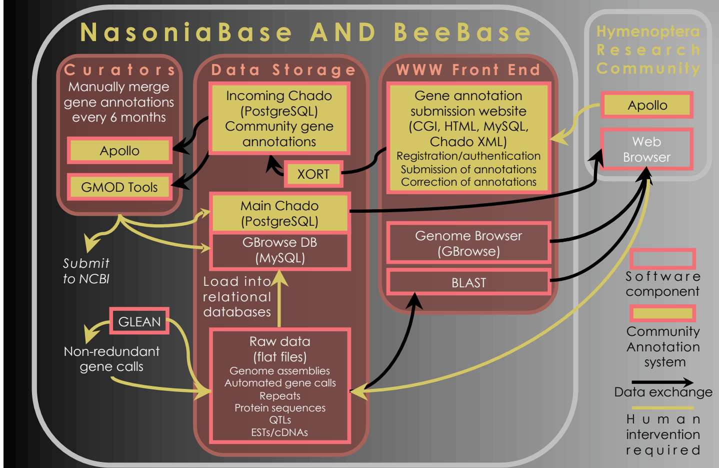
United States Department of Agriculture
National Institute of Food and Agriculture

THE HYMENOPTERA GENOME DATABASE

Mónica C. Muñoz-Torres, Justin T. Reese, Christopher P. Childers, Anna K. Bennett,
Jaideep P. Sundaram, Donald C. Vile and Christine G. Elsik.
GEORGETOWN UNIVERSITY, DEPARTMENT OF BIOLOGY, WASHINGTON, DC 20057

ABSTRACT

The Hymenoptera Genome Database (HGD, http://HymenopteraGenome.org) is an informatics resource supporting genomics of hymenopteran insect species. It currently provides access to genome sequences and annotation for honey bee, *Apis mellifera* (http://BeeBase.org) and the parasitoid wasp, *Nasonia vitripennis* (http://NasoniaBase.org). Honey bee is the most important pollinator of food crops and is a useful model for social behavior and immunity. *Nasonia* has a valuable role in agricultural research as a model for beneficial parasitoid wasps, which are used to control insect pests. The combination of these two genomes into a single resource has enhanced the value of genomic data for each species by facilitating cross-species comparisons. In addition to providing a central location for hymenopteran genomics data, HGD includes the genomes of three bee pathogens: *Ascosphaera apis*, *Nosema ceranae*, and *Paenibacillus larvae*. Genome viewers include tracks for predicted genes, manually annotated genes, linkage markers, transposable elements, SNPs, and alignments of protein homologs and ESTs. The honey bee comparative map viewer displays comparisons between linkage maps and genome assembly. HGD supports community gene annotation of the bee and wasp genomes using a remote connection to the Chado database by Apollo Genome Annotation client software. HGD web pages are implemented using the Drupal content management platform, an open-source content management platform with several features specifically developed for manipulating genomic data.



DATA EXCHANGE IN THE HYMENOPTERA GENOME DATABASE

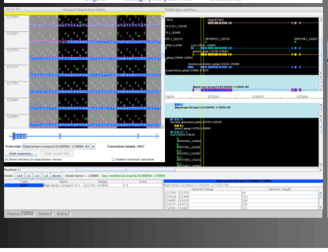
COMMUNITY ANNOTATION

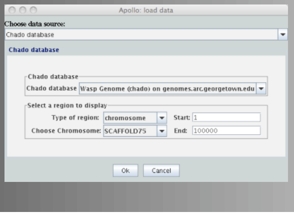
A Chado (GMOD) database allows researchers to use the Apollo Annotation Editor installed on their computer to connect directly to the NasoniaBase server to import gene evidence, such as predicted genes and EST alignments. Community annotators submit their gene models to NasoniaBase via the submission website.


Nasonia Annotations

You are logged in as:
ce75@georgetown.edu

Choose a Chado-XML formatted file to upload
(File should have an .xml extension)




