

# Shorebirds and avian influenza viruses

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Very little is known about the viruses circulating within and between shorebird species. The Southeastern Cooperative Wildlife Disease Study (SCWDS) at the College of Veterinary Medicine, University of Georgia, USA, is currently investigating the prevalence of avian influenza viruses (AIV) in those shorebirds that migrate across the eastern half of the United States.

AIV have been found in more than 90 species of wild birds but do not appear to cause noticeable disease or mortality. Unlike the human form, AIV occurs in the digestive system of birds and is spread via faeces. AIV has the potential to mutate and cross species lines potentially infecting other animals such as swine, horses, and domestic poultry. Virus eradication efforts on swine and poultry farms are costly, and no continent (except Antarctica) has been spared the expense of cleaning up after an outbreak.

Until recently, it was generally believed that humans could be infected with influenza of avian origin only after the virus had undergone numerous mutations through another host, such as swine. However, scientists are alarmed by the recent direct transmission of AIV from domestic birds to humans. The first recognized case occurred in Hong Kong in 1997 when 6 out of 18 people known to have been infected died from an influenza infection transmitted directly from domestic poultry to humans. In addition, there have been numerous accounts of genetic exchange between viruses normally restricted to either birds or mammals. During the last 30 years, most avian influenza research has focused on the Anseriformes. The limited data on AIV in Charadriiformes suggest that influenza infections in shorebirds differ seasonally and genetically. For instance, prevalence rates in waterfowl are highest in the Northern Hemisphere in autumn whereas in shorebirds they appear to be highest in spring.

Our research attempts to understand the epidemiology of AIV in shorebirds migrating across the eastern half of the United States. Because of domestic animal and public health concerns, it is important to determine how the virus is transmitted and maintained in shorebirds in relation to species, time, and location. Beginning in April 2000, we collected cloacal swabs from shorebirds cannon-netted or mist-netted by several collaborators. The majority of our sampling ended

in September 2001. Over 3,000 shorebirds have been sampled during spring and autumn migration from over 10 locations in the United States. Additionally, we sampled shorebirds wintering at one location in Argentina.

We test each sample by inoculating specific pathogen-free eggs with a small amount of medium in which each cloacal swab was collected. If the virus is present, it will proliferate in the eggs over the course of 72 hours. Viruses are initially detected as a result of their ability to haemagglutinate (bind with) red blood cells. Further classification, or sub-typing, of the virus is performed serologically to determine the specific surface proteins called haemagglutinin and neuraminidase. The genetics of these viruses are studied more intensively by the Southeast Poultry Research Laboratory, Agricultural Research Service, US Department of Agriculture, to determine potential pathogenicity in other animals and their relationship with other known avian and mammalian influenza viruses.

One of our primary interests at SCWDS is investigating the prevalence of infection and viral sub-type diversity among species and locations. For instance, is there a sub-type difference between species? Are some sub-types more frequently isolated at a particular location? Answers to these questions may help us understand whether such differences relate to species, migration patterns, habitat preferences, or other factors. It is hoped that a better understanding of the risk associated with these viruses will benefit shorebird conservation efforts, as well as public and domestic animal health alike.

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