Gramene
SINCE 2001

Plant comparative genomics
Making agricultural data FAIR

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

https://www.gramene.org

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.

Tools

Browse
Download
BLAST
Pathways
Expression
CLIMtools

MAIZE Gramene
maize-pangenome.gramene.org

Rel #3 (July 2023)
Maize genomes: 41
Gene trees: 36K

GRAPEVINE Gramene
vitis.gramene.org

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

ORYZA Gramene
oryza.gramene.org

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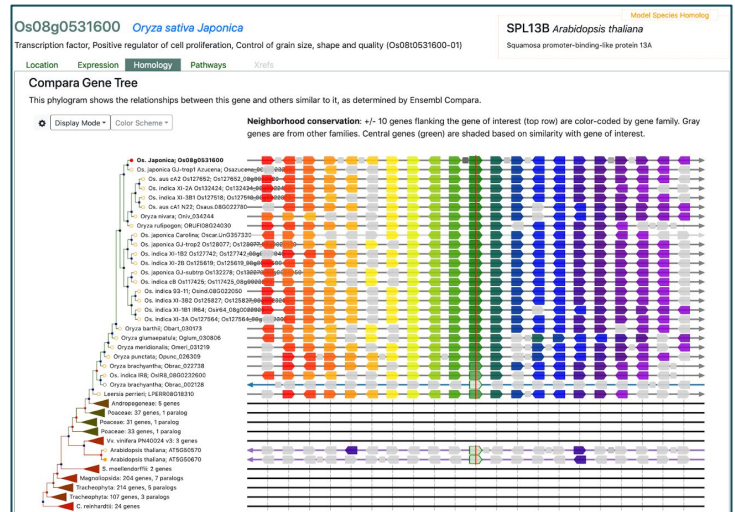Gene trees: 38K

SORGHUM BASE
sorghumbase.org

Rel #6 (June 2023)
Sorghum genomes: 29
Gene trees: 43K
>90M SNPs & EMS mutations
Publications DB &
research highlights

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.

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

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

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CLIMtools

Environment × Genome × Phenotype Associations

SINCE 2021

https://www.gramene.org/CLIMtools

Version 2 (May 2022)
Arabidopsis accessions: 2999
Oryza accessions: 658 Indica & 253 Japonica
Climate Variables: 473 Arabidopsis & 413 Oryza

Climate GWAS and TWAS
RiboSNitch† prediction

AraCLIM V2

Interactive spatial analysis web tool via a database of local Arabidopsis environments

OryzaCLIM V1

What is the local environment of sequenced landraces?

CLIMGeno

Genetic variation associated with an environmental variable of interest

GenoCLIM

Environmental variation associated with a gene or variant of interest. *What is the GxE of my gene of interest?*

T-CLIM_V2

Association between natural variation in transcript abundance of a gene and an environmental variable

† RiboSNitches are SNPs that change RNA structure between the reference and the alternative SNP.

ClimTools: Ferrero-Serrano *et al* (2022)
10.1186/s13059-022-02656-4
Oryza ClimTools: Ferrero-Serrano *et al* (bioRxiv)
10.1101/2023.05.10.540241

CERES Solar insolation spring (W/m2): 106.25
SRTM 90m Digital Elevation Database v4.1 (m): 1472

CERES Solar insolation spring (W/m2)

Latitude.csv Results for Chromosome 1
Rollover for more info. Drag chart area to zoom. Click point for zoomed annotated plot.

USDA   NSF   Gramene   CSH   PennState