



SorghumBase: Public Genetic and Genomic Database for the Sorghum Community

Nicholas Gladman
ASPB, August 2023



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SorghumBase is a Community Knowledge-base

- New database resource!
- **Genetic, Genomic, Variation, Expression, and Metabolic Data and Visualizations**
- Our stakeholders are geneticists, genomicists, molecular biologists, and breeders
- Working toward breeding resource development
- FAIR
- Release 6 (June 2023)

Scientific Advisory Board



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Tuinstra



Stephen
Kresovich

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

Welcome To Sorghumbase

Genomic Resources for the Sorghum Research Community



Genetic Variation

[Explore the Impact of Variants on Gene Structure](#)



Gene Expression

[Access Curated Gene Expression Data](#)



Pathways

[Plant Reactome Pathways on Community Reference Genomes](#)



News

[Relevant developments in Sorghum research.](#)



Tools

[Gene Search, Genome Browser, BLAST](#)



Events

[Upcoming Meetings and Conferences](#)

Search Views Are Completely Integrated

Short Root

Close X

Genes 404 terms [Website 4 matches](#)

Plant Ontology: anatomy

ROOT APICAL MERISTEM (6) LATERAL ROOT (17) LATERAL ROOT PRIMORDIUM (11) ROOT PRIMORDIUM (22) PRIMARY ROOT TIP (3) PRIMARY ROOT (11)

LATERAL ROOT TIP (2) ROOT CAP (8) ROOT TIP (54) ROOT ELONGATION ZONE (6)

InterPro: Family

ROOT_CAP (280) GLV2 (89) RPD1-LIKE (31) NPH3-LIKE (41) NAKR1/2/3 (183) SHORT-ROOT (8) RUS_FAM (216) NAKR2/3 (2) BPS1_PLN (976) RGF1/2/3 (34)

Trait ontology

ADVENTITIOUS ROOT LENGTH (8) ROOT WEIGHT (15) ROOT THICKNESS (13) ROOT HAIR LENGTH (19) ADVENTITIOUS ROOT NUMBER (8) ROOT VOLUME (1)


ROOT NUMBER (59) ROOT SHAPE (14) ROOT DRY WEIGHT (5) ROOT LENGTH (167)

Gene Ontology: biological process


LATERAL ROOT MORPHOGENESIS (68) POST-EMBRYONIC ROOT MORPHOGENESIS (70) LATERAL ROOT DEVELOPMENT (208) LATERAL ROOT FORMATION (54)

TRICHOBLAST DIFFERENTIATION (291) ROOT MERISTEM GROWTH (16) ATRICHOBLAST DIFFERENTIATION (1) ROOT CAP DEVELOPMENT (24) BASIPETAL AUXIN TRANSPORT (24)


ACROPETAL AUXIN TRANSPORT (4)



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SorghumBase Hosts Community Publications

Short Root

Genes 404 terms

Website 4 matches

Posts 1

Events 0

Papers 3

SbPho2, Phosphorus Starvation Signaling Gene, Identified in Sorghum and Shown to be Involved in Regulating the Uptake of Multiple Nutrients

Sorghum mutant, sbpho2, exhibits leaf necrosis and short roots, and is likely involved in phosphate accumulation and root architecture alteration.

Monday, June 5, 2023

[Read more](#)



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[Explore the Impact of Variants on Gene Structure](#)



News

[Relevant developments in Sorghum research.](#)



Gene Expression

[Access Curated Gene Express](#)



Tools

[Gene Search, Genome Brows](#)

SORGHUMBASE NEWS ENGAGE GENOMES TOOLS RESEARCH ABOUT

SORGHUMBASE ARTICLES

SbPho2, Phosphorus Starvation Signaling Gene, Identified in Sorghum and Shown to be Involved in Regulating the Uptake of Multiple Nutrients

