Gramene

SINCE 2001

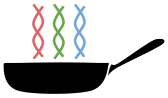
Plant comparative genomics

Making agricultural data FAIR

Findable **A**ccessible **I**nteroperable **R**eusable

https://www.gramene.org

Rel #68 (Dec. 2023)	Species with genetic variation: 19
Plant genomes: 150	Species with baseline gene expression: 23
Gene family trees: 157K	Curated rice pathways: 339
Pairwise DNA alignments: 279	Species with orthology-based pathway projections: 130
Synteny maps: 80	Support for community curation of gene structures



PanGenomes

For each pan genome site, gene trees were built with a minimum of 7 outgroup species. Expression data and pathways are available for the reference genomes.

Tools

- Browse
- Download
- BLAST
- Pathways
- Expression
- CLIMtools

ORYZA Gramene

oryza.gramene.org

Rel #8 (Aug. 2024)
Rice genomes: 28
Gene trees: 38K
46M SNPs, QTLs, RFLPs, SSRs

MAIZE Gramene

maize-pangenome.gramene.org

Rel #4 (Feb. 2024)
Maize genomes: 37
Gene trees: 35K

SORGHUM BASE

sorghumbase.org

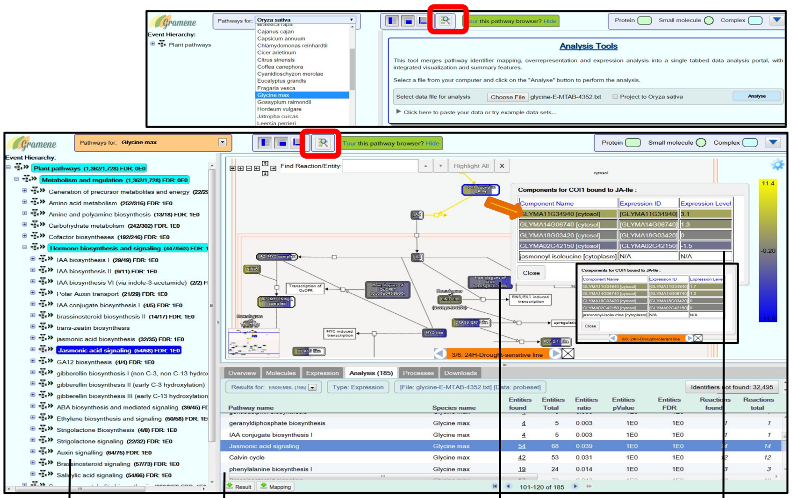
Rel #9 (January 2025)
Sorghum genomes: 88
Gene trees: 45K
BTx623: 59M SNPs & EMS mutations
Tx2783: 32.5M SNPs in Publications DB & research highlights

GRAPEVINE Gramene

vitis.gramene.org

Rel #4 (Jan. 2024)
Grape genomes: 31
Gene trees: 33K

Comparative pathway analysis of JA signaling in rice vs 4 species in Gramene's Plant Reactome



This tool merges pathway identifier mapping, overrepresentation and expression analysis into a single tabbed data analysis portal, with integrated visualization and summary features.

Select a file from your computer and click on the "Analyse" button to perform the analysis.

Select data file for analysis: Choose File glycine-E-MTAB-4352.txt ☐ Project to Oryza sativa Analyse

▶ Click here to paste your data or try example data sets...

