

Resource Summary Report

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Tribolium castaneum Genome Project

RRID:SCR_002848

Type: Tool

Proper Citation

Tribolium castaneum Genome Project (RRID:SCR_002848)

Resource Information

URL: <http://www.hgsc.bcm.tmc.edu/content/red-flour-beetle-genome-project>

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Description: This portal provides information about the Tribolium castaneum Genome Project. The Tribolium castaneum genome sequence and its analysis has been published in Nature, two companion journal issues (IBMB and DGE) and numerous other publications listed below. The red flour beetle, Tribolium castaneum, a common pest that is also a genetic model for the Coleoptera. The genome has been sequenced to 7-fold coverage using a whole genome shotgun approach and assembled using the HGSC's assembly engine, Atlas, with methods employed for the Drosophila pseudoobscura genome assembly. Approximately 90% of the genome sequence has been mapped to chromosomes in collaboration with Dick Beeman (USDA ARS) and Sue Brown (Kansas State University). Access to the Data :- Genome Assembly: The long term home of the Tribolium genome is Beetlebase. Tcas 3.0 is now available in GenBank and on our FTP site. Note there are no restrictions of any kind on the Tribolium data as it has been published. Version 2 of the assembly, Tcas_2.0 is available for download using the FTP Data link in the sidebar. The assembly is described in detail in the README in that directory. T.cas_1.0 was a preliminary genome assembly that did not include large insert paired end information and has been moved to a previous assemblies folder. A genboree browser of the Tcas2.0 sequence is available here: There are also links to the genboree browser from the blast results (at the bottom of each reported HSP) if you use the blast server on this page. The original linear scaffold file, Tcas2.0/linearScaffolds/Tcas20050914-genome, posted on the ftp site did not include singleton contigs from the assembly and thus did not fully reflect the tribolium genome sequence, missing ~4.4Mb of sequence in 1860 contigs and reptigs or approximately 2.5% of the assembled sequence. A corrected Tcas20051011-genome file containing these missing sequences is now available on the ftp site. The blast databases have also been updated to reflect this change. All other data is correct, and not affected by this change. :- BLAST Searches: The BLAST link is located in the sidebar. :* Linearized chromosome and unplaced scaffold sequences :* Assembled contigs :* Bin0 unassembled reads and Repeat reads Traces are available from the NCBI Trace Archive by using the

link in the sidebar, or by using NCBI MegaBLAST with a same species or cross species query. Sponsors: Funding for this project has been provided by the National Human Genome Research Institute (NHGRI U54 HG003273), which is part of the National Institutes of Health (NIH), and the U.S. Department of Agriculture's Agricultural Research Service (USDA ARS Agreement No. 58-5430-3-338).

Synonyms: Tribolium

Resource Type: data or information resource, database, portal, topical portal

Keywords: genetic, chromosome, coleoptera, drosophila, genome, model, pest, red flour beetle, sequence, tribolium castaneum

Availability: Free, Freely available

Resource Name: Tribolium castaneum Genome Project

Resource ID: SCR_002848

Alternate IDs: nif-0000-25607

Old URLs: <http://www.hgsc.bcm.tmc.edu/project-species-i-Tribolium%20castaneum.hgsc?pageLocation=Tribolium%20castaneum>

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260821T193654+0000

Ratings and Alerts

No rating or validation information has been found for Tribolium castaneum Genome Project.

No alerts have been found for Tribolium castaneum Genome Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Rosenberger DW, et al. (2026) Tribolium flour beetles are strongly attracted to decomposing wood, their putative historical habitat, over flour. Scientific reports, 16(1).

Li R, et al. (2026) DeBCR: a sparsity-efficient framework for image enhancement through a deep-learning-based solution to inverse problems. Communications engineering, 5(1), 25.

Gao YF, et al. (2025) Chromosome-level genome assembly of the longhorn beetle *Arhopalus rusticus* (Coleoptera: Cerambycidae). *Scientific data*, 12(1), 1171.

Lomheim HJ, et al. (2025) Comparative Embryology and Transcriptomics of *Asellus infernus*, an Isopod Crustacean From Sulfidic Groundwater. *Evolution & development*, 27(3), e70014.

Žikić V, et al. (2024) Effect of γ -cypermethrin and pirimiphos-methyl on wing morphology of *Tribolium castaneum* (Herbst) and *T. confusum* Jacquelin du Val: a comparative study. *Environmental science and pollution research international*, 31(1), 895.

Linz DM, et al. (2023) Transcriptomic exploration of the Coleopteran wings reveals insight into the evolution of novel structures associated with the beetle elytron. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 340(2), 197.

Holditch Z, et al. (2020) Priority determines *Tribolium* competitive outcome in a food-limited environment. *PloS one*, 15(7), e0235289.

Leite DJ, et al. (2016) Pervasive microRNA Duplication in Chelicerates: Insights from the Embryonic microRNA Repertoire of the Spider *Parasteatoda tepidariorum*. *Genome biology and evolution*, 8(7), 2133.

Odman-Naresh J, et al. (2013) A lepidopteran-specific gene family encoding valine-rich midgut proteins. *PloS one*, 8(11), e82015.

Posnien N, et al. (2011) Candidate gene screen in the red flour beetle *Tribolium* reveals *six3* as ancient regulator of anterior median head and central complex development. *PLoS genetics*, 7(12), e1002416.