SorghumBase Team / 5 June 2023

Phosphorous (Pi) availability significantly affects sorghum production. Although many regions have soil with abundant phosphorus, some developing countries have significant phosphorus growth and yield limitations due to low Pi fertilizer access or application. Inefficient application of exogenous Pi also increases costs and pollution. Scientists from Liaoning Academy of Agricultural Sciences in Shenyang, China investigated Pi signaling to gain insight into breeding Pi-efficient sorghum. Gong et al. (2023) and Hu et al. (2021) demonstrated that *Arabidopsis* and rice plants with mutations in *PHO2* accumulated two to four times more Pi in their shoots than their wild-type counterparts. The present study examines this phenotype in sorghum. Zhu et al. identified *sbpho2* mutants in an EMS population and mapped the trait to an E2 conjugase gene (SbPho2:0050228100), a putative orthologue of the rice and *Arabidopsis* *PHO2* genes. The researchers then compared the root architecture of *sbpho2* mutant sorghum plants to rice *opho2* mutants and found that while the rice mutants showed normal lengths of primary roots (Izu et al., 2011) under both Pi-sufficient and Pi-deficient conditions, the sorghum mutants showed reduced primary root growth. However, under Pi starvation conditions sorghum mutant's primary and adventitious root elongation ratios were higher than those of the wild type. These Pi starvation experiments, as well as the transformation of SbPHO2 in the rice *opho2* mutant, indicate that, in sorghum, SbPHO2 is associated with root architecture and Pi accumulation in the shoots. The researchers also found that the concentration of Nitrogen, in addition to the concentrations of other nutrients, were decreased in the *sbpho2* mutant and, conversely, the concentrations of potassium, iron, sodium, calcium, and zinc were increased. This is consistent with the alteration of the expression of several nitrate-, potassium- and other metal element-related genes in *sbpho2*. The results show that *PHO2* plays an important role in Pi starvation signaling.

SorghumBase Examples:

Gene: SBPHO2_0050228100

Variant table

Variant ID	Chr	Ref	Alt	Gene	Struc	Struc	Struc	Struc	Struc	Struc
HLA_000000000.0	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.1	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.2	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.3	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.4	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.5	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.6	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.7	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.8	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'
HLA_000000000.9	1	A	G	SbPho2	UTR	5'	UTR	5'	UTR	5'

Figure 1: Table of likely-disruptive EMS-induced variants impacting the PHO2 transcript in BTx623.

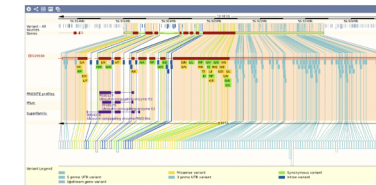


Figure 2: Image view of all EMS-induced and natural variants in the PHO2 gene model. The majority of variation occurs in the 5' UTR region.

Reference:

Zhu Z, Qu X, Li D, Zhang L, Wang C, Cong L, Bai C, Lu X. SBPHO2, a conserved Pi starvation signalling gene, is involved in the regulation of the uptake of multiple nutrients in sorghum. *Plant Sci.* 2022 Dec 5;327:111556. PMID: 36481362. DOI: 10.1016/j.plantsci.2022.111556. [Read more](#)

Search for Publications, Gene, Germplasm & Ontologies

sexton

Genes 0 terms Website 3 matches

Posts 0 Events 0 Papers 3

Antimicrobial Activity of Sorghum Phenolic Extract on Bovine Foodborne and Mastitis-Causing Pathogens.
Schnur SE, Amachawadi RG, Baca G, Sexton-Bowser S, Rhodes DH, Smolensky D, Herald TJ, Perumal R, Thomson DU, Nagaraja TG

Crop modeling defines opportunities and challenges for drought escape, water capture, and yield increase using chilling-tolerant sorghum.
Raymundo R, Sexton-Bowser S, Ciampitti IA, Morris GP

Current status and prospects of herbicide-resistant grain sorghum (*Sorghum bicolor*).
Pandian BA, Sexton-Bowser S, Prasad PV, Jugulam M
grass weeds, herbicide resistance, sorghum, stewardship

nitrogen

Genes 188 terms Website 21 matches

Posts 1 Events 0 Papers 20

Validation of QTL mapping and transcriptome profiling for identification of candidate genes associated with nitrogen stress tolerance in sorghum.
Gelli M, Kondrachineva A, ...

