Climate change suggests a shift of H5N1 risk in migratory birds

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ABSTRACT

Migratory birds are considered to have played an important role in the spread of highly pathogenic avian influenza H5N1. However, how bird species are expected to modify their wintering sites in response to climate change, and in turn affect the geographic distribution of the risk associated with H5N1 outbreaks, is unknown. We explored the association between past climate variability and H5N1 outbreaks that were attributed to migratory birds from 2005 to 2009. We then predicted the distribution of risk associated with H5N1 outbreaks based on future climate change scenarios. Overlapping the probabilities of bird distribution and H5N1 outbreaks produced final emergence risk. Our results suggest that minimum daily temperature in the winter (−15 to −11 °C, 15 to 17 °C) and maximum daily temperature in the summer (12 to 15 °C, 30 to 35 °C) governed wild bird migratory routes, while high mean air pressure and low mean specific humidity in the winter impacted the outbreaks of H5N1 among migratory birds. By the end of 2030, Europe may be at higher risk for H5N1 outbreaks in January and February. Northern Africa and Southern and Western Asia will likely be a higher risk for H5N1 outbreaks from April to June. Our findings suggest a potential shift in H5N1 risk from Southeast Asia to the western part of the world due to climate change. The results of this study could be used to inform policy in the area of H5N1 outbreak detection and preparedness.

1. Introduction

Highly pathogenic avian influenza (HPAI) A subtype H5N1 virus was first isolated from a goose farm in Guangdong Province, China in 1996 (Claas et al., 1998). It is epizootic in several bird species, principally across Southeast Asia (Webster, 2004). Clade 2.2 of the virus spread globally throughout Europe, the Middle East and Africa after first appearing in Asia in 2005 (Chen et al., 2006; Webster and Govorkova, 2006; Scotch et al., 2013; Li et al., 2014). Because of the high lethality and virulence of H5N1, its endemic presence, its increasingly large host reservoir, and its significant rate of mutation, it is currently one of the world's greatest pandemic threats (Gambotto et al., 2008; Tsang et al., 2005).

It is commonly accepted that migratory birds are the natural reservoir of influenza A viruses, and waterfowl are the primary reservoir of low-pathogenic avian influenza (LPAI) viruses (Olsen et al., 2006). Evidence supporting the role of migratory birds in the spread of HPAI H5N1, especially the Anseriformes and Charadriiformes, emerged when almost 10,000 migratory birds infected with H5N1 died at the Qinghai Lake nature reserve in central China in 2005, and a series of outbreaks occurred in Europe in early 2006 (Chen et al., 2005). Based on the whole-genome analyses of low pathogenic avian influenza isolates collected in Alaska from the

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northern pintail (*Anas acuta*), which migrates between North America and Asia, phylogenetic analysis suggested that wild birds could transfer influenza viruses (AIVs) intercontinentally (Koehler et al., 2008).

HPAI H5N1-infected migratory birds have been found in several European countries, but local outbreaks were smaller in size and intensity compared with the situation observed in China and Southeast Asia (Globig et al., 2009; Ward et al., 2008). This pattern suggests that some wild birds are able to spread AIVs over long distances to previously unaffected areas (Olsen et al., 2006). In experimental studies, wild species of ducks, geese and swans have shown the ability to replicate and shed H5N1 for several days without showing clinical or pathologic signs of disease (Kim et al., 2009). Among the species studied, mallards (*Anas platyrhynchos*), mute swans (*Cygnus olor*), cackling geese (*Branta hutchinsii*), and bar-headed geese (*Anser indicus*) pose a greater risk for HPAI H5N1 transmission (Brown et al., 2006, 2008a,b; Keawcharoen et al., 2008). Some wild birds may be partially immune to HPAI H5N1 due to previous exposure to LPAI viruses (Seo et al., 2002). Specifically, a previous infection with subtype H9N2 could confer partial protection against HPAI H5N1 (Khalenkov et al., 2009). Data obtained by satellite telemetry revealed that white-faced whistling ducks (*Dendrocygna viduata*) survived HPAI H5N2 infection and were able to migrate for at least 655 km. This finding suggests that long distance dispersal of HPAI H5N2 by migratory ducks is possible (Munster and Fouchier, 2009). Based on one of the largest datasets available for migratory and resident wild birds sampled on HPAI H5N1 infection in Thailand, a nonhomogeneous birth and death statistical model was used to reveal the relationship between poultry and wild bird outbreaks. The result indicated that the transmission efficiency of HPAI H5N1 among poultry was 1.7 times higher in regions where infected wild birds had been detected compared with regions without infected wild birds (Keawcharoen et al., 2011). In addition, waterfowl may transfer the virus mechanically during long distance migration, and feathers infected with HPAI H5N1 could also be a source of environmental contamination with high viral loads (Uriarte et al., 2011; Yamamoto et al., 2010).

