

## The space–time clustering of highly pathogenic avian influenza (HPAI) H5N1 outbreaks in Bangladesh

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### SUMMARY

Bangladesh faced two epidemic waves of highly pathogenic avian influenza (HPAI) H5N1 in two consecutive years. The peaks of the waves were observed in February–July 2007 and January–April 2008, respectively. We examined the spatial and temporal patterns of the 293 outbreaks in 143 subdistricts in 2007 and 2008. Global clustering assessed by *K*-function was seen at distances 150–300 km between subdistricts. Significant local clusters were detected by space–time scan statistics. In both waves, significant primary clusters of HPAI outbreaks were identified in the central part of the country dominated by commercial production systems and in the northwestern part primarily in backyard production systems. Secondary clusters varied from the northwestern part in 2007 and the southern part in 2008. The findings are highly relevant for the successful planning and implementation of control, prevention and surveillance strategies by highlighting areas where detailed investigations should be initiated.

**Key words:** Bangladesh, clustering, epidemiology, subdistricts, H5N1 avian influenza.

### INTRODUCTION

Avian influenza caused by highly pathogenic avian influenza (HPAI) virus subtype H5N1 has had enormous and serious consequences on animal and public health and socio-economic issues primarily in Asia. Since 2003 more than 60 countries have experienced

HPAI (H5N1) outbreaks [1, 2]. Although most of the countries succeeded in clearing the virus in the initial phase of the outbreak, the virus persists in southeastern and southern Asian countries including Bangladesh, Egypt, Indonesia and Vietnam ([http://www.fao.org/ag/againfo/programmes/en/empres/maps\\_2009.html](http://www.fao.org/ag/againfo/programmes/en/empres/maps_2009.html)). In these countries year-round sporadic outbreaks are still recorded in poultry. So far, this zoonotic virus has been the cause of 440 human infections in 15 different countries with 262 fatalities since 1997 [3]. Initially, poultry production was the main target of the virus with large numbers of culled

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animals and losses in domestic and international markets. As a consequence the livelihood of poultry stakeholders has experienced significant negative effects during the outbreak period.

Bangladesh experienced the first HPAI outbreak on 15 January 2007 and the country was officially declared HPAI H5N1 positive on 22 March 2007 [4, 5]. Despite implementation of different control measures including movement control, the outbreaks continued with 68 outbreaks in 2007 and 225 outbreaks in 2008. A total of 1.7 million poultry were culled as part of the control measures, causing huge economic losses for the country [6]. In May 2008 the only human case was reported without fatality [7, 8]. Although no further human cases have been recorded following this case the virus still persists causing intermittent poultry outbreaks in different geographical areas of the country [1]. Therefore, HPAI control in poultry is a priority in Bangladesh.

According to the Food and Agricultural Organization of the United Nations (FAO) there are four types of poultry production sectors: (1) industrial and integrated production, (2) large-scale commercial production, (3) small-scale commercial production, and (4) backyard production [9]. Bangladesh has all of these production systems but small-scale commercial production (type 3) and backyard production (type 4) predominate. Of the 222 million total poultry population about 50% are backyard and reared in the scavenging system on the homesteads of villagers. Commercial farming is mostly located in the urban and peri-urban regions of the country where the supply facilities for the inputs of farming and marketing of the products operate smoothly [10]. Bangladesh has observed H5N1 outbreaks in both commercial and backyard poultry production systems from the beginning of the avian influenza (AI) epidemic.

The veterinary services in Bangladesh are available at a lower administrative level of subdistricts (*upzila*). The Department of Livestock Services (DLS) under the supervision of the chief veterinary officer (Director General, DLS) provides veterinary services through the *upzila* livestock offices [11]. Currently, DLS has no nationwide active animal disease surveillance programme. The passive surveillance programme solely depends on the report of the *upzila* livestock officer (ULO) to the directorate. Thus, an improvement of services primarily involving active surveillance, disease control programmes and more resources is strongly needed at the subdistrict level in Bangladesh.

Understanding of clustering and spreading mechanisms of diseases provides information for disease control and prevention strategies. Space–time pattern of clustering of HPAI outbreaks in Bangladesh might be the basis for identifying areas where more investigations can be initiated in order to explore the entrenchment and spreading sources of the virus. Advances within the area of spatial epidemiology, particularly spatial statistics and spatial software have created opportunities to examine the in-depth pattern of disease over space and time. Hence, different methods for detection of disease clusters become ‘state of the art’ for outbreak investigation. Significant clusters have been observed in disease outbreaks, e.g. sleeping sickness [12], SARS [13], and zoonotic diseases, e.g. West Nile virus [14], bovine spongiform encephalopathy [15], and brucellosis [16]. Spatial and temporal patterns in previous HPAI outbreaks have been investigated in Thailand [17], Vietnam [18, 19] and Italy [20]. However, such patterns were not systematically examined for HPAI outbreaks in Bangladesh. Moreover, differences of the poultry husbandry and agro-ecology between Bangladesh and other southeastern Asian countries make it prudent to investigate space–time clusters for HPAI outbreaks in Bangladesh.

Mechanisms of spread and persistence of H5N1 virus remain unexplored in the HPAI epidemic of Bangladesh as in many other countries. However, in order to improve planning and implementation of control and prevention strategies such information is essential.

