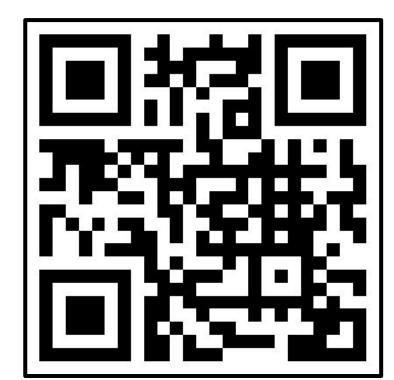


Gramene 2023: A comparative resource on plant reference genomes, pan genomes and plant reactome pathways.



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VERSATILE SEARCH INTERFACE & PAN-GENOME SITES

Homology view

Shows inferred evolutionary histories from Compara, integrated with

functional domain information from InterPro.

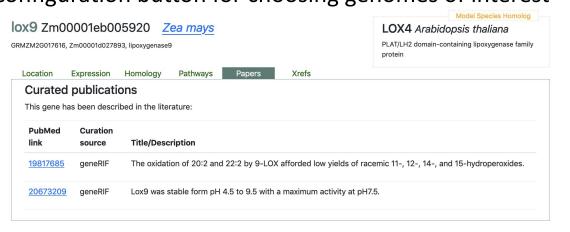
Alignment Overview

Highlights Gramene's homepage has been reimplemented for easy deployment across

- our sites. • Search results integrate six data types as embedded views: Location,
- Expression, Homology, Pathways, Papers & Cross-References.
- The Homology view allows zooming in (Multi-alignment view) and out (Neighborhood conservation) from the Alignment Overview of a gene family
- Integration of gene functions described in the literature (354 Z. mays, 4006 O. sativa, 7184 A. thaliana), see Papers tab.

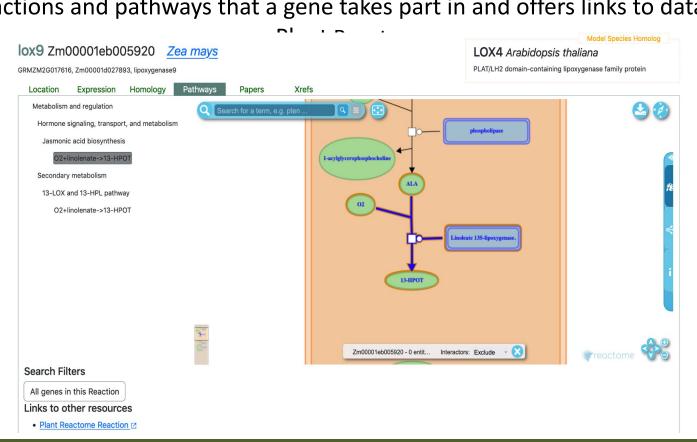
Updated layout

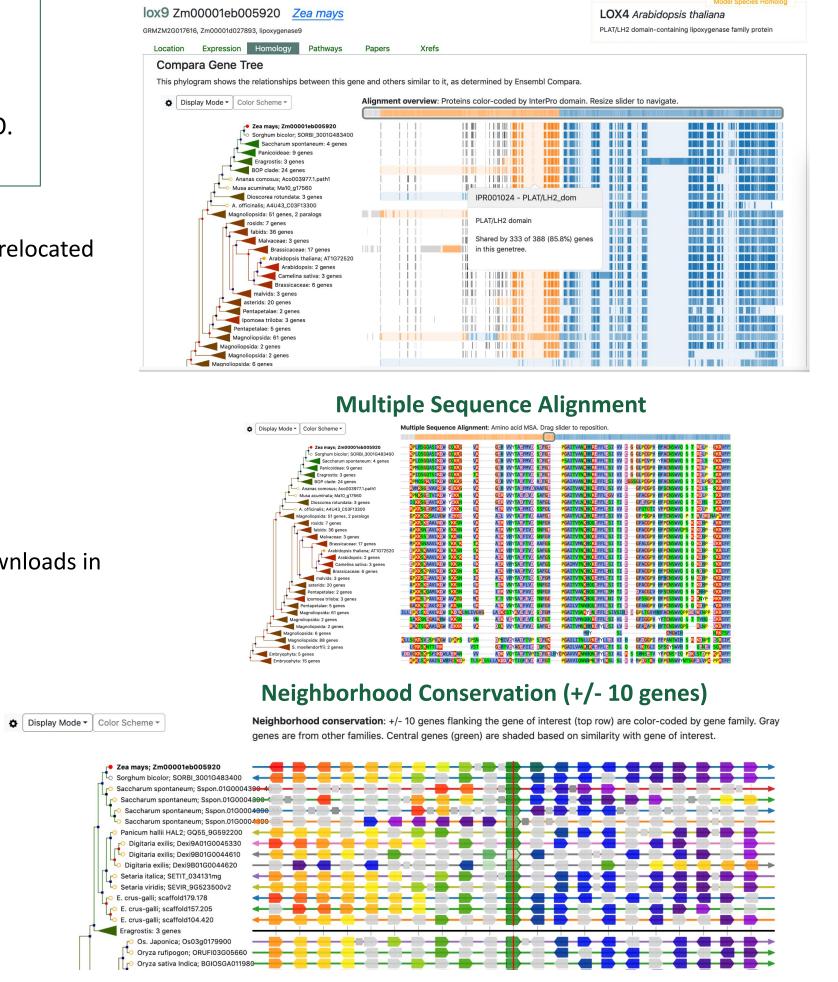
New Papers tab. More control over search filters, automatically pruned species tree, relocated configuration button for choosing genomes of interest

