CottonGen: Updates to the Cotton Community Database for Genomics, Genetics and Breeding Research

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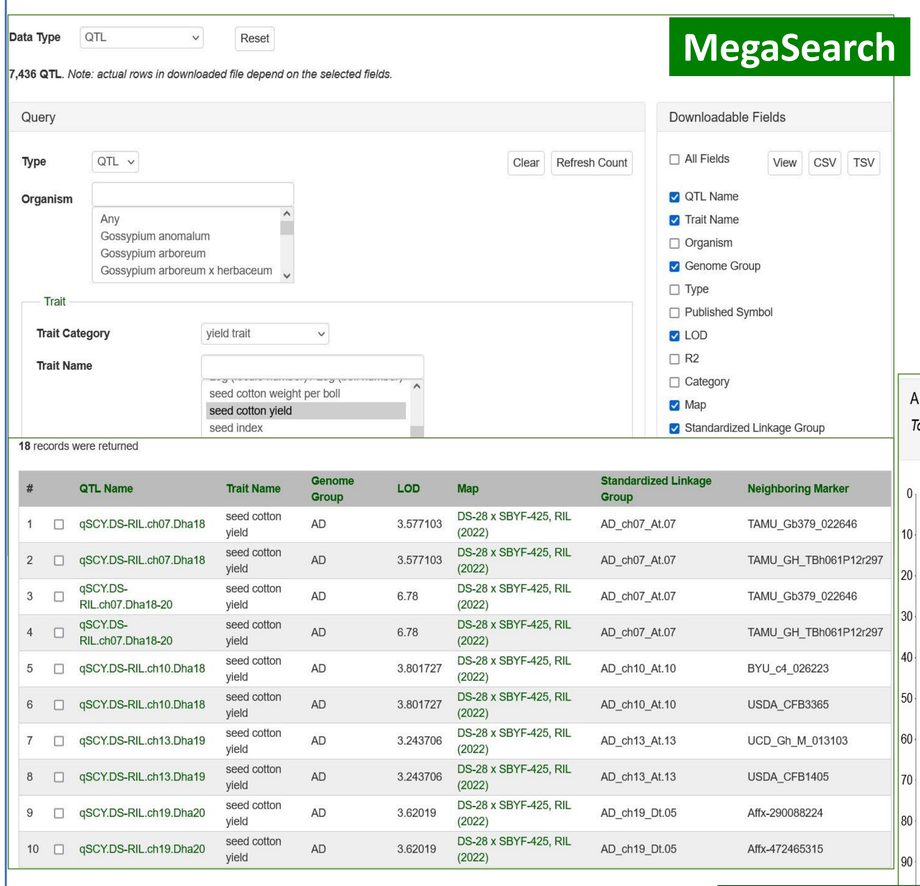
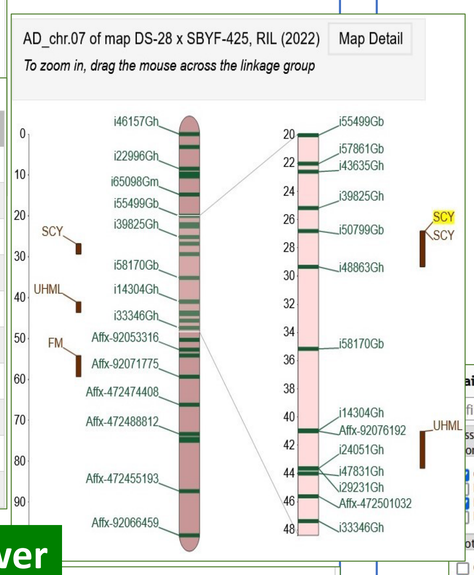
ABSTRACT

Established in 2012 through a merger of CottonDB and the Cotton Marker Database, CottonGen is the established genomics, genetics and breeding database for the cotton community. It provides a comprehensive collection of data, various analysis tools, Breeding Information Management System (BIMS), and links to external resources of interest to cotton researchers. CottonGen currently contains 53 (21 tetraploids and 33 diploids) annotated genome sequences; 5,725,571 genes/transcripts, 117 genetic maps; 665,269 markers; 7,199 QTLs; 20,187 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; 540,171 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, and MegaSearch, a powerful search engine, both with recently added new features and functions. All the data are integrated within the database and can easily be queried through its various search engines. Serving as a portal for communication, CottonGen also houses all ICGI information for the community.

