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Comparative epidemiology of human infections with avian influenza A(H7N9) and A(H5N1) viruses in China

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Abstract

Background—The novel influenza A(H7N9) virus recently emerged, while influenza A(H5N1) virus has infected humans since 2003 in mainland China. Both infections are thought to be predominantly zoonotic. We compared the epidemiologic characteristics of the complete series of laboratory-confirmed cases of both viruses in mainland China to date.

Methods—An integrated database was constructed with information on demographic, epidemiological, and clinical variables of laboratory-confirmed A(H7N9) and A(H5N1) cases that were reported to the Chinese Center for Disease Control and Prevention up to May 24, 2013. We described disease occurrence by age, sex and geography and estimated key epidemiologic parameters.

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Findings—Among 130 and 43 patients with confirmed A(H7N9) and A(H5N1) respectively, the median ages were 62y and 26y. In urban areas, 74% of cases of both viruses were male whereas in rural areas the proportions were 62% for A(H7N9) and 33% for A(H5N1). Among cases of A(H7N9) and A(H5N1), 75% and 71% reported recent exposure to poultry. The mean incubation periods of A(H7N9) and A(H5N1) were 3.1 and 3.3 days, respectively. On average, 21 and 18 contacts were traced for each A(H7N9) case in urban and rural areas respectively; compared to 90 and 63 for A(H5N1). The hospitalization fatality risk was 35% (95% CI: 25%, 44%) for A(H7N9) and 70% (95% CI: 56%, 83%) for A(H5N1).

Interpretation—The sex ratios in urban compared to rural cases are consistent with poultry exposure driving the risk of infection. However the difference in susceptibility to serious illness with the two different viruses remains unexplained, given that most A(H7N9) cases were in older adults while most A(H5N1) cases were in younger individuals.

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Introduction

Since February 19, 2013 when the first patient infected with the novel influenza A(H7N9) virus from an avian source showed symptoms, mainland China has reported 130 laboratory-confirmed cases as of May 24, 2013. This virus apparently exhibits low pathogenicity in avian species¹ contrasted with severe human disease.² Such divergent inter-species manifestation differs from A(H5N1), another influenza virus of direct avian origin, which is highly pathogenic in both humans and birds.³ Another immediately striking feature of A(H7N9) is the relatively rapid accumulation of laboratory-confirmed cases in humans, even though phylogenetic⁴ and epidemiologic^{5, 6} evidence point to predominantly zoonotic transmission. In contrast A(H5N1), similarly an exclusive zoonosis with very few exceptions, has caused only 43 laboratory-confirmed cases since the symptom onset date of November 23, 2003 in mainland China's first patient.

To improve understanding of these different viral characteristics and to inform public health control measures for both co-circulating viruses, we compared key epidemiologic parameters of the complete series of laboratory-confirmed human influenza A(H7N9) and A(H5N1) cases in mainland China to date.

Methods

Subjects

In China, all laboratory-confirmed A(H7N9) cases, and all laboratory-confirmed A(H5N1) cases, are reported to the Chinese Center for Disease Control and Prevention (China CDC) through a national system for reporting notifiable infectious diseases. Case definitions, surveillance for identification of A(H7N9) and A(H5N1) cases, and laboratory test assays are described in previous reports.⁶⁻⁹ A joint field investigation team comprising staff of local or provincial level CDC and/or the China CDC conducted field investigations of the laboratory-confirmed cases of A(H7N9) virus infection. All confirmed A(H5N1) cases were interviewed by a trained team from the China CDC except two military cases. Demographic, epidemiological and basic clinical data on A(H7N9) and A(H5N1) cases were collected on standardized forms. Investigations were generally initiated within 24 hours of diagnosis of suspected A(H7N9) and A(H5N1) virus infection, clinical circumstances permitting.

An integrated database was constructed by China CDC, with detailed epidemiologic information on each laboratory-confirmed influenza A(H7N9) and A(H5N1) case reported

to China CDC by May 24 2013. Information used in the present analysis included the age, sex, place of residence, number and type of contacts traced, symptoms at illness onset, underlying medical conditions associated with an increased risk of influenza complications,¹⁰ and dates of illness onset, hospital admission, death or discharge, plus dates of potential exposures to domestic or retail animals and visits to live poultry markets.

Ethical Approval

It was determined by the National Health and Family Planning Commission that the collection of data from both A(H5N1) and A(H7N9) cases was part of a continuing public health investigation of an emerging outbreak and was exempt from institutional review board assessment.

