

## Social Network Analysis of Livestock Movements for Enhancing Foot-and-Mouth Disease Control in Korea

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**Introduction:** Transportation of live animals is one of the most important modes of transmission of infectious disease including foot-and-mouth diseases (FMD). According to epidemiological investigation report on 2014-2015 FMD outbreaks in Korea, the majority of secondary outbreaks were caused by the movement of pigs with subclinical stage and contact via contaminated vehicles. Furthermore, slaughterhouses were implicated in the global spread of FMD virus during the epidemics. In this context, in-depth knowledge of the structure of direct and indirect contacts between slaughterhouses is paramount for understanding the dynamics of FMD transmission. Registration of livestock is mandatory in Korea since 2013. However, social network structure of the vehicle movements to slaughterhouses in Korea remains unclear. The aim of this study was to configure social network topology of vehicle movements between slaughterhouses for better understanding of how slaughterhouses are potentially connected and to explore whether transmission of FMD outbreaks can be explained by network properties constructed in the study.

**Materials and Methods:** Movement data of cattle and pigs during the period from 1st of September 2014 to 28th of February 2015, as well as demographic information related to livestock holdings were provided from the Animal and Plant Quarantine Agency. Contact data were originated from the national KAHIS (KAHIS, Korean Animal Health Integrated System) database, which tracks the route of an individual vehicle movements using Global Positioning System (GPS). Of these, movement data on December 2014 were excluded from the network analysis, since movement pattern may not normal due to standstill of FMD outbreak on 3 December 2014. Finally, we created 5 monthly directed networks based on the frequency and chronology of on- and off-slaughterhouse vehicle movement events. In the network, a node represented a slaughterhouse and an edge (link) denoted a vehicle movement between two slaughterhouses.

**Results:** Final data contained information on a total of more than 5.6 million (average 1.1 million per month) animal movements among 75 slaughterhouses included in the study. For each of the 5 studied networks, the network structures were characterized by small-world properties, with a short mean distance, high clustering coefficient,

and short diameter. In addition, single large strong component was observed in each of created network, and this component included 94.4-100% of network nodes. The characteristic of hub and spoke type structures were not identified. Structural vulnerability of the network suggest that once a livestock disease is introduced in a slaughterhouse within the cohesive component, it can spread to all other slaughterhouses in the component.

**Conclusions:** From an epidemiological perspective for infectious disease management, the empirically- derived small-world networks could assist decision-makers on the higher potential for a large FMD epidemic within the livestock industry and for rapid spread of the disease across long distance despite standstill of animal movements, given an incursion of the virus in any slaughterhouse in the country. A prompt restriction of vehicle movement among livestock facilities is utmost important to stop a future spread attributable to FMD virus irrespective of geographical boundaries. Future studies required to determine the types of networks structure at province level, leading to better understanding and interpretation of outbreak data and more appropriate biosecurity decisions. This research was supported by Animal Disease Management Technology Development (C1012360-01-01) Ministry of Agriculture, Food and Rural Affairs.

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## Spatial Sampling Design for Active Surveillance of Highly Pathogenic Avian Influenza (HPAI) of Wild Birds

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**Introduction:** In Korea, after the first confirmation of highly pathogenic avian influenza (HPAI) in 2003 from chickens, five large outbreaks have recorded in poultry farms until December 2015. Epidemiological studies for all outbreaks revealed that wild birds migrating from surrounding countries was implicated with the primary source of HPAI virus (HPAIV) introduction. In response to these concerns by government authority (Animal and Plant Quarantine Agency, APQA), the catchment of wild birds and testing program as part of ongoing national active surveillance program, initiated in 2007, has continued implemented to understand the role of wild birds in the dynamics of HPAIV infection and to enhance the possibility of early detection. During 2007-2015, a total of 10,235 birds were captured nationwide

in habitats and its environs. However, surveillance design and sampling in the context of wild bird population still present major challenges in that current sampling design used for identifying sampling locations was not designed to solve spatial sampling problems related to spatially autocorrelated data. The overall goal of wild bird surveillance is intended to select geographic sites that adequately represented habitats throughout the country taken logistically and financially constraint into account. In this paper we review the current wild bird catchment program and present a computer application(written in visual basic) that utilizes spatial sampling algorithm to identify wild bird capture sites compiled over broad geographic locations in the country.