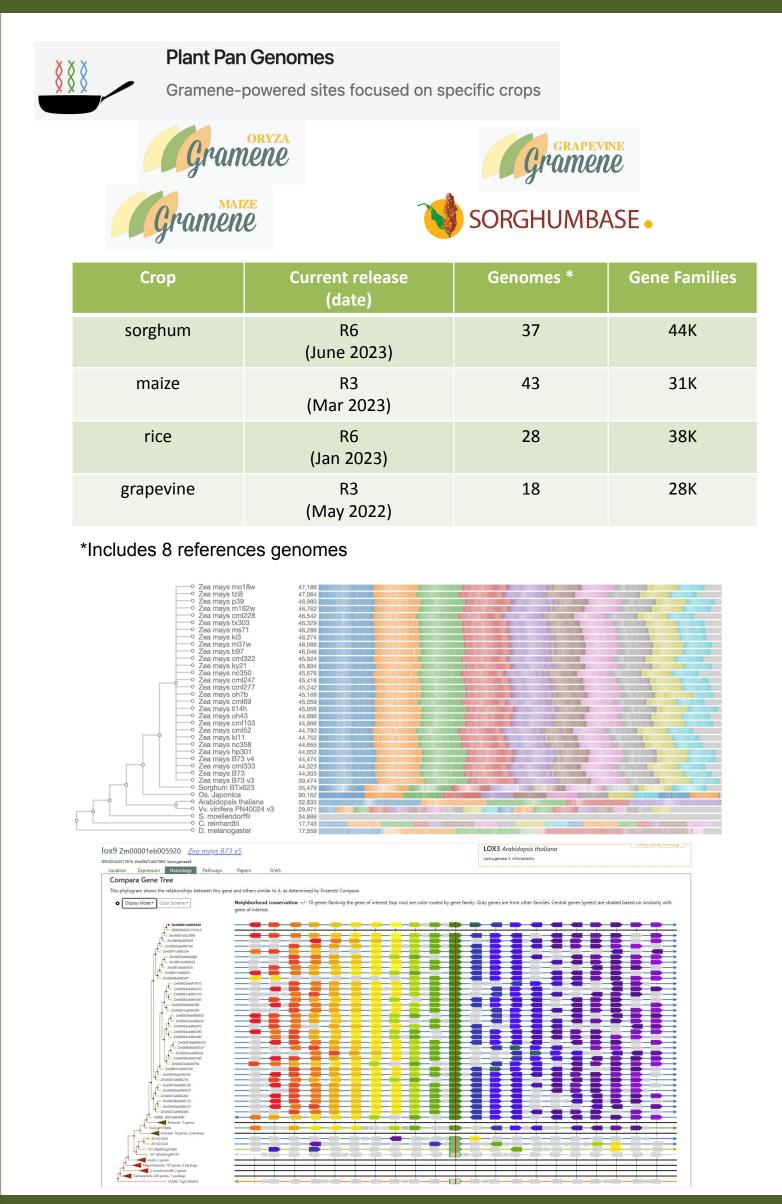


Pathways view

Shows the reactions and pathways that a gene takes part in and offers links to data downloads in





