

PROGRAM ACTIVITY REPORT (PAR)



AVIAN INFLUENZA IN MONGOLIA

The NWDP has been collaborating with colleagues in Mongolia to collect samples from wild birds for highly pathogenic avian influenza (HPAI) virus surveillance this past summer. This is the 3rd year of a collaborative project with the Mongolian Academy of Sciences, Colorado State University and the National Wildlife Disease Program. Mongolia is where a number of migratory bird die-offs have occurred due to highly pathogenic H5N1 avian influenza in recent years, primarily involving the bar-headed goose, *Anser indicus*. The bar-headed goose was the principle species involved in the well-known HPAI H5N1 wild bird outbreak at Qinghai Lake in North-central China in 2005, as well as a die-off at Erkhel Lake in Mongolia in 2006. Both sites are in the Central Asian flyway. The Qinghai Lake event was the first documented large scale die-off of wild birds due to highly pathogenic avian influenza H5N1. Prior to Qinghai Lake, wild birds were thought to be primarily asymptomatic carriers of HPAI. Thousands of bar-headed geese died at Qinghai Lake, about 10% of the entire population which is now estimated at about 36,000 birds.

Mongolia presents unique advantages for the study of avian influenza in wild birds. About 70% of the bar-headed goose population breed on Mongolia's vast mosaic of grasslands and wetlands



Sampling swans at Khar Us Lake, western Mongolia
(photo by Nyambayar Battbayar)

each year. The natural ecology of avian influenza in wild birds can be studied in isolation from interactions with domestic fowl because there are almost no commercial domestic poultry or backyard poultry in Mongolia. In addition, large numbers of other waterfowl and shorebirds breed or pass through Mongolia during annual seasonal migrations along the Central Asian flyway. In the palearctic zone, the East Asian-Australian flyway bridges the gap between the Central Asian flyway and the North

American Pacific flyway. Thus, through flyway interactions, there is potential for HPAI H5N1 to cross into the North American Pacific flyway via wild bird movements.

Since 2009 biologists with the Wildlife Science Conservation Center and the Institute of Biology at the Mongolian Academy of Sciences, have collected approximately 2000 samples from birds and small mammals, including tracheal swabs, fecal samples, serum, and tissues. The samples are packed in nitrogen vapor shippers and shipped from Mongolia to CSU, where they are tested for AIV. Samples contents are assayed by RT-PCR in a Biosafety Level 3 laboratory at CSU. Positive samples are further characterized by virus isolation methods and genetic sequencing. Several sequences from this project have been described and accessioned in Genbank.

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The original artwork on this page was created by the National Wildlife Disease Program's Erika Kampe and Sarah Goff