ORYZA Gramene

Plant comparative genomics
Making agricultural data FAIR

https://oryza.gramene.org

28 Oryza genomes, closely related Leersia, 6 outspecies

Release #6 (January 2023)
- Rice genomes: 28
- Gene family trees: 37K
- 30 synteny maps
- Curated gene annotations for > 4K genes from RAP-DB and NCBI's geneRIF made searchable
- List of publications associated with curated genes in search results
- 3 pairwise whole-genome alignments
- Baseline gene expression studies on IRGSP1: 10
- Curated pathways IRGSP1: 320 including lignin & metabolite biosynthesis

Oryza PanGenome

Left panel: Whole-Genome Alignment region comparison view between Nipponbare, Sorghum and Maize

Tools

Browse | Download | BLAST

Pathways | Expression | Variation

ATCGAGCT
ATCCAGCT
ATCGAGAT

Synteny between
Nipponbare IRGSP chr1 and
US Carolina Gold contigs

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

Gene Neighborhood conservation view provides insights on gene structural variations

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.

Community Engagement

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

THE UNIVERSITY OF ARIZONA — COLLEGE OF AGRICULTURE & LIFE SCIENCES

KAUST
King Abdullah University of Science and Technology

DEPARTMENT OF AGRICULTURE 1898

CGIAR

IRRI

USDA Agricultural Research Service

CSH

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

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Rel #66 (Dec. 2022)
Plant genomes: 128
Gene family trees: 152K
Pairwise DNA alignments: 278
Synteny maps: 79

Species with genetic variation: 15
Species with baseline gene expression: 28
Curated rice pathways: 320
Species with orthology-based pathway projections: 120
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.

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Rel #6 (Jan. 2023)
Rice genomes: 28
Gene trees: 38K

MAIZE Gramene
maize-pangenome.gramene.org

Rel #2 (July 2021)
Maize genomes: 26
Gene trees: 31K

GRAPEVINE Gramene
vitis.gramene.org

Rel #3 (May 2022)
Grape genomes: 18
Gene trees: 28K

SORGHUM BASE
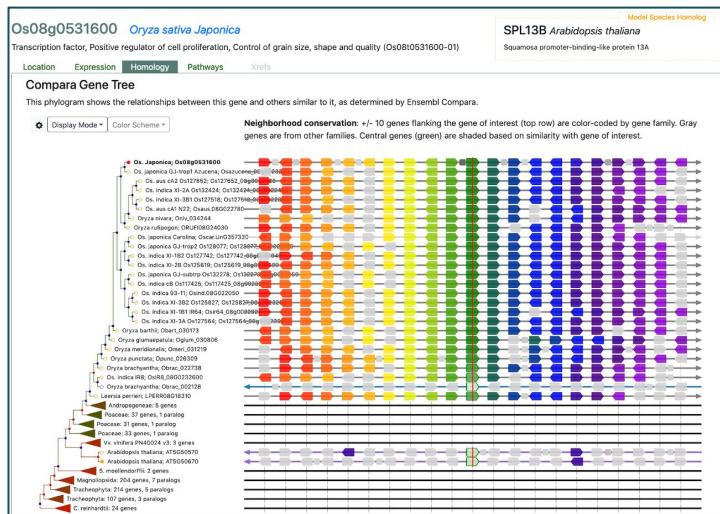sorghumbase.org

Rel #5 (Dec. 2022)
Sorghum genomes: 28
Gene trees: 44K
61M SNPs and EMS mutations
Publications DB & research highlights

Contact us for data integration, training and support or to partake in our community curation projects:
https://www.gramene.org/feedback

Tools

Browse
Download
BLAST
Pathways
Expression
CLIMtools

Neighborhood Conservation View. This view allows researchers to identify structural variants and presence/absence variation in a conserved region. For each gene in the tree 10 flanking genes are displayed and color coded by gene family or shaded based on similarity to the gene of interest.

USDA   CSH   EMBL-EBI   OSU   OICR Ontario Institute for Cancer Research

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