

Avian influenza H5N1 viral and bird migration networks in Asia

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The spatial spread of the highly pathogenic avian influenza virus H5N1 and its long-term persistence in Asia have resulted in avian influenza panzootics and enormous economic losses in the poultry sector. However, an understanding of the regional long-distance transmission and seasonal patterns of the virus is still lacking. In this study, we present a phylogeographic approach to reconstruct the viral migration network. We show that within each wild fowl migratory flyway, the timing of H5N1 outbreaks and viral migrations are closely associated, but little viral transmission was observed between the flyways. The bird migration network is shown to better reflect the observed viral gene sequence data than other networks and contributes to seasonal H5N1 epidemics in local regions and its large-scale transmission along flyways. These findings have potentially far-reaching consequences, improving our understanding of how bird migration drives the periodic reemergence of H5N1 in Asia.

bird migration | HPAI H5N1 | viral migration | network | satellite tracking

Migratory birds play important roles in the geographic spread of various zoonotic agents (1). Among these agents, the avian influenza viruses (AIVs) have been shown to be transmitted over long distances during the seasonal migration of birds (2, 3). Wild waterfowl, in particular, are considered the natural reservoir of low-pathogenic avian influenza (LPAI) viruses and have been shown to spread LPAI viruses along migratory flyways in Asia, Africa, and the Americas (4–7). However, one of the fundamental unknowns remaining is the role played by wild birds in the regional spread of AIV (8–11).

Highly pathogenic avian influenza (HPAI) H5N1 first appeared in Asia in 1996 (12), and subsequently spread to Europe, the Middle East, and Africa, causing many human casualties and major economic loss in the booming Asian poultry sector. Despite the low transmissibility of HPAI H5N1 from birds to humans and from humans to humans, the high fatality rate reported in humans after the onset of the epidemic and the potential for H5N1 to become pandemic through migratory bird flyways raised serious concerns (13). The Qinghai lineage of H5N1, in particular, expanded from Qinghai to Eurasia and into the Indian subcontinent and northern and central Africa along migratory flyways. It was also shown experimentally that some species of birds shed the virus before the onset of clinical signs or with no clinical signs (14, 15). This suggests that the large-scale transmission of H5N1 by migratory birds could potentially go undetected. Using satellite telemetry, Gaidet et al. reported that one infected white-faced whistling duck (*Dendrocygna viduata*) survived HPAI H5N2 infection and was able to migrate

for at least 655 km, when tracked with a satellite transmitter for 47 d (16). Other studies have shown that the direction of the geographic spread of HPAI H5N1 is consistent with the major bird migration routes (17, 18). A number of studies have also suggested that long-distance migration may lead to immunosuppression in birds and migratory performance is negatively affected by viral infections (19–21). However, it should be noted that HPAI H5N1 is rarely reported in living and healthy wild birds (22–24).

Recently, HPAI H5N1 clade 2.3.2, the dominant subclade in Asia, was detected in migratory birds during their migration in Mongolia, South Korea, and Japan, and was shown to be associated with wild waterfowl infections (25–27). Furthermore, an isolate of HPAI H5N1 from a common buzzard (*Buteo buteo*) in Bulgaria showed close genetic proximity to clade 2.3.2.1 isolates from wild birds in the Tyva Republic and Mongolia, suggesting

Significance

Highly pathogenic avian influenza virus H5N1 first emerged in Asia and subsequently unfolded into the first avian influenza panzootic, causing major economic losses in the poultry sector. However, we still do not understand the regional long-distance transmission and seasonal patterns of H5N1. In this study, we addressed this issue by combining H5N1 outbreak records, whole-genome sequences of viral samples, and satellite tracking data for four species of migratory birds in Asia. We show that timing of H5N1 outbreaks and viral migration are closely associated with known bird migration routes. The flyway is the major viral transmission barrier to the intracontinental spread of H5N1 by migratory birds in Asia, whereas geographic distances within the flyways have little effect on H5N1 transmission.

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Table 1. Statistically supported migration rates of H5N1 viruses jointly estimated from all gene segments

Area A	Area B	Rate	Indicator	BF
MO	NEA	0.91 (0.16–1.84)	>0.90	>100
QH	MO	1.99 (0.33–4.11)	>0.90	>100
SC	SEA	1.82 (0.51–3.48)	>0.90	>100
MO	SC	0.28 (0.05–0.58)	>0.90	>100
SC	NEA	0.22 (0.03–0.47)	>0.90	>100
MO	SA	0.96 (0.02–2.25)	0.78	88.29

MO, Mongolia; NEA, northeast Asian, i.e., Japan and Korea; QH, Qinghai; SA, South Asia; SC, southern China; SEA, Southeast Asia. Rate: viral migration rate. BSSVS was used to reduce the number of parameters to those with significantly nonzero transition rates. Areas A and B were the locations connected by nonzero rates. BF > 100 indicates decisive support for migration between locations; $30 \leq \text{BF} \leq 100$ indicates very strong support; $10 \leq \text{BF} \leq 30$ indicates strong support; and $6 \leq \text{BF} \leq 10$ indicates substantial support. Only statistically supported migrations with indicator values >0.50 and BF > 30 are shown. The indicator is the posterior probability of observing nonzero migration rates in the Bayesian sampled trees. HA, hemagglutinin; NA, neuraminidase; NP, nucleoprotein; NS, nonstructural gene; MP, matrix proteins; PA, PB1, and PB2, RNA polymerases.

nonzero rates, the significant nonzero migration rates remained unchanged (*SI Appendix, Table S5*).

The viral migration network was jointly estimated from all eight viral gene segments in a single analysis (Fig. 3*A*). It was insensitive to the sample sizes in the main migration paths (*SI Appendix, Table S8*). The gene flow structures were similar to the bird migration network (Fig. 3*B*), for the gene flow between South Asia, Qinghai, and Mongolia (the CA flyway) and for the gene flow through southern China, Mongolia, Japan, and the Republic of Korea (the EA flyway). The EA-1 and EA-2 flyways were defined by the migration routes. EA-1 started at Hong Kong and progressed through southern China, the Republic of Korea, and Japan. EA-2 started at Poyang Lake and progressed through southern China, the Republic of Korea, and Mongolia. The linkage between southern China and Japan–Korea was not strongly supported by the Bayes factor (BF), perhaps because there were gaps in the viral sampling in these two areas. Most of the isolates from southern China were clustered in 2003–2008, whereas the samples from Japan–Korea were clustered in 2009–2011. The migration rates were higher within the flyways than between the flyways (two tailed *t* tests, $P < 0.01$; *SI Appendix, Fig. S6*). The flyways yielded largely congruent results, and the level of gene flow within a flyway was usually higher than that between flyways (3).

Coincidence Between Viral Transmission and Bird Migration Networks.

The network of HPAI H5N1 gene flow in Asia was built based on a phylogenetic analysis (Fig. 4). Using randomization tests, we showed that the observed gene flow was best explained using a flyway-based random network (FRN), either within the CA or the EA flyway, rather than by a purely random network (RN) including all geographic locations (Fig. 5*A* and Table 2). The significance of this result was assessed with a two-tailed *t* test ($P < 0.01$). These results reject the hypothesis of random mixing between flyways and suggest that migratory flyways act as a major barrier to the intracontinental spread of HPAI H5N1. Within each FRN, 1,000 random networks were created and compared with the network of bird migrations to reveal potential alternative transmission routes that might better explain the observed gene flow. The results of this analysis showed that the bird migration network best explained the pattern of gene flow in both the EA and CA flyways (Fig. 5*B*, Table 2, and *SI Appendix, Fig. S7*). For example, the trajectory Nepal–Qinghai–Mongolia–Bangladesh–India is a likely network for the CA flyway and is consistent with the observed bird migration pattern. The bird migrations were more complex in the EA flyway, and two different flyways were identified: the EA-1 flyway, Hong Kong–Guangdong–Shantou Special Economic Zone–

Zhejiang–Republic of Korea–Eastern Siberia–Japan; and the EA-2 flyway, Poyang Lake–Hubei, Hunan–Mongolia–Republic of Korea. Both networks are consistent with the observed migration networks and also showed a good fit with the gene flow in the EA flyway (Fig. 5*B*, Table 2, and *SI Appendix, Fig. S7*).

Finally, the inclusion of bird migration histories (Fig. 4*B*) in the migration networks outperformed the measurement of genetic and spatial divergences when viral migration histories were not considered (Table 2 and *SI Appendix, Fig. S8*). This was not unexpected because spatial distance measurements that ignore the history of viral migration may fail to reveal the underlying spatial-genetic pattern. In particular, the cycle of bird migrations best described the viral gene flow, and geographic distance had little effect on viral transmission along the flyway. This suggests that spatial distance is not a major ecological barrier to gene transfer within a flyway. Our network analysis consistently demonstrated that migratory birds and HPAI H5N1 share the same migration network, and that the virus could have evolved and spread along the bird migratory pathways in Asia. A randomization analysis of subsets of isolates throughout the FRN analysis revealed weak correlation between the number of isolates per locality and the spatial-genetic coefficient (*SI Appendix, Fig. S9*).

Discussion

Our study provides unique insight into the association between viral transmission networks, bird migration networks, and the timing of H5N1 outbreaks in Asia. Our results showed that in the period 2003–2012, the regular migration of the HPAI H5N1 virus occurred between migratory avian flyways and that bird migrations coincided with the peaks of HPAI H5N1 epidemics. This suggests that the annual epidemic lags for H5N1 outbreaks are associated with bird migrations along these flyways. The robustness of our findings on the gene flow dynamics of HPAI H5N1 was tested against 1,000 artificially generated random networks. The network analysis performed in this study indicated that the spread of clades 2.3.2 of HPAI H5N1 probably shared the same geographic pattern as the network of bird migrations.

Dozens of studies have discussed the spatiotemporal distribution of H5N1 and the potential effect of covariates on the distribution of its epidemics (29, 30). In this study, we have shown with a wavelet analysis that the temporal lags between epidemics are associated with the flight duration between successive locations along flyways. Our results further support a strong correlation between bird migration speed and epidemic velocity (Fig. 2). We combined satellite tracking data with a phylogenetic analysis to study the spatiotemporal spread of HPAI H5N1 across Asia. We have demonstrated how migration history can be associated with genetic distance and how transmission networks can be inferred from genetic information using a statistical framework. Our analyses demonstrate that the spread of HPAI H5N1 correlates with bird migration networks. Four bird vector species for H5N1 were used to analyze the bird migration

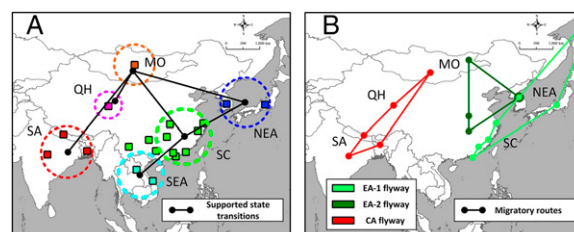


Fig. 3. Viral migration and bird migration networks in Asia. (A) Supported state transitions of HPAI H5N1 clades 2.3.2. (B) The migration routes of the four main bird species [bar-headed goose (*Anser indicus*), swan goose (*Anser cygnoides*), ruddy shelduck (*Tadorna ferruginea*), and northern pintail (*Anas acuta*)] in the Central Asian (CA, red line), East Asian–Australasian 1 (EA-1, starting at Hong Kong, green line), and East Asian–Australasian 2 flyways (EA-2, starting at Poyang Lake, dark green line).

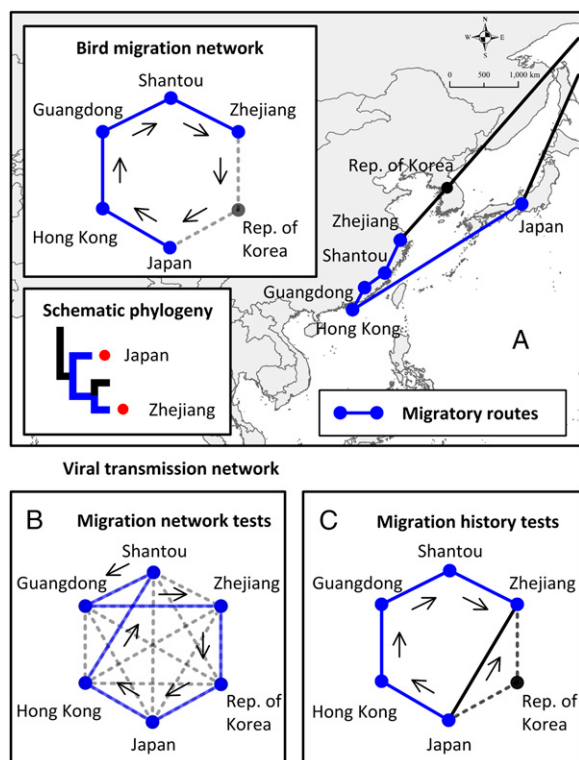


Fig. 4. Viral gene flow and bird migration network. (A) The bird migration network along the East Asian–Australasian 1 flyway (EA-1, starting at Hong Kong), and the associated partial phylogeny describing the relationship with the viral strains from Japan and Zhejiang Province. (B) Example of randomly generated viral migration networks. Viral migration was assumed to follow an underlying migration process along an unobserved network. A total of 1,000 random networks were created in each flyway. (C) Migration history tests were implemented by measuring spatial distances together with the migration history (blue line) or without the migration history (direct spatial distance measurement from Japan to Zhejiang, black line). The hexagon and edges represent the possible network graph of the locations (nodes) in the flyway. The migration routes are illustrated by blue lines.

patterns and represented the major flyways in Asia well. We observed that the contribution of each bird species to the gene flow network was generally consistent with the migration pattern of each species: northern pintail (*A. acuta*) along the EA-1 flyway, swan goose (*A. cygnoides*) along the EA-2 flyway, bar-headed goose (*A. indicus*), and ruddy shelduck (*T. ferruginea*) along the CA flyway. The viral samples used in this study were recovered from most Asian countries in which HPAI H5N1 has been circulating throughout the last decade (31, 32). Because isolates from wild birds constituted a large proportion of the total samples, these viral samples provide a good opportunity to estimate the relationship between the transmission patterns of HPAI H5N1 and bird flyways (SI Appendix, Fig. S10).

Several important limitations of the present analysis should be noted. First, satellite tracking data on wild bird migrations were not available for some areas located along the flyways, in particular in Southeast Asia, where H5N1 is known to be endemic. Second, the birds' behavior and migration routes might have been affected by the solar-powered GPS trackers. Third, all of the isolates from clades 2.3.2 from Southeast Asia and Yunnan, Guangxi, and Guizhou Provinces in China were taken from poultry samples (SI Appendix, Fig. S10) and showed a close genetic association, so they were excluded from the analysis. Fourth, information on the sampling locations of the isolates from Mongolia was unavailable, and the potential habitats of the birds were scattered across different locations in the country

(Fig. 1A). Finally, no gene reassortment was considered in the analysis. Gene reassortment may influence the evolutionary rate of the virus and therefore affect the performance of our models. Furthermore, the rates of sequence evolution were insensitive to coalescent models among the branches of the clade 2.3.2 viruses (SI Appendix, Table S6). Future surveillance efforts should include more frequent and geographically extensive sampling of HPAI H5N1 to improve our knowledge of the association between the spread of the H5N1 virus and bird migration (33).

It has been suggested that the poultry trade, illegal bird trade, and wild bird smuggling may play important roles in the global dispersal of H5N1 (34–36). Therefore, bird migration networks may not be the only route by which H5N1 is transmitted (17). As shown in SI Appendix, Fig. S11, the isolates from wild birds constituted only 20% of the samples isolated along the Asia flyways (SI Appendix, Table S7), and the bird migration network was not the optimal network explaining the patterns of gene flow for all clades. Therefore, we infer that the bird migration network may not be the main route of dispersal for all of the clades, but is one of several underlying transmission networks. Moreover, although some of the H5N1 viruses were isolated from wild birds, their presence may have been the immediate result of a previous outbreak in poultry, and vice versa. This bias is inevitable because of the current sampling strategy. In our analysis, we considered isolates from poultry and from H5N1 outbreaks in poultry based on the most reasonable assumption. However, to address the uncertainties in the model, we require a better surveillance strategy in future studies.

