

## VOLUME 28, NO. 3 Fall 2010

### In Search of Bat Splats

Droppings may yield genetic secrets of flying foxes

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It is dusk in the South Pacific. Flying foxes rise into the pink-orange sky and cruise above the forest canopy in search of food. As the forest settles into nighttime mode, daytime distractions drift away. The temperature falls (at least a bit), the flies go to sleep, and I have a quiet moment to reflect on why I am here in the Mariana Islands, preparing to crawl around collecting bat feces. Later, in a DNA-analysis lab, I'll use these samples to develop a much-needed method for understanding flying foxes without having to capture or handle these magnificent but threatened bats.

I have been studying fruit bats, primarily the large flying fox (*Pteropus vampyrus*) and golden-capped fruit bat (*Acerodon jubatus*), in the Philippines since 1997. I recently expanded my research to include the Marianas flying fox (*Pteropus mariannus*). Like most endangered flying foxes, the species I study are found on islands in Southeast Asia and the South Pacific, where travel is difficult and research is rare.

In the Philippines, I spent years collecting population and distribution data on the remaining colonies of the largest bats in the world. Interpreting the data is tricky, however, because we lack basic information about the bats' population structure.

Conserving these flying foxes requires answers to two crucial questions: Are colonies of a flying fox species on scattered islands connected or are they isolated populations? And how small can these colonies get before their survival is put at imminent risk? We can't resolve these questions yet, but we have taken a giant step toward answering them.

Historically, the answer to the first question seems simple: The mere fact that colonies exist on a number of islands across an archipelago, such as the Philippines or the Marianas, suggests they are all part of a connected "metapopulation."

Over many years, there probably was enough movement among the islands for the scattered colonies to remain part of the same species. But how has the introduction of people changed the rules? Are migrations more dangerous now because of hunting pressure or limited habitat? Documenting the connections among populations will help managers understand the new dynamic and identify islands on which conservation efforts should focus.

The second question, on population size, is especially critical. Flying fox colonies in the Philippines once numbered in the hundreds of thousands and were found on every major island. Now few colonies remain, and they are mere shadows of historic sizes — often fewer than 5,000 individuals.

When wildlife populations fall below a certain threshold, they can enter a negative-feedback loop. They become susceptible to chance genetic or environmental impacts, which shrink the population further and increase susceptibility even more, and so on in what biologists call an "extinction vortex." That frightening name fits the



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consequences.

Virtually any species can collapse into an extinction vortex, but the threshold varies by species and ecosystem. In the Philippines, we know that most flying fox populations are small. But we don't know if these populations have fallen so far that they could face an impending crash. In the Mariana Islands, populations are even smaller, but they are a different species. Are these numbers similar to historic populations? Might some island colonies already face becoming too small? Effective conservation and management depends on answering these questions.

Genetic analysis is used on some species to explore critical conservation issues. But I had sworn off using genetics with fruit bats because it traditionally required tissue samples, which means capturing bats. From earlier fieldwork, I have the scars to prove how difficult it is to catch even one flying fox, let alone the numbers required to answer population-level questions.

Plus, capture clearly causes stress among these large bats. It had been suggested that I pay hunters to collect bats for research, but paying for dead bats was certainly not the message I wanted to send to local communities.

I had been working on fruit-bat research and conservation in the Philippines for more than nine years before I realized what now seems obvious: fecal samples might provide flying fox DNA without putting the bats at risk.

(Fruit-bat poop, by the way, is not considered guano and has no generally accepted name. "Splat," a term occasionally found in scientific literature, seems quite descriptive, so I am using it.)

Splats are easy to collect and do not require capturing, handling or harming flying foxes. The promise of splats as a benign source of flying fox DNA was exciting, so I applied for " and received " a Bat Conservation International Student Research Scholarship to give it a try.

But implementing a new idea is rarely easy. Although genetic-research labs had been using fecal samples to extract DNA (from cells sloughed off the intestines) for scores of species, many of my academic advisors were skeptical that the process would work for flying foxes. They noted that food passes quickly through the guts of these bats and the amount of feces is small, so the chance of finding sufficient intestinal cells seemed unlikely.

As I was becoming discouraged, however, a mentor suggested I contact bat biologist Gary McCracken, a well-known geneticist and now a BCI Board Member. McCracken assured me that the idea could work and said he had done it in unpublished lab experiments a few years earlier.

So on my next trip to the Philippines, I collected splats from two flying fox species by spreading plastic sheets under roost trees that contained only the targeted species. Flying fox colonies in the Philippines may contain several species of bats, but they are often segregated in the roosts.

I delivered the samples to the genetics lab at the University of Montana, where my colleagues spent the past year tweaking their fecal DNA-extraction kits to obtain and analyze fruit-bat DNA from the tiny splats.

The news came in an email in May: the process works!

Much remains to be done, of course, as we optimize the protocol for using fruit-bat splats as a source of genetic material. Our success came with mitochondrial DNA, which is useful for such basic issues as identifying species. Mitochondria are energy-producing structures outside the cell's nucleus and the small strands of DNA they contain are distinct from nuclear DNA, which comprises the chromosomes.

We plan to develop procedures for finding and using nuclear DNA, which provides much finer detail, including identifying individual bats. We also hope to learn exactly what's required for good samples with current analytical tools. But we have cleared our biggest hurdle by demonstrating that bat splats can be used for DNA analyses. Now we can begin answering critical questions about the conservation of flying foxes.

It is dark in the forest and most of the bats have left the trees. I put on my headlamp and follow my trail markers to the roost where I spread plastic sheets the night before. I scrape a day's worth of bat splats into small paper bags and encase each one in a plastic wrap. Scraping splats may sound less glamorous than capturing bats, but I find it exciting. These little droppings may hold answers that can help us save these remarkable bats from slipping away forever.

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