

Overview

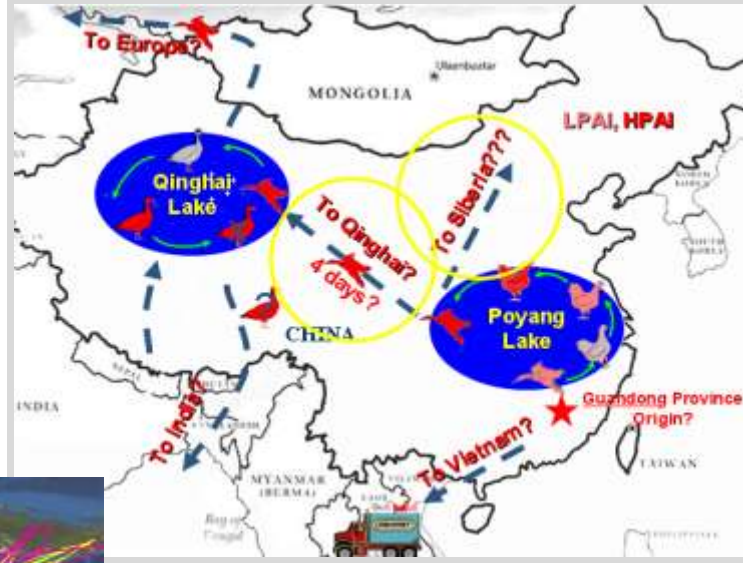
- Beginning in 2007, USGS Patuxent Wildlife Research Center (PWRC) and Western Ecological Research Center (WERC) developed a Wild Bird Avian Influenza Program to improve the scientific understanding of the intensely debated topic regarding wild birds and highly pathogenic avian influenza (HPAI) circulation.
- Under partnership with the United Nations Food and Agriculture Organization, we study wild bird host ecology in relation to HPAI risk factors to better understand how wild birds might be involved in HPAI transmission.
- To date, we have marked more than 500 waterfowl of 23 species with satellite transmitters to study movement patterns in relation to disease factors. The work spans 12 countries and the 4 main flyways of Eurasia (East African – West Asian, Black Sea - Mediterranean, Central Asian, and East Asian flyway).



Waterfowl migrations from 12 countries, 23 species, and >550 individuals as part of the [USGS – UNFAO Avian Influenza Program](#).

Focal Area: Qinghai and Poyang Lakes, China

Victims and Vectors: Movement of Avian Influenza In Poultry and Wild Birds



- Before 2005, H5N1 was only found in domestic poultry or wild birds in close proximity to poultry.
- The outbreak at Qinghai Lake during Spring 2005, killed > 6000 wild birds in an area devoid of domestic poultry, sparking debate on the role wild birds play in the spread and persistence of H5N1 along migration corridors.
- Qinghai Lake: China's largest saltwater lake; important breeding and migration site for waterbirds; site of largest H5N1 outbreak in wild birds in a region devoid of domestic poultry
- Poyang Lake: China's largest freshwater lake; important wintering grounds for waterbirds; densely populated agricultural region allowing for intermixing of wild and domestic birds
- Chen et al. 2006 hypothesized H5N1 transmitted from Poyang Lake to Qinghai Lake via migratory waterfowl – our findings do not support this hypothesis.

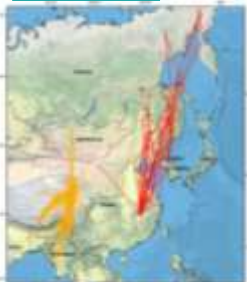


Using satellite telemetry to study wild bird movements in relation to HPAI. Ruddy shelduck, *Tadorna ferruginea* (above) and bar-headed goose, *Anser indicus* (right).

Prior to this work, most studies on HPAI movements were based on virology data alone.

Our ecological and epidemiological studies provide new information that counter some of the hypothesized movements proposed in earlier virology papers.

[Takekawa et al. 2010 Avian Diseases](#)



Contrary to Chen et al. 2006 – no migratory connection between Poyang and Qinghai Lakes

[Prosser et al. 2009, Ibis](#)



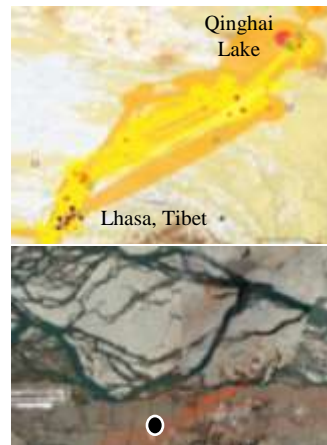
RESULTS



We documented for the first time a migratory link between Qinghai and Mongolia H5N1 outbreak regions (Prosser et al. 2009, left) in contrast to hypothesized disease movements based on molecular phylogeographies (Wallace et al. 2007, above).

[Prosser et al. 2011, PLoS ONE](#)

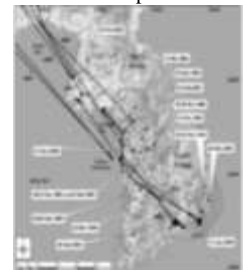
Wild birds & H5N1, Central Asia Flyway



Spatial and temporal concordance between wild bird movements and H5N1 sources Top: Bar-headed goose (BHGO) migration between QHL and Lhasa; Bottom: BHGO and H5N1 outbreaks, Lhasa wintering grounds

[Newman et al. 2009, PLoS ONE](#)

Korea – Whooper Swans



[Takekawa et al. 2010 Avian Diseases](#)

China/Russia – 8 waterfowl spp.



Unlike results from the Central Asian flyway, we did not find temporal concordance between H5N1 outbreaks and wild bird movements in the East Asian Flyway.