Our results indicate that the transmission of HPAI H5N1 is strongly associated with bird migrations. This calls for increased collaboration between the countries located along the same flyways. Based on the complex dynamics of viral transmission identified in this study, we suggest that future efforts to control HPAI H5N1 should not only include regional surveillance, but

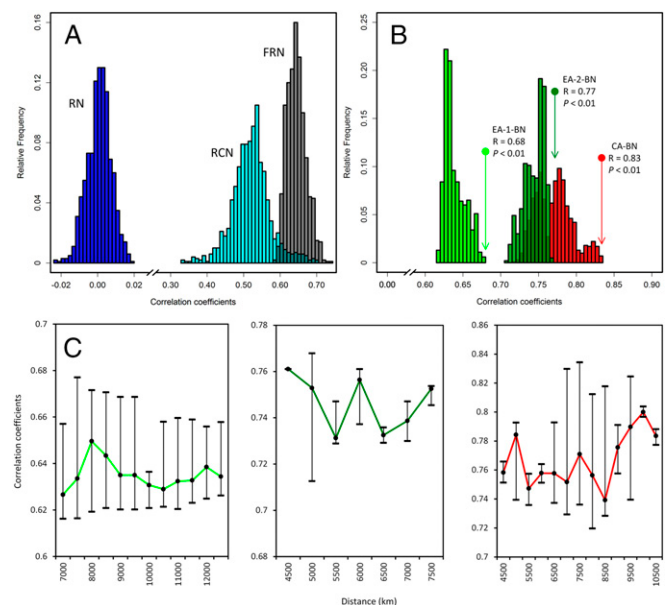


Fig. 5. Correlation of the gene flow network with randomly generated networks of HPAI H5N1 clade 2.3.2. (A) Histogram of the correlation coefficients; blue bars represent the purely random network model, cyan bars represent the random categorized network model, and gray bars are flyway-based random networks. (B) Histogram of the correlation coefficients for the flyway-based random networks and bird migration networks: green, East Asian–Australasian 1 flyway (starting at Hong Kong); dark green, East Asian–Australasian 2 flyway (starting at Poyang Lake); and red, Central Asian flyway. Each test is based on 1,000 random networks. (C) Correlation coefficients for each flyway-based network against the total perimeter of the network. Box indicates the maximum and minimum range; black point represents the median.

Table 2. Randomization test and bird migration results for the network contribution to patterns of HPAI H5N1 gene flow

Model	Migration history	R	P	R mean	R SD
RN*	With	—	—	0.01	0.01
FRN†	With	—	—	0.69	0.01
RCN	With	—	—	0.52	0.05
EA-1-RN*	With	—	—	0.64	0.01
EA-1-BN†	With	0.68	<0.01	—	—
EA-1-BN*	Without	0.64	<0.01	—	—
EA-2-RN*	With	—	—	0.74	0.01
EA-2-BN†	With	0.77	<0.01	—	—
EA-2-BN*	Without	0.76	<0.01	—	—
CA-RN*	With	—	—	0.77	0.02
CA-BN†	With	0.83	<0.01	—	—
CA-BN*	Without	0.80	<0.01	—	—

RN, random network; FRN, flyway random network; EA, East Asian-Australasian flyways; EA-1, the migration started at Hong Kong; EA-2, the migration started at Poyang Lake; CA, Central Asian flyways; RCN, randomly categorized network; BN, bird migration network. Migration history, measuring spatial distance with or without migration history. R is the spatial-genetic correlation coefficient, mean is the average R value, and SD is the SD of 1,000 random networks.

*Randomization tests, virus transmission was assumed to follow a random network.

†Migration network tests, virus transmission was assumed to follow the bird migration network.

*Migration history tests, virus transmission was assumed without migration history (Fig. 4C), but the cycle length of network was included.

that flyway-based strategies should be implemented, involving all of the countries affected by potential HPAI H5N1 outbreaks. A similar effort is also required to coordinate preventive and intervention strategies, to improve vaccination and prevent nonuniform vaccination policies, which could result in the silent spread of the virus. Vaccination is a key component in the control of HPAI H5N1 in China, Vietnam, and Egypt. However, it seems that such strategies produce unpredictable results (37, 38). Both the evolutionary rates of the virus and the number of positively selected sites were higher in virus populations in countries using an avian influenza vaccine for H5N1 (39). Furthermore, the H5N1 virus can replicate in clinically healthy vaccinated birds (37). Therefore, it is likely that the selection pressure resulting from vaccination influences the viral ecology in countries located along the migratory flyways.

Materials and Methods

Data Collection. The HPAI H5N1 outbreak data were obtained from the Food and Agriculture Organization of the United Nations and the World Organization for Animal Health. The information included the dates and locations of outbreaks, and the host species. The records from both sources were combined and all duplicate reports were removed. Our database contains information on 17,250 independent outbreaks, collected between December 2003 and April 2012 in Asia. Although this dataset contains the most comprehensive outbreak records available, some outbreaks may have gone unreported because a passive surveillance system was used.

The satellite tracking data on wild bird migrations along the EA flyways and CA flyway were collected by the United States Geological Survey. There are four stages in the annual cycles of migratory birds: nonbreeding, spring migration breeding, postbreeding, and autumn migration. The annual cycles are reflected in the time series data. We selected four species of birds as representative of the migrations that occur in the study area: the northern pintail (*A. acuta*), swan goose (*A. cygnoides*), ruddy shelduck (*T. ferruginea*), and bar-headed goose (*A. indicus*) (SI Appendix, Table S1). This choice was based on the population abundances in the study area, the type of clinical symptoms displayed when infected with the HPAI H5N1 virus, and the birds' virus shedding capacities (14, 40, 41). The arrival dates, departure dates, and flight durations between locations were extracted from the GPS tracking data for each bird species (provided in SI Appendix, Table S3).

The nucleotide sequences of HPAI H5N1 were obtained from the GenBank database, hosted by the National Center for Biotechnology Information, on October 31, 2012 (42). All segments were aligned using the default settings

in MUSCLE v3.5 (43). The dataset sizes were as follows: HA, $n = 2,379$ (alignment length of 1,656 nucleotides); NA, $n = 196$ (1,410 nt); PB2, $n = 196$ sequences (2,277 nt); PB1, $n = 194$ (2,271 nt); PA, $n = 196$ (2,148 nt); NP, $n = 196$ (1,494 nt); MP, $n = 200$ (982 nt); and NS, $n = 196$ (838 nt). The 142 H5N1 sequences were combined with the nucleotide sequences (excluding partial sequences <70% of the full-length sequence) of all influenza A viruses available in GenBank. The final numbers of sequences of the H5N1 viruses for the EA flyways and CA flyway are given in SI Appendix, Table S2.

Each H5N1 sequence was assigned a geographic area according to its province/country of isolation (SI Appendix, Tables S3 and S4). The spatial distance between each pair of countries/provinces was calculated from the latitude and longitude of each state/province center. We collected and analyzed 297 sequences of viruses from clades 2.3.2 that were isolated in 2003–2012 (Fig. 1B) in these regions (Fig. 1C), including China ($n = 120$), Bangladesh ($n = 15$), India ($n = 7$), Japan ($n = 41$), Laos ($n = 6$), Mongolia ($n = 21$), Nepal ($n = 10$), the Republic of Korea ($n = 39$), and Vietnam ($n = 38$). The sequences from China were categorized according to locations (Fig. 1B).

Phylogenetic Analysis. Neighbor-joining trees of the H5N1 HA sequences were constructed using a GTR + I + Γ_4 model in PAUP v4.0b10 (44). The best nucleotide substitution model was selected with the Akaike information criterion and a hierarchical likelihood ratio test in ModelTest (45, 46). To assess the robustness of the tree topology, a set of 100 pseudoreplicates was generated and used in bootstrap analyses with the maximum likelihood (ML) method implemented in PHYML (47) and the neighbor-joining method implemented in PAUP v4.0b10. These trees were highly congruent to those produced with PAUP above. The sequences associated with clades 2.3.2 were included in our analyses (SI Appendix, Table S2).

Estimates of Viral Migration Through Discrete Geographic Regions. We used a nonreversible continuous-time Markov chain model to estimate the migration rates between regions along flyways and the general patterns of regional circulation of the H5N1 virus. This analysis was restricted to the six geographic regions identified above. In this analysis, the constant size, exponential growth, and Bayesian skyline coalescent prior were used with a strict and uncorrelated lognormal relaxed molecular clock, and a general time-reversible (GTR) nucleotide substitution model in BEAST v2.1 (48). The performance of each combination was compared using BFs (SI Appendix, Table S6) (49). We performed three independent analyses of 50–100 million generations. These analyses were combined after the removal of an appropriate burn-in (10–20% of the samples in most cases), with 5,000 generations sampled from each run for a total of 15,000 trees and parameter estimates.

BSSVS was used to infer the phylogeographic diffusion processes under a parsimonious scenario (50). BSSVS searches for the transition rates that are zero, depending on the evidence in the data, and efficiently infers the ancestral locations (51). For the BSSVS, we assumed a Poisson prior, which assigns a 50% prior probability to the minimal rate configuration. A mean Poisson prior of 0.693 was used in this analysis (50, 52). The binary indicator (I) and BF were used to explore the state space. If the rate is zero, it is impossible to directly diffuse from one location to another. The BF test was used to determine which diffusion links were statistically significant based on the standard BSSVS protocol (49).

The supported state transitions of gene segments were recovered from the independent Bayesian analyses, which indicated the potential persistence of a virus in a metapopulation mixing between geographic regions. The viral migration network was jointly estimated from all eight gene datasets in a single analysis even though the taxon number for each gene dataset was not identical (53). Within-flyway rate estimates were compared with between-flyway rate estimates to measure the viral diffusion patterns. To investigate any possible bias arising from the uneven sample sizes at each location, we performed a sensitivity test using increasingly larger random subsets of isolates (from 50%, 60%, 70%, and 80–90% of the original dataset) throughout the BSSVS procedure, with 50 replicates for each gene (SI Appendix, Table S8).

Network Analyses to Determine Viral Gene Flow and Migration. Under the assumption that viruses circulate across a fixed network with a mutation rate-drawn from an underlying normal distribution (estimated with BEAST), then the spatial distance measured in the migration history could reflect the genetic distance between all possible pairs of viral samples in the network. Also, the differences in sampling times among the same or distinct localities can be transformed into the number of viral spread cycles within the network (SI Appendix, SI Materials and Methods, and Eq. S3). The GTR + I + Γ_4 substitution model was used to estimate the pairwise genetic distances between sequences, and the possibly underestimated migration distances of the ancestral virus were identified and were not included (SI Appendix, SI Materials and Methods, and Fig. S12).

Phylogeographic models were constructed to determine the extent of the viral gene flow that was influenced by bird migration and to explore the ML transmission network, based on the assumption that the data arise from an underlying migration process along an unobserved network. Our model can be described as follows: (i) A thousand RN models incorporate all of the sampling locations in a homogenous network. FRN models incorporate all of the locations within an existing flyway, either CA or EA, according to their sampling locations. All of the scenarios of viral migration between flyways, including the east-west migration paths between Mongolia and northeast Asia, and Qinghai and southern China are considered to display viral migration between the EA and CA flyways, due to the fact that the flyways intersect in this region. Randomly categorized networks (RCNs), incorporate localities that were randomly categorized into any of the flyways, regardless of their actual sampling locations, but corresponding to the number of locations along the EA and CA flyways. (ii) Random networks were created to find the best-fitting network for each flyway, which best explained the pattern of gene flow, and then compared with the bird migration network. A total of 1,000 RNs were created in each flyway, as for the FRN and RCN model, but the EA flyway was divided into the EA-1 flyway (starting at Hong Kong) and EA-2 flyway (starting at Poyang Lake). The spatial distances were considered as the routines of bird migration within flyway (Fig. 4A). (iii) Spatial distances, using direct measurements (simple measurements of spatial distances between strains in which the viral migration history was not considered) or measurements with the migration history (the spatial distance traveled by

the viral ancestors is summed), were compared between geographic locations in the FRN model. All networks were one directional and each node was passed only once.

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Supporting Information Appendix

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SI Materials and Methods

Geographical and avian species information

Each HPAI H5N1 virus sequence was assigned a discrete geographical state according to its province/country of isolation. The East Asian-Australasian flyway includes China (Guangdong, Guangxi, Guizhou, Hunan, Hubei, Hong Kong, Shantou, Shanghai, Yunna, Zhejiang), Japan, Republic of Korea, Mongolia. The Central Asian flyway includes India, Nepal, Bangladesh, China (Qinghai Lake), Mongolia.

Hosts were classified according to the list of species affected by H5N1 avian influenza from the U. S. Geological Survey National Wildlife Health Center. Each of gene was examined from its source of article (1-28).

Migratory bird data

The satellite tracking data on wild bird migration along East Asian-Australasian Flyway and Central Asian Flyway was collected from United States Geological Survey (USGS). We distinguished four stages in migratory birds' annual cycle: nonbreeding, spring migration breeding–post breeding and autumn migration. Considering the population in study area, the clinical symptoms after infected by HPAI H5N1 virus and the capability of shedding viruses, we have chosen four major species groups of wild birds in our data set: Northern Pintail (*Anas acuta*), Swan Goose (*Anser cygnoides*), Ruddy Shelduck (*Tadorna ferruginea*) and Bar-headed

Goose (*Anser indicus*) (Table S1). We extracted arrival and departure date in each location of each bird. Then the flight time between locations of different species was calculated (Table S2).

Arrival and departure date in each location of each bird was extracted. The flight time from A region to B region is defined as the average of the longest time difference and the shortest time difference between locations.

$$D_L = T_{(d,B)} - T_{(a,A)} \quad [S1]$$

$$D_S = T_{(a,B)} - T_{(d,A)} \quad [S2]$$

Where D_L is the longest time difference, $T_{(d,B)}$ is the departure date in B region, $T_{(a,A)}$ is the arrival data in A region. D_S is the shortest time difference, $T_{(a,B)}$ is the arrival data in B region, $T_{(d,A)}$ is the departure date in A region.

Wavelet Approach

A wavelet analysis was used to investigate and quantify the temporal evolution of time series with different rhythmic components (29, 30). The wavelet transform decomposes signals over dilated and translated functions, the “mother wavelet”, which can be expressed as the function of two parameters: the time position and the scale of the wavelets relative to the frequency. A phase analysis was used to

characterize the association between signals, which can show whether the presence of a particular frequency at a given time in the disease corresponds to the presence of that same frequency at the same time. The phase angle difference can provide information on the sign of the relationship or the time lag separating the disease and climate series. Wavelet coherence allows us to quantify the statistical relationships between two time series (signals), which can provide local information about where two nonstationary signals are correlated in a particular period. The phase angle difference can then provide information on the sign of the relationship, or on the time lag separating the two time series (31).

Here, a wavelet coherence analyses was performed to quantify the statistical association between the national (or provincial for China) H5N1 outbreak time series located within each flyway. The wavelet coefficients, corresponding to periods ranging from 0.8 to 1.2 years, were used to reconstruct filtered time series corresponding to the annual outbreaks in each country (or province for China). The phase difference was also used to determine the order in which successive districts were affected by the annual epidemic and to evaluate the instantaneous temporal lag between epidemics at different locations (32). All significance levels were based on 1000 bootstrapped series. We performed all the analyses in Matlab (version 6.5, MathWorks, Natick, MA, USA).

Estimates of Viral Migration through Discrete Geographic Regions

We used a non-reversible continuous-time Markov chain model to estimate the migration rates between regions along flyways and the general patterns of regional circulation of the H5N1 virus. This analysis was restricted to the six geographic regions identified above. In this analysis, the constant size, exponential growth, and Bayesian skyline coalescent prior were used with a strict and uncorrelated lognormal (UCLN) relaxed molecular clock, and a general time-reversible (GTR) nucleotide substitution model in BEAST v2.1 (33). The performance of each combination was compared using Bayes factors (BFs; Table S6) (34). We performed three independent analyses of 50–100 million generations. These analyses were combined after the removal of an appropriate burn-in (10%–20% of the samples in most cases), with 5,000 generations sampled from each run for a total of 15,000 trees and parameter estimates.

BSSVS was used to infer the phylogeographic diffusion processes under a parsimonious scenario (35). BSSVS searches for the transition rates that are zero, depending on the evidence in the data and efficiently infers the ancestral locations (36). For the BSSVS, we assumed a Poisson prior, which assigns a 50% prior probability to the minimal rate configuration. A mean Poisson prior of 0.693 was used in this analysis (35, 37). The binary indicator (*I*) and BF were used to explore the state space. If the rate is zero, it is impossible to directly diffuse from one location to another. The BF test was used to determine which diffusion links were statistically significant based on the standard BSSVS protocol (34). To assess the influence of this

prior choice, a sensitivity analysis with respect to larger Poisson prior means was performed.

The supported state transitions of gene segments were recovered from the independent Bayesian analyses, which indicated the potential persistence of a virus in a metapopulation mixing between geographic regions. The viral migration network was jointly estimated from all gene datasets in a single analysis even though the taxon number between each gene dataset was not identical (38). Isolates from Mongolia showed genetic association with both EA and CA groups, besides flyways intersect in this region. The east-west migration paths between Mongolia and northeast Asian, Qinghai and South China, were considered as viral migration between EA and CA flyways. Within-flyway rate estimates were compared with between-flyway rate estimates to measure the viral diffusion patterns. To investigate any possible bias arising from the uneven sample sizes at each location, we performed a sensitivity test using increasingly larger random subsets of isolates (from 50%, 60%, 70%, 80% to 90% of the original dataset) throughout the BSSVS procedure, with 50 replicates for each gene.

