



CottonGen: An Integrated Web Database for Cotton Genomics, Genetics and Breeding Data

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Jing Yu^{1*}, Sook Jung¹, Chun-Huai Cheng¹, Stephen Ficklin¹, Taein Lee¹, Ping Zheng¹, Don Jones², Richard Percy³, Dorrie Main^{1*}

1. Washington State University 2. Cotton Incorporated 3. USDA-ARS * corresponding authors: jing.yu@wsu.edu, dorrie@wsu.edu

Abstract

CottonGen (<http://www.cottongen.org>) is a curated web-based relational database providing a central repository and data-mining resource for genomics, genetics, and breeding data of cotton. CottonGen contains whole genome sequences and annotation of both *G. raimondii* and *G. arboreum* - the ancestors of tetraploid commercial cottons, the unigenes for the family and the genera, gene sequences from NCBI, genetic maps, trait loci, germplasm, marker diversity, breeding, and publication data. All predicted genes of the whole genome sequence, unigenes and NCBI genes have been further annotated by homology to genes in other species, InterPro protein domains, GO terms and KEGG pathway terms. Whole genome sequences and annotation including genes, mRNAs, markers, re-sequencing data, NCBI sequences and homologous genes from other species, can be viewed through GBrowse and JBrowse. Pathway data can also be accessed through the CottonCyc Pathways. New querying functionality includes an advanced marker search, gene search, publications search and a sequence retrieval tool. Data submission templates, tutorials and a frequently asked questions section have also been added. Future development will include implementation of a breeder's toolbox, and addition of synteny, gene/genome curation tools as well as more map, marker and trait data.

Function Overview

Genomes: *G. raimondii* and *G. arboreum* genome sequence assemblies and functional annotations (predicted genes, expression data, InterPro, GO terms, and KEGG assignments).

Maps: 49 map data sets with 34,559 loci consisting of 44 genetic, 2 association, 1 bin, 1 consensus, and 1 *in-silico* maps, which covers cotton genome groups AD, A, D, and G.

Markers: Over 265,000 genetic markers consisting of 3,541 RFLPs, 78,340 SSRs, 183,035 SNPs, etc.

Germplasm: Over 15,000 germplasm including populations or individual entries identified from nearly 50k names or entries obtained from 14 collections from United States, Uzbekistan, and China.

Trait: 107,889 trait scores from USDA GRIN, China and Uzbekistan germplasm evaluations.

Images: 12,269 digital images from the USDA-ARS National Cotton Germplasm Characterization Project.

BLAST: Search for sequence similarity matches; select the best target sequence database and alignment parameters for your search.

CMap: Search and view mapped genes, markers, and QTLs using the comparative mapping viewer CMap.

CottonCyc: Browse the cotton predicted pathways generated by PathwayTools using the JGI v2.0 *G. raimondii* genome gene models.

GBrowse and JBrowse: Browse and search genes, markers, expressed sequences, and other structural genomics features on the *G. raimondii* (D5) and *G. arboreum* (A2) genomes using the genome browsers GBrowse and JBrowse.

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Web Site www.cottongen.org

General | Help | Data | Search | Tools | ICGI | Community

Function overview, work progress, usages, and CottonGen presentations | Data downloads & submissions, or browse Data in CottonGen | Conferences, employment & mailing list achieves

Achievements

CottonGen's 1st Year Progress
CottonDB on WSU servers | Tripal instance created | Develop ICGI website | Add CottonDB data in Chado | Web page development | Setting Queries

CottonGen's 2nd Year New Features and New Data
D5 genome assemblies & annotations | ICGI election system & website | Trait, QTL, Publication searches | Data download, submission, FAQ, Tutorials | New SSR and SNP markers | China & UZ germplasm evaluations | ARS digital images

CottonGen's 3rd Year ... New Tools and WGS data
SSR marker redundancy & sequence clarification | CottonCyc & JGI-D5 pathways | 50k new SSRs and 150k new SNPs | JBrowse | WGS & GMAP data | Implement genome synteny browser

Search Markers

- All markers
 - Search for marker source information. A table of...
 - Search for mapped markers. A table of all marker...
 - Search markers on nearby loci. A list of all loci th...
 - Advanced Marker Search. Search markers in eith...
- Mapped markers with sequences
 - Browse or search by map name. A table listed by...
 - Browse or search by chromosome number. A tab...
 - Browse or search by Genome Group. A table liste...

