HUMAN AVIAN INFLUENZA IN INDONESIA: ARE THEY REALLY CLUSTERED?

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Abstract. Understanding the epidemiology of human H5N1 cases in Indonesia is important. The question of whether cases are clustered or not is unclear. An increase in clustered cases suggests greater transmissibility. In the present study, 107 confirmed and 302 suspected human H5N1 cases in Indonesia during 2005-2007 were analyzed for spatial and temporal distribution. Most confirmed cases (97.2%) occurred on two main islands (Java and Sumatera). There were no patterns of disease occurrence over time. There were also no correlations between occurrence patterns in humans and poultry. Statistical analysis showed confirmed cases were clustered within an area on Java island covered by 8 districts along the border of three neighboring provinces (Jakarta, West Java, and Banten). This study shows human H5N1 cases in Indonesia were clustered at two sites where there was a high rate of infection among poultry. These findings are important since they highlight areas of high risk for possible human H5N1 infection in Indonesia, thus, preventive measures may be taken.

Keywords: human H5N1, cluster H5N1, spatial analysis, temporal analysis

INTRODUCTION

The influenza A virus subtype H5N1, commonly known as "bird flu" or avian influenza (AI) has never been proven to be transmissible from human to human, however there are concerns the virus could mutate leading to a global pandemic. Indonesia has the largest number of human cases of H5N1. This could cause the country to become an epicenter of an H5N1 pandemic. Identification of the actual distribution of human H5N1 cases in Indonesia is critically important, since an increase in clustered cases could suggest greater transmissibility of the virus (The Writing Committee of WHO Consultation on Human Influenza, 2005; Wong and Yuen, 2006; Kandun *et al*, 2008).

Opinions vary on whether human H5N1 virus infections in Indonesia have a cluster pattern. All human H5N1 cases have been among blood relatives, suggesting a possible genetic predisposition toward susceptibility to H5N1 virus infection. A cluster of 8 cases, of whom 7 were

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fatal, occurred in Karo, North Sumatera. Mathematical modelling (Yang *et al*, 2007) showed significant clustering. Whether the virus is capable of sustaining human to human transmission is still unproven, thus H5N1 clustering among humans in Indonesia remains controversial.

This study attempts to identify geographical clusters and describe the temporal distribution of human H5N1 infections in Indonesia.

MATERIALS AND METHODS

Ethic statement

Ethical clearance to conduct this study statement was given by the Indonesian Health Ethics Committee. No informed consent was obtained from participants since the data were obtained retrospectively from health offices and analyzed anonymously.

Study design

This was a retrospective study describing the spatial and temporal distribution of poultry and human H5N1 virus infections in Indonesia during 2005-2007. This study employed secondary data gathered from provincial health offices, district health offices, and public health centers in provinces in which human H5N1 infections occur. Other sources were the Indonesian Ministry of Health, Ministry of Agriculture, National Institute of Health Research and Development, Central Management Unit of Avian Influenza and the World Health Organization.

Study population and size

A total of 107 confirmed H5N1 infections identified from June 2005 to December 2007 and an additional 302 suspected cases of H5N1 infection from 12 provinces in Indonesia were selected as the study population. These cases resided in 38 districts of 12 provinces on Sumatra, Java, Bali and Sulawesi islands. Suspected cases only included those from four provinces of the upper (Banten and DKI Jakarta) and lower (East Java and South Sumatera) quartiles based on human H5N1 prevalence. The addition of suspected cases was necessary to increase the number of point locations for spatial autocorrelation.

Method of data collection

All confirmed and suspected cases (total of 409 cases) in Indonesia (Fig 3) were used to assess for possible geographical clustering. The coordinates of the residences of each case were taken using a global positioning device (GarminMap CX7, Germany). Demographic factors, such as age, sex and date of onset for each case, were also recorded.

Data processing and analysis

Analysis consisted of descriptive statistics and evaluation of the extent of the observed pattern of human H5N1 cases. The coordinates were entered and considered both as points and areas of settlement depending on the type of analysis. Arc View version 3.3 and Geoda 095i were used to perform the analyses. Analysis started by describing the spatial means or average locations of the cases. Another descriptive analysis for point location was spatial standard distance. The 409 cases were divided into three groups by year of incidence, 2005, 2006 and 2007, to assess movement of the spatial standard distance throughout the study period, thus revealing movement of infection over time.

To identify clusters of human H5N1 infection, quadrant analysis was performed in order to evaluate changes in point density over space. Square quadrats were chosen as the sampling units and the size of quadrats was chosen following the

formula of Griffith and Amrhein (1991). The Kolomogorov-Smirnov (K-S) test was then carried out to test differences in patterns of observed cases and the theoretical frequency of distribution.