Virus Gene Flow and Migration Analyses

We assumed that if the virus circulated and spread across a fixed network, and the mutation rates are drawn from an underlying normal distribution (estimated with BEAST), then the spatial distance measured with migration history could reflect its

genetic distance between all possible pairs of viral samples in the network, and the difference in sampling time among the same or distinct localities can be transformed into the number of viral spread cycles within the network (*SI Appendix, Materials*). The GTR + I + Γ_4 substitution model was employed to estimate the pairwise genetic distances between sequences.

To characterize the differences in rates of nucleotide substitution per site and per year across the tree, the BEAST program that employs Bayesian Markov chain Monte Carlo (MCMC) approach (39) was used. Model selection analyses were first undertaken to select a statistically appropriate evolutionary model. The Constant size, Exponential growth and Bayesian skyline coalescent prior were utilized with the strict and uncorrelated lognormal (UCLN) relaxed molecular clocks, the general time-reversible (GTR) nucleotide substitution model. We performed three independent analyses of 50 to 100 million generations. These analyses were combined after the removal of an appropriate burn-in (10–20% of the samples in most cases), with 5,000 generations sampled from each run for a total of 15,000 trees and parameter estimates. Then the relationship was computed as:

$$D_{ij} = (t_i - t_j) \times d_{\text{cycle}} + d_{ij, \text{migration}} \quad [\text{S3}]$$

$$G_{ij} = \frac{D_{ij}}{v} \times E_{ij} \quad [\text{S4}]$$

Where G_{ij} is the genetic distance between the sequence i and j , D_{ij} represent the spatial distance measured with migration history between sampling location of the virus i and j . E is the evolutionary rate that followed a normal distribution, v is the spread velocity. And t is the sampling time, d_{cycle} and $d_{ij,migration}$ represent cycle length of network and the spatial distance measured with migration history of sampling location, respectively. The pairwise genetic distance which is larger than the maximum possible divergence for virus isolated within one year along flyways were not included due to a possible underestimated migration distance of ancestral virus. The results indicated that the possible underestimated migration distance take account for 5.10% (642/12585) among pairwise distances for viral samples along the three flyways (Fig. S12).

Phylogeographic models were constructed to determine the extent of the viral gene flow that was influenced by bird migration and to explore the ML transmission network, based on the assumption that the data arise from an underlying migration process along an unobserved network. (i) A thousand random network models (RN; incorporating all the sampling locations as a homogenous network), flyway random network models (FRN; incorporating all the locations within an existing flyway according to their real sampling locations, either CA or EA, and including the scenarios of viral migration between flyways, the east–west migration paths between Mongolia and northeast Asia, and Qinghai and southern China are considered to show viral migration between the EA and CA flyways, due to the flyways intersect in this

region), and randomly categorized networks (RCN; in which localities were randomly categorized into any of the flyways, regardless of their real sampling locations, corresponding to the number of locations in EA and CA flyways) were generated. (ii) Random networks were created to find the best-fitting network for each flyway, which best explained the pattern of gene flow, and then compared with the bird migration network. A total of 1000 RNs were created in each flyway, as for the FRN and RCN model, but the EA flyway was divided into the EA-1 flyway (starting at Hong Kong) and EA-2 flyway (starting at Poyang Lake). The spatial distances were considered as the routines of bird migration among flyway (Fig. 4A). (iii) Spatial distances, using direct measurements (simple measurements of spatial distances between strains in which the viral migration history was not considered) or measurements with the migration history (the spatial distance travelled by the viral ancestors is summed), were compared between geographic locations in the FRN model. All networks were one directional and each node was passed only once.

Sample size of random network determination

There are a huge number of possible networks by random combination. It is difficult to analyze all the possible scenarios and, on the other hand, too small samples may lead to inaccurate prediction. Therefore, a proper sample size of random networks is of great significance for inferring the distribution. In the present study, the sample size n was computed as:

204

$$n = \left[\frac{Z_{\alpha/2} \sigma}{E} \right]^2 \quad [S5]$$

205

206 Where E is the margin of error and σ is the population standard deviation. Z represents

207 the critical value, the positive Z value that is at the vertical boundary for the area of

208 $\alpha/2$ in the right tail of the standard normal distribution.

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- 293 38. Bahl J, *et al.* (2013) Influenza A virus migration and persistence in North American wild
294 birds. *PLoS Pathog* 9(8):e1003570.
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SI Figures

Number of outbreaks

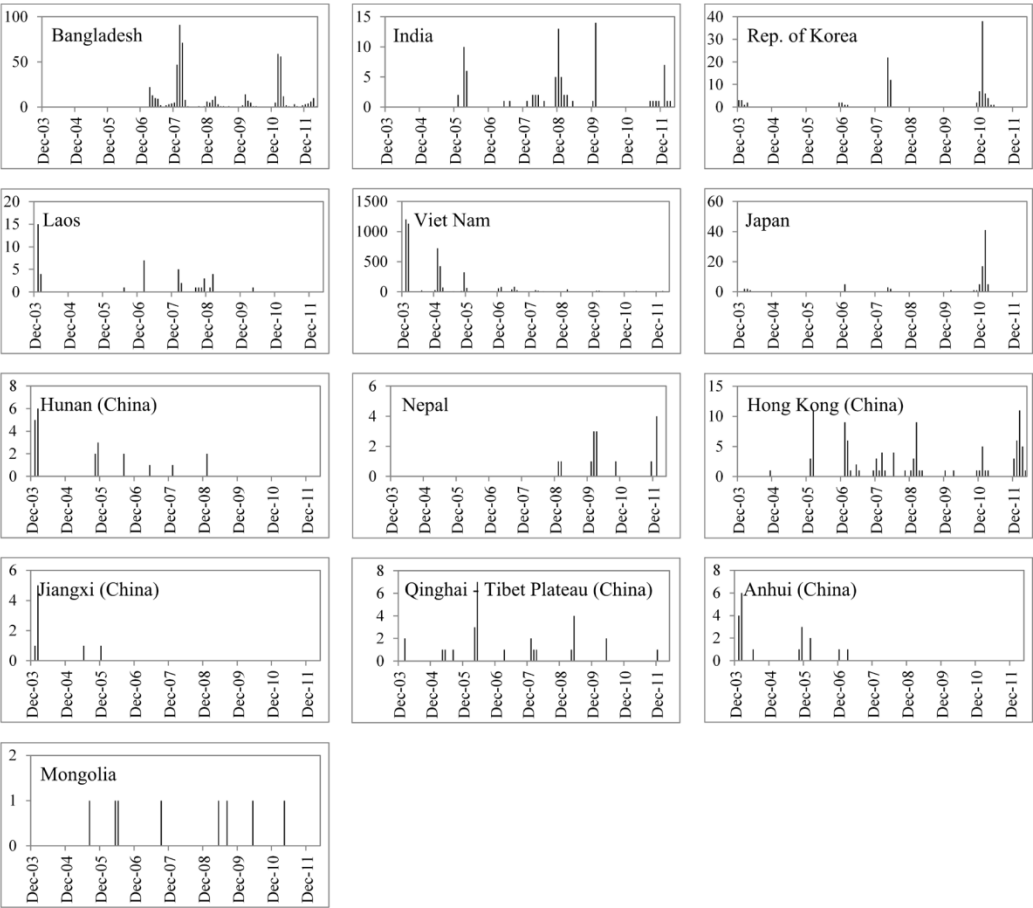
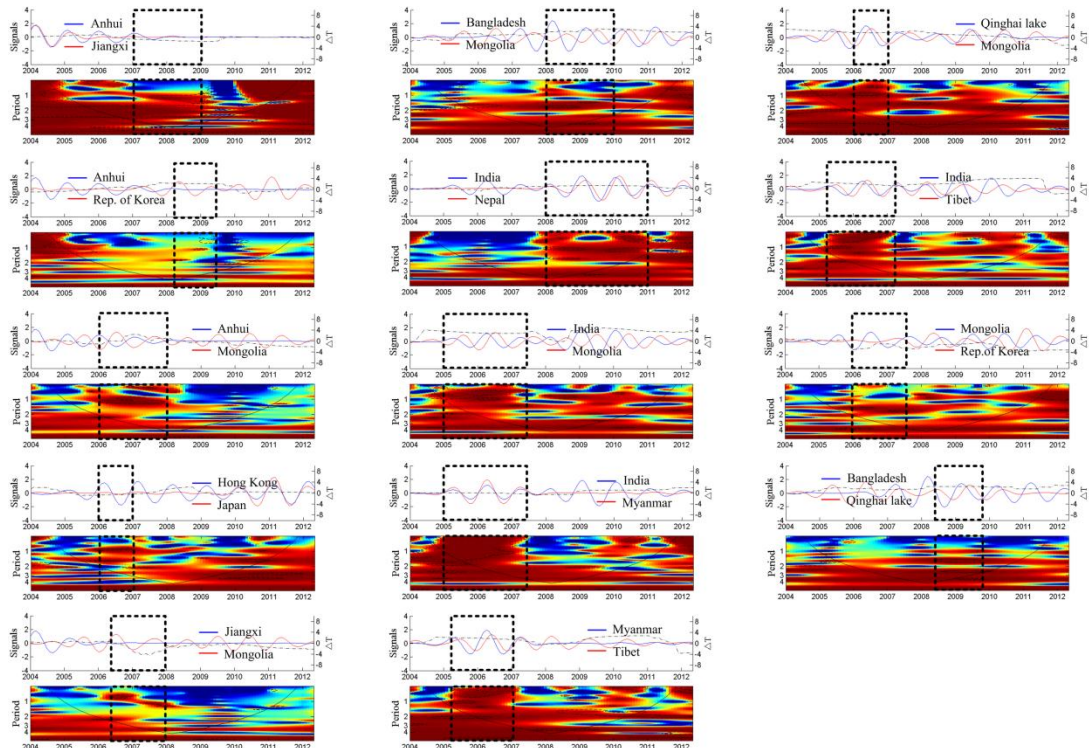


Fig. S1. Monthly H5N1 outbreaks of countries or areas in flyway, 2003-2012

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310 **Fig. S2.** Filtered incidence and phase differences between epidemics at different
 311 locations along the same flyways. The incidence series are square root transformed,
 312 and all series are normalized. Phase evolutions computed in the 0.8-1.2-y period band.
 313 In the coherence power spectra (x-axis: time in year; y-axis: period in year), power is
 314 coded from low value, in dark blue, to high value, in dark red. The black dashed lines
 315 shows 5% significance level, computed on 1,000 bootstrapped series. The inner area,
 316 within the cone of influence (black line), indicates the region not influenced by edge
 317 effects. Black dashed boxes represents the period of time where coherency is
 318 significant, when interpretation of analysis was possible.

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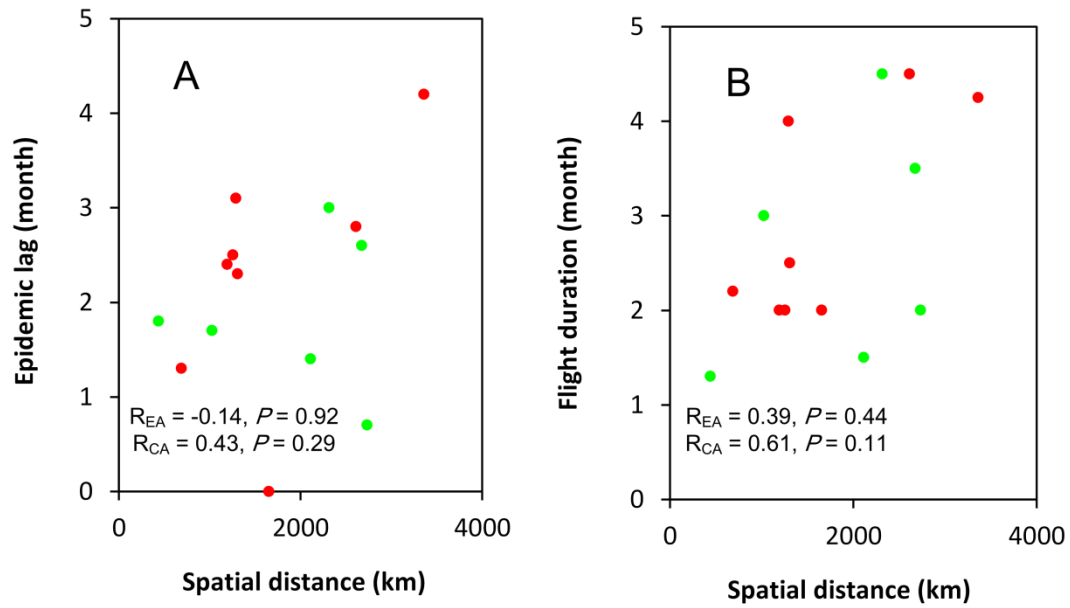


Fig. S3. Temporal relationships between epidemic lag, flight duration, and spatial distance along flyways in Asia. (A) Scatterplot of the mean annual lags between epidemics against the spatial distances between regions. (B) Average flight times during the migration of four bird species (bar-headed goose [*Anser indicus*], swan goose [*Anser cygnoides*], ruddy shelduck [*Tadorna ferruginea*], and northern pintail [*Anas acuta*]) against the spatial distances between regions (green: East Asian–Australasian flyway; red: Central Asian flyway).

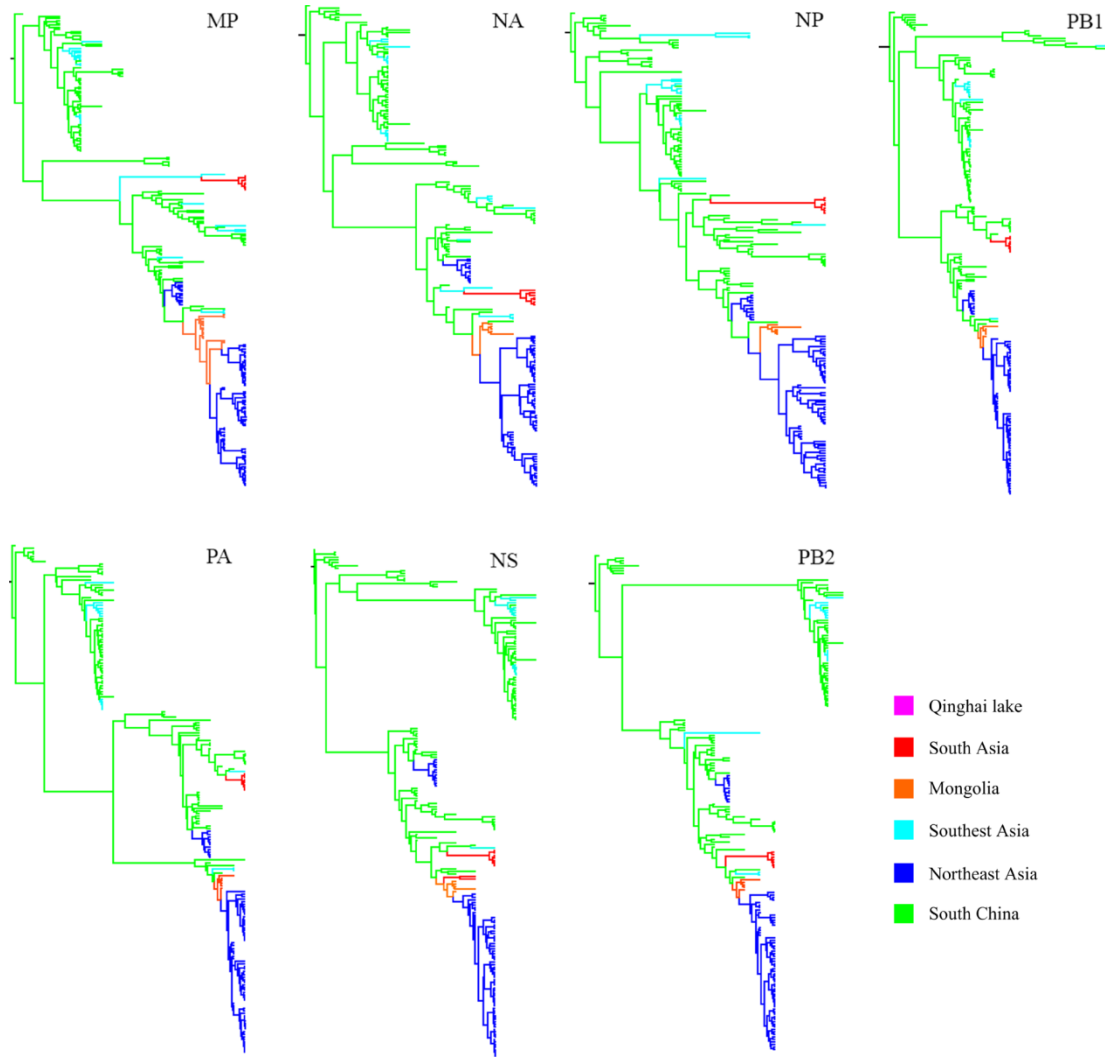


Fig. S4. Temporally structured maximum clade credibility phylogenetic tree showing the genes of the clade 2.3.2 HPAI H5N1 virus, branches are colored according to the place of sampling as shown in the legend box. There are 221, 194, 196, 196, 196, 200, and 196 gene sequences of NA, PB1, PB2, PA, NP, MP, NS separately, were available for reconstruction of the corresponding phylogeny (Table S2), therefore the taxon number between each gene dataset was not identical.

