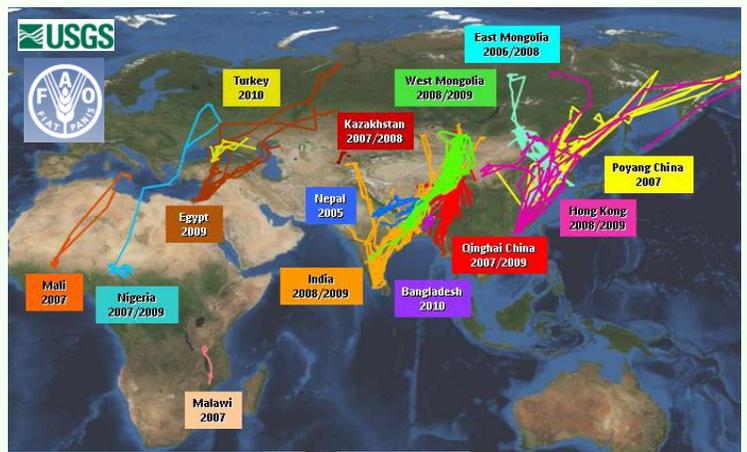


USGS Wild Bird Avian Influenza Program - Studies from Endemic Regions of Eurasia

Satellite Telemetry

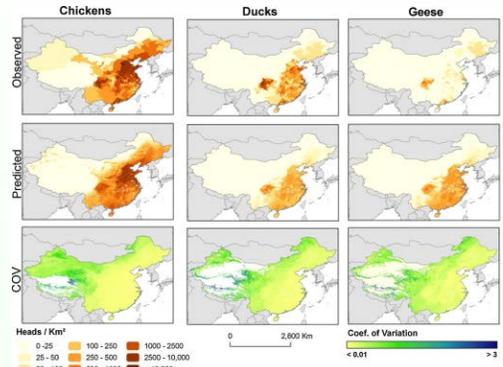
- Beginning in 2007, USGS Patuxent Wildlife Research Center (PWRC) and Western Ecological Research Center (WERC) developed a Wild Bird Avian Influenza Program to improve the scientific understanding of the intensely debated topic regarding wild birds and highly pathogenic avian influenza (HPAI) circulation.
- 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 650 waterfowl of 24 species with satellite transmitters to study movement patterns in relation to disease factors. The work spans 11 countries and the 4 main flyways of Eurasia (East African – West Asian, Black Sea - Mediterranean, Central Asian, and East Asian flyway)



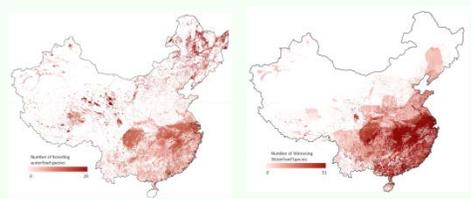
Using satellite telemetry to study wild bird movements in relation to HPAI. Ruddy shelduck (*Tadorna ferruginea*) (left), and bar-headed goose, (*Anser indicus*) (right).

Disease Risk Modeling

- Using remote sensing, spatial, and statistical approaches to modeling H5N1 transmission risk between wild and domestic bird populations and incorporating uncertainty within the modeling process.

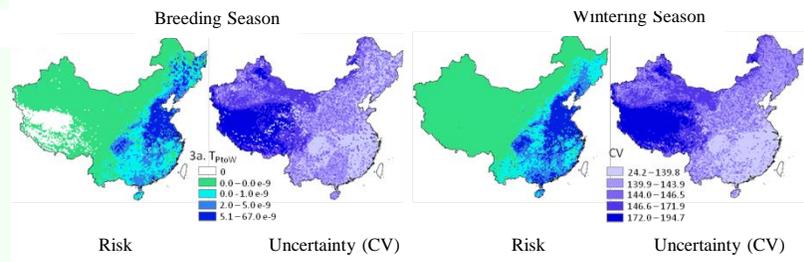


1 km resolution Poultry distribution models, Prosser et al. 2011, *Agriculture, Ecosystems, and Environment*



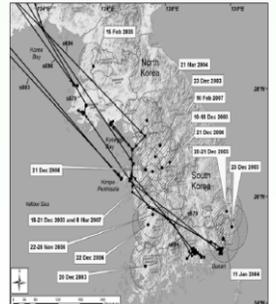
Anatidae Waterfowl distribution models (30 breeding and 37 wintering species, Prosser et al. (In Review)

H5N1 transmission risk between poultry and wild waterfowl populations Prosser et al. 2013 *Frontiers in Public Health*

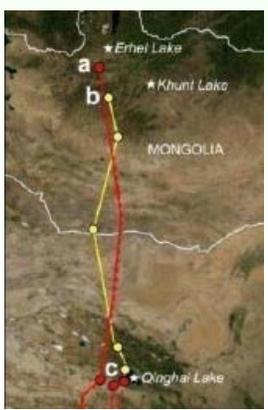


- Prior to this work, most studies on HPAI movements were based on virology data alone.
- Our studies provide new information that counter some hypothesized movements proposed in prior studies and stress the need for a combined approach of virology and ecology of wild host species.

Newman et al. 2009, *Plos One*



Migration of swans from Mongolia to Korea show spatial proximity to outbreaks; however timing of movements does not support hypothesis of wild bird involvement.

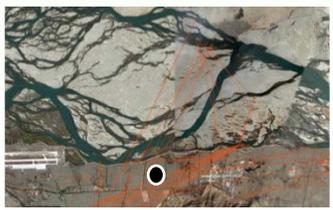
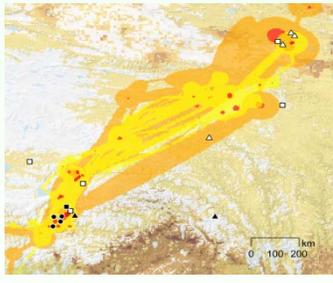


Prosser et al. 2009, *Ibis*



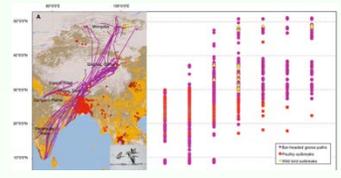
We documented for the first time a migratory link between Qinghai and Mongolia H5N1 outbreak regions (Prosser et al. 2009, left) in contrast to hypothesized disease movements based on molecular phylogeographies (Wallace et al. 2007, above).

Prosser et al. 2011, *Plos One*



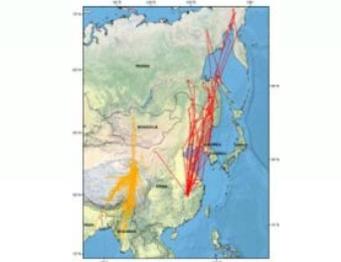
Spatial and temporal concordance between wild bird movements and H5N1 sources showing the potential of wild birds to transport H5N1 within the Central Asian Flyway. Top: Bar-headed goose (BHGO) migration between QHL and Lhasa, Tibet; Bottom: BHGO and H5N1 outbreaks, Lhasa wintering grounds.

Newman et al. 2012, *Plos One*



Positive correlation between waterfowl movements and H5N1 outbreaks in Central Asian Flyway.

Takekawa et al. 2010 *Avian Diseases*



Contrary to Chen et al. 2006 – no migratory connection between Poyang and Qinghai Lakes. Unlike results from the CAF, temporal concordance between H5N1 outbreaks and wild bird movements were not observed in the East Asian Flyway.