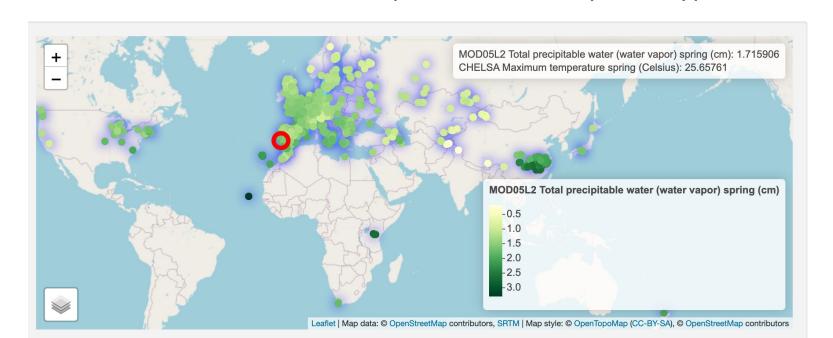


CLIMTOOLS

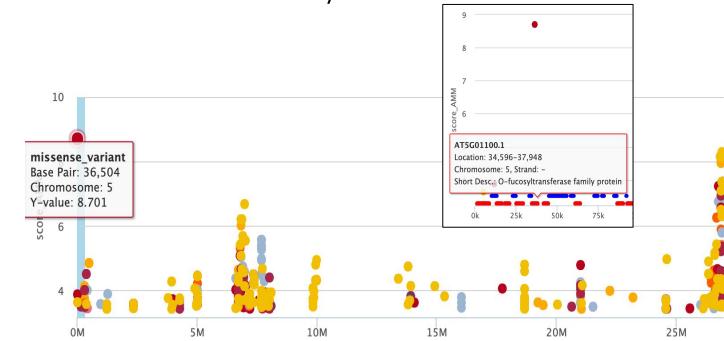


https://gramene.org/CLIMtools

CLIMtools is a set of interactive web-based databases of the environment × genome associations and correlations between the local environment and a pool of curated phenotypes.



Global distribution of germplasm climate data Map view shows locations where specific germplasm were collected color coded by climate variables.



Explore genome-wide associations with climate data Interactive plot shows variants colored by consequence type and overlapping genes

GENOMES, PATHWAYS & EXPRESSION

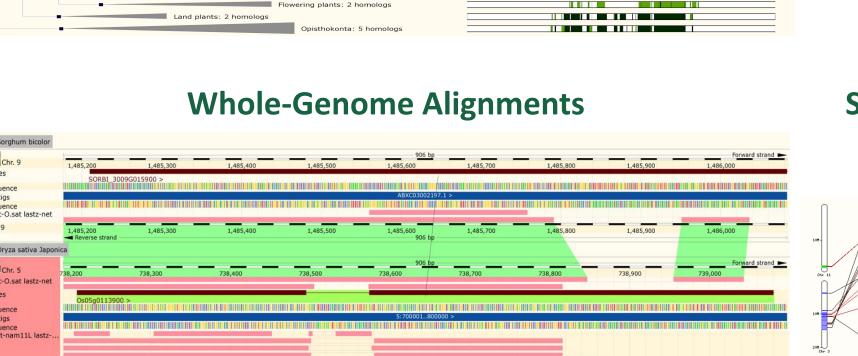
different data points

OMICs data analysis

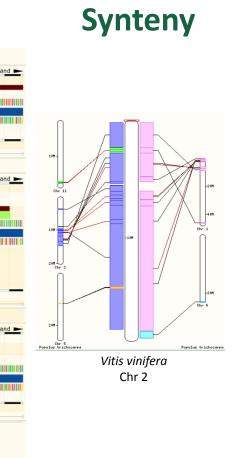
Diverse Reference Genomes







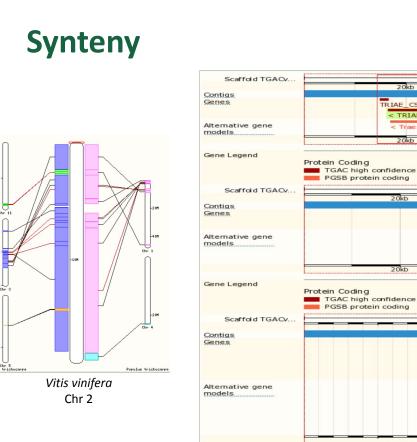
Whole-Genome Alignment region comparison view between Nipponbare, Sorghum and Maize