The second method of analysis used was the Nearest Neighbor Analysis, which applied the concept of area per point (or spacing), to compared the observed average distance between neighboring points to that of a random pattern. The randomness of points could then be expressed $R = \frac{r^{obs}}{r^{exp}}$; where r^{obs} and r^{exp} represent the observed and expected correlations between two points, respectively (Clark and Evans, 1954).

The next step on the analysis was to test for spatial autocorrelation using Geoda to analyze the interdependence between values of a variable at different geographic locations and the degree of spatial clustering for all cases. Significant positive spatial autocorrelations indicate points with similar characteristics tend to be near each other, or clustered.

To identify clustering, Moran I was applied using the random permutation procedure of Monte Carlo, with statistical significance set at $p=0.010$.

The probability of local clustering, which considered the variability of spatial autocorrelation over the study regions, was calculated using LISA (Local Inference Spatial Autocorrelation). This measurement can identified spatial autocorrelation on a local scale. There are four possibilities for local autocorrelation: high-high area (an area and its neighbors had high numbers of events); low-low area (an area and its neighbors had low numbers of events); high-low area (an area with high numbers of events surrounded by areas with low numbers of events) and low-high (an area with low number of events surounded by areas with high numbers of events).

RESULTS

Spatial and temporal analysis of H5N1 infection among poultry

Secondary data gathered from the central management unit for the Avian Influenza (CMUAI) Department of Agriculture, showed the Indonesian H5N1 outbreak among poultry in Indonesia started in August 2003. The first cases occurred in two provinces on the island of Java: Banten and Central Java. In the following month, Lampung, the southernmost province on Sumatra Island, was affected. Outbreaks among poultry continued to proliferate toward the northwest then to the east. The most distant provinces were affected later in time.

By December 2003, 12 provinces had been affected by the disease. The number of affected provinces continuously increase during 2004, 2005, 2006 and 2007 with 18, 19, 24 and 27 provinces being affected, respectively. By December 2007 poultry from 32 out of 33 provinces had been affected by the virus at least once. In total, 197 districts and municipalities were affected. The only province not affected was North Maluku. Java and Sumatra were the two most affected islands from the H5N1 outbreak among poultry. All provinces on those islands were affected with varying prevalences, although not all districts were hit. The only two provinces which were not affected by the disease by the end of December 2007 were North Maluku, and Gorontalo (Fig 1).

The H5N1 trend among poultry from 2005 to 2007 had no significant increase or decrease in number of cases. However, human H5N1 cases had several peaks with the highest being in mid 2006 (Fig 2).
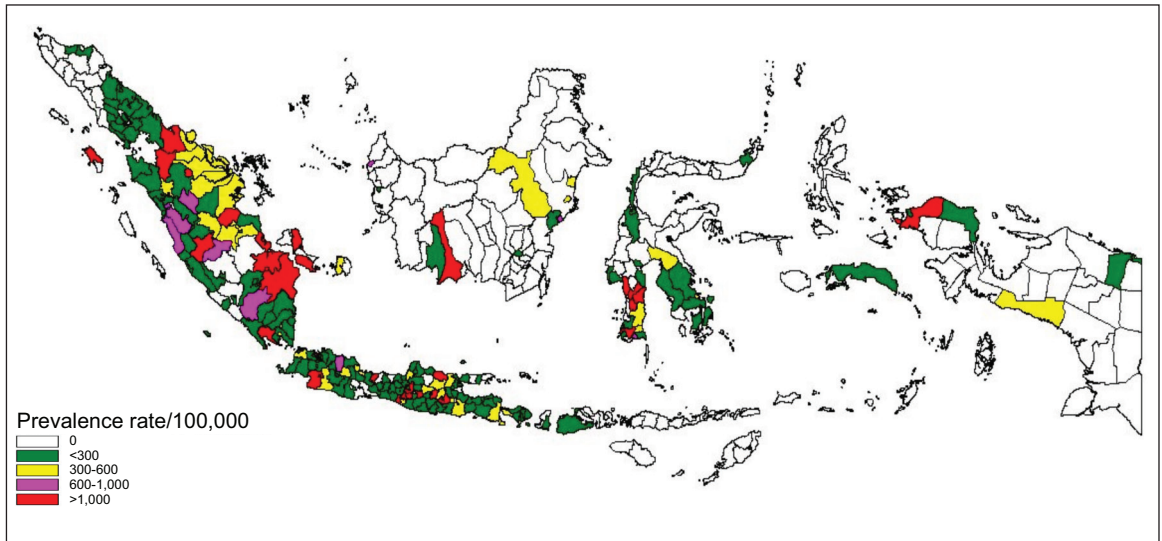
Fig 1–Prevalence rates of H5N1 infection among poultry in Indonesia during 2005-2007.
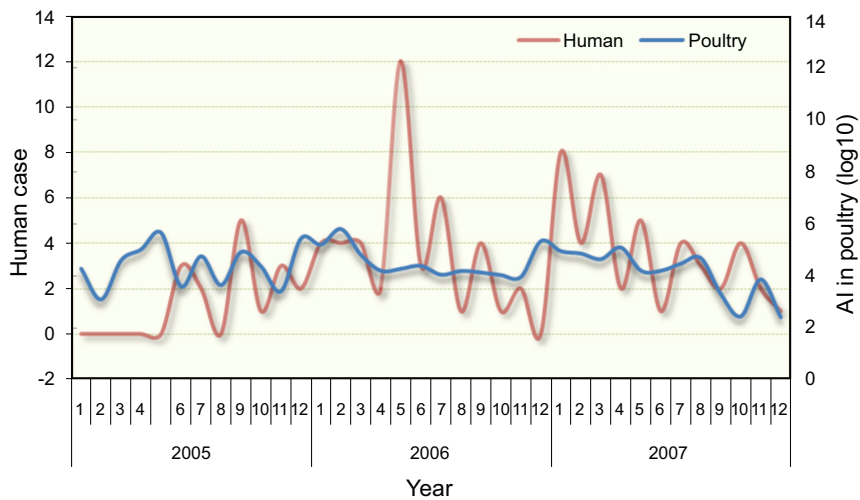

