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NMRC Researchers Sequence Bat Genomes and Gain Insights That Could Potentially Be Used to Mitigate Viral Infections in Humans

SILVER SPRING, Md. – A team of researchers from the Naval Medical Research Center (NMRC) worked with international partners to sequence the genome of two bat species. This sequence data could eventually be used to mitigate viral infections in humans and lead to vaccines for deadly viruses. The study was published December 20, 2012, online in *Science*.

Over the past decade and longer, bats have been implicated as reservoirs of a number of deadly viruses. Until recently little was known of the bat's immune system and or why bats can carry viruses like Nipah, Hendra, Ebola and others that kill mammals like horses, cats, and humans and yet not get sick.

“We sequenced the entire genome of two very different bats and did comparisons between the two and with other mammals,” said Dr. Kimberly Bishop-Lilly, deputy head of NMRC's Biological Defense Research Directorate Genomics Program. “We found that there are some key differences in genes that affect the bat's immune system and the way it deals with DNA damage. These differences may have come about as a byproduct of the evolution of flight. For instance, we found differences in a gene called c-rel, which plays a role in the innate immune system and in DNA damage response, which is a target for virus-interactions.”

Researchers are beginning to see that there are some key differences between a bat's immune system and that of a human. The more they investigate those differences the closer they will get to coming up with novel antiviral strategies for people.

Bishop-Lilly pointed out that bats are very ancient mammals and have some unique characteristics like flight, hibernation, and echolocation. At the time the NMRC researchers began their work only one bat genome sequence was available, the *Myotis lucifugus*, the little brown bat, which hasn't been shown to be a vector for any of the very deadly emerging viruses. The researchers then sequenced the genome of the giant flying fox, a kind of bat that has been shown to carry those types of viruses, as well as the genome of

another bat, *Myotis davidii*, and made a comparison to learn more about what gives the bat the ability to carry a deadly virus without getting sick.

“Genomic research is very valuable to biomedical research because all the traits that make up a person, essentially all the traits that influence a person’s susceptibility to a given disease, are encoded in their genome,” said Bishop-Lilly. “It is essentially the blueprint for health and diseases. The more we understand the genetic basis for health and diseases, the more possibilities there are for designing drugs to treat or prevent diseases. By studying how traits, like the bat’s innate immunity, have evolved in the genome, we can come up with creative new ways to prevent or treat viral infections.”

Collaborating with researchers from the Uniformed Services University of the Health Sciences in Bethesda, Md., the Australian Animal Health Laboratory, the Beijing Genomics Institute, the Wuhan Institute of Virology, and the University of Copenhagen, the NMRC team made significant progress and the results of the study, “Comparative analysis of bat genomes provides insight into the evolution of flight and immunity,” have been published in *Science* online.

“This study opens the door for further investigation into the relatively unique biology of bats and how their bodies interact with microbes,” said Bishop-Lilly. “Our hope is that other scientists can build upon these findings through further comparative genomics and that our findings together will hopefully lead to the design of antiviral drugs in the future.”

There are a wide range of applications for genomic research, from discovering novel disease-causing microorganisms, to characterizing individual’s genomes and coming up with specific therapies. At NMRC researchers are currently using genomic research to address other areas as well by looking for biomarkers of bioweapons exposure in humans with the aim of developing new assays, characterizing strain collections, and developing bioinformatics pipelines to help make high-throughput sequencing fieldable.

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