



Modelling the distribution of domestic ducks in Monsoon Asia

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ARTICLE INFO

Article history:

Received 2 December 2010

Received in revised form 11 April 2011

Accepted 25 April 2011

Available online 24 May 2011

Keywords:

Livestock mapping

Domestic ducks

Monsoon Asia

Regression models

Highly pathogenic avian influenza

ABSTRACT

Domestic ducks are considered to be an important reservoir of highly pathogenic avian influenza (HPAI), as shown by a number of geospatial studies in which they have been identified as a significant risk factor associated with disease presence. Despite their importance in HPAI epidemiology, their large-scale distribution in Monsoon Asia is poorly understood. In this study, we created a spatial database of domestic duck census data in Asia and used it to train statistical distribution models for domestic duck distributions at a spatial resolution of 1 km. The method was based on a modelling framework used by the Food and Agriculture Organisation to produce the Gridded Livestock of the World (GLW) database, and relies on stratified regression models between domestic duck densities and a set of agro-ecological explanatory variables. We evaluated different ways of stratifying the analysis and of combining the prediction to optimize the goodness of fit of the predictions. We found that domestic duck density could be predicted with reasonable accuracy (mean RMSE and correlation coefficient between log-transformed observed and predicted densities being 0.58 and 0.80, respectively), using a stratification based on livestock production systems. We tested the use of artificially degraded data on duck distributions in Thailand and Vietnam as training data, and compared the modelled outputs with the original high-resolution data. This showed, for these two countries at least, that these approaches could be used to accurately disaggregate provincial level (administrative level 1) statistical data to provide high resolution model distributions.

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1. Introduction

Maps of livestock distribution are a concise way to visualize and analyze large census datasets. They have a wide variety of applications such as assessing the risk of zoonotic disease, food safety management, determination of the potential daily protein production capacity, monitoring of the land-use changes, assessment of the environmental risk associated with animal production (Wint and Robinson, 2007).

The highly pathogenic avian influenza (HPAI) H5N1 virus that first appeared in southern China in the late 1990s (Li et al., 2004) is one of the most significant recent epizootics which has had dramatic consequences on smallholders' livelihoods and poultry

production in many countries (Brown, 2010). To date, the human death toll of these events remains moderate despite the very high mortality rates observed in wild and domestic fowl (World Health Organization, October 2010: 507 cases reported, 302 deaths confirmed).

Domestic ducks play a significant role in the epidemiology of HPAI H5N1 virus. First, experimental studies have demonstrated that they can be apparently healthy carriers of the HPAI H5N1 virus and have even been referred to as the "Trojan horse of the avian flu" (Kim et al., 2009). Domestic ducks have been shown to survive HPAI H5N1 virus infections and excrete large quantities of the virus without showing clinical signs of disease (Hulse-Post et al., 2005). As a result, domestic ducks may play a determinant role in the transmission of the virus during the movement of flocks between different feeding locations. Studies have shown that the distribution of HPAI H5N1 virus in parts of Asia is heavily influenced by the distribution of duck farming systems (Gilbert et al., 2007). More specifically, the density of ducks has been found to be a key variable for the predicting of the presence of HPAI H5N1 virus in Thailand (Gilbert

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et al., 2006), Vietnam (Pfeiffer et al., 2007), over the Mekong region (Gilbert et al., 2008), and even at the global scale (Hogerwerf et al., 2010).

However, despite the importance of ducks in HPAI H5N1 transmission, data on domestic duck populations derived from national censuses are often incomplete and vary considerably in resolution between countries. Some countries such as Thailand and Vietnam that produce large quantities of duck meat and eggs have undertaken massive survey campaigns (e.g. X-ray survey in Thailand involving 400,000 inspectors) following the HPAI H5N1 virus epidemics of 2004 and have very high resolution data reported at administrative levels 3 and 4 (e.g. Thailand: county and village level). In some other countries where HPAI H5N1 is of concern, however, data are available at best only at administrative levels 1 and 2. A striking example is China, which hosts more than 75% of the world's domestic duck population (FAOSTAT, 2010), yet species level duck data are available only at the provincial level (administrative level 1). In the Chinese province of Xinjiang, for example, there is only one figure provided for the entire 600,000 km². At this time modellers lack comprehensive and accurate information relative to the domestic duck population density and location. Ideally such information could be modelled at fine spatial resolution by applying an appropriate *disaggregation* methodology to the existing data. Various disaggregation techniques have been explored and applied with relative success to a wide range of livestock species (Wint and Robinson, 2007; Neumann et al., 2009; Gerber et al., 2005). To our knowledge, however, no previous attempts have focused on the geographical distribution of domestic ducks specifically in Monsoon Asia, a region of particular concern for the persistence of HPAI H5N1 virus. In this study we present a statistical modelling procedure inspired by earlier efforts to map livestock distributions (Wint and Robinson, 2007) and specially adapted to the case of domestic ducks. The methodology was applied to disaggregate reported domestic duck data to a 1 km × 1 km continuous population density surface across 14 countries.