Fig 2–Trend of avian influenza infections among humans and poultry in Indonesia during 2005-2007. The number of infected poultry are presented as log10 of the actual value.

A similar study was carried out during the same time period from September 2005 to May 2007, with an average of 5 cases occurring each month and from June to December 2007 with an average of 3 cases occuring each month, despite the control measures put in place (Sedyaningsih *et al*, 2008).

Table 1
Distribution of human H5N1 cases in Indonesia by province, during
June 2005-December 2007.

Province	Island	Human population density/km^2	Confirmed No. (%)	Suspected No. (%)
DKI Jakarta	Java	13,400	27 (25.2)	153 (50.7)
Banten	Java	1,016	22 (20.6)	51 (16.9)
West Java	Java	1,033	18 (16.8)	0
Central Java	Java	951	9 (8.4)	0
North Sumatra	Sumatra	158	8 (7.5)	0
East Java	Java	726	7 (6.5)	87 (28.8)
Riau	Sumatra	52	7 (6.5)	0
West Sumatra	Sumatra	100	3 (2.8)	0
Lampung	Sumatra	197	2 (1.9)	0
Bali	Bali	599	2 (1.9)	0
South Sumatra	Sumatra	59	1 (0.9)	11 (3.6)
South Sulawesi	Sulawesi	133	1 (0.9)	0
Total			107 (26.2)	302 (73.8)

Distribution of human cases

The majority of H5N1 cases in Indonesia occured in Jakarta Province (25.2%) followed by two neighboring provinces Banten (20.6%) and West Java (16.8%). Ninety-seven point two percent of confirmed cases (n=104) were found on the two main islands of Java (77.5%) and Sumatera (19.7%) (Table 1). Only 2.8% of confirmed cases (n=3) were documented from two other islands: Bali (n=2) and Sulawesi (n=1).

The number of human H5N1 cases correlate positively (p=0.01) with population density (Table 1). The higher the population, the greater the number of cases of human H5N1. Jakarta Province, with a population density of 13,400 persons/km^2 had the largest number of confirmed cases (27).

Of the total 409 confirmed (n=107) and suspected (n=302) cases, the median age was 16 years old (range 0-80; SD=17) (Table 2). The age group with the largest percentage of cases was the 11-20 year old age group (27.1%) and followed by 21-30 year old (25.2%) and <10 years old (22.4%) age groups. Suspected cases were most commonly found among children <10 years old (43.3%); this number decreased with increasing age. The differences by age group were significant (p<0.001).

In both confirmed and suspected cases, the number of males was nearly three times higher than females; however this difference was not significant (p=0.499).

When spatial and temporal data for human and poultry H5N1 cases were overlapped, there were no similarities in patterns for either confirmed or suspected cases (Fig 2).

