



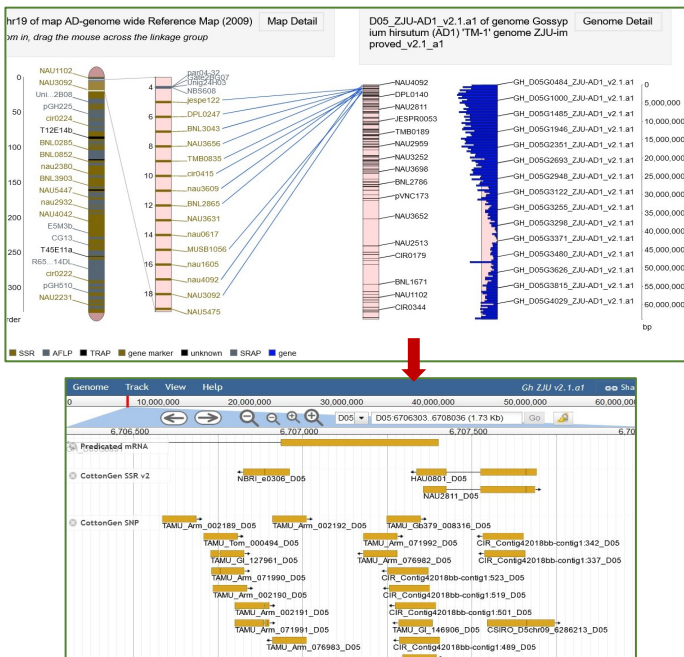
Welcome to the first issue of the CottonGen newsletter in 2021. This newsletter is issued to inform users about **new or updated data and tools in CottonGen**. In addition to new and updated data, each issue will provide more information on data or tools on the **featured tool/data** section.

New Genome Assemblies

Data from **six new whole genome assemblies** have been added to CottonGen. It includes data from [G. rotundifolium \(K12\)](#), new versions of [G. arboreum \(A2\)](#) and [G. raimondii \(D5\)](#), [Gossypium stocksii \(E1\)](#), [Gossypium thurberi \(D1-5\)](#) and [Gossypium davidsonii \(D3D-8\)](#). Access data from [Gene Search](#), [MegaSearch](#), [Synteny Viewer](#), [JBrowse](#), [BLAST](#) as well as the individual genome pages linked above.

Genome comparison in MapViewer

[Marker correspondence view](#) is available between genetic maps and genome scaffold/chromosomes with hyperlinks to JBrowse.



MapViewer with genome view and links to JBrowse

New Marker, QTL, Trait, and Mutant data

Newly added data includes 11921 SWU SSRs and some RT-PCR marker and primers, 276 QTLs and 11,127 trait data of yield and qualities, and 208 cotton mutants. Search [Marker](#), [QTL](#), and [Mutants](#) and view them in [MapViewer](#). Mutants can be searched in QTL/MTL search page by setting type as MTL (Mendelian Trait Loci).

NCGC trait descriptor rating scales updated

The list of [NCGC Standardized Descriptor Rating Scales](#) and relevant trait scores in CottonGen. New or updated descriptors rating scales are boll variation, bract size, canopy type, ease of germination, hair variation, leaf lacinate, nectary variation, stand establishment, uniformity, usability. [Trait Descriptor Search](#) gives information of definition (some with panel or illustration images), datasets & germplasm that have scores in CottonGen.

The screenshot shows the 'Search Trait Descriptors' interface. The search term 'petal' is entered, and the results show two records. A red arrow points to the 'petal color' descriptor. To the right, a grid of images illustrates various petal colors: WHITE (5), CREAM (1), LIGHT YELLOW (3), YELLOW (2), RED (4), GOLDEN (7), PINK (8), and LIGHT BLUE (6).

