Do contrasting patterns of migration movements and disease outbreaks between congeneric waterfowl species reflect differing immunity?

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Abstract

Long-distance migrations influence the dynamics of host-pathogen interactions and understanding the role of migratory waterfowl in the spread of the highly pathogenic avian influenza viruses (HPAIV) is important. While wild geese have been associated with outbreak events, disease ecology of closely related species has not been studied to the same extent. The swan goose (Anser cygnoides) and the bar-headed goose (Anser indicus) are congeneric species with distinctly different HPAIV infection records; the former with few and the latter with numerous records. We compared movements of these species, as well as the more distantly related whooper swan (Cygnus cygnus) through their annual migratory cycle to better understand exposure to HPAIV events and how this compares within and between congeneric and noncongeneric species. In spite of their record of fewer infections, swan geese were more likely to come in contact with disease outbreaks than bar-headed geese. We propose two possible explanations: i) frequent prolonged contact with domestic ducks increases innate immunity in swan geese, and/or ii) the stress of high-elevation migration reduces immunity of bar-headed geese. Continued efforts to improve our understanding of species-level pathogen response is critical to assessing disease transmission risk.

Introduction

Long-distance migrations in wildlife co-determine the dynamics of host-pathogen interactions (Altizer et al., 2011). The role migration plays in the host-pathogen relationship can be extremely complex, with migration presenting an opportunity for a disease to spread across a landscape while also potentially reducing prevalence via death during travel or allowing healthy individuals to separate from infected individuals or regions (Altizer et al., 2011; Risely et al., 2018). Migration can even be an important part in the life cycle of a pathogen due to reduced immune function (Owen & Moore, 2008; Hawley & Altizer, 2011) and increased exposure of the host across the migratory route (Fritzsche & Høyé, 2016; Leung & Koprivnikar, 2016), or by animals being together in dense congregations thereby facilitating disease transmission (Hill...
et al., 2012; Fritzsch & Hoye, 2016; van Dijk et al., 2018). However, despite the complex and compelling relationship between wildlife migrations and the potential pathogens these animals carry, relatively few studies have examined how annual migration movements affect the transmission and evolution of pathogens within host populations (Hall et al., 2014; Verhagen et al., 2015). A prime example of this dearth of information is found in wild waterfowl whose migration is a well-known ecological phenomenon; yet, the relationship between migration and disease spread is not well understood.

Traditional amplification routes of avian influenza viruses include direct or indirect transmission of the non-lethal, low-pathogenic avian influenza virus (LPAIV) from wild bird reservoirs to highly-dense populations such as farmed poultry. This transmission is often facilitated by agricultural practices with low biosecurity (Takekawa et al., 2010a and b; Fearnley, 2015), such as grazing domestic ducks in marshes where they can comingle with migratory wild birds. This viral flow is demonstrated by the amplified infection prevalence of locally circulating LPAIVs observed concurrent with the arrival of migratory waterfowl (Lisovskiy et al., 2018; Verhagen et al., 2015). Once introduced to highly concentrated poultry herds in domestic facilities, LPAIVs can easily mutate into a highly pathogenic virus, which can have dramatic impacts on affected poultry farms (Wallace, 2016).

The emergence of the Asian lineage HPAI H5N1 virus marked the evolution of the highly pathogenic avian influenza viruses (HPAIV) spill-over from poultry to wild birds and the environment. For instance, the HPAIV H5N1 outbreak at Qinghai Lake in 2005 killed over 6000 wild migratory waterfowl, more than 90% of which were bar-headed geese (Anser indicus) (Chen et al., 2005; Liu et al., 2005). Subsequent research has suggested that, much like the introduction of LPAIV from wild birds to domestic poultry, spill-over of HPAIV from domestic poultry to wild birds is likely facilitated by agricultural practices (Hénaux & Samuel, 2011; Prosser et al., 2016; Stallknecht et al., 1990) that enable co-occurrence of the virus and its avian hosts in wetlands (Prosser et al., 2016; Takekawa et al., 2010a). Thus, areas with high concentrations of domestic ducks and geese as well as migratory waterfowl, such as southeast China (Prosser et al., 2013), are especially prone to outbreaks of HPAIV and can serve as disease hotspots (Gilbert et al., 2012; Cappelle et al., 2014). However, once HPAIV spill-over into the environment, it is not limited to these high-risk areas. Research indicates that some waterfowl species can migrate while infected with HPAIV (Hill et al., 2012), which strengthen the potential for long-distance dispersal (Altizer et al., 2011; Verhagen et al., 2015).