Statistical Methods

We plotted the geographic locations of cases, and conducted descriptive analyses of the dates of illness onset and the characteristics of participants. We analysed the number and type of contacts traced for each case, by type of case and exposure history. Close contacts were defined as individuals known to have been within 1m, or had direct contact with respiratory secretions or faecal material, of a patient with laboratory-confirmed A(H7N9) or A(H5N1) virus infection any time from the day before the onset of illness to when the case was isolated in the hospital or died.^{6, 11} We used survival analysis techniques to estimate time-delay distributions including the incubation period (infection to illness onset), illness onset to admission, onset to laboratory confirmation, admission to death, and admission to discharge.^{12, 13} We compared alternative parametric distributions including gamma, Weibull and lognormal distributions with non-parametric estimates, and selected the best parametric distribution based on the Akaike Information Criterion.¹⁴

Confirmed cases and their relatives were interviewed to ascertain exposure histories to poultry and swine, as well as environmental exposures, during the 14 days prior to illness onset.^{6, 15, 16} We estimated the incubation period based on dates of reported close contact with live poultry as the proxy for infection, and in sensitivity analyses we explored estimates based on reported exposures to any live animals, and on reported visits to live poultry markets (thus accounting for the possibility of infection by environmental contamination). Information on potential exposures was typically collected for each of the preceding 14 days, but some cases had repeated exposures and our analysis explicitly allowed for the interval censoring in the exposure data.¹⁴ In this analysis we could not include cases that reported recent live poultry exposure but could not recall the exact dates of exposures.

While the case fatality risk (i.e. the risk of death among cases¹⁷) has often been used as an important measure of the seriousness of infection, the estimated case fatality risk can be highly dependent on the definition of a “case” and can sometimes be misinterpreted. Instead, here we chose to investigate the hospitalization fatality risk, i.e. the risk of death among hospitalized cases, for two reasons. First, mild infections are less likely to have been detected, both for A(H7N9) and A(H5N1), and therefore the risk of death among medically-attended and laboratory-confirmed cases would be quite different, potentially by orders of magnitude, to the symptomatic case fatality risk (i.e. the risk of death among symptomatic cases of A(H7N9) virus infection). Second, mild cases identified through sentinel influenza-like illness surveillance or contact tracing should have a substantially lower risk of mortality than serious cases admitted with pneumonia, and a single estimated case fatality risk would misrepresent this heterogeneity. We therefore estimated the hospitalization fatality risk using a non-parametric approach that accounted for the competing risks of death or discharge, as well as right-censoring of the outcomes of patients still hospitalized.¹⁸ We estimated 95% confidence intervals for the hospitalization fatality risk by using bootstrap estimates of the

asymptotic variance with 1000 replications.¹⁸ All statistical analyses were conducted using R version 3.0.1 (R Foundation for Statistical Computing, Vienna, Austria).

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Results

As of May 24 2013 a total of 130 cases of laboratory-confirmed A(H7N9) virus infection have been officially announced with illness onset dates between February 19 and May 3 2013. A total of 43 cases of laboratory-confirmed A(H5N1) virus infection have so far been reported in mainland China with the last case documented on February 9 2013, with illness onset dates between November 23 2003 and February 3 2013. Whereas A(H5N1) cases have been distributed across most parts of China, A(H7N9) cases in mainland China were initially concentrated in the Yangtze river delta in eastern China, with the most recent cases being detected radially away from the initial epicenter to the south and north (Figure 1).

Ninety-three (72%) of the A(H7N9) cases occurred in residents of urban areas. In contrast, the incidence rate of the A(H5N1) cases peaked in 2006, and 24 (56%) of the cases occurred in rural residents (Figure 1, Figures 2A and 2C). Thirty three (77%) of the A(H5N1) cases occurred in the winter months November through February (Figure 2B). There was a marked difference in the age and sex distributions of cases overall and by location of residence (Figure 3).

In urban areas, cases were more common in males: the male:female ratio for A(H7N9) was 2.9:1 and for A(H5N1) it was 2.8:1. In rural areas, the male:female ratio was 1.6:1 for A(H7N9) and 0.5:1 for A(H5N1). Whereas more than half (71/130, 55%) of the A(H7N9) cases occurred in persons at least 60 years of age (median age = 62y), A(H5N1) cases were predominantly young adults (Figure 3, Table 1).