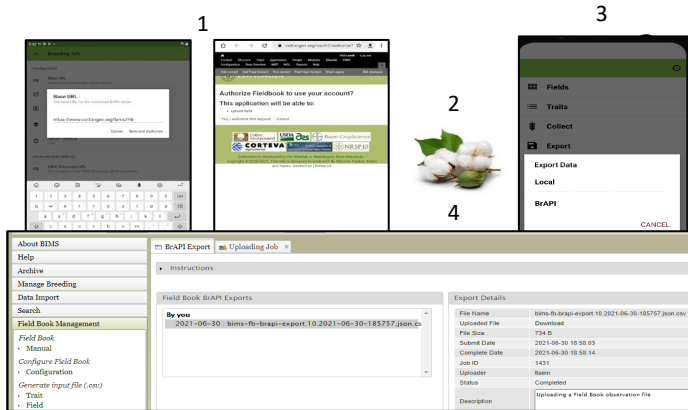
#	Descriptor	Category	Trait	Definition
1	petal color	morphological trait	petal color	petal color descriptor code definitions from three datasets: a) NCC 7=golden; 8=pink; 9=seg/off type; b) CN_COT Corolla color. Code 6=pink, 7=red, 8=purple; c) UZ_COT: Petal color. Code Definition 7=Bicolor.
2	petal spot	morphological trait	petal spot	petal spot descriptor code definitions from two datasets: a) NCC 1=Absent, 9=Present.

Trait descriptor search



BIMS is made BrAPI compliant

The [Breeding Information Management System \(BIMS\)](#) in CottonGEN is made [BrAPI](#) compliant. BrAPI is a web service API specification for communicating plant breeding data. With this new functionality, BIMS users can import data in Field Book app to BIMS just by clicking buttons!



1. Connect to BIMS from Field Book App and receive an input file through BrAPI
2. Collect phenotype data.
3. Export phenotype data to BIMS.
4. View data in BIMS!

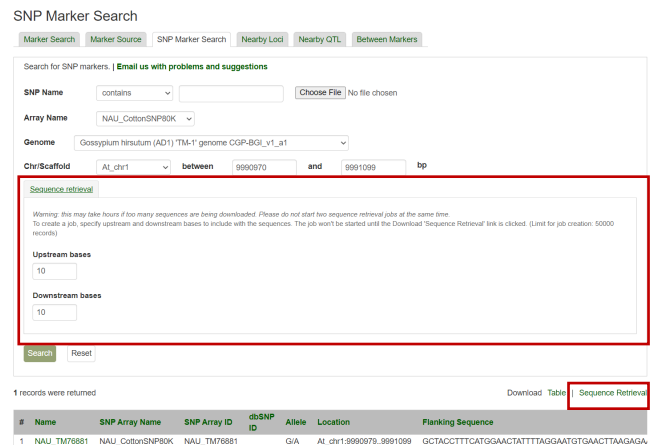
A manuscript on BIMS has been published ([Jung et al. 2021](#)). Visit BIMS website [breedwithbims.org](#), join the [BIMS Mailing List](#) and follow us on [Twitter](#) for more information!

COTTONGEN DATA

Genomes 48 of 26 species (AD,A,D,B,E,F,G,K)	Genes/mRNAs 1,520 K/2,404 K	Transcripts/Refs 5.8 B/214 K
Genetic Maps 115	QTLs/MTLs 6,772/208	Markers 587,004
Genotypes 25,164,549	Phenotypes 539,975	Germplasm 19,725
Images 45,214	Publications 16,371	Contacts 645

Retrieve Sequences around SNPs and Genes

Sequence retrieval with user-defined length of upstream and downstream available in [Marker Search](#) and [Gene Search](#)! Users can filter the list of genes and markers or load a file with gene names or marker names before retrieving sequences around them.



SNP search page with sequence retrieval option

More..

- **New Search for Images** available
- **G. raimondii transposable element (TE)** sequences available
- **Genes linked to gene family tree** data in [PhyloGenes](#). Check out an [example gene page](#).