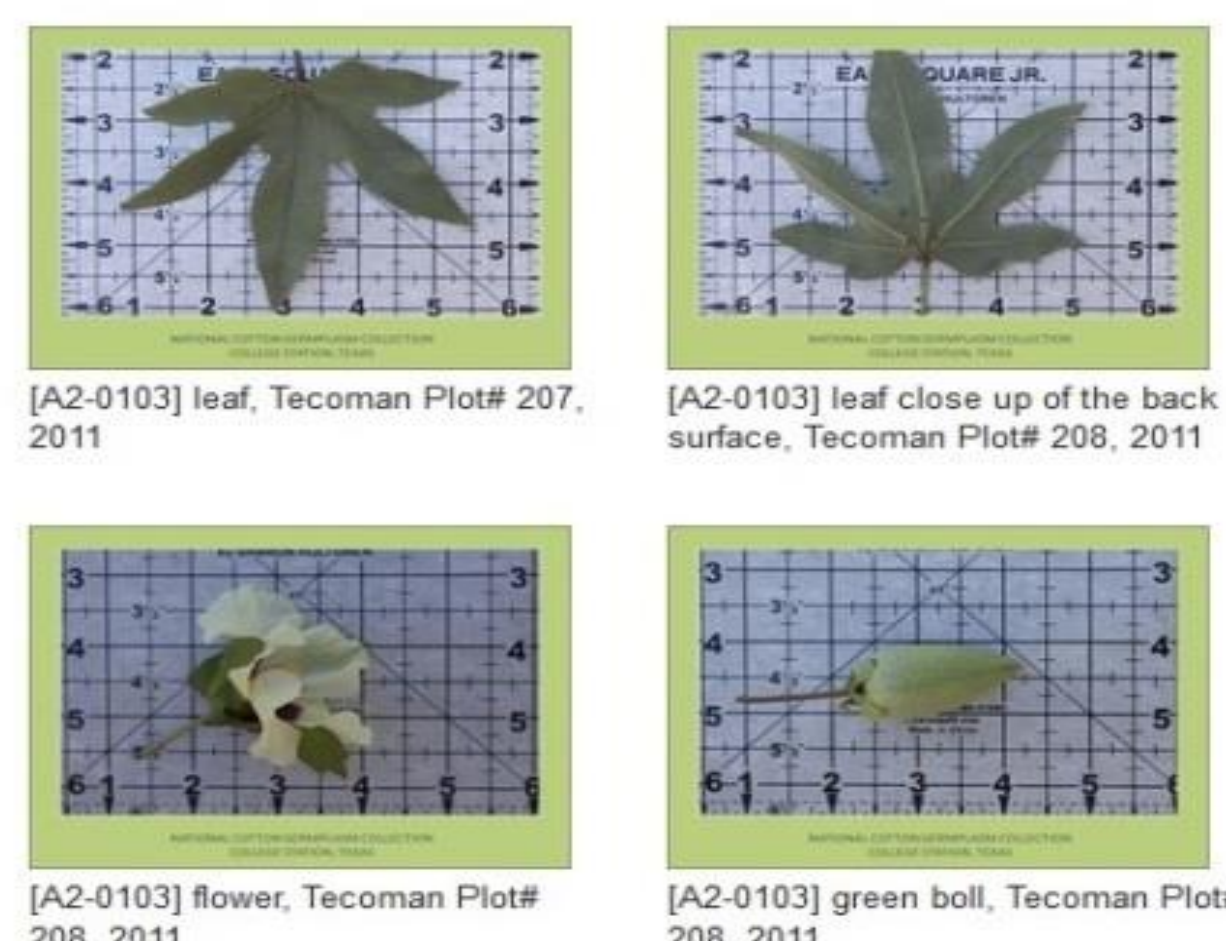
Marker Details

Name	TMB0364
Alias	TMF14 TMB0334 TMB0364=TMB0334 TML20
Genbank ID	BV679351
Type	SSR
Probe	N/A
Species	Gossypium hirsutum
Germplasm	TM-1
Source Sequence	N/A
Source Type	genomic
Repeat Motif	(CA) ₉
PCR Condition	Annealing temperature: 55
Primer 1	TMB0364_F: GGCACACCGGT...
Primer 2	TMB0364_R: TTGCATGACCAA...
Product Length	227

