

# Birds of all feathers and global flu diversity

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A member of the Wildlife Conservation Society surveillance team prepares to release a whooper swan on a Mongolian lake following sample collection and fitting of a neck collar, part of ongoing health and migration studies. Credit: Martin Gilbert

A group of international scientists have completed the first global inventory of flu strains in birds by reviewing more than 50 published studies and genetic data, providing new insight into the drivers of viral

diversity and the emergence of disease that can ultimately impact human health and livelihoods.

The research, published in the journal *PLOS ONE* and performed as part of the USAID PREDICT project, identified over 116 avian [flu strains](#) in wild [birds](#). This is roughly twice the number that were found in domestic birds, and more than ten times the number found in humans.

Additionally, an analysis of studies that sampled more than 5,000 birds suggested some regions may have more viral diversity than others.

Avian [flu](#) outbreaks come with no warning. In 2013, an H7N9 avian flu strain caused a deadly outbreak in people in China. This surprised virologists, as the strain had never before caused disease in humans. To date, there have been more than 300 clinical cases of H7N9 with a 33 percent mortality rate. This year, another strain known to infect birds, H10N8, has caused human cases for the first time.

As was the case in the H7N9 outbreak, most direct bird-to-human spillover events (when a virus jumps from one species to another) of avian flu can be traced back to human contact with domestic poultry. Although avian flu strain diversity often originates in wild birds, it is the mixing of viruses among poultry, pigs, and people that substantially heightens the disease risk in humans.

In an effort to improve preparedness, scientists are looking to better understand and monitor the diversity of all [avian flu](#) viruses – not just those known to cause disease. Completing the first global inventory of flu strains in birds is a key step in building that understanding.

"This snapshot of the world of flu virus diversity in birds is the outcome of many years of ecology and evolution, as viewed through the lens of surveillance methods utilized by scientists from around the world," said study lead and Wildlife Conservation Society (WCS) Associate Director

of Wildlife Epidemiology, Dr. Sarah Olson.

Understanding the natural diversity of viruses is critically important to identifying health risks. But authorities face a challenge, both in focusing efforts in the right places, and adequately financing surveillance to describe global flu diversity. To address this, the authors introduced a new method, which borrows on approaches used by ecologists, to estimate the diversity of flu viruses in a particular location. With this approach, health authorities can design surveillance programs to detect a given percentage of flu virus diversity.

The scientists also looked at patterns of flu diversity in different bird hosts. Mallards carry the highest number of strains at 89 and ruddy turnstones were second with 45. The more a strain was shared across wild bird types, the more likely it was to be found in domestic birds, a risk factor for spillover events. They also noted that some strains could be specific to certain bird types. For example, gulls and shorebirds (Charadriiformes) carried ten strains that have not been identified in any other bird order.

According to Dr. Olson, "This inventory isn't about blaming [wild birds](#), but it allows us to map what we know, and informs our understanding of what drives viral diversity and the emergence of rare viral strains that can infect people. Given that [flu viruses](#) can jump from domestic poultry to people, ongoing efforts at improving biosecurity at poultry farms and markets remain key to outbreak prevention."

**More information:** "Sampling strategies and biodiversity of influenza A subtypes in wild birds," [dx.plos.org/10.1371/journal.pone.0090826](https://doi.org/10.1371/journal.pone.0090826)

Provided by Wildlife Conservation Society

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