



# SORGHUMBASE.

## Summer Newsletter • August 2026

Quarterly Community Update | April – July 2026

Welcome to the Summer 2026 edition of the SorghumBase newsletter! This quarter brought new platform features, notable publications, and a busy calendar of community activity – here are the highlights.

**86** new papers • **11** research highlights • **13** news items • **24** community events

**New on the site:** TBrowse gene tree viewer, expression visualization, gene attributes, ontology enrichment, and user gene lists with data export.

**In the works:** Release 11 – four new and five updated genome annotations – plus 15 new curated RNA-seq expression studies

Over the last few months the SorghumBase team has rolled out several new features across the website

- **AlphaFold** protein structures with SIFT scores are now available in the SorghumBase EnsEMBL genome browser.
- **User gene lists** and the **data exporter** extend the gene search interface, making it easy to create and share gene lists and export a wide range of gene attributes.
- **Expression visualization**: Select any set of baseline expression samples to build customized expression profiles for the genes in your search results, displayed as a heatmap or parallel-coordinates plot paired with a data table. Dragging along the sample axes of the parallel-coordinates plot creates expression-based filters.
- **Gene attributes**: A dynamic table displays up to 5,000 genes from the current search, with prototype attributes that summarize expression by tissue and flag stress conditions under which each gene is activated or repressed. These attributes can also be applied as search filters.
- **Ontology enrichment**: Identifies ontology terms and other hierarchical controlled-vocabulary annotations that are statistically overrepresented in your search results.
- **TBrowse**: Our new viewer for gene trees, species trees, and associated data now powers the taxonomic distribution of gene search results and is the default gene-tree viewer in the Homology tab. More interactive than the previous TreeViz, it supports pruning and regrowing branches, swapping child nodes, filtering the tree with a query string, and customizing the layout of each display zone..

Watch demonstrations of TBrowse and the other new features at

<https://sorghumbase.org/videos>

## SorghumBase Release 11

SorghumBase Release 11 is in preparation and will deliver four new and five updated genome annotations, refreshed protein-coding gene trees, and additional gene search features.

## Expanded Gene Expression Resources

In collaboration with the EMBL-EBI Expression Atlas, we have prioritized 15 new RNA-seq studies for curation, validation, and configuration for baseline and differential expression analysis. New in final quality control, these datasets will be released through the Expression Atlas and then integrated into the SorghumBase Expression portal – giving the community high-quality, FAIR-compliant expression data across a wide range of tissues, developmental stages, genotypes, and experimental conditions, linked directly to SorghumBase gene pages.

**86 papers added to the database**

**Browse publications**

**11 research highlights published**

**Read the highlights**

**13 news items posted**

**Catch up on the news**

**24 events community events listed**

**See upcoming events**

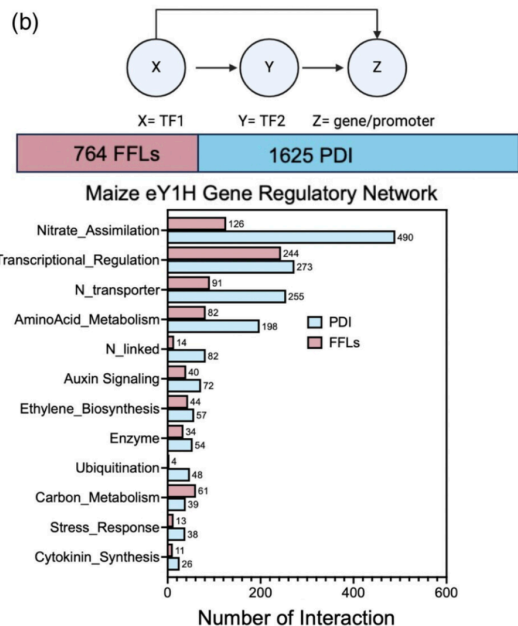


Research Highlight

## **A Global Sorghum Pangenome Reference Reveals Genetic Variation Underlying Adaptation and Crop Improvement**

[READ POST](#)

(a) **Maize eY1H Gene Regulatory Network**



Gene regulatory network analysis revealed the transcription factor interactions and conserved network motifs that control nitrogen uptake and metabolism in maize. Read more at [SorghumBase](#).

### More Publications from the Team

In collaboration with the Plant Cell Atlas team, Dr. Sunita Kumari and Dr. Doreen Ware co-authored “A Single-Cell Blueprint for Cellular Diversity in the Green Lineage,” a review published in *Current Biology* that examines how comparative single-cell approaches are revealing the gene regulatory networks and evolutionary mechanisms behind cellular diversity – and the key challenges and opportunities for building comprehensive plant cell atlases for fundamental biology and crop improvement.

