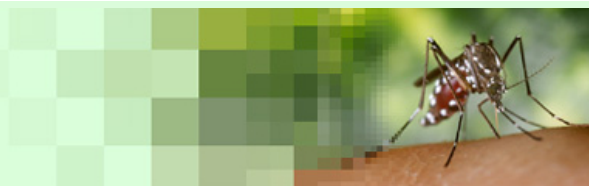# The VectorBase Newsletter
Issue 11 - Spring 2011

News

Funding Opportunity

The NIAID-funded VectorBase invites research investigations called Driving Biological Projects (DBPs) from organizations housing experimental laboratories having expertise and knowledge in working with arthropod vectors of human pathogens. We anticipate making two awards of up to $600K each by April 1, 2012. A two page Letter of Intent (LOI) is due August 1, 2011. Full proposals will be solicited by invitation only, with a deadline of November 1, 2011. See the full solicitation from the VectorBase site[1] and send questions to vector@nd.edu.

Anopheles Genomes Cluster

Samples are now in sequencing at the Broad Institute for the NHGRI/NIAID-supported project, "Genome Analysis of Vectorial Capacity in Major Anopheles Vectors of Malaria Parasites". VectorBase looks forward to working together with the Broad and members of the vector community to process and host these new genomes and their meta-data. Please visit VectorBase often for project information, updates, and data as they become available.

Genomes and Data

Rhodnius prolixus

An early pre-release of the *Rhodnius prolixus* genome is available. This annotation includes: repeat masking, ESTs and RNA-seq transcriptome alignments, UniProt peptide alignments, Genscan based gene models and an transcriptome derived geneset.

Kissing bug

Further data sets will be added in the coming months with the expected pre-release of the first genebuild for the June release.

Glossina morsitans

The genome of the Tsetse fly, *Glossina morsitans morsitans*, has been sequenced and assembled by the Wellcome Trust Sanger Institute. A pre-release of the assembly will be available in the June release. Like the *Rhodnius* pre-release this will contain align-

Tsetse fly

ments of transcriptome and peptide data and *ab initio* gene predictions.

Next-generation RNA-seq

VectorBase now contains next-generation transcriptome sequence data sets (RNA-seq). Over the past few releases we have added data from 9 Anopheline species available for querying via the BLAST server and as data tracks served to the *Anopheles gambiae* browser via DAS. Further, the genome browser is now capable of displaying community members' own indexed BAM files for all species.
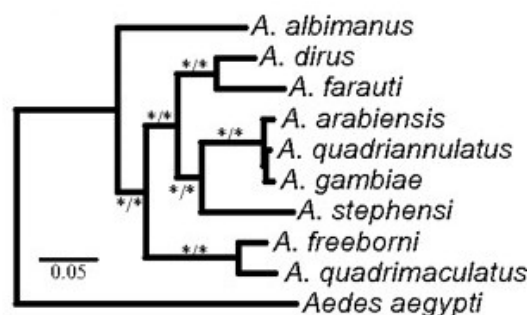
As more data sets become available VectorBase will continue to make these available to the community. A major update for *Aedes aegypti* is due for the June release including 1.3 M Roche 454 reads and 41 M Illumina reads from the Short Read Archive (SRA). We encourage our communities to contact us early to discuss visualization of newer generation sequencing data sets through VectorBase including resequencing data.

[1] http://www.vectorbase.org/Other/News/?id=140

Upcoming Outreach

VectorBase staff will be attending a number of meetings in the coming months giving workshops, talks or posters. If you are attending any of the following look out for us and come chat about vector genomics.

7th Annual BioMalPar Conference, Biology and Pathology of the Malaria Parasite
EMBL Heidelberg, Germany 16-18th May 2011
http://embl.de/training/events/2011/BMP11-01

5th Annual Arthropod Genomics Symposium Arthropod Genomics 2011: Exploring Diversity, Relating Similarity
Kansas City, USA, June 9 - 12, 2011
http://www.k-state.edu/agc/symp2011/

Journées Ouvertes en Biologie, Informatique et Mathématiques (JOBIM 2011)
Paris, France, June 28 - July 1, 2011
http://www.pasteur.fr/JOBIM2011

Fifth International Meeting on "Molecular and Population Biology of Mosquitoes and Other Disease Vectors"
Kolymbari, Crete, Greece, 24-30 July 2011
http://www.anobase.org/conferences/home_2011.html

Social Networks

We're still on Twitter[2] and Facebook[3]!

The VectorBase Editors.
newsletter@vectorbase.org

VectorBase Top Tip – Variant Effect Predictor

Did you know you can predict the effect of variants within the vector genomes? A variant effect predictor is available through the 'Manage your data' button found in the left hand navigation menu of the genome browser. Users can upload a text file containing the variation data in a tab-separated format (chromosome, start, end, allele, strand) and the predictor will return the consequence of this variation with information about the affected gene and transcript, any amino acid changes and whether this variation is currently in the database. Full documentation relating to both input and output file formats can be found at http://www.vectorbase.org/info/website/upload/var.html.

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[2] http://twitter.com/vectorbase
[3] http://facebook.com/vectorbase