Improving abiotic stress tolerance in sorghum: focus on the nutrient transporters and marker-assisted breeding.
Maharajan T, Krishna TPA, Kiriyanthan PM, Janacimuthu S, Cesar SA

Nitrogen deficiency results in changes to cell wall composition of sorghum seedlings.
Divai PP, Miyamoto T, Awano T, Takada R, Tobimatsu Y, Umezawa T

BTX623

Genes 0 terms Website 65 matches


Posts 8 Events 0 Papers 57


Whole-genome sequencing of 400 Sorghum Association Panel (SAP) accessions establishes a crucial resource for dissecting genomic diversity in sorghum
Boatwright and coworkers generated about 44 million genetic variants in 400 SAP accessions using whole-genome sequencing.
Friday, February 11, 2022 [Read more](#)

Sorghum bicolor RTx430
Sorghum bicolor RTx430, a grain sorghum inbred commonly used as pollinator in hybrid production, whose genome is known to be rich in repeats, was assembled and annotated by (Deschamps et al. 2018).
Tuesday, July 6, 2021 [Read more](#)

Chromosome-scale assembly of the sorghum Tx430 genom using Nanopore sequencing and DLS optical mapping
A new chromosome-scale assembly of the sorghum genome was generated by combining Nanopore sequencing with DLS optical mapping. In this paper, published in this week's Nature Communications issue Oxford Nanopore sequences generated on a MinION sequencer and combined them with
Sunday, July 19, 2020 [Read more](#)

SorghumBase Contains EMS-induced and Natural Variant Resources



SORGHUM BASE BLAST Help Feedback Genome Browser Release Notes f Search Sorghumbase... 

Sorghum bicolor ssp. bicolor BTx623 (Sorghum_bicolor_NCBv3) Location: 3:69,827,192-69,830,766 Gene: **SORBI_3003G385900** Trans: SORBI_3003G385900.1 Jobs

Gene-based displays

- Summary
 - Splice variants
 - Transcript comparison
 - Gene alleles
- Sequence
 - Secondary Structure
 - Gene families
 - Literature
- Plant Compara
 - Genomic alignments
 - Gene tree
 - Gene gain/loss tree
 - Orthologues
 - Paralogues
- Pan-taxonomic Compara
 - Gene Tree
 - Orthologues
- Ontologies
 - GO: Biological process
 - GO: Cellular component
 - GO: Molecular function
- Phenotypes
- Genetic Variation
 - Variant table
 - Variant image
 - Structural variants
- Gene expression
- Regulation
- External references
- Supporting evidence
- ID History
 - Gene history
 - Gramene Search

[Configure this page](#) [Custom tracks](#) [Export data](#) [Share this page](#)

Gene: SORBI_3003G385900

Description hypothetical protein

Location [Chromosome 3: 69,827,192-69,830,766](#) reverse strand.

About this gene This gene has 1 transcript ([splice variant](#)), [39 orthologues](#) and [11 paralogues](#).



Transcripts [Show transcript table](#)

Summary

Gene type Protein coding


Annotation method Protein coding genes annotated in [ENA](#)


[Go to Region in Detail for more tracks and navigation options \(e.g. zooming\)](#)


Drag/Select:  


