

Spatio-temporal analysis of HPAI(H5N1) in Bangladesh



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Background and objective:

Bangladesh faced the first outbreak of (HPAI) H5N1 in February 2007 and the outbreaks are still ongoing. Understanding of clustering and spreading mechanism of HPAI outbreaks in Bangladesh might be the basis to identify areas where more investigations can be initiated to explore entrenching and putative spreading sources of the virus. The objective of the present study was to identify space-time clusters of the HPAI outbreaks at subdistrict level in Bangladesh to support existing surveillance and to suggest empirical strategies for HPAI control.

Materials and methods :

For the purpose of our study, a subdistrict was considered infected if it had at least one officially confirmed [1] outbreak within period of interest. The rest of the subdistricts were considered as non-infected. The centroids of the subdistricts were considered as the coordinates of respective subdistricts.

Temporal distribution: We constructed the epidemic curve for affected subdistricts in relation to the production system by plotting the number of infected subdistricts identified per day as a function of time. We applied a temporal moving average of the affected subdistricts to get the stationary time series.

Spatial 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 and Ersbøll [2]. The method overcomes the assumption of CSR, limits edge effects and exclude the size of the study area which cause estimation problems due to mountains, lakes and irregular coastal lines.

Space-time clustering: We employed the scan statistics [3] to detect significant clusters of HPAI at subdistrict level with a Bernoulli model with inclusion of 15% of the population using the daily infection status in subdistricts over the study period. The scan statistics was carried out by SaTScan (Ver 8.0, Martin Kulldorff and Information Management Services, <http://www.satscan.org>).

Results and Discussion:

Temporal trends showed that in each of the waves an increasing number of outbreaks occurred between January and May (Figure 1) when the temperature is low in Bangladesh. This time period is preceded by the migration period of the migratory birds in the early winter (November and December). It suggests a possible initial role of migratory bird for the introduction of the virus. Global clustering assessed by the *K*-function was seen at distances 150-300km between subdistricts (Figure 2). Significant local clusters were detected by the 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 among backyard production systems. Secondary clusters varied from the north western part in 2007 and the southern part in 2008 (Figure 3). The most likely clusters (primary) formed in subdistricts by different production type systems were independent and showed good agreement over the space. This indicates the source of introduction and local spreads. The formation of the secondary clusters is indicative for the long distance spread. We believe, like in Vietnam, within-country infection transmission in Bangladesh was driven by movement of the poultry and poultry products rather than the multiple introductions or spread by wild birds.

The findings are highly relevant for the successful planning and implementation of control, prevention and surveillance strategies by highlighting the areas where detailed investigations should be initiated.

References:

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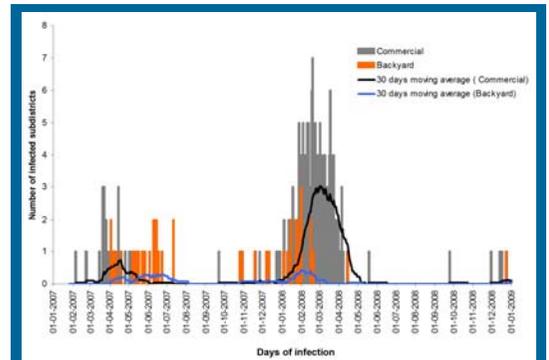


Figure 1. Epidemic curve of infected subdistricts of HPAI outbreaks in Bangladesh (2007- 2008) for commercial and backyard flocks.

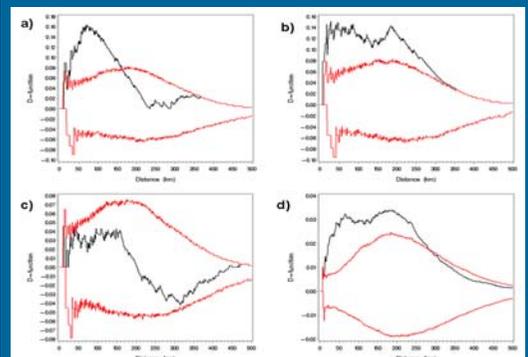


Figure 2. Estimated D-function (—) with 95% simulation envelop (---) of HPAI outbreaks in Bangladesh for backyard (a, first and c, second wave) and commercial (b, first and d, second wave) production systems. HPAI outbreaks in Bangladesh, 2007-2008.

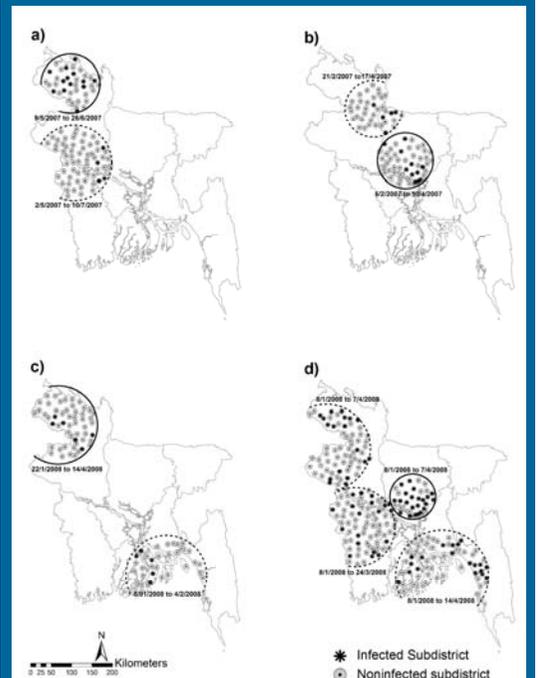


Figure 3. Location of the primary (—) and secondary clusters (---) of HPAI outbreaks in Bangladesh by backyard (a, first and c, second wave) and commercial (b, first and d, second wave) production systems.