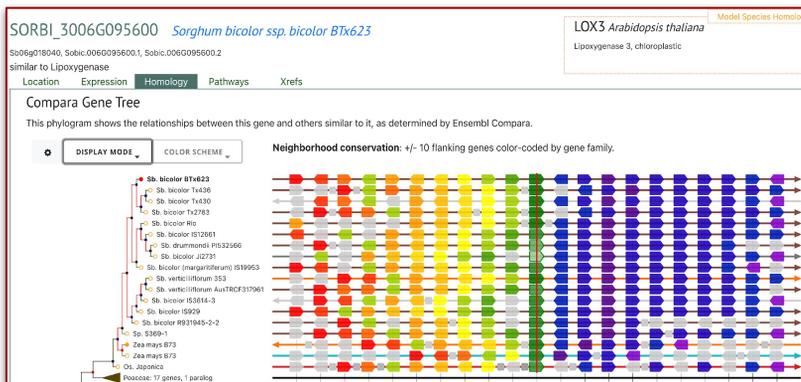


Contact us to highlight your research, integrate your data & get personalized training and support:
<https://www.sorghumbase.org/feedback>

Gene Neighborhood conservation view provides insights on gene structural variations



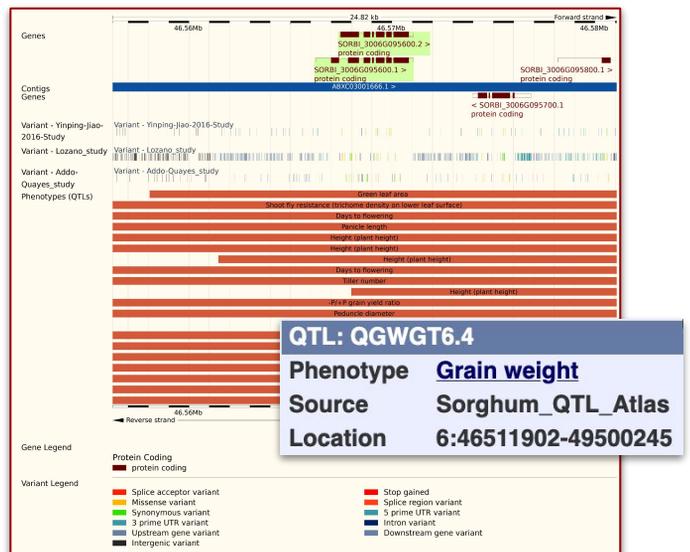
The "Gene Neighborhood" is derived from gene trees, based on protein alignments. The view displays 10 flanking genes color coded by gene family or shaded based on similarity to the gene of interest, providing insights on gene structural variants or presence/absence genes.

Release #5 (Dec. 2022)

- Sorghum news, events, job postings
- Sorghum publications: 574
- Sorghum genomes: 28 (10 CP-NAM)
- Gene family trees: 44K
- Synteny maps: 84
- Whole-genome alignments: 3
- Genetic Variation: 61M single-nucleotide variants; 23.7K loss of func. (LOF) genes
- 44M SNPs, 5M indels, 18835 LOF genes, 400 SAP (Boatwright 2022)
- 13.1M SNPs, 4641 LOF genes, 499 lines TERRA-MEPP & TERRA-REF panels (Lozano 2021)
- EMS: 4.3M SNPs, 9673 LOF genes from 2 populations (Jiao 2016 & Addo-Quaye 2018)
- 6K Atlas QTLs: >150 studies on 223 traits
- Baseline gene expression studies (BTx623): 8
- Pathways based on rice projections (BTx623): 269 including lignin & metabolite biosynthesis



QTLs are available as tracks on Genome Browser



- What else do we do?**
- Community engagement and training
 - Research highlights
 - Support for data standards
 - Integrate access via data federation

Cite SorghumBase: Gladman *et al* (2022) [10.1007/s00425-022-03821-6](https://doi.org/10.1007/s00425-022-03821-6)



Community Engagement Initiatives

Sorghum Reference Genomes

- Working group established in 2019
- Prioritized germplasms for reference maps
- Set standards: metadata, naming conventions
- Practical Haplotype Map (**Sorghum v2 2023**)

