COTTONGEN

COTTON DATABASE RESOURCES

April 2026

Welcome to the 2nd issue of the CottonGen newsletter in 2026. This newsletter is issued to inform users about **new or updated data and tools in CottonGen**. In addition to new and updated data, each issue will provide more information on data or tools in **the featured tools/data** section.

What's New in CottonGen?

Short video tutorials – BIMS

- How to make customized columns in BIMS templates (*2:09 min*): Describes how to make customized columns in templates, such as phenotype, accession, cross, and package, and how to search data using the custom categories.
- How to import image data in BIMS (*2:41 min*): Learn how to import image files of specific phenotypic samples.

Whole Genome Data

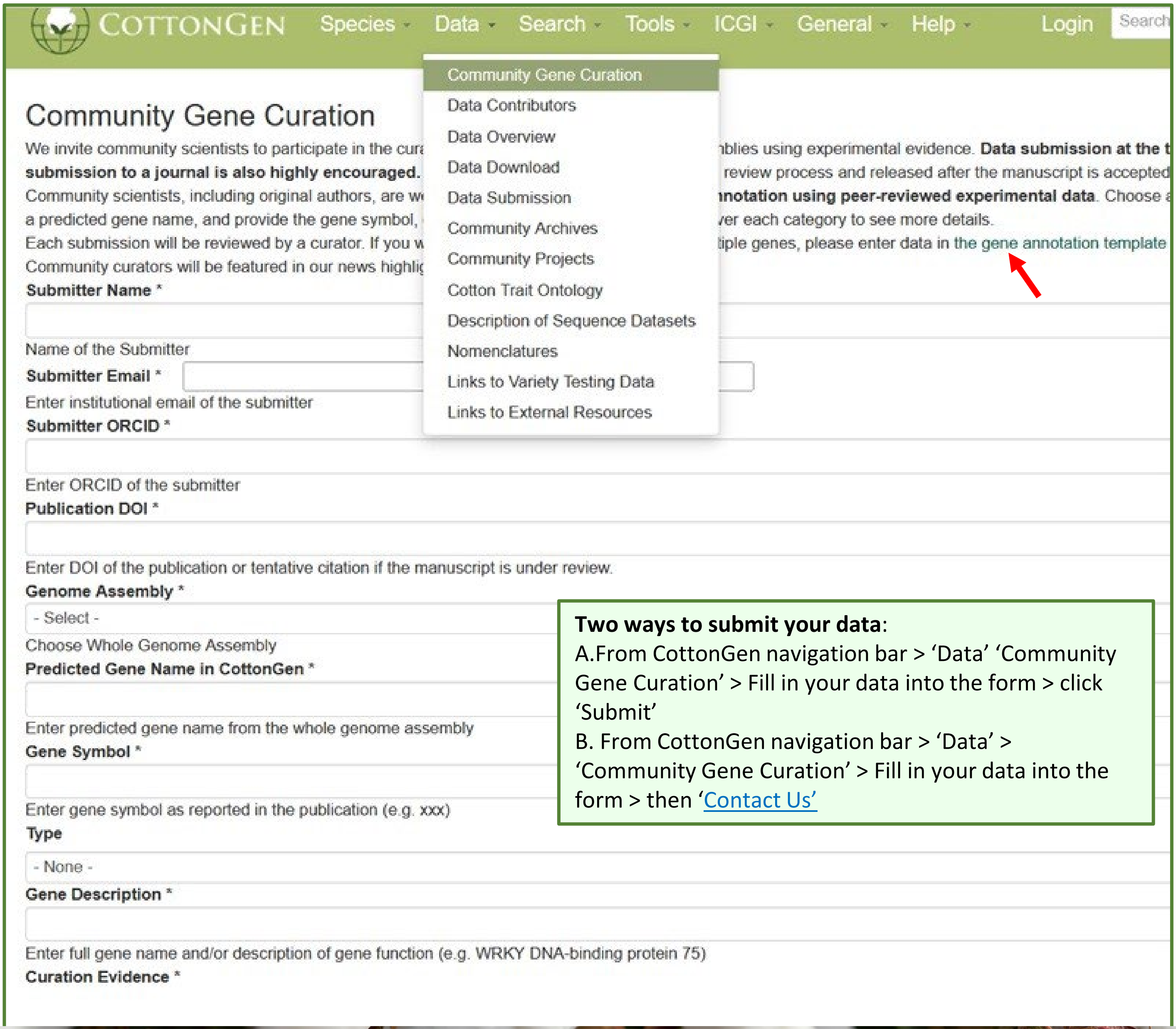
- *Gossypium arboreum* (A2) 'ZB-1' genome ZSTU_v1 (Sun R, *et al.* Scientific Data.)
- The CottonGen Team has added functional annotations, marker sequence alignments, within CottonGen's tools of BLAST, JBrowse, and Synteny Viewer.