Around two thirds of cases reported recent exposure to poultry for both A(H7N9) and A(H5N1) (Table 1), most commonly through visiting a live poultry market for A(H7N9) or exposure to sick or dead poultry for A(H5N1). Symptoms at illness onset were relatively similar between the two viruses, with fever and cough being the most frequently reported symptoms, but less frequently so for A(H5N1) (Table 2). The average number of contacts traced for each A(H5N1) case was much greater than for each A(H7N9) case (Table 3). For A(H7N9) cases, 2554 close contacts were reported and all of them were traced, almost half being healthcare-associated contacts. 21 contacts developed acute fever or respiratory symptoms during medical surveillance period of 7 days after last exposure to A(H7N9) cases without appropriate personal protective equipment. Close contacts who developed febrile respiratory illness were transferred to a designated hospital for diagnosis and treatment, and respiratory specimens and/or paired sera were collected for laboratory testing. Four of the ill contacts were laboratory confirmed as cases of A(H7N9) virus infection. The mean number of contacts traced of A(H7N9) cases was higher for urban (20.3) compared to rural (17.9) residents (Table 3).

Information on dates of recent exposures to live poultry were available for 32 (25%) A(H7N9) and 27 (63%) A(H5N1) cases. Weibull models were found to have the best fit to the incubation period distributions for A(H7N9) and A(H5N1). We estimated the mean incubation period for A(H7N9) to have mean 3.1 (95% CI: 2.6, 3.6) days and standard

deviation 1.4 days, with 95th percentile 5.5 days. For A(H5N1), we estimated the incubation period to have mean 3.3 days (95% CI: 2.7, 3.9) and standard deviation 1.5 days, with 95th percentile 6.0 days (Figure 4A). In sensitivity analyses, estimated incubation period distributions for A(H7N9) and A(H5N1) based on contact with any live animals or visits to live poultry markets were very similar (data not shown).

The onset-to-admission interval was also similar for the two viruses (Figure 4B): it was estimated for 123 A(H7N9) cases to have mean 4.2 days (95% CI: 3.7, 4.9) based on the best-fitting gamma distribution, while for all 43 A(H5N1) cases it was estimated to have median 4.9 days (95% CI: 3.9, 5.9) based on the best-fitting Weibull distribution. For the onset to laboratory confirmation delays, lognormal models fitted best, and the distributions were similar for the two viruses (Figure 4C). For A(H7N9) the median onset to laboratory confirmation delay was 8.3 days (95% CI: 7.3, 9.5) and for A(H5N1) the mean was 10.7 days (95% CI: 9.1, 12.7).

We estimated the respective hospitalization fatality risks excluding 7 A(H7N9) cases classified as “mild” and allowing for unresolved outcomes in 17 A(H7N9) cases that are currently still in hospital.¹⁹ Among 123 hospitalized A(H7N9) cases and 43 hospitalized A(H5N1) cases, we respectively estimated that the hospitalization fatality risks were 35% (95% CI: 25%, 44%) and 70% (95% CI: 56%, 83%). Almost all laboratory-confirmed A(H5N1) virus infections had resulted in recovery or death within three to four weeks of admission, but duration of hospital stay was typically longer for A(H7N9) cases (Figure 4D, Figure 4E). The median time from hospitalization to death for A(H7N9) cases was 12.0 days, compared to 5.7 days for A(H5N1) cases based on best-fitting lognormal distributions (Figure 4D). Among cases who survived, the median time from hospitalization to discharge was 41.7 days for A(H7N9) cases while it was 18.7 days for A(H5N1) cases based on best-fitting Weibull distributions (Figure 4E).

Discussion

Here we present the comparative epidemiology of human influenza A(H7N9) and A(H5N1) virus infections in China. While both viruses are of avian origin, and neither has yet acquired the ability for sustained human-to-human transmission, there are stark differences in the epidemiology to date.²⁰ Whereas most confirmed A(H7N9) and A(H5N1) cases reported exposure to live poultry (Table 1), the type of exposure was very different in urban and rural locations. This is clearly illustrated in Figure 3, where the male:female ratio is much higher in urban than rural areas for both viruses. This observation is most consistent with sex-based differences in exposure rather than differences in immunity. In particular, the male:female ratio is highest for cases in Shanghai compared to other urban areas (data not shown), anecdotally this is the Chinese city where men may have the greatest frequent retail exposures to live poultry than women.²¹

