CottonGen: A Central Data Repository and Analysis Resource for the Cotton Community
www.cottongen.org

Beltwide Cotton Conferences
January 10-12, 2023
New Orleans Marriott

WASHINGTON STATE UNIVERSITY
World Class. Face to Face.

Jing Yu[1], Sook Jung[1], Chun-Huai Cheng[1], Taein Lee[1], Ping Zheng[1], Katheryn Buble[1], James Crabb[1], Jodi Humann[1], Heidi Hough[1],

Don Jones[2], J. Todd Campbell[3], Josh Udall[4], Dorrie Main[1]

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

Abstract

CottonGen is a genomics, genetics and breeding database for the cotton community. It provides a comprehensive collection of data, various analysis tools, Breeding Information Management System, and links to external resources of interest to cotton researchers. CottonGen currently contains 55 (21 tetraploids and 33 diploids) annotated genome sequences; 5,725,571 genes/transcripts, 117 genetic maps; 690,386 markers; 7,436 QTLs; 20,177 germplasm; metabolic pathways for 13 species (AD1-AD5, A, B, D, E, F, G, K, and kirkii); 31,148,121 SNP and 14,284 SSR genotype measurements; 540,457 phenotype measurements (mainly from RBTN and NCGC projects), 45,155 images (mainly of NCGC); and synteny data for 53 genomes with links to genes, mRNA, orthologs and function. Analysis and visualization tools in CottonGen include the genome browser JBrowse, Synteny Viewer, MapViewer, CottonCyc, BLAST+, BIMS (the Breeding Information Management System), and MegaSearch, a powerful search engine, both with recently added new features and functions. All the data are integrated within CottonGen and can easily be queried through various CottonGen's search engines. In this presentation, examples of using CottonGen search engines to find marker/QTL/trait/Genome location and integration among them.

MegaSearch to find all markers that associate with seed cotton yield, have genetic map position on Chromosome 23, and identify their genomic locations.

Step1. Go to CottonGen's MegaSearch, select 'Data Type' = Marker

View Search Result. Genome locations are hyperlinked to a genome browser. In example below, click on green text at red arrow, then its genome location in JBrowse view appears above

Step2. In sections of 'Genetic Position' and 'Trait', select 'Standardized Linkage Group' and 'Trait' of interest (red arrows), then from 'Downloadable Field', select contents that you want to 'View' or 'Download'

Download Search Result. Click on 'CSV' to download data as comma-separated values table (below).

BIMS to store, manage, archive and analyze public or private breeding data (genotype/phenotype/germplasm)

Choose a program or a trial to view stats for each trait

Select trials and compare their trait measurements

Search specific region of micronaire and save the result

BIMS ONLINE WORKSHOP WILL BE SCHEDULED, WE WILL SEND OUT A NOTICE SOON

Acknowledged with Thanks

cotton COTTON INCORPORATED · USDA ARS · Bayer CropScience · CORTEVA agriscience · SAAESD · NRSP10 CROP DATABASE RESOURCES · The Cotton Research Community