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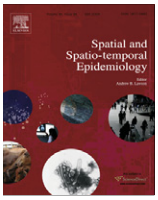

Spatio–temporal analyses of highly pathogenic avian influenza H5N1 outbreaks in the Mekong River Delta, Vietnam, 2009

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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.

1. Introduction

Highly pathogenic avian influenza (HPAI) H5N1 is a contagious disease of poultry characterized by high mortality and a wide host range (OIE, 2002; Swayne, 2008). Since 2003 outbreaks of HPAI have been common in many countries throughout Asia. Although HPAI outbreaks have been brought under control in many countries, eradication has not been achieved and in some areas the disease has become endemic. Control and prevention of the disease requires a proactive approach, particularly in areas where poultry are kept under backyard and free-ranging systems (Tiensin et al., 2005). Despite massive control efforts involving movement restrictions, culling of affected stock and vaccination, outbreaks of HPAI H5N1 continue to occur in Vietnam (DAH, 2009a).

Poultry production in Vietnam is characterized by small individually-owned flocks. Poultry movement in Vietnam is complex (compared with other Asian countries) involving large numbers of small holders moving stock to and from traders, neighbors and local markets. Movement patterns are influenced by the type of poultry product being traded and where they originate from. For instance, poultry products (meat and eggs) are mainly sold in local markets in lowland areas, whereas farm-gate sales are characteristic in midland and highland areas. Broilers and eggs can be sold to traders at farm gates and local markets (Tung, 2006). Bicycles and motorbikes are commonly used to transport poultry and poultry product to and from markets due to the ease with which they can move through narrow and congested road systems. An additional feature, with particular relevance to the epidemiology of HPAI, relates to the use of field running ducks, that is ducks moved from one location to another in the major rice growing areas

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(particularly in the south of the country) for the purpose of grazing on insects, snails and leftover rice grains. In addition to the accepted transmission mechanisms (local spread from infected flocks and long distance spread via movement of birds) the control of HPAI in Vietnam is complicated by the involvement of field running duck movements (Henning et al., 2009a). Selection of disease control measures should rely on a good understanding of the main transmission pathways of HPAI. Surveillance systems should target identification of important local and long-distant transmission pathways for HPAI in this area.

In Vietnam a number of spatial and spatio–temporal analyses of HPAI H5N1 outbreaks have been conducted to characterize the geographic distribution and quantify the spatial and temporal spread of HPAI H5N1 outbreaks at the commune level (Pfeiffer et al., 2007; Henning et al., 2009b; Minh et al., 2009). An inter-commune transmission model was developed by Walker et al. (2010) to quantify the spatial and temporal dynamics of the spread of HPAI H5N1 infection, indicating a substantial decrease in the transmissibility of infection between communes after vaccination. In all previous studies, in the absence of detailed data defining flock location, commune centroids have been used to represent the point location of outbreaks. This represents a simplification of the data that has the potential to obscure some of the more subtle features of disease spread mechanisms.

The aim of this study was to provide insight into the spatio–temporal patterns of HPAI H5N1 outbreaks in the Mekong River Delta and to quantify between-household transmission characteristics. In contrast to earlier epidemiological studies of HPAI H5N1 in Vietnam, the observational unit in this study was the household. Findings from this work should help to better understand the spread mechanisms of HPAI H5N1 in Vietnam.

2. Materials and methods

2.1. Study area and study period

The geographical area of interest for this study comprised the 337 communes within four provinces (Soc Trang, Hau Giang, Bac Lieu and Ca Mau) in the Mekong River Delta of Vietnam (Fig. 1). Poultry were kept by 269,755 households in the study area. The median number of households keeping poultry per commune was 414 (interquartile range [IQR]: 199–978 households) (DAH, 2009b). Between 1 January and 12 March 2009 inclusive, 38 commune-level outbreaks of HPAI H5N1 were recorded in 5 provinces in the Mekong River Delta. Of these, 37 commune-level outbreaks (97%) occurred in the four contiguous provinces defined as the study area.

2.2. Outbreak definition

In this study, a household-level outbreak was defined as both an index case household and subsequent households where poultry showed clinical signs of HPAI H5N1 during the outbreak period. In Vietnam, a commune-level outbreak of HPAI H5N1 was defined as a commune that had at least one household with poultry showing clinical signs of disease and laboratory confirmation of HPAI H5N1 using RRT-PCR (real-time reverse transcriptase polymerase chain reaction). The first diagnosed household in a commune was defined as the index case for that commune. Subsequent flocks in the same commune showing typical clinical signs of disease, as prescribed by the Department of Animal Health of Vietnam (DAH, 2004), were considered to be HPAI H5N1 infected and culled without laboratory diagnosis. It is thought that more than 90% of samples collected from HPAI suspected poultry in the Mekong River Delta are subsequently diagnosed as being positive with H5N1 using RRT-PCR (Tran D. Quy, personal communication). A commune was declared free of disease 21 days after the last clinically affected poultry were destroyed (MARD, 2007; DAH, 2008). The period from the detection of the index household outbreak to the declaration of disease freedom was defined as the outbreak period.

2.3. Data collection

In Vietnam, the routine HPAI H5N1 surveillance program relies on poultry farmers recognizing sick or dead poultry in a flock and then reporting the details of these events to commune veterinarians. In 2009 a case-control study was conducted to identify risk factors associated with outbreaks of HPAI H5N1 in the Mekong River Delta.

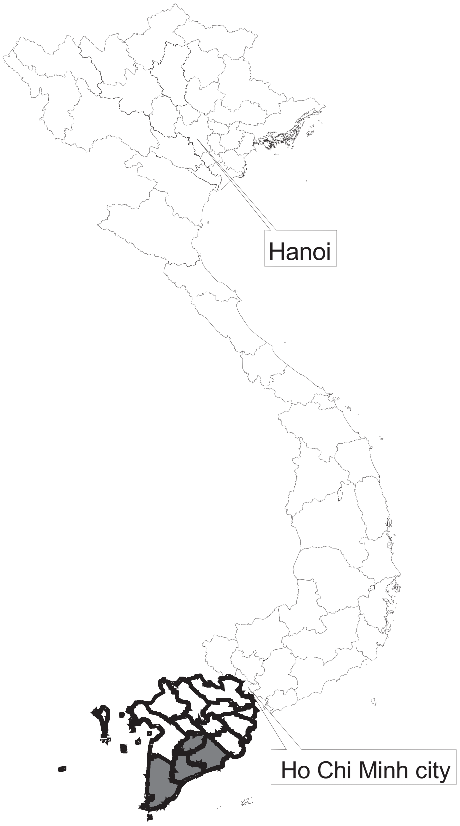

Fig. 1. Map showing provincial boundaries (thin lines, $n = 63$) of Vietnam and the Mekong River Delta (thick lines, $n = 13$), and locations of the four studied provinces (shaded).