

UF veterinary researchers discover new virus linked to death of Australian snakes

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A University of Florida researcher and colleagues in Australia and Germany have discovered what might be a deadly new snake virus.

Dubbed the “Sunshine [virus](#)” because of its discovery in Australia’s Sunshine Coast region, the organism causes nervous system and respiratory disease and is the first of its kind to be identified. Although it is in the same overall family as other viruses that affect snakes and lizards, the Sunshine virus doesn’t fit into existing subgroups of viruses.

The discovery, described online and in the upcoming October 2012 print edition of the journal *Infection, Genetics and Evolution*, might help scientists better understand the biology and origin of an important group of disease-causing organisms and inform efforts to prevent future outbreaks.

“Understanding the ecology and diversity of infectious diseases of wildlife is critical,” said co-author James Wellehan, an assistant professor of zoological medicine at the UF College of Veterinary Medicine. “While medicine has traditionally waited for big outbreaks to cause large numbers of deaths and then dealt with new diseases reactively, an understanding of what viruses are out there and how they can be expected to behave allows us to be proactive, being aware of and monitoring agents of potential concern.”

The emergence in recent years of deadly new viruses that attack humans has raised concerns regarding transmission between wildlife, livestock

and humans. For example, the Hendra and Nipah viruses caused high rates of death in Australia and Indonesia in the 1990s, not just among horses and pigs but also among humans.

The quest to identify the new virus started as an investigation of the cause of a 2008 disease outbreak in a privately owned Australian collection of 70 pythons. As more and more animals became sick, showing signs of pneumonia, depression, lethargy and abnormal behavior such as “star gazing” — staring up at things — they were all eventually euthanized.

The researchers had great difficulty detecting the elusive virus and struggled to identify the category in which it belonged.

“We screened more than 450 samples, including swabs, tissues and blood for snake viruses,” said lead author Timothy Hyndman, a lecturer and graduate student at Murdoch University in [Australia](#). “It was very frustrating. After two and a half years, we finally isolated something. A year later, we figured out what it was.”

The researchers infected snake heart cells with virus collected from tissues of the affected snakes and found that it caused the cells to become abnormally large and have more than one nucleus, the cell’s command center.

Using sophisticated techniques for analyzing large numbers of genetic sequences at the same time, the researchers identified several that had limited similarity to known viruses in large genetic databases. They used this information to put together the genetic blueprint of the Sunshine virus. Statistical analyses that allow construction of a “family tree” showed that the Sunshine virus belonged to a family called paramyxovirus. That family contains some of the most significant disease-causing agents in animals and humans, according to the National

Center for Biotechnology Information. Measles, mumps and canine distemper are all in the family.

But unlike all known snake and lizard viruses in that family, the new virus did not fit into a subgroup called ferlavirus. The new virus is only distantly related to those viruses.

“This is the first non-ferlavirus paramyxovirus to be discovered from a reptile,” Hyndman said. “In the previous 40 years, reptilian paramyxoviruses were all very similar until this one was discovered.”

Previously known members of the virus family have grouped into two subfamilies. The Sunshine virus fell outside both of those known groups. Inclusion of Sunshine virus in the family tree analysis showed that viruses thought to be in the same subfamilies might not actually share recent ancestors, the researchers said.

“The two subfamilies may need to be split up into distinct families,” Wellehan said.

Although it is likely that the virus was responsible for the outbreak of disease in the collection of pythons, that has not been proved irrefutably.

The study shows off how sophisticated gene sequencing technology can be used to characterize mysterious new viruses and possibly speed up public health responses to outbreaks in humans, animals and plants, the researchers said.

“This virus was invisible to prior technologies,” said Eric Delwart, director of molecular virology at the Blood Systems Research Institute and an adjunct professor of laboratory medicine at the University of California, San Francisco, who was not involved in the study. “Besides providing assays to help track and control outbreaks of this new snake

virus, the study highlights the enhanced ability of scientists to rapidly identify novel pathogens.”

Provided by University of Florida

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