

Hitting snooze on the molecular clock: Rabies evolves slower in hibernating bats

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The rate at which the rabies virus evolves in bats may depend heavily upon the ecological traits of its hosts, according to researchers at the University of Georgia, the U.S. Centers for Disease Control and Prevention and Katholieke Universiteit Leuven in Belgium. Their study, published May 17 in the journal *PLoS Pathogens*, found that the host's geographical location was the most accurate predictor of the viral rate of evolution. Rabies viruses in tropical and sub-tropical bat species evolved nearly four times faster than viral variants in bats in temperate regions.

"Species that are widely distributed can have different behaviors in different geographical areas," said Daniel Streicker, a postdoctoral associate in the UGA Odum School of Ecology and the study's leader. "[Bats](#) in the tropics are active year-round, so more rabies [virus transmission](#) events occur per year. Viruses in [hibernating bats](#), on the other hand, might lose up to six months' worth of opportunities for transmission."

Understanding the relationship between host ecology and viral evolution rates could shed light on the transmission dynamics of other viruses, such as influenza, that occur across regions, infect multiple [host species](#) or whose transmission dynamics are impacted by anthropogenic change.

The team's findings could eventually help [public health officials](#) better predict when rabies virus transmission could happen in different environments and as environments change, but Streicker cautions that more research into the rabies [virus genome](#) and bats' overwintering

ecology is needed.

"If viral evolution is faster, it could potentially lead to greater [genetic diversity](#) in crucial parts of the [viral genome](#) that allow it to shift hosts," he said. "For rabies, we don't yet know what those are, so identifying them will be key. Similarly, before understanding whether climate change will speed viral evolution, we need a better idea of how environmental changes will influence host ecology and behavior."

Evolutionary biologists have long recognized that molecular evolution proceeds in a largely clock-like manner, with mutations accumulating at a fairly constant rate over time. This "molecular clock" allows for powerful inferences—from dating the origins of species to the origins of epidemics. However, the rate at which the clock ticks varies dramatically among species; much research has focused on what causes these differences.

For RNA viruses such as rabies, understanding the rate variability has practical implications, since faster evolution can enable viral emergence in new species or allow a virus to evade its host's immune defenses. However, nearly all past studies compared viruses of completely different families and were therefore limited to focusing on viral structural traits. Since few opportunities existed to study the evolution of similar viruses in different host species, the role of the host had been almost completely neglected.

Streicker set out to better understand the tempo of the evolution of rabies viruses in bats, and specifically what, if any, role the host species played.

To conduct the study, Streicker and his colleagues compiled a database of rabies virus genetic sequences from infected bats in the U.S. and South America, representing 21 different variants of the virus. They also

collected information on the biology and ecology of the different bat species that served as viral hosts. They looked at the evolutionary history of the different bat species; their overwintering behavior (whether the bats hibernated, went through periods of torpor or remained active during the winter); their metabolic rates; and their migration habits (whether they engaged in long distance migration). They also classed the bats by climatic region and whether they were solitary or roosted in colonies.

Their analysis of this enormous database revealed extreme variability in the rate of evolution in different rabies viruses, comparable to the differences seen between viruses of entirely different families. The analysis also suggested that viral genetic traits were not chiefly responsible for this variation since rates seemed to shift freely throughout the ancestral history of the [rabies virus](#) as it jumped into new [bat species](#).

"Earlier studies led to the conclusion that viral genomic traits are driving the evolution rate," Streicker said. "It turns out that's not the whole story. In this case, host biology plays an important role."

The trait that best correlated with the rate of viral evolution was not the host's evolutionary history. It was its climatic region, which affects the bats' behavior.

Rabies in tropical bats goes through more generations per year than in temperate bats, a mechanism also hypothesized to accelerate how quickly the molecular clock ticks in free-living tropical plants and animals. The rapid evolution in rabies viruses provided the researchers with an opportunity to examine one of the mechanisms thought to drive the differences in evolution and species diversity across latitudes from the poles to the tropics.

"This is just another example of how the fast pace of [evolution](#) in RNA viruses makes them exceptional tools for understanding simultaneously ecological and evolutionary processes," Streicker said.

More information: For the study, "Rates of viral evolution are linked to host geography in bats," see [dx.plos.org/10.1371/journal.ppat.1002720](https://doi.org/10.1371/journal.ppat.1002720)

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