Though previous work has addressed many questions regarding the spatial-temporal correlations between waterfowl migration and HPAIV outbreaks (Newman et al., 2009; Si et al., 2009; Verhagen et al., 2014), phylogenetic relationships among outbreaks (Tian et al., 2015; Xu et al., 2016), and outbreak drivers (Gilbert et al., 2007; Prosser et al., 2013), there are no studies we are aware of comparing HPAIV outbreak patterns in congeneric migratory waterfowl species. The swan goose (Anser cygnoides) and the bar-headed goose provide an ideal opportunity for examining avian influenza in congeneres as these species both breed in Mongolia (Batbayar et al., 2013) and co-occur in some areas but follow separate migration routes (Batbayar, 2013). During the autumn migration, swan geese use northeast China and the Yalu River Estuary as important stopover sites (Batbayar et al., 2013) on their way to over-wintering in the Yangtze River lowlands via the East Asian-Australasian Flyway. In contrast, the bar-headed goose stopover at Qinghai Lake and wetlands on the Qinghai Plateau in the Central Asian Flyway (Takekawa et al., 2017) before migrating to southern Tibet or India. Additionally, while passive and active surveillance indicate that swan geese are generally infected infrequently and in low numbers (Kou et al., 2009; Welte & Terán, 2004), bar-headed geese have been regularly documented in HPAIV outbreaks from 2004-2017. This suggests species differences, either with respect to exposure to, or immunity against, HPAIV (Welte & Terán, 2004; Chen et al., 2005; Takekawa et al., 2010b). In this study, we compare migratory movements of the bar-headed goose and the swan goose and examine HPAIV outbreak patterns along their migration routes. We also contrast their movements to those of two whooper swan (Cygnus cygnus) populations to: i) provide comparison with a different genus of waterfowl that migrates along comparable habitats; and ii) examine whether HPAIV outbreak patterns between and within waterfowl species are correlated with the variable densities of domestic ducks. We discuss mechanisms that may contribute to differences in outbreak patterns and transmission, such as migration strategies and immunity.

Materials and methods

Tracking data

We obtained global positioning system (GPS) data tracking bar-headed goose and swan goose from the U.S. Geological Survey (USGS) and the Food and Agriculture Organization of the United Nations (FAO). In addition, we acquired data and for swan goose from the Department of Earth System Science at Tsinghua University, Beijing, China and included movement data of two whooper swan populations: one migrating between Mongolia and South Korea (USGS-FAO) and the other between Russia and Japan (Shimada et al., 2014). These different migration corridors overlap with high and low poultry density areas, respectively, which enables within-species comparison.

The USGS-FAO information included a total of 18 swan goose, 38 bar-headed goose, and 10 whooper swans captured in overwintering and breeding areas (Table 1); the Tsinghua University sample 44 swan goose marked in overwintering and breeding areas (Xu et al., 2016); and the Shimada et al. (2014) data concerned a total of 47 whooper swans captured in eastern Hokkaido and north-eastern Honkou, Japan. The GPS and ARGOS platform transmitting terminals (see Table 1 for further information) were programmed to record locations at 2-hour intervals for swan goose and whooper swans and at 4-hour intervals for bar-headed goose. Additional information can be found in the Table 1 and in previous papers (Newman et al., 2009, 2012; Batbayar et al., 2013; Shimada et al., 2014; Xu & Si, 2019; Xu et al., 2019).

Migration route estimations

We used dynamic Brownian Bridge Movement Models (dBBM) to measure utilization distributions (UD) of the tracked populations (Kranstauber et al., 2012). The dBBMI assumes heterogeneous GPS tracks and thereby estimates UD with a sliding window of GPS locations for detecting behavioural changes. We used a resolution of 10 km with a sliding window encompassing 23 locations with a margin of 11 locations and a location error of 23
m (Palm et al., 2015). We set the time step at 8 locations for swan goose and whooper swans and at 4 locations for bar-headed goose covering a 16-h period.

Because tracking durations varied among individuals, we weighted their individual UD by multiplying all raster values by the number of tracking days. Population-level UDs were calculated from the sum of weighed individual UDs, and we generated 90% cumulative probability contours to circumscribe their main use areas including breeding, stopover, and wintering areas (Si et al., 2018; Xu et al., 2019). We used 99% cumulative probability contours to represent migration routes (Palm et al., 2015).

Because original tracking data for the Russia-Japan whooper swans were not available, we extracted coordinates for the main areas of wintering, stopover, and breeding sites from published maps (Shimada et al., 2014) via geo-referencing and created buffer zones around each of these geo-referenced sites with a radius of 32.5 km, i.e., an average maximum foraging distance for waterfowl (Johnson et al., 2014).

**Poultry density measurements**

We obtained densities of domestic ducks from the Livestock Geo-Wiki (https://livestock.geo-wiki.org/home-2/). To evaluate the differences among migratory populations and their contact probability with poultry, we summarized densities of domestic ducks and chickens from each raster cell in sites used along their migration routes, derived from tracking data from 2004-2017. Differences in poultry densities in areas of different migratory populations were tested with Bonferroni corrected post-hoc tests (Dunn, 1961).