Therefore, the objective of the present study was to identify space–time clusters of HPAI outbreaks at the subdistrict level in Bangladesh to support existing surveillance and to suggest empirical strategies for HPAI.

## MATERIALS AND METHODS

### Outbreak data and data management

Data on outbreaks of HPAI were collected from the website of the World Animal Health Organization (OIE) [1]. All laboratory-confirmed outbreaks were officially reported by DLS Bangladesh to OIE. Clinical AI cases were initially reported by farmers to a state veterinary surgeon working at the subdistrict livestock office (i.e. the ULO) who then examined the sick chickens on farm. If AI was suspected, dead chickens were collected and sent to the National

Reference Laboratory for Avian Influenza (NRL-AI) in Bangladesh. The virus was confirmed in tracheal samples from chickens on the suspected farms by the NRL-AI by RT-PCR using a primer set HA oligo-5' (5'-ACACATGCYCARG ACATACT-3') and HA oligo-3' (5'-CTYTGRTTYAGTGTTGATGT-3') described by Lee *et al.* [21]. Biswas *et al.* [4] described in detail HPAI case-reporting in chickens, laboratory techniques employed at the NRL-AI and diagnostic reconfirmation of the virus in some representative samples sent to the Veterinary Laboratory Agency in the UK.

For administrative purposes Bangladesh is divided into six divisions, 64 districts and 481 subdistricts [22]. We concentrated our study at subdistrict level with a subdistrict of Bangladesh as the study unit. The location used for the subdistricts was the centroid of the respective subdistricts. Coordinates for the centroids were calculated from the subdistrict-level digital map in ArcMap 9.2 (Environmental System Research Institute, USA). Coordinates were converted from latitude/longitude to Cartesian UTM coordinates using the WGM84 ellipsoid and UTM zone 46. We performed data management with SAS version 9.1 (SAS Institute Inc., USA).

Of the 481 subdistricts we excluded 17 due to lack of data availability regarding centroids resulting in a sample of 464 subdistricts. A subdistrict was considered as infected (case) if it had at least one officially confirmed outbreak within the period of interest. The rest of the subdistricts were considered as non-infected (control).

### Descriptive analysis

We constructed the epidemic curve for affected subdistricts in relation to the production system. We plotted the number of infected subdistricts identified per day as a function of time. A subdistrict with one or more laboratory-confirmed case(s) for a particular day was considered as an infected subdistrict. In construction of the epidemic curve of the affected subdistricts we applied a temporal moving average of the affected subdistricts. The latter method removes the dependency of frequency at some specific temporal points and transforms the frequencies into a continuous form. We used a window size of 30 days based on visual inspection of the smoothed plot. Finally, we calculated the prevalence of HPAI-infected subdistricts stratified by production systems.

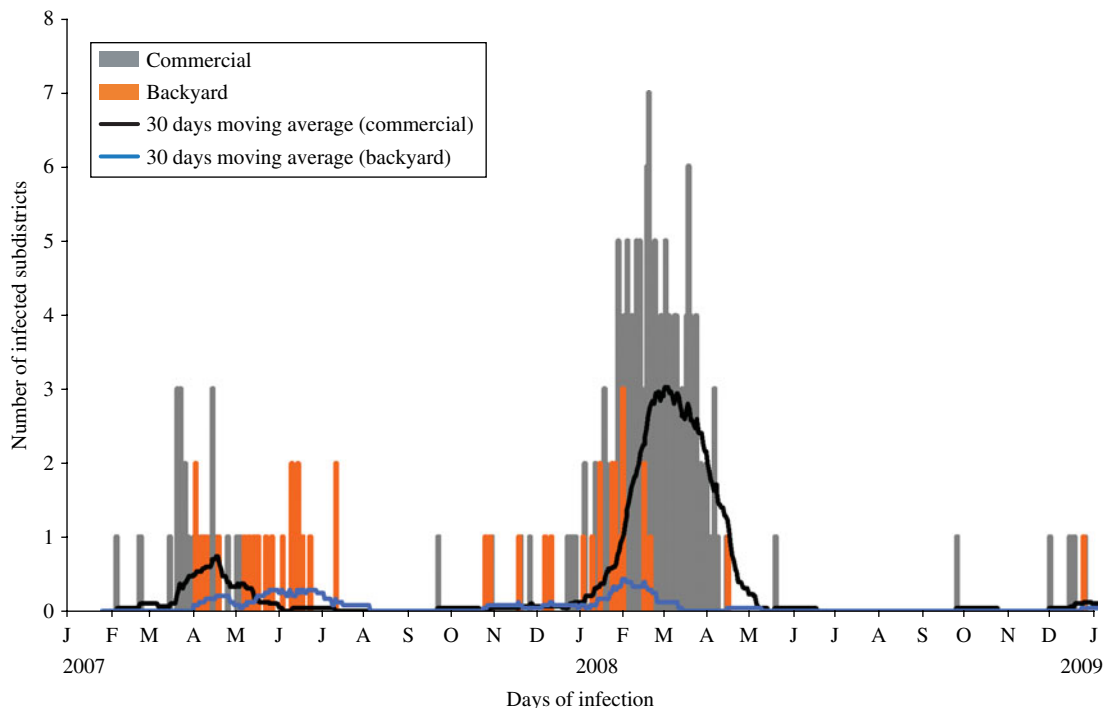
### Cluster analysis

To examine clustering of HPAI outbreaks at sub-district level in Bangladesh we used two approaches. First, we evaluated global spatial clustering using *K*-function analysis for each wave and production type. Second, in order to identify the exact location of clusters, we applied local cluster detection technique using scan statistics.

