



The VectorBase Newsletter

Issue 14 – February 2014

New Data ¹

28 genomes and counting

We currently host 28 genomes and more are coming soon. For a complete list of our current species please visit www.vectorbase.org/genomes. In this page you can also check if either the assembly or gene set of your favorite organism has been updated.



Biomphalaria glabrata

Our most recent updates include the genome of *Biomphalaria glabrata*, new assemblies for *Aedes aegypti* Liverpool, *Anopheles stephensi* Indian and *A. darlingi* Coari, and a new gene set for *Glossina morsitans* Yale.

Anopheles 16 genomes project

In September of 2008 funding was approved to sequence and assemble the genomes and transcriptomes of 13 *Anopheles* species. This project was inspired by very ambitious goals:

- improved understanding of vectorial capacity,
- the application of that understanding toward reducing malaria disease burden.

An updated list of the 16 species that are now part of the project is available at <https://olive.broadinstitute.org/projects/anopheles>. Production sequencing began in spring 2011. Initial draft genome assemblies were finished in 2013. Transcriptome assemblies, genome assemblies, and gene models were recently “frozen” and variant discovery and community analysis started.

All 16 reference genomes are inside VectorBase www.vectorbase.org/info/about/species.html, and community gene annotation is now underway. More details about the project can be found in Neafsey et al 2013 following this link: <http://www.ncbi.nlm.nih.gov/pubmed/23708298>.

Submit to VectorBase

You are encouraged to contact us to:

- Link genes to publications: To link one or a few genes please use this form <https://www.vectorbase.org/>

[content/publication-submission](#). For batch submission, send us the info in an Excel spreadsheet.

- Annotate genes with the Community Annotation Portal (CAP): Submit your gene models in GFF3 format using this link <https://www.vectorbase.org/cap>
- Add transcript or protein data: This type of data can be displayed on the Expression Browser, Genome browser or Population Biology Browser (PopBio). Priority will be given to published (or about to be published) data submitted already in Ensembl, NCBI or the DDBJ.

Outreach

VectorBase Scientific User Group

On February 3rd, 2014 we had our first (online) group meeting, please follow this link to meet the group members, www.vectorbase.org/sug. The benefits and expectations for the user group are:

- Learn about VectorBase’s new data and new tools and resources, and provide feedback
- Suggest new features and help test them
- Provide input on outreach plans and opportunities

Thank you very much to all the users that volunteer to participate in this group. Your input is very much appreciated.

Callout for your pictures

Do you want to share your pictures for our Images section? Go to <https://www.vectorbase.org/image-gallery> and look at what we have and what are we missing. If you would like to contribute and share your pictures **free of copyright**, please send us a link to your work. As with the other images, your name will be associated with each one of the pictures in VectorBase.

Tutorials, practice exercises, sample files and videos

Visit the page <https://www.vectorbase.org/tutorials> to learn how to better use VectorBase. If you are not very familiar with the page or need to show the basics to a new member in your lab, we recommend the “Tour” and “An overview of VB tools and resources”.

¹For more details about what is new on VectorBase please make sure to visit our latest release notes at <https://www.vectorbase.org/releases>. Remember, VectorBase is updated every two months!

In our last release, VB-2013-12, we included practice exercises and sample files to make it easier for you to learn. More video tutorials will be incorporated this year, too. If you have any suggestions about topics not covered in the tutorials, please let us know.

VectorBase Hands-on Workshop

Are you attending the American Society of Tropical Medicine and Hygiene (ASTMH) 63rd Annual Meeting this year? If you are, please mark your calendars and extend your stay for a couple of extra nights: our next workshop will be before the meeting on **Nov 1-2, 2014, in New Orleans, Louisiana, USA.**

The goal of the workshop is to present an overview of the VectorBase website and offer a training and data analysis opportunity. Seating will be limited to 30 people and priority will be given to scientists from disease-endemic countries. Previous VectorBase workshop attendees are not

eligible. More details will come soon.



Top Tip: As a registered user, your past BLAST, ClustalW, and HMMER jobs will be saved and viewable on your user page if you are logged in. To see them go to the homepage, log in and then click on your name in the top right corner. Look for the “Your jobs” section with (bullet point) instructions for using the interface at the bottom.

The screenshot shows a user interface for managing past jobs. At the top, there are tabs for "ClustalW", "HMMER", and "blastn". Below each tab is a list of jobs with columns for job ID, date, species, and status. There are also "Edit" buttons for each job. At the bottom of the page, there is a list of instructions:

- Click on a tool name above to view your past jobs
- Click on the job number to view your results in a new tab
- Press the star button next to a job to save it long term
- Click it again to allow it to expire
- The edit button may be used to give your job a custom description

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