Apollo: load data

Choose data source: Chado database

Chado database

Chado database: Wasp Genome (chado) on genomes.arc.georgetown.edu

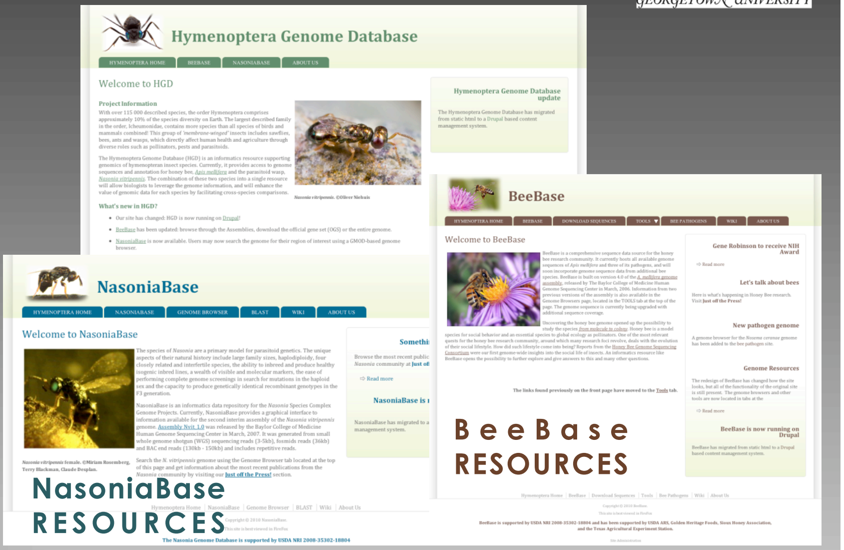
Select a region to display

Type of region: chromosome

Start: 1

Choose Chromosome: SCAFFOLD75

End: 100000


Hymenoptera Genome Database

Welcome to HGD

Project Information

With over 115 000 described species, the order Hymenoptera comprises approximately 10% of the species diversity on Earth. The largest described family in the order, Icheumonidae, contains more species than all species of birds and mammals combined! This group of *'membrane-winged'* insects includes sawflies, bees, ants and wasps, which directly affect human health and agriculture through diverse roles such as pollinators, pests and parasitoids.

The Hymenoptera Genome Database (HGD) is an informatics resource supporting genomics of hymenopteran insect species. Currently, it provides access to genome sequences and annotation for honey bee, *Apis mellifera* and the parasitoid wasp, *Nasonia vitripennis*. The combination of these two species into a single resource will allow biologists to leverage the genome information, and will enhance the value of genomic data for each species by facilitating cross-species comparisons.

Nasonia vitripennis. ©Oliver Niehuis

What's new in HGD?

- Our site has changed: HGD is now running on Drupal!
- BeeBase has been updated: browse through the Assemblies, download the official gene set (OGS) or the entire genome.
- NasoniaBase is now available. Users may now search the genome for their region of interest using a GMOD-based genome browser.

Hymenoptera Genome Database update

The Hymenoptera Genome Database has migrated from static html to a Drupal based content management system.

NasoniaBase

Welcome to NasoniaBase

The species of *Nasonia* are a primary model for parasitoid genetics. The unique aspects of their natural history include large family sizes, haplodiploidy, four closely related and interfertile species, the ability to inbreed and produce healthy isogenic inbred lines, a wealth of visible and molecular markers, the ease of performing complete genome screenings in search for mutations in the haploid sex and the capacity to produce genetically identical recombinant genotypes in the F3 generation.

NasoniaBase is an informatics data repository for the *Nasonia* Species Complex Genome Projects. Currently, NasoniaBase provides a graphical interface to information available for the second interim assembly of the *Nasonia vitripennis* genome. Assembly Nvit_1.0 was released by the Baylor College of Medicine Human Genome Sequencing Center in March, 2007. It was generated from small whole genome shotgun (WGS) sequencing reads (3-5kb), fosmids reads (36kb) and BAC end reads (130kb - 150kb) and includes repetitive reads.

Search the *N. vitripennis* genome using the Genome Browser tab located at the top of this page and get information about the most recent publications from the *Nasonia* community by visiting our **Just off the Press!** section.

Nasonia vitripennis female. ©Miriam Rosemberg, Terry Blackman, Claude Desplan.

Browse the most recent public *Nasonia* community at **Just of**

Read more

NasoniaBase has migrated to a management system.

NasoniaBase RESOURCES

Copyright © 2010 NasoniaBase.
This site is best viewed in FireFox

The Nasonia Genome Database is supported by USDA NRI 2008-35302-18804

BeeBase

Welcome to BeeBase

BeeBase is a comprehensive sequence data source for the honey bee research community. It currently hosts all available genome sequences of *Apis mellifera* and three of its pathogens, and will soon incorporate genome sequence data from additional bee species. BeeBase is built on version 4.0 of the *A. mellifera* genome assembly, released by The Baylor College of Medicine Human Genome Sequencing Center in March, 2006. Information from two previous versions of the assembly is also available in the Genome Browsers page, located in the TOOLS tab at the top of the page. The genome sequence is currently being upgraded with additional sequence coverage.

Uncovering the honey bee genome opened up the possibility to study the species *from molecule to colony*. Honey bee is a model species for social behavior and an essential species to global ecology as pollinators. One of the most relevant quests for the honey bee research community, around which many research foci revolve, deals with the evolution of their social lifestyle. How did such lifestyle come into being? Reports from the Honey Bee Genome Sequencing Consortium were our first genome-wide insights into the social life of insects. An informatics resource like BeeBase opens the possibility to further explore and give answers to this and many other questions.

The links found previously on the front page have moved to the Tools tab.

Gene Robinson to receive NIH Award

Read more

Let's talk about bees

Here is what's happening in Honey Bee research. Visit **Just off the Press!**

New pathogen genome

A genome browser for the *Nosema ceranae* genome has been added to the bee pathogen site.

