Estimating the per-contact probability of infection by highly pathogenic avian influenza virus during the 2003 epidemic in The Netherlands

A. Ssematimba[1,2], A.R.W. Elbers[1] , T.J. Hagenaars[1] and M.C.M. de Jong[2]

Introduction

Estimates of the per-contact probability of transmission of Highly Pathogenic Avian Influenza (HPAI) virus between flocks are important for the design of better control and biosecurity strategies.

Objective

To estimate the probability of a farm being infected with HPAI virus through a given contact from an infectious farm.

Materials and Methods

We use the data on traced farm contacts (that were not necessarily part of the outbreak control) collected during the epidemic. For each contacted farm, we extracted all its potentially infectious contacts.

- Each farm was characterized by a binary infection status (i.e., response variable)
- A generalized linear model with a binomial distribution and the explanatory variables (contacts) linked by a cloglog function is fitted.
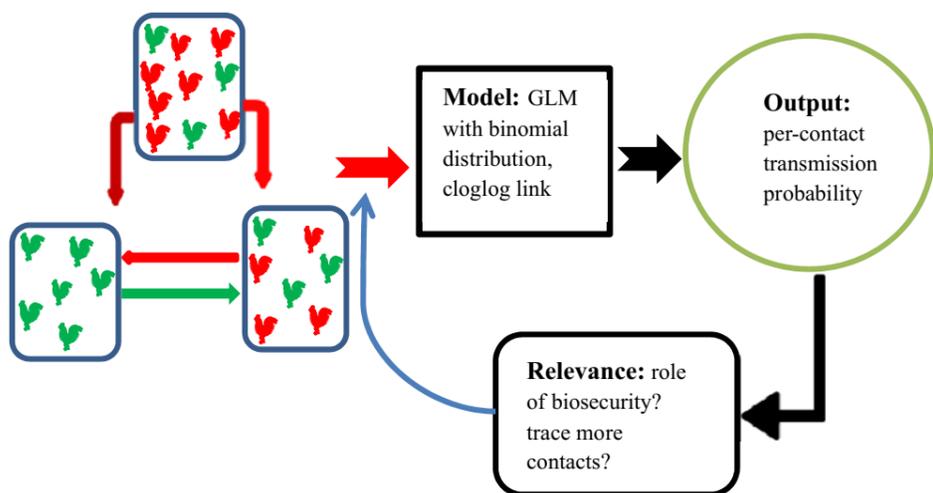
Fig. 1. Schematic view of the approach of this study

Results

The estimated probabilities (with their accompanying 95% CI) are presented in Table1 and the distribution of (merged) contact-distances is presented in Fig. 2.

Table1: The estimated per-contact transmission probabilities (95% CI)

Variable	Total no. of contacts (no. successful)	Per-contact transmission probability (95% CI)	P-value
Feed contact	267 (101)	0.444 (0.387 - 0.499)	0.00
Egg contact	81 (69)	0.761 (0.681 - 0.840)	0.00
Rendering contact	40 (36)	0.776 (0.646 - 0.890)	0.05
Material and manure contact	13 (11)	0.813 (0.565 - 0.965)	0.13
Advisor and dealer contact	15 (12)	0.738 (0.494 - 0.919)	0.35
Person and family contact	17 (12)	0.739 (0.499 - 0.915)	0.37

*AIC: 351.78, Residual deviance: 339.78 on 267 degrees of freedom
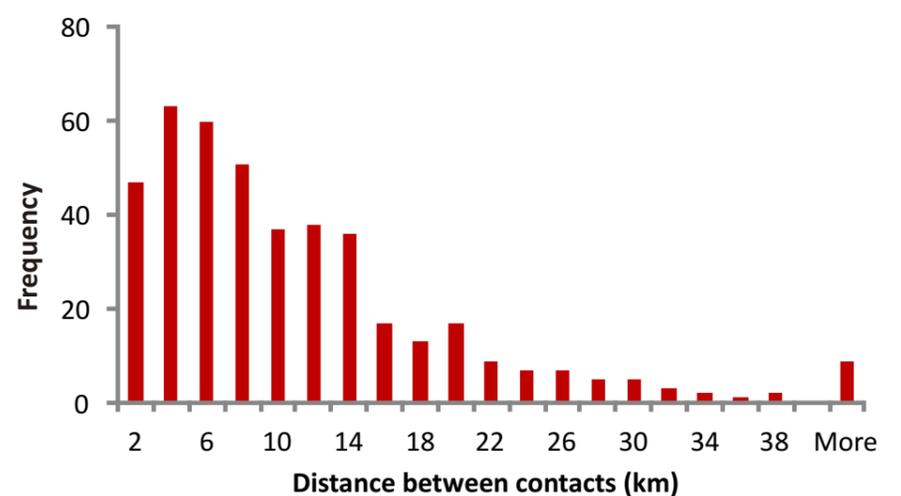
Fig. 2. The distribution of merged infectious contacts

Discussion and conclusions

At least one potentially infectious contact was determined for 128 (out of 241) infected and 145 uninfected farms. There is a need to better understand the possible mechanisms of untraced transmission.

The per-contact probabilities obtained here are higher than 0.037 i.e., the upper estimate of the per person-visit transmission probability for the contacts that were part of the outbreak control (te beest et al., *ZPH, 2010*). These contacts were subjected to thorough biosecurity hence the low estimate.

- This discrepancy provides a scientific support to improve biosecurity measures linked to the contacts

Relevance: These estimates can be used to inform studies, such as epidemiological models, that evaluate the impact of improved biosecurity and minimized contact-frequency in controlling HPAI virus spread.

Next step: To estimate the per-farm distance-dependent probability of infection by the merged contacts.

[1] Central Veterinary Institute (CVI), part of Wageningen UR
PO Box 65, 8200 AB Lelystad, The Netherlands
Tel. +31 320 238 852
e-mail: amos.ssematimba@wur.nl
www.cvi.wur.nl

[2] Quantitative Veterinary Epidemiology,
Department of Animal Sciences,
Wageningen University,
P.O. Box 338, 6700 AH Wageningen, The Netherlands