The *K*-function is a global measure to detect clustering of events in spatial point process. Like all other global measures it can evaluate overall the spatial autocorrelation and clustering. The hypothesis of no clustering also known as complete spatial randomness (CSR) is often tested using a homogenous Poisson process for the null-hypothesis *K*-function. In our analysis we used the centroid of the subdistricts as the location of the infected subdistricts which are fixed locations in space. The centroids of the subdistricts are not randomly distributed. To resolve the problem of non-randomly distributed locations we used the simulation method of the null-hypothesis *K*-function developed by Ersbøll & Ersbøll [23]. This method not only overcomes the assumption of CSR of the centroid locations but also limits edge effects and excludes the size of the study area which causes estimation problems due to mountains, lakes and irregular coastal lines. We simulated the *K*-function for infected subdistricts from a random sampling of the subdistrict locations. Random samples were drawn from a random distribution which was generated by Monte Carlo (MC) simulations based on the exact locations of the subdistricts. The difference between the simulated and empirical *K*-functions (the so-called *D*-function) was plotted together with the 95% simulation envelop as a function of distance. Presence of global clustering was indicated when the *D*-function curve crossed the 95% simulation envelop.

We employed scan statistics [24, 25] to detect significant clusters of HPAI at subdistrict level with a Bernoulli model using the daily infection status in subdistricts over the study period. The scan statistics was carried out by SaTScan (version 8.0, Martin Kulldorff and Information Management Services; <http://www.satscan.org>).

The space-time cluster analysis searches, locates and tests for the significance of space-time clusters. The search was performed by using cylindrical moving windows of variable size in the study area and over the period of interest. The scan statistics count



**Fig. 1.** Epidemic curve of infected subdistricts of HPAI outbreaks in Bangladesh (2007–2008) for commercial and backyard flocks.

the number of expected and observed infected subdistricts for each window. A cluster of subdistricts is identified when there are a greater number of observed infections than expected. The likelihood ratio test was used to test the significance of the clusters. The *P* value for test of significance was obtained from MC simulations (999 permutations).

Initially, we carried out a purely spatial analysis of HPAI outbreaks for commercial and backyard production systems, separately. For this analysis the circular base [centred in each of the locations (sub-district) of the window which represented the spatial dimension], was allowed to include up to 50% of the total population. Spatio-temporal cluster analysis was performed with a cylindrical spatio-temporal search window centred in each location with the base representing space and height representing time. The spatial dimension was allowed to include up to 50% of the population and the temporal window was allowed to include 50% of the study period. We analysed circular clusters with no geographical overlapping, with inclusion of 15% and 25% of the population for purely spatial and spatio-temporal clusters; 50% of the temporal observations were included in the window for spatio-temporal cluster analysis.

## RESULTS

### Descriptive analysis

From February 2007 to December 2008, a total of 148 (31%) out of 481 subdistricts were officially confirmed positive for HPAI infection.

The epidemic of HPAI in Bangladesh is characterized by two distinct waves between February 2007 and May 2008 (Fig. 1). The first wave began in February, peaked in March and ended in early July 2007. After that almost 2 months passed without any officially confirmed cases. The second wave started sporadically in September and continued to November 2007. The epidemic started in December 2007, peaked in February and ended in April 2008. After the second wave there were still some sporadic officially confirmed cases in Bangladesh. The moving average indicated the first wave was between April and July 2007 and the second wave was between January and April 2008. The analyses were performed for the two waves individually.

In the first wave 29 (6.03%) subdistricts and in the second wave 115 (23.90%) subdistricts were infected. Infected flocks were mostly found in the subdistricts of central (Dhaka Division) and northwestern part (Rajshahi Division) of Bangladesh. The prevalence

Table 1. Descriptive analysis given by number of outbreaks, number of subdistricts with at least one outbreak, subdistrict prevalence and corresponding 95% confidence limits for HPAI outbreaks in backyard and commercial productions systems, Bangladesh 2007–2008

	First wave		Second wave	
	Backyard	Commercial	Backyard	Commercial
$n_{\text{outbreaks}}$	20	24	22	208
$n_{\text{SD}+}$	16	15	18	109
Prevalence	0.033	0.031	0.037	0.227
95% CI	0.019–0.054	0.018–0.051	0.022–0.059	0.190–0.267

$n_{\text{outbreaks}}$ , Number of outbreaks;  $n_{\text{SD}+}$ , number of subdistricts with at least one outbreak; Prevalence, subdistrict level prevalence ( $n=481$ ); 95% CI, 95% confidence limits.

