

The VectorBase Newsletter

Issue 9 – July 2010



News

Release cycle

Until recently, new data were added to VectorBase on an *ad-hoc* basis. We decided to have a regular bi-monthly release cycle, and the first release was in April this year. This release was a test, invisible to most users, and no data were changed. However, our second release has brought a big change: a new style genome browser!

Releases are named by the year and month of their release date, e.g. VB-2010-06. An e-mail will be sent to our mailing list with release notes describing what's new. Unfortunately we will be unable to keep an archive site of previous releases, but you will still be able to access the data as flat files.

AnoEST retirement

Due to the rapid influx of new data, VectorBase is no longer able to maintain the legacy AnoEST resource. It will remain available, but unsupported, for the foreseeable future. Similar functionality is available within the VectorBase genome browser. More details can be found on our [forum](#)¹, where your comments are welcome.

Data updates

Pediculus humanus

The gene set for the body louse, *Pediculus humanus*, is now available at [VectorBase](#)²! Browse the gene set, check for orthologs to other VectorBase species, blast your sequences against the *Pediculus* transcripts/proteins.

The annotation is available for download as a GFF file and as fasta files.

The genome paper has also been published this month (Kirkness *et al*, PNAS, 2010). It describes the body louse genome and its link with the primary bacterial endosymbiont, *Candidatus Riesia pediculicola*.

IDOMAL

The first version of IDOMAL (Infectious Disease Ontology Malaria), the Malaria ontology, covers both clinical and epidemiological aspects of the disease, as well as vector biology. IDOMAL, will form part of a suite of ontologies that will be used to drive IT tools and databases specifically constructed to help control malaria and, later, other vector-borne diseases. This suite already consists of the ontology described here as well as the one on insecticide resistance (MIRO) that has been available for some time. Additional components are being developed and introduced into IDOMAL. [IDOMAL](#)³ is available through VectorBase.

RNA-seq differential expression studies

We have started to receive differential expression data from groups working with RNA-seq “next generation” technology. As a preliminary step (towards full integration into VectorBase), we have made the data available through a simple web application and via DAS to gene pages. The first experiment of this kind in VectorBase measures the transcriptional response of *Aedes aegypti* larvae to six pollutants and insecticides. Follow [this link](#)⁴ and follow the on-screen instructions (located in the left menu) to set up the “NextGen” Expression External Data source.

Tool updates

Genome browser

In order to stay in sync. with Ensembl, VectorBase has now moved to the latest Ensembl Genome Browser! The new look is more intuitive and has numerous additional features. Navigation was made easier, with three tabs for location, gene and transcript, and a left side menu to move between data categories. Managing your data (DAS) and configuring the page have also been simplified.

The data remain unchanged; the links have been

³<http://www.vectorbase.org/GetData/Downloads/?type=Ontology>

⁴http://www.vectorbase.org/Aedes_aegypti/Gene/ExternalData?db=core:g=AAELO01063

¹<http://bit.ly/9xkelJ>

² http://www.vectorbase.org/Pediculus_humanus

rationalised (VectorBase address + species name) but the 'old' addresses will be redirected to the new ones so any bookmarked links will still be valid.

Search

Along with the new genome browser comes a greatly improved search facility. You can now search by gene name, description, VectorBase identifiers or external identifiers (such as UniProt), community symbols (Anopheles) and variation IDs (Anopheles). There is also a search box available on each page in the Genome Browser, so you can quickly move from gene to gene.

Tutorials

To help transition to the new Genome Browser, we have written a Genome Browser tutorial and updated our other tutorials.

Tutorials are short and are meant to give a quick introduction to specific VectorBase functionalities.

Check out the Help Wiki for the [list of tutorials](#)⁵ available!

Call to the community!

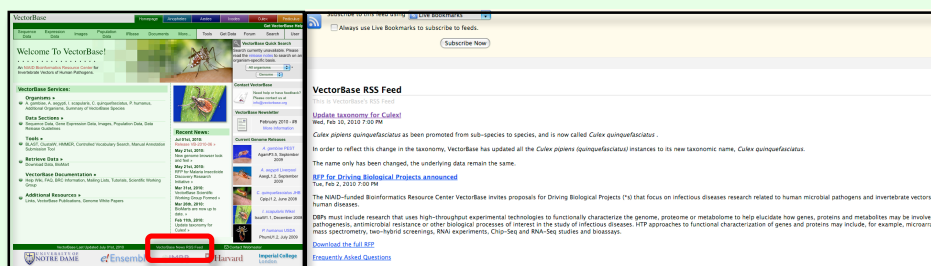
VectorBase is looking to make more cross-references from the curated gene predictions to external resources. If you maintain a vector-related resource and would like to see linkouts from VectorBase then please get in contact with us. The minimal required information is a formatted text file mapping VectorBase gene or transcript identifiers to identifiers in your resource and a URL template. Files should be versioned to a VectorBase geneset and we will maintain the links until such time as the geneset is updated when we will contact you about updating the mapping file.

The VectorBase Editors.
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VectorBase top tip

Did you know that you can follow VectorBase news by subscribing to our [RSS Feed](#)⁶? All news stories about the data and tools relevant to your research will automatically populate the feed as our team posts them.

Subscribe in 5 secs. by clicking the 'RSS Feed' link at the bottom of the VectorBase home page and following the instructions on your web browser.



⁵http://www.vectorbase.org/Help/VectorBase_tutorials

⁶<http://www.vectorbase.org/news-rss.xml>