- Plant pathways (1,362/1,728) FDR: 0E0
  - Metabolism and regulation (1,362/1,728) FDR: 0E0
    - Generation of precursor metabolites and energy (22/2
    - Amino acid metabolism (252/316) FDR: 1E0
    - Amine and polyamine biosynthesis (13/18) FDR: 1E0
    - Carbohydrate metabolism (242/302) FDR: 1E0
    - Cofactor biosyntheses (192/246) FDR: 1E0
    - Hormone biosynthesis and signaling (447/563) FDR: 1
      - IAA biosynthesis I (29/49) FDR: 1E0
      - IAA biosynthesis II (9/11) FDR: 1E0
      - IAA biosynthesis VI (via indole-3-acetamide) (2/2) F
      - Polar Auxin transport (21/29) FDR: 1E0
      - IAA conjugate biosynthesis I (4/5) FDR: 1E0
      - brassinosteroid biosynthesis II (14/17) FDR: 1E0
      - trans-zeatin biosynthesis
      - jasmonic acid biosynthesis (32/35) FDR: 1E0
      - Jasmonic acid signaling (54/68) FDR: 1E0
      - GA12 biosynthesis (4/4) FDR: 1E0
      - gibberellin biosynthesis I (non C-3, non C-13 hydro
      - gibberellin biosynthesis II (early C-3 hydroxylation)
      - gibberellin biosynthesis III (early C-13 hydroxylation
      - ABA biosynthesis and mediated signaling (39/45) FD
      - Ethylene biosynthesis and signaling (50/58) FDR: 1E
      - Strigolactone Biosynthesis (4/8) FDR: 1E0
      - Strigolactone signaling (22/32) FDR: 1E0
      - Auxin signalling (64/75) FDR: 1E0
      - Brassinosteroid signaling (67/73) FDR: 1E0
      - Salicylic acid signaling (54/66) FDR: 1E0

Components for COI1 bound to JA-Ile :

Component Name	Expression ID	Expression Level
GLYMA11G34940 [cytosol]	[GLYMA11G34940]	3.1
GLYMA14G06740 [cytosol]	[GLYMA14G06740]	1.3
GLYMA18G03420 [cytosol]	[GLYMA18G03420]	0
GLYMA02G42150 [cytosol]	[GLYMA02G42150]	-1.5
jasmonoyl-isoleucine [cytoplasm]	N/A	N/A

Components for COI1 bound to JA-Ile :

Component Name	Expression ID	Expression Level
GLYMA11G34940 [cytosol]	[GLYMA11G34940]	1.7
GLYMA14G06740 [cytosol]	[GLYMA14G06740]	1.3
GLYMA18G03420 [cytosol]	[GLYMA18G03420]	0
GLYMA02G42150 [cytosol]	[GLYMA02G42150]	0
jasmonoyl-isoleucine [cytoplasm]	N/A	N/A

Pathway name	Species name	Entities found	Entities Total	Entities ratio	Entities pValue	Entities FDR	Reactions found	Reactions total
geranyldiphosphate biosynthesis	Glycine max	4	5	0.003	1E0	1E0	1	1
IAA conjugate biosynthesis I	Glycine max	4	5	0.003	1E0	1E0	1	1
Jasmonic acid signaling	Glycine max	54	68	0.039	1E0	1E0	14	14
Calvin cycle	Glycine max	42	53	0.031	1E0	1E0	12	12
phenylalanine biosynthesis I	Glycine max	19	24	0.014	1E0	1E0	3	3

Events with enrichment statistics

Download pathway enrichment data and mapped gene loci

Use arrows to view expression from different data points

Data for unmapped gene loci

Contact us for data integration, training and support or to partake in our community curation projects:

https://www.gramene.org/feedback

Cite Gramene:
Tello-Ruiz *et al* (2021) 10.1093/nar/gkaa979

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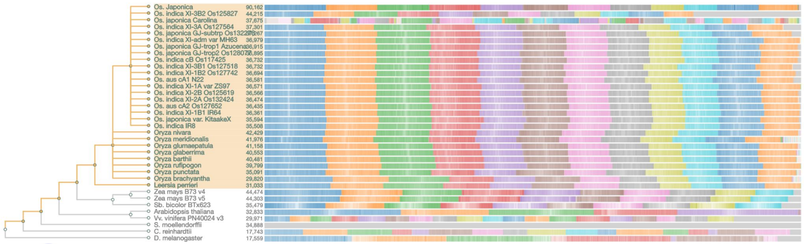
ORYZA Gramene