23.57 kb Forward strand


69.82Mb 69.83Mb 69.84Mb

Genes.  SORBI_3003G3857001 > protein coding

Contigs.  ABXC03000724.1 >

Genes.  < SORBI_3003G385800.1 protein coding


 < SORBI_3003G385900.1 protein coding

 < SORBI_3003G386000.1 protein coding

69.82Mb 69.83Mb 69.84Mb

Reverse strand

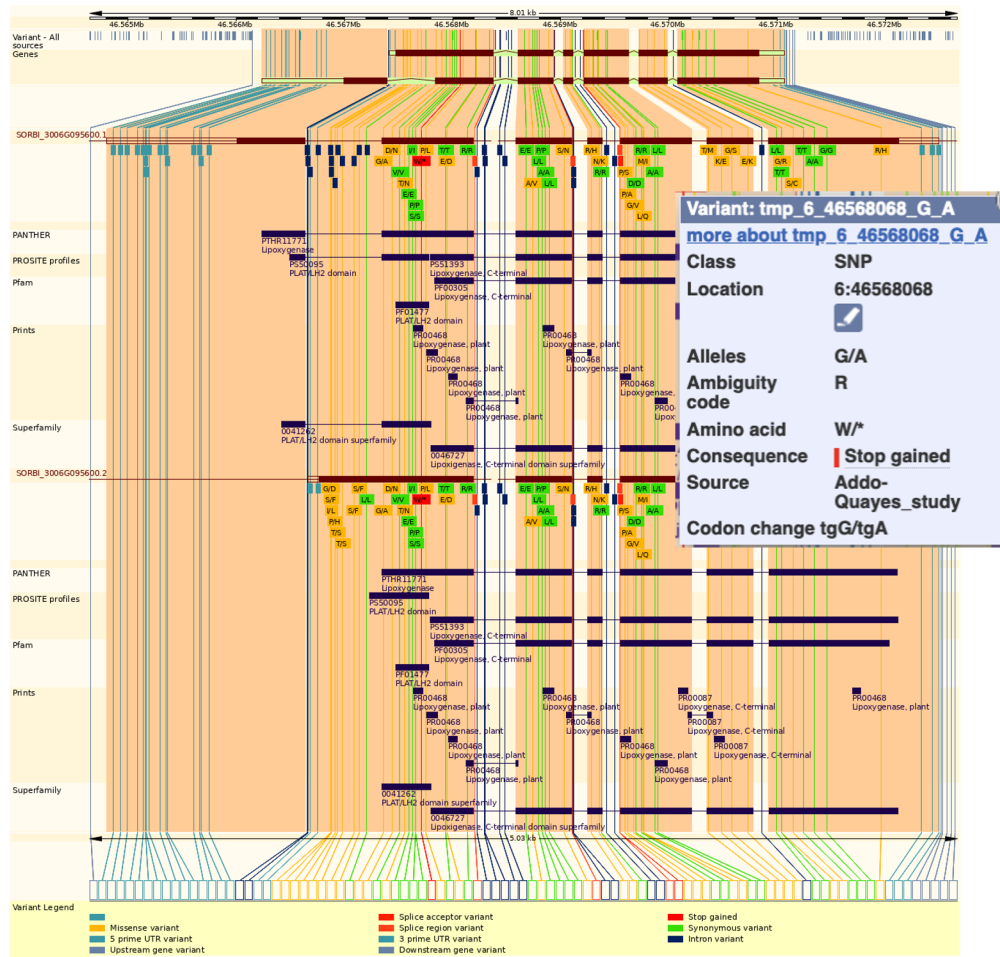
Gene Legend

Protein Coding  protein coding

Configuring the display

Tip: use the "Configure this page" link on the left to show additional data in this region.

Variant Image: Find Disruptive SNPs in Gene Model



Variant Table: Filterable View for SNP



SORGHUM
BASE

BLAST Help Feedback Genome Browser Release Notes

Search Sorghumbase...



Sorghum bicolor ssp. bicolor BTx623 (Sorghum_bicolor_NCB1v3) Location: 3:69,827,192-69,830,766 Gene: SORBI_3003G385900 Trans: SORBI_3003G385900.1 Jobs

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- Ontologies
 - GO: Molecular function
 - GO: Biological process
 - GO: Cellular component
- Phenotypes
- Genetic Variation
 - Variant table**
 - Variant image
 - Structural variants
 - Gene expression
 - Regulation
 - External references
 - Supporting evidence
- ID History
 - Gene history
 - Gramene Search

Configure this page

Custom tracks

Export data

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Gene: SORBI_3003G385900

Description hypothetical protein
Location [Chromosome 3: 69,827,192-69,830,766](#) reverse strand.
About this gene This gene has 1 transcript ([splice variant](#)), [39 orthologues](#) and [11 paralogues](#).
Transcripts [Show transcript table](#)

Variant table

Variant table ✕
This table shows known variants for this gene. Use the 'Consequence Type' filter to view a subset of these.