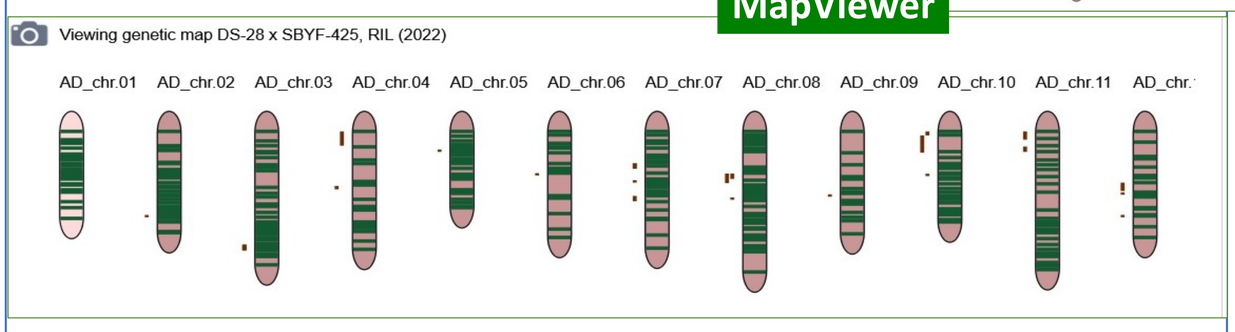
GENETIC TOOLS



- New MegaSearch interfaces for map, marker and QTL searches and data downloads
- MapViewer tool to view and interact with genetic maps