Spatial and temporal analysis of H5N1 infections in humans

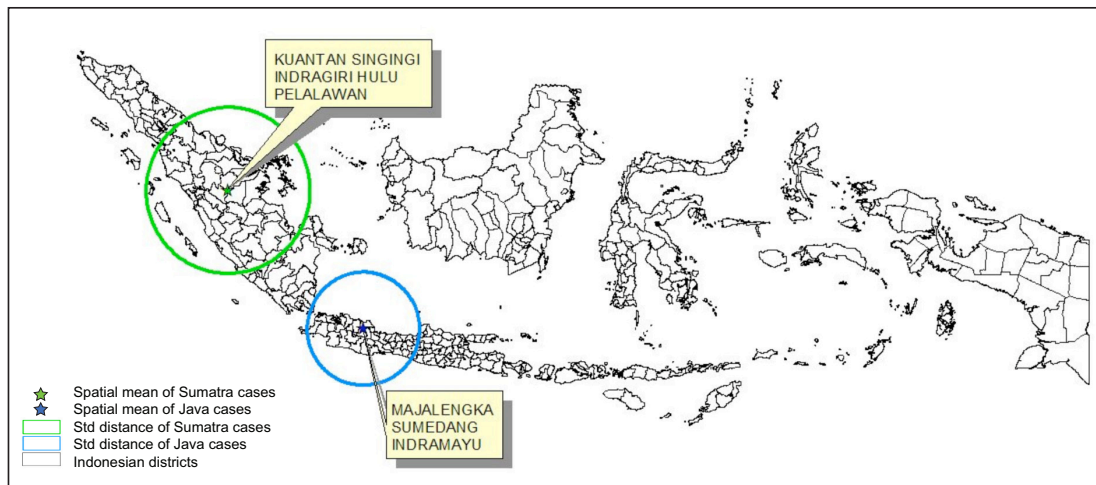During June 2005 - December 2007 107 confirmed human H5N1 cases were

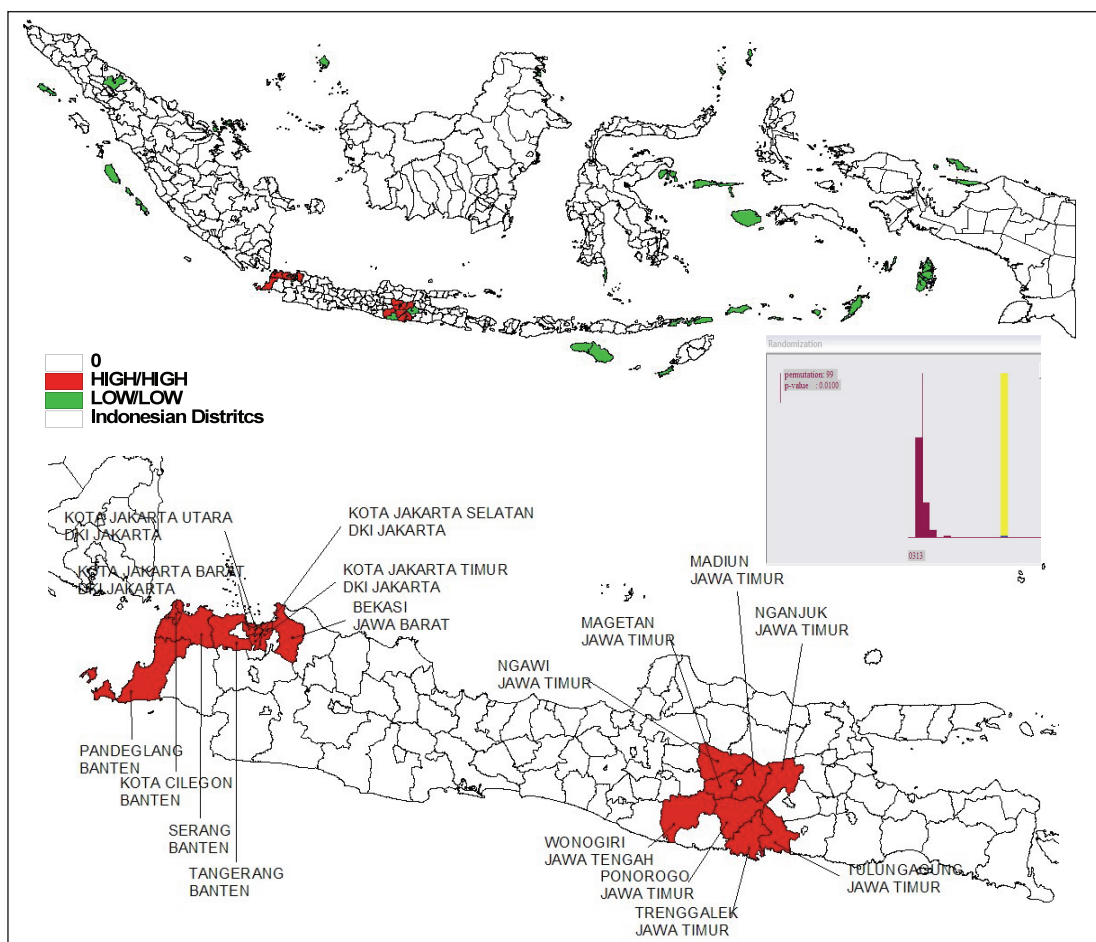Fig 3–Location of spatial means of confirmed and suspected human H5N1 cases for Java and Sumatra cases.

