Exome Sequencing of Five Lemur Species from a Captive Colony

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Lemurs are a group of primates only found on the island of Madagascar off the southeast coast of Africa. They are thought to have arrived at Madagascar about 60 million years ago via a rafting event from the African coast that carried the ancestor of living lemurs to the island. An adaptive radiation followed the primordial lemur’s arrival in Madagascar, as the relative absence of major predators and competitors on the island at the time provided many niches to be filled. Today, there are over 100 recognized species of lemurs on Madagascar. Lemurs have also retained several morphological traits, like the presence of a wet nose and small brain size, that are considered ancestral in the evolutionary history of primates. The combination of retained ancestral features, unique traits that lemurs have evolved during their isolation in Madagascar, and the wide diversity of lemur species has drawn the attention of many researchers, conservationists, scholars, and natural historians interested in primate evolution.

There has been a lot of work done examining the evolutionary biology, behavior, morphology, and ecological features of lemurs and lemur populations. This grant is helping me make my own addition to what is known about lemurs by adding a wealth of genetic information about five different lemur species. Specifically, I acquired blood samples from two individuals, a male and a female, from each of four brown lemur species (*Eulemur ruffifrons*, *E. rubriventer*, *E. flavifrons*, and *E. fulvus*) and one species of sifaka (*Propithecus coquereli*) from the Duke Lemur Center at Duke University (Figure 1). After extracting DNA from these blood samples at Dr. Jason Kamilar’s Comparative Primatology Laboratory here at UMass, I send the extracted DNA to the Yale Center for Genome Analysis (YCGA) at Yale University. At the YCGA, the DNA samples underwent exome sequencing. Exome sequencing is a type of genetic sequencing that targets all of the coding region of the genome which are all the genes that code for proteins in the body. While the exome only makes up 2% of the genome, in humans this still amounts to some 20,000 genes! Exome sequencing is an affordable approach for getting a lot of genetic data on genomic regions with well-researched and annotated functional properties. After all, proteins are the building blocks of everything in the body and underlie all of its manifold physiological processes. Thus, the data I now have on hand have lots of important lessons to teach us about how brown lemurs and sifakas have evolved on the genetic level.

Fig. 1 The five lemur species I had sequenced. From left to right: Coquerel’s sifaka (*P. coquereli*), the red-fronted brown lemur (*E. ruffifrons*), the red-bellied lemur (*E. rubriventer*), the blue-eyed black lemur (*E. flavifrons*), and the common brown lemur (*E. fulvus*). Pictures are not my own and from Wikipedia

The great news is that the quality control measures I ran on the sequence data I received from the YGCA show that my samples produced high quality data. This is really exciting because it shows that
exome capture methodologies designed for humans can yield high quality exome sequence data from primate species that have been diverged form humans for over 60 million years. In fact, these data are among the first lemur exomes sequenced and might be the first exomes ever sequenced for the four brown lemur species I sampled. All this high-quality data however, means that I have millions of bits of genetic sequences that I have to put together. Exome sequencing relies on fragmenting full DNA sequences into small pieces to clone and then sequence in parallel. What I am working on now is mapping all of these “reads” to a reference genome that was recently sequenced for the Coquerel’s sifaka. By using the Coquerel’s sifaka genome as a scaffold, I’ll be able to piece together my exomes and then begin to examine how the brown lemur and sifaka species I sampled differ in their protein-coding genes. While I am primarily interested in genes related to different neural circuits and processes, I’ll be able to use these data to explore the evolution of many other biological processes in lemurs.