

Nickbakhsh, S.,<sup>1</sup> Matthews, L.,<sup>1</sup> Dent, J.E.,<sup>2</sup> Arnold, M.,<sup>3</sup> Reid, S.W.J.<sup>4</sup> and Kao, R.R.<sup>1</sup>

<sup>1</sup>Boyd Orr Centre for Population and Ecosystem Health, University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK; <sup>2</sup>Department of Mathematics and Statistics, University of Strathclyde, 16 Richmond Street, Glasgow, G1 1XQ, UK; <sup>3</sup>Veterinary Laboratories Agency, New Haw, Surrey, KT15 3NB, UK; <sup>4</sup>Royal Veterinary College, University of London, Hawkshead Lane, North Mymms, Hatfield, Hertfordshire, AL9 7TA, UK.

## Introduction

Explicit examinations of the impact of local population dynamics, and their interaction with the temporal dynamics of network links, are few. Using the example of highly pathogenic avian influenza (HPAI) in British poultry, the implications of variability in farm-level transmission dynamics for virus spread at the population-level was demonstrated.

## Methods

### 1. Catching-company data:

Temporally explicit movement data was obtained from one major catching company in England: 44,758 individual on-to-farm visits across 950 days, for 68 catching-teams and 415 poultry farms (~91% were broiler chicken producers).<sup>1</sup>

### 2. S-E-I-R deterministic within-flock transmission model:

A Susceptible-Exposed-Infected-Removed model was used representing HPAI transmission in broiler chickens. An additional 'F' class allowed the build-up of infectious faecal material over time (eq.1). A mortality threshold (MT) – as a proportion of the initial flock size – triggered outbreak detection and inhibition of on-to-farm visits.<sup>2</sup>

$$\frac{dS}{dt} = -S\left(\beta_a \frac{I}{n} + \beta_f \frac{F}{n}\right)$$

$$\frac{dE}{dt} = S\left(\beta_a \frac{I}{n} + \beta_f \frac{F}{n}\right) - \delta E$$

$$\frac{dI}{dt} = \delta E - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

$$\frac{dF}{dt} = \varepsilon I - \sigma F$$

$\beta_a$  = transmission rate via aerosol /bird /hour  
 $\beta_f$  = transmission rate via infectious faeces /bird /hour  
 $\beta_a + \beta_f$  = total infection pressure  
 $n$  = flock size (poultry count/ number of houses)  
 $\delta$  = rate of infectiousness onset /bird /hour  
 $\gamma$  = HPAI induced mortality rate /bird /hour  
 $\varepsilon$  = faecal excretion rate/ bird/ hour  
 $\sigma$  = rate of decay of infectious faeces /bird /hour

eq.1

### 3. Simulating a range of outbreak scenarios:

A wide range of outbreak scenarios were considered, represented by different  $R_0$  values calculated as the dominant eigenvalue of the Next Generation Matrix for the ODE system (eq.1); range = 3-38, corresponding to time-to-detections of ~2-10 days.

### 4. Quantifying farm-level transmission potential (TP):

$TP_i$  represented the farm-level potential for personnel, vehicles and equipment to become exposed to HPAI during an on-to-farm visit:

$$TP_i = \sum_{t=1}^{t_{\max}} F_{i,t} \cdot \kappa_{i,t}$$

eq.2

$F_{i,t}$  = amount of infectious faecal material for farm  $i$  on day  $t$

$\kappa_{i,t}$  = total number of slaughterhouse loads for farm  $i$  on day  $t$

### 5. Farm-level predictors of TP:

To generate a farm-level "risk" profile, demographic and between-farm network connectivity<sup>3</sup> factors predictive of  $TP$  were identified using multivariable linear regression.

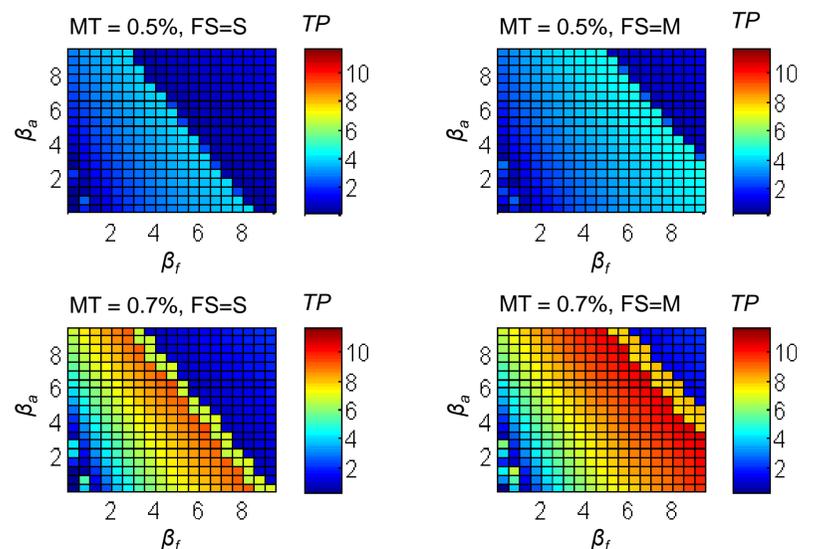
### 6. TP and national-level impact:

