Assessment of Virus Movement Across Continents: Evaluating Virus Transmission and Shared Migration Pathways Between Whooper Swans and Northern Pintails

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In April and May 2008, dead or dying Whooper Swans infected with the highly pathogenic H5N1 virus were found at three sites in northern Japan, including two locations on the island of Hokkaido. Detection of H5N1 on Hokkaido marks the closest occurrence of highly pathogenic H5N1 to North America, and demonstrates that the range of the virus is still expanding in east Asia. This was the first occurrence of H5N1 in Japan since March 2007, and was the first time that the virus had been found solely in a migratory waterbird, rather than domestic poultry. The virus isolate from Japanese swans had a 99.7% genetic similarity to an H5N1 strain found in infected poultry in South Korea. The recent occurrence of the virus solely in Japanese swans, and the genetic similarities between Japanese and Korean H5N1 strains strongly suggests that migratory birds may have been responsible for this recent movement of the virus between countries. However, little is known about migration routes of Whooper Swans in east Asia.

The areas in Japan where H5N1 was detected in swans are important wetland habitats for numerous migratory waterbirds, making interspecific virus transmission possible. Of 53 Northern Pintails marked with satellite transmitters by the USGS (Derksen et al. 2008) and the University of Tokyo in 2008, 8 (15%) used the same sites where H5N1 was detected in swans (Figure 1). Most pintails were present at those sites during the reported outbreaks. Thus some of the Northern Pintail population in Japan was potentially exposed to the H5N1 virus. Northern Pintails can be exposed to H5N1 and remain healthy, yet shed the virus orally and via feces (Brown et al. 2006), making it possible for them to spread H5N1 across geographic regions. Importantly, the occurrence of H5N1 in Whooper Swans came at a time when a substantial number of waterbirds were initiating their northward migration, increasing the possibility for geographic spread of the virus. One pintail marked with a satellite transmitter migrated approximately 1000 km within 10 days after departing a site where H5N1 was detected in swans, and two birds ultimately migrated >3000 km to eastern Russia. A pintail marked by USGS in Japan in 2008 migrated to St. Lawrence Island, Alaska on 23 June, the first observed direct movement of a radiomarked pintail between Japan and Alaska.

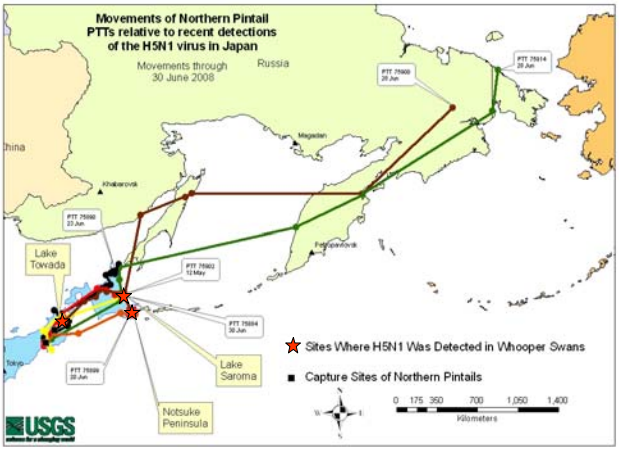

Figure 1. Movements of radiomarked Northern Pintails relative to sites where H5N1 was detected in Whooper Swans.

Figure 2. Whooper Swans and Northern Pintails at a Japanese winter area.

Interspecific virus transmission between Whooper Swans and Northern Pintails in Japan needs to be evaluated, as does the extent to which these species share migration pathways and breeding areas. Understanding virus transmission between swans and pintails is especially important given that Whooper Swans and Northern Pintails frequently aggregate at the same winter and migration habitats (Figure 2), and because some individuals of both species likely migrate to Japan from the Korean Peninsula, where H5N1 is persistent. Viral transmission from swans to pintails could result in the spread of viruses to North America either via transcontinental migration of pintails, or through contact between Asian and North American pintails on shared breeding areas in Russia. Further, North American pintails and other species that migrate to eastern Russia could come into contact with Whooper Swans during nesting or molt.

We propose to collaborate with Japanese scientists to study phylogenetic characteristics of low pathogenic viruses found in Whooper Swans and Northern Pintails that winter sympatrically in Japan. An assessment of shared low pathogenic viruses will enable us to determine the extent to which swans and pintails exchange viruses. Genetic

comparison of Asian viruses to those found in North American pintails will enable us to evaluate whether interspecific virus transmission between Whooper Swans and Northern Pintails could contribute to intercontinental movement of viruses. Swan and pintail feces collected by Japanese biologists as part of H5N1 surveillance will provide a source for low pathogenic viruses used for genetic sequencing. Sequencing of low pathogenic viruses found in Japanese pintails is ongoing at Kitasato University in Japan, and we are collaborating with University faculty to facilitate that effort. This effort will complement our recent genetic sequencing of low pathogenic viruses from Northern Pintails in Alaska and California (Koehler et al. 2008).

In addition, we propose to work with Japanese colleagues to mark Whooper Swans in Japan with satellite transmitters in 2009 to study their migration and breeding distribution. Because we have comparable satellite telemetry data from Northern Pintails marked in Japan, we will be able to directly measure overlap between the two species distributions at different times during migration and breeding. This will help us estimate the likelihood that Whooper Swans and Northern Pintails will come into contact and potentially exchange viruses after their departure from winter areas. These data will enable us to map the distribution of Whooper Swans on Asian breeding areas, and to assess the likelihood that North American pintails or other migrants will occur in those areas. This project is also timely because it will be conducted shortly after the Alaska Science Center has completed satellite telemetry studies of Tundra Swan migration in western Alaska. That study will provide an indication of movement of Tundra Swans between Alaska and eastern Russia, and result in data that could be useful to assess the likelihood of contact between Tundra and Whooper Swans.

The combined use of satellite telemetry and genetic assessment of low pathogenic viruses has been useful to demonstrate that Northern Pintails from Japan and North America share a broad area of overlap in eastern Russia, and that transcontinental exchange of virus genetic material has occurred (Koehler et al. 2008). This study will broaden our understanding of potential pathways by which avian influenza viruses move between continents, and help us assess the likelihood that the H5N1 virus will reach North America via migratory birds. Understanding these viral transmission pathways can help prioritize future surveillance sampling efforts (Flint et al. 2007, Ip et al. 2008).

Literature Cited

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