Climate change is likely to influence the geographical distribution and transmission intensity of disease (Gething et al., 2010; Wu et al., 2014). Satellite imagery, global climate models (GCM), meteorological data, and species distribution models can be used in combination to predict the future distribution of disease vectors and hosts (Michishita et al., 2012a,b; Xu et al., 2004, 2006).

Climate change may additionally influence HPAI H5N1 evolution and host behaviour, thereby modifying the periodicity, prevalence, and intensity of HPAI H5N1 transmission (Herrick et al., 2013). On one hand, several studies have shown that climate conditions and climate indices can influence the timing of migration and the distribution of migratory birds (Cotton, 2003; Forchhammer et al., 2002; Sillett et al., 2000). Among these variables, temperature was found to have a strong statistical correlation with bird distribution (Root, 1988; Root and Schneider, 1993). In particular, winter temperatures are closely associated with waterfowl movement. The congregation of waterfowl along the 0 °C isotherm likely contributed to the geographical spread of HPAI H5N1 outbreaks in migratory birds in Europe during the winter of 2005–2006 (Reperant et al., 2010). On the other hand, it has been shown that AIVs can persist for an extended period of time in water, especially at low temperatures (Brown et al., 2007, 2009; Stallknecht et al., 1990). In extremely cold conditions, high-energy expenditure and limited access to food can also make potential hosts more susceptible to AIVs. Predicting the impact of climate change on the distribution of HPAI H5N1 outbreak risks will inform disease prevention policy and preparedness.

In this study we explored the potential impact of climate change on the distribution of HPAI H5N1 infection risk in three steps. First, we investigated the impact of climate on the spatial distribution of migratory birds and the occurrence of H5N1 outbreaks among migratory birds. Second, the monthly spatial distribution of migratory birds and H5N1 outbreaks were derived and estimated globally based on the current climate. Finally, we used future climate scenarios based on conservative greenhouse gas emissions to predict the risk of HPAI H5N1 outbreaks among migratory birds for each month and construct global risk maps up until the year 2030.

2. Material and methods

2.1. HPAI H5N1 outbreak data

HPAI H5N1 outbreak data from 2005 to 2009 were obtained from the Food and Agriculture Organization (FAO) of the United Nations and the World Organization for Animal Health (OIE). The data include the date and location of the outbreak, the subtype of AIV, and the host species (domestic or wild). To build an integrated dataset, we combined the two data sources and removed all duplicate reports. Our dataset included 902 independent records of outbreaks in wild birds spanning from January 2005 to April 2009.

An HPAI H5N1 outbreak in wild birds is defined as one or more cases of HPAI H5N1 in wild birds within a 100 km area that was free of HPAI H5N1 outbreaks in poultry in the current and preceding months (Reperant et al., 2010). Using this definition, wild bird outbreaks that may have resulted from an infected poultry outbreak were excluded. Data were pooled by calendar month.

2.2. Migratory bird data

Data on wild bird migration and migration paths were derived from the work of Gaidet et al. (2010) from United States Geological Survey (USGS), the Raptor Research Group of Taiwan (RRGT) and the Royal Society for the Protection of Birds (RSPB). This geocoded data include migratory bird ringing and satellite tracking data. The migration flyways covered in this study are the Black Sea/Mediterranean Flyway, the East Asian–Australasian Flyway, the Central Asian flyway and the West Asian–East African Flyway. Data were pooled by calendar month.

2.3. Climate data

The modern era retrospective-analysis for research and applications (MERRA) dataset is a re-analysis climate database managed by the NASA Goddard Earth Observing System Data Assimilation System Version 5 (GEOS-5). The MERRA climate data are generated by combining all available global surface observations every 3 h and interpolating the results to a continuous surface. It produces estimates of global climate variables ten meters above the land surface, with a resolution of 0.5° latitude by 0.6° longitude. Daily averages of surface incident shortwave flux (radiation), air temperature, specific humidity, precipitation, and air pressure were used in this study. The 5-year monthly mean temperature, monthly standard deviation of temperature, mean minimum temperature, mean maximum temperature, monthly cumulative precipitation, mean air pressure, mean specific humidity and monthly cumulative radiation were calculated on a global scale.

To derive robust estimates of future climate conditions, we used the climate projections (Table S1) derived from downscaled monthly outputs of 20 different global circulation models (GCMs) (Table S2), based on the representative concentration pathways (RCP) 4.5 emission scenario. We used the year 2030 as the reference year for prediction of the same climate variables extracted from the MERRA dataset.