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Issue 10|January 2024

Welcome to the 1st issue of the CottonGen newsletter in 2024. This newsletter is issued to inform users about **new or updated data and tools in CottonGen and provides a summary of the number of users, citations, and data over the years.**

COTTONGEN

COTTON DATABASE RESOURCES

What's New in CottonGen?

Short video tutorial

 <u>How to view correspondences between genomes</u> and genetic maps (2:47 mins)

New Genome Data

 <u>Gossypium hirsutum</u> (AD1) 'PSC355' genome <u>USDA_v1</u> data (COHEN 2023. <u>Nematode-resistance</u> <u>loci in Upland cotton genomes are associated with</u> <u>structural differences.</u>) with CottonGen's functional annotations, marker and RefTran alignments, protein homologies.

Conference Presentations

- Presented at the Cotton Improvement Conference in <u>2024 Biltwide Cotton Conference</u> and workshops at the <u>2024 Plant and Animal Genome Conference</u> (PAG-31). Click the links below to view detailed information:
 - <u>CottonGen presentations</u> (at Biltwide Cotton or PAG-31)
 - <u>Database or Tool-related presentations</u> (at PAG-31)

New Data

- 1986 GWAS data for fiber qualities (*Thyssen 2019*, <u>Whole genome sequencing of a MAGIC population</u> identified genomic loci and candidate genes for major fiber quality traits in upland cotton (Gossypium hirsutum L.)
- Two maps with 3579 SLAF markers and 96 key fiber-related QTLs (Wang 2016, <u>Phenotypic variation</u> analysis and QTL mapping for cotton (Gossypium hirsutum L.) fiber quality grown in different cottonproducing regions) and 206 fiber-quality QTLs (Wang 2020, <u>Identification of candidate genes for key fibre-</u> related QTLs and derivation of favourable alleles in Gossypium hirsutum recombinant inbred lines with G. barbadense introgressions)
- Map with 7708 SNP markers and 17 QTLs for plant height traits (*Ma 2019*, <u>QTL analysis and candidate</u> gene identification for plant height in cotton based on an interspecific backcross inbred line population of <u>Gossypium hirsutum × Gossypium barbadense</u>)
- 50 QTLs for verticillium wilt resistance genes (*Bolek 2005, <u>Mapping of verticillium wilt resistance genes in</u> <u>cotton</u>)*
- 78K SSR markers identified from AD1-NBI genome (*Wang 2015, <u>Genome-wide mining, characterization,</u> <u>and development of microsatellite markers in Gossypium species</u>) available at both CottonGen Marker and JBrowse (name with prefix 'AD1-NBI_SSR')*
- New gene annotation from microPublication biology (Zirkel 2023, Gossypium hirsutum gene of unknown function, Gohir.A02G039501.1, encodes a potential DNA-binding ALOG protein involved in gene regulation)

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CottonGen by the Numbers

The database has seen growth in the number of users, citations, and data over the years. Let's look at the numbers! First, let's look at usage. The number of users has grown and the number of times they visit the site (Session) and the number of pages they view (Pageviews) each visit is growing.

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|--------------------------|----------|-----------|--------|-----------|--|--|--|--|--|--|
| Year | Sessions | Pageviews | Users | Countries | | | | | | |
| 2023 | 63,602 | 657,182 | 25,970 | 161 | | | | | | |
| 2022 | 64,182 | 399,080 | 32,043 | 177 | | | | | | |
| 2021 | 55,902 | 340,700 | 28,048 | 164 | | | | | | |
| 2020 | 44,505 | 321,846 | 21,215 | 151 | | | | | | |
| 2019 | 43,269 | 302,699 | 22,124 | 147 | | | | | | |
| 2018 | 33,965 | 278,885 | 13,146 | 153 | | | | | | |
| 2017 | 30,430 | 212,204 | 11,176 | 138 | | | | | | |
| 2016 | 26,221 | 155,207 | 9,748 | 145 | | | | | | |
| 2015 | 18,056 | 101,672 | 8,523 | 134 | | | | | | |
| 2014 | 15,666 | 90,994 | 7,914 | 132 | | | | | | |
| 2013 | 7,474 | 43,776 | 3,850 | 93 | | | | | | |
| 2012 | 6,378 | 46,279 | 2,137 | 51 | | | | | | |

CottonGen Usage by Year

Last, let's look at the amount of data that has been added over the last 10 years. The amount of genetic data (markers, maps, QTL) has grown steadily. This year we started adding GWAS data. We are adding data as it is published and featured. All Be on the lookout for the new additions! The number of **peer-reviewed manuscripts** citing CottonGen is growing as more data, analyses, and tools are added. Primary citations are manuscripts that cite CottonGen directly. Secondary citations are the number of times the primary citations were cited. Since 2012, CottonGen has been cited in **958** publications, with **18,975** secondary citations. Thank for citing CottonGen! Your paper and papers that cited yours can be accessed <u>here</u>!

<u>CottonGen Citations</u> over the last 10 Years

| Year | Primary Citations | Secondary Citations | | |
|------|--------------------------|---------------------|--|--|
| 2023 | 149 | 156 | | |
| 2022 | 139 | 692 | | |
| 2021 | 142 | 1,476 | | |
| 2020 | 103 | 2,094 | | |
| 2019 | 172 | 6,887 | | |
| 2018 | 84 | 3,206 | | |
| 2017 | 77 | 2,870 | | |
| 2016 | 39 | 1,232 | | |
| 2015 | 29 | 2,851 | | |
| 2014 | 19 | 1,297 | | |

Growth in Major CottonGen Data Types since 2013 and the last Year

| Year | Genomes | Genes | mRNA | Maps | Markers | QTL | GWAS |
|------|---------|-----------|-----------|------|---------|-------|-------|
| 2023 | 72 | 3,291,541 | 4,043,446 | 123 | 783,033 | 7,589 | 4,107 |
| 2022 | 55 | 2,496,604 | 3,199,165 | 117 | 690,386 | 7,228 | NA |
| 2013 | 2 | 37,505 | 118,243 | 50 | 23,000 | 304 | NA |

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