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 parasitoids, 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 homology 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.

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/Haplotyping block, Gbrowse interface, gene expression annotation query with cross-species comparison functions, and Api-Nasonia Synteny Browser. 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.

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