Filter ✕ SIFT: All ✕ Consequences: Splice acceptor vari...(5/26) ▼ Filter Other Columns

Show/hide columns								Search...	
Variant ID	Chr: bp	Alleles	Class	Source	Conseq. Type	AA	AA coord	Transcript	
tmp_3_69827957_C_T	3:69827957	C/T	SNP	USDA_Lubbock_EMS	Stop gained	W*	677	SORBI_3003G385900.1	
tmp_3_69827964_G_A	3:69827964	G/A	SNP	USDA_Lubbock_EMS	Stop gained	Q*	675	SORBI_3003G385900.1	
tmp_3_69828296_G_C	3:69828296	G/C	SNP	SAP_Boatwrigth_t_study	Stop gained	Y*	591	SORBI_3003G385900.1	
tmp_3_69828503_C_T	3:69828503	C/T	SNP	USDA_Lubbock_EMS	Stop gained	W*	522	SORBI_3003G385900.1	
tmp_3_69829703_G_A	3:69829703	G/A	SNP	USDA_Lubbock_EMS	Stop gained	Q*	196	SORBI_3003G385900.1	
tmp_3_69830063_C_T	3:69830063	C/T	SNP	USDA_Lubbock_EMS	Stop gained	W*	107	SORBI_3003G385900.1	
tmp_3_69830123_C_T	3:69830123	C/T	SNP	USDA_Lubbock_EMS	Stop gained	W*	87	SORBI_3003G385900.1	
tmp_3_69827422_C_G	3:69827422	C/G	SNP	Lozano_study	Missense variant	K/N	855	SORBI_3003G385900.1	
tmp_3_69827469_C_T	3:69827469	C/T	SNP	USDA_Lubbock_EMS	Missense variant	E/K	840	SORBI_3003G385900.1	
tmp_3_69827478_G_A	3:69827478	G/A	SNP	Addo-Quayes_study	Missense variant	R/C	837	SORBI_3003G385900.1	
tmp_3_69827492_G_A	3:69827492	G/A	SNP	Addo-Quayes_study	Missense variant	P/L	832	SORBI_3003G385900.1	

Coordinating With EVA For Stable Variant IDs



- Collect and centralize data, easy to find, share, organize, maintain (FAIR)
- Reduce redundancy, stable unique identifier for each unique genetic locus
- Crosslink to other data archival resources
- NCBI dbSNP & EVA provided 'ss' & 'rs' identifiers for human and non human species

Identifier type	Example	Description
-----------------	---------	-------------

ssID	ss335	Submitted SNP ID assigned by dbSNP or EVA.
------	-------	--

rsID	rs334	Reference SNP ID assigned by dbSNP or EVA. ssIDs of the same variant type that colocalise are combined to give an rsID for that locus.
------	-------	--

Sorghum Community Mapping Panel Working Group

- Develop a domestic provider for genotyping US sorghum germplasm
- We have finished probe design
- Currently in validation phase (breeding material, populations, and landraces)
- Anticipate creation of PlexSeq array in ~6 months (AgriPlex)
- Final array marker selection based on feedback from breeders with most useful markers for US breeding germplasm

SorghumBase Has Community Curation Functions

Sorghum bicolor ssp. *bicolor* BTx623

SORBI_3001G394400

Sb01g037340, Sobic.001G394400

similar to Phytochrome B

Location Expression Homology Pathways Papers Xrefs

Model Species Homolog

PHYB *Arabidopsis thaliana*

Phytochrome B

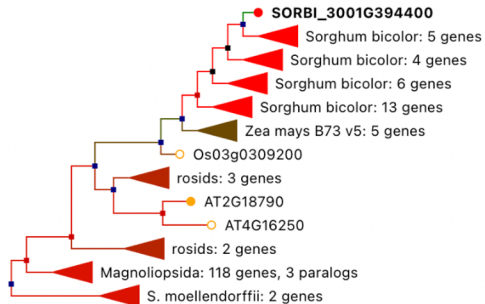
Compara Gene Tree

This phylogram shows the relationships between this gene and others similar to it, as determined by Ensembl Compara.