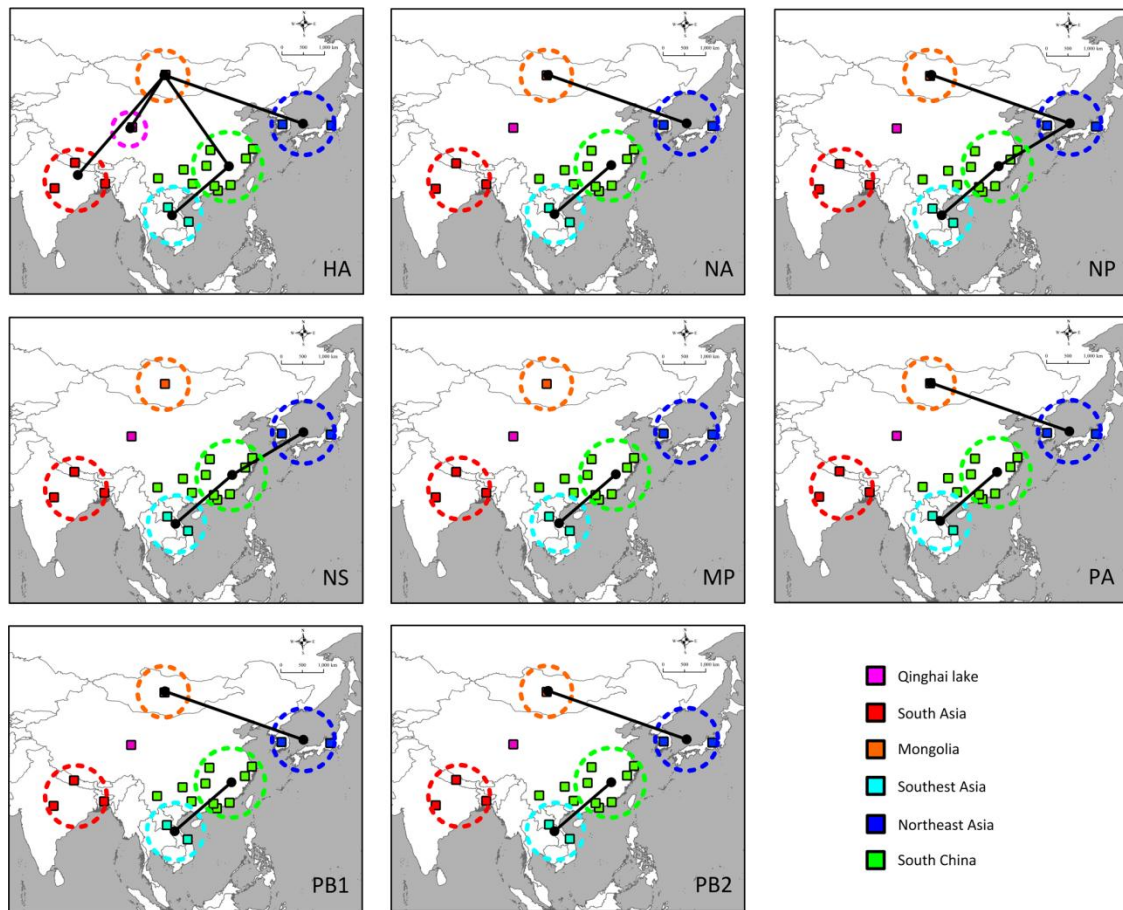


Fig. S5. Supported state transitions of the internal genome segments of clade 2.3.2

HPAI H5N1 virus. Geographic regions are indicated by color.

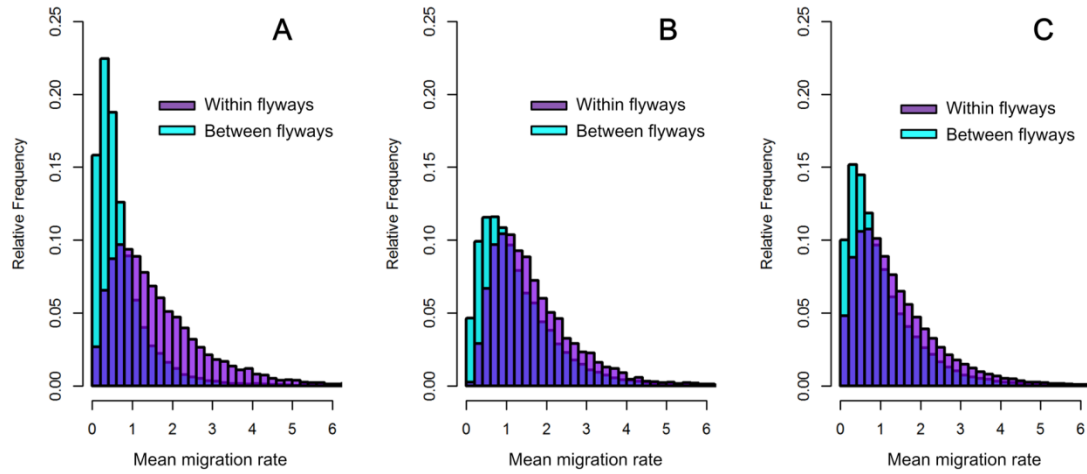


Fig. S6. Density distribution of mean statistically supported migration rates per Markov chain Monte Carlo step; mean within-flyway migration rates and mean between-flyway migration rates jointly estimated from (A) HA, (B) NA, and (C) whole-genome segments.

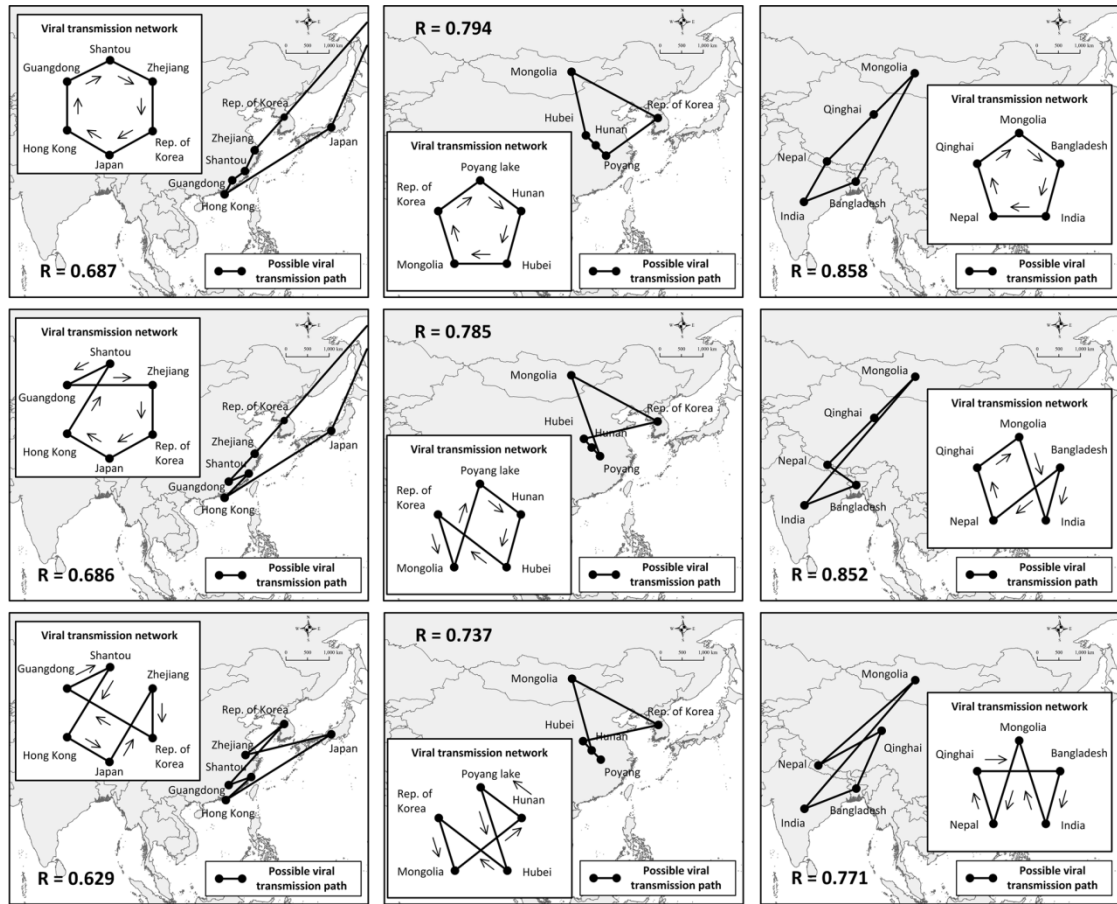


Fig. S7. Comparison of viral transmission networks. Columns of panels show different flyways, the first column plots the East Asian-Australasian-1 (starting from Hong Kong) flyway, the second column plots the East Asian-Australasian-2 (starting from Poyang lake) flyway, and the third column plots the Central Asian flyway. Rows of panels show different networks, the first row plots the possible transmission network, the second row plots the second best transmission network, and the third row plots the networks, with similar perimeter to bird migration network.

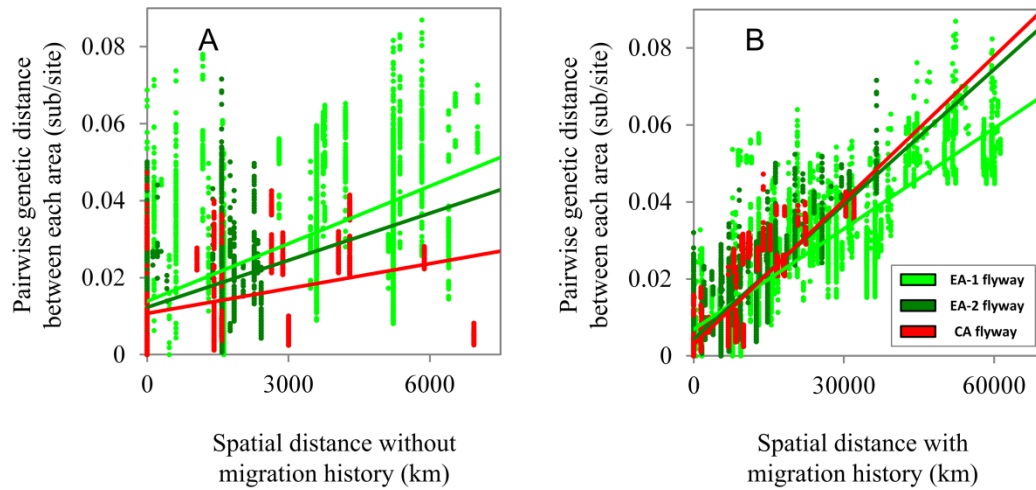


Fig. S8. Spatial–genetic correlation in the spread of H5N1 HPAIV. (A) Pairwise genetic distances for all possible pairs of viral samples versus their spatial distances without migration history and cycle length of network; (B) Pairwise genetic distances for all possible pairs of viral samples versus their spatial distances with migration history in bird migration network. Central Asian (CA, red points), East Asian-Australasian-1 (EA-1, green points) and East Asian-Australasian-2 (EA-2, dark green points) flyways.

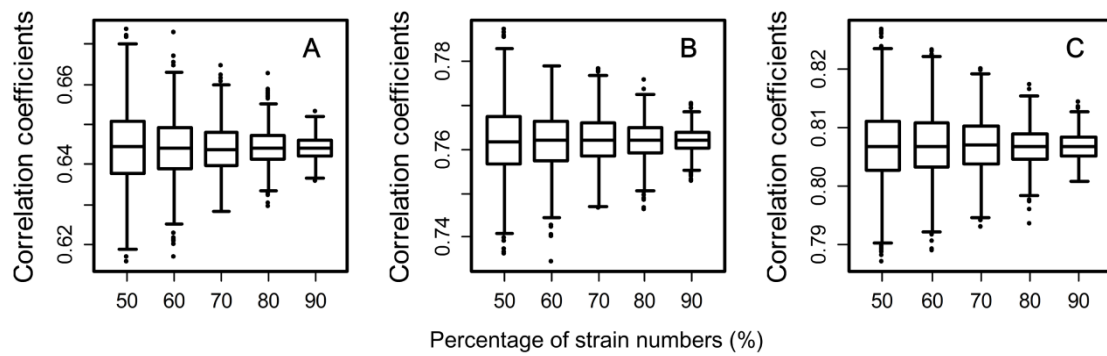


Fig. S9. Spatial–genetic correlation in the spread of H5N1 clade 2.3.2 virus after individual isolates were randomly removed. Variable proportions of isolates were randomly selected to constitute the bird migration network, from which the spatial–genetic coefficient of determination (R^2) was calculated. Each box is based on 1000 replicates. (A) East Asian–Australasian-1 flyway (starting at Hong Kong); (B) East Asian–Australasian-2 (starting at Poyang Lake); (C) Central Asian flyway.

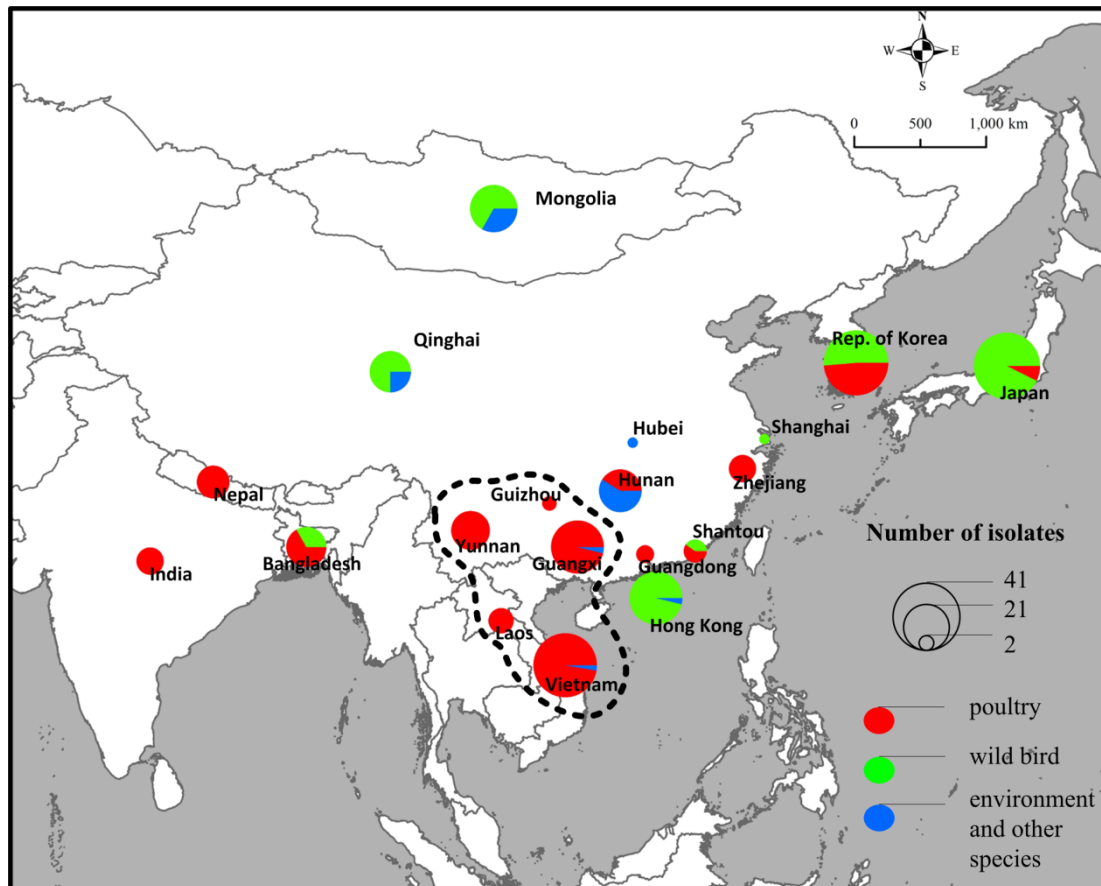


Fig. S10. Geographic sources of clade 2.3.2 HPAI H5N1 virus used in this study.

There was no available satellite tracking data on migration across the area with dashed lines. There were no clade 2.3.2 HPAI H5N1 viruses isolated from wild birds in these areas. Hosts were classified according to the list of species affected by H5N1 avian influenza from the U. S. Geological Survey National Wildlife Health Center. Each of gene was examined from its source of article.

