with Ensembl Genomes, for each reference genome, we incorporate community annotation from primary sources and enrich this information with a series of standardized functional analyses (e.g., InterProScan, GO and PO assignments). Evolutionary histories are provided by Compara phylogenetic gene trees and complemented by analyses of whole genome alignments. Gramene has also positioned itself as a resource for genome variation data in food crops including three *Arabidopsis* species, rice, maize, sorghum, wheat, and barley.

Pathways & Networks

The Plant Reactome (http://plantreactome.gramene.org) is a new platform for the comparative analysis of plant metabolic and regulatory networks, produced in collaboration with the Human Reactome Project. The October release of Plant Reactome includes 305 metabolic and signaling pathways for 97 plant species including maize, rice, three Arabidopsis species, grape, tomato, Brassicas, and other crucifers.

Gramene also produces and hosts or mirrors metabolic pathways databases and visualization tools in the BioCyc collection. These are now hosted at CyVerse (http://pathway.iplantcollaborative.org).

Outreach

Meet us at key scientific meetings including Plant Biology, PAG, and Maize Genetics. We also participate in several Research Coordination Networks to understand community needs, and to establish and promote common data exchange formats.

Web Services

- Gramene Mart for custom data dumps
- Public MySQL & DAS servers
- RESTful APIs

Cite Us

Tello-Ruiz *et al* (2018). Gramene 2018: unifying comparative genomics and pathway resources for plant research. NAR 46 (D1): D1181

Contact us

feedback@gramene.org

Like our Facebook page!

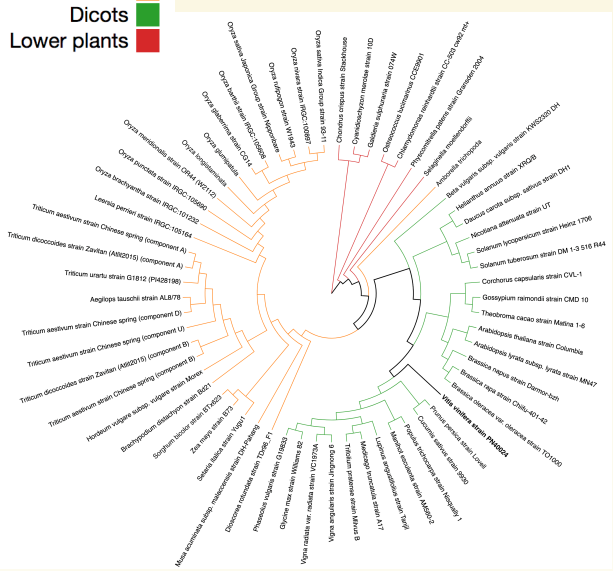
Twitter @GrameneDatabase

Funding

Current work is being supported by the NSF Plant Genome Research Resource grant award #1127112 and the USDA-ARS #1907-21000-030-00D.

Gramene

Monocots
Dicots
Lower plants

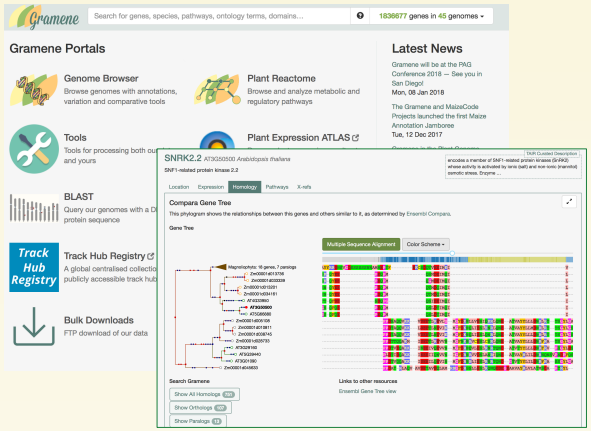


New: Coffee, hot pepper, artichoke, liverwort, tef & durum wheat. **Updated:** Chocolate tree.

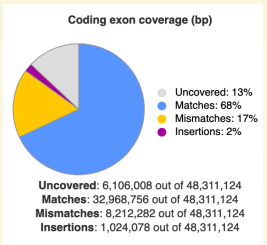
Comparative Genomics Across the Plant Kingdom

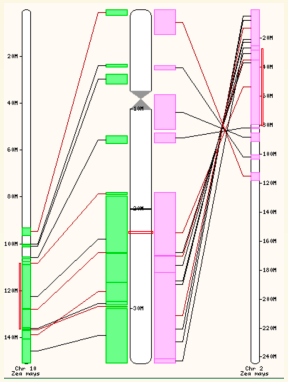
http://www.gramene.org

Gramene continues to grow! Now at 67 reference genomes and pathways for 97 species, including crops, model organisms and lower plants (build 62). Together these serve as a reference resource for comparative analyses, for the broad scientific community, in support of basic and translational research which impact societal interests in food security, energy production, and mitigating the effect of climate change.

