Work Completed

- ➢ New or updated Data
    - *G. barbadense* 3-79 (AD2_NBI) genome sequence made available on CottonGen JBrowse, includes:
        - o Genome sequence Assembly and annotation
        - o CottonGen all marker sequence alignments
        - o CottonGen unigene v1.0 alignments
        - o PlantGDB cotton unigene alignments
        - o J. Udall 2012 Unigene contig alignments
        - o NCBI cotton dbest sequence alignments
        - o Cacao theobroma v1.1 protein homologies and alignments
        - o Arabidopsis thaliana TAIR10 protein homologies and alignments
        - o Oryza sativa MSU v7.0 protein homologies and alignments
        - o Glycine max v1.0 protein homologies and alignments
        - o Vitis vinifera protein homologies and alignments

    - Marker and Maps
        - o Added TAMU CottonSNP63K AD genome intra species map (7,171 loci)
        - o Added TAMU CottonSNP63K AD genome inter species map (19,191 loci)
        - o Added CSIRO MCU-5 × Siokra 1–4, RIL SNP map (1244 loci and 4 QTLs)
        - o Reloadeded 40,796 SNP marker data and sequences to fix bug caused by system upgrade
        - o Added 10,521 TAMU Gb379 SNPs to chado
        - o Added new cotton trait categories to chado
        - o Added a new project page for the TAMU Cotton63KSNP Array
        - o Added UCD SNP/InDel and TM-1x3-79 map genotype data
        - o Added ARS-CS NCGC SSR genotypic data, contains 204,776 genotypic scores from 104 SSRs screened on 1969 germplasm
        - o Reloaded UCD SNP/InDel data to fix bug caused by system upgrade
        - o Reloaded USDA CFB SNP data to fix bug caused by system upgrade
        - o Map/marker/qtl data extracted and curated from 12 publications and added to data templates for upload to CottonGen

- ➢ Tools and Website
    - CottonCyc
        - o Analyzed and added a new CottonCyc pathaways for the AD1-BGI genome
        - o Updated the D5-JGI CottonCyc pathways by using PathwayTools version 19.5
    - GBrowse_Syn
        - o Conducted Synteny analysis between D5-JGI and A2-BGI and made available on GBrowse_Syn
    - JBrowse
        - o Fixed problem with the *G. raimondii* JGI protein homology data and updated data on Data Download page
    - Other
        - o Fixed the broken link between CottonGen germplasm and USDA-GRIN

- ➢ Conferences and Presentations
  - • Prepared and presented CottonGen at the ICGI 2016 Conference
  - • Released the first CottonGen biannual newsletter

- ➢ Usage in Q2 of 2016: 7,216 visits by 3,340 unique viewers from 108 countries who viewed 38,274 pages.

Work in Progress and plan in Q3, 2016

- • Creating CottonGen reference transcriptome using public RNASeq and EST data
- • Continue on the development of CottonGen BIMS to provide better interfaces and also converting to Tripal to share with other databases
- • Adding germplasm type to all germplasm in chado
- • Adding more map, marker and QTL data: We are continuously adding more map, marker and QTL data from publications to keep up-to-date database.
- • Developing further terms for Trait Ontology to describe cotton traits.