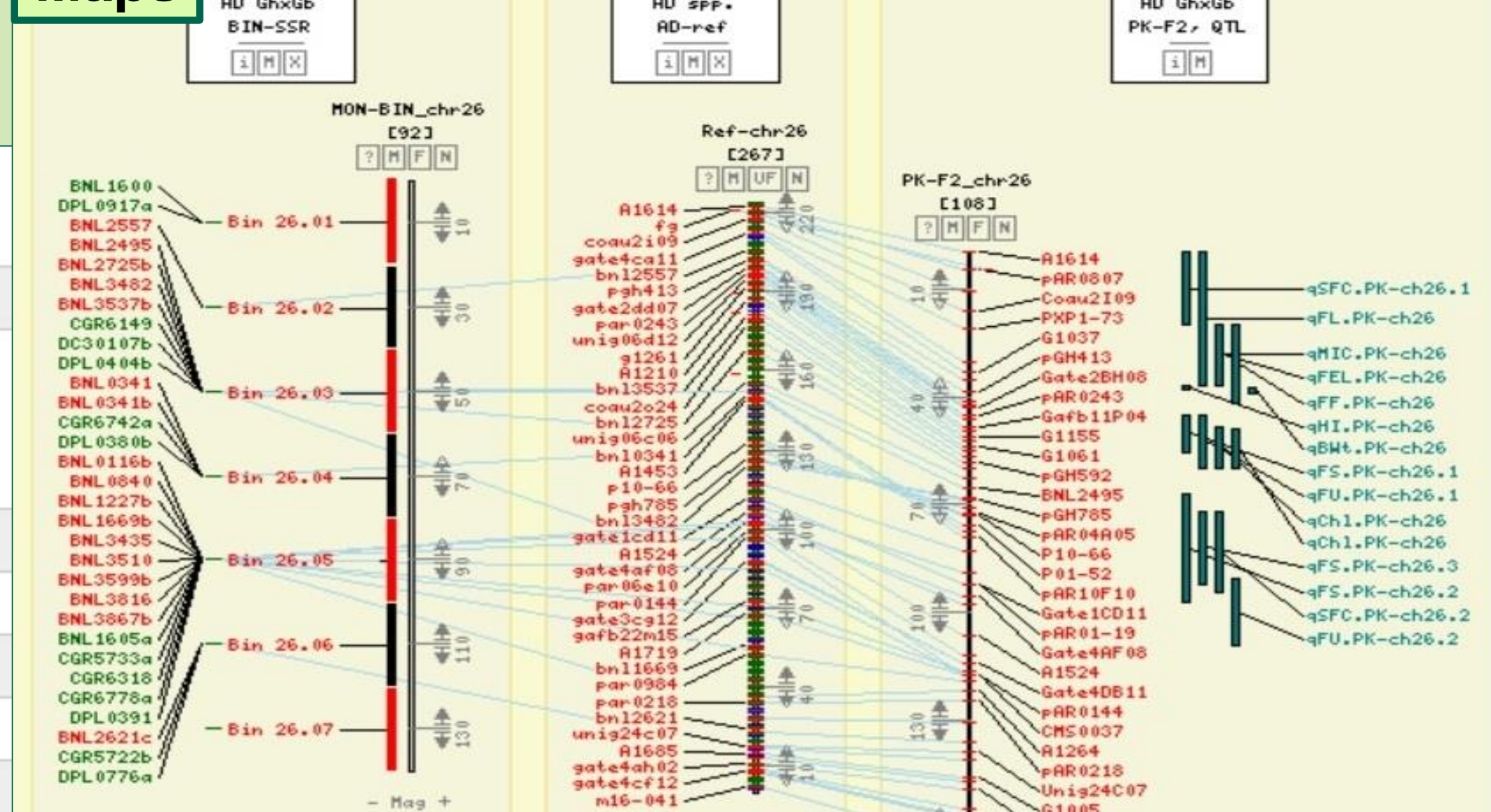
Germplasm Details

Name	TM-1
Alias	Texas-marker 1 (TM1) [view all 17]
Type	undefined
Species	<i>Gossypium hirsutum</i>
In Collection	[view all 3]
Description	genetic standard line
Origin	USDA-ARS-SPARC-CGRU
Pedigree	derived from the cultivar Deltap
Maternal Parent of	TM-1 x 3-79, F2 [view all 6]
Paternal Parent of	7235 x TM-1, RIL
Phenotypic Data	[view all 163]
Genotypic Data	[view all 2516]
Map	[view all 6]
DNA Library	[view all 13]
Sequence	[view all 48417]

Germplasm Images



Maps



QTL Details

QTL Label	qFL_HP-ch14
Published Symbol	qFLchr14
Trait Name	Fiber_length
Trait Alias	length. Fiber.
Trait Study	HP-F2-3-2007
Population	Handan-208 x Pima-90, F2:3
Female Parent	Handan-208
Male Parent	Pima 90
Colocalizing Marker	N/A
Neighboring Marker	m7e11-360 BNL1059
LOD	3.82
Additivity Dominance Ratio	0.17
R2	0.134

Genome

CottonCyc *G. raimondii* Pathway: TCA cycle II (plants and fungi)

Genome JGI v2.0 (annot v2.1): 162 kbp from Chr03:6,192,586..6,354,585

Trait Descriptors and Rating Scale

Descriptor	Description Code or Rating Scale	0	1	2	3	4	5
Boll Color*		green	dark green	light green	red	sun	
Boll Glanding	glandless*	medium	light	heavy	seg/off type		
Boll Nectaries	absent	present	reduced	inactive	seg/off type		
Boll Pitting		smooth	light pitted	inatted	very pitted	seg/	
Boll Point	Moderately pointed	pointed	blunt	seg/off type			
Boll Shape		Oval	round	cone	cone-oval	seg/	
Boll Size		medium	large	small	seg/off type	extr	
Bract Color		green	red	sun red	seg/off type		