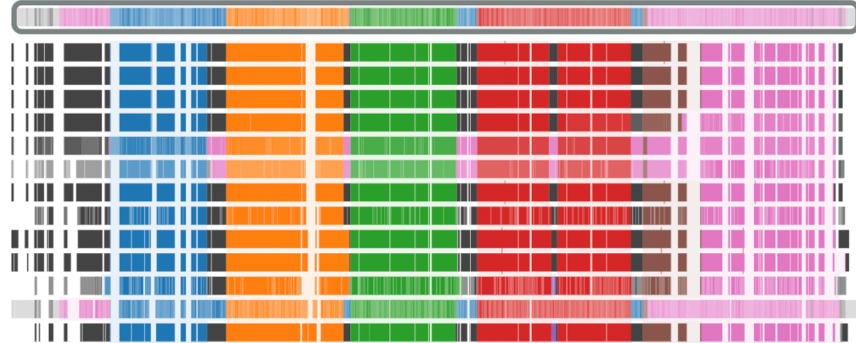


DISPLAY MODE

COLOR SCHEME



Alignment overview: Proteins color-coded by InterPro domain. Resize slider to navigate.



Search Filters

GENE TREE | HOMOLOGS 162

GENE TREE | ORTHOLOGS 41

GENE TREE | PARALOGS 4

Links to other resources

- [Ensembl Gene Tree view](#)
- [Curate](#)

Gene Tree Triage Interface

This is the gene tree containing **SORBI_3001G394400**. Description: **similar to Phytochrome B**.

Curation Instructions

Mark genes as okay or flag genes that you think might have issues and choose a reason from the drop down menu. When finished, enter your email address and submit.

The reason for flagging a gene model is optional, but you may indicate whether there is a gain (G), loss (L) or no change (__) in the beginning, middle, and end of the gene model.

For example **L,_,_** means there is a loss at the 5' end.

Display Mode

Alignment overview: Proteins color-coded by InterPro domain. Resize slider to navigate.