Other New Data

- The authors re-sequenced 336 G. barbadense accessions and identified 16 million SNP and conducted a genome-wide association study (GWAS) of 15 traits including fiber quality, yield, disease resistance, maturity, and plant architecture. *(Zhao N, et al. Genomic and GWAS analyses demonstrate phylogenomic relationships of Gossypium barbadense in China and selection for fiber length, lint percentage, and Fusarium wilt resistance.)*
- A multi-parent advanced generation inter-cross (MAGIC) population of 550 recombinant inbred lines (RILs) together with their 11 Upland cotton parents with a total of 473,516 polymorphic SNP markers was used to identify quantitative trait loci (QTL) for drought tolerance (DT) and salt tolerance (ST) at the seedling stage based on two replicated greenhouse tests. *(Abdelraheem A, et al. GWAS reveals consistent QTL for drought and salt tolerance in a MAGIC population of 550 lines derived from intermating of 11 Upland cotton (Gossypium hirsutum) parents.)*
- A genome-wide as-sociation study of 5 fiber quality traits across multiple field environments identified a total of 512 qtls (main-effect QTLs) and 94 qtlEs (QTL-by-environment interactions) related to fiber quality, of which 292 qtls and 57 qtlEs colocated with previous studies. *(Song X, et al. Combined genome and transcriptome analysis of elite fiber quality in Gossypium barbadense.)*
- A linkage map harboring 192 SSRs was constructed from the CRI-G6 population (Acala 1517 × Dezhou 047) using mixed-model-based composite interval mapping (MCIM) method. The map was used to detect quantitative trait loci (QTLs) associated with cotton yield traits in 3 environments. *(Zhao N, et al. QTL Analysis on Yield and Its Components in Recombinant Inbred Lines of Upland Cotton.)*

You are invited to Join the Community Gene Curation

We invite community scientists to participate in the curation of genes from whole genome assemblies using experimental evidence. Data submission at the time of manuscript submission to a journal is also highly encouraged. The data will be held privately during the review process and released after the manuscript is accepted for publication. Below shows how to send your ‘Gene Curation’ data.



Community Gene Curation

We invite community scientists to participate in the cura … nblies using experimental evidence. **Data submission at the t**
submission to a journal is also highly encouraged. … review process and released after the manuscript is accepted
Community scientists, including original authors, are w … **nnotation using peer-reviewed experimental data**. Choose a
a predicted gene name, and provide the gene symbol, … ver each category to see more details.
Each submission will be reviewed by a curator. If you w … tiple genes, please enter data in the gene annotation template
Community curators will be featured in our news highlig

Submitter Name *

Name of the Submitter

Submitter Email *

Enter institutional email of the submitter

Submitter ORCID *

Enter ORCID of the submitter

Publication DOI *

Enter DOI of the publication or tentative citation if the manuscript is under review.

