

# What can we say from the death of layer chickens? Estimating within-flock HPAI (H5N2) dynamics using an Approximate Bayesian Computation framework

## Introduction

- In early 2015, outbreaks of H5N2 clade 2.3.4.4 highly pathogenic avian influenza (HPAI) were detected in commercial poultry in the upper Midwestern states of the United States. The unprecedented scope of the outbreak highlighted gaps in the epidemiological understanding of this novel HPAI in commercial flocks.
- It was unclear how the complex population structure present in caged layer operations may affect the spread of the virus within barns.
- Objective:** To infer the epidemiological characteristics of how H5N2 clade 2.3.4.4 HPAI virus spread within table egg layer operations during the 2015 Iowa outbreak.



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## Method

- We fitted a stochastic, individual-based, Susceptible-Infectious-Recovered (SIR) within-flock model over the observed daily incident mortalities of caged layers for six H5N2-infected table egg layer operations in Iowa (Fig 1A).

- The flock size of the selected barns ranged from 62,000 to 308,800 birds, with a median of 104,500 birds. In each barn, the population structure was considered based on a double-sided multiple-tier cage system, with rows of 209 to 244 cages and 5 to 9 birds per cage. Number of cages in rows and number of birds in cages depended on the total population size and kept consistent stock density around 20,000 birds per block (Fig 1B).

- Transmission is through direct (i.e. between birds of the same cage or of contiguous cages) and indirect (homogeneous mixing process) contacts (Fig 1c). Probability  $M_i$  of infection for susceptible birds in cage  $i$  is:

$$M_i = 1 - \exp\left(-\left[\beta_w \frac{y_i}{N_i} + \beta_w \sum_{j \neq i} \frac{\rho_{ij} y_j}{N_j} + \beta_b \frac{1}{N_{tot}} \sum_{j \neq i} y_j\right] \times \Delta t\right)$$

with  $y_i$  and  $y_j$ : number of infected birds in cage  $i$  and  $j$  ( $i \neq j$ );  $N_i$  and  $N_{tot}$ : number of birds in cage  $i$  and in the whole barn;  $\rho_{ij}$ : contiguity between cages.

- The infectious period was assumed following an Erlang distribution of mean  $1/\mu_i$  and shape  $k_{inf}$ . A constant mortality rate  $r_M$  was introduced to account for management practices.

- Parameter Inference using Approximate Bayesian Computation employing sequential Monte Carlo (ABC-SMC) algorithm [1,2].

- Model was fitted over each longitudinal mortality record independently or together, selecting particles based on the  $R^2$  coefficient between observations and predictions.

## Key findings

- Taken together, posterior median estimates of direct ( $\beta_w$ ) and indirect ( $\beta_b$ ) transmission rates were 11.4 (95% Cr. I. 4.8 to 18.3) and 6.8 (95% Cr. I. 2.1 to 9.6) per infectious chicken per day, respectively (Figs 2A-B).
- The spread of H5N2 in table egg layer operations was characterised by a long median infectious period  $1/\mu_i = 13.9$  days (95% Cr. I. 8.6 to 17.5 days, Fig 2c).
- The model estimates that approximately 10-16 days would elapse between a virus introduction and detection of clinical signs (Fig 2D).

## Conclusion

- The median estimates of infectious period for H5N2 clade 2.3.4.4 was greater than what was reported for other subtypes, suggesting that this H5N2 virus was not well adapted to chickens upon initial introduction to layer flocks.
- Although these estimates are based on a small number of operations, inferences highlight the importance of indirect/fomite transmission.

Figure 1. Cage layout and model structure.

(A) Cumulative number of mortalities recorded daily in each barn used for model fitting. (B) Basic schematic of a multi-tier cage system for table egg layer hens. Each tier is composed of two rows of multiple cages. (C) Potential transmission routes of H5N2 between table egg layers from two separated rows of cages.

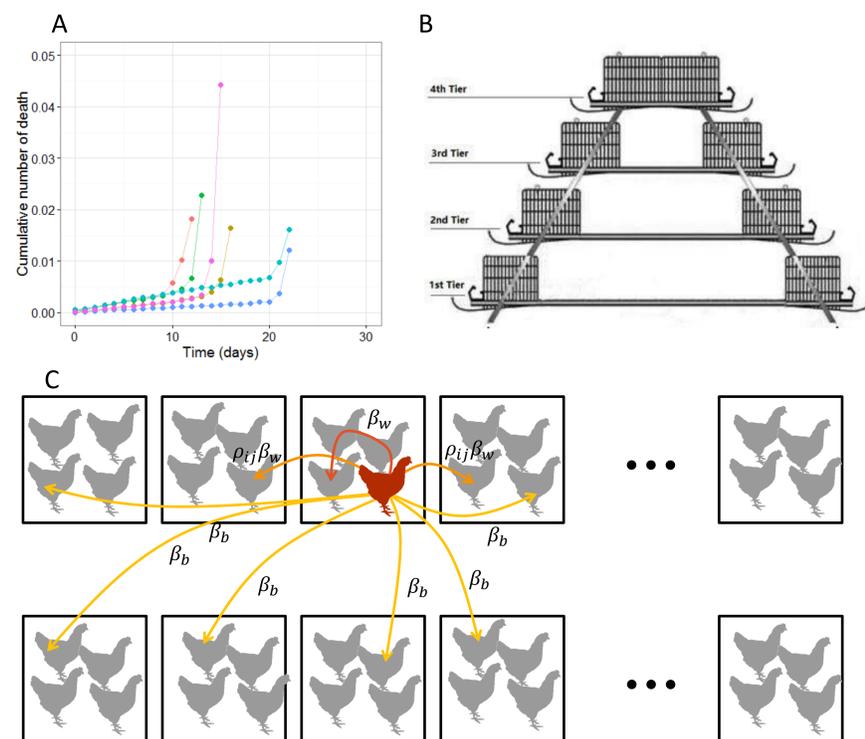


Figure 2. Model inferences

(A) Estimates of the within-cage transmission rate  $\beta_w$ . (B) Estimates of the between-cage transmission rate  $\beta_b$ . (C) Estimates of the mean infectious period  $1/\mu_i$ . In A to C, points are median estimates when inferences are made for each barn separately, whereas solid lines are those when inferences are made over all barns together. (D) Inferred number of days required to detect disease introduction for each barn. Error bars and dashed vertical lines in A to C represent 95% credible interval. Dashed line in D shows the median duration of disease detection computed for all barns. Size of the dots in A to C varies as a function of the size of each barn.

