



CottonGen, a Central Platform to Facilitate Knowledge Discovery in Cotton Research

www.cottongen.org



Jing Yu¹, Sook Jung¹, Chun-Huai Cheng¹, Taemin Lee¹, Ping Zheng¹, Katheryn Buble¹, Jodi L. Humann¹,

James Crabb¹, Heidi Hough¹, B. Todd Campbell², Don C. Jones³, Josh Udall⁴, and Dorrie Main¹

1. Washington State University, Pullman, WA, 2. USDA-ARS, Florence, SC, 3. Cotton Incorporated, Cary, NC, 4. USDA-ARS, College Station, TX

Abstract

CottonGen (www.cottongen.org) integrated significantly more data in 2019: New whole genome assembly data include those from 5 diploids (*G. arboreum*, *G. raimondii*, *G. turneri*, *G. austral*, *Gossypoides kirkii*) and 5 tetraploids (*G. hirsutum*, *G. barbadense*, *G. mustelinum*). Cotton sequences, curated from NCBI, has also been updated and now contains over 53K new genes and over 205K new proteins. Seven new (*G. arboreum*, *G. barbadense*, *G. turneri*, *G. kirkii*, *G. austral*, *G. mustelinum*) or updated (*G. hirsutum*) pathways are available from CottonCyc database. 282 cotton trait descriptors, developed from QTL publications and evaluation data, have been submitted to Crop Ontology (www.cropontology.org). Other new data added in 2019 include 8000 non-fiber traits and 5,000 new fiber trait data from RBTN, 321 QTLs, 594 QTL trait data, 2,230 SSR markers collected from peer-viewed publications. New and updated tools include the interactive and customizable search tool, MegaSearch and new functionalities including SNP genotype data management in BIMS.

Resources @CottonGen_news

Key Features

- Easy-to-use search interfaces for retrieving data on markers, genes, transcripts, sequences, QTLs, and traits
- JBrowse and Syntenic Viewer with genome comparisons with orthologs data
- MapViewer for interactive map viewing of genetic maps
- BIMS, Breeder Data Management and Analysis System
- Assembled and annotated reference transcriptome (RefTrans) which is searchable using BLAST
- PathwayCyc with eight species (5 diploids and 3 tetraploids)

Available Data

- 20 whole genome sequences for 8 diploid and 12 tetraploid cotton
- 575,844 genetic markers and 111 genetic maps
- 5,522 QTLs, 12,337 images, and 19,563 germplasm
- 25,227,605 genotype scores and 383,431 phenotype scores