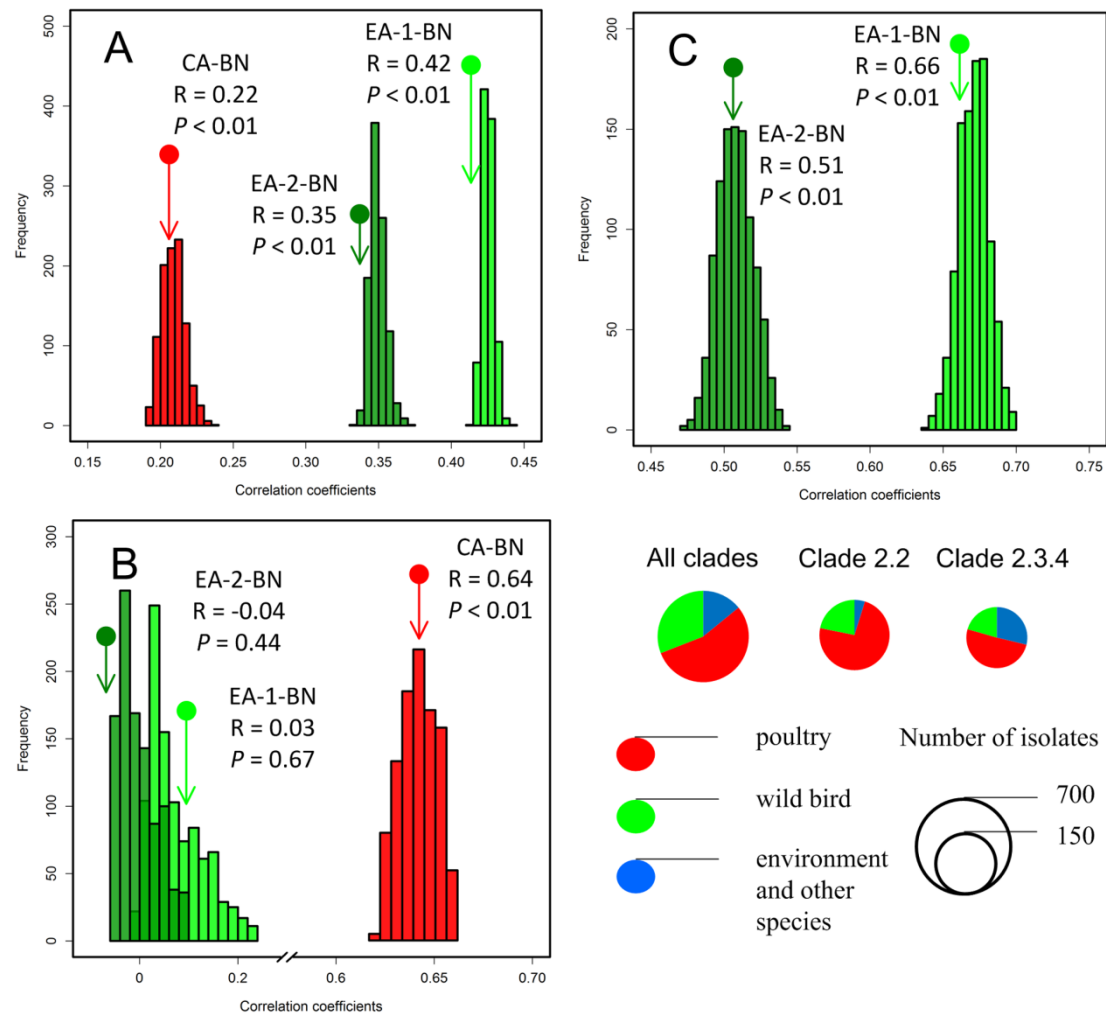


Fig. S11. Correlation of gene flow network with randomly generated networks of (A) all clades, (B) clade 2.2, and (C) clade 2.3.4 virus. Green, dark green and red bars represent East Asian-Australasian-1 (starting from Hong Kong), East Asian-Australasian-2 (starting from Poyang Lake) and Central Asian flyways, respectively. Each test is based on 1000 random networks. Consider the sample size, sample distribution, coverage, clade 2.2 and clade 2.3.4 virus were treated as an independent dataset in FRN analysis. Due to the data limitation, the FRN analysis could not be conducted in clade 2.3.4 virus in CA flyway.

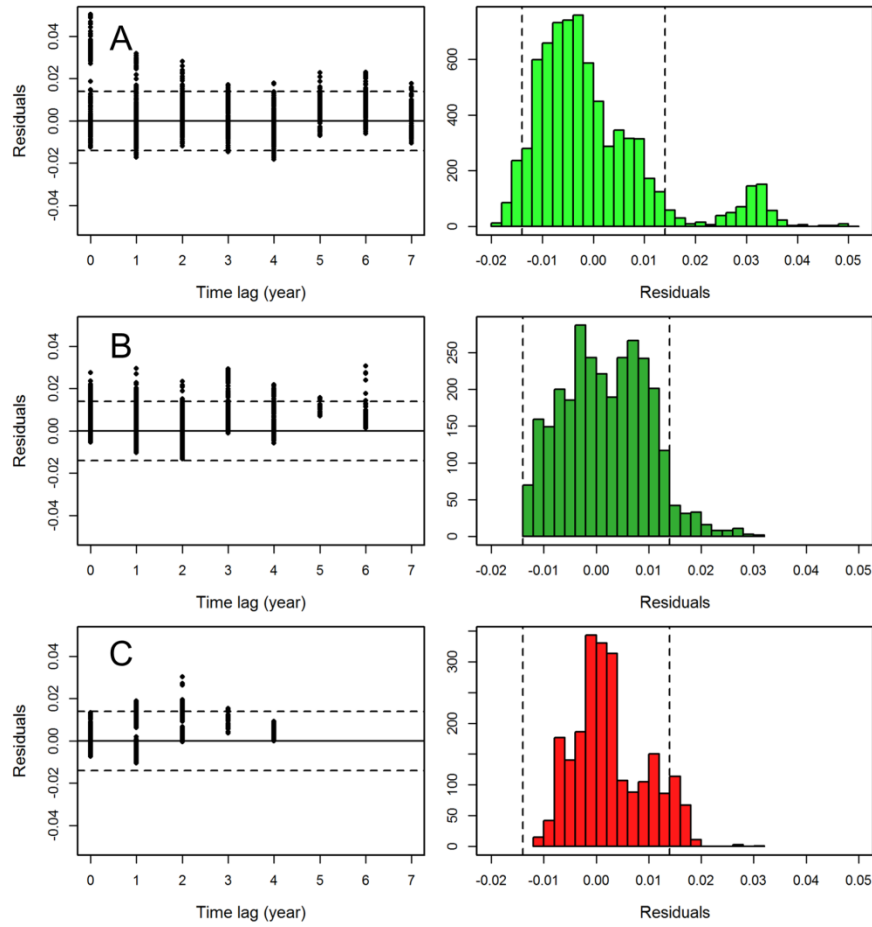


Fig. S12. Residuals of pairwise genetic distances for virus isolated along flyways through different time lengths. The dot lines indicated 95% upper limit of mutation rate inferred by BEAST. (A) Residuals of pairwise genetic distances for virus isolated between years along East Asian-Australasian-1 flyway (Hong Kong started); Histogram of residuals are shown to the right of the scatter plot. (B) Residuals of pairwise genetic distances for virus isolated between years along East Asian-Australasian-2 (Poyang lake started). (C) Residuals of pairwise genetic distances for virus isolated between years along Central Asian flyways.

410 **SI Tables**

411 **Table S1. Species of satellite-tracked birds.**

Species	Latin name	Data source	Time	Flyway
Bar-headed Goose	<i>Anser indicus</i>	USGS	2007-2012	Central Asian Flyway
Swan Goose	<i>Anser cygnoides</i>	USGS	2006-2010	East Asian-Australasian Flyway
Ruddy Shelduck	<i>Tadorna ferruginea</i>	USGS	2007-2012	Central Asian Flyway
Northern Pintail	<i>Anas acuta</i>	USGS	2007-2012	East Asian-Australasian Flyway

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415 **Table S2. Sequences used in this study, clade 2.3.2 and clade 2.3.2.1**

Virus	GenBank Accession Number							
	HA	NA	PB1	PB2	PA	NP	MP	NS
A/duck/China/E319-2/03	AY518362	AY518363	AY518366	AY518367	AY518365	AY518364	AY518361	AY518360
A/Ph/ST/44/2004	AY651366	AY651478	AY651700	AY651756	AY651645	AY651533	AY651426	AY651590
A/chicken/Guangdong/178/04	AY737296	AY737299	AY737294	AY737293	AY737295	AY737297	AY737298	AY737300
A/chicken/Guangxi/2448/2004	DQ320894	DQ321026	DQ321289	DQ320828	DQ321223	DQ321091	DQ320960	DQ321157
A/chicken/Guangxi/2461/2004	DQ320895	DQ321027	DQ321290	DQ320829	DQ321224	DQ321092	DQ320961	DQ321158
A/grey_heron/Hong_Kong/728/2004	DQ320923	DQ321055	DQ321318	DQ320857	DQ321252	DQ321120	DQ320989	DQ321186
A/grey_heron/Hong_Kong/837/2004	DQ320924	DQ321056	DQ321319	DQ320858	DQ321253	DQ321121	DQ320990	DQ321187
A/silky_chicken/Shantou/475/2004	CY028961	CY029260	CY029257	CY029256	CY029258	CY029259	CY029261	CY029262
A/duck/Guangdong/23/2004	HM172116	HM172210	HM172387	HM172432	HM172321	HM172230	HM172140	HM172300
A/duck/Guangxi/351/2004	DQ320877	DQ321009	DQ321272	DQ320811	DQ321206	DQ321074	DQ320943	DQ321140
A/duck/Guangxi/380/2004	DQ320878	DQ321010	DQ321273	DQ320812	DQ321207	DQ321075	DQ320944	DQ321141
A/Chicken/Shantou/810/05	DQ095626	DQ095666	DQ095746	DQ095766	DQ095726	DQ095686	DQ095646	DQ095706
A/Chinese_pond_heron/Hong_Kong/18/2005	DQ320925	DQ321057	DQ321320	DQ320859	DQ321254	DQ321122	DQ320991	DQ321188
A/Owston'scivet/Vietnam/1/2005	EF124794	EF124796	EF124800	EF124801	EF124799	EF124797	EF124795	EF124798
A/Quail/Shantou/911/05	DQ095627	DQ095667	DQ095747	DQ095767	DQ095727	DQ095687	DQ095647	DQ095707
A/chicken/Guangdong/1/2005	EU874899	EU874900	EU874903	EU874902	EU874897	EU874898	EU874901	EU874904
A/chicken/Guangxi/3154/2005	DQ992718	EF124279	EF123977	DQ992651	EF124732	EF124430	EF124128	EF124581
A/chicken/Guangxi/3791/2005	DQ992724	EF124285	EF123983	DQ992657	EF124738	EF124436	EF124134	EF124587
A/chicken/Guangxi/604/2005	DQ320898	DQ321030	DQ321293	DQ320832	DQ321227	DQ321095	DQ320964	DQ321161
A/chicken/Guiyang/2147/2005	DQ992751	EF124210	EF123908	DQ992582	EF124663	EF124361	EF124059	EF124512
A/chicken/Guiyang/2173/2005	DQ992752	EF124211	EF123909	DQ992583	EF124664	EF124362	EF124060	EF124513
A/chicken/Viet_Nam/10/2005	CY016867	CY016869	CY016873	CY016874	CY016872	CY016870	CY016868	CY016871
A/chicken/Viet_Nam/14/2005	EF535027	--	--	--	--	--	--	--
A/chicken/Viet_Nam/17/2005	CY017059	CY017061	CY017065	CY017066	CY017064	CY017062	CY017060	CY017063
A/duck/Yunnan/4400/2005	DQ992797	EF124293	EF123991	DQ992665	EF124746	EF124444	EF124142	EF124595
A/duck/Yunnan/4589/2005	DQ992799	EF124295	EF123993	DQ992667	EF124748	EF124446	EF124144	EF124597
A/duck/Yunnan/5251/2005	DQ992803	EF124213	EF123911	DQ992585	EF124666	EF124364	EF124062	EF124515
A/duck/Yunnan/5820/2005	DQ992806	EF124214	EF123912	DQ992586	EF124667	EF124365	EF124063	EF124516
A/duck/Yunnan/5877/2005	DQ992807	EF124297	EF123995	DQ992669	EF124750	EF124448	EF124146	EF124599
A/duck/Yunnan/6607/2005	DQ992812	EF124216	EF123914	DQ992588	EF124669	EF124367	EF124065	EF124518
A/goose/Guangxi/3017/2005	DQ992716	EF124277	EF123975	DQ992649	EF124730	EF124428	EF124126	EF124579
A/goose/Guangxi/3316/2005	DQ992719	EF124280	EF123978	DQ992652	EF124733	EF124431	EF124129	EF124582
A/goose/Guangxi/345/2005	DQ320896	DQ321028	DQ321291	DQ320830	DQ321225	DQ321093	DQ320962	DQ321159
A/goose/Guangxi/3714/2005	DQ992722	EF124283	EF123981	DQ992655	EF124736	EF124434	--	EF124585
A/goose/Yunnan/3720/2005	DQ992795	EF124291	EF123989	DQ992663	EF124744	EF124442	EF124140	EF124593
A/goose/Yunnan/4129/2005	DQ992796	EF124292	EF123990	DQ992664	EF124745	EF124443	EF124141	EF124594
A/goose/Yunnan/4494/2005	DQ992798	EF124294	EF123992	DQ992666	EF124747	EF124445	EF124143	EF124596
A/goose/Yunnan/4804/2005	DQ992800	EF124296	EF123994	DQ992668	EF124749	EF124447	EF124145	EF124598
A/goose/Yunnan/6027/2005	DQ992808	EF124298	EF123996	DQ992670	EF124751	EF124449	EF124147	EF124600
A/goose/Yunnan/6368/2005	DQ992811	EF124215	EF123913	DQ992587	EF124668	EF124366	EF124064	EF124517