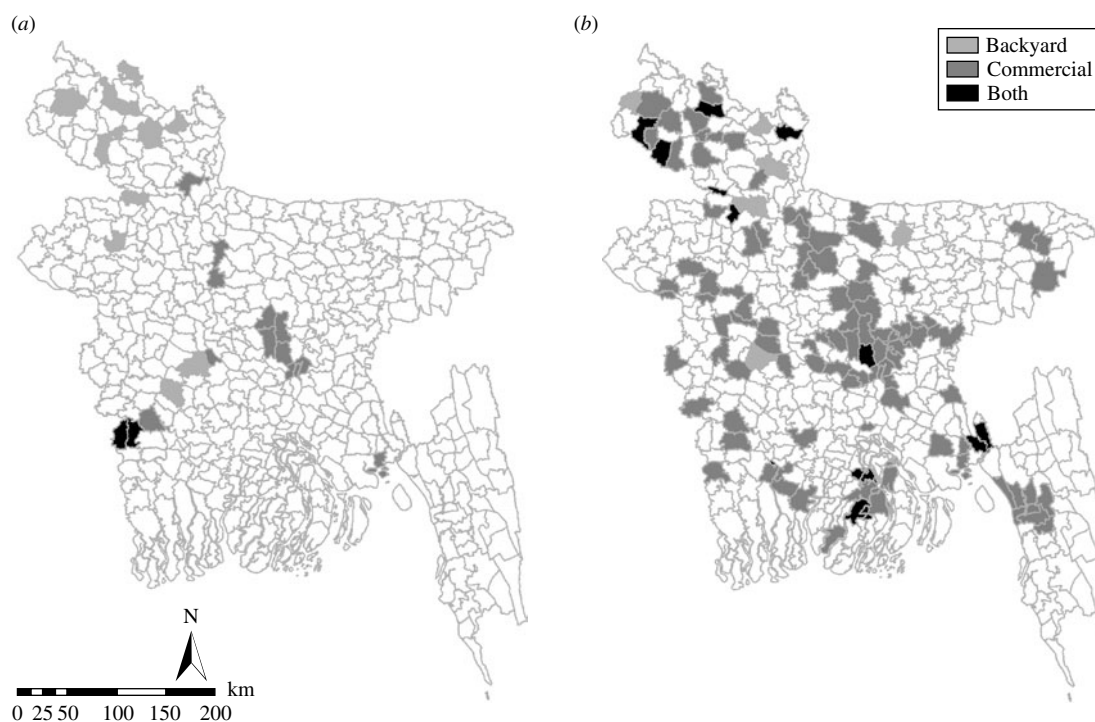


Fig. 2. Geographical distribution of HPAI-infected subdistricts in (a) first wave and (b) second wave for commercial and backyard production systems. HPAI outbreaks in Bangladesh, 2007–2008.

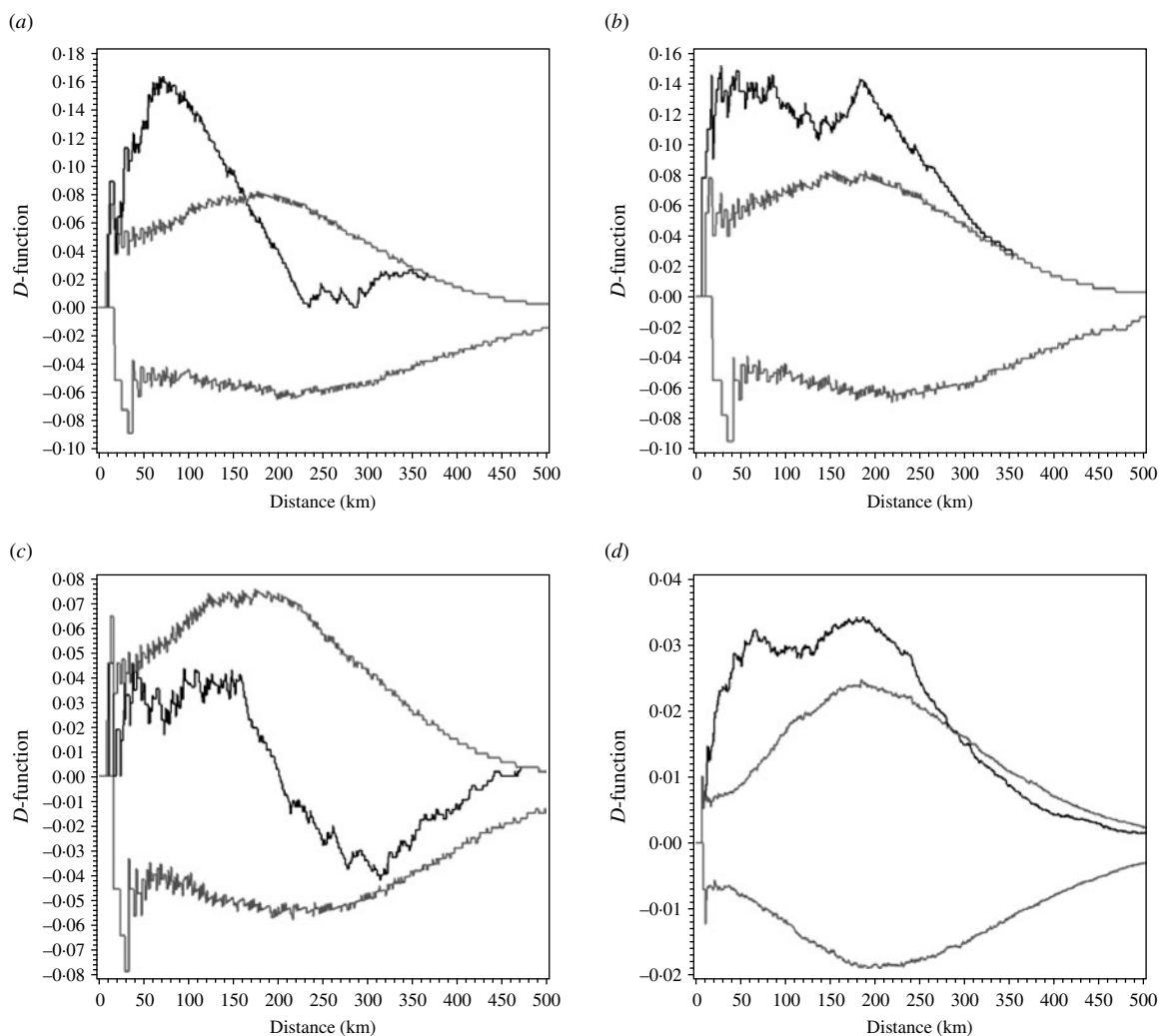
of infected subdistricts was 3.3% and 3.1% in the first wave in backyard and commercial flocks, respectively (Table 1). In the second wave, the prevalence was 3.7% and 22.7% in backyard and commercial flocks, respectively (Table 1). The spatial distribution of the infected subdistricts for the two waves is shown in Figure 2. In the first wave HPAI was identified in both backyard and commercial flocks. In the