The methodology relies on the use of agro-ecological predictors providing information on both bioclimatic and anthropogenic factors which are assumed to affect the geographical distribution of duck farming. The central hypothesis is that robust statistical relationships can be established between domestic duck population density and these agro-environmental predictors, and that these relationships can be used to disaggregate the administrative level distribution of domestic duck data across Monsoon Asia.

2. Materials and methods

We aimed to obtain the most recent duck data at the finest possible administrative level within Monsoon Asia. This required data to be compiled at different administrative levels depending on sources available. Table 1 provides details of the reported statistics used. The absolute numbers of ducks per reporting unit were converted into densities (birds km⁻²) by dividing the number of birds by the area of land considered suitable for duck production. This step was important to prevent densities from being underestimated in administrative units containing vast areas of land unsuitable for duck production (e.g. Xinjiang province, China). The suitability mask for ducks was modified from the original GLW monogastric livestock (pigs and poultry) mask (Wint and Robinson, 2007). We took a conservative approach in suitability masking by excluding only the most unsuitable areas for duck production (extreme high elevations, tundra, ice and deserts, for example, see Table S4 in Prosser et al. (in this issue)). The resulting dependent (y) variable data are referred to as 'training data'.

Two main groups of predictors were included. First, eco-climatic predictors derived from Fourier transformed MODIS

Imagery (<http://modis.gsfc.nasa.gov/>) over the period 2001–2005 (Scharlemann et al., 2008) and second, anthropogenic variables.

The Global MODIS Imagery is a compilation of images of the surface of the earth taken every 8 or 16 days for different channels of reflectance. These images are then composited over a period of time to generate a time series for each channel. The different channels are subject to atmospheric corrections and used in combination to define bioclimatic indices such as the Normalized Difference Vegetation Index (NDVI) or Land Surface Temperature (LST); variables that are expected to be of relevance in explaining the spatial distributions of livestock species (Wint and Robinson, 2007) and associated animal diseases (Hay et al., 2006; Sinka et al., 2010).

The Fast Fourier Transform (FFT) is a widespread ordination method used in ecology to summarize the information contained in a time-series in a way that is directly subject to interpretation (which is not always the case of other ordination methods such as the principal component analysis). The resulting output of the FFT is an image with each pixel being attributed the value of the Fourier coefficients (phase or amplitude) of the time series for the different harmonics of the signal. In this study we used the values of the amplitude and phase of the first to third harmonic, describing, respectively, the amplitude and the delay of the annual, bi-annual and tri-annual biological cycles for the channels listed in Table 2.

Domestic livestock production is constrained by natural limitations such as food availability, temperature, aridity and access to water, which can be captured through statistical relationships with the eco-climatic predictors. But production is also driven by human activities and related to factors such as population density, demand and access to production inputs (feeds, services, etc.) and output markets. As these factors are suspected to explain a substantial share of the spatial variability of domestic duck distribution in specific areas, we also used a set of anthropogenic predictor variables including human population density (Balk et al., 2006), distance to the nearest road (Dobson et al., 2000) and travel time to major cities (Nelson, 2008; Table 2).

The first step of the modelling procedure consisted of the spatial sampling of duck density data. However, because of the high heterogeneity in spatial resolution of the reported training data from different countries, applying a sampling scheme of equal density was not ideal. Applying a density related sampling scheme to take advantage of high resolution training data in some countries would have resulted in a large proportion of data points being associated with the same, single duck density value reported within an administrative unit. Conversely, using a low density of sampling points would not take full advantage of the higher resolution data available in other areas.

We therefore used a stratified sampling approach that included at least one point per administrative unit with training data and, beyond that, an average of 20 points per decimal degree across our analysis extent (Supplementary information, Fig. S3). Twenty-five random sets of sample points were created in order to bootstrap the analysis – each containing 75% of points used to train the statistical models (model set) and 25% for model validation (test set).

A forward inclusion multiple regression approach was developed using log-transformed duck densities as the dependent variable (to normalize duck densities). This involved the iterative inclusion of each predictor, paired with its quadratic term to account for non-linear relationships. Starting from a null-model, the algorithm searched for and included the pair of predictors that resulted in the best reduction in Akaike Information Criterion (AIC) (Burnham and Anderson, 2002; Whittingham et al., 2006). This process continued until the improvement in AIC was less than 1% (Fig. 1). As a measure to prevent over-fitting, we limited the maximum number of pairs of predictors to one for every 15 sampling points from different administrative units. The coefficients of the model were then applied to the imagery to obtain the log-

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