# Migratory Birds, domestic poultry and avian influenza

The persistence and recurrence of H5N1 avian influenza in endemic regions can largely be blamed on movement and infection by migratory birds. Trade in poultry, poultry products and caged birds, and movement of wild birds also account for H5N1 prevalence in these areas. Several recent outbreaks of avian influenza have suggested strong evidence of migratory birds playing a role in transmitting the virus over long distances.



In a paper published last week in the *SIAM Journal on Applied Mathematics*, authors Lydia Bourouiba, Stephen A. Gourley, Rongsong Liu, and Jianhong Wu analyze the interaction between non-migratory poultry and migratory birds in order to investigate the role of the latter in the spread of H5N1.

Although avian influenza rarely infects humans, occasional cases of human infection have been observed since the late nineties.  Moreover, it is a huge problem in the poultry industry since infected flocks can cause a drain on resources and threaten food supply. It can also result in significant reduction in wild bird populations, which is of great ecological concern.

"How the interaction of a migratory bird species with domestic poultry contributes to the spread and persistence of the highly pathogenic H5N1 virus is a question of profound importance to the control of avian influenza spread, and to the effort of mitigating the impact of the disease on the domestic poultry industry," says corresponding author Stephen Gourley, researcher in the Department of Mathematics at the University of Surrey. "Answering this question requires a truly interdisciplinary approach involving collaborations from different fields. Mathematical modeling can play a significant role in solving such a complex problem in which experiments are difficult and surveillance data is limited."

In order to determine how migratory birds might contribute to disease in poultry, the authors first analyze the susceptibility of migratory birds to infection by using a model to trace their path along flyways. "Patches" represent 4 locations: breeding and wintering sites, and layovers on outgoing and return routes where birds stop to rest and feed. The migration flyway is expressed mathematically by a one-dimensional closed curve starting and ending at the breeding patch. Reaction-advection equations describe the migration of birds along this flight path.



The Common Teal - Photo courtesy of birdskorea.org

The quantity of birds susceptible to infection is calculated by determining the density of susceptible birds along the flying route. The time of journey for the susceptible birds is the distance between each patch divided by their mean flight velocity. In-flight mortalities are also accounted for in the equation. Assuming that migratory birds can only contract the virus while in patches (and not while in transit), the probability of infection of a bird is determined based on its contact rate with infected migratory birds and infected poultry, and time spent in a patch. The time of stay depends on several factors, such as the rate at which birds enter the patch, length and duration of their journey, energy consumed on their incoming flight, and the nourishment required to proceed.
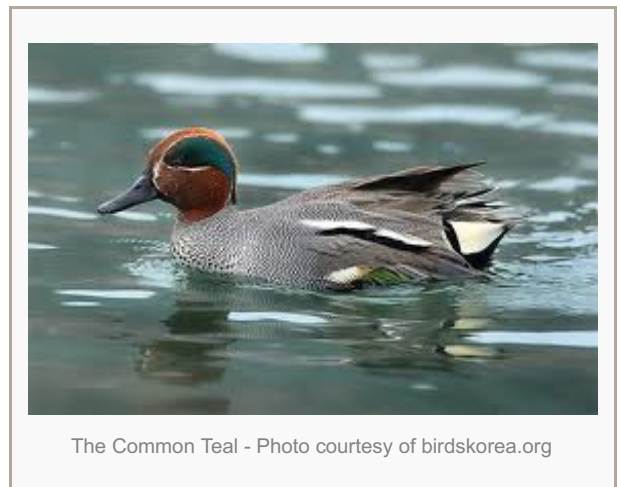
The model factors in the observation that birds encounter very different conditions at different stages on their

migration route. In reality, migratory birds have more than a single stopover in their fall and spring routes; these are lumped together as one each for the sake of simplicity. The population of poultry on each patch is assumed to be a constant, as is the length of the flyway and average flight velocity.



The Common Teal in flight - Photo courtesy of orientalbirdimages.org

Using their model, the authors analyze the dynamics of migratory Common Teals and their interaction with farmed poultry in the Poyang Lake area of China. Their simulations demonstrate that the arrival of migratory birds in winter can introduce avian influenza to poultry in disease-free periods. Once the flu becomes endemic in the wintering location, the result is sustenance of the flu in migratory birds themselves. "It is amazing that our model, which starts from surprisingly simple assumptions, can predict when there will be an outbreak of the disease, and how limited data from the Chinese Poyang Lake region can be used to parametrize and validate the model," says Gourley.

Future research should be focused on finding tools that can predict peak disease times, according to the researchers. "Some of our computer simulations suggest that peak disease activity will not always occur in a regular predictable pattern," Gourley explains. "Irregular intervals from peak to peak pose significant challenges for future theoretical research. Tools that can estimate peak times will be important for designing effective surveillance and for planning intervention strategies."

In addition, integrating such research with data from international migratory bird surveillance and commercial poultry trade can shed more light on these interactions on a global scale. Many national and international organizations are involved in these efforts. The United States Geological Survey (USGS) has been working in partnership with the United Nations Food and Agricultural Organization (UN FAO) to study the role of wild birds in the geographic spread of H5N1.

"It would be great to have more information about global surveillance of migratory birds and commercial poultry trading so that [our] model can be expanded to understand the disease spread along the network of migratory flyways and commercial trading," says Gourley. "This shows the importance of continuing and enhancing the current work of the UN FAO and the US Geological Survey."

Source:

*The interaction of Migratory Birds and Domestic Poultry and its role in sustaining Avian Influenza*

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