

Discovery of a hepatitis C-related virus in bats may reduce outbreaks in humans

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Viral hepatitis affects more than 500 million people worldwide and is a cause of liver failure and liver cancer. While vaccines are available for hepatitis A and B, this is not the case for hepatitis C, which affects as much as two percent of the population in the U.S. Scientists today are reporting discovery of a virus related to hepatitis C in Asian bats, which may provide insights into the origins of the hepatitis C virus and into the mechanisms by which infectious diseases move from other species to humans.

The full study findings are published online in the publication *PLoS Pathogens*.

Transmitted by [blood transfusion](#) or [sexual intercourse](#), hepatitis C is a common cause of [liver failure](#). Viruses related to hepatitis C, known as GB-viruses, have previously been found only in primates. Now, using cutting-edge molecular techniques, an international team of investigators has identified a GB-virus in *Pteropus giganteus* bats in Bangladesh. The work was completed at the Center for Infection and Immunity (CII) at Columbia University's Mailman School of Public Health, led by W. Ian Lipkin, MD; the International Centre for [Diarrheal Disease](#) Research in Bangladesh; 454 Life Sciences, a Connecticut-based division of Roche Corporation; and the Wildlife Trust in New York City. Using [gene sequencing](#) methods, the investigators confirmed the viral genetic material in the serum of five of 98 bats, and in the saliva of one, to be related to GBV-A and -C viruses. Further analysis of the two identified strains, tentatively named GBV-D, suggests that *P. giganteus* bats are a

natural reservoir for this virus. According to the research team, the fact that bat saliva can contain GBV-D [nucleic acids](#) provides a biologically plausible mechanism for this agent to be transmitted from infected bats to other hosts, including humans.

Bats are often important hosts for emerging infectious disease agents with significant impact on human health including rabies, ebola, Marburg, hendra, nipah, and SARS viruses. Opportunities for transmission to humans are particularly prominent in countries like Bangladesh, where people live in close association with bats.

"This discovery underscores the importance of international programs focused on microbe hunting in hot spots of emerging infectious diseases," said Dr. Ian Lipkin, John Snow Professor of Epidemiology and director of the CII. "Finding this novel flavivirus in bats significantly broadens the host range of GB-like agents and may provide insights into the origins of [hepatitis C](#)," added Thomas Briese, PhD, lead molecular biologist on the team and Mailman School associate professor and associate director of CII.

"The Indian subcontinent and South Asia are areas where we are ardently working to identify the next possible pandemic disease," stated Peter Daszak, President of Wildlife Trust. "Identification of the natural reservoir of a virus, even if it may not directly infect people, is critical to surveillance and reducing the risk of outbreaks of infectious disease," noted Jonathan Epstein, associate vice president of Conservation Medicine Programs at Wildlife Trust.

Provided by Columbia University's Mailman School of Public Health

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