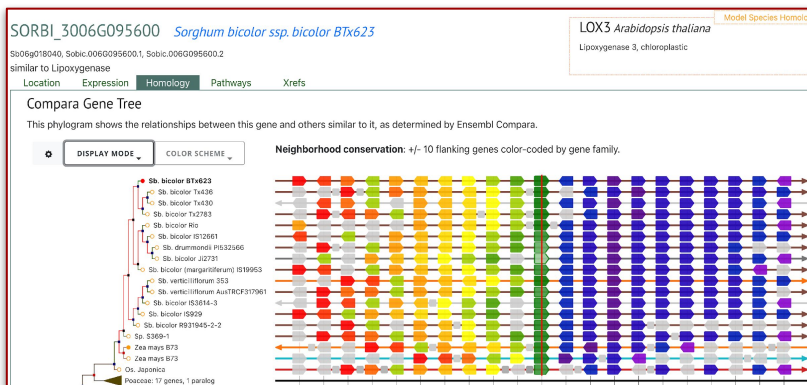


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Tools

- Browse
- Download
- BLAST
- Pathways
- Expression
- Variation

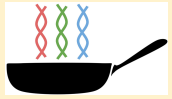
Gene Neighborhood conservation view provides insights on gene structural variations



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 #6 (June 2023)

Discover the latest in sorghum research!

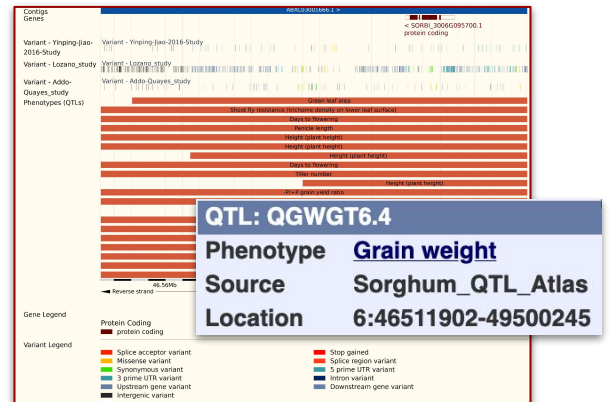


PanGenomes

- Sorghum genomes: 29 (6 SAP, 11 BAP, 10 CP-NAM, BTx623: NCBI_v3 & JGI_v5)
- Curated genes from GeneRIF & RAP-DB with PubMed links and searchable TO/PO terms
- Genetic Variation:
 - BTx623: 59M variants; >27K LOF genes
 - 46M SNPs (SAP, TERRA-REF, TERRA-MEP, etc.)
 - 13M EMS-induced mutations
 - Tx2783: 32.5M SNPs, 400 SAP lines
- 6K Atlas QTLs; 148 traits are now searchable
- Baseline gene expression studies (BTx623): 8
- Pathways based on rice projections (BTx623): 268
- Gene family trees: 43K
- Synteny maps: 83
- Whole-genome alignments: 15
- Sorghum publications: 782
- Sorghum news, events, job postings

Visit SorghumBase today for a wealth of resources and tools to enhance your research

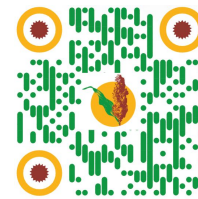
OZ Sorghum Atlas QTLs are available as a track in the genome browser



Explore our Additional Services

- 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)



Sorghum Reference Genomes

- Working group established in 2019
- Prioritized germplasm for reference maps
- Practical Haplotype Map (2023-24)

Sorghum Community Marker Panel

- Working Group established in August 2022
- Target: Develop a marker panel for US germplasm – <https://shorturl.at/abgqU>
- Review existing genotyping technologies
- Validation of panel with relevant germplasm in progress