COTTONGEN TOOLS

BIMS For breeders	BLAST For sequence search/alignment	CottonCyc For metabolic pathways
Map Viewer For genetic map view/comparison	Primer3 For designing PCR primers	Synten Viewer For search/view syntenic blocks among genomes

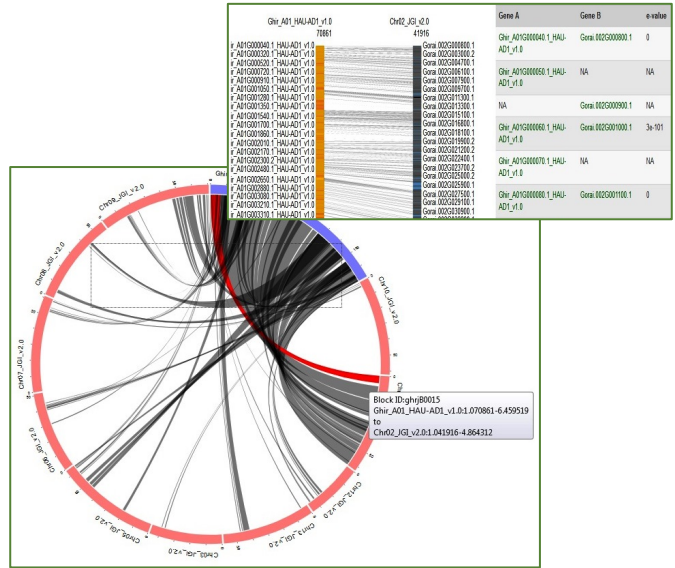
Genome Synteny Viewer

One of the additional analyses that CottonGEN does with provided genome data is a synteny comparison between the genomes. The analysis is conducted with [MCSanX](#) and displayed using the [Tripal Syntenic Viewer](#) module.

Using the [simple web interface](#), select the first genome and a chromosome or scaffold, and then select one or more genomes to compare against. The pairwise comparison data is displayed in a circus plot and syntenic blocks can be selected and viewed in a more detailed, linear side-by-side view.

In the detailed view, there is also an accompanying table that lists the corresponding mRNAs and has hyperlinks to the corresponding mRNA feature page on CottonGEN. Each mRNA feature page has the associated sequences and details about homology to the Swiss-Prot protein and InterPro protein family databases.

For more details on how to use the PathwayCyc tool, watch the video on the MainLab Bioinformatics [YouTube channel](#).



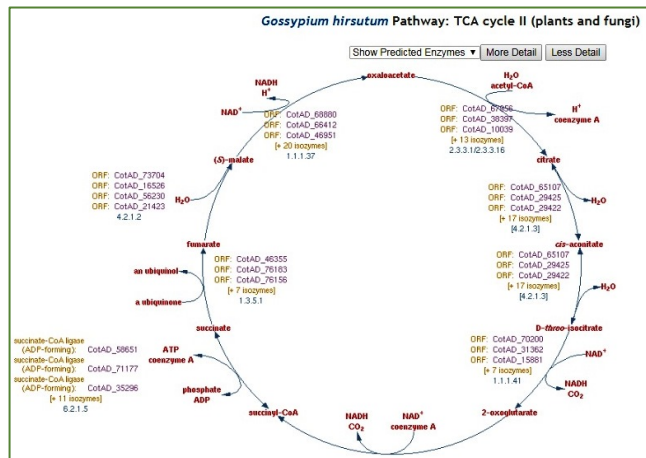
Syntenic plot of Chromosome 1 from *Gossypium hirsutum* (AD1) 'TM-1' genome compared to the *Gossypium raimondii* (D5) genome.

PathwayCyc

Genomes added to CottonGEN are also analyzed with [Pathway Tools](#) to identify metabolic pathways. The data is then displayed with an embedded instance of the software on CottonGEN under the [CottonCyc tool](#).

Users can also overlay data from transcriptomics or metabolomics experiments onto the cellular overview graphic. The pathways that have corresponding data are color coded to show over- or under-expression.

CottonCyc accounts can also be requested to allow users to upload, sort, and save data using the SmartTables feature. For more details on how to use the PathwayCyc tool, watch the video on the MainLab Bioinformatics [YouTube channel](#).



An example PathwayCyc diagram from the *G. hirsutum*

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