

Anna Blenda, blenda@clemson.edu, Department of Genetics and Biochemistry, Clemson University, Biosystems Research Center, 51 New Cherry Street, Clemson, SC, 29634, USA

Preetham Yellambalase, preetham@genome.clemson.edu, Department of Genetics and Biochemistry, Clemson University, Biosystems Research Center, 51 New Cherry Street, Clemson, SC, 29634, USA

Michael Palmer, mbp@clemson.edu, Clemson University Genomics Institute, Clemson University, Biosystems Research Center, 51 New Cherry Street, Clemson, SC, 29634, USA

Roy Cantrell, RCantrell@cottoninc.com, Cotton Incorporated, Cary, NC, 27513, USA

Dorrie Main, dorrie@wsu.edu, Department of Horticulture and Landscape Architecture, Washington State University, WA, 99164, USA

The Cotton Microsatellite Database (CMD) (<http://www.cottonssr.org>) is a curated database resource providing centralized access to the largest collection of publicly available cotton SSRs. Microsatellite markers can be used in various applications including gene tagging, genome mapping, selecting progeny for a desired phenotypic trait, localizing qualitatively as well as quantitatively inherited traits, pedigree analysis, variety protection, and introgressing novel genes into breeding germplasm from exotic germplasm. The novelty of the CMD is in its specific orientation toward researchers involved in molecular marker development and application to cotton breeding. It is being actively used by the international cotton community, and can be viewed as an important vehicle toward increased collaboration among academic, government and industry cotton scientists, both nationally and worldwide. The CMD Advisory Board includes 5 scientists from the USDA, 1 researcher from academia, and 6 representatives from international companies. The present collection of 3,610 SSRs in CMD was generated through collaboration with major cotton research groups from the USA, France and China. Currently, the cotton SSRs from 9 projects deposited in the CMD are represented by 2,285 EST-SSRs and 1,325 genomic SSRs, of which 2 are chloroplast-derived and 192 are BAC-derived. CMD provides a suite of online tools for data mining and comparative analysis. Future development of the CMD will focus on the establishment of a standard nomenclature for cotton SSRs, adding new microsatellite data from both public and private sources, enhanced SSR data mining and analysis capabilities, such as full sequence processing facilities, and provision of a quarterly newsletter for the cotton community. Annotation of SSRs will include further classification using gene ontology and KEGG terms.