second wave most outbreaks were seen in commercial flocks.

### Global clustering

We performed  $K$ -function analysis by wave and production type. The results of the  $K$ -function analysis are presented in Figure 3. The results indicate global





**Fig. 3.** Estimated  $D$ -function (—) with 95% simulation envelop (---) of HPAI outbreaks in Bangladesh for backyard [(a) first wave, (c) second wave] and commercial [(b) first wave, (d) second wave] production systems. HPAI outbreaks in Bangladesh, 2007–2008.

clustering of subdistricts in both waves in the commercial production system. Clustering was seen within distances of 250–300 km in the two waves. Conversely, global clustering of the outbreaks, within a distance of 150 km, was evidenced in the backyard production system only in the first wave.

#### Local clusters

Results of the space–time cluster analysis according to wave and production types are represented in Table 2. Location of the clusters with up to a maximum of 15% of the population included in the scanning window and the maximum of the temporal scanning window set to 50% of the study period, and the time precision set to 1 week is shown in Figure 4. The

primary cluster for commercial poultry was in the central part of the country in both first and second waves. The primary cluster of the backyard poultry was in the northwestern part of the country. In both production systems the location of the primary cluster remained unchanged in both waves of the epidemic. The secondary clusters varied in number and location over space and time.

#### DISCUSSION

The temporal and spatial patterns of HPAI outbreaks that occurred in backyard and commercial chicken production systems in the two epidemic waves during 2007 and 2008 in Bangladesh were described as accentuating the clustering of the outbreaks in space.

Table 2. Significant clusters of HPAI outbreaks of Bangladesh by production system and waves

Wave (type)	Pop.	Cluster	Radius (km)	Time period	O (E)	RR	LR	<i>P</i>
First wave (backyard)	15	P	67·76	9 May 2007–26 June 2007	13 (0·56)	65·00	46·45	0·001
		S	83·84	2 May 2007–10 July 2007	4 (0·17)	29·00	13·02	0·003
	25	P	99·44	9 May 2007–10 July 2007	15 (0·64)	90·60	55·12	0·001
		S	35·43	4 Apr. 2007–17 Apr. 2007	3 (0·13)	27·35	9·69	0·049
Second wave (backyard)	15	P	85·56	22 Jan. 2008–14 Apr. 2008	6 (0·27)	31·07	19·59	0·001
		S	84·88	8 Jan. 2008–4 Feb. 2008	5 (0·22)	29·19	16·18	0·001
	25	P	155·14	22 Jan. 2008–14 Apr. 2008	7 (0·31)	33·21	23·06	0·001
		S	120·27	8 Jan. 2008–4 Feb. 2008	6 (0·27)	31·07	19·59	0·001
First wave (commercial)	15	P	61·72	21 Feb. 2007–17 Apr. 2007	20 (1·40)	33·14	60·27	0·001
		S	62·00	5 Feb. 2007–10 Apr. 2007	6 (0·42)	17·07	16·46	0·001
	25	P	72·68	5 Feb. 2007–17 Apr. 2007	25 (1·76)	51·00	78·77	0·001
Second wave (commercial)	15	P	48·27	8 Jan. 2008–7 Apr. 2008	70 (25·94)	3·55	78·26	0·001
		S	102·05	8 Jan. 2008–14 Apr. 2008	36 (13·34)	3·05	37·86	0·001
		S	99·03	8 Jan. 2008–7 Apr. 2008	31 (11·49)	2·99	32·33	0·001
		S	95·13	8 Jan. 2008–24 Mar. 2008	25 (9·26)	2·93	25·81	0·001
	25	P	79·85	8 Jan. 2008–7 Apr. 2008	91 (33·72)	4·01	106·11	0·001
		S	144·89	8 Jan. 2008–14 Apr. 2008	45 (16·68)	3·16	48·06	0·001