Our deduction has at least *prima facie* validity in that the age distribution of urban A(H7N9) cases is consistent with increasing exposure to retail poultry with age.^{22, 23} Whereas some of the rural A(H5N1) cases have occurred in areas with low population density and were associated with exposure to backyard live poultry or handling of slaughtered poultry,²⁴ most of the rural cases of A(H7N9) occurred in people who live on the outskirts of urban areas and were exposed to retail poultry in live poultry markets; few A(H7N9) cases were exposed to backyard poultry (Table 1). The preponderance of females among the rural A(H5N1) cases may be due to greater exposures to rearing, slaughtering and cooking backyard poultry.⁷ The characteristics of A(H5N1) cases in China were similar to A(H5N1) cases in other countries in the region (Table 4).

The estimated mean incubation period for A(H7N9) of around three days is much lower than previously reported,⁶ which prompted public health authorities to extend the period of medical surveillance for close contacts of confirmed cases from one week initially to 10 days currently.²⁵⁻²⁷ Of note, the present findings concur with those estimated by an entirely different method based on inference from the time series of cases.²⁸ The clarification of the incubation period distribution has important implications. Current case definitions should be updated since incubation periods as long as 8 to 10 days are very unlikely. Quarantine or medical surveillance for close contacts need not last longer than one week since more than 95% of cases would present within seven days of infection. Accurate estimates of the incubation period distribution can help estimate epidemic potential in the event an avian influenza virus emerges that is efficiently transmissible in humans.

There has been substantial interest in the case fatality risk associated with A(H7N9) virus infection. Because estimates of the laboratory-confirmed case fatality risk may misinterpreted as estimates of the symptomatic case fatality risk, although they differ substantially, we focused on the hospitalization fatality risk i.e. the risk of death among hospitalized cases.¹⁹ We found the hospitalization fatality risk of A(H7N9) to be around 35%, much lower than for A(H5N1). The hospitalization fatality risk of 70% for A(H5N1) was similar to other reports from the region except for Vietnam (Table 4),²⁹⁻³⁵ and higher than estimates from Egypt perhaps because of differences in the viral clade or differences in speed of hospital admissions and levels of care.^{35, 36}

The longer average duration of hospitalization for A(H7N9) before death (Figure 4) may be a reflection of advances in medical care which can sustain life for longer, but could also indicate slower disease progression. However, we did not examine detailed clinical information in this report given a separate nationally-based effort already under way. The relatively long onset to admission intervals and onset to laboratory-confirmation intervals for A(H7N9) with respective medians of 4.2 days and 8.3 days currently (Figures 4B and 4C) could be reduced in order to permit more timely thus more effective treatment with antivirals.^{29, 31} If preliminary testing can indicate influenza A virus infection either by rapid point-of-care tests or by RT-PCR, this could permit early antiviral treatment before the subtype is known.

Authorities traced more than 2554 close contacts to date with only 4 potentially secondary infections detected, and those 4 specific clusters could either be a result of limited human-to-human transmission or a common source of infection.⁶ The high average number of contacts traced for each case (Table 3), particularly for A(H5N1) cases who tended to be younger and therefore had more household and community contacts and care involving multiple hospitals with larger medical teams, indicates the potential difficulty that would be faced in a future outbreak of an avian influenza virus that is more transmissible between humans. The higher mean number of contacts for urban compared to rural residents is a reflection of the higher connectivity associated with urban living and the larger medical teams found in tertiary referral hospitals in large cities.

There are a number of limitations to our analyses. First, we have compared laboratory-confirmed cases of A(H7N9) and A(H5N1), and it is possible that some cases of influenza A(H7N9) and A(H5N1) virus infection have not been ascertained, particularly those that occurred earlier in the respective epidemics, for example because of lack of access to laboratory testing in some areas. Almost all laboratory-confirmed A(H7N9) cases had serious illness including pneumonia, and all A(H5N1) cases had pneumonia. Laboratory confirmation of a small number of A(H7N9) virus infections with mild to moderate disease is suggestive of a larger number of mild to moderate cases.⁸ In addition, as of May 24, 17 A(H7N9) cases are still in hospital, and the current A(H7N9) outbreak may yet not have

ended which could lead to some bias in the follow-up data. Second, our estimates of the incubation period are based on a subset of 32 cases with information on single or repeated exposures, while accurate and complete information on exposures can be difficult to ascertain. The lack of exposure data for some cases could have biased the estimates of the incubation period distribution.

