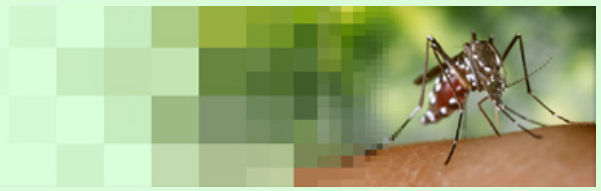


The VectorBase Newsletter

Issue 12 - Autumn/Fall 2011



News

Genome projects approved

VectorBase has been informed that the NIH/NIAID vector genome working group has approved two new projects. One will sequence the mite vector of scrub typhus, *Leptotrombidium deliense*, and provide additional genome and transcriptome sequencing of *Ixodes scapularis* and related ticks. The second will target genomes of 11 *Simulium* (black fly) species, including the major *S. damnosum* siblings, *S. woodii*, *S. ochraceum* and *S. vittatum*. White papers for both projects can be found under “Additional Resources” on the VectorBase site.

New data & resources

Pre-sites

To provide faster access to upcoming genomes, we have recently introduced preliminary sites, called “pre-sites”.

These contain preliminary gene annotations, transcriptome and proteome alignments and represent a snap shot of the annotation process at a given time. The rationales for presenting such data are to give more frequent updates on the annotation and to engage the community much earlier in the process. Releases are data-driven, rather than time-driven, and as such pre-sites, are updated independently of the bi-monthly release cycle.

Because these data are preliminary, they are not archived and non-searchable. While we strongly encourage the community to use them, we advise not to rely on the identifiers, as these will not be tracked.

To date, we have been providing pre-sites for two species: *Rhodnius prolixus* and *Glossina morsitans*.

Rhodnius prolixus pre-site

The 0.5 gene set has been released for *R. prolixus*; it was built using the Ensembl annotation pipeline¹. It is accessible via the [genome browser](#), for [BLAST search](#) and [downloading](#). Additional features such as RNA-seq and protein similarities, *ab initio* predictions and EST-build genes are also available in the genome browser.

Glossina morsitans pre-site

The 0.5 gene set has been released for *G. morsitans* and is our first annotation using the MAKER pipeline², rather than the more traditional Ensembl pipeline. It is currently undergoing some analysis from the *Glossina* community so we only provide gene models via [BLAST](#) and the [genome browser](#). *Ab initio* gene models, transcriptome and proteome alignments are also accessible via the genome browser, and assembly can be found in the [download section](#). We welcome any help from the community, so please contact us if you would like to be involved in the manual annotation process!

Unified population data

During the summer, VectorBase unveiled its “beta” population biology web resource³. Our aim is to bring together all population-based studies (field or lab) into one database so that geographic, experimental, phenotypic and genotypic characteristics can be queried, analysed and visualised. For now, it is possible to browse the mosquito field samples that were originally made available in VectorBase’s IRBase and AgPopGenBase resources, along with 60 samples from the Neafsey et al. SNP-chip paper⁴. Comments and suggestions from the community are welcome at any stage in the development of this resource.

¹<http://www.ensembl.org/info/docs/genebuild/index.html>

²Cantarel et al., *Genome Res.* 2008 Jan;18(1):188-96.

³<http://funcgen.vectorbase.org/PopulationBETA>

⁴<http://www.sciencemag.org/content/330/6003/514.abstract>

Upcoming Outreach

Attending TropMed Philly?

Visit us in the exhibits area at the ASTMH 60th Annual Meeting in Philadelphia, December 4-8, 2011. Representatives of VectorBase will be part of a shared exhibit along with several other NIH/NIAID Bioinformatics Resource Centers. VectorBase representatives will answer questions, demo VectorBase, help with queries and distribute materials.

VectorBase workshops

Our staff will be running a 2-day VectorBase workshop at the Liverpool School of Tropical Medicine (Liverpool, UK) in November. This event is now fully subscribed, but we invite other labs and institutes to host VectorBase workshops. You are free to select the topics you would like us to cover. If you are interested, please contact us at info@vectorbase.org for more details.

Social Networks

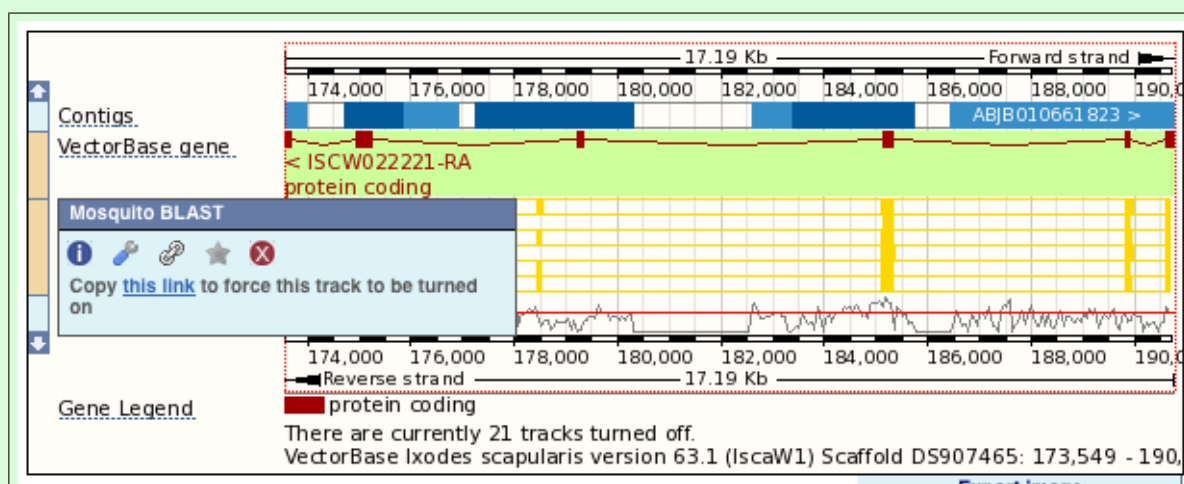
We're still on Twitter⁵ and Facebook⁶!

The VectorBase Editors.

newsletter@vectorbase.org

VectorBase Top Tip – Switch on a genome browser track via email

It is now possible to send a link via email which will turn on a specified track in the recipient's genome browser. This saves explaining to your colleagues and collaborators how to "Configure this page...". Simply mouse-over the track name and then the chain-link icon in the popup. Then copy the URL (right mouse-click menu in most web browsers). Here is the (shortened) [link from the graphic below \(goo.gl/WL1pf\)](http://goo.gl/WL1pf) to prove that it works.



⁵<http://twitter.com/vectorbase>

⁶<http://facebook.com/vectorbase>