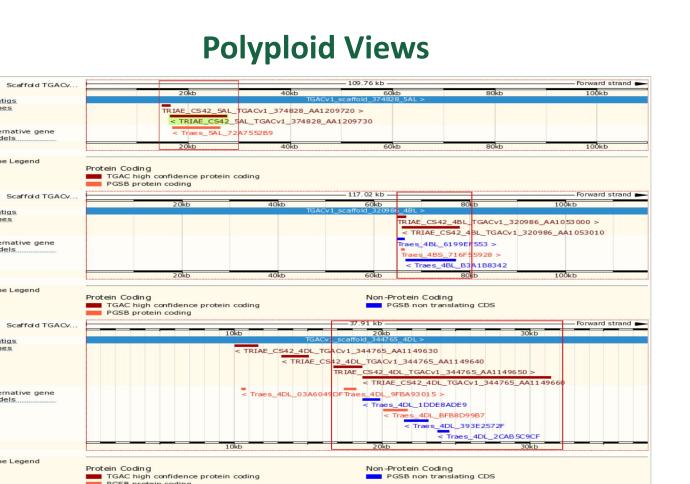
Salicylic acid signaling (54/66) FDR: 1E0

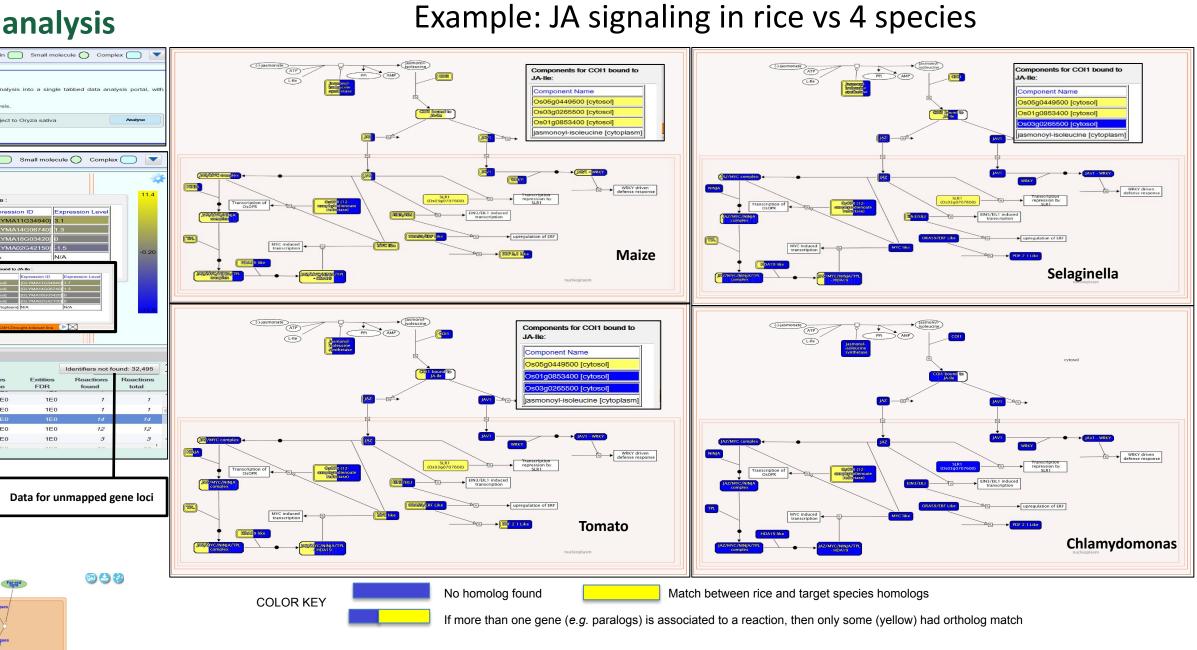
Download pathway Enrichment

data and mapped gene loci

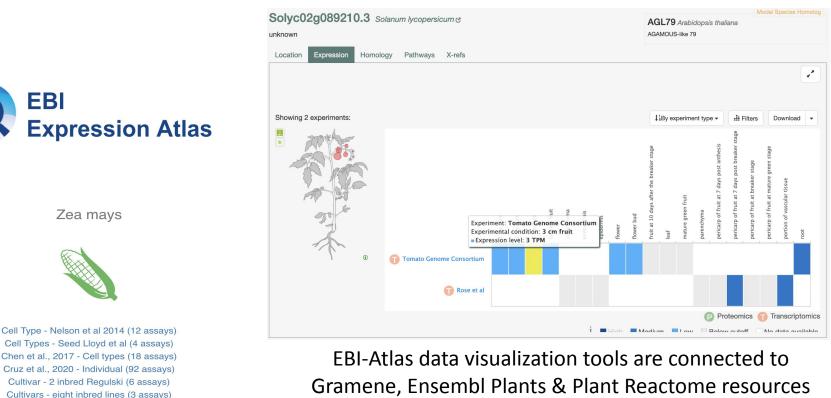


Interactor Overlay





Comparative pathway analysis



ranscription profiling by array of seedlings from two maize inbred lines (Ye478 and Han21)under drought stress, re-watering after drought, or normal watering conditions Microarray 1-colour mRNA rganism: Zea mays Array Design(s): Affymetrix GeneChip Maize Genome Array [Maize] eference(s): 19953304 (Filter by genes in paper) Select genome browser to view tracks Gramene genome browser Ensembl Genomes genome browser noderate drought moderate drought severe drought severe drought severe drought severe drought severe drought in "re-watering" vs "re-watering" vs stress' vs'control stress' vs'control in "Han21" in "Ye478" in "Ye478" in "Ye478" in "Ye478" in "Ye478" in "Ye478" in Zm00001d032610 Zm.622.1.S1_at Zm00001d028647 Zm.11928.1.A1_s_at downregulated Zm00001d029630 Zm.8801.1.A1_at

Zm00001d022965 Zm.1313.1.A1_s_at Zm00001d004389 Zm.18651.1.A1_at

Gramene is developed in collaboration with Ensembl Plants, and leverages the Ensembl & Reactome platforms

BUILD 66 HIGHLIGHTS

- •128 plant reference assemblies including 14 new genomes added in the past year.
- •Gene models with functional & structural annotations.
- •Protein-based gene trees with 152K gene families (5.1M input proteins) provide access to orthologs and paralogs and the ability to transverse across species.
- •278 whole-genome alignments between each genome and a reference monocot (e.g., rice) and dicot (e.g., grape) genomes & 79 synteny maps.
