

CottonDB Enhancement

YU Jing¹, KOHEL Russell², HINZE Lori², FRELICHOWSKI James²,

XU Zhan-you¹, YU John Z², PERCY Richard²

(1. *Texas A&M University / Crop Germplasm Research Unit, USDA-ARS-SPARC, College Station, Texas 77845, USA*; 2. *Crop Germplasm Research Unit, USDA-ARS-SPARC, College Station, Texas 77845, USA*)

CottonDB (www.cottondb.org) was initiated in 1995. It is a database that contains genomic, genetic, and taxonomic information for cotton (*Gossypium* spp.). It serves both as an archival database and as a dynamic database, which incorporates new data and user resources. CottonDB is maintained at the Southern Plains Agricultural Research Center in College Station, TX. The project includes a website and database creating a repository of information for over 450,000 gene, EST, and contig sequences; genetic and physical map data; nearly 10,000 DNA primers; and 9,000 germplasm accessions. Tens of genetic maps and data of trait studies have been updated. The 13-year-old database is now being migrated to a new database architecture, and the new user interface provides a more intuitive approach to searching. Several graphical interfaces have been or will be implemented. CMap viewer, developed by Gramene, has been used to facilitate comparative genomics in CottonDB by allowing users to align and compare all maps in CottonDB; web BLAST server, developed by NCBI, complemented by 18 cotton and Arabidopsis nucleotide and protein sequence databases, is used for comparing gene and protein sequences against others in public databases; web FPC Viewer, developed by Arizona Genomics Institute, has been used for displaying cotton BAC clone contigs and cotton physical maps and for the assembly of sequence ready clones for large scale sequencing projects; and GBrowse, developed by GMOD, will provide a user-friendly interface for physical maps and allow users to annotate map data. An overview of current accessions, new features, and planned additions will be presented. An open invitation is extended to the research community to make suggestions, contribute data, and develop tools to improve the performance and utility of this public database.