

Spatio-temporal analyses of highly pathogenic avian influenza H5N1 outbreaks in the Mekong River Delta, Vietnam, 2009

Phan Q. Minh, Mark A. Stevenson, Chris Jewell, Nigel French, Birgit Schauer

Abstract

This paper presents the results of spatio-temporal analyses and epidemic modelling of HPAI H5N1 outbreaks that occurred in four provinces of the Mekong River Delta, Vietnam between January and March 2009. Significant spatio-temporal interaction of disease risk was observed within a distance of 10 km and 12 days following the detected onset of clinical signs. We estimate that the household-to-household infection rate within a commune was approximately 50 times greater than the household-to-household infection rate between communes. Our findings show that the predominant mechanism of infection transfer was local spread. A comparison of disease control procedures and veterinary capacity in communes with relatively high and low infection rates should help to identify procedures essential for effective outbreak management in this area of Vietnam.

Keywords

- HPAI;
- Poultry;
- Spatio-temporal interaction;
- Disease transmission;
- Vietnam

Figures and tables from this article:



Fig.1. Map showing provincial boundaries (thin lines, $n = 63$) of Vietnam and the Mekong River Delta (thick lines, $n = 13$), and locations of the four studied provinces (shaded).

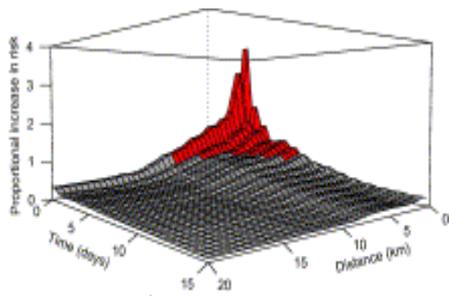


Fig.2. Spatio-temporal interaction of HPAI risk among household-level outbreaks ($n = 164$) in four provinces of the Mekong River Delta, Vietnam between 1 January and 12 March 2009. The red shaded area shows the distance-time separations where the proportional increase in risk attributable to space-time interaction was greater than one.

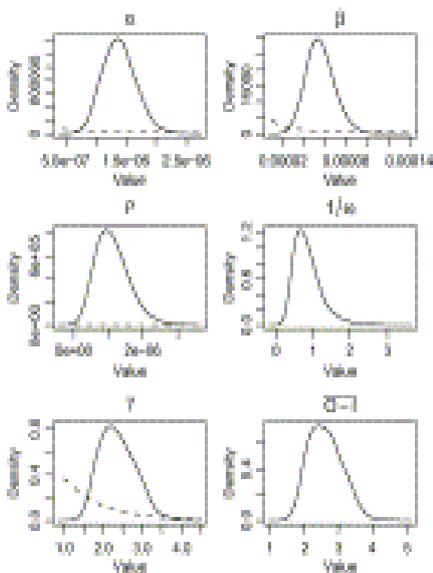


Fig.3. Graphs showing the probability density functions of the background rate of infection (α), the household-to-household infection rate within the commune (β), the household-to-household infection rate between communes (ρ), the commune-level random effect ($1/\omega$), the rate parameter of the Gamma distribution of the time from infection to observation of the clinical signs (γ), and the time from infection to observation of the clinical signs ($\theta - 1$). Dotted lines indicate the prior distributions for the parameters. A value of $\beta = 0.00005$ means that the rate of household-to-household infection transmission within the commune was 0.00005 infections per individual per day.

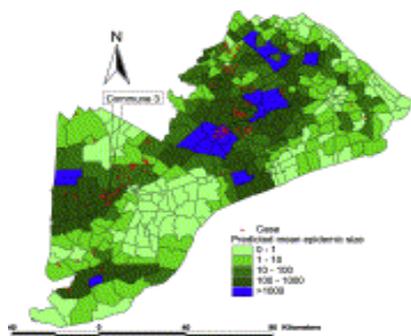


Fig.4. Spatio-temporal analyses of HPAI H5N1 outbreaks in the Mekong River Delta, Vietnam, January to March 2009. Map of the study area showing: (1) locations of HPAI-infected households ($n = 164$), and (2) the mean predicted epidemic size in each commune ($n = 337$). Boundaries of communes are shown as black lines. The estimated origin of the epidemic (commune 3) is indicated.

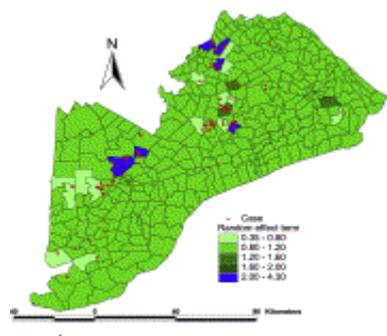


Fig.5. Spatio-temporal analyses of HPAI H5N1 outbreaks in the Mekong River Delta, Vietnam, January to March 2009. Map showing: (1) locations of HPAI-infected households ($n = 164$), and (2) the posterior mean of the commune level random effects. The random effect allows spatial

heterogeneity in infectivity, thus partially accounting for commune-level overdispersion in the data. Boundaries of communes are shown as black lines.

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