

VOLUME 27, NO. 4 Winter 2009

Food Forensics

New technology uses DNA to reveal what's on the menu for bats

Robin Floyd and Elizabeth Clare

What bats eat is a critical “ and surprisingly complicated “ aspect of bat conservation. Deciphering a bat's dietary needs is essential for figuring out the species' role in the mosaic of biodiversity and for establishing conservation priorities. When bats consume damaging or dangerous insect pests, that knowledge is key to answering one of the public's most common questions about bat conservation: why should I care?

People are generally familiar with the idea that many bats eat insects. But "insects" is a very broad group, with at least a million species. Scientists need more detail. What kinds of insects are bats eating? Do they hunt only for favorite prey, or just devour everything they find? Such details are extremely important for conservation planning.

While the question may seem simple, definitive answers can be very tough to obtain. For many years, we have been missing this very basic knowledge about most insect-eating bats for the simple reason that their feeding behavior is very difficult to observe. Bats hunt at night, fly fast and pursue prey that are often too small for human observers to track. A common alternative to direct observation is to reconstruct bats' diets by collecting and examining their feces (guano). By carefully teasing apart guano pellets under a microscope, digested prey fragments can often be recovered. But many insects are small and soft, and bats tend to chew their food thoroughly, so researchers typically retrieve only degraded scraps of insect bodies, which can make precise identification problematic. We might know that the bats ate beetles or moths, but greater detail than that was often impossible.

Until now.

Insect fragments in guano contain tiny amounts of genetic material. Technological innovations now allow scientists to analyze those traces of DNA to precisely identify the insects that left them “ just as CSI detectives analyze blood from a crime scene. With this information, we can now gain a remarkably detailed picture of a bat's dinner menu.

In a study described in the journal *Molecular Ecology*, our team of researchers based at the University of Guelph and the University of Western Ontario in Canada used these methods to examine the detailed diet of the eastern red bat (*Lasiurus borealis*). Our results demonstrate that this approach, called DNA barcoding, can be extremely effective.

This technique of using discrete DNA sequences to identify digested food remains has been used successfully in various animals, but not with bats. Every living thing carries its full set of genes in every cell of its body. Research has demonstrated that, for the purpose of simply telling species apart, you don't need to examine all the genes “ a time-consuming and expensive process. Barcoding works by selecting a small region of DNA that varies a bit by species but is mostly constant within each species and can therefore be used as a species marker or signature, much as a barcode in a supermarket quickly identifies specific products. The goal is a consistently reliable method of species identification that is relatively quick and inexpensive.



 [View PDF version](#)
[5.77 MB]

The region chosen for the standardized DNA barcode is part of a gene called cytochrome oxidase I (COI). Required for metabolizing oxygen, this gene is present in all animals but varies by species. So, given even a tiny fragment of an animal, such as a leg or a hair, we can read its genetic barcode. But that alone does not reveal its species. To determine that, we must compare what we find against a list of barcodes attached to specific species and find a match.

That is the role of the International Barcode of Life (iBOL) project, a major research program that is building a global database of barcode sequences with the ambitious goal of a universal DNA-based identification system. It is a huge task, given the many millions of species in the world. Among the tools created to assist iBOL is the Barcode of Life Data Systems (BOLD), a growing Internet database that already contains barcodes for more than 65,000 identified species.

BOLD, which also includes pictures, maps, taxonomy data and links to museums and expert information, functions as a genetic encyclopedia of biodiversity. It was an essential tool in our study of DNA sequences extracted from bat guano in Ontario, Canada, and undoubtedly will be a vital part of ecological research around the world.

We used mist nets to capture eastern red bats, isolating each one in a cloth bag for about 30 minutes before releasing it. We then gathered the guano pellets left in the bags. Back in the lab, we used fine forceps to dissect these pellets under a microscope and collect tiny fragments of insect bodies. DNA was extracted from each of these fragments, and a portion of the COI gene was sequenced. The sequence “our barcode” from each fragment was compared against the sequences in the BOLD database to search for a species-identifying match.

Since the global DNA barcoding campaign is still a rather new enterprise (it was first proposed by Dr. Paul Hebert of the University of Guelph in 2003), we were not able to find exact matches for all the insects we encountered. We were very successful, nonetheless, with some surprises in the results. The study produced nearly 800 separate barcode sequences from the guano of 56 individual bats. These sequences grouped into 127 distinct species that could be identified.

The results produced a number of insights into the feeding behavior of eastern red bats. First, and least surprisingly, moths constitute about 60 percent of their diet “consistent with what was already known about eastern red bats.

More intriguing, however, were some of the moth species that showed up on the list. These included a number of significant pests, such as gypsy moths, tent caterpillars and cone worms, which damage forest trees, as well as orchard and garden pests including shuckworm moths, codling moths and members of the genus *Acrobasis*.

Also notable were insects that did not turn up in our lists of prey. Moths of the arctiid family are abundant in areas where our red bats were foraging, yet they were entirely absent from the DNA-based dietary survey. This is especially interesting because many moths in this family have evolved adaptations that should help them avoid capture by bats, including the ability to hear ultrasonic bat calls and to produce high-frequency sounds that might confuse bat echolocation. Our findings offer additional evidence that arctiid defenses against bats are quite effective.

Besides moths, barcoding revealed several other groups that had not previously been cited

as prey for eastern red bats, including mayflies, net-wings and caddisflies. We even found an occasional non-insect “two species of spider.

This study clearly demonstrates the value of DNA barcoding for dietary analysis in insectivorous bats. As the barcode database continues to expand its list of identified insects, the accuracy and detail of guano analysis will improve. And these same techniques likely will be applicable to other bat groups, such as the fruit eaters, pollinators, carnivores and vampires.

This new ability to identify organisms from fragmentary remains opens up many new avenues for research in ecology. It greatly increases the precision with which we can examine species interactions and understand how ecosystems work and how best to conserve them.

ELIZABETH CLARE received her undergraduate degree from the University of Western Ontario. She is finishing a Ph.D. in molecular evolution and ecology at the University of Guelph, Canada, under the supervision of Paul Hebert and M. Brock Fenton (of the University of Western Ontario). ROBIN FLOYD received his Ph.D. from the University of Edinburgh, UK. He is a postdoctoral researcher in the lab of Teresa Crease at the University of Guelph. Elizabeth Clare is expanding her work with DNA barcoding with financial support from a 2009 BCI Student Research Scholarship to study resource partitioning among insect-eating bats in tropical Costa Rica.

All articles in this issue:

- ▶ [Armed Rangers and Harsh Lands](#)
- ▶ [Food Forensics](#)
- ▶ [Chasing Migratory Tree Bats](#)
- ▶ [Steppe Bats of Mongolia](#)
- ▶ [BCI's New Leader](#)
- ▶ [News & Notes](#)