A/quail/Guangxi/575/2005	DQ320897	DQ321029	DQ321292	DQ320831	DQ321226	DQ321094	DQ320963	DQ321160
A/quail/Viet_Nam/15/2005	CY017051	CY017053	CY017057	CY017058	CY017056	CY017054	CY017052	CY017055
A/chicken/Vietnam/TY25/2005	EU118135	EU118144	--	--	--	--	--	--
A/chicken/Vietnam/TY31/2005	EU118136	EU118127	--	--	--	--	--	--
A/chicken/Yunnan/chuxiong01/2005	EU635874	EU635875	--	--	--	--	--	--
A/duck/Guangxi/2926/2005	DQ992715	EF124276	EF123974	DQ992648	EF124729	EF124427	EF124125	EF124578
A/duck/Guangxi/3085/2005	DQ992717	EF124278	EF123976	DQ992650	EF124731	EF124429	EF124127	EF124580
A/duck/Guangxi/3364/2005	DQ992720	EF124281	EF123979	DQ992653	EF124734	EF124432	EF124130	EF124583
A/duck/Guangxi/3548/2005	DQ992721	EF124282	EF123980	DQ992654	EF124735	EF124433	EF124131	EF124584
A/duck/Guangxi/3741/2005	DQ992723	EF124284	EF123982	DQ992656	EF124737	EF124435	EF124133	EF124586
A/duck/Guangxi/3819/2005	DQ992725	EF124286	EF123984	DQ992658	EF124739	EF124437	EF124135	EF124588
A/duck/Guangxi/4016/2005	DQ992726	EF124287	EF123985	DQ992659	EF124740	EF124438	EF124136	EF124589
A/duck/Guangxi/4184/2005	DQ992727	EF124288	EF123986	DQ992660	EF124741	EF124439	EF124137	EF124590
A/duck/Guangxi/4196/2005	DQ992728	EF124289	EF123987	DQ992661	EF124742	EF124440	EF124138	EF124591
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A/duck/Guangxi/793/2005	DQ320899	DQ321031	DQ321294	DQ320833	DQ321228	DQ321096	DQ320965	DQ321162
A/duck/Guangxi/951/2005	DQ320900	DQ321032	DQ321295	DQ320834	DQ321229	DQ321097	DQ320966	DQ321163
A/duck/Hunan/1265/2005	DQ320911	DQ321043	DQ321306	DQ320845	DQ321240	DQ321108	DQ320977	DQ321174
A/duck/Hunan/1608/2005	DQ320912	DQ321044	DQ321307	DQ320846	DQ321241	DQ321109	DQ320978	DQ321175
A/duck/Hunan/1652/2005	DQ320913	DQ321045	DQ321308	DQ320847	DQ321242	DQ321110	DQ320979	DQ321176
A/duck/Lang_Son/201/2005	GU186724	GU186726	GU186730	GU186731	GU186729	GU186727	GU186725	GU186728
A/duck/Viet_Nam/12/2005	CY016883	CY016885	CY016889	CY016890	CY016888	CY016886	CY016884	CY016887
A/duck/Vietnam/201/2005	EU930884	EU930886	EU930890	EU930891	EU930889	EU930887	EU930885	EU930888
A/duck/Vietnam/203/2005	EU930900	EU930902	EU930906	EU930907	EU930905	EU930903	EU930901	EU930904
A/duck/Vietnam/204/2005	EU930908	EU930910	EU930914	EU930915	EU930913	EU930911	EU930909	EU930912
A/duck/Vietnam/206/2005	EU930924	EU930926	EU930930	EU930931	EU930929	EU930927	EU930925	EU930928
A/duck/Vietnam/568/2005	DQ320939	DQ321070	DQ321333	DQ320874	DQ321267	DQ321135	DQ321005	DQ321201
A/Muscovy_duck/Vietnam/1455/2006	CY029535	CY029537	CY029533	CY029532	CY029534	CY029536	CY029538	CY029539
A/duck/Yunnan/1126/2006	DQ992813	--	--	--	--	--	--	--
A/peregrine_falcon/Hong_Kong/5211/2006	CY036045	CY036047	CY036043	CY036042	CY036044	CY036046	CY036048	CY036049
A/pheasant/Shantou/2239/2006	DQ992782	EF124212	EF123910	DQ992584	EF124665	EF124363	EF124061	EF124514
A/duck/Guangxi/89/2006	DQ992741	EF124209	EF123907	DQ992581	EF124662	EF124360	EF124058	EF124511
A/Daurian_starling/Hong_Kong/1532/2007	CY036181	CY036183	CY036179	CY036178	CY036180	CY036182	CY036184	CY036185
A/chicken/Huabei/0513/2007	JQ809274	--	--	--	--	--	--	--
A/chicken/Hunan/3/2007	GU182142	GU182144	GU182140	GU182139	GU182141	GU182143	GU182145	GU182146
A/environment/Dongting_Lake/Hunan/5-41/2007	GQ290463	--	--	--	--	--	--	--
A/environment/Hunan/5-25/2007	GU182198	GU182200	GU182196	GU182195	GU182197	GU182199	GU182201	GU182202
A/environment/Hunan/5-32/2007	GU182206	GU182208	GU182204	GU182203	GU182205	GU182207	GU182209	GU182210
A/grey_heron/Hong_Kong/3088/2007	CY036213	CY036215	CY036211	CY036210	CY036212	CY036214	CY036216	CY036217
A/house_crow/Hong_Kong/5288/2007	CY036189	CY036191	CY036187	CY036186	CY036188	CY036190	CY036192	CY036193
A/little_egret/Hong_Kong/8550/2007	CY036197	CY036199	CY036195	CY036194	CY036196	CY036198	CY036200	CY036201
A/little_egret/Hong_Kong/8863/2007	CY036205	CY036207	CY036203	CY036202	CY036204	CY036206	CY036208	CY036209
A/peregrine_falcon/Hong_Kong/1143/2007	CY036093	CY036095	CY036091	CY036090	CY036092	CY036094	CY036096	CY036097
A/pika/Qinghai/GRL/2007	GQ227380	GQ227381	GQ227376	GQ227378	GQ227377	GQ227375	GQ227382	GQ227379

A/pika/Qinghai/HMH/2007	GQ227367	GQ227369	GQ227368	GQ227370	GQ227374	GQ227372	GQ227371	GQ227373
A/pika/Qinghai/QW/2007	GQ227391	GQ227394	GQ227397	GQ227398	GQ227396	GQ227392	GQ227393	GQ227395
A/pika/Qinghai/SHK/2007	GQ227383	GQ227389	GQ227384	GQ227386	GQ227385	GQ227388	GQ227390	GQ227387
A/red-billed_starling/Hong_Kong/4925/2007	CY036165	CY036167	CY036163	CY036162	CY036164	CY036166	CY036168	CY036169
A/common_buzzard/Hong_Kong/9213/2007	CY036221	CY036223	CY036219	CY036218	CY036220	CY036222	CY036224	CY036225
A/common_magpie/Hong_Kong/5052/2007	CY036173	CY036175	CY036171	CY036170	CY036172	CY036174	CY036176	CY036177
A/duck/Hunan/3/2007	GU182150	GU182152	GU182148	GU182147	GU182149	GU182151	GU182153	GU182154
A/black-crowned_night_heron/Hong_Kong/659/2008	CY036229	CY036231	CY036227	CY036226	CY036228	CY036230	CY036232	CY036233
A/chicken/Hunan/8/2008	GU182158	GU182160	GU182156	GU182155	GU182157	GU182159	GU182162	GU182161
A/chicken/Korea/Gimje/2008	GQ412053	GQ412064	GQ412039	GQ412033	GQ412045	GQ412057	GQ412069	GQ412075
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A/chicken/Korea/YAQ173/2008	GQ412056	GQ412066	GQ412042	GQ412036	GQ412048	GQ412060	GQ412072	GQ412078
A/chicken/Laos/LPQ001/2008	CY041047	--	--	--	--	--	--	--
A/chicken/Laos/OX005/2008	CY041048	--	--	--	--	--	--	--
A/chicken/Laos/XDM006/2008	CY041049	--	--	--	--	--	--	--
A/chicken/Viet_Nam/TMU009/2008	CY095689	CY095690	--	--	--	--	CY095691	--
A/environment/Hunan/6-45/2008	GU182190	GU182192	GU182188	GU182187	GU182189	GU182191	GU182193	GU182194
A/environment/Hunan/7-73/2008	GU182174	GU182176	GU182172	GU182171	GU182173	GU182175	GU182177	GU182178
A/great_egret/Hong_Kong/807/2008	CY036237	CY036239	CY036235	CY036234	CY036236	CY036238	CY036240	CY036241
A/grey_heron/Hong_Kong/1046/2008	CY036245	CY036247	CY036243	CY036242	CY036244	CY036246	CY036248	CY036249
A/house_crow/Hong_Kong/7677/2008	AB517661	AB517662	--	--	--	--	--	--
A/magpie_robin/Hong_Kong/1097/2008	CY036253	CY036255	CY036251	CY036250	CY036252	CY036254	CY036256	CY036257
A/magpie_robin/Hong_Kong/1897/2008	CY036261	CY036263	CY036259	CY036258	CY036260	CY036262	CY036264	CY036265
A/whooper_swan/Akita/1/2008	AB436736	AB436735	AB436732	AB436731	AB436733	AB436734	AB436737	AB436738
A/whooper_swan/Aomori/1/2008	AB458239	AB458241	AB458237	AB458236	AB458238	AB458240	AB458242	AB458243
A/whooper_swan/Aomori/2/2008	AB458247	AB458249	AB458245	AB458244	AB458246	AB458248	AB458250	AB458251
A/whooper_swan/Hokkaido/1/2008	AB436550	AB436552	AB436548	AB436547	AB436549	AB436551	AB436553	AB436554
A/whooper_swan/Hokkaido/2/2008	AB436902	AB436904	AB436900	AB436899	AB436901	AB436903	AB436905	AB436906
A/duck/Hunan/8/2008	GU182166	GU182168	GU182164	GU182163	GU182165	GU182167	GU182169	GU182170
A/duck/Korea/JEQ149/2008	GQ412052	GQ412067	GQ412043	GQ412037	GQ412049	GQ412061	GQ412073	GQ412079
A/duck/Korea/NSQ263/2008	GQ412054	GQ412068	GQ412044	GQ412038	GQ412050	GQ412062	GQ412074	GQ412080
A/Guangxi/1/2009	CY098744	CY098746	CY098742	CY098741	CY098743	CY098745	CY060162	CY098747
A/Muscovy_duck/Vietnam/18151/2009	JN055364	--	--	--	--	--	JN055394	--
A/Muscovy_duck/Vietnam/18152/2009	JN055368	--	--	--	--	--	--	--
A/Muscovy_duck/Vietnam/18153/2009	JN055369	--	--	--	--	--	--	--
A/bar-headed_goose/Mongolia/X25/2009	AB521999	AB522000	--	--	HM006729	--	--	--
A/bar-headed_goose/Mongolia/X53/2009	HM006730	AB523769	AB523765	AB523764	HM006731	AB523768	AB523770	AB523771
A/bar-headed_goose/Mongolia/X54/2009	AB523366	AB523367	--	--	--	--	--	--
A/brown-headed_gull/Qinghai/1/2009	HQ020367	--	--	--	--	--	--	--
A/brown-headed_gull/Qinghai/2/2009	HQ020368	--	--	--	--	--	--	--
A/environment/Chang_Sha/1/2009	JN543373	--	--	--	--	--	--	--
A/environment/Chang_Sha/2/2009	JN543374	--	--	--	--	--	--	--
A/environment/Chang_Sha/25/2009	JN543378	--	--	--	--	--	--	JN558603

A/environment/Chang_Sha/3/2009	JN543375	--	--	--	--	--	--	--
A/feral_pigeon/Hong_Kong/3409/2009	AB557629	AB557630	--	--	--	--	--	--
A/great_black-headed_gull/1/2009	HQ020369	--	--	--	--	--	--	--
A/great_black-headed_gull/Qinghai/2/2009	HQ020370	--	--	--	--	--	--	--
A/great_black-headed_gull/Qinghai/3/2009	HQ020371	--	--	--	--	--	--	--
A/great_black-headed_gull/Qinghai/4/2009	HQ020372	--	--	--	--	--	--	--
A/great_black-headed_gull/Qinghai/5/2009	HQ020373	--	--	--	--	--	--	--
A/great_black-headed_gull/Qinghai/6/2009	HQ020374	--	--	--	--	--	--	--
A/great_cormorant/Qinghai/1/2009	HQ020375	--	--	--	--	--	--	--
A/great_crested-grebe/Qinghai/1/2009	CY063318	CY063320	CY063316	CY063315	CY063317	CY063319	CY063321	CY063322
A/grey_heron/Hong_Kong/779/2009	AB517663	AB517664	--	--	--	--	--	--
A/herring_gull/Mongolia/833T/2009	CY098291	--	--	--	--	--	--	--
A/large_billed_crow/Hong_Kong/885/2009	AB521161	AB521162	--	--	--	--	--	--
A/oriental_magpie_robin/Hong_Kong/9298/2009	AB557633	AB557634	--	--	--	--	--	--
A/ruddy_shelduck/Mongolia/911T/2009	CY098293	--	--	--	--	--	--	--
A/ruddy_shelduck/Mongolia/X42/2009	HM006736	AB523761	AB523757	AB523756	HM006737	AB523760	AB523762	AB523763
A/ruddy_shelduck/Mongolia/X63/2009	AB523368	AB523369	--	--	--	--	--	--
A/swan/Shanghai/10/2009	JF975561	JF975563	JF975559	JF975558	JF975560	JF975562	JF975564	JF975565
A/water/Hunan/7/2009	CY098853	CY098855	CY098851	CY098850	CY098852	CY098854	CY098856	CY098857
A/whooper_swan/Mongolia/4/2009	HM006741	--	--	--	--	--	--	--
A/whooper_swan/Mongolia/5/2009	HM006742	--	--	--	--	--	--	--
A/whooper_swan/Mongolia/6/2009	HM006743	AB520710	AB520706	AB520705	HM006744	AB520709	AB520711	AB520712
A/whooper_swan/Mongolia/7/2009	HM006745	--	--	--	--	--	--	--
A/whooper_swan/Mongolia/8/2009	HM006746	AB517668	--	--	--	--	--	--
A/whooper_swan/Mongolia/9/2009	HM006747	--	--	--	--	--	--	--
A/chicken/Vietnam/20346/2009	JN055371	--	--	--	--	--	JN055396	--
A/chicken/Vietnam/20388/2009	JN055373	--	--	--	--	--	--	--
A/chicken/Vietnam/20389/2009	JN055377	--	--	--	--	--	--	--
A/chicken/Vietnam/20390/2009	JN055374	--	--	--	--	--	--	--
A/chicken/Vietnam/20392/2009	JN055375	--	--	--	--	--	--	--
A/chicken/Vietnam/20395/2009	JN055376	--	--	--	--	--	--	--
A/chicken/Vietnam/20396/2009	JN055372	--	--	--	--	--	--	--
A/chicken/Vietnam/27265/2009	JN055379	JN055393	--	--	--	--	JN055397	--
A/common_goldeneye/Mongolia/X59/2009	AB522001	AB522002	--	--	--	--	--	--
A/common_goldeneye/Mongolia/X60/2009	HM006733	AB523777	AB523773	AB523772	HM006734	AB523776	AB523778	AB523779
A/crested_myna/Hong_Kong/1178/2009	AB521163	AB521164	--	--	--	--	--	--
A/duck/Vietnam/27329/2009	JN055385	--	--	--	--	--	--	--
A/duck/Vietnam/27339/2009	JN055387	--	--	--	--	--	--	--
A/duck/Vietnam/27354/2009	JN055386	--	--	--	--	--	JN055399	--
A/duck/Vietnam/27372/2009	JN055389	--	--	--	--	--	--	--
A/duck/Vietnam/27373/2009	JN055388	--	--	--	--	--	--	--
A/duck/Vietnam/27374/2009	JN055390	--	--	--	--	--	--	--
A/duck/Vietnam/27386/2009	JN055391	--	--	--	--	--	--	--
A/Hong_Kong/6841/2010	HQ636461	HQ636462	HQ652629	HQ652630	HQ652628	HQ652626	HQ636463	HQ652627

A/Hubei/1/2010	CY098758	CY098760	CY098756	CY098755	CY098757	CY098759	CY098761	CY098762
A/baikal_teal/Korea/Q524/2010	JN807976	JN808028	JN807919	JN807892	JN807946	JN808000	JN808075	JN808099
A/bar-headed_goose/Qinghai/1/2010	HQ020364	--	--	--	--	--	--	--
A/chicken/Korea/Iksan/2010	JN807979	JN808038	JN807935	JN807918	JN807957	JN808026	JN808072	JN808092
A/chicken/Nepal/105/2010	JN613388	--	--	--	--	--	--	--
A/chicken/Nepal/111/2010	JN613387	--	--	--	--	--	--	--
A/chicken/Nepal/115/2010	JN613386	--	--	--	--	--	--	--
A/chicken/Nepal/2-53/2010	JN613390	--	--	--	--	--	--	--
A/chicken/Nepal/5-1cl/2010	JN613389	--	--	--	--	--	--	--
A/chicken/Nepal/81/2010	JN613385	--	--	--	--	--	--	--
A/chicken/Nepal/A135/2010	JN613383	--	--	--	--	--	--	--
A/chicken/Nepal/A136/2010	JN613384	--	--	--	--	--	--	--
A/great_crested_grebe/Qinghai/1/2010	HQ020376	--	--	--	--	--	--	--
A/hooded_crane/Kagoshima/4612J008/2010	AB677931	AB677933	AB677929	AB677928	AB677930	AB677932	AB677934	AB677935
A/mallard/Korea/1195/2010	HQ695910	HQ695911	HQ695913	HQ695912	HQ695914	HQ695915	HQ695916	HQ695917
A/mandarin_duck/Korea/K10-480/2010	JF699672	JF699676	--	--	--	--	--	--
A/mandarin_duck/Korea/K10-483/2010	JF699673	JF699677	--	--	--	--	--	--
A/mandarin_duck/Korea/K10-485/2010	JF699674	JF699678	--	--	--	--	--	--
A/mandarin_duck/Korea/Q525/2010	JN807993	JN808052	JN807941	JN807900	JN807949	JN808001	JN808079	JN808106
A/tundra_swan/Mongolia/1T/2010	CY098292	--	--	--	--	--	--	--
A/tundra_swan/Tottori/12-002/2010	AB677923	AB677925	AB677921	AB677920	AB677922	AB677924	AB677926	AB677927
A/whooper_swan/Mongolia/1/2010	AB569348	AB569350	AB569346	AB569345	AB569347	AB569349	AB569351	AB569352
A/whooper_swan/Mongolia/11/2010	AB569607	AB569608	--	--	--	--	--	--
A/whooper_swan/Mongolia/21/2010	AB569609	AB569610	--	--	--	--	--	--
A/whooper_swan/Mongolia/7/2010	AB569353	AB569354	--	--	--	--	--	--
A/duck/Hokkaido/WZ101/2010	AB612909	AB612911	AB612907	AB612906	AB612908	AB612910	AB612912	AB612913
A/duck/Hokkaido/WZ83/2010	AB612901	AB612903	AB612899	AB612898	AB612900	AB612902	AB612904	AB612905
A/duck/Korea/Cheonan/2010	JN807985	JN808043	JN807933	JN807909	JN807950	JN808005	JN808063	JN808090
A/duck/Lao/463/2010	CY098337	CY098339	--	CY098336	--	CY098338	CY098340	--
A/duck/Lao/469/2010	CY098344	CY098346	--	CY098342	CY098343	CY098345	CY098347	CY098348
A/duck/Lao/471/2010	CY098352	CY098354	CY098350	CY098349	CY098351	CY098353	CY098355	CY098356
A/duck/Nepal/DTS22/2010	JN613379	--	--	--	--	--	--	--
A/duck/Nepal/DTS24/2010	JN613380	--	--	--	--	--	--	--
A/Mallard_duck/Korea/W401/2011	JN202558	JN202562	JN202570	JN202572	JN202568	JN202564	JN202560	JN202566
A/Mallard_duck/Korea/W404/2011	JN202559	JN202563	JN202571	JN202573	JN202569	JN202565	JN202561	JN202567
A/baikal_teal/Korea/Q34/2011	JN807975	JN808033	JN807923	JN807893	JN807952	JN808022	JN808074	JN808085
A/black_headed_gull/Hong_Kong/07035-1/2011	JQ922566	--	--	--	--	--	--	--
A/chicken/Aichi/T1/2011	AB675740	AB684120	AB684117	AB684116	AB684118	AB684119	AB684121	AB684122
A/chicken/Bangladesh/11rs1984-16/2011	JQ409048	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-17/2011	JQ409049	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-18/2011	JQ409050	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-19/2011	JQ409051	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-22/2011	JQ409052	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-33/2011	JQ409056	--	--	--	--	--	--	--