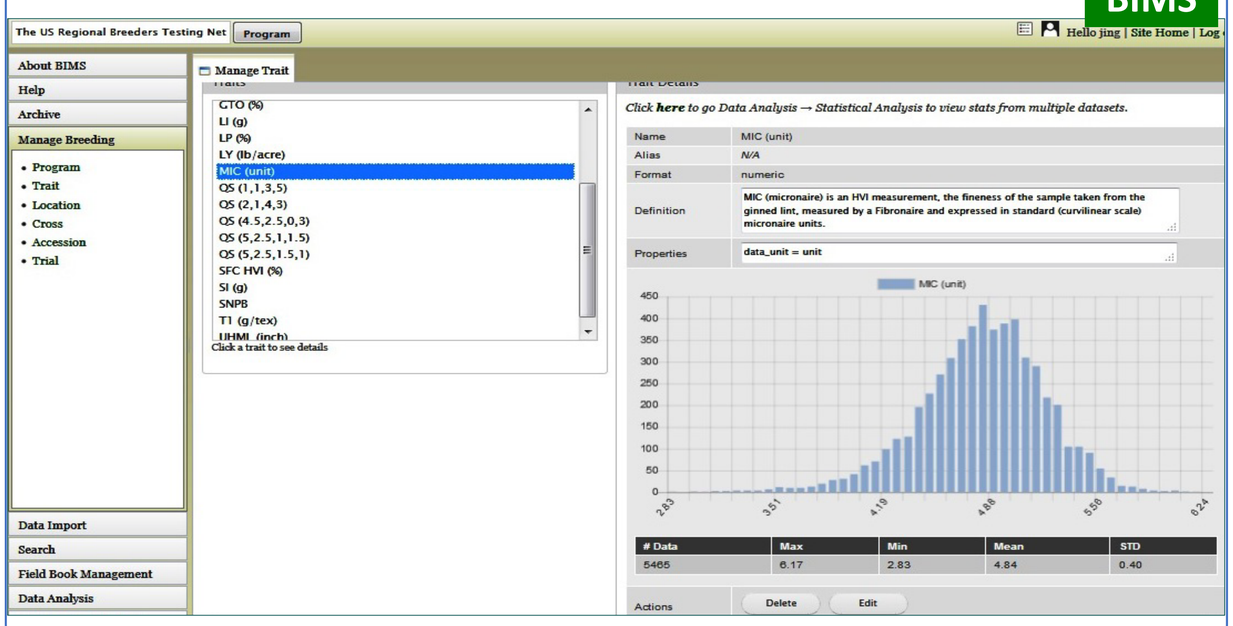


MapViewer



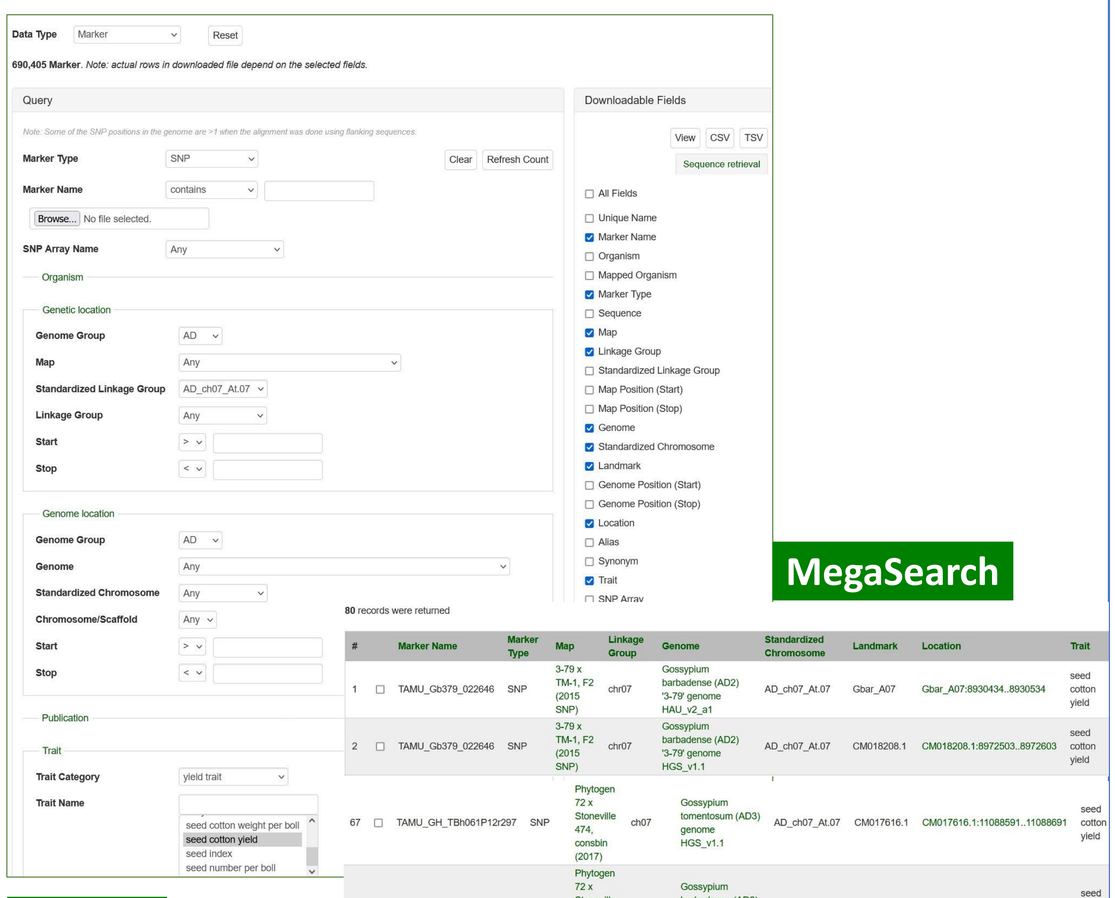
BREEDING TOOLS

- Breeding Information Management System (BIMS) available to breeders through CottonGen
- Allows to store, manage, archive and analyze public or private breeding data
- Multiple users can manage each program and upload data
- Compatible with Android app Field Book for electronic data collection and with BrAPI
- comparable with public data