https://oryza.gramene.org

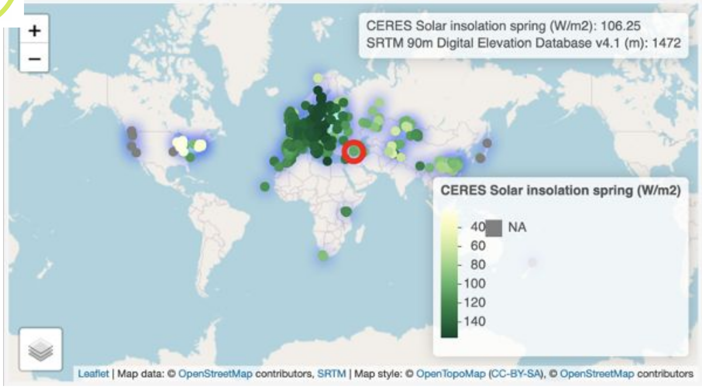
Plant comparative genomics

Making agricultural data FAIR

28 Oryza genomes, closely related Leersia, 6 outspecies



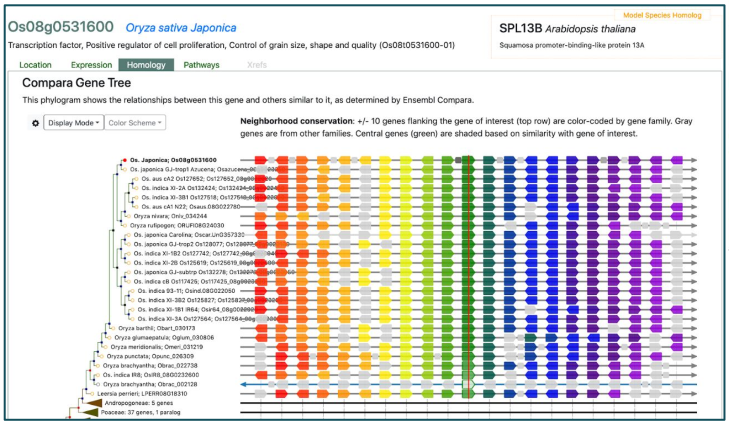
Oryza CLIMtools: Interactive spatial analysis web tool via a database of local Oryzae environments



- What is the GxE of my gene of interest? → **GenoCLIM**
- What is the local environment of sequenced landraces? → **OryzaCLIM**
- What is the GxE for my environmental variable of interest? –> **CLIMGeno Japonica / Indica**

Ferrero-Serrano et al (2024)

Gene Neighborhood conservation view provides insights on gene structural variations


Os08g0531600 *Oryza sativa Japonica*

Transcription factor, Positive regulator of cell proliferation, Control of grain size, shape and quality (Os08t0531600-01)

Model Species Homolog

SPL13B *Arabidopsis thaliana*

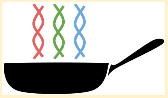
Squamosa promoter-binding-like protein 13A

Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

Neighborhood conservation: +/- 10 genes flanking the gene of interest (top row) are color-coded by gene family. Gray genes are from other families. Central genes (green) are shaded based on similarity with gene of interest.

The “Gene Neighborhood” is derived from gene trees, based on protein alignments. The view displays 10 flanking genes color coded by gene family or shaded based on similarity to the gene of interest, providing insights on gene structural variants or presence/absence genes.

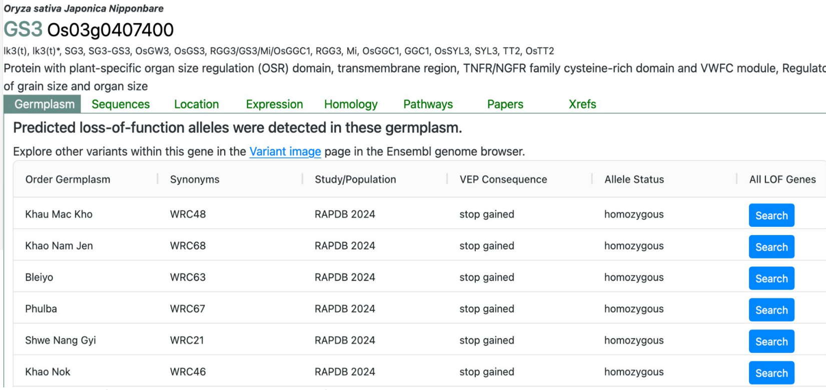


Release #8 (August 2024)

