The VectorBase Newsletter Issue 13 - Summer 2012

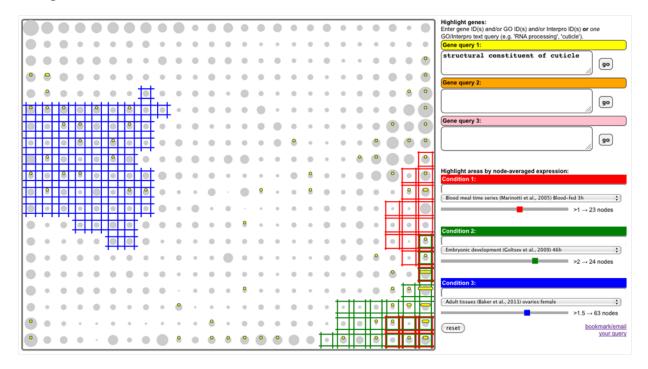
New data and resources

VectorBase Expression Map

VectorBase stores many high-throughput microarray (a.k.a. DNA chip) datasets which measure the relative amounts of thousands of *Anopheles gambiae* and *Aedes aegypti* gene product with respect to various experimental factors, such as tissues/organs, developmental stages and pathogens. Each experiment provides a wealth of information but, until now, a big picture "all genes, all factors" analysis has not been readly available. Such a holistic, or "systems", view of gene expression could greatly accelerate knowledge discovery and hypothesis generation from mosquito gene expression data.

In our updated VectorBase Expression Map (Mac-Callum et al. 2011) ¹ each A. gambiae and A. aegypti gene is assigned to one of 500 clusters. Because genes within a cluster have similar expression profiles, and the clusters are arranged on a rectangular grid, this resource is a powerful visualization tool for casual exploration and knowledge discovery. For example, we show in the figure below a query asking: Which genes are highly expressed in *A. gambiae* shortly after ingestion of a blood meal?

Two regions of the map are highlighted in red. Examination of the clusters soon reveals that one region is dominated by high levels of expression in late embryonic development (green highlighting) and also genes involved in cuticle formation (yellow symbols). Thus in just a few minutes we can begin to hypothesize that one response to the blood meal is to remodel the cuticle in order to accomodate the large increse in volume. The map shows two further modes of behavior for cuticle genes: they are either constitutively expressed (in all experiments performed so far) or are expressed in the ovaries (blue highlighting).



New website coming soon!

The VectorBase developers have been busy creating a new website with improved search and navigation, as well as a more consistent look and feel.

During the transition period of several months, both new and old sites will run in parallel. Your feedback is very welcome at any time.

¹BMC Genomics. Dec: 12:620

New data for Rhodnius prolixus

An enhanced gene build for *Rhodnius prolixus* has been included as part of the VB-2012-04 release. The high number of trascripts has been reduced. Submit your annotations to VectorBase Community Annotation Portal (CAP), the next gene set will include the community gene models!

At the present time, the following data are available: repeats, EST alignments, RNA-seq alignments, peptide alignments, full length cD-NAs, Lagerblad gene models (clustered 454 sequences), consensus set with 16,122 genes and 16,134 trascripts, Genscan models, SNAP models, ncRNAs and pseudogenes.

Note that VectorBase provides a **BLAST** service to compare your sequence against the *R. prolixus* supercontigs, trascripts and peptides.

Outreach

VectorBase FREE workshops

We invite labs and institutes to host free Vector-Base 1-2 day 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.

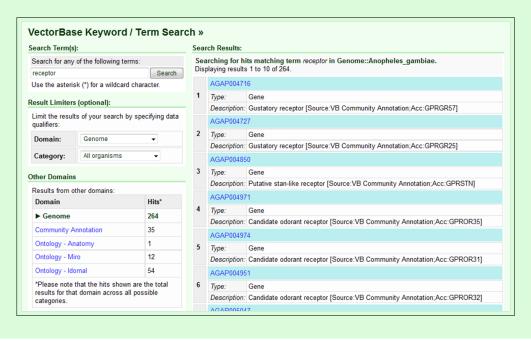
Facebook² and Twitter³

Post your comments, questions, suggestions or tweets!

The VectorBase Editors. newsletter@vectorbase.org

VectorBase top tip - New search engine at VectorBase

Searching via the main page or at the dedicated search page now searches VectorBase's genome, expression, community annotation, ontology, and population data. Searching any one of domains mentioned will return the results for that domain and provide links and the total number of results found across all possible domains. This should make findings data in VectorBase easier and promote grater connectivity between the various domains and genomic browsers.



²www.facebook.com/VectorBase

³www.twitter.com/vectorbase