A/chicken/Bangladesh/11rs1984-34/2011	JN795925	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-40/2011	JQ409057	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-43/2011	JQ409058	--	--	--	--	--	--	--
A/chicken/Bangladesh/11rs1984-45/2011	JQ409059	--	--	--	--	--	--	--
A/chicken/India/CA0301/2011	CY089472	CY089473	CY092122	CY092121	CY092123	CY092124	CY092125	CY092126
A/chicken/India/CA0302/2011	CY089474	CY089475	CY092128	CY092127	CY092129	CY092130	CY092131	CY092132
A/chicken/India/CA0303/2011	CY089468	CY089469	CY092134	CY092133	CY092135	CY092136	CY092137	CY092138
A/chicken/India/CL03485/2011	CY089470	CY089471	CY092140	CY092139	CY092141	CY092142	CY092143	CY092144
A/chicken/India/TR0383/2011	CY089476	CY089477	CY092116	CY092115	CY092117	CY092118	CY092119	CY092120
A/chicken/Korea/Asan90/2011	JN807977	JN808040	JN807925	JN807911	JN807972	JN808009	JN808076	JN808102
A/chicken/Korea/IC546/2011	JN807978	JN808044	JN807934	JN807907	JN807970	JN808018	JN808068	JN808081
A/chicken/Korea/PT412/2011	JN807980	JN808045	JN807938	JN807910	JN807966	JN808010	JN808056	JN808100
A/chicken/Korea/SJ378/2011	JN807981	JN808031	JN807929	JN807898	JN807965	JN808023	JN808055	JN808088
A/chicken/Korea/YS171/2011	JN807982	JN808034	JN807931	JN807894	JN807954	JN808013	JN808078	JN808086
A/chicken/Mie/1/2011	AB675741	AB684194	AB684191	AB684190	AB684192	AB684193	AB684195	AB684196
A/chicken/Miyazaki/M6/2011	AB675739	AB684099	AB684096	AB684095	AB684097	AB684098	AB684100	AB684101
A/duck/Vietnam/OIE-2533/2011	AB700635	AB700637	AB700633	AB700632	AB700634	AB700636	AB700638	AB700639
A/duck/Vietnam/QT801/2011	JN986881	JX826585	--	--	--	--	--	--
A/duck/Vietnam/QT802/2011	JN986882	JX826586	--	--	--	--	--	--
A/duck/Zhejiang/213/2011	JN646713	JN646727	JN646699	JN646692	JN646706	JN646720	JN646734	JN646741
A/duck/Zhejiang/224/2011	JN646714	JN646728	JN646700	JN646693	JN646707	JN646721	JN646735	JN646742
A/duck/Zhejiang/2242/2011	JN646715	JN646729	JN646701	JN646694	JN646708	JN646722	JN646736	JN646743
A/duck/Zhejiang/2243/2011	JN646716	JN646730	JN646702	JN646695	JN646709	JN646723	JN646737	JN646744
A/duck/Zhejiang/2244/2011	JN646717	JN646731	JN646703	JN646696	JN646710	JN646724	JN646738	JN646745
A/duck/Zhejiang/2245/2011	JN646718	JN646732	JN646704	JN646697	JN646711	JN646725	JN646739	JN646746
A/duck/Zhejiang/2248/2011	JN646719	JN646733	JN646705	JN646698	JN646712	JN646726	JN646740	JN646747
A/eurasian_eagle_owl/Korea/Q133/2011	JN807989	JN808029	JN807926	JN807914	JN807951	JN808024	JN808066	JN808087
A/eurasian_eagle_owl/Korea/Q178/2011	JN807973	JN808037	JN807920	JN807897	JN807967	JN808017	JN808073	JN808103
A/eurasian_eagle_owl/Korea/Q182/2011	JN807974	JN808032	JN807932	JN807899	JN807947	JN808019	JN808077	JN808104
A/eurasian_eagle_owl/Korea/Q196/2011	JN807990	JN808027	JN807943	JN807896	JN807958	JN808020	JN808070	JN808097
A/eurasian_sparrowhawk/Korea/Q94/2011	JN807991	JN808046	JN807937	JN807904	JN807971	JN808014	JN808080	JN808082
A/goshawk/Tochigi/64/2011	AB676810	AB676812	AB676808	AB676807	AB676809	AB676811	AB676813	AB676814
A/great_drested_grebe/Hyogo/2802E082/2011	AB677899	--	--	--	--	--	--	--
A/greater_scaup/Hokkaido/2/2011	AB621349	AB621350	AB675550	AB675549	AB675551	AB675552	AB675553	AB675554
A/greater_scaup/Hokkaido/28/2011	AB629702	AB629703	AB676796	AB676795	AB676797	AB676798	AB676799	AB676800
A/mandarin_duck/Kochi/3901C005/2011	AB677891	AB677893	AB677889	AB677888	AB677890	AB677892	AB677894	AB677895
A/mandarin_duck/Korea/K10-515/2011	JF699675	JF699679	--	--	--	--	--	--
A/mandarin_duck/Korea/Q2/2011	JN807992	JN808050	JN807921	JN807901	JN807968	JN808016	JN808069	JN808107
A/mandarin_duck/Miyazaki/22M807-1/2011	AB677875	AB677877	AB677873	AB677872	AB677874	AB677876	AB677878	AB677879
A/mandarin_duck/Nagasaki/4202A023/2011	AB677867	AB677869	AB677865	AB677864	AB677866	AB677868	AB677870	AB677871
A/mandarin_duck/Oita/4402B056/2011	AB677859	AB677861	AB677857	AB677856	AB677858	AB677860	AB677862	AB677863
A/owl/Tokushima/3602A023/2011	AB677883	AB677885	AB677881	AB677880	AB677882	AB677884	AB677886	AB677887
A/peregrine_falcon/Aichi/2302O017/2011	AB677915	AB677917	AB677913	AB677912	AB677914	AB677916	AB677918	AB677919
A/peregrine_falcon/Aomori/7/2011	AB629713	AB629715	AB629711	AB629710	AB629712	AB629714	AB629716	AB629717

A/peregrine_falcon/Kyoto/2602A009/2011	AB677907	AB677909	AB677905	AB677904	AB677906	AB677908	AB677910	AB677911
A/peregrine_falcon/Tochigi/15/2011	AB617579	AB617581	AB617577	AB617576	AB617578	AB617580	AB617582	AB617583
A/pheasant/Korea/PT411/2011	JN807994	JN808048	JN807939	JN807908	JN807955	JN808007	JN808057	JN808098
A/pintail/Hokkaido/1/2011	AB621345	AB621346	AB675556	AB675555	AB675557	AB675559	AB675561	AB675562
A/quail/Korea/GC395/2011	JN807995	JN808030	JN807930	JN807917	JN807948	JN808011	JN808060	JN808096
A/tufted_duck/Fukushima/16/2011	AB629698	AB629699	AB675583	AB675582	AB675584	AB675585	AB675586	AB675587
A/tufted_duck/Fukushima/2/2011	AB615237	AB615239	AB615235	AB615234	AB615236	AB615238	AB615240	AB615241
A/tufted_duck/Fukushima/4/2011	AB675503	AB675505	AB675501	AB675500	AB675502	AB675504	AB675506	AB675507
A/tufted_duck/Fukushima/5/2011	AB675536	AB675538	AB675534	AB675533	AB675535	AB675537	AB675539	AB675540
A/tufted_duck/Fukushima/7/2011	AB675544	AB675546	AB675542	AB675541	AB675543	AB675545	AB675547	AB675548
A/tufted_duck/Yamaguchi/3502B007/2011	AB677851	AB677853	AB677849	AB677848	AB677850	AB677852	AB677854	AB677855
A/tundra_swan/Fukushima/207/2011	AB629700	AB629701	AB676784	AB676783	AB676785	AB676786	AB676787	AB676788
A/turkey/Korea/DDC518/2011	JN807996	JN808047	JN807940	JN807905	JN807956	JN808015	JN808061	JN808084
A/whooper_swan/Hamanaka/2011	CY110738	CY110740	CY110736	CY110735	CY110737	CY110739	CY110741	CY110742
A/whooper_swan/Hokkaido/13-21/2011	AB629708	AB629709	AB676816	AB676815	AB676817	AB676818	AB676819	AB676820
A/whooper_swan/Hokkaido/13-27/2011	AB629704	AB629705	AB676790	AB676789	AB676791	AB676792	AB676793	AB676794
A/whooper_swan/Hokkaido/3/2011	AB620022	AB620023	AB675566	AB675565	AB675567	AB675569	AB675571	AB675572
A/whooper_swan/Hokkaido/4/2011	AB610972	AB610974	AB610970	AB610969	AB610971	AB610973	AB610975	AB610976
A/whooper_swan/Hokkaido/6/2011	AB621347	AB621348	AB675574	AB675573	AB675575	AB675577	AB675579	AB675580
A/whooper_swan/Hokkaido/A13/2011	AB629706	AB629707	AB676822	AB676821	AB676823	AB676824	AB676825	AB676826
A/whooper_swan/Korea/Q28/2011	JN807998	JN808041	JN807922	JN807913	JN807963	JN808008	JN808058	JN808089
A/wild_bird/Korea/IS18/2011	JN807999	JN808053	JN807927	JN807902	JN807960	JN808006	JN808071	JN808105
A/common_Ketrel/Korea/Q197/2011	JN807983	--	--	--	--	--	--	--
A/common_pochard/Shimane/5502B024/2011	AB677843	AB677845	AB677841	AB677840	AB677842	AB677844	AB677846	AB677847
A/crow/Bangladesh/11rs1984-11/2011	JN795913	--	--	--	--	--	--	--
A/crow/Bangladesh/11rs1984-12/2011	JN795914	--	--	--	--	--	--	--
A/crow/Bangladesh/11rs1984-13/2011	JN795915	--	--	--	--	--	--	--
A/crow/Bangladesh/11rs1984-14/2011	JN795916	--	--	--	--	--	--	--
A/crow/Bangladesh/11rs1984-15/2011	JN795917	--	--	--	--	--	--	--
A/duck/India/02AF1/2011	CY089413	CY089415	CY089411	CY089410	CY089412	CY089414	CY089416	CY089417
A/duck/India/02CA10/2011	CY089421	CY089423	CY089419	CY089418	CY089420	CY089422	CY089424	CY089425
A/duck/Korea/AS117/2011	JN807984	JN808051	JN807936	JN807906	JN807962	JN808004	JN808067	JN808093
A/duck/Korea/IC360/2011	JN807986	JN808049	JN807928	JN807895	JN807964	JN808002	JN808062	JN808094
A/duck/Korea/NJ83/2011	JN807987	JN808039	JN807945	JN807916	JN807969	JN808012	JN808064	JN808095
A/duck/Korea/YA54/2011	JN807988	JN808035	JN807924	JN807903	JN807953	JN808021	JN808065	JN808101
A/duck/Quangngai/1037/2011	JQ898146	--	--	--	--	--	--	--

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419 **Table S3. Information on satellites tracking birds**

Flyway	Region A	Region B	MIN	MAX	AVE	Species	PTT*
Central Asian flyway (CA)	Bangladesh	India	-	-	0	Bar-headed Goose	41592BG/85784BG
	India	Bangladesh	-	-	0	Bar-headed Goose	85784BG
	India	Nepal	3	4	4.5	Bar-headed Goose	85722BG/85777BG/85784BG
	India	Qinghai	-	-	0	Bar-headed Goose	85777BG
	India	Tibet	0	3	1.5	Bar-headed Goose	85784BG
	Mongolia	Qinghai	2	6	4	Bar-headed Goose	41592BG/85722BG/85781BG/85784BG
	Nepal	India	-	-	0	Bar-headed Goose	85784BG
	Nepal	Tibet	0	1	0.5	Bar-headed Goose	85722BG/85777BG
	Qinghai	Mongolia	0	1	0.5	Bar-headed Goose	85722BG/85777BG/85784BG
	Qinghai	Tibet	0	1	0.5	Bar-headed Goose	41592BG/85722BG/85781BG/85784BG
	Tibet	Bangladesh	-	-	1	Bar-headed Goose	41592BG
	Tibet	India	0	1	0.5	Bar-headed Goose	85722BG/85777BG/85784BG/85781BG
	Tibet	Qinghai	0	2	1	Bar-headed Goose	85722BG/85784BG
CA (India – Mongolia)	Bangladesh	India	3	5	4	Ruddy Shelduck	97734RS
	India	Bangladesh	-	-	0	Ruddy Shelduck	97734RS
	India	Mynamar	-	-	0	Ruddy Shelduck	74810RS
	India	Tibet	0	3	1.5	Ruddy Shelduck	74810RS/97741RS/97734RS
	Mongolia	Qinghai	3	6	4.5	Ruddy Shelduck	74810RS
	Mynamar	India	-	-	4	Ruddy Shelduck	74810RS
	Mynamar	Tibet	3	4	3.5	Ruddy Shelduck	74810RS
	Qinghai	Mongolia	0	2	1	Ruddy Shelduck	74810RS/97741RS/97734RS
	Qinghai	Tibet	1	3	2	Ruddy Shelduck	74810RS
	Tibet	India	0	6	3	Ruddy Shelduck	74810RS/97734RS
	Tibet	Mynamar	0	1	0.5	Ruddy Shelduck	74810RS
CA (Qinghai – India)	Bangladesh	India	0	4	2	Ruddy Shelduck	82127RS/74821RS
	India	Bangladesh	0	5	2.5	Ruddy Shelduck	82127RS/74821RS
	India	Mynamar	-	-	0	Ruddy Shelduck	82121RS
	India	Tibet	-	-	0	Ruddy Shelduck	82127RS/74821RS/82121RS
	Mynamar	India	-	-	4	Ruddy Shelduck	82121RS
	Qinghai	Tibet	2	4	3	Ruddy Shelduck	82127RS/82121RS
	Tibet	India	-	-	0	Ruddy Shelduck	82127RS/82121RS
	Tibet	Qinghai	0	1	0.5	Ruddy Shelduck	82127RS/82121RS
East Asian-Australasian Flyway (Poyang lake – Mongolia)	Anhui	Jiangxi	0	2	1	Swan Goose	82107SG/82111SG/G585SG
	Anhui	Mongolia	1	2	1.5	Swan Goose	82107SG/82111SG/G585SG
	Jiangxi	Anhui	1	5	3	Swan Goose	82107SG/82111SG/G585SG
	Mongolia	Anhui	3	7	5	Swan Goose	82111SG/G585SG
	Mongolia	North Korea	2	5	3.5	Swan Goose	82107SG/82111SG/G585SG
	North Korea	Anhui	1	4	2.5	Swan Goose	82107SG/82111SG/G585SG
East Asian-Australasian	Anhui	North Korea	-	-	1	Northern Pintail	44815NP
	HK	Jiangxi	-	-	3	Northern Pintail	44815NP

tralasian	HK	North Korea	-	-	3	Northern Pintail	91268NP
flyway	HK	South Korea	4	2	3	Northern Pintail	91268NP/95377NP
	Japan	HK	-	-	2	Northern Pintail	91268NP
	Jiangxi	Anhui	-	-	0	Northern Pintail	44815NP
	North Korea	Japan	6	7	6.5	Northern Pintail	44815NP/91268NP
	North Korea	South Korea	-	-	7	Northern Pintail	95377NP

420 *PTT, Platform Terminal Transmitters.

