The VectorBase Newsletter
Issue 10 – October 2010

News

Driving Biological Projects

A few months ago, VectorBase invited proposals for Driving Biological Projects (DBPs), funded by NIH/NIAID, these projects should use high-throughput experimental technologies to functionally characterize the genome, proteome or metabolome of vector species.

Two projects were selected:
Comparative Neurotranscriptome of *Aedes aegypti*
Physical Reference Maps for Vector Genome Assembly

The data generated will be made available through VectorBase.

The next call should be announced in about 14 months (Jan.2012). More information is available on the [VectorBase website](http://www.vectorbase.org/Other/News/?id=125)[1].

Culex genome paper

The paper relating the sequencing, annotation and analysis of the *Culex quinquefasciatus* genome has been published this month in Science (Arensburger *et al.,* 2010). As well as giving an overview of the genome structure and of the gene content, it presents a comparison of the three mosquito genomes and shows that increase in *Culex* gene number is partially due to a gene family expansion.

A companion paper (Bartholomay *et al.*, 2010) describes *Culex* responses to infection by diverse pathogens, and compares these responses in the three mosquitoes.

Data updates
Release: VB-2010-10

Anopheles gambiae M & S

A genome browser is now available for the *Anopheles gambiae* [M](http://www.vectorbase.org/Anopheles_gambiaeM/Info/Index) and [S](http://www.vectorbase.org/Anopheles_gambiaeS/Info/Index) forms[2,3]. At the moment it only contains repeats and EST alignments. The next release (Dec.2010) will bring Genscan gene models and UniProt mapping. Gene sets built from *An. gambiae* PEST are currently being produced and should be released early 2011.

An article published this month in Science (Lawniczak *et al.*, 2010) details the analysis of the M and S forms and reports widespread and heterogeneous genomic divergence, suggesting a well advanced speciation process and raising a challenge in identifying genes critical to this initiation.

In a parallel collaboration between Imperial College London and the Broad Institute, the M and S sequences were used to design a 400K Affymetrix SNP-array. This SNPchip was used to survey large population structure in an article from the same issue of Science (Neafsey *et al.*, 2010).

The latest *An. gambiae* PEST genome browser already features the 400K SNP locations used on the array and future releases (from Dec.2010) will contain the genotypes described in the paper. Further data sets will be incorported as they become available as this array is being made publically available by Affymetrix.

Link to external resources

Mosquito genes from all 3 species are now linked to a new external reference: the Insect immune-related gene and gene family resource, ImmunoDB.

The mosquito genomes have also been masked with transposable elements from the transposable element database TEFam.

Tool updates

Contact form

A new contact form can be found on the main page under the " Communications" section. Why not use it to send us your comments about our website?
- what do you like? or don't like?
- which data types you would like to see?
- which tools you would like to use?
- how to improve our service?
- or tell us anything else you have to say!

Feel free to leave your email address if you'd like to receive a response from the VectorBase staff or leave that field blank to comment anonymously.

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[1] http://www.vectorbase.org/Other/News/?id=125
[2] http://www.vectorbase.org/Anopheles_gambiaeM/Info/Index
[3] http://www.vectorbase.org/Anopheles_gambiaeS/Info/Index

RSS feeds

We are pleased to announce expanded RSS services, now accessible from the "Communication" section of the VectorBase home page. VectorBase RSS includes four new feeds, providing information on (i) our presence at scientific gatherings, (ii) publications, (iii) releases, and (iv) job positions relevant to our user community. Subscribe to stay up to date on the latest VectorBase developments!

If you want to post a job advert via our job RSS feed, please contact ***info@vectorbase.org***.

Community outreach

Interaction data

We are regularly asked why VectorBase do not show interaction data. The simple answer is that there aren't that many publicly available. So if you have hold of some interaction data, whether within the host itself or between host and pathogen, please submit them to an interaction archive database, or even better, to the [International Molecular Exchange Consortium](#)[4] (IMEx). We will then link to these resources and show your data!

South African IRBase node

IRbase is now in use at the National Health Laboratory Service of South Africa (Dr. Lizette Koekemoer). The system is used to store, search, and map their own insecticide resistance data using a web interface for both end users and curators. Data will be transferred to the VectorBase public repository at a later point.

Do you also have insecticide resistance data you would like to share publicly? No need to install IRBase locally – just contact us and we will let you know how to do so.
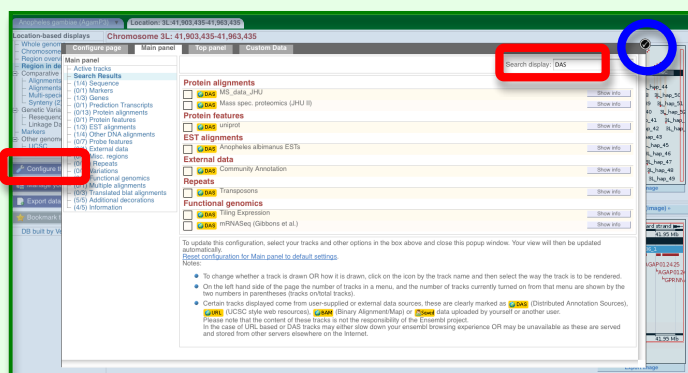
Facebook

After [Twitter](#)[5], VectorBase is now on [Facebook](#)[6]. Like us and we will keep you updated with news from the buzzing world.

The VectorBase Editors.
newsletter@vectorbase.org

VectorBase top tip

Did you know that from the genome browser, you can search the large number of available tracks in the "Configure this page" popup window. For example, enter DAS in the top right text box and all the DAS tracks are listed. Don't forget to click the tick symbol in the top right hand corner when you're done selecting/deselecting tracks.

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[4] http://www.imexconsortium.org/

[5] http://www.twitter.com/vectorbase

[6] http://www.facebook.com/VectorBase