

## Genomes & Diversity

Gramene currently hosts 53 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 analyses. These include functional annotation by InterProScan and classification using controlled vocabularies (e.g., GO and PO). Evolutionary histories are provided by Compara phylogenetic gene trees and complemented by analyses of whole genome alignments. In recent years, Gramene has also positioned itself as a resource for genome variation data in food crops including Asian and African rice, maize, sorghum, wheat, barley, grape and tomato.

## 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 February release of Plant Reactome includes 264 metabolic, regulatory, developmental and signaling pathways for 75 plant species including rice, Arabidopsis, maize, Brassicas, and other crucifers.

Gramene also produces and hosts or mirrors metabolic pathway 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 PAG, the Maize Genetics Conference, and ASPB's Plant Biology. 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 API

## 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](mailto:feedback@gramene.org)

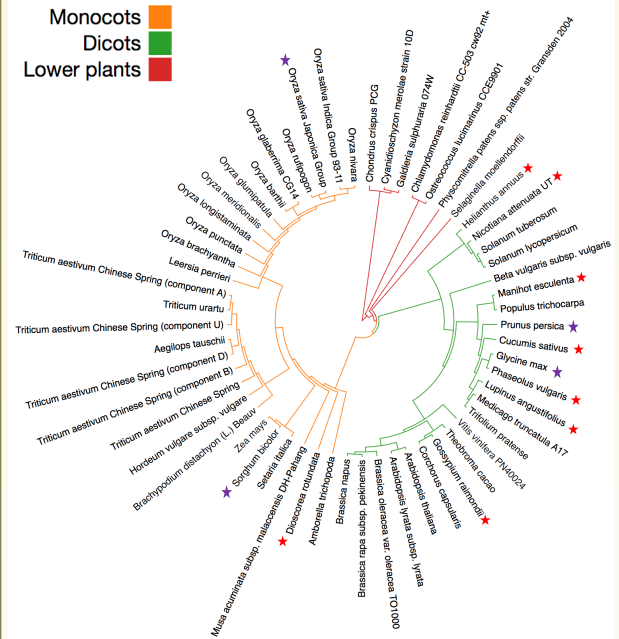
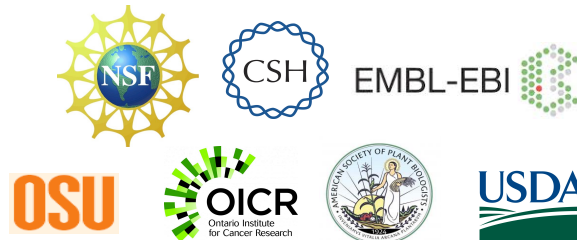
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## Funding

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



★ New

★ Updated

## Comparative Genomics Across the Plant Kingdom

<http://www.gramene.org>

Gramene continues to grow! Now at 53 reference genomes and pathways for 75 species, including crops, model organisms and lower plants (build 56). 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.

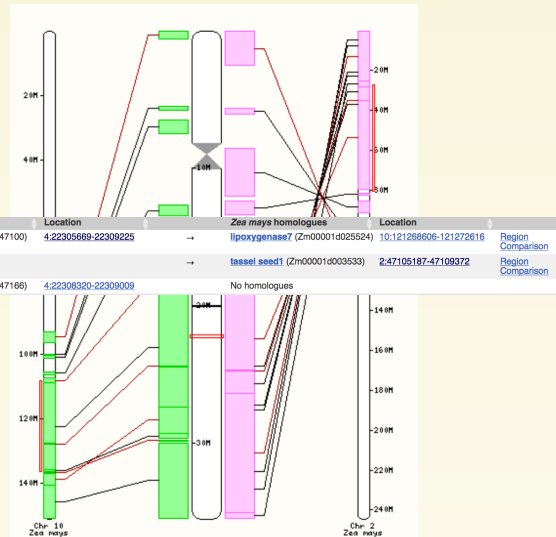
**Gramene** Search for genes, species, pathways, ontology terms, domains... 2075935 genes in 53 genomes

**Gramene Portals**

- Genome Browser**: Browse genomes with annotations, variation and comparative tools
- Plant Reactome**: Browse and analyze metabolic and regulatory pathways
- Tools**: Tools for processing both our data and yours
- BLAST**: Query our genomes with a DNA or protein sequence
- Gramene Mart**: An advanced query interface powered by BioMart
- Track Hub Registry**
- Multiple Sequence Alignment**: Amino acid MSA, Drag slider to reposition.

**Latest News**

- Gramene Workshop at the 2018 Maize Genetics Meeting in Saint-Malo, France Tue, 08 Mar 2018
- Gramene webinar Feb 27, 2018: Plant Reactome pathway updates and new features Mon, 15 Feb 2018
- Gramene release # 56b: updates to Plant Reactome Thu, 01 Feb 2018
- The Gramene Database build 56 is out with 8 new plant genomes!
- Gramene will be at the PAK Conference 2018 -- See you in San Diego!