- •A new <u>CLIMtools</u> portal brings interactive web-based views of Environment x Genome associations, RiboSNitch prediction, and correlations between the local environment and a pool of curated
- Genetic variation amounts to >238 M markers including SNPs, QTLs, SSR/RFLPs and EMS-induced variants.
- •336 curated rice pathways and orthology-based projections for
- 120 species allow inter-species comparisons (Plant Reactome).
- •Baseline and differential expression data sets from 982 experiments and 28 reference plant species (Expression Atlas).
- •Read more: https://www.gramene.org/news

COMMUNITY ENGAGEMENT



- Download a quick start Gramene pamphlet and other e-learning materials:
- http://www.gramene.org/outreach
- Subscribe to <u>Gramene's mailing list</u> Gramene's You Tube channel
- Follow Gramene in Social Media:











Zea mays

Cell Type - Nelson et al 2014 (12 assays Cell Types - Seed Lloyd et al (4 assays)

Cruz et al., 2020 - Individual (92 assays)

Cultivar - 2 inbred Regulski (6 assays)

Cultivars - eight inbred lines (3 assays)

Meng et al, 2017 - Age (24 assays) Organism Part - Chang et al 2012 (4 assay

Pang et al., 2018 - Cultivar (291 assays)

Seed development - Chen et al (65 assays)

huai Wang et al, 2014 - Organism part (6 assar

Thatcher et al., 2014 - Cultivar (94 assays

Tissues - 4 Chettoor et al (11 assays Tissues - 6 Wang (36 assays) Tissues - Stelpflug et al (267 assays Tissues - Walley et al (68 assays) Wang et al 2014 - Sampling site (75 assay

Want et al., 2020 - Cultivar (40 assays)

Liu et al., 2020 - Organism part (20 assays)

NAM Consortium Group, B73 genome - Organism par (21 assays)

Maize is one of 28 plant species with

Downregulated onl

gene expression data in EBI-Atlas