Genome Assembly *

- Select -

Choose Whole Genome Assembly

Predicted Gene Name in CottonGen *

Enter predicted gene name from the whole genome assembly

Gene Symbol *

Enter gene symbol as reported in the publication (e.g. xxx)

Type

- None -

Gene Description *

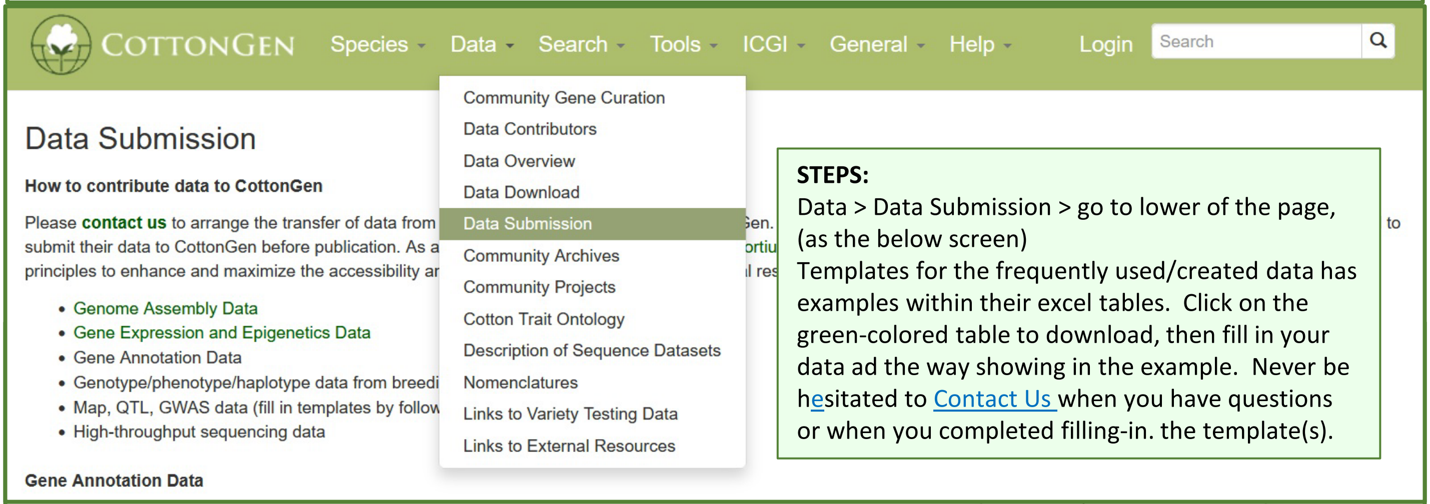
Enter full gene name and/or description of gene function (e.g. WRKY DNA-binding protein 75)

Curation Evidence *

Two ways to submit your data:
A.From CottonGen navigation bar > ‘Data’ ‘Community Gene Curation’ > Fill in your data into the form > click ‘Submit’
B. From CottonGen navigation bar > ‘Data’ > ‘Community Gene Curation’ > Fill in your data into the form > then ‘Contact Us’

Submit Other Types Data

With new publications appearing almost daily, direct submission accelerates the curation process compared to manual extraction from journals. Submit data at the time of manuscript submission to a journal is also highly encouraged. Below lists the templates for all different types of data, some of them with filled in example to show how to fill in data there.