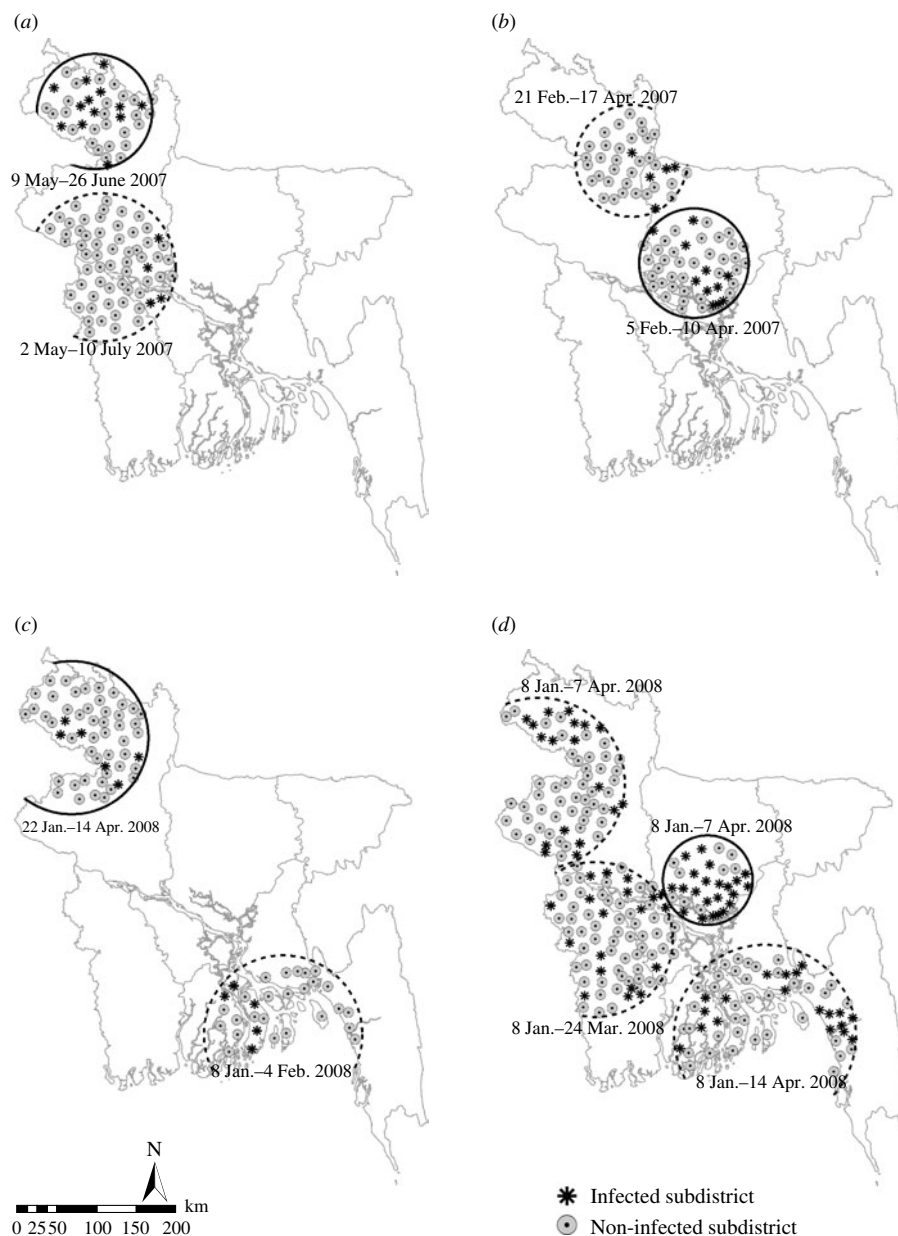
Pop., Population scanned; P, primary; S, secondary; O, observed subdistricts (infected); E, expected subdistricts (infected); RR, relative risk; LR, likelihood ratio; *P*, *P* value for likelihood ratio.

The temporal trend showed that in each of the waves an increasing number of outbreaks occurred between January and May, when the temperature in Bangladesh is low. This almost coincided with the period that was identified as the high-risk period for other southeastern Asian countries [18, 26]. This time period is preceded by the bird migratory period in early winter (November and December). It suggests a possible initial role of migratory birds for the introduction of the virus. This is substantiated by phylogenetic analysis of the H5N1 strains obtained from Bangladesh where it appears that a single introduction of the virus followed by only minor mutations might have occurred in both commercial and backyard poultry. Moreover, comparative sequence information of HPAI (H5N1) isolates from Bangladesh and other countries revealed that all the Bangladeshi isolates belong to clade 2·2 of the Qinghai lineage. Of the clade 2·2 viruses, the Bangladeshi isolates of both backyard and commercial chicken origin resemble those from Kuwait, Mongolia, Russia and Afghanistan than those of India [27]. Because the country has no poultry trade link with any of these countries it can be hypothesized that the virus might have been introduced into Bangladesh by the migratory birds before the first wave commenced. However, the role of the Indian isolates in the introduction of HPAI (H5N1) virus in Bangladesh can not

entirely be ruled out. As the lower temperatures enhance the persistence of the virus [28] it could have persisted in the environment and continued to spread following initial introduction. However, persistence of the virus in an as yet unidentified reservoir, e.g. ducks, could also be a possibility.