**Plant Reactome**  
Gramene Pathways

Pathways for: *Oryza sativa*

- Cellular processes** (c145) PDR: 160
- Catabolic** (c139)
- Metabolism and regulation** (c148) PDR: 160
- Generation of precursor metabolites and energy** (c127)
- Amino acid metabolism** (c137) PDR: 160
- Amino and polyamine biosynthesis** (c137)
- Carbohydrate metabolism** (c103) PDR: 160
- Lipid metabolism** (c142) PDR: 160
- Nucleotide biosynthesis, signaling, and flow** (c141) PDR: 160
- RNA biosynthesis I** (c140) PDR: 160
- RNA biosynthesis II** (c139) PDR: 160
- AA biosynthesis I** (c138) PDR: 160
- AA biosynthesis II** (c137) PDR: 160
- Transcription** (c136) PDR: 160
- Cytosines** (c135) PDR: 160
- Cytosines I** (c134) PDR: 160
- Cytosines II** (c133) PDR: 160
- Secondary metabolite biosynthesis** (c132) PDR: 160
- Fatty acid and lipid metabolism** (c131) PDR: 160
- Energetic metabolism** (c130) PDR: 160
- Nucleotide metabolism** (c129) PDR: 160
- Response to stress** (c128) PDR: 160
- Phenylpropane metabolism** (c127) PDR: 160
- Long ray regulated expression of Bolognes** (c126) PDR: 160
- Transition from vegetative to reproductive stages** (c125) PDR: 160

New homepage & improved search capabilities including new expression & pathways panels, pruning of gene trees to show selected species, highlighted protein domain structure, and zooming to nucleotide level

### Duplicate maize regions show co-synteny with rice

Plant Reactome hosts curated rice pathways and homology-based projections to 75 species, including maize, black bean, wheat, sorghum, barley, chickpea, soybean, tomato, potato, banana, grape, orange, pepper, and coffee. Gene expression views from ATLAS available in both, the genome and pathway browsers

**Zea mays (AGPv4)**

Location: 6:85,061,295-85,065,162

Gene: **yellow endosperm1** *Zm00001d036345*

**Gene-based displays**

- Summary
- SNP variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Gene families
- Plant Compara
- Genomic alignments
- Gene tree
- Gene genealog tree
- Orthologues
- Paralogues
- Plan-taxonomic Compara
- Gene Tree
- Orthologues
- Ontologies
- Phenotypes
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID history
- Gene history

**Gene expression**

Showing 3 experiments:

1lib experiment type:   **Filters** Download

Experiment: **Wang** Experimental condition: **tassel** Expression level: **41 TPM**

High Medium Low Below cutoff No data available

**Explore this variant**

- Genomic context
- Genes and regulation
- Flanking sequence
- Genotype frequency
- Phenotype data

Variant: **EMS**

Allele: frequency (count) Genotype: frequency (count)

Population: Sorghum\_EMS\_mutant\_population G: 0.998 (501) A: 0.002 (1) GIG: 0.996 (250) AIG: 0.004 (1)

Sample genotype: **TTCATCT**

Flanking sequence: **ATTTCATT CCGGCGTG TCGATCT**

Variant: **G**

Consequence: **missense variant**

Gene: **SRD6**

Transcript strand: **+**

Allelic variation: **+**

Consequence Type: **missense variant**

Position in transcript: **200 bp upstream**

Position in cds: **200 bp upstream**

Annotation: **5' UTR** **ORF** **3' UTR**

Gene ID: **SRD6**

Gene Symbol: **SRD6**

Gene Name: **SRD6**

Gene Description: **Dominant gene variant**

Gene Synonyms: **SRD6**

Gene Ontology: **SRD6**

Gene Family: **SRD6**

Gene Tree: **SRD6**

Gene Genealogy: **SRD6**

Gene Orthology: **SRD6**

Gene Paralogy: **SRD6**

Gene Variation: **SRD6**

Gene Image: **SRD6**

Gene Structural Variants: **SRD6**

Gene Expression: **SRD6**

Gene Regulation: **SRD6**

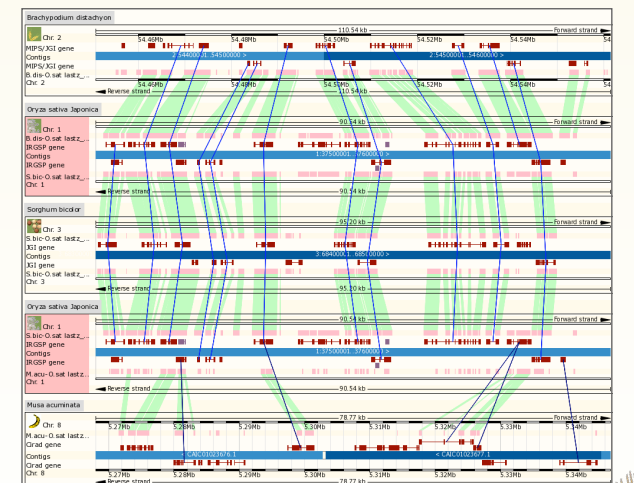
Gene External References: **SRD6**

Gene Supporting Evidence: **SRD6**

Gene ID History: **SRD6**

Gene Gene History: **SRD6**

Configure this page



ATLAS data visualization tools are connected to Gramene, Ensembl Plants and Plant Reactome resources

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

The multi-species view shows alignments in the context of gene annotations across multiple species