Sorghum BreedBase Platform

- Prototyping and evaluation March 2022
- Open-source, web-based portal for communication and data sharing among the breeders, researchers, and stakeholders in the global sorghum community
- Integrates breeding data management and analysis tools:
 - **Breeding-focused:** Pedigrees, Field Trials, Phenotypes, Genotyping Trials, Germplasm Accessions and Lots, Image/Spectral Datasets, and more...
 - **Genomics resources:** GWAS, Genomic Prediction, Linear Mixed Modeling, Population Structure (PCA), and Kinship and Clustering

Sorghum Community Marker Panel

- Currently soliciting germplasms and markers for prototyping the panel
- Target Region: USA (Domestic Use)
- Working Group established in August 2022 under the auspices of the Sorghum Crop Germplasm Committee (CGC). Members from Academics, Government and Industry
- Direct outcome of the CGC meeting held at SICNA 2022 at Dallas-Fort Worth, TX

Sorghum BreedBase Platform (Beta)

Manage Locations

[Upload New Locations]

| Column visibility | Copy | Excel | CSV | PDF | Print | Search: | | | | |
|-------------------|-------------------|--------------|----------------------|----------|-------|---------|----------|-------------|----------|-------------------------|
| ID | Name | Abbreviation | Country | Program | Type | Lat | Long | Altitude(m) | Trials | Nearest NOAA Station ID |
| 78 | Williamson County | WILT | USA United States of | TAMU-KSU | Field | 30.713 | -97.4427 | 180 | 0 trials | GHCND:USC00300381 |
| 31 | Victoria County | | | | | | | | | |
| 88 | Thomas County | | | | | | | | | |

Trial Details

View and edit basic information about the experiment.

[Edit Trial Details](#)

| | |
|---|--|
| Trial Name | 19_THOKS_TxKH |
| Breeding Program | TAMU-KSU |
| Trial Location | Thomas County (United States of America) |
| Year | 2019 |
| Stock Type Being Evaluated In This Trial | accession |
| Number of Stocks in This Trial | 100 |
| Trial Type | phenotyping_trial |



19_THOKS_TxKH SGN177

| | |
|---------------------------|--------|
| Plot Width (m) | 1.8 |
| Plot Length (m) | 5.2 |
| Size (ha) | 0.2898 |
| Will Be Genotyped | no |
| Will Be In Crosses | no |

Search Accessions and Plots

Name Search

Stock Name or Description:

Stock Type:

Advanced Search

Search Results

View Another Property:

Show entries

| Stock Name | Stock Type | Organism | Synonyms | Submitters | Organization |
|---------------|------------|-----------------|----------|---------------|--------------|
| A03040/R17117 | accession | Sorghum bicolor | | Jales Fonseca | |
| A03040/R17161 | accession | Sorghum bicolor | | Jales Fonseca | |

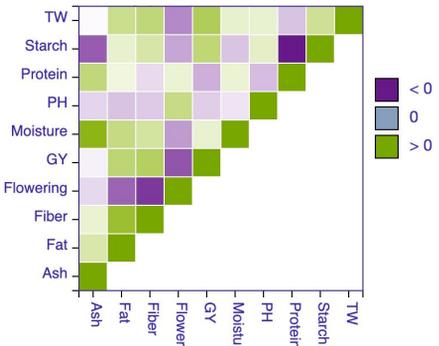
Raw Data Statistics

Display:

Show rows

| Trait | Mean | Min | Max | Std Dev | CV | Count | Percent Missing | Histogram |
|-------------------|------|------|------|---------|--------|-------|-----------------|-----------|
| Ash STO:0005644 | 1.33 | 1.10 | 1.52 | 0.08 | 6.18% | 199 | 0.50% | |
| Fat STO:0007856 | 2.55 | 0.27 | 3.39 | 0.52 | 20.38% | 199 | 0.50% | |
| Fiber STO:0006674 | 1.67 | 1.38 | 1.98 | 0.11 | 6.31% | 199 | 0.50% | |
| | | | | | | 100 | 50.00% | |

Phenotypic correlation analysis (Pearson)



Legend: ■ < 0, ■ 0, ■ > 0

Anova

Grain Yield Run ANOVA

ANOVA result: GY

| | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(> F) |
|---------------|--------|---------|-------|-------|---------|---------|
| germplasmName | 351.19 | 3.55 | 99 | 100 | 4.25 | 0 |

Download: [\[Anova table\]](#) | [\[Model summary\]](#) | [\[Model diagnostics\]](#) | [\[Adjusted means\]](#)













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