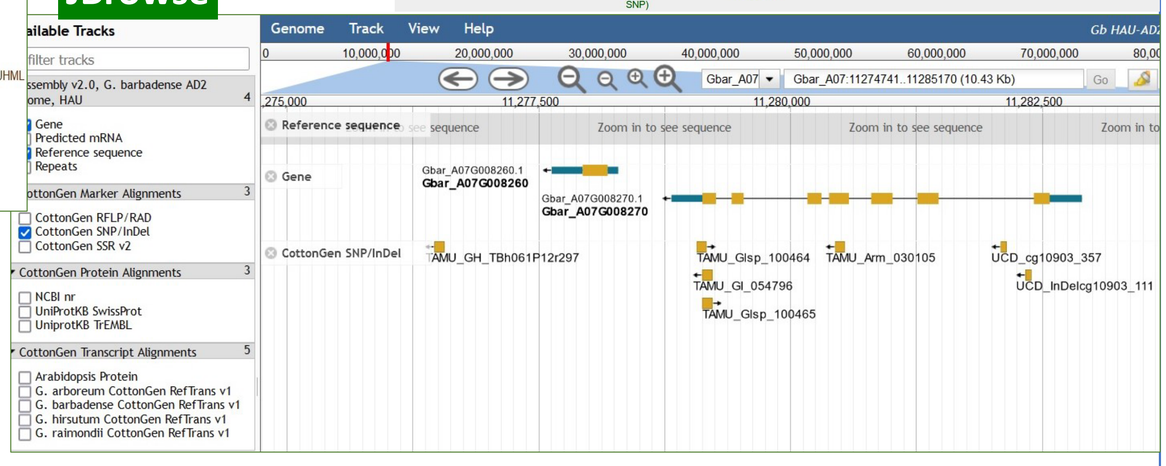
GENOMIC TOOLS

- Genome sequences available to search using BLAST tool and mRNA and genes can be searched using MegaSearch
- JBrowse displays the genome assemblies with links to more information about gene, mRNA, marker, and transcript features
- Explore the metabolic pathways of genomes and overlay transcriptomics and metabolomics data using PathwayCyc tool
- Synteny Viewer to view genome syntenic blocks and Ortholog/Paralog MegaSearch as another way to explore the data

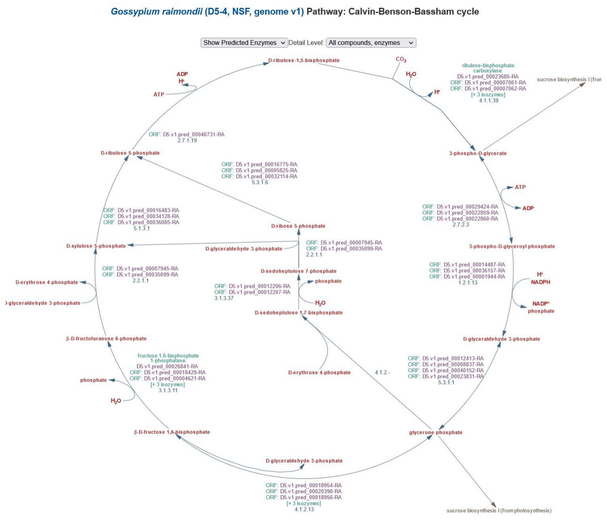


MegaSearch

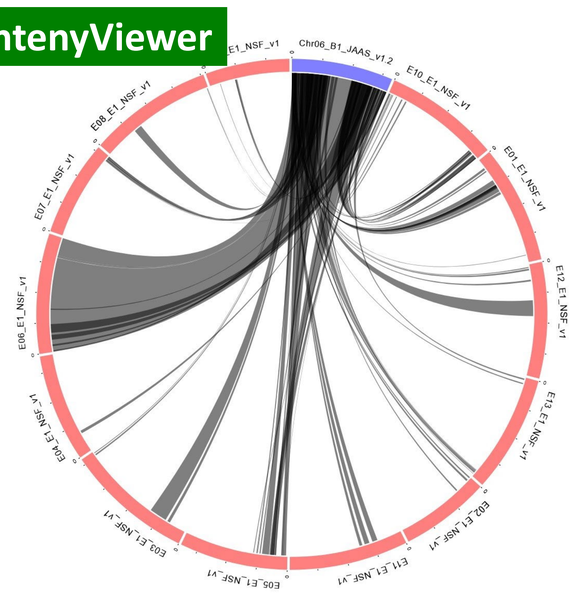
JBrowse



CottonCyc



SyntenyViewer



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