Resource Summary Report

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Honey Bee Genome Project

RRID:SCR_002890
Type: Tool

Proper Citation

Honey Bee Genome Project (RRID:SCR_002890)

Resource Information

URL: http://www.hgsc.bcm.tmc.edu/content/honey-bee-genome-project

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Description: The HGSC has sequenced the honey bee, Apis mellifera. The version 4.0 assembly was released in March 2006 and published in October 2006. The genome sequence is being upgraded with additional sequence coverage. The honey bee is important in the agricultural community as a producer of honey and as a facilitator of pollination. It is a model organism for studying the following human health issues: immunity, allergic reaction, antibiotic resistance, development, mental health, longevity and diseases of the X chromosome. In addition, biologists are interested in the honey bee's social organization and behavioral traits. This project was proposed to the HGSC by a group of dedicated insect biologists, headed by Gene Robinson. Following a workshop at the HGSC and a honey bee white paper, the HGSC began the project in 2002. A 6-fold coverage WGS, BAC sequence from pooled arrays, and an initial genome assembly (Amel_v1.0) were released beginning in 2003. This has been a challenging project with difficulty in recovering AT-rich regions. The WGS data had lower coverage in AT-rich regions and BAC data from clones showed evidence of internal deletions. Additional reads from AT enriched DNA addressed these underrepresented regions. The current assembly Amel_4.0 was produced with Atlas and includes 2.7 million reads (1.8 Gb) or 7.5x coverage of the (clonable) genome. About 97% of STSs, 98% of ESTs, and 96% of cDNAs are represented in the 231 Mb assembly. About 2,500 reads were also produced from a strain of Africanized honey bee and SNPs were extracted. These were released in dbSNP and the NCBI Trace Archive. Analysis of the genome by a consortium of 20 labs has been completed. This produced a gene list derived from five different methods melded through the GLEAN software. Publications include a main paper in Nature and up to forty companion papers in Genome Research and Insect Molecular Biology. Sponsors: Sequencing of the honey bee is jointly funded by National Human Genome Research Institute (NHGRI) and the Department of Agriculture (USDA). Multiple drones from the same queen (strain DH4) were obtained from Danny Weaver of B.

Weaver Apiaries. All libraries were made from DNA isolated from these drones. The honey bee BAC library (CHORI-224) was prepared by Pieter de Jong and Katzutoyo Osoegawa at the Children's Hospital Oakland Research Institute.

Synonyms: Honey Bee

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

Keywords: gene, agricultural, allergy, antibiotic, apis mellifera, array, behavioral, biologist, chromosome, development, disease, genome, heath, honey bee, human, immunity, insect, mental heath, organism, pollination, reaction, resistance, sequence, trait

Funding:

Resource Name: Honey Bee Genome Project

Resource ID: SCR_002890

Alternate IDs: nif-0000-25604

Old URLs: http://www.hgsc.bcm.tmc.edu/project-species-i-Apis%20mellifera.hgsc?pageLocation=Apis%20mellifera

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250516T053648+0000

Ratings and Alerts

No rating or validation information has been found for Honey Bee Genome Project.

No alerts have been found for Honey Bee Genome Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zeng X, et al. (2020) Genome sequencing of deep-sea hydrothermal vent snails reveals adaptions to extreme environments. GigaScience, 9(12).

Schatton A, et al. (2018) FoxP in bees: A comparative study on the developmental and adult

expression pattern in three bee species considering isoforms and circuitry. The Journal of comparative neurology, 526(9), 1589.

Wu YM, et al. (2018) Draft genomes of two blister beetles Hycleus cichorii and Hycleus phaleratus. GigaScience, 7(3), 1.

Moda LM, et al. (2013) Nutritionally driven differential gene expression leads to heterochronic brain development in honeybee castes. PloS one, 8(5), e64815.