What’s New in CottonGen?

**Outreach**

- [How to Use the Expression Heatmap Tool](#) (2:23 mins)

**Upcoming PAG Database Workshop**

- NRSP10 Database Workshop featuring CottonGen Database, Jan. 14, 1:30-3:40 PM.
- International Cotton Genome Initiative (ICGI) Workshop, Jan 14, 4:00-6:10 PM

**Tool Improvements**

- Heatmap tool for visualizing gene expression
- GWAS added to updated QTL/GWAS search

**New Data**

- 2126 GWAS data for agronomic ([Du 2019](#)) and root system traits ([Cui 2022](#))
- Gene Expression data from a root system study ([Cui 2022](#)), a Root-Knot nematode resistance study ([Ojeda-Rivera 2022](#)), and V. dahliae resistance study ([Dong 2019](#))
- Added RBTN 2022 fiber trait data
- A new community project [iCottonQTL – An R/Shiny Web App for Streamlining Cotton Genetic Mapping](#)

**New Genome Data/Functional Analysis**

Eleven new diploid genomes and annotation datasets.

4 of them were submitted by CAAS-CRI ([Xu, 2023](#)):
- *[G. harknessii](D2-2) genome CRI_v1]*
- *[G. klotzschianum](D3-k) genome CRI_v1]*
- *[G. gossypioides](D6) genome CRI_v1]*
- *[G. trilobum](D8) genome CRI_v1]*

The other 7 collected from publication ([Wang, 2022](#)):
- *[G. herbaceum](A1) 'ZhongCao1' genome HAU_v1]*
- *[G. herbaceum](A1) 'A1a wild' genome HAU_v1]*
- *[G. anomalum](B1) genome HAU_v1]*
- *[G. sturtianum](C1) genome HAU_v1]*
- *[G. stocksii](E1) genome HAU_v1]*
- *[G. longicalyx](F1) genome HAU_v1]*
- *[G. bickii](G1) genome HAU_v1]*

CottonGen’s functional annotations were added to all the above genomes, too.
GWAS result table shows the data that you chose. From the result table, you can go to pages like GWAS, marker, gene, trait, MapViewer, and JBrowser.

GWAS Marker Gene Page

GWAS Page

GWAS Marker Page

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Funded by: Cotton Inc.; USDA-ARS; Bayer CS; CORTEVA; USDA National Research Project (NRSP10)