Support for Data Standards

- Genetic Variation Working Group with USDA biocurators since Nov. 2021

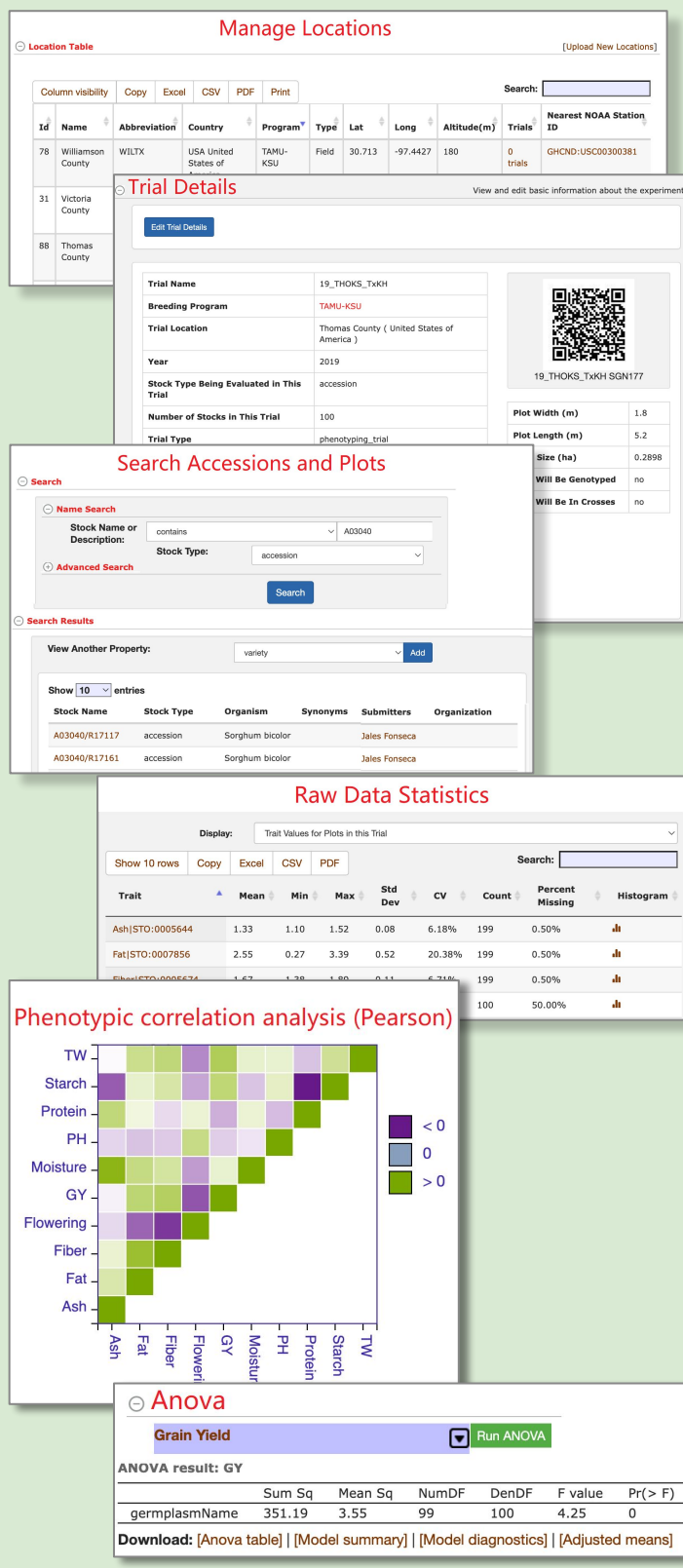
Sorghum BreedBase Platform

- Prototyping and evaluation March 2022
- Open-source, web-based portal for communication & data sharing among breeders, researchers, and stakeholders in the global sorghum community
- Integrates breeding data management & analysis tools
- Collaborators: TAMU, ARS, Breeding Insight, BreedBase
 - **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

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Sorghum BreedBase Platform (Beta)



Manage Locations

Location Table [Upload New Locations]

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

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

Search Accessions and Plots

Name Search: Stock Name or Description: contains A03040
 Stock Type: accession

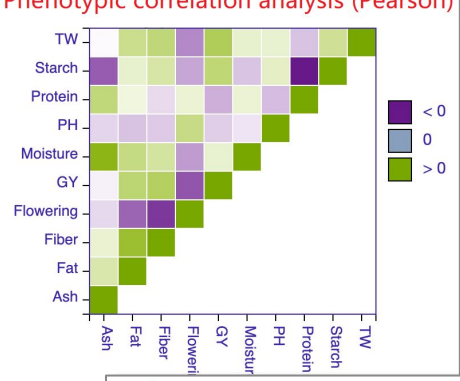
Search Results

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

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	1.90	0.11	6.31%	199	0.50%	
						100	50.00%	

Phenotypic correlation analysis (Pearson)



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]