Fig 4–Significant clusters of human H5N1 infection (confirmed and suspected; n=409) in Indonesia.

Table 2
Distribution of human H5N1 cases by age group and sex (n=409) during
June 2005-December 2007.

Characteristics	Confirmed (n=107)	Suspected (n=302)	p-value
Age (years)			
≤ 10	24 (22.4)	131 (43.3)	<0.001
11-20	29 (27.1)	53 (17.5)	
21-30	27 (25.2)	42 (13.9)	
31-40	19 (17.8)	35 (11.7)	
41-50	8 (7.5)	14 (4.7)	
≥ 51	0	27 (8.9)	
Sex			
Male	142 (74.1)	160 (73.6)	0.499
Female	55 (25.9)	52 (26.4)	

Values in the parenthesis is percent

reported from 12 provinces. The first human H5N1 case was reported in Banten in mid 2005 followed by cases in DKI Jakarta and Lampung. A total of 16 human H5N1 infections occurred within these three provinces during the last two quarters of 2005. Until May 2006, cases were confined to DKI Jakarta, Banten and West Java, then later during the same month, cases occured in a family cluster in North Sumatra. In 2006, there were a total of 47 human H5N1 cases reported. In 2007, 44 human H5N1 cases were reported.

Geographically the spatial means and the spatial standard distances moved westward. The spatial standard distances of human H5N1 infections increased from 2005 to 2006 and decreased from 2006 to 2007 (Table 3). Spatial means for confirmed and suspected human H5N1 cases during 2005-2007 were localized to Karawang District, Banten Province.

A separate analysis of the cases in Sumatra and Java (Fig 3) showed the means of the cases in Sumatra occurred along the border of three districts: Pelalawan, Indragiri Hulu and Kuantan Singgingi of Riau Province. For all the cases in Java, the means were located in the districts Majalengka, Indramayu and Sumedang of West Java Province.

Point pattern analysis

Quadrat analysis. Quadrat analysis showed human H5N1 infections in Indonesia during June 2005-December 2007 were significantly clustered (Table 4) both for pooled data or separated data for Java and Sumatra.

Nearest Neighbor statistic

The results of the Nearest Neighbor statistic showed similar outcomes, in which all suspected and confirmed human H5N1 cases were found to be significantly clustered (R statistic close to 0). Similar results were found when the data were analyzed separately in Sumatra and Java (Table 5).

Moran I and local autocorrelation

Quadrat and Nearest Neighbor analyses treat all points in the distribution as

Table 3

Spatial means and standard distance of human H5N1 infections during 2005-2007.

Year	Spatial means	Standard distances	Diameters in km
2005	(106.487, -6.095)	0.6279	136.86
2006	(106.034, -4.746)	5.4889	1,099.44
2007	(106.611, -4.847)	4.9280	1,227.17

Table 4

Result of Quadrat analysis for all cases (n=409), Java and Sumatra cases.

Location of cases	K-S statistic (D)	Critical value
Jawa cases only	0.902	0.328*
Sumatra cases only	0.844	0.521*
All 409 cases	0.924	0.294*

*Statistically significant with p<0.05.

if they are the same, meaning the points are not distinguishable except for their locations. To include analysis of the attributes of each point, knowing different geographic locations rarely have identical characteristics, spatial autocorrelation was performed. The results of global and local autocorrelation are listed below.

A significant Moran I statistic test for confirmed and suspected human H5N1 cases (p=0.010) meant nearby districts tended to have similar H5N1 infection prevalence levels. Fig 4 shows that the first local human H5N1infection cluster consisted of 10 districts within three provinces: Jakarta, Banten, and West Java. Five districts, Jakarta Utara, Jakarta Selatan, Jakarta Barat, Jakarta Timur, and Jakarta Pusat, were within DKI Jakarta Province. Bekasi District was in West Java Province, and 4 districts, Pandeglang, Kota Cilegon, Serang and Tangerang were in Banten Province.

The second human H5N1 cluster was located along the border of Central and East Java. There was only one district (Wonogiri) in Central Java Province and seven districts (Ponorogo, Trenggalek, Tulungagung, Ngawi, Magetan, Madiun and Nganjuk) in East Java Province affected.

To narrow down the cluster analysis, Moran I and local autocorrelation analyses were carried out separately among the 107 confirmed cases. The result shows (Fig 5) there was only one cluster area instead of two, as it appreared with suspected cases were included. The cluster covered a total of 8 districts: 5 districts (Jakarta Utara, Jakarta Selatan, Jakarta Barat, Jakarta Timur, and Jakarta Pusat) in Jakarta Province, 2 districts (Bogor and Bekasi) in West Java Province, and 1 district (Tangerang) in Banten Province.