**Highly pathogenic avian influenza viruses outbreak assessments**

We obtained confirmed HPAIV outbreaks from 2004-2017 through EMPRES-i (Welte & Terán, 2004). We assumed an outbreak window of 30 days (i.e., where the outbreak observation date is the median date) during which the virus may be transmitted to wild migratory birds that visit the outbreak areas with an incubation period of 21 days plus a disinfection period of 9 days (Si et al., 2009). We extracted GPS locations for tracked individuals during each outbreak window and examined the distribution of distances between these locations and HPAIV outbreaks. Differences among cumulative distributions were tested with a Kolmogorov-Smirnov test (Frank & Massey, 1951). We ran the analysis in R 3.4.3 (R Development Core Team, 2016) and QGIS 2.18 (QGIS Development Team, 2015).

**Results**

The marked swan geese bred in north-eastern Mongolia used the Yalu River Estuary at the border of China and North Korea as a stopover site and overwintered in the Yangtze River Lowlands of southern China including Poyang Lake. Bar-headed goose bred in north-western Mongolia and migrated over the Gobi Desert and the Qinghai-Tibetan Plateau. Eight of the 36 bar-headed geese crossed the Himalayas and overwintered in India, whereas the rest of the marked bar-headed goose overwintered near Lhasa, China. The breeding grounds for the population of whooper swans marked by the USGS-FAO were near the Mongolia-Russia border and they migrated to southern South Korea for overwintering. The other whooper swan population was located in north-eastern Russia and southern Japan (Figure 1).

There were no HPAIV outbreaks concerning swan goose in the EMPRES-i database between 2004 and 2017, but 11 HPAIV outbreaks in bar-headed goose and 37 in whooper swans (Table 2). The HPAIV outbreaks in bar-headed goose occurred in Mongolia, around Qinghai Lake, and in the Lhasa River Valley, while HPAIV outbreaks in whooper swans mainly occurred in Japan (Figure 1C). There were fewer HPAIV outbreaks, i.e. outbreaks in domestic and wild birds along the migration route for swan goose compared with the other species. A total of 20 HPAIV outbreaks occurred along the migratory route of the swan goose, whereas 48 outbreaks occurred along the migration route of the bar-headed goose (Table 2). 67 outbreaks occurred along the migratory route of the whooper

### Table 1. Summary of marked bird population data.

| Population of individuals | Number of tracking capture | Year of data | Capture location | GPS transmitter | Data source |
|---------------------------|---------------------------|-------------|-----------------|----------------|-------------|
| **Swan goose** A. cygnoides | 18 | 1211 | 2006, 2008 | Khaichiin Tsagaan Lake, Khorin Tsagaan Lake and Khokh Lake, Mongolia | Solar-powered Argos-GPS platform transmitter terminals* | USGS/FAO |
| **Swan goose** A. cygnoides | 44 | 435 | 2015, 2016 | Hulun Lake, China | GPS-GSM solar-powered loggers° | Tsinghua University |
| **Whooper swan** C. cygnus | 10 | 820 | 2006 | Khorin Tsagaan Nuur and Delger Tsagaan Lake, Mongolia | Solar-powered Argos-GPS platform transmitter terminals* | USGS/FAO |
| **Whooper swan** C. cygnus | 47 | 1380 | 2009, 2010 | Lake Kussharo, Lake Izunuma-Uchinuma | Solar- and battery-powered Argos-GPS platform transmitter terminals* | Shimada et al. (2014) |
| **Bar-headed goose** A. indicus | 38 | 788 | 2008, 2009 | Terkhiin Tsagaan Lake, Mongolia, Chilika Lake, East India, Kootthakulum Bird Sanctuary, South India | Solar-powered Argos-GPS platform transmitter terminals* | USGS/FAO |

*Platform transmitting terminals: Microwave Telemetry, Inc., Columbia, MD, USA; °GPS-GSM, Global Positioning System - Global System for Mobile Communications. The transmitters were IBIS series, Ecotone Telemetry, Gymia, Poland and necked HIQNG series, Huan Global Messenger Technology Co. Ltd., Xiangtan, China; The GPS and ARGOS transmitters were programmed to record GPS locations at 2-hour intervals for swan goose and whooper swans and 4-hour intervals for bar-headed goose.
Swans from Mongolia, and 44 outbreaks occurred in the sites of whooper swans in Russia and Japan (Table 2).

Swan geese were closer to outbreak locations than bar-headed geese and whooper swans within a radius of 500 km around outbreak events (Figure 2D). Densities of domestic ducks in both the stopover, breeding and wintering sites and migration routes of the swan geese were also higher than those for bar-headed geese (Figure 2A and B). Densities of domestic ducks in the 90% cumulative probability contours of the Mongolia-South Korean whooper swan population was higher compared to those in Russia and Japan (Figure 2C), but the number of outbreaks was higher for the Russia-Japan population (Table 2).