Curate: click to flag genes

okay flag

okay

okay

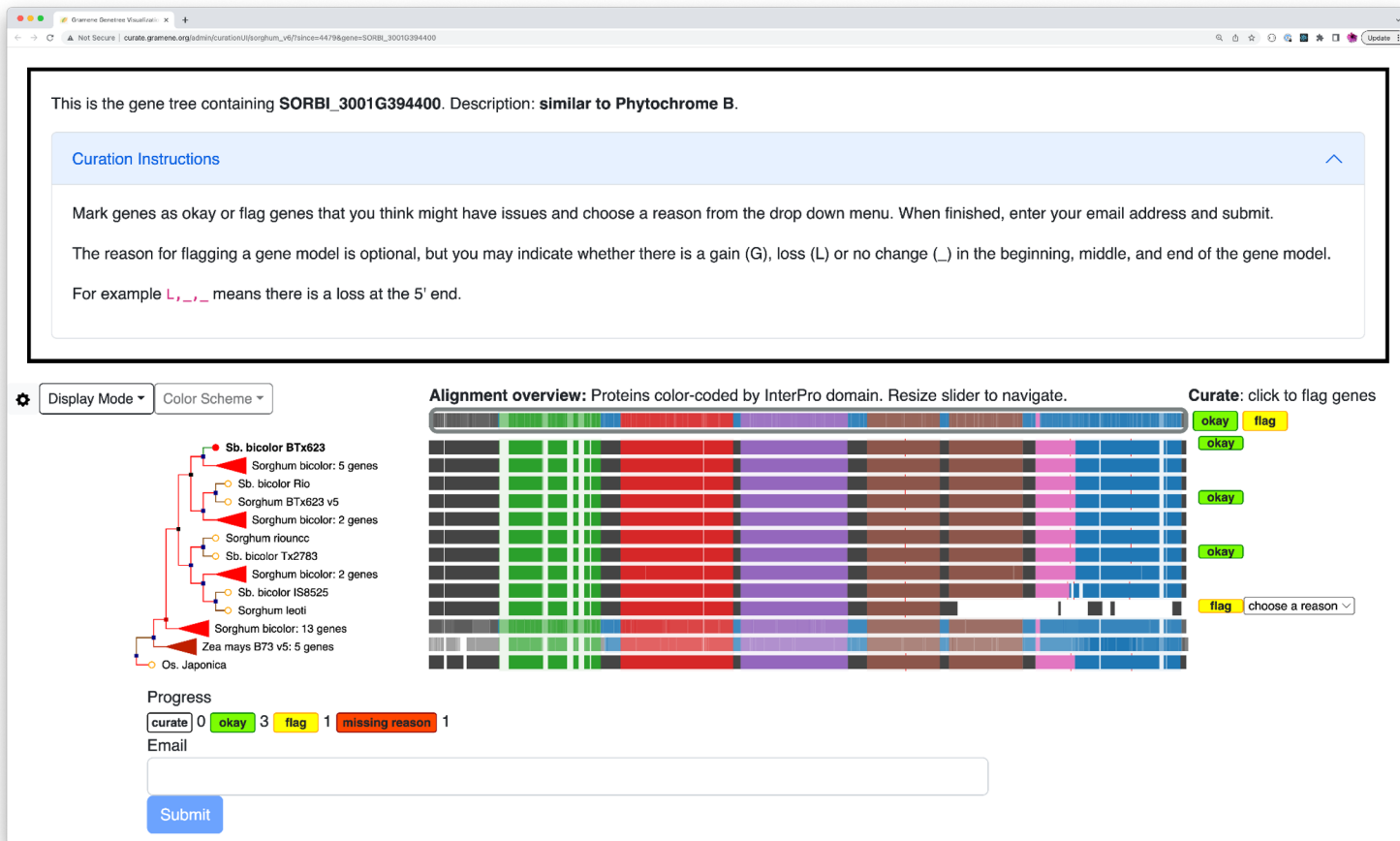
okay

flag choose a reason

Progress

curate 0 okay 3 flag 1 missing reason 1

Email



Student curators

Apollo



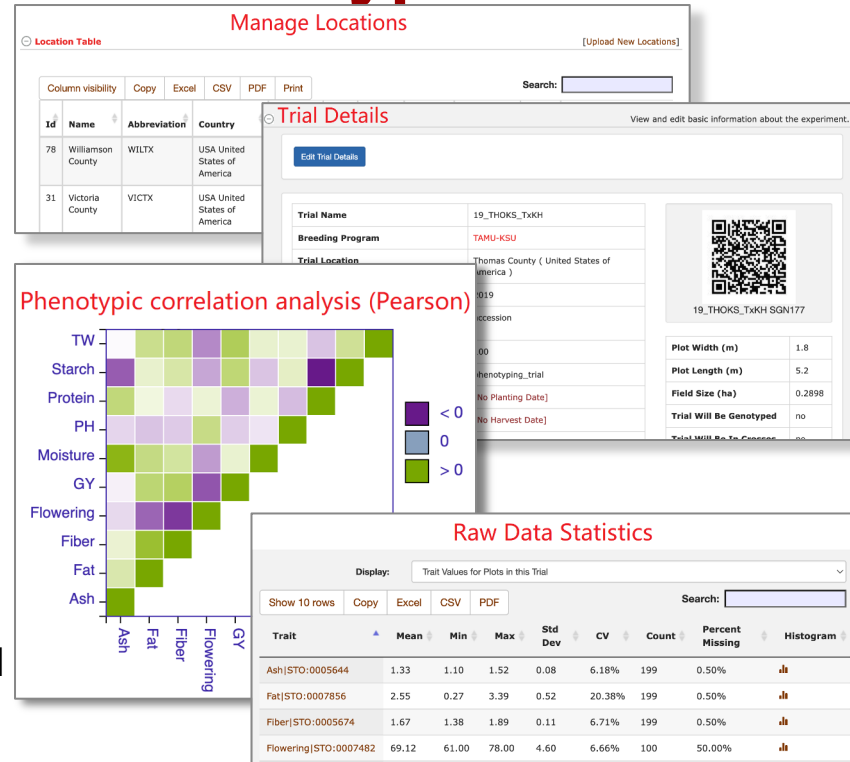
Updated genes

Release updates



Supporting Breeding and Phenotype Data

- Evaluating use of BreedBase to host sorghum data
- Web-based portal for sorghum breeders, researchers, and stakeholders
- Integrates phenotypic data management and breeding tools
- **Phenotype and Breeding datasets:** Pedigrees, Field Trials, Phenotypes, Genotyping Trials, Germplasm Accessions and Lots, Image/Spectral Datasets, etc.
- **Analysis Workflows:** GWAS, Genomic Prediction, Linear Mixed Modeling, Population Structure (PCA), and Kinship and Clustering



Future Plans for 2023-2024

- 3-4 releases per year
 - Extend current data types while adding new functionality
- Stable identifiers for genetic variation (rsIDs)
- Direct access to GRIN germplasm genotypes
- Continued evaluation of BreedBase to support management of phenotype and breeding data
- Finish community mapping panel and coordinate with working group towards phenotype data standards

Community Engagement Is Our Priority!

contact@sorghumbase.org

- Mailing list
 - Visit www.sorghumbase.org to join!
- Events (<https://www.sorghumbase.org/events>)
- Training guides and videos (<https://www.sorghumbase.org/guides>)
- **1-on-1 training is always available**
- Training opportunities
 - Navigating and using website