Our findings show human H5N1 infections in Indonesia were geographically clustered in two areas: Banten Province
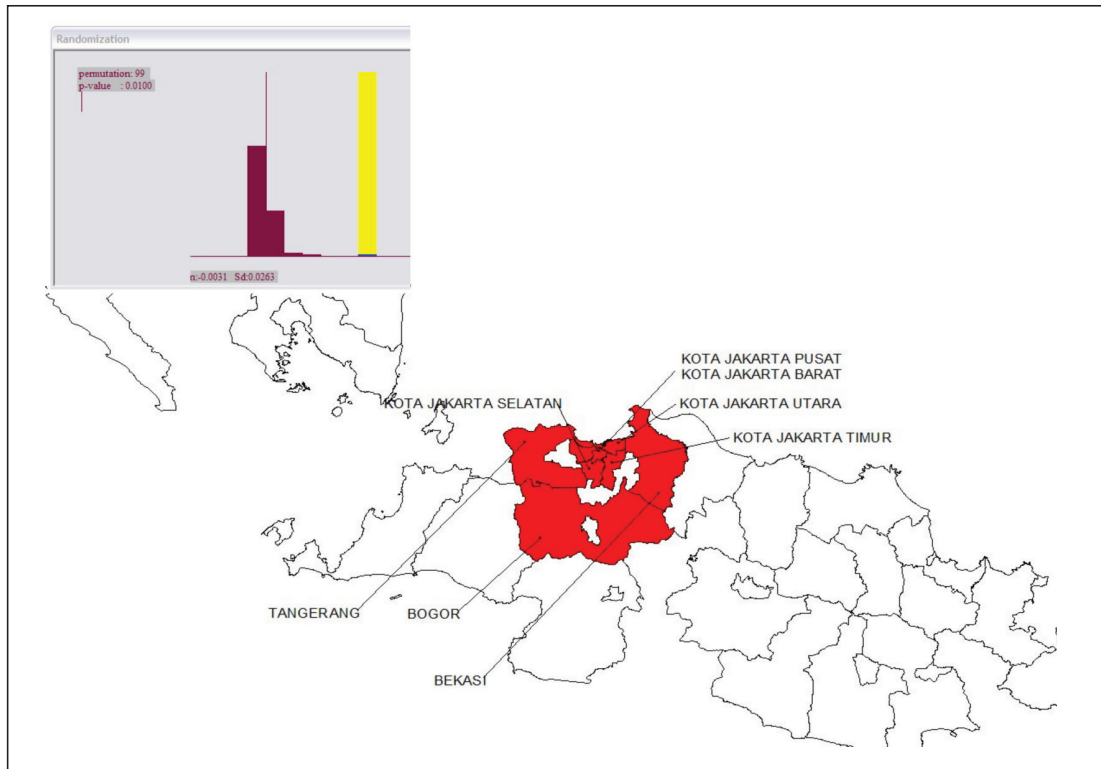
Fig 5–Significant clusters of only confirmed human H5N1 cases (*n*=107) in Indonesia during 2005-2007.

and along the border of Central and East Java Provinces. These areas have a high human population density and a high poultry population density. During the three year study period, outbreaks of H5N1 infection among poultry were also found in these areas, although data were only available from sector 3 (small scale chicken farms) and sector 4 (backyard farming). Large scale commercial farms (sectors 1 and 2) were also found to have high numbers of attacks during the outbreak, yet data regarding poultry infections within these two sectors is not made available even to the Indonesian Livestock Service department. There were no clear patterns of human H5N1 cases among humans or poultry during 2005-2007. In other words, the infection can occur regardless of season.

Spatial analysis of the data regarding human H5N1 infections in Indonesia should results in further research concentrating on a comprehensive explanation for the outbreaks, which is beyond the scope of this study. The large number of poultry H5N1 infections in provinces with large numbers of commercial poultry farms (sectors 1 and 2) indicates the H5N1 virus may have penetrated these 2 sectors (commercial circuit) causing outbreaks in sectors 3 and 4. Limited data from sectors 1 and 2 should cause the Indonesian Department of Livestock to impose a stricter regulations and enforcement of these regulations in these two sectors, in order

Table 5
Results of Nearest Neighbor snalysis for all cases (*n*=409), Java and Sumatra cases.

Location	Observed neighbor distance	Expected neighbor distance	R statistic with Donnely correction
Java cases only	2.005	8.885	0.219*
Sumatra cases only	13.961	46.923	0.275*
All cases	2.954	24.579	0.118*

*Statistically significant with $p<0.05$.

to allow livestock officials to obtain access to these results of evaluating animal health and monitoring.

