



## About CottonGen

CottonGen initiated in 2013 from the consolidation of CottonDB and the Cotton Marker Database (CMD). Since then, it has expanded to include transcriptome, annotated genome sequence, marker-trait-locus and breeding data, as well as enhanced tools for easy querying and visualizing research data and has become a centralized database containing genomics, genetics, and breeding data and analysis tools for cotton. Annotated genome sequences are available to view and search and there is also information about genetic maps, molecular markers, and QTL. If you are a breeder who needs to manage private breeding program data, access to the Breeding Information Management System (BIMS) can be requested. Visit us at www.cottongen.org to see everything that is available. Each issue of the newsletter will focus on a different type of data and what features are available. Short monthly how-to videos are available from the site.

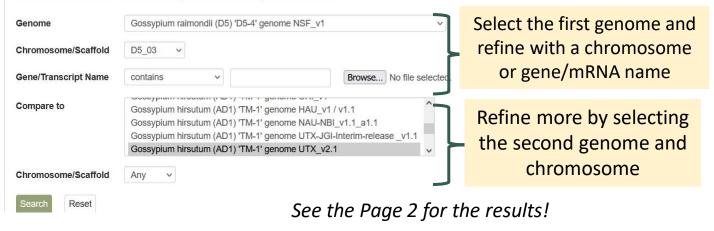
## New Ortholog/Paralog Search

While ortholog and paralog data are stored in our database as part of the <u>MCScanX</u> synteny analysis are viewable in the <u>Synteny</u> <u>Viewer</u> tool, there was not a way to search that data directly. To remedy this, we have designed the new <u>Search Orthologs and</u> <u>Paralogs</u> feature. See the diagram below for details on how to use it.

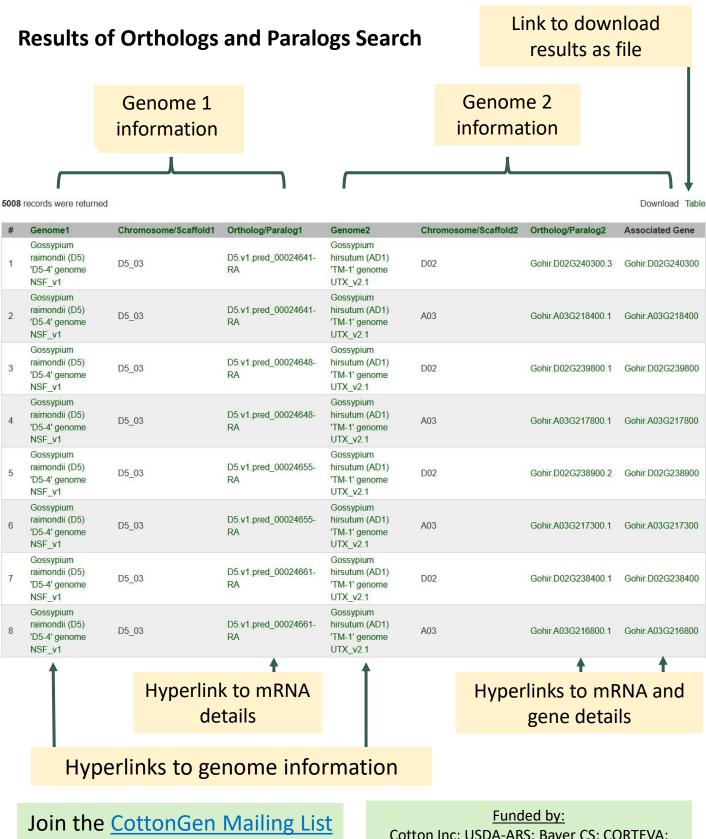
Remember that clicking on mRNA names opens the details page for that mRNA where you can see all the functional annotation details. Can't find your genome on the list in the new search? Only genomes that are within the Synteny Viewer are currently available. The missing genomes will be added soon. Please <u>contact us</u> with feedback.

## Search Orthologs and Paralogs

Retrieve orthologs/paralogs that are detected using MCScanX (Wang et al. 2012) using default settings. Sequences in ortholog/paralog columns between different assemblies/annotations of the same species represents potentially the same genes. In most cases, mRNA transcripts were used in the analysis and genes were used only when mRNAs are not available. The result table provides associated gene names as well.



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