Data Overview

**Genomes**: *G. raimondii* and *G. arboreum* genome sequence assemblies and functional. Annotations including genes, GO, InterPro, and KEGG assignments.

**Maps**: 49 maps with 34,559 loci covering cotton genome groups AD, A, D, and G.

**Markers**: Over 265,000 genetic markers consisting of 3,541 RFLPs; 78,340 SSRs and 183,035 SNPs

**Germplasm**: Over 15,000 germplasm including populations or individual entries identified from nearly 50,000 names obtained from 14 collections from the US Uzbekistan, and China.

**Traits**: 107,889 trait scores from USDA GRIN, China and Uzbekistan germplasm evaluations

**Images**: 12,269 digital images from the USDA-ARS National Cotton Germplasm Characterization Project

**Literature**: 15,425 articles from journals, conferences, book chapters, and theses.

Coming Soon ...

- **GBrowse-Syn**: view synteny between related genomes
- **The Cotton Breeders Toolbox**: search the national cotton variety trials data
- **Evaluation Data**: search the ARS College Station germplasm evaluation data
- **SNP Data**: more whole genome SNP data

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About CottonGen

CottonGen is the genomics, genetics and breeding database developed to facilitate basic, translational and applied research in cotton. It is built using the open-source Tripal database infrastructure, providing access to publicly available cotton data and tools for easy querying, visualizing and downloading of research data.

Providing a hub for community communication, CottonGen is fully integrated with the International Cotton Genome Initiative website. It maintains the ICGI membership database, information for the ICGI biennial international research conferences and biennial elections. CottonGen is developed by Mainlab Bioinformatics at WSU (www.bioinfo.wsu.edu).

**Tools**

- **BLAST**: Search for sequence similarity against all the publicly available cotton sequence databases.
- **CMap**: Search and view mapped genes, markers, and QTLs using Compare maps.
- **CottonCyc**: Browse the PlantCyc and KEGG pathway databases for cotton, using Pathway Tools and the JGI v2.0 *G. raimondii* genome gene models.
- **GBrowse and JBrowse**: Browse and search genes, markers, expressed sequences, etc. on *G. raimondii* (D5) and *G. arboreum* (A2) genomes using GBrowse or JBrowse.
- **Search Interfaces**: Search by gene, QTL, trait evaluation, marker, germplasm, publication.