**Discussion and conclusions**

We compared HPAIV outbreak patterns between two congeneric species, the swan geese and the bar-headed geese and found that there were no recorded HPAIV outbreaks in the former but multiple outbreaks in latter. Contrary to our expectations, swan geese were found closer to outbreak areas than bar-headed geese during HPAIV outbreaks. Also, areas used by swan geese had significantly higher duck densities than areas used by bar-headed geese that were often reported in outbreaks. Although the swan geese were more likely to be present in HPAIV outbreak areas during migration, they had a lower chance of being infected with...
HPAIVs. However, the bar-headed geese were less likely to contact HPAIV outbreaks during migration but had multiple HPAIV outbreaks. We postulate two possible explanations for this: i) frequent contact and long contact history with domestic ducks might cause greater levels of innate immunity in swan geese; and/or ii) the high elevation Himalayan migration of bar-headed geese could compromise their immunity resulting in greater vulnerability to HPAIV infection.

Firstly, wild birds that have frequent contacts with domestic birds are less often found in outbreaks because they may have greater levels of immunity from frequent exposure to poultry (Brown et al., 2008; Nemeth et al., 2013; Pantin-Jackwood et al.,

Table 2. Summary of outbreaks in different bird populations.

| Population                               | Outbreaks in the study populations | Outbreaks in other species* |
|------------------------------------------|------------------------------------|-----------------------------|
| Swan goose                               | 0                                  | 20                          |
| Bar-headed goose                         | 11                                 | 48                          |
| Whooper swan (Mongolia-S. Korea)         | 0                                  | 67                          |
| Whooper swan (Russia-Japan)              | 37                                 | 44                          |

*In wild birds and poultry birds using the study species’ migration corridor, the whooper swan populations were included to provide a comparison of one species with two different migration routes.
2017). Migratory individuals have larger immunological organs than resident birds (Moller & Erritzoe, 1998) due to frequent exposure to pathogens during migration (Brown et al., 2008). The whooper swan population that had a higher probability of contact with domestic ducks had no HPAIV outbreak records, whereas the whooper swan population that had a lower probability of contact with domestic ducks was associated with more HPAIV outbreaks (Figure 2). This is consistent with our findings for differences between swan geese and bar-headed geese, as birds with a higher probability of contacting poultry had fewer HPAIV outbreaks (Takekawa et al., 2010b). Furthermore, swan geese have a long contact history with domestic ducks in East Asia (Darwin, 1859; Niu, 2016), which might be a selective driver for higher levels of innate immunity (Moller & Erritzoe, 1998). In addition, domestic swan geese is a common poultry species in this region, meaning that viruses circulating in domestic poultry may also be better adapted to this species and thereby counteract any enhanced immunity from increased exposure.

Secondly, although bar-headed geese are well-known victims of HPAIV outbreaks in the wild (Chen et al., 2005; Takekawa et al., 2010b), only 2 of 8 bar-headed geese died in experimental HPAI H5N1 infections (Brown et al., 2008; Nemeth et al., 2013). This mortality rate (25%) is lower compared with other waterfowl species (Brown et al., 2008; Moller & Erritzoe, 1998) indicating that, in non-migration conditions, bar-headed geese may be less vulnerable to HPAI H5N1 infection than other species. However, migrating over the Himalayas and the associated stress of long flight and scaling heights may decrease the immune responses of these geese. Migration is an energetically costly strategy, increasing the metabolic rate 10 times (Battley & Piersma, 2005), a cost that has to be balanced against other expenses, such as immune responses (Altizer et al., 2011; van Dijk & Matson, 2016). For example, migratory barn swallows (Hirundo rustica) (Johnson et al., 1970; Hylocichla mustelina) (Owen & Moore, 2006) have been found to be immunocompromised compared with non-migratory conspecific ones. The long-distance, high-altitude migration strategy of bar-headed geese is indeed energetically challenging (Hawkes et al., 2011). Some bar-headed goose populations migrate shorter distances between Qinghai Lake and Lhasa, but they need to allocate more energy to withstand the harsh Tibetan climate (Takekawa et al., 2017). Energetically costly migration at high altitudes suppresses immune the immune system (Bishop et al., 2015; van Dijk & Matson, 2016) increasing the vulnerability of bar-headed geese to disease.

In light of these findings, we suggest that more comparative studies should be conducted to examine innate immunological differences among migratory waterfowl species, testing whether contact with domestic ducks stimulate the innate immune reactions against HPAIVs. Furthermore, we suggest physiological studies to investigate whether migration suppresses immune responses. These efforts can be helpful for understanding the HPAIV outbreak pattern and improving our understanding of pathogen dispersal via migratory hosts.

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