Data Submission

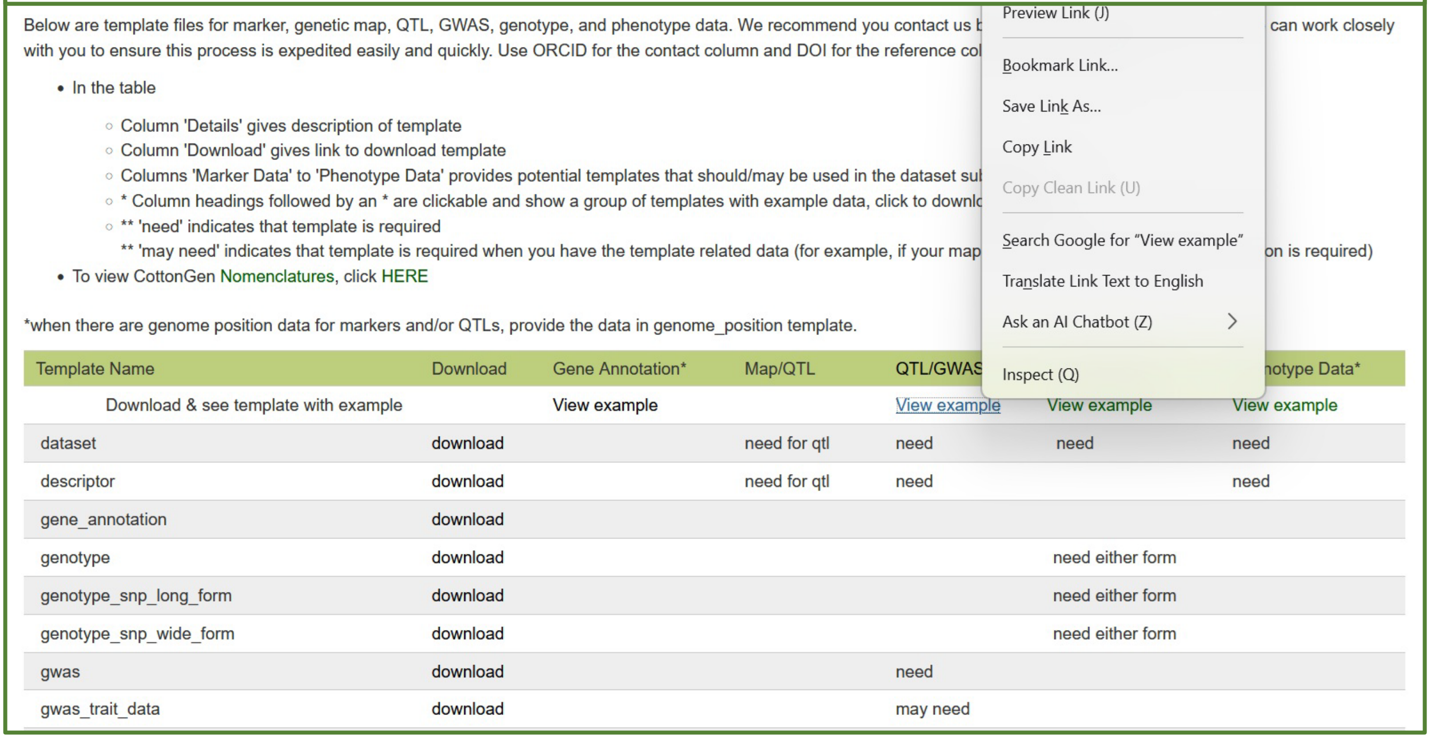
How to contribute data to CottonGen

Please **contact us** to arrange the transfer of data from … Gen. … to submit their data to CottonGen before publication. As a … ortiu … principles to enhance and maximize the accessibility ar … l res

- Genome Assembly Data
- Gene Expression and Epigenetics Data
- Gene Annotation Data
- Genotype/phenotype/haplotype data from breedi
- Map, QTL, GWAS data (fill in templates by follow
- High-throughput sequencing data

Gene Annotation Data

STEPS:
Data > Data Submission > go to lower of the page, (as the below screen)
Templates for the frequently used/created data has examples within their excel tables. Click on the green-colored table to download, then fill in your data ad the way showing in the example. Never be hesitated to Contact Us when you have questions or when you completed filling-in. the template(s).



Below are template files for marker, genetic map, QTL, GWAS, genotype, and phenotype data. We recommend you contact us b … can work closely with you to ensure this process is expedited easily and quickly. Use ORCID for the contact column and DOI for the reference col

- In the table
  - Column 'Details' gives description of template
  - Column 'Download' gives link to download template
  - Columns 'Marker Data' to 'Phenotype Data' provides potential templates that should/may be used in the dataset sul
  - * Column headings followed by an * are clickable and show a group of templates with example data, click to downlo
  - ** 'need' indicates that template is required
    ** 'may need' indicates that template is required when you have the template related data (for example, if your map … on is required)
- To view CottonGen Nomenclatures, click HERE

*when there are genome position data for markers and/or QTLs, provide the data in genome_position template.

Template Name	Download	Gene Annotation*	Map/QTL	QTL/GWAS		notype Data*
Download & see template with example		View example		View example	View example	View example
dataset	download		need for qtl	need	need	need
descriptor	download		need for qtl	need		need
gene_annotation	download					
genotype	download				need either form	
genotype_snp_long_form	download				need either form	
genotype_snp_wide_form	download				need either form	
gwas	download			need		
gwas_trait_data	download			may need		