

# Hidden viruses thrive in desert wildlife

## ASU researchers uncover viruses in lovebirds and bobcats, shedding light on how pathogens move through Arizona's ecosystems

By Richard Harth, ASU News  
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As the sun rises over the Sonoran Desert, bright green lovebirds gather noisily around backyard feeders. At dusk in the Arizona foothills, bobcats slip silently through dry washes and rocky crags.

These familiar animals seem worlds apart — one urban and social, the other solitary and elusive. But new research from Arizona State University shows they share something unexpected: previously unknown viruses quietly circulating in their bodies.

In two new studies, researchers used modern genomic tools to explore the hidden viral world in unexpected places. Together, the studies offer a snapshot of viral diversity in desert wildlife and demonstrate how scientists track viruses across hosts, environments and time.

Virologist [Arvind Varsani](#) and his colleagues, including ornithologist [Kevin McGraw](#), identified previously unknown viruses in Phoenix's feral lovebirds. In a separate case study, they uncovered novel viruses associated with a wild Arizona bobcat in collaborative work with [Arizona Game and Fish Department](#).

The research traces where these viruses came from and how long they've circulated in Arizona, and it explains why understanding them now is important.

"In these studies, we partner with both local and international scientists to carry out exciting research on these iconic animals," says Varsani, corresponding author of the new studies. "Collaborative, multidisciplinary research enables us to break discipline-specific silos, execute scientific inquiry faster and learn new techniques from each other that lead to new insights."

The research was conducted by lead authors [Simona Kraberger](#) and [Ayla Žuštra](#), both members of the [Varsani lab](#). Varsani is a researcher with the [Biodesign Center for Fundamental and Applied Microbiomics](#), the [Center of Evolution and Medicine](#) and the [School of Life Sciences](#) at ASU.

### Healthy birds, hidden viruses

[One study](#) focused on feral rosy-faced lovebirds — bright green parrots that have become a familiar sight in Phoenix after escaping or being released from the pet trade decades ago. Although these birds appear healthy and thrive in urban neighborhoods, little was known about the viruses they carry.

Researchers collected samples from dozens of lovebirds across multiple sites in the Phoenix area and screened them for DNA viruses. These are viruses that encode their genetic information in DNA rather than RNA. While both types of viruses can cause diseases, they infect and reproduce in different ways.

The results revealed a surprisingly rich viral landscape. Many birds carried beak and feather disease virus (BFDV), a type of circovirus. Circoviruses have circular DNA and commonly infect birds and pigs. BFDV is known to cause severe disease in some parrot species. Yet in these lovebirds, the virus does not appear to cause illness.

Genetic analysis showed that the BFDV strains found in Phoenix lovebirds were closely related to viruses seen elsewhere in the world. This suggests they arrived with imported pet birds and have persisted locally for years, possibly decades.

The team also found a previously unknown adenovirus in the birds. Adenoviruses are a common group of viruses that, in humans, can cause respiratory infections, stomach bugs, pink eye and more. They are also common in birds.

To understand how these viruses are related and how long they have been present, the researchers used Bayesian phylogenetic analysis — a statistical approach that builds evolutionary trees from viral genomes. Rather than simply identifying which viruses are present, this method helps estimate when different viral lineages diverged and how they likely spread through populations.

The findings show that feral lovebirds serve as long-term hosts for multiple viruses, offering scientists a valuable opportunity to study viral persistence and evolution in a stable, urban wildlife population.

“When we study viral communities in wildlife, we are able to learn so much more than just disease associations — we can uncover clues about the host population history, behavior and movement, and how viruses persist and evolve in their hosts,” Kraberger says.

The research appears in the journal *Virology*.

## **A bobcat case study**

[The second study](#) took a very different approach. Instead of sampling many animals, researchers conducted an in-depth case study of a bobcat that had already died and was examined postmortem. The adult male, found northeast of the Phoenix area, had died from traumatic injuries unrelated to disease.

The team analyzed all genetic material in the samples using metagenomic sequencing, a technique that reads DNA from everything present at once — host tissue, parasites, bacteria and viruses. Unlike traditional tests that look only for specific organisms chosen in advance,

metagenomics reveals what's there without prior assumptions, making it especially powerful for discovery.

The analysis revealed four previously unknown circovirids, members of a family of small DNA viruses related to circoviruses. Importantly, the viruses were not all found in the bobcat's tissues. Some appeared in fecal material, while others were detected only in a tapeworm recovered from the animal, suggesting they may infect parasites rather than mammals.

If so, those viruses could act as molecular “tags,” allowing scientists to track tapeworm life cycles and food-web connections that are otherwise difficult to observe. Because the viruses evolve alongside their parasite hosts, their genetic signatures can reveal where parasites have moved — even when the parasites themselves are hard to detect.

“Typically, research on viruses focuses on infection and disease outcome,” Žuštra says. “Here, we approached the research from a more unconventional angle and looked at viruses as a tool to discover interactions or patterns we may not have been able to see otherwise.”

The study appeared in the journal *Viruses*.

## **Two methods, one larger picture**

Although the studies examined different animals using different approaches, they complement each other. Metagenomics answers the question “what's here?” — casting a wide net to detect genetic material from many organisms at once. Phylogenetic analysis answers “where did it come from, and how did it move?” — placing viruses into an evolutionary and geographic context.

Together, these tools allow researchers to move beyond simple detection and toward a deeper understanding of viral ecology.

## **Why viral diversity matters**

Viruses are often associated with disease, but most viruses do not cause obvious illness. Some may even play beneficial roles in regulating ecosystems or shaping immune systems. In humans, for example, about 8% of the genome consists of remnants of ancient viral infections, embedded over millions of years of evolution.

Understanding viral diversity in wildlife is challenging, especially compared with bacteria or larger parasites. Viruses mutate quickly, exchange genetic material and frequently jump between hosts. That complexity makes it difficult to predict which viruses might pose future risks, but also makes baseline surveillance essential.

By documenting viruses already present in common species, researchers can better recognize changes when they occur. In a rapidly growing desert city where wildlife, pets and people increasingly intersect, this knowledge may prove particularly valuable.

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*This story originally appeared on [ASU News](#).*

## Main image



Beneath feathers and fur, a hidden viral world comes into focus through genomic research on Arizona's lovebirds and bobcats. Graphic by Jason Drees/ASU

## Text image(s)





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