Genome Resources

The redesign of BeeBase has changed how the site looks, but all of the functionality of the original site is still present. The genome browsers and other tools are now located in tabs at the

Read more

BeeBase is now running on Drupal

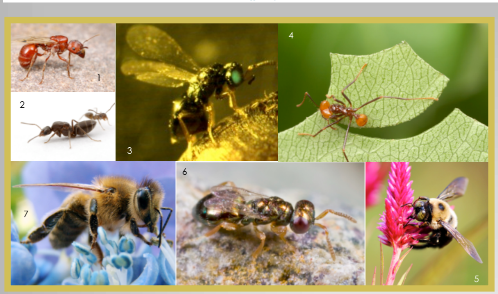
BeeBase has migrated from static html to a Drupal based content management system.

BeeBase RESOURCES

Copyright © 2010 BeeBase.
This site is best viewed in FireFox

BeeBase is supported by USDA NRI 2008-35302-18804 and has been supported by USDA ARS, Golden Heritage Foods, Sioux Honey Association, and the Texas Agricultural Experiment Station.

Site Administration




BeeBase

Apis mellifera Pathogens

Ascosphaera apis *Nosema ceranae* *Paenibacillus larvae*

Ascosphaera apis

Resources	Genome Browser on scaffold coordinates (n = 1649)
Description	Larval pathogen; causitive agent of chalkbrood disease
Sequencing Group	Baylor College of Medicine
NCBI Phylogenetic Classification	*Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiomycetidae; Onygenales; Ascosphaeraceae; Ascosphaera; Ascosphaera apis USDA-ARSEF 7405* (Taxonomy ID: 392613)
Publication	Qin X, Evans JD, Aronstein KA, Murray KD, Weinstock GM. Genome sequences of the honey bee pathogens Paenibacillus larvae and Ascosphaera apis. Insect Mol Biol. 2006 Oct;15(5):715-8. PubMed PMID: 17069642.

New pathogen genome!

A genome browser for the *Nosema ceranae* genome has been added to the site.

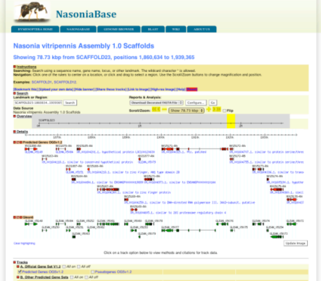
New data added for P. larvae!

Six new data tracks have been added to the *Paenibacillus larvae* Genome Browser.

Read more

HONEY BEE PATHOGENS

GENOME BROWSERS AND WIKI SITES

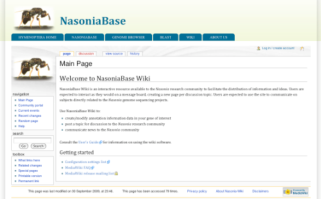

NasoniaBase

Nasonia vitripennis Assembly 1.0 Scaffolds

Showing 78.73 kbp from SCAFFOLD23, positions 1,860,634 to 1,939,365

Instructions
Searching: Search using a sequence name, gene name, locus, or other landmark. The wildcard character * is allowed.
Navigation: Click one of the rulers to center on a location, or click and drag to select a region. Use the Scroll/Zoom buttons to change magnification and position.

Examples: SCAFFOLD1, SCAFFOLD12.


NasoniaBase

Main Page

Welcome to NasoniaBase Wiki

NasoniaBase Wiki is an interactive resource available to the *Nasonia* research community to facilitate the distribution of information and ideas. Users are expected to interact as they would on a message board, creating a new page per discussion topic. Users are expected to use the site to communicate on subjects directly related to the *Nasonia* genome sequencing projects.

SUMMARY

The Hymenoptera Genome Database includes BeeBase (http://BeeBase.org) and NasoniaBase (http://NasoniaBase.org). BeeBase resources currently include honey bee Gbrowse for different assemblies and superscaffolds, BLAST and PSI-BLAST websites, a CMAP comparative map viewer, honey bee pathogen Gbrowse, and a sequence query and download webpage. NasoniaBase includes a genome browser, Apollo annotation database, and annotation community submission website. Future plans include QTL viewer, SNP/Haplotype block Gbrowse interface, gene expression annotation query with cross-species comparison functions, and *Apis-Nasonia* Synteny Broswer. In addition, genes will be annotated with GO terms, and new GO terms will be developed for Hymenoptera species. Gene pages will be developed with annotations, database cross-references, links to other insect MODs, NCBI, Entrez Gene, NCBI Homologene, OrthoMCL, Uniprot, and internal connections to genome viewer, gene expression, SNP and phenotype information.

FUNDING: NRI 2008-35302-18804 from the USDA National Institute of Food and Agriculture.

Picture Credits: 1. *Pogonomyrmex barbatus*. Alexander Wild, www.alexanderwild.com. **2**. *Linepithema huumile*, Alexander Wild. **3**. *Nasonia vitripennis* female. Miriam Rosemberg, Terry Blackman, Claude Desplan. **4**. *Atta cephalotes*. Alexander Wild. **5**. *Bombus terrestris*. Endangered Bees, http://library.thinkquest.org/07aug/02034/home.html. **6**. *Nasonia vitripennis* female. Oliver Niehuis. **7**. *Apis mellifera*. Wikimedia Commons.