DISCUSSION

We determine the space-time patterns of human H5N1 infection in Indonesia using Quadrat analysis, Nearest Neighbor analysis and a test for spatial autocorrelation. Up to present, clustering of human cases in Indonesia is defined as two or more cases in a blood relative. There have been no studies of geographical clustering of cases. This study of all human H5N1 infections in Indonesia during June 2005-December 2007 found about one-fourth of cases occurred within ten family clusters of blood relatives (Sedyaningsih *et al*, 2007; Kandun *et al*, 2008).

The epidemiology of human H5N1 infections, in terms of age and sex distribution found in the present study is similar to that reported by neighboring countries (Mounts *et al*, 1999; Dinh *et al*, 2006). In our study the median age of cases was 16 years and most cases were <20 years old (Table 2). Other studies (The Writting Committee of the WHO on Human Influenza, 2005; Peiris *et al*, 2007) have reported median ages ranging from 16 to 18 years old and that younger age groups were more sensitive to the disease than adults and the elderly. The higher incidence in children may suggest an age dependent host susceptibility toward H5N1 infection. A wide range of ages with H5N1 infection (two months to 80 years old) was found in our study. These results agree with a study by Goicoechea *et al* (2007) who reported the age distribution may be due to variations in risk behavior or age related host resistance.

One risk behavior commonly found in Asian countries, particularly Indonesia, is backyard farming, whether as a hobby or for small income generation for the family (Government of Indonesia, 2004; Perez-Brena and Casas, 2004; Dinh *et al*, 2006; Kung *et al*, 2007; Sedyaningsih *et al*, 2007). Certain birds, such as the Arabian chicken, fighting cock, Guinea fowl and singing birds are often raised as pets. This is found not only in rural, but in urban areas as well, such as DKI Jakarta.

The high incidence of human H5N1 infections in children may be due to greater exposure to poultry around the house compared to adults. Small children spend most of their time at home, playing with the birds. Those who practice backyard farming often do not follow basic hygiene measures. In many households the different species are mixed with wild birds.

Another explanation for human H5N1 infections is the presence of a receptor recognized by the H5N1 virus (2,3-linked sialic acid) that is expressed in the lower respiratory tract. In children this receptor may be expressed in the upper airways, increasing the chance of infection. 2,3-linked sialic acids are homogeneously distributed in human fetal lung and the expression of these receptors appears to decreased with age (Witayathawornwong, 2006; Wong and Yuen, 2006).

Human H5N1 virus infections followed similar patterns to poultry. Infections among poultry first appeared in Banten and Central Java, then moved northwest to Lampung and North Sumatra and finally eastward to East Java and Bali. Computation of spatial means and spatial standard distances among human H5N1 cases (Table 3) showed an increase in numbers of case and spread to northern Sumatra. Unfortunately, changes in standard distance only describe the distribution of human cases.

Banten and Central Java Provinces are the epicenters for both human and poultry H5N1 infections. Since the end of 2004 H5N1 infections among poultry have moved toword the northwest and later eastward, putting an increasingly larger number of humans at risk. Over a three year period (2005-2007) Jakarta and Central Java were the two provinces with the highest prevalence of human H5N1 infections. Data obtained from provincial livestock offices show large poultry farms (sectors 1 and 2) are concentrated on Java Island. There are 10 large enterprises (primary poultry breeders), that are the main stock suppliers for nearly all the commercial poultry farms in Indonesia. These companies also have their own meat and egg production units. A study done by Sumiarto in 2007 reported 70% of the total poultry population is located in Java. The larger the population of poultry, the greater the chances of the disease spreading to consumer districts. Our unpublished mapping data of H5N1 infection movement among poultry indicate districts closer to Java had the disease earlier than those further away.

The Moran I and local autocorrelation test for confirmed cases (n=107) indicate there was a cluster of cases in eight neighboring districts (Fig 4). These districts share a common border and large numbers of human H5N1 cases. This reflects the potential role of environmental factors. One explanatory factor is the number of infected poultry in these districts which transmit the disease to humans (zoonosis). Another study (Simanjuntak *et al*, 2007) reported that during a two year period (2005-2007) Central and East Java had the largest number of poultry outbreaks (26), followed by West Java and Banten (14). Outbreaks involving significant numbers of animals were characterized by penetration of infection into commercial farms. These usually included industrially reared poultry, but also included other poultry traded, including semi-commercial and backyard farming (Capua and Marangan, 2007). This could explain the large number of human H5N1 infections in the two clusters shown in Fig 4 (pooling confirmed and suspected cases).