Coate JE, Doyle JJ, Farmer A, Huang SC, Kajala K, Kenchanmane Raju SK, Kumari S, Palfalvi G, Radin I, Singh P, Stata M, Ware D, Yao Q, Nikolov LA. A single-cell blueprint for cellular diversity in the Green Lineage. *Current Biology*. 2026 Jun 8;36(11):R577-R589. doi: 10.1016/j.cub.2026.04.003.

Scientists from Cold Spring Harbor Laboratory, EMBL-EBI, USDA-ARS, and partner institutions in the AgBioData consortium demonstrated the value of standard reference SNP identifiers (rsIDs) for agricultural genomics, anchored by the submission of 47 million sorghum and 10 million soybean variants to the European Variation Archive. Standardized rsIDs allow variants generated on different assemblies and genotyping platforms to be harmonized across studies, and they improve interoperability with functional prediction tools, pan-genome resources, and breeding platforms. The authors outline practical adoption strategies — seeding variant catalogs from existing GWAS datasets, lightweight annotation workflows, and FAIR-compliant submission guides — while noting remaining challenges around legacy SNP nomenclature, polyploid and under-studied crops, and breeder-facing software. Widespread rsID adoption is a foundational step toward FAIR agricultural genomics, enabling long-term data reuse, large-scale meta-analysis, and more efficient use of genomic information in crop improvement.

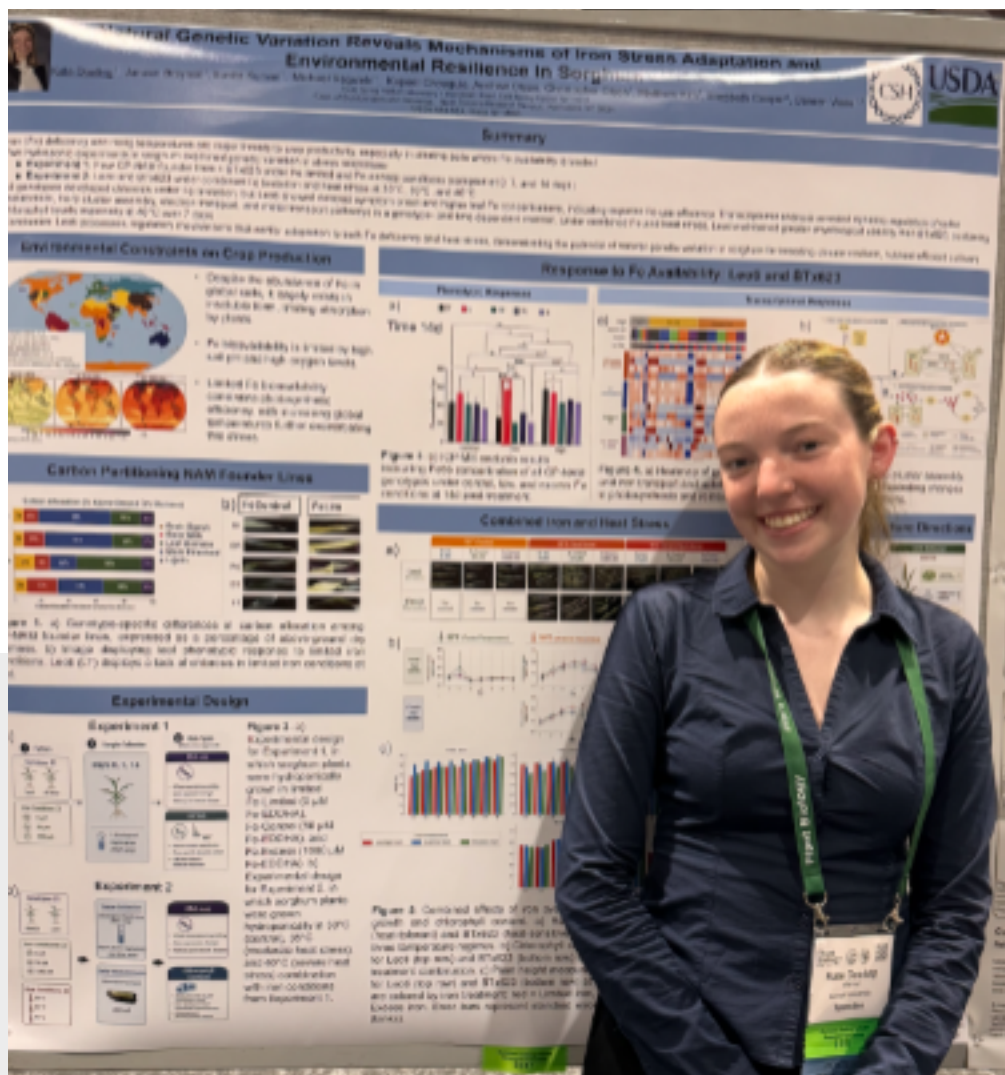
Tello-Ruiz MK, Cezard T, Andorf C, Balyan S, Bassil NV, Beier S, Bushakra JM, Chang TH, Chougule K, Cobo-Simón I, Dyer S, Elisk CG, Gladman N, Harrison M, Humann J, Kim C, Kumar V, Nandety RS, Nelson R, Olson A, Sen TZ, Sheehan MJ, Wei S, Ware D. (2026) Adoption of Standard Reference SNP Identifiers in Agricultural Genomics for Interoperability and Data Reuse. *Scientific Data*. doi:10.1038/s41597-026-07208-0.