 - Community curation of gene structure
 - Metadata and sample submission
 - Content management system
- Working Groups
 - Community Mapping Panel, Reference Genomes
 - Phenotype (future working group)

Community Collaborators



THE UNIVERSITY
OF QUEENSLAND
AUSTRALIA



GIFS

Growing science for life

CLEMSON
UNIVERSITY

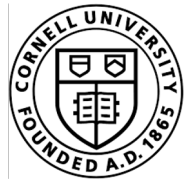


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Service

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SorghumBase Team



Nick Gladman
Leadership



Doreen Ware
Leadership



Kapeel Chougule
Genome Annotation
& Data Resources



Marcela K. Tello-Ruiz
Communication &
Data Resources



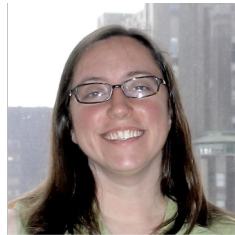
Andrew Olson
Architecture &
Infrastructure



Sunita Kumari
Communication &
Data Resources



Zhenyuan Lu
Workflows &
Data Resources



Audra Olson
Communication



Vivek Kumar
Infrastructure &
Data Resources



Peter Van Buren
Systems Engineer



Sharon Wei
Infrastructure &
Data Resources

Acknowledgements

Ware Lab 2023



Presence @ ASPB 2023:

- Bioinformatics Workshop - Organizer: Sunita Kumari
 - Gramene by Sunita Kumari
 - SorghumBase by Nick Gladman
- Posters:
 - **#500-08**: Gramene
 - **#700-09**: SorghumBase
 - **#800-56**: DAP-seq - Audrey Fahey
 - **#500-24**: NUE GRN - Janeen Braynen
 - **#1100-19**: QPSI - Sunita Kumari
 - **#800-64**: GRAS TFs - Nick Gladman

We gratefully acknowledge support from USDA-ARS-8062-21000-041-00D



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