

Dear colleagues —

You may recall endorsing proposals to the NIH and Wellcome Trust for continued funding of microbial, pathogen and vector informatics resources. **We are pleased to report that these projects have now been renewed**, in the form of an integrated Bioinformatics Resource Center contract from the NIH covering vector, fungal and parasite resources ([VectorBase](#), [FungiDB](#), [EuPathDB](#)), and two allied Resource Grants from the Wellcome Trust focusing on fungi and kinetoplastid parasites. These awards will allow us to continue loading the ever-increasing volume of Omic-scale datasets available for microbial eukaryotes, hosts and vectors into a new and improved **VEuPathDB database**, ensuring that this information is Findable, Accessible, Interoperable, and Reusable [FAIR]. A press release is available [here](#).

Changes planned for the coming months include:

- Full integration of VectorBase and the EuPathDB family of databases, providing increased data-loading efficiency, improved query & analysis capabilities, a common platform for viewing and interrogating host, vector, and pathogen datasets, and scalable infrastructure for comparative genomic analysis.
- Improved annotation functionality, to effectively capture expert knowledge, *via* 'User Comments' attached to any record, and a common Apollo annotation platform for community contributors and professional curators alike.
- Expanded harmonization of semantic terms across all sites, leveraging ontologies to facilitate biologically-accurate description of sample information, including clinical and phenotypic analyses.
- New workflows expanding the ability of users to analyze their own datasets (RNAseq mapping, mutant identification, *etc*), and integrate these private datasets with public data available in VEuPathDB.

Some additional notes:

- All component database names ([FungiDB](#), [PlasmoDB](#), [TriTrypDB](#), [VectorBase](#), *etc*) will remain active.
- The [VEuPathDB](#) Project (Vector & Eukaryotic Pathogen Bioinformatics Resources) incorporates staff from all previous projects & institutions.
- No new data will be released as we merge our infrastructure over the coming six months, but we will continue to load new data in anticipation of the first integrated release, projected for March 2020.
- We continue to welcome input from all of our diverse user communities ... if you have specific questions, or wish to participate more actively in providing advice, please email [help@VEuPathDB.org](mailto:help@VEuPathDB.org)
- In order to help assess the usage of informatics resources, please continue to cite VEuPathDB resources in your publications, *e.g.* "putative secreted kinases were identified by querying [ToxoDB.org](#)", "sequences were downloaded from [FungiDB.org](#)", "data presented here are available at [VectorBase.org](#)", *etc*. If these resources are essential to your work, you may also wish to provide acknowledgement in your publications & slide presentations (logos are available [here](#)).
- The Bill & Melinda Gates Foundation has requested a proposal for expanding [ClinEpiDB.org](#), which relies upon VEuPathDB infrastructure to accommodate large-scale clinical, field & epidemiological datasets; we look forward to integrating these resources with genomic databases.
- As always, we look forward to feedback from database users, *via* the '[Contact Us](#)' link on all of our web sites, face-to-face discussions at major meetings, *etc*.

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**... on behalf of the entire VEuPathDB team!**