

Hepatitis c-like viruses identified in bats and rodents

As many as one in 50 people around the world is infected with some type of hepacivirus or pegivirus, including up to 200 million with hepatitis C virus (HCV), a leading cause of liver failure and liver cancer. There has been speculation that these agents arose in wildlife and jumped species to infect humans; however, little was known about their distribution in other species.

In two new papers published in the journals *mBio* and *Proceedings of the National Academy of Sciences*, investigators at the Center for Infection and Immunity (CII) at Columbia University's Mailman School of Public Health report the discovery of hepaciviruses and pegiviruses—close relatives of HCV—in rodents and bats. The viruses are similar to those that infect humans and may therefore provide insights into the origins of HCV, as well as the mechanisms behind animal-to-human transmission. It may also enable development of new animal systems with which to model HCV pathogenesis, vaccine design, and treatment.

Both discoveries were made using high-throughput sequencing and other molecular methods for pathogen discovery pioneered at CII. Both represented multicenter global efforts.

As reported in *mBio*, Amit Kapoor, PhD, and colleagues screened more than 400 wild-caught rodents. Molecular analysis revealed the presence of hepaciviruses and pegiviruses closely related to those found in humans. "Importantly, the rodent hepaciviruses contained sequences that are thought to play a role in liver infection in HCV," says Dr. Kapoor, lead author of the study and assistant professor of Pathology and Cell Biology at Columbia University Medical Center. "We also found instances of a single animal infected with multiple hepaciviruses."

Such co-infections have also been observed with HCV in humans, suggesting that the immune response to HCV is different than with most viral infections—a finding that has implications for vaccine design. "It also supports the potential use of rodent hepaciviruses in developing models for human disease," says W. Ian Lipkin, MD, John Snow Professor of Epidemiology and director of the CII.

Researchers from Rockefeller University, University of Edinburgh, University of Copenhagen, University of New Mexico, North Carolina College of Veterinary Medicine, Pennsylvania State University and the National Institutes of Health contributed to the study. Results appear online in *mBio*.

In a second study led by P. Lan Quan, PhD, molecular assays of 1,615 bats collected worldwide led to the identification of 83 novel hepaciviruses and pegiviruses, representing an infection rate of nearly 5%. "The broad prevalence, unprecedented diversity, and worldwide distribution of these novel viruses suggest that bats are a major and ancient reservoir for both hepaciviruses and pegiviruses, and provide insights into the evolutionary history of HCV and human pegiviruses," says Dr. Quan, associate research scientist at the Center for Infection and Immunity.

Source: Columbia University's Mailman School of Public Health