Oryza PanGenome

- Rice genomes: 28
- Gene family trees: 38K
- 30 pairwise synteny maps
- 3 pairwise whole-genome alignments
- Genetic variation: 46M SNPs, RFLPs, SSRs
- Geno-Pheno associations: QTLs, SVs & CLIMtools
- Baseline gene expression studies on IRGSP1: 15
- Differential gene expression studies EBI-Atlas: 95
- Curated single-cell expression studies EBI-Atlas: 3
- Curated pathways IRGSP1: 339 including lignin & metabolite biosynthesis

New in Gene Search: Germplasm Table View


Oryza sativa Japonica Nipponbare

GS3 Os03g0407400

Ik3(t), Ik3(t)*, SG3, SG3-GS3, OsGW3, OsGS3, RGG3/GS3/Mi/OsGGC1, RGG3, Mi, OsGGC1, GGC1, OsSYL3, SYL3, TT2, OsTT2

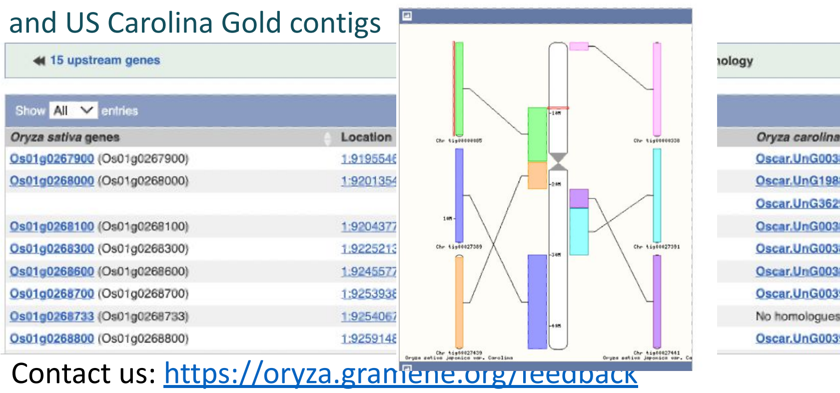
Protein with plant-specific organ size regulation (OSR) domain, transmembrane region, TNFR/NGFR family cysteine-rich domain and VWFC module, Regulato of grain size and organ size

Predicted loss-of-function alleles were detected in these germplasm.

Explore other variants within this gene in the Variant image page in the Ensembl genome browser.

Order Germplasm	Synonyms	Study/Population	VEP Consequence	Allele Status	All LOF Genes
Khau Mac Kho	WRC48	RAPDB 2024	stop gained	homozygous	Search
Khao Nam Jen	WRC68	RAPDB 2024	stop gained	homozygous	Search
Bleiyo	WRC63	RAPDB 2024	stop gained	homozygous	Search
Phulba	WRC67	RAPDB 2024	stop gained	homozygous	Search
Shwe Nang Gyi	WRC21	RAPDB 2024	stop gained	homozygous	Search
Khao Nok	WRC46	RAPDB 2024	stop gained	homozygous	Search

Synteny between IRGSP chr1 and US Carolina Gold contigs


Synteny between Oryza sativa (Geng/Japonica-temp var. Nipponbare) c

15 upstream genes

Show All entries

Oryza sativa genes	Location	Oryza carolina
Os01g0267900 (Os01g0267900)	1:9195546	Oscar.UnG003
Os01g0268000 (Os01g0268000)	1:9201354	Oscar.UnG198
		Oscar.UnG362
Os01g0268100 (Os01g0268100)	1:9204377	Oscar.UnG003
Os01g0268300 (Os01g0268300)	1:9225213	Oscar.UnG003
Os01g0268600 (Os01g0268600)	1:9245577	Oscar.UnG003
Os01g0268700 (Os01g0268700)	1:9253938	Oscar.UnG003
Os01g0268733 (Os01g0268733)	1:9254067	No homologues
Os01g0268800 (Os01g0268800)	1:9259148	Oscar.UnG003

Contact us: https://oryza.gramene.org/feedback

Wei et al. GrameneOryza: A Comprehensive Resource for Oryza Genomes, Genetic Variation, and Functional Data. *Submitted manuscript.*

Community Engagement

- Engagement and training
- Support for data standards
- Integrated access via data federation

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Department of Agriculture 1898

CGIAR

IRRI

USDA ARS Agricultural Research Service

CSH

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