BAT CONSERVATION INTERNATIONAL

bats

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Saving Malaysia's Fruit Bats

Research group led by former BCI student scholar promotes education and coexistence

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Pale spear-nosed bat (*Phyllostomus discolor*)

Photo: Jose Gabriel Martinez Fonseca

FEATURES

DEPARTMENTS

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NEWS & UPDATES

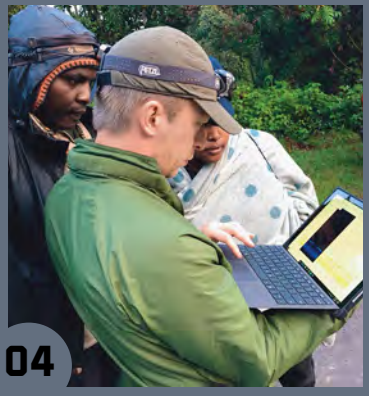

Photo: Dr. Winifred Frick

ON THE COVER

Protecting Malaysia's bats by providing education to farmers and tourists.

Photo: Sanjitpaal Singh / Jitspics.com

bat chat
A conversation with a noted expert

Gene Genius

Researcher and BCI science advisory committee member unveils new knowledge about bat genomes

by Shaena Montanari

Dr. Liliana Dávalos is one of BCI's science advisory committee members and a professor of conservation biology at Stony Brook University in New York. She earned her Ph.D. in ecology, evolution, and environmental biology from Columbia University and now runs a lab focused on the study of molecular evolution and tropical biology. Dr. Dávalos is part of the research team that published an article in *Nature* focusing on what high-quality genomes reveal about evolutionary adaptations of bats.

Photo: Dr. Winifred Frick

▲ Dr. Liliana Dávalos shows off some of the test tubes used in the sequencing project.

Why did you start researching bats?

Like so many young organismal biologists, I was seduced and enchanted by birds, and that's what I wanted to study. But when I was applying to graduate school, I did not hear back from the ornithologists and instead heard back from one researcher, Dr. Nancy Simmons, who later became my advisor. She said she would work with me if I would consider a project about bats instead. I already had some familiarity with bats from fieldwork. The field of bat researchers was a lot smaller at the time, and there were many opportunities to have a great impact with research.

The *Nature* study you worked on recently compares whole genomes of bats. How does sequencing whole genomes help you understand more about characteristics of bats, such as disease tolerance?

I think the No. 1 thing we can do with whole genomes is study gene content with much greater precision. As we get better and better genomes, we understand that evolution through gene duplication and gene loss is important. To understand more about gene families (sets of similar genes) that are critical for immunity and sensory systems in mammals, we need really good whole genomes to study.

What did you learn about the relationship between bats and viruses in this recent study?

One of the key things that was discovered in this paper is that there are ancient viral insertions in the genome. From that, we can infer that over millions of generations, bats have been exposed to unique viruses that other mammals have never been exposed to before. We find insertions in the genome from viruses that have, as of now, only been found circulating in birds. That is a remarkable finding because it tells us something about the history of what viruses bats have been dealing with for a long time.

What types of themes and questions do you think will guide your future research?

I think we are going to take the bats in the lab. In some cases, that means the whole bat, but also through immortalized cell lines for bats, which are still uncommon. These types of resources exist in mouse models—you can order particular mouse cell lines from a catalog that mimic a particular disease to study in a lab. Future research will entail the development of a much greater variety of these cell lines for bats. Outside of the lab, we also want to do more field studies like track and monitor bat metabolism, health, and disease, all of which used to be difficult to do but are now becoming less expensive.