

# Integrated systematics: barcoding, biosurveillance and biosystematics

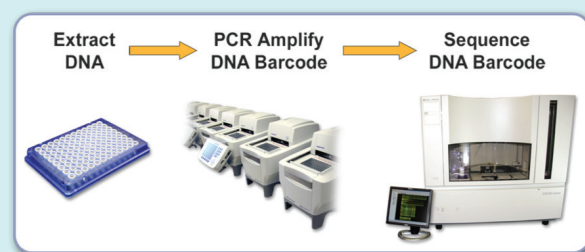
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*Molecular sequence data is increasingly easy to generate, but is most powerful when integrated with a strong taxonomic platform and the biological data necessary to interpret and leverage the knowledge.*

The Walter Reed Biosystematics Unit (WRBU) promotes integrated approaches to accurately identify biomedically important arthropods (mosquitoes, ticks, fleas, black flies, sand flies, mites) and assess their role in the transmission of disease. Leaning heavily on the taxonomic expertise within the Unit, and our unbridled access to the U.S. National Collection, WRBU heads the global Mosquito Barcoding Initiative, which links the methods and knowledge of traditional taxonomists with modern molecular genetic approaches. The Mosquito Barcoding Initiative (MBI) dataset, available through the Barcode of Life Database (BOLD; [boldsystems.org](http://boldsystems.org)), comprises unique species-diagnostic mtDNA COI sequence data (“DNA barcodes”) from over 70,000 individuals representing 1,400 species. DNA reference libraries are also being generated for key global vectors of sand flies, horse flies, ticks, mites, and fleas.

WRBU combines the power of molecularly identified vectors with the WRBU VectorMap platform (currently the world’s largest curated vector distributional database, with over 600,000 entries) with expert biological and ecological knowledge to document, model, and generate quality and actionable vector hazard predictions.

## THE BARCODING CYCLE PROCESS



WRBU has compiled the largest vouchered mosquito DNA barcode database in the world—facilitating rapid, accurate identification of species and cryptic and novel taxa in species complexes.

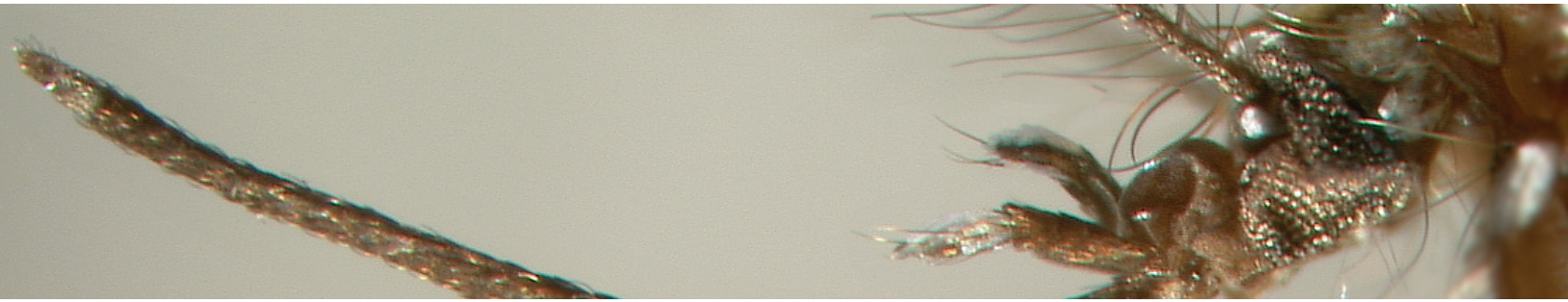
## FORWARD-FACING VECTOR IDENTIFICATION PLATFORMS

### Vector Eye

In partnership with Johns Hopkins University, WRBU is developing an app to identify key vector species from the camera of a smartphone. The algorithm, based on facial recognition software, is trained with field-collected (and suitably imperfect) specimens that are retrospectively identified using DNA barcodes.

### Vector Detector

WRBU is developing new and powerful tools to identify, incriminate, and document vectors. These include multiplex assays on the robust, field-ready



MagPix platform using DNA barcoding and whole genome data. Assays run on this platform can detect up to 50 different targets in a single reaction. We are currently developing the Vector Detector platform to include all 16 global *Aedes* fever virus vectors and dengue, Zika, chikungunya and yellow fever. This now allows simultaneous detection of multiple pathogens and vectors, substantially improving the data-to-decision pipelines essential to timely entomological intelligence detection and effective interventions.

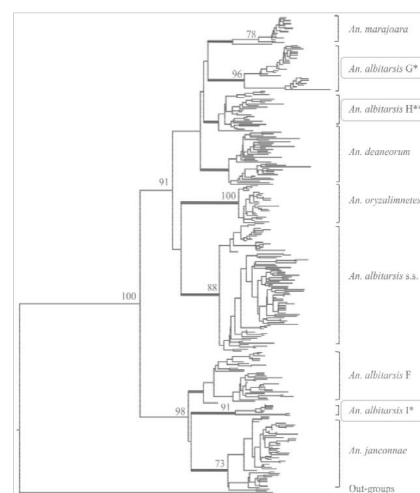
WRBU is a leading advocate for the integration of whole-genome approaches to more effectively address the challenges of understanding vectors and their pathogens to help mitigate their impacts. DNA sequence data from freshly collected samples are being combined with archive museum samples, including the United States National Collections that WRBU curates through a formal partnership with the Smithsonian Institution - National Museum of Natural History (NMNH). These curated, archived voucher samples document past and current genetic variation, as well as changing distributions, and are invaluable resources for future researchers using new powerful new technologies. DNA and genetic resources are stored long-term in the Smithsonian Institution's biorepository.

## PHYLOGENOMICS

As costs involved with whole genome sequences decrease, the ability to provide maximal genetic data on all study species becomes increasingly possible. Together with researchers at the North Carolina State University, WRBU has been awarded an NSF grant to determine the internal relationships within the family Culicidae, using 1,000 genomes. Our approach is highly systematic, with genomes garnered from topotypic

exemplars of each genus and subgenus to generate a robust phylogenetic framework for our functional genomes studies. We rely heavily on the U.S. National Collection to provide these keystone species, and have generated many whole genomes from old pinned museum specimens. Efforts are underway to sequence all mosquito vector species, as well as biomedically important tick species.

Available biotechnologies surrounding whole genome sequencing are rapidly changing our ability to document past events, to understand current biological patterns, and to use futuristic "gene-editing" approaches to address a variety of challenging biological issues. In order for these approaches to be effective, they need to incorporate detailed understanding of the life history of the species involved. Having a strong phylogenomic understanding of the evolution of mosquito groups, coupled with associated bionomic characteristics, allows us to interrogate and determine the genetic basis of key bionomic characters—including adult life strategies and host preferences, immature feeding habitats, and habitat salinity tolerances—allowing us to profile those genes and gene regions associated with disease agent transmission competence.



Molecular approaches accelerate the discovery of new species.

