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Short communication

# Within-flock transmission of H7N1 highly pathogenic avian influenza virus in turkeys during the Italian epidemic in 1999–2000

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ABSTRACT

Highly pathogenic avian influenza (HPAI) viruses show different disease dynamics between virus strains and host species, and therefore epidemic field data are very valuable. This study used field data of the HPAI H7N1 epidemic which affected Northern Italy in 1999–2000. Field mortality data was back-calculated into a S-I-format to estimate the transmission rate parameter $\beta$, indicating the number of birds infected per infectious bird per time unit. The bird-infectious period was assumed to be 2 days, and all birds were assumed to die after this infectious period. The estimated $\beta$ for HPAI H7N1 virus transmission in turkeys was 1.43 (95% CI: 1.17–1.74). Farm risk factors such as flock size and age of the turkeys did not influence the estimated transmission rate parameter.

## 1. Introduction

Highly pathogenic avian influenza (HPAI) viruses cause severe mortality among poultry flocks, and therefore huge economical damage to the poultry sector. Control of HPAI epidemics has proven to be difficult in densely populated poultry areas (Boender et al., 2007; Bowes et al., 2004; Capua et al., 2002; Stegeman et al., 2004).

Transmission dynamics, such as the transmission rate parameter $\beta$ (number of birds infected per infectious bird per time unit) and the $R_0$ (number of secondary infections in a susceptible population) give insight in how fast and extensive a virus spreads, and can be implemented in simulation models to evaluate the effect of control measures (for example Savill et al., 2006). Field data are very valuable for studying within-flock dynamics, but are rarely available in sufficient detail. So far, $\beta$ and $R_0$ have been estimated from field data for HPAI H5N1 virus in Thailand (Tiensin et al., 2007) and HPAI H7N7 virus in The Netherlands (Bos et al., 2009). These studies showed that two different epidemics have different disease dynamics. There are indications that besides environmental factors and strain differences, host species-specific characteristics also influence disease dynamics, and therefore it is important to analyse any available epidemic data to the full extent.

In Italy, a HPAI H7N1 epidemic caused the death of over 13 million birds and the infection of 413 flocks in 1999–2000 (Capua et al., 2002). This epidemic provided the opportunity to further study HPAI virus transmission, taking into account the effect of host species and virus strain. Data on daily mortality and farm characteristics had been collected on infected farms and used in this study to estimate the within-flock transmission rate parameter $\beta$ for HPAI H7N1 virus in meat type turkeys and broilers.

## 2. Material and methods

### 2.1. Data

Daily mortality data and farm characteristics were collected from infected turkey and broiler premises during

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**Table 1**
Descriptive characteristics of the farms included in the study.

| | $n$ | # Birds present on farm | | | Age in weeks at depopulation | | |
|---|---|---|---|---|---|---|---|
| | | Minimum | Median | Maximum | Minimum | Median | Maximum |
| Turkeys (all farms) | 45 | 3680 | 13,500 | 35,204 | 4 | 12 | 19 |
| Turkeys (farms with one house) | 23 | 3680 | 12,000 | 31,760 | 4 | 9 | 19 |
| Broilers (all farms) | 6 | 33,160 | 50,243 | 78,900 | 5 | – | 8 |
| Broilers (farms with one house) | 4 | 33,160 | 50,243 | 56,150 | 5 | – | 8 |

the Italian HPAI H7N1 epidemic in 1999–2000. From these farms, 51 farms had sufficient data (i.e. daily mortality on at least 20 consecutive days) available for this study, consisting of 45 meat type turkey farms and 6 broiler farms. However, only farms with one poultry house were used (23 meat type turkey farms and 4 broiler farms), to assure the estimated parameter values were really within-flock parameters. In this study one flock is defined as a group of birds kept under the same conditions in one house; all birds were raised on the floor with litter. Because the main interest of this study was the transmission rate parameter $\beta$, only the mortality data most likely related to HPAI were taken into account. Therefore, the last 20 daily observations before depopulation related to HPAI diagnosis were included in this study. Farm characteristics included poultry species, age of the birds at depopulation and initial flock size.

### 2.2. Method

The study followed the method previously described by Bos et al. (2009). In short: the daily mortality data were back-calculated to fit a S-I-format, in which birds were either susceptible (S) or infectious (I). The length of the bird-infectious period ($T_I$) was based on the results of challenge experiments with HPAI H7N1 virus in turkeys (unpublished data) and set at 2 days. After this $T_I$ birds died and were removed. Birds were considered a case (C) 1 day before their infectious period. For the flocks included in the analysis, each day-record in the back-calculated database contained the number of S, I or dead (D) birds, as well as the total number of birds present ($N$) and the number of cases per day.

The back-calculated data were analysed using the GENMOD procedure in SAS®, version 9.1, with a binomial distribution of the outcome ($C(t)/S(t)$), a complementary log–log link function, and flock inserted as repeated subject. The offset was set at $\log(I(t)/N(t))$.

Covariates were included for the age of the birds in weeks at depopulation (as a continuous variable) and flock size at the start of the production cycle (smaller or larger than the median), as these were believed to influence within-flock transmission. Models were compared by means of a likelihood-ratio test.

### 2.3. Sensitivity analyses

There was uncertainty about the length of the infectious period ($T_I$). To consider the influence of the parameter $T_I$, sensitivity analyses were performed with $T_I$ set at 1 and at 4 days. To study the effect of farms with multiple houses, these farms were analysed separately and together with the one-house farms. To justify the decision to only use the last 20 observations, the model was also run with the last 10 and the last 30 observations (when available) of a flock. Furthermore, flocks with little increase in mortality were removed to study their influence on the transmission rate parameter. Finally, a sensitivity analysis was performed for influence of poultry species, by including day-records of the broiler flocks and species as a covariate.

## 3. Results

### 3.1. Descriptives

See Table 1 for the descriptives of the dataset. The number of meat type turkeys per flock is generally lower than the number of broilers per flock, i.e. the medians are 12,000 and 50,243 birds. The age at depopulation in meat type turkeys varied from 4 to 19 weeks; in broilers the age at depopulation was 5–8 weeks.

### 3.2. Transmission dynamics

Table 2 shows the results of the uni- and multivariable models for flocks with meat type turkeys only. The inclusion of flock size into the model significantly improved the model fit, although the two categories (smaller or larger than the median of 12,000 turkeys) did not differ significantly. Inclusion of the age of the turkeys in weeks did not improve model fit, neither did a multivariable model with flock size and age fit the data better.

The point estimate for the transmission rate parameter $\beta$ for the basic model was 1.43 (95% CI: 1.17–1.74) per infectious turkey per day, and $R_0$ was estimated to be 2.9 (Table 3). From Table 3 it can also be seen that the model is quite robust; only a change in the length of the infectious period significantly changes the point estimate of $\beta$ from 2.20 (95% CI: 1.75–2.77) to 1.02 (95% CI: 0.85–1.22) per turkey per day, for 1 and 4 days of length, respectively. Inclusion of farms with multiple poultry houses, inclusion of more or less observations and exclusion of farms with little mortality, all do not have a relevant influence on the value of $\beta$.

In the four broiler farms the transmission rate parameter $\beta$ was 1.19 (95% CI: 0.93–1.52), as estimated from the basic model with broiler records added. This was not significantly different from transmission in turkeys, which might be a result of low power.