We performed our cluster analysis based on the waves and the production systems. Although we assumed that there was only a single introduction of H5N1 in Bangladesh, the transmission pattern is very different in the two different production systems. Previously, it has been demonstrated that the management and risk factors related the spread of HPAI in the commercial and backyard production systems are very different [5, 29]. Furthermore, the prevalence of infected subdistricts varied geographically. The subdistricts which mainly experienced infection in the commercial production system were located in the central part of the country and subdistricts primarily experiencing outbreaks in the backyard production system were located in the northwestern part of the country.

The simultaneous application of *K*-function analysis and the spatial scan statistics improved our understanding of the geographical location of HPAI occurrence in Bangladesh. Our study revealed the presence of significant clusters during two different waves. The most likely clusters (primary) formed in



**Fig. 4.** Location of the primary (—) and secondary clusters (- - -) of HPAI outbreaks in Bangladesh by backyard [(a) first wave, (c) second wave] and commercial [(b) first wave, (d) second wave] production systems.

subdistricts by different production systems were independent and showed good agreement over space. This indicates the source of introduction and local spreads. Human activities and risky behaviour of the farmers could have played important roles in the local spreading mechanism [4, 30]. We used exploratory maps to visualize the relationship between human and poultry density and the HPAI-infected subdistricts. As in previous investigations in Thailand [17] and Vietnam [19] we found that the outbreaks clustered in the high-density areas for both poultry and humans.

The formation of secondary clusters is indicative of the long distances that the virus may be spread. We believe, as in Vietnam, within-country infection transmission in Bangladesh was driven by movement of poultry and poultry products rather than multiple introductions or spread by wild birds [19].

In the current surveillance system detection of HPAI firmly depends on the clinical signs of the disease, including high mortality in the flock. Due to the high mortality rate of HPAI and the government's compensation plan, the risk of underreporting of



clinical cases is considered to be negligible, but can not entirely be ruled out particularly for backyard flocks where flock sizes are very small and such flocks might have been wiped out before clinical signs became noticeable. Moreover, asymptomatic cases might have gone undiagnosed. In addition, ducks have been demonstrated to be able to act as a 'silent reservoir' of infection as they may be infected without showing clinical signs. This could complicate the epidemiology further. Because of the underreporting of cases in backyard chickens, asymptomatic cases and silent reservoirs the apparent number of the positive subdistricts could be lower than the true number, which also increases the chance of a higher number of subdistrict cases in the cluster analysis. Such misclassification could bias the results to an underestimation of the subdistrict level prevalence and the extension of the clusters (number or size of the clusters or both).

Simultaneous application of temporal, spatial and spatio-temporal approaches to HPAI outbreaks revealed additional information which otherwise would not be available from the traditional epidemic curve to identify the mode of spread. This approach ensured information simultaneously regarding time and space which is essential for the planning of appropriate control and targeted surveillance. Application of the relevant approaches explored useful information for the HPAI outbreaks of Thailand, Italy and Vietnam [17–20]. Further investigations of the direction of spread, e.g. Romanian outbreaks [31] and ecological niches of HPAI will provide additional information for future surveillance and control programmes.

## DECLARATION OF INTEREST

None.

