

Cotton Marker Database (CMD) as an Enhanced Resource for Cotton Research Community

BLENDA Anna¹, LEE Taein², SURYANARAYANA Anilkumar¹,
MAIN Doreen², JONES Don³

(1. *Department of Genetics and Biochemistry, Clemson University, Biosystems Research Center, 51 New Cherry Str., Clemson, SC 29634, USA*; 2. *Department of Horticulture and Landscape Architecture, Washington State University, 45 Johnson Hall, Pullman, WA 99164, USA*; 3. *Agricultural Research Division, Cotton Incorporated, 6399 Weston Parkway, Cary, NC 27513, USA*)

Recently, thousands of SSR and now SNP markers have been discovered in cotton. Each of these markers provides a valuable molecular tool applying genetic and genomic research to cotton improvement. Cotton DNA marker database (CMD) continues to serve as a molecular marker resource for the cotton research community (<http://www.cottonmarker.org>). The current collection of cotton SSR markers publicly available through CMD is 8,915 and the number continues to grow. Currently, several CMD features were added or improved to enhance the database importance as a resource for cotton researchers. In February 2008, all CMD data was uploaded into a redesigned and significantly improved database schema incorporating data tables for the new type of cotton markers (SNP), as well as fsa files of panel screened data for visual display. All the data displayed is available to download. The BLAST, FASTA, and CAP3 servers on CMD now offer expanded parameter options so users can tailor their searches more precisely, and the significant similarity searches are significantly faster. To increase a collaboration effort with CottonDB, a link to the CottonDB record of the CMD SSRs was added to the View SSR pages. Further, search publication function has been added to the CMD, as well as e-mail publication alerts. The addition of SNP markers will include displaying the SNP-containing consensus sequence with the SNP highlighted, as well as displaying the individual sequences that are part of the consensus sequence (where possible). In addition, future development will focus on the establishment of a standard nomenclature for cotton SSRs and SNPs, collecting of all available genetic maps data, annotation of genetic traits/genes in cotton linked to the CMD SSRs/SNPs, improving the tools and functionality of the web interface, such as an advanced search site with options for search/display categories. When the cotton physical map is available, users also will be able to retrieve the anchored BAC clones containing the SSRs of interest through the anchored BACs page in the map viewer. With cotton genome sequencing in progress, the CMD also will focus on enhanced SSR and other markers data mining and analysis capabilities such as full sequence processing facilities.