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Researchers identify first known relatives of rubella virus

Bethesda, Md. – An international research team recently discovered two new animal viruses that are the first known relatives of the rubella virus, which could ultimately impact global efforts to eliminate the virus. These findings were published Oct. 7 in *Nature*.

The study, “Relatives of rubella virus in diverse mammals,” was performed in the laboratory of Dr. Kimberly Bishop-Lilly, director of the Genomics & Bioinformatics Department at the Biological Defense Research Directorate, Naval Medical Research Center (NMRC) in Frederick, Md, and a graduate of the Uniformed Services University (USU). Bishop-Lilly advised Dr. Adrian Paskey on this project. Paskey was an Emerging Infectious Diseases (EID) student at USU at the time she was conducting this research, and is now a postdoctoral fellow with the Centers for Disease Control and Prevention (CDC). The discovery was also part of a large collaborative effort between many other academic partners as well as several German labs and institutes, who were studying bats in Kibale National Park in Uganda and mice and ill animals at a zoo in Germany.”

Rubella, also known as “German measles,” is caused by a respiratory virus with symptoms of skin rash and fever, and it can result in birth defects, miscarriages and stillbirths if it infects pregnant women. Between 1964 and 1965, a rubella epidemic affected over 12 million people the USA. The first rubella vaccine became available in 1969 and the virus had been eliminated in the U.S. by 2004. Today, rubella still circulates in some parts of the world but is considered to be a prime target for global eradication by the World Health Organization. Many children around the world are vaccinated against rubella, along with measles and mumps. The combined “MMR” vaccine is safe and effective.

The team of researchers found two new animal viruses that are the first known relatives of rubella virus: ruhugu virus (in western Uganda) and rustrela virus (in northern Germany). The ruhugu virus was found in cyclops leaf-nosed bats, a common species of insect-eating bat that lives in hollow trees across Equatorial Africa. Half of bats were infected, possibly indicating that these bats are natural carriers of the virus. The rustrela virus was found in yellow-necked field mice, a common species of rodent that lives in a variety of habitats across Europe and Asia. Half of the mice were infected, which could indicate that these mice are natural carriers of the virus.

It is not known whether the new viruses can infect humans and there is no evidence that humans have been infected with these viruses. Likewise, there is no evidence that rubella virus can infect animals. Rustrela virus caused the deaths of a donkey, a capybara, and a kangaroo at a zoo in Germany, indicating that these types of viruses can “jump” into new species and cause disease. Based on their findings, the authors think rubella has a zoonotic origin.

“This makes sense because many human viruses originated in animals. We don’t know if rubella virus originally came from a bat, a mouse, or another mammal, or when it made the ‘jump’ into humans,” Paskey said.

The authors also emphasized the importance of ecosystem conservation as a tool to prevent situations where people and animals come into close contact, possibly allowing viruses to “jump” across species.

Collaborations on the study included the Navy Medical Research Center, along with the University of Wisconsin, the Integrated Research Facility at the National Institute of Allergy and Infectious Diseases (NIAID), the Institute of Diagnostic Virology, Institute of Novel and Emerging Infectious Diseases, Department of Experimental Animal Facilities and Biorisk Management, Friedrich-Loeffler-Institut (Germany), State Office for Agriculture, Food Safety and Fisheries (Germany), and the German Center for Infection Research.

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To read the full study, visit <https://www.nature.com/articles/s41586-020-2812-9>.

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