# THE HYMENOPTERA GENOME DATABASE

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**USDA**
United States Department of Agriculture
National Institute of Food and Agriculture

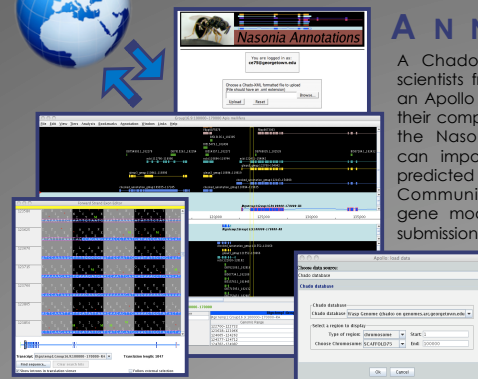GEORGETOWN UNIVERSITY · 17 89

## HGD IN A NUTSHELL

The **HYMENOPTERA GENOME DATABASE** (HGD) is a relational database that implements open-source software and components, providing access to curated data **CONTRIBUTED BY** an extensive, active research **COMMUNITY**. HGD contains up-to-date versions of the **GENOME ANNOTATIONS** for honey bee and its pathogens (http://BeeBase.org), jewel wasps (http://NasoniaBase.org), and a portal to the genomes of six species of ants. Together, these species cover approximately 200 MY in the phylogeny of Hymenoptera, allowing to **LEVERAGE** genetic, genome sequence, and gene expression **DATA**, as well as the biological knowledge of related model organisms. HGD has **SUPPORTED** five dispersed manual **ANNOTATION EFFORTS** with research contributions from almost 80 institutions in 14 countries. Community-based annotation efforts are made possible thanks to a **REMOTE CONNECTION** to a Chado database via the **APOLLO** Genome Annotation client software. Curated data at HGD includes predicted and annotated gene sets supported with evidence tracks such as ESTs/cDNAs, small RNA sequences and GC composition domains. Data at HGD can be **QUERIED** using genome browsers and / or BLAST/PSI-BLAST servers, and it may also be downloaded to perform **LOCAL SEARCHES**. We encourage the public to access and contribute data to HGD at:

## http://HymenopteraGenome.org

## DATA EXCHANGE IN THE HYMENOPTERA GENOME DATABASE

### Genome Databases

**Curators**
Manually merge gene annotations every 6 months
- Apollo
- GMOD Tools

Submit to NCBI

- GLEAN
Non-redundant gene calls

**Data Storage**
Incoming Chado (PostgreSQL) Community gene annotations
XORT
Main Chado (PostgreSQL) | GBrowse DB (MySQL)
Raw data (flat files)
Genome assemblies
Automated gene calls
Repeats
Protein sequences
QTLs
ESTs/cDNAs

Load into relational databases

**WWW Front End**
Gene annotation submission website (CGI, HTML, MySQL, Chado XML)
Registration/authentication
Submission of annotations
Correction of annotations
Genome Browser (GBrowse)
BLAST

### Hymenoptera Research Community
- Apollo
- Web Browser

Software component

Community Annotation system
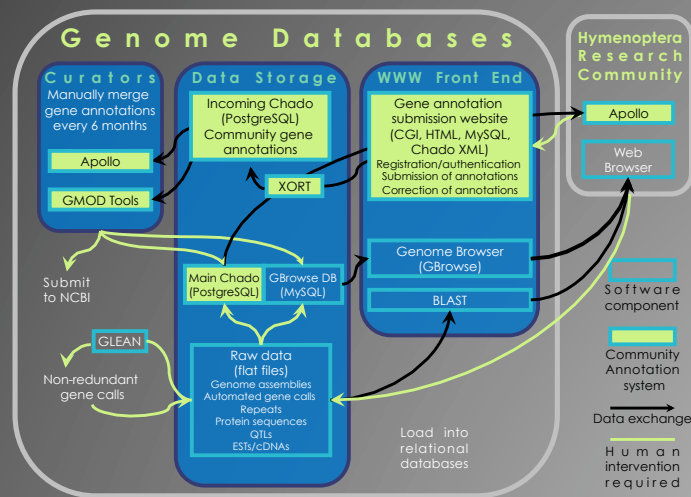
Data exchange

Human intervention required

## COMMUNITY ANNOTATION

A Chado (GMOD) database allows scientists from around the world to use an Apollo Annotation Editor installed on their computers and connect directly to the NasoniaBase server. Researchers can import gene evidence, such as predicted genes and EST alignments. Community annotators submit their gene models to NasoniaBase via the submission website.
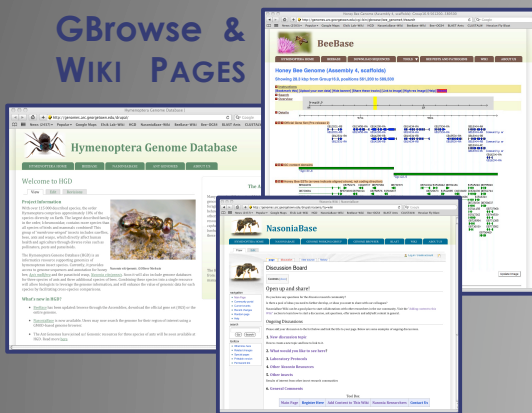
## 200 million years in the phylogeny of Hymenoptera

## GBrowse & WIKI PAGES

## AVAILABLE RESOURCES

The Hymenoptera Genome Database includes BeeBase, NasoniaBase and the Ant Genomes Portal. BeeBase resources currently include honey bee GBrowse for assemblies and superscaffolds, BLAST, PSI-BLAST, a CMAP comparative map viewer, honey bee pathogen GBrowse, and a sequence query and download webpage. NasoniaBase includes a genome browser, an Apollo annotation database, and an 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 containing 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 will be developed.

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