Our estimates of biological parameters, such as the incubation period and to some extent the hospitalization fatality risk, should generalize to other countries. Other parameters such as the onset to admission delay and the onset to laboratory confirmation delay may also depend on health services and surveillance capacity, while the age and sex distribution of cases would also depend on patterns in exposure that could differ in other locations.

In conclusion, we have reported estimates of important epidemiological parameters and distributions of A(H7N9). However many important questions remain. The differences in age distribution of laboratory-confirmed A(H7N9) and A(H5N1) cases are intriguing; presumably immunity associated with different histories of influenza virus exposures plays an important role in addition to differences in exposure patterns. While we have reported the hospitalization fatality risk, the symptomatic case fatality risk remains to be determined and it is possible that a large portion of the ‘clinical iceberg’ of infection has remained undetected to date. The warm season has now begun in China, and no new laboratory-confirmed human A(H7N9) cases have been identified since May 8. If A(H7N9) follows a similar pattern to A(H5N1) (Figure 2B), it is possible that the A(H7N9) epidemic may reappear in the fall. This potential lull should be an opportunity for discussion of definitive preventive public health measures, and optimization of clinical management, as well as capacity building in the region given the possibility that A(H7N9) may spread outside China's borders.

Panel: Research in Context

Systematic review—We searched PubMed on May 27 2013, with the terms “A(H7N9)” or “H7N9” or “A(H5N1)” or “H5N1”. We also searched articles in press and available online at international medical and infectious disease journals. Our search did not reveal any reports of human infections with avian influenza A(H7N9) virus before 2013. A total of 628 laboratory-confirmed influenza A(H5N1) virus infections in humans have been reported to the World Health Organization by April 28 2013,³⁰ including 45 from China since 2003 (43 from mainland China and 2 from Hong Kong Special Administrative Region). The majority of A(H5N1) cases occurred in children and young adults reporting recent exposure to live poultry (Table 4).^{31, 33, 34, 36} Preliminary reports of A(H7N9) epidemiology included three hypotheses for the increased incidence rate of laboratory-confirmed A(H7N9) in men compared to women: greater risk of exposure in men, worse prognosis for infected men than infected women, and differential health seeking behaviors.²⁰

Interpretation—Our study showed that the higher incidence rate of A(H7N9) cases in men was more apparent in urban than rural areas, and the increased risk for men was also observed for A(H5N1) in urban areas (Figure 3). This is more consistent with exposure playing a major role in risk of infection, although we cannot rule out the possibility of differences in immunity or health care seeking behaviors. The majority of cases of both viruses reported recent exposure to poultry (Table 1) and there is good evidence of the low human-to-human transmissibility given extensive contact tracing efforts and very low numbers of potential secondary cases identified. Some of the epidemiologic parameters were similar for both viruses (Figure 4 panels A-C), while hospitalized cases of A(H5N1) had a higher risk of fatality (70% vs 35%) and more rapid disease progression (Figure 4D). Given

the seasonal pattern in human infections with influenza A(H5N1) virus in China (Figure 2B), we must be prepared for A(H7N9) to reappear later this year.

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Figure 1.

Geographical distribution of 130 and 43 laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) viruses respectively in urban and rural areas of mainland China, with dates of illness onset between November 25 2003 and May 3 2013. Provinces are shaded according to population density, and A(H7N9) and A(H5N1) cases with more recent calendar dates of illness onset are represented by symbols with darker shades.

Figure 2.

Occurrence of laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) viruses over calendar time. Panels (A) and (B) show the number of laboratory-confirmed cases of infection with avian influenza A(H5N1) virus among urban and rural residents by calendar year and calendar month of illness onset, respectively. Panel (C) shows the number of laboratory-confirmed cases of infection with avian influenza A(H7N9) virus by week of illness onset.

Figure 3.

Panels (A) and (B) compare the age and sex profiles of laboratory-confirmed cases of infection with avian influenza A(H7N9) and A(H5N1) viruses. Panels (C) and (D) show the age and sex profiles for A(H7N9) and A(H5N1) cases in residents of urban areas. Panels (E) and (F) show the age and sex profiles for A(H7N9) and A(H5N1) cases in residents of rural areas.

Figure 4.

Comparisons of time-delay distributions for laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) viruses. Panel (A) shows the estimated incubation period distributions i.e. the days from infection to illness onset. Panel (B) shows the days from illness onset to admission. Panel (C) shows the days from illness onset to laboratory confirmation of A(H7N9) virus infection. Panels (D) and (E) show the days from admission to death and days from admission to discharge, respectively.