DKI Jakarta was found to have a cluster of human H5N1 cases based on cluster analysis for confirmed cases. Although there are no commercial poultry enterprises registered within this province, DKI Jakarta is known as the end market for this business. Poultry (mostly live and some carcasses) come from many suppliers outside the province. The situ-

ation is worsened by a lack of bio-security measures among collectors and slaughter house operators, particularly, traditional slaughter houses.

Another plausible explanation for clustered areas is interstate population and poultry movement. There is no single port of entry since poultry are brought in by land transportation accross all borders. Some areas with few or no human H5N1 cases are secluded islands, such as Sumba, South Maluku and some islands west of Bengkulu with minimal marketing chains. Movement of infected poultry, movement of contaminated equipment, vehicles and penetration of contaminated infectious organic material into other areas may also be sources of infection.

A study by Green *et al* (2006) explained the mix of circulating influenza strains and protective immunity among local people within these areas may cause influenza infection clustering. Further studies are needed to confirm this.

REFERENCES

Capua I, Marangon, S. Control and prevention of avian influenza in an evolving scenario. *Vaccine* 2007; 25: 5645-52.

Clark PJ, Evans FC. Distance to nearest neighbour as a measure of spatial relationships in population. *Ecology* 1954; 35: 445-53.

Dinh PN, Long HT, Tien NT, *et al*. Risk factors for human infection with avian influenza A H5N1, Vietnam, 2004. *Emerg Infect Dis* 2006; 12: 1841-7.

Goicoechea M, Pawitan JA, Dudley JP, *et al*. Human H5N1 Influenza. *N Engl J Med* 2007; 356: 1375-7.

Green SK, Ionides EL, Wilson ML. Patterns of influenza-associated mortality among US elderly by geographic region and virus subtype, 1968-1998. *Am J Epidemiol* 2006; 4: 316-26.

Griffith DA, Amrhein CG. Statistical analysis for geographers. Englewood Cliffs, NJ: Prentice-Hall, 1991.

Government of Indonesia. Indonesian law 32/2004. Amendment of Law 22/1999 on Regional Government. Jakarta: Goverment of Indonesia, 2004.

Kandun IN, Tresnaningsih E, Purba WH, *et al*. Factor associated with case fatality of human H5N1 virus infections in Indonesia. *Lancet* 2008; 372: 744-9.

Kung NY, Morris RS, Perkins NR, *et al*. Risk for infection with highly pathogenic influenza A virus (H5N1) in chickens, Hong Kong, 2002. *Emerg Infect Dis* 2007; 13: 412-8.

Mounts AW, Kwong H, Izurieta HS, *et al*. Case-control study of risk factors for avian influenza A (H5N1) disease, Hong Kong, 1997. *J Infect Dis* 1999; 180: 505-8.

Peiris JSM, de Jong MD, Guan Y. Avian influenza virus (H5N1): a threat to human health. *Clin Microbiol Rev* 2007; 20: 243-67.

Perez-Brena P, Casas I. [Avian influenza A (H5N1) infectious in both birds and humans in South-Eastern Asian countries]. *Enferm Infecc Microbiol Clin* 2004; 22: 412-8.

Sedyaningsih ER, Isfandari S, Setiawaty V, *et al*. Epidemiology of cases of H5N1 virus infection in Indonesia, July 2005-June 2006. *J Infect Dis* 2007; 196: 522-7.

Sedyaningsih ER, Isfandri S, Soendoro T, Supari SF. Towards mutual trust, transparency and equity in virus sharing mechanism: The avian influenza case of Indonesia. *Ann Acad Med* 2008; 6: 482-8.

Simanjuntak G, Purba W, Lingga J, Kisyanto Y. Current situation of avian influenza in Indonesia. Paper presented at the Joint International Tropical Medicine Meeting. Bangkok: Faculty of Tropical Medicine, Mahidol University, November 29-30, 2007.

Sumiarto B, Arifin B. Overview on poultry sector and HPAI situation for Indonesia with special emphasis on the Island of Java - Background paper. 2007. [Cited 2011 Jan

16]. Available from: URL: www.ifpri.org

Witayathawornwong P. Avian influenza A (H5N1) infection in a child. *Southeast Asian J Trop Med Public Health* 2006; 37: 684-9.

Wong SSY, Yuen K-y. Avian Influenza virus infections in humans. *Chest* 2006; 129: 156-68.

The Writing Committee of the World Health Organization Consulation on Human Influenza AH. Avian influenza A (H5N1) infections in humans. *N Engl J Med* 2005; 353: 1374-85.

Yang Y, Halooran, EM, Sugimoto, J, Longini, IM. Detecting human to human transmission of avian influenza (H5N1). *Emerg Infect Dis* 2007: 1-14.