

# Bats are the major reservoir of coronaviruses worldwide

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A researcher examines a *Pipistrellus hesperidus*, or Dusky Pipistrelle bat, collected in Uganda. Credit: Kirsten Gilardi, UC Davis

Results of a five-year study in 20 countries on three continents have found that bats harbor a large diversity of coronaviruses (CoV), the

family of viruses that cause Severe Acute Respiratory Syndrome Coronavirus (SARS) and Middle East Respiratory Syndrome Coronavirus (MERS). Findings from the study—led by scientists in the USAID-funded PREDICT project at the Center for Infection and Immunity (CII) at Columbia University's Mailman School of Public Health and the University of California, Davis' One Health Institute in the School of Veterinary Medicine—are published in the journal *Virus Evolution*. PREDICT is a globally coordinated effort to detect and discover viruses of pandemic potential and reduce risk for future epidemics.

With the cooperation of local governments, researchers sampled and tested 19,192 [bats](#), rodents, non-human primates, and humans in areas where the risk of animal-to-human transmission is greatest, including sites of deforestation, ecotourism, and animal sanctuaries. The researchers identified 100 different CoVs and found that more than 98 percent of the animals harboring these viruses were bats, representing 282 [bat species](#) from 12 taxonomic families. Extrapolating to all 1,200 bat species, they estimate a total of 3,204 CoV are carried by bats worldwide, most of which have yet to be detected and described. They also found that CoV diversity correlated with bat diversity with high numbers of CoVs concentrated in areas where there are the most bat species, suggesting CoVs coevolved with or adapted to preferred families of bats.

"This study fills in a huge gap in what we know about the diversity of coronaviruses in animal hosts," says first author Simon Anthony, assistant professor of Epidemiology in CII. "Charting the geographic and genetic diversity of coronaviruses in animals is a critical first step towards understanding and anticipating which specific viruses could pose a threat to human health."

## **The First Step to Identifying Suspect Viruses**

The researchers used consensus PCR, a cost-effective technique that targets a small section of the viral genome—sufficient to locate the position of each [virus](#) in the family tree of all CoVs. To go a step further, researchers are using more powerful genome-wide sequencing to take a detailed look at those viruses that resemble known threats to humans. In a study published in April, they reported that a MERS CoV-like virus did not have the genetic prerequisites to jump to humans—a sign that MERS-CoV had evolved to become more capable of transmission. A similar effort is now underway to sequence viruses similar to SARS-CoV.

## **Regional Variation in Risk of Virus "Jumping" Outside Its Genus**

Researchers report preliminary evidence that CoVs in bats in Latin America were less likely than CoVs in Africa and Asia to "jump" outside their genus or family, potentially a sign of relatively lower risk of bat-to-human transmission on that continent. However, the authors caution that these regional differences may reflect variation in the ecology of bats in the various areas, and more work needs to be done to understand this.

## **Bats Play an Important Role**

The researchers say their findings should not be interpreted as a call to cull bats. Bats play an important role in the ecosystem, and most of the coronaviruses they carry are harmless to humans. Additionally, culling may have unintended consequences: destabilizing host ecology can actually increase risk for disease transmission, as seen in studies of Marburg and rabies viruses.

"Our goal is to shed light on the ecology of virus-host interactions to

better understand and address the conditions that give rise to outbreaks like SARS and MERS," says senior author Tracey Goldstein, associate professor at the One Health Institute at the University of California, Davis.

Provided by Columbia University's Mailman School of Public Health

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