**Materials and Methods:** Geographic information system(GIS) has been used for spatial sampling design for active surveillance of HPAI in wild birds and its habitats when a sampling frame is unavailable and location is important for data collection (1, 2). Accordingly, we analyzed APQA database regarding records of wild birds capture retrieved from 2007-2015 to assess the status of historic sampling locations using ArcGIS (ver 10, ESRI, USA). Data were analyzed for each of 9 provinces including 8 municipalities. Geocoding was performed with the help of Google Earth to determine the precise coordinates of the farm locations and Kernel density mapping was accomplished with ArcGIS.

**Results:** Of 10,235 wild birds captured, 34.5% were from Chungnam, followed by Cheonbuk(30.6%), Gyeonggi (14.3%), Chungbuk (6.8%), Gyeongnam (6.3%), Cheonnam (5.9%), Kangwon (0.7%), Gyeongbuk (0.5%), and Jeju island (0.4%). The majority (57.6%) of sampling sites was situated on the west coast region of Korea (Cheonnam, Cheonbuk, Chungnam, Gyeonggi), which is co-incident with main migratory route of the birds. However, these locations accounted for only 45.6% of 195 NIBR monitoring sites, indicating that current sampling locations are geographically biased to limited areas at substantial cost. There were large differences between the sampling sites and geographic locations of wild birds isolated with HPAIV.

**Conclusions:** Due to the variability of wild bird population at major migration sites in Korea, a robust sampling strategy is necessary to collectively identify appropriate sites. Random spatial sampling scheme offers an alternative technique that could reduce opportunities for bias in sampling site selection compared to simple random method. Our study highlights areal sampling design that are needed to explore the distribution of targeted bird population with spatially clustered at some regions on introduction of HPAIV into Korean poultry premises via wild birds. This study was financially supported by the Animal and Plant Quarantine Agency (Project code: Z-1543068-2014-14-01).

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#### P-003

### Spatiotemporal Distribution of Migratory Bird Species with Potential Transmission of Highly Pathogenic Avian Influenza

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**Introduction:** Describing seasonal and spatial distribution of migratory birds is of crucial importance for the development of effective conservation strategy, and of great interest for the control of highly pathogenic avian influenza (HPAI) involving migratory birds (1). Epidemiological studies for 5 large HPAI outbreaks occurred in Korea during 2003-2015 revealed that wild birds migrating from surrounding countries was assumed to had key role in the HPAI virus (HPAIV) introduction. Further, more than 60 HPAI positive cases from wild birds and fecal samples were reported during the epidemics. According to the statistics of National Institute of Biological Resources (NIBR), over 1 million water birds are migrating South Korea annually, with more than 200 species. However, important aspects of species richness of wintering migrants, local abundance, species at domestic habitats, breeding performance and elevation preferences are still poorly understood, although the way in which migratory birds are distributed across these factors is a question of ecological and conservation importance. In this paper, distribution of migratory bird species during winter migration or stopover were quantified over 3 years and analyzed in conjunction with a variety of ecological variables to understand the annual variation in species, habitat use (monitoring site), local abundance, and spatial pattern, based on NIBR survey reports.

**Materials and Methods:** Since 1999 the NIBR has been conducted standardized wild bird survey each year to identify the number and dominant species of migratory birds and to monitor the main wintering and staging ground for 195 major monitoring sites. From the annual reports of 2012-2014, attribute variables for each monitoring site such as numbers of birds by species, order, and province were retrieved and constructed in Microsoft Excel. Data analyses were performed using the SAS software version 9.4. Geocoding and Kernel density mapping was accomplished with ArcGIS (ESRI). All data were mapped using the latitude and longitude coordinate system, based on the Korea central-belt.

**Results:** The number of species reached 1,079,956 in 2012