Table 1

Characteristics of laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) viruses in mainland China.

Characteristic	Influenza A(H7N9) (n=130)	Influenza A(H5N1) (n=43)
Median age, y (inter-quartile range)	62 (47, 73)	26 (19, 35)
Male (%)	92 (71%)	22 (51%)
Presence of at least one underlying medical condition* (%)	50/111 (45%)	5/41 (12%)
Urban residence	93 (72%)	19 (47%)
Rural residence	37 (28%)	24 (53%)
<i>Possible source of infection</i>		
Any exposure to poultry	92/123 (75%)	29/41 (71%)
Occupational exposure to live poultry	6 (5%)	4 (9%)
Visited live poultry market	43/84 (51%)	23/41 (56%)
Exposed to sick/dead poultry	3/123 (2%)	16/41 (39%)
Exposure to backyard poultry	19/71 (27%)	21/41 (51%)

* Only underlying medical conditions associated with a high risk for influenza complications¹⁰ were counted here, including: chronic respiratory disease, asthma, chronic cardiovascular diseases, diabetes, chronic liver disease, and chronic renal disease.

Table 2

Comparison of symptoms at illness onset of laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) viruses respectively in mainland China with available data.

Symptoms	A(H7N9) (n=85) n (%)	A(H5N1) (n=37) n (%)
Fever 38°C	67 (79%)	24 (65%)
Cough	60 (71%)	20 (54%)
Sputum	28 (33%)	12 (32%)
Chills	17 (20%)	13 (35%)
Fatigue	18 (21%)	9 (24%)
Arthralgia	15 (18%)	12 (37%)
Shortness of breath	11 (13%)	3 (8%)
Sore throat	8 (9%)	2 (5%)
Coryza	3 (4%)	5 (14%)
Nasal congestion	3 (4%)	3 (8%)
Headache	3 (4%)	7 (19%)
Chest pain	2 (2%)	1 (3%)

Table 3

Average numbers of close contacts traced for laboratory-confirmed cases of human infection with avian influenza A(H7N9) and A(H5N1) in mainland China with available data.

Location and type of exposure*	Mean number of close contacts traced					
	A(H7N9) (n=106)			A(H5N1) (n=41)		
	n	Healthcare	Others [†]	n	Healthcare	Others [†]
<i>Urban residence</i>						
Occupational exposure to live poultry	71	11.2	9.8	17	69.9	19.9
Exposure to retail live poultry	3	23.7	7.3	1	67.0	42.0
Exposure to live poultry elsewhere	28	14.8	8.0	13	70.4	20.2
No known exposure	27	9.1	11.3	2	87.5	13.0
	13	4.9	10.7	1	31.0	9.0
<i>Rural residence</i>						
Occupational exposure to live poultry	35	6.7	11.6	24	27.7	35.1
Exposure to retail live poultry	3	9.1	6.9	3	5.7	19.0
Exposure to live poultry elsewhere	11	12.8	12.9	8	34.0	31.4
No known exposure	20	3.3	11.7	13	28.8	41.1
	1	0.0	10.0	0	-	-

*Types of exposure were ordered by risk level and categorized to be mutually exclusive by excluding overlapping cases with higher risk of exposure. "Exposure to poultry elsewhere" includes exposure to backyard poultry.

[†]Other contacts includes family and community contacts. Missing data were imputed by assuming the same ratio between healthcare and other contacts in the same category.

Table 4

Comparison of epidemiologic characteristics of laboratory-confirmed A(H5N1) cases reported in China and other countries.

Characteristic	China (n=43)	Vietnam ^{31, 32} (n=67)	Thailand ³³ (n=25)	Indonesia ³⁴ (n=127)	Egypt ³⁶ (n=63)
Calendar years of illness onset	2003-13	2004-06	2004-06	2005-08	2006-09
Median age, y (range)	26 (2-62)	25 (16-42)	18 (1-68)	20 (2-67)	10 (1-75)
Male, %	51%	55%	64%	50%	36%
Presence of at least one underlying medical condition, %	12%	-	16%	-	-
Any recent exposure to poultry, %	71%	64%	100%	82%	71%
Hospitalization fatality risk, %	70%	39%	68%	82%	39%
Median duration of hospitalization for fatal cases, days	6	5	6	3	7
Median duration of hospitalization for non-fatal cases, days	21	16	13	-	-

“-”: information not available