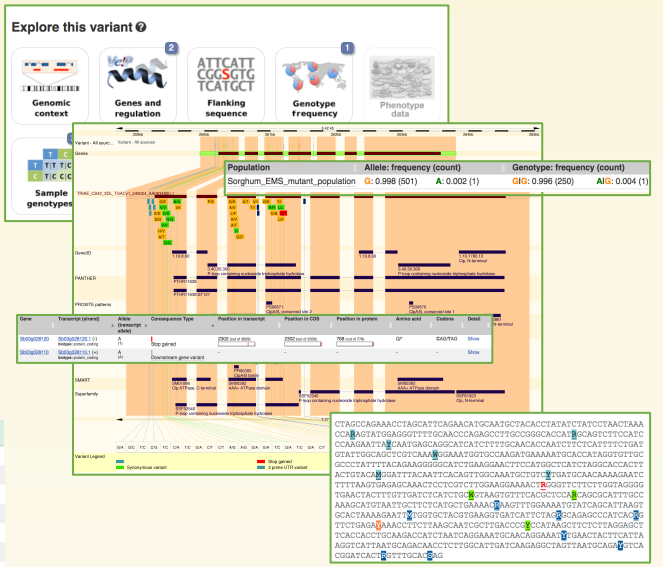


Robust search capabilities include new expression & pathways panels, pruning of gene trees to show selected species, highlighted protein domain structure, and zooming to nucleotide level.





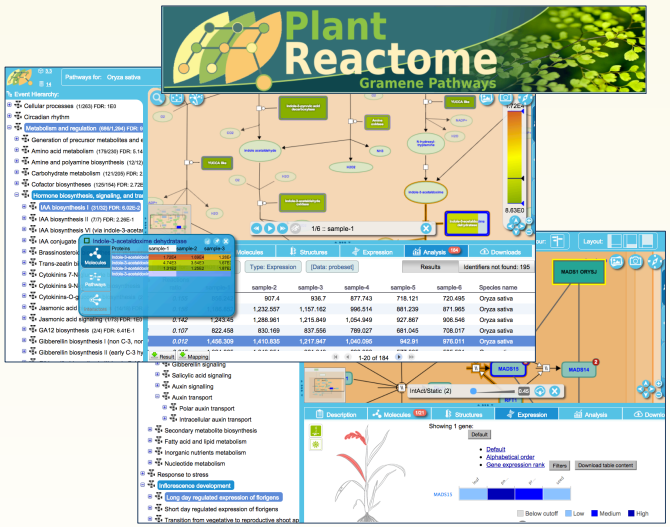
Cereals Comparative Genomics. Browse whole-genome alignments between *O. sativa* Japonica & 66 species (left): exon coverage for rice & grape, and 18 synteny maps (below).



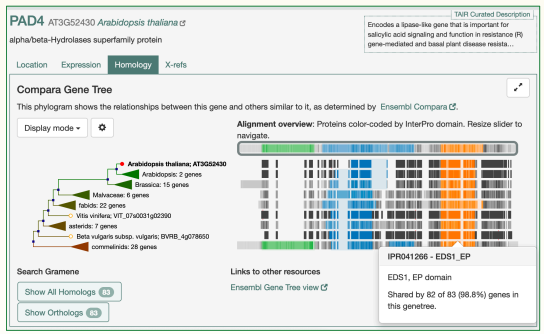
View, mine, and download SNP and structural diversity and their consequence on gene/transcript function. Featured above is EMS-induced variation in sorghum.

Oryza sativa genes	Location		*Zea mays* homologues	Location	
SPH (Os04g0447100)	4:22304995-22309225	→	tassel seed1 (Zm00001d003533)	2:47105187-47109372	Region Comparison
		→	lipoxygenase7 (Zm00001d025524)	10:121268606-121272616	Region Comparison

Gene-level co-synteny defines *homeologs* between monocot reference genomes rice chr4 and maize.



Plant Reactome hosts curated rice pathways and homology-based projections to 97 species, including three species of *Arabidopsis*, grape, orange, strawberry, banana, tomato, potato, pepper, and coffee. Gene expression views from ATLAS available in both genome and pathway browsers.



Phylogenetic tree view for *Arabidopsis thaliana* PAD4, an alpha/beta-hydrolase using Gramene's integrated search. Pruning by species is enabled. Protein domains are color-coded, showing conservation throughout the eukaryotic lineage.

Wheat polyploid views and whole-genome alignments in the context of gene annotations across multiple species.