To explore whether a farm's propagation risk corresponded to potential outbreak extent at the national-level, a farm's  $TP$  was cross-classified with their between-farm network connectivity estimate.

## Results

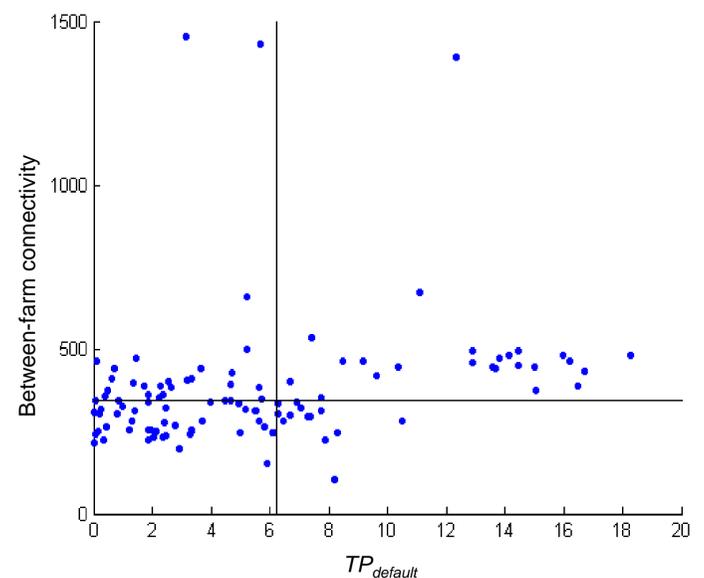
•  $TP$  scaled with the build-up of infectious faeces, peaking at high transmissibility ( $R_0 \sim 25-30$ ) then dropped rapidly – earlier disease detection reduced the opportunity for catching-team visits (Figure 1).

•  $TP$  was sensitive to small changes to the assumed mortality threshold (MT) and flock size (FS; S = 'small', ~4,500-14,000 birds; M = 'medium', ~14,000-28,000 birds).



**Figure 1.** Mean transmission potentials ( $TP$ ) across all farms ( $n=108$ ) for pairwise combinations of the infection pressure parameters ( $\beta_a$  and  $\beta_f$ ), showing increases to flock size (FS) and assumed mortality threshold (MT).

• Between-farm connectivity was the best predictor of  $TP$  (coefficient=0.004, 95% CI=0.001-0.006,  $p=0.004$ ,  $R^2=0.68$ ). However, 32% of farms had a relatively high potential impact at the national-level, despite a relatively low  $TP$  (top left quadrant, Figure 2).



**Figure 2.** Cross-classifying each farm's  $TP$  with a measure of their network connectivity.  $TP_{\text{default}}$  = farm-level  $TP$  computed for a mid-range infection pressure. Horizontal and vertical lines represent median values of between-farm connectivity and  $TP_{\text{default}}$  respectively.

## Conclusion

The interaction between group-level transmission dynamics and the pattern of on-to-farm movement events has important implications for disease transmission dynamics – only small changes to parameters increased the risk for the propagation of HPAI virus infection. However, this farm-level risk did not correspond to the potential impact at the national-level in all cases.

## References

- Dent et al. (2011) *BMC Veterinary Research*, 7:59.
- Savill et al. (2008) *Journal of the Royal Society Interface*, 5:1409-1419.
- Nickbakhsh et al. (2011) *BMC Veterinary Research*, 7:66.

## Acknowledgements

We thank Defra and the Animal Health & Veterinary Laboratories Agency for providing the data, Lucy Snow for her contribution to collation of the catching-company data and ICHAIR, through the Scottish Research Council, for funding. R.R.K. is funded by a Wellcome Trust Senior Research Fellowship.