SorghumBase team members Dr. Doreen Ware, Dr. Sunita Kumari, and Kate Dooling joined more than 1,200 plant scientists, educators, and students at the ASPB/CSPB Plant Biology 2026 meeting in Ottawa, Canada. Through a workshop, exhibit booth, and poster presentations, the team showcased SorghumBase and Gramene as community-driven, FAIR, and AI-ready plant genomics resources, presented research on iron stress adaptation in sorghum, and built new collaborations across the global plant science community.

Drs. Ware and Kumari also took part in the 2026 Plant Cell Atlas (PCA) Core Network Participant Meeting at the Donald Danforth Plant Science Center in St. Louis, Missouri, which reviewed five years of achievements by the PCA Research Coordination Network, set priorities for the Year 6 extension, and addressed the initiative's long-term sustainability. They contributed to discussions on community collaboration, data standards, and FAIR, interoperable resources for single-cell plant genomics.



AgBioData consortium presenters, including Drs. Doreen Ware and Sunita Kumari, at the ASPB/CSPB Plant Biology 2026 meeting in Ottawa.



Kate Dooling, presenting on iron stress adaptation in sorghum

The ASPB Northeastern Section meeting gave early-career scientists a chance to connect with collaborators and spark new research questions, featuring 15 oral and 34 poster presentations from high school students through professors, plus keynotes by Dr. Hong Ma, on the control of RNA splicing and exon–intron structure across angiosperms, and Dr. Guillermo Jimenez-Aleman, on fatty acids and a dual defense mechanism in plants. The Ware lab took home both postdoctoral talk awards: Dr. Janeen Braynen won first place for “Integrating Transcriptomics and Ionomics to Dissect Iron Use Efficiency and Heat Stress Responses in Sorghum,” and Dr. Lydia Tressel took second place for “Pre-domestication Dynamics of a Key Regulator Gene for Seed Dormancy in Barley.”



Award winners Dr. Janeen Braynen and Dr. Lydia Tressel with colleagues at the ASPB Northeastern Section meeting.

Dr. Nick Gladman represented SorghumBase at the National Association of Plant Breeders annual meeting in College Station, Texas — an excellent showcase for the advances of US crop breeders and for the resources that Gramene and SorghumBase offer them. In his keynote, USDA REE Under Secretary Dr. Scott Hutchins outlined agency priorities, including genotyping and phenotyping the seed collections of the National Plant Germplasm System.

## Meet the SorghumBase Team at the Global Sorghum Conference

Join us at the Global Sorghum Conference, September 14–18, 2026, at Texas Tech University in Lubbock, Texas. This international event will showcase sorghum's role as *The Resource Conserving Crop™* through scientific presentations, networking, and field tours. Kick off the conference at our workshop on **September 14, “Discover, Connect, and Contribute: Exploring SorghumBase Resources for the Global Sorghum Community,”** where the team will share updates on community data resources and gather your feedback. And stop by the SorghumBase booth to meet the team, explore the latest features, and talk through your research — whether you'd like to submit data, access genomic and phenomic resources, or learn how SorghumBase can support your work. We're happy to arrange one-on-one discussions during the conference.

### GET INVOLVED

Submit your work for a SorghumBase Research Highlight

Meet the team at the Global Sorghum Conference

Contact us to contribute gene function, expression, or genetic variation data

### QUICK LINKS

[SorghumBase Home](#)[Release Notes](#)[Research Highlights](#)[Publications](#)[Contact Us](#)

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