## REFERENCES

1. **World Organization for Animal Health (OIE)**. Update on highly pathogenic avian influenza in animals ([http://www.oie.int/downld/avian%20influenza/A\\_AI-Asia.htm](http://www.oie.int/downld/avian%20influenza/A_AI-Asia.htm)), Paris, 2009. Accessed 15 July 2009.
2. **Alexander DJ**. Summary of avian influenza activity in Europe, Asia, Africa, and Australasia, 2002–2006. *Avian Diseases* 2007; **51** (1 Suppl): 161–166.
3. **World Health Organization (WHO)**. Cumulative number of confirmed human cases of avian influenza A/(H5N1) reported to WHO, 31 August 2009. ([http://www.who.int/csr/disease/avian\\_influenza/country/cases\\_table\\_2009\\_08\\_31/en/index.html](http://www.who.int/csr/disease/avian_influenza/country/cases_table_2009_08_31/en/index.html)), Geneva, 2009. Accessed 24 September 2009.
4. **Biswas PK, et al.** Avian influenza outbreaks in chickens, Bangladesh. *Emerging Infectious Diseases* 2008; **14**: 1909–1912.
5. **Biswas PK, et al.** Risk factors for infection with highly pathogenic influenza A virus (H5N1) in commercial chickens in Bangladesh. *Veterinary Record* 2009; **164**: 743–746.
6. **Ministry of Fisheries and Livestock (MOFL)**. Government of the People's Republic of Bangladesh, daily bird flu situation (<http://www.mofl.gov.bd/>), Dhaka, 2009. Accessed 24 September 2009.
7. **World Health Organization (WHO)**. Cumulative number of confirmed human cases of avian influenza A/(H5N1) reported to WHO, 28 May 2008 ([http://www.who.int/csr/disease/avian\\_influenza/country/cases\\_table\\_2008\\_05\\_28/en/index.html](http://www.who.int/csr/disease/avian_influenza/country/cases_table_2008_05_28/en/index.html)), Geneva, 2008. Accessed 24 September 2009.
8. **ICDDR, B**. First confirmed human infection with avian influenza A (H5N1) virus in Bangladesh. *Health and Science Bulletin* 2008; **6**: 2–6.
9. **Food and Agriculture Organization (FAO)**. Animal health. In: *A Global Strategy for Prevention and Control of Highly Pathogenic Avian Influenza* ([http://www.fao.org/ag/againfo/resources/en/pubs\\_ah.html](http://www.fao.org/ag/againfo/resources/en/pubs_ah.html)), p. 13. Rome, 2007. Accessed 24 September 2009.
10. **Dolberg F**. Poultry sector country review: Bangladesh, pp. 19–20. Food and Agricultural Organization of the United Nations (FAO) (<ftp://ftp.fao.org/docrep/fao/011/ai319e/ai319e00.pdf>). Rome, 2009. Accessed 24 September 2009.
11. **Department of Livestock Services (DLS), Ministry of Fisheries and Livestock (MOFL)**. Government of the People's Republic of Bangladesh, Organogram. (<http://www.dls.gov.bd/organogram.htm>), Dhaka, 2009. Accessed 24 September 2009.
12. **Berrang-Ford L, et al.** Spatial analysis of sleeping sickness, southeastern Uganda, 1970–2003. *Emerging Infectious Diseases* 2006; **12**: 813–820.
13. **Lai PC, et al.** Understanding the spatial clustering of severe acute respiratory syndrome (SARS) in Hong Kong. *Environmental Health Perspectives* 2004; **112**: 1550–1556.
14. **Ruiz MO, et al.** Environmental and social determinants of human risk during a West Nile virus outbreak in the greater Chicago area, 2002. *International Journal of Health Geographics* 2004; **3**: 8.
15. **Stevenson MA, et al.** Descriptive spatial analysis of the epidemic of bovine spongiform encephalopathy in Great Britain to June 1997. *Veterinary Record* 2000; **147**: 379–384.
16. **Fosgate GT, et al.** Time-space clustering of human brucellosis, California, 1973–1992. *Emerging Infectious Diseases* 2002; **8**: 672–678.
17. **Tienson T, et al.** Ecologic risk factor investigation of clusters of avian influenza A (H5N1) virus infection in Thailand. *Journal of Infectious Diseases* 2009; **199**: 1735–1743.

18. **Pfeiffer DU, et al.** An analysis of the spatial and temporal patterns of highly pathogenic avian influenza occurrence in Vietnam using national surveillance data. *Veterinary Journal* 2007; **174**: 302–309.
19. **Minh PQ, et al.** Spatio-temporal epidemiology of highly pathogenic avian influenza outbreaks in the two deltas of Vietnam during 2003–2007. *Preventive Veterinary Medicine* 2009; **89**: 16–24.
20. **Mulatti P, et al.** Spatial analysis of the 1999–2000 highly pathogenic avian influenza (H7N1) epidemic in northern Italy. *Avian Diseases* 2007; **51** (1 Suppl.): 421–424.
21. **Lee MS, et al.** Identification and subtyping of avian influenza viruses by reverse transcription-PCR. *Journal of Virological Methods* 2001; **97**: 13–22.
22. **Bangladesh Bureau of Statistics (BBS).** *Statistical Pocket Book of Bangladesh: 2008*. (<http://www.bbs.gov.bd/>), Dhaka, 2008. Accessed 24 September 2009.
23. **Ersbøll AK, Ersbøll BK.** Simulation of the K-function in the analysis of spatial clustering for non-randomly distributed locations – exemplified by bovine virus diarrhoea virus (BVDV) infection in Denmark. *Preventive Veterinary Medicine* 2009; **91**: 64–71.
24. **Kulldorff M, Nagarwalla N.** Spatial disease clusters: detection and inference. *Statistics in Medicine* 1995; **14**: 799–810.
25. **Kulldorff M.** A spatial scan statistics. *Communication in Statistics – Theory and Method* 1997; **26**: 1481–1496.
26. **Park AW, Glass K.** Dynamic patterns of avian and human influenza in east and southeast Asia. *Lancet Infectious Diseases* 2007; **7**: 543–548.
27. **Islam MR, et al.** Phylogenetic analysis of highly pathogenic avian influenza (H5N1) virus isolates of first two waves in Bangladesh. *Bangladesh Journal of Livestock Research* 2008; **15**: 1–6.
28. **Shortridge KF, et al.** Characterization of avian H5N1 influenza viruses from poultry in Hong Kong. *Virology* 1998; **252**: 331–342.
29. **Biswas PK, et al.** Risk for infection with highly pathogenic influenza A virus (H5N1) in backyard chickens in Bangladesh. *Emerging Infectious Diseases* 2009; **15**: 1931–1936.
30. **Capua I.** Avian influenza: We have the chance to make a difference. *Veterinary Journal* 2007; **174**: 213–214.
31. **Ward MP, et al.** Geostatistical visualisation and spatial statistics for evaluation of the dispersion of epidemic highly pathogenic avian influenza subtype H5N1. *Veterinary Research* 2008; **39**: 22.