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Short communication

Transmission parameters of highly pathogenic avian influenza (H7N1) among industrial poultry farms in northern Italy in 1999–2000

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Abstract

We estimated between-farm transmission parameters of the highly pathogenic avian-influenza (HPAI) epidemic that struck the poultry industry of northern Italy (including turkeys, layer hens, broilers, gamebirds, and waterfowl) from December 1999 through April 2000. We estimated the average number of susceptible farms that were infected with HPAI virus by each infectious farm during a day (β) with a generalised linear model (GLM). The HPAI's reproductive ratios (R_h; the average number of new infected farms (IFs) that were caused by an infectious farm) were calculated separately for the regions of Lombardy and Veneto, where 382 out of 413 (92.5%) of IFs were located. In both regions, R_h decreased to ~1 during the second month of the epidemic (showing that its containment had been initiated). Subsequently, during the last two months of the epidemic, β and R_h were reduced to 0.04/day and 0.6, respectively, in Veneto and to 0.07/day and 0.8 in Lombardy. The reduction of the susceptible population through strict control measures, including pre-emptive slaughter of at-risk poultry flocks, was implemented to a greatest extent in Veneto and this might have been associated with a more rapid control of the epidemic in this region than in Lombardy.

Keywords: Avian influenza; Epidemic; Italy; Reproductive ratio; Generalised linear model

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1. Introduction

Highly pathogenic avian influenza (HPAI) can cause severe losses to poultry industries and poses a threat to public health (Capua, 2006). Epidemiological analyses of data from HPAI

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epidemics provide estimates of the effects of risk factors that can be used to identify categories of animals, farm types or geographic areas on which to focus interventions to reduce the risk of the infection. The effects of disease-control measures that were adopted in the past should also be evaluated to provide scientific evidence for the control of new epidemics.

The effects of risk factors were estimated by using multivariable Cox regression on data from an HPAI epidemic that led to the destruction of 16 million birds in the winter of 1999–2000 in Italy (Capua and Marangon, 2000). The epidemic was caused by a H7N1 subtype virus that originated, by mutation, from a low-pathogenic avian-influenza (LPAI) virus, which circulated among poultry farms in the spring. The hazard of the disease was significantly greater in Lombardy than in Veneto (hazard ratio = 3.4, 95% confidence interval: 2.4, 4.8), the two northern regions where 382 out of 413 (92.5%) of the infected farms (IFs) occurred. Proximity ($\leq$1.5 km) to previous IFs, turkey as the bird species (as compared to layer hens, broilers, gamebirds, and waterfowl), and size $>$ 18,000 birds were other risk factors that were positively associated with the hazard of HPAI at the farm level (Mannelli et al., 2006).

Methods such as multivariable Cox regression were originally developed to study chronic diseases and, when applied to HPAI, did not provide measures of the virus transmission between infectious and susceptible farms (de Jong, 1995). Conversely, the transmission of infectious agents between animal farms can be quantified by dividing farms into classes according to a susceptible-infectious-removed (SIR) model, and by calculating the parameter β as the average number of susceptible farms that were infected with the disease agent by each IF during a time unit. The infection's reproductive ratio (R_h; the average number of new IFs that were caused by an IF) can be obtained by multiplying β by the average duration of IFs' infectious periods (Stegeman et al., 1999; Bouma et al., 2003). Following the HPAI epidemics that struck The Netherlands in 2003 (Elbers et al., 2004; Fouchier et al., 2003), generalised linear models (GLM) were used to estimate β and R_h, which were subsequently compared in two regions before and after HPAI notification. It was concluded that the containment of HPAI was achieved through a reduction in the number of susceptible farms by depopulation of infected areas (Stegeman et al., 2004).

In this study we estimated between-farm HPAI transmission parameters during the Italian 1999–2000 epidemic. Our objective was to generate hypotheses on the effects of different HPAI-control scenarios in Lombardy and Veneto; we used methods that were specifically developed for quantifying transmission of infectious agents.

2. Material and methods

We carried out our analyses on a data-base (provided by the Istituto Zooprofilattico delle Venezie, Padova; IZSV) of poultry farms of Lombardy and Veneto. The database included dates of stocking and of slaughter of bird farms, and dates of detection of clinical signs of HPAI. In addition to clinical signs, isolation of HPAI virus and post-mortem lesions were criteria for case-definition that were applied according to the EU legislation (CEC, 1992). Therefore, in this study, we considered IFs that were officially recorded at the national reference centre for avian influenza at the IZSV.

For each day throughout the entire epidemic, new IFs were counted on the day of the detection of clinical signs, whereas farms that were stocked with birds as part of the regular production cycle and had no sign of HPAI were counted as susceptible. Moreover, the number of infectious farms during each day corresponded to IFs in their temporal risk window (TRW). An IF's TRW is the time interval during which clinical signs of disease can be detected in another farm following transmission from the IF (Taylor et al., 2004). In our calculation, we