421 MIN, the minimum flight time from Region A to B of satellite tracking birds;

422 MAX is the maximum flight time, and AVE is the average flight time.

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424 **Table S4. Summary of the sequences associated with clade 2.3.2 and 2.3.2.1 listed**
 425 **by location/gene/year**

Location	Year	HA	NA	PB1	PB2	PA	NP	MP	NS
Bangladesh	2011	15	-	-	-	-	-	-	-
Guangdong (China)	2004	2	2	2	2	2	2	2	2
	2005	1	1	1	1	1	1	1	1
Guangxi (China)	2004	4	4	4	4	4	4	4	4
	2005	20	20	20	20	20	20	19	20
	2006	1	1	1	1	1	1	1	1
	2009	1	1	1	1	1	1	1	1
Guizhou (China)	2005	2	2	2	2	2	2	2	2
Hong Kong (China)	2004	2	2	2	2	2	2	2	2
	2005	1	1	1	1	1	1	1	1
	2006	1	1	1	1	1	1	1	1
	2007	9	9	9	9	9	9	9	9
	2008	6	6	5	5	5	5	5	5
	2009	5	5	-	-	-	-	-	-
	2010	1	1	1	1	1	1	1	1
Hubei (China)	2011	1	-	-	-	-	-	-	-
	2010	1	1	1	1	1	1	1	1
Hunan (China)	2005	3	3	3	3	3	3	3	3
	2007	5	4	4	4	4	4	4	4
	2008	4	4	4	4	4	4	4	4
	2009	5	1	1	1	1	1	1	2
India	2011	7	7	7	7	7	7	7	7
Japan	2008	5	5	5	5	5	5	5	5
	2010	4	4	4	4	4	4	4	4
	2011	32	31	31	31	31	31	31	31
Laos	2008	3	-	-	-	-	-	-	-
	2010	3	3	1	3	2	3	3	2
Mongolia	2009	16	10	4	4	5	4	4	4
	2010	5	4	1	1	1	1	1	1
Nepal	2010	10	-	-	-	-	-	-	-
Qinghai (China)	2007	4	4	4	4	4	4	4	4
	2009	10	1	1	1	1	1	1	1
	2010	2	-	-	-	-	-	-	-
Shanghai (China)	2009	1	1	1	1	1	1	1	1
Shantou (China)	2004	2	2	2	2	2	2	2	2
	2005	2	2	2	2	2	2	2	2
	2006	1	1	1	1	1	1	1	1
South Korea	2008	6	6	6	6	6	6	6	6
	2010	8	8	5	5	5	5	5	5

	2011	25	24	23	23	23	23	23	23
Unknown location (China)	2003	1	-	-	-	-	-	-	-
	2007	1	-	-	-	-	-	-	-
Viet Nam	2005	14	13	11	11	11	11	11	11
	2006	1	1	1	1	1	1	1	1
	2008	1	1	-	-	-	-	1	-
	2009	18	1	-	-	-	-	4	-
	2011	4	3	1	1	1	1	1	1
Yunan (China)	2005	13	13	12	12	12	12	12	12
	2006	1	-	-	-	-	-	-	-
Zhejiang (China)	2011	7	7	7	7	7	7	7	7

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Table S5. Sensitivity analysis of the expected number of migration rates for HPAI H5N1 clade 2.3.2 based on the HA gene.

	Prior Mean	Posterior median	BCI*	$I > 0.5$ and BF > 3†	Estimated log marginal likelihood (SE)
Log(2)		7	5-8	5‡	-10365.28 (0.72)
1		7	5-9	5‡	-10366.80 (0.78)
5		10	7-13	5‡	-10368.58 (0.59)
10		12	9-15	5‡	-10372.81 (1.82)

* BCI, Bayesian credible intervals of the inferred number of rates.

† I , binary indicator; BF, Bayes factor.

‡ The statistically significant migration paths remained unchanged in these tests.

436 **Table S6. Statistical performance of molecular evolutionary models**

Molecular clock model	Coalescent prior	Estimated rate of evolution*	Estimated marginal likelihood	Bayes factor‡					
				Constant		Exponential		BSP	
				Relaxed	Strict	Relaxed	Strict	Relaxed	Strict
Relaxed	Constant size	5.83 (4.79-6.84)	-10281.4	-	71.41	2.46	70.78	0.015	85.80
Strict	Constant size	5.00 (4.47-5.56)	-10453.2	-71.41	-	-68.94	-0.62	-71.42	14.39
Relaxed	Exponential	5.73 (4.87-6.61)	-10286.1	-2.46	68.94	-	68.32	-2.48	83.33
Strict	Exponential	5.00 (4.46-5.59)	-10454.2	-70.78	0.62	-68.32	-	-70.80	15.01
Relaxed	BSP	5.74 (4.52-6.79)	-10283.1	-0.015	71.42	2.48	70.80	-	85.81
Strict	BSP	5.03 (4.52-5.57)	-10457.2	-85.80	-14.39	-83.33	-15.01	-85.81	-

437 n/a, not applicable.

438 *Units are 10^{-3} substitutions per nucleotide per year.

439 †A measure of the variation in evolutionary rate among phylogeny branches.

440 BSP, Bayesian Skyline Plot.

441 ‡The posterior probability and Bayes factor based on the marginal likelihoods of the models was
 442 used to choose the most suitable model for the data. The strength of the evidence against H0 was
 443 evaluated as $2\ln\text{BF} < 2$ = no evidence; 2–6 weak evidence; 6–10 strong evidence; and > 10 very
 444 strong evidence. A negative $2\ln\text{BF}$ indicated evidence in favour of H0. Only values of ≥ 10 were
 445 considered significant.

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448 **Table S7. Sequences used in this study**

ID	Country	Year	clade	Strain
DQ371928	China	2005	2.3.4	A/Anhui/1/2005
CY098668	China	2006	2.3.4	A/Anhui/1/2006
CY098681	China	2007	2.3.4	A/Anhui/1/2007
DQ371929	China	2005	2.3.4	A/Anhui/2/2005
EF553329	China	2006	7	A/Anhui/T2/2006
FJ573468	Bangladesh	2008	2.2.2	A/Bangladesh/207095/2008
CY088769	Bangladesh	2011	2.2.2	A/Bangladesh/3233/2011
DQ095612	China	2005	2.2	A/Bar-headed Goose/Qinghai/59/05
DQ095615	China	2005	2.2	A/Bar-headed Goose/Qinghai/60/05
DQ095620	China	2005	2.2	A/Bar-headed Goose/Qinghai/62/05
DQ095622	China	2005	2.2	A/Bar-headed Goose/Qinghai/65/05
DQ095623	China	2005	2.2	A/Bar-headed Goose/Qinghai/67/05
DQ095619	China	2005	2.2	A/Bar-headed Goose/Qinghai/75/05
EF587277	China	2003	7	A/Beijing/01/2003
CY098709	China	2009	2.3.4	A/Beijing/1/2009
DQ095616	China	2005	2.2	A/Brown-headed Gull/Qinghai/3/05
DQ835313	China	2006	2.3.4	A/China/GD01/2006
EU263981	China	2006	2.3.4	A/China/GD02/2006
AY651353	Hong Kong	2003	9	A/Ck/HK/2133.1/2003
AY651357	Hong Kong	2003	1	A/Ck/HK/FY157/2003
AY651354	Hong Kong	2003	1	A/Ck/HK/NT93/2003
AY651356	Hong Kong	2003	1	A/Ck/HK/SSP141/2003
AY651355	Hong Kong	2003	9	A/Ck/HK/WF157/2003
AY651364	China	2004	2.3.1	A/Dk/HN/303/2004
DQ095629	China	2005	2.3.4	A/Duck/Fujian/1734/05
DQ320922	China	2005	2.2	A/Environment/Qinghai/31/2005
FJ492882	China	2005	2.3.4	A/Fujian/1/2005
FJ492883	China	2007	2.3.4	A/Fujian/1/2007
DQ095628	China	2005	9	A/Goose/Shantou/1621/05
DQ100557	China	2005	2.2	A/Great black headed gull/Qinghai/1/2005
DQ095614	China	2005	2.2	A/Great black-headed gull/Qinghai/2/2005
FJ492884	China	2006	2.3.4	A/Guangdong/01/2006
CY098702	China	2008	2.3.4	A/Guangdong/1/2008
CY098655	China	2006	2.3.4	A/Guangdong/2/2006
DQ842489	China	2006	2.3.4	A/Guangzhou/1/2006
DQ992780	China	2006	2.2	A/Guinea fowl/Shantou/1341/2006
AY575869	Hong Kong	2003	1	A/HK/212/03
EF541401	Hong Kong	2004	1	A/Hong Kong/213/2003
CY098641	China	2004	2.3.4	A/Hubei/1/2006
FJ492879	China	2004	2.3.4	A/Hunan/1/2006
CY098688	China	2004	2.3.4	A/Hunan/1/2008
CY098723	China	2004	2.3.4	A/Hunan/1/2009
CY098751	China	2004	2.3.4	A/Hunan/2/2009
EU311220	India	2004	1	A/India/m777/2007
CY036077	Hong Kong	2007	2.3.4	A/Japanese white-eye/Hong Kong/737/2007

EU434694	China	2007	2.3.4	A/Jiangsu/2/2007
KC784948	China	2007	2.3.4	A/Jiangsu/4/2007
KC784946	China	2008	2.3.4	A/Jiangsu/6/2008
FJ492885	China	2005	2.3.4	A/Jiangxi/1/2005
CY098716	China	2009	2.3.4	A/shandong/1/2009
CY098634	China	2006	2.3.4	A/Shanghai/1/2006
EF137706	China	2006	2.3.4	A/Shenzhen/406H/2006
FJ492881	China	2006	2.3.4	A/Sichuan/1/2006
CY098603	China	2006	2.3.4	A/Sichuan/2/2006
CY098648	China	2006	2.3.4	A/Sichuan/3/2006
FJ492886	China	2006	2.2	A/Xinjiang/1/2006
CY098730	China	2009	2.3.4	A/Xinjiang/1/2009
FJ492880	China	2006	2.3.4	A/Zhejiang/1/2006
DQ643809	China	2006	2.3.4	A/Zhejiang/16/2006
GU050317	Hong Kong	2007	2.3.4	A/avian/Hong Kong/0719/2007
GU050310	Hong Kong	2007	2.3.4	A/avian/Hong Kong/2065/2007
GU050333	Hong Kong	2007	2.3.4	A/avian/Hong Kong/2372/2007
DQ137873	China	2005	2.2	A/bar-headed goose/Qinghai/0510/05
HM172085	China	2006	2.2	A/bar-headed goose/Qinghai/1-HVRI/2006
HQ020365	China	2007	2.2	A/bar-headed goose/Qinghai/2/2007
HM172454	China	2005	2.2	A/bar-headed goose/Qinghai/3/2005
DQ822563	China	2006	2.2	A/bar-headed goose/Qinghai/F/2006
FJ461725	China	2007	2.2	A/bar-headed goose/Qinghai/F/2007
HM172087	China	2006	2.2	A/bar-headed goose/Tibet/8/2006
AY651373	Hong Kong	2003	1	A/black headed gull/HK/12.1/2003
DQ100554	China	2005	2.2	A/black-headed goose/Qinghai/1/2005
DQ100555	China	2005	2.2	A/black-headed goose/Qinghai/2/2005
DQ100556	China	2005	2.2	A/black-headed gull/Qinghai/1/2005
DQ822564	China	2006	2.2	A/black-headed gull/Qinghai/3/2006
AY741213	China	2004	6	A/blackbird/Hunan/1/2004
CY036109	Hong Kong	2007	2.3.4	A/blue magpie/Hong Kong/1993/2007
CY036141	Hong Kong	2007	2.3.4	A/chestnut munia/Hong Kong/2442/2007
AY830774	China	2004	9	A/chick/Macheng/2004
FJ784842	China	2007	2.3.4	A/chicken/Anhui/1089/2007
HM172095	China	2004	9	A/chicken/Anhui/39/2004
EF553330	China	2006	9	A/chicken/Anhui/T5/2006
EU008592	China	2006	9	A/chicken/Anhui/T6/2006
FJ839920	India	2008	2.2.2	A/chicken/Assam/140187/2008
GU066389	India	2008	2.2.2	A/chicken/Assam/142007/2008
HQ156765	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/1151-10/2010
HQ156776	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/1151-11/2010
HQ156760	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/1151-9/2010
JQ409047	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-10/2010
JN795910	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-2/2011
JN795918	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-20/2011
JN795919	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-21/2011
JN795920	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-23/2011
JQ409053	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-24/2011
JQ409054	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-25/2011

JQ409055	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-26/2011
JN795921	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-27/2011
JN795922	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-28/2011
JN795923	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-29/2011
JN795924	Bangladesh	2011	2.3.4	A/chicken/Bangladesh/11rs1984-30/2011
JN795926	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-35/2011
JN795927	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-36/2011
JN795928	Bangladesh	2011	2.3.4	A/chicken/Bangladesh/11rs1984-37/2011
JQ409043	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-4/2010
JN795929	Bangladesh	2011	2.2.2	A/chicken/Bangladesh/11rs1984-44/2011
JN795911	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-5/2010
JN795912	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-6/2010
JQ409044	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-7/2010
JQ409045	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-8/2010
JQ409046	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/11rs1984-9/2010
CY043380	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/362/2007
CY043378	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/363/2007
CY043381	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/364/2007
CY043376	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/376/2007
CY043377	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/380/2007
CY043355	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/382/2007
CY043375	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/394/2007
CY043366	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/490/2007
CY043379	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/531/2007
KF888416	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/9636/2010
JN679058	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/BL-4/2007
JQ609542	Bangladesh	2010	2.2.2	A/chicken/Bangladesh/BL-470/2010
CY043374	Bangladesh	2009	2.2.2	A/chicken/Bangladesh/CD-08(09)BL-418/2009
CY043361	Bangladesh	2008	2.2.2	A/chicken/Bangladesh/CD-48-BL-165/2008
CY043369	Bangladesh	2008	2.2.2	A/chicken/Bangladesh/CD-590(08)-BL-410/2008
CY043372	Bangladesh	2008	2.2.2	A/chicken/Bangladesh/CD586-08-BL-409/2008
CY043362	Bangladesh	2008	2.2.2	A/chicken/Bangladesh/FD(B)-120-BL-148/2008
CY043359	Bangladesh	2007	2.2.2	A/chicken/Bangladesh/FDIL(G)-502/2007
CY066004	Bhutan	2010	2.2.2	A/chicken/Bhutan/248006/2010
CY066012	Bhutan	2010	2.2.2	A/chicken/Bhutan/248007/2010
CY063473	Bhutan	2010	2.2.2	A/chicken/Bhutan/248009/2010
CY063481	Bhutan	2010	2.2.2	A/chicken/Bhutan/248015/2010
KC631944	China	2011	2.3.4	A/chicken/China/JX/2011
HM172096	China	2007	2.3.4	A/chicken/Fujian/1/2007
DQ992822	China	2005	2.3.4	A/chicken/Fujian/10039/2005
DQ992823	China	2005	2.3.4	A/chicken/Fujian/10313/2005
DQ320876	China	2005	9	A/chicken/Fujian/1042/2005
DQ992824	China	2005	2.3.4	A/chicken/Fujian/10567/2005
DQ992828	China	2005	2.3.4	A/chicken/Fujian/11933/2005
DQ992830	China	2005	2.3.4	A/chicken/Fujian/12239/2005
DQ992831	China	2006	2.3.4	A/chicken/Fujian/584/2006
HM172075	China	2004	9	A/chicken/Gansu/44/2004
AY609312	China	2004	2.5	A/chicken/Guangdong/174/04
AY737289	China	2004	2.3.1	A/chicken/Guangdong/191/04

EU243146	China	2005	7	A/chicken/Hebei/126/2005
DQ343150	China	2005	7	A/chicken/Hebei/326/2005
EU243126	China	2005	7	A/chicken/Hebei/706/2005
HM172081	China	2009	7.2	A/chicken/Hebei/A-8/2009
DQ080022	China	2004	6	A/chicken/Henan/01/2004
AY950232	China	2004	9	A/chicken/Henan/12/2004
FJ784843	China	2006	2.3.4	A/chicken/Henan/1362/2006
AY950234	China	2004	9	A/chicken/Henan/16/2004
AY950231	China	2004	9	A/chicken/Henan/210/2004
HM172080	China	2006	7.2	A/chicken/Henan/A-7/2006
DQ992836	Hong Kong	2006	2.3.4	A/chicken/Hong Kong/282/2006
KC784945	Hong Kong	2003	9	A/chicken/Hong Kong/369/2003
KF169906	Hong Kong	2008	2.3.4	A/chicken/Hong Kong/8825-2/2008
DQ992841	Hong Kong	2006	2.3.4	A/chicken/Hong Kong/947/2006
GU052486	Hong Kong	2006	2.3.4	A/chicken/Hong Kong/D-06-0947/2006
EF670482	China	2004	9	A/chicken/Hubei/14/2004
FJ784851	China	2007	2.3.4	A/chicken/Hubei/2856/2007
FJ784853	China	2007	2.3.4	A/chicken/Hubei/3002/2007
AY684706	China	2004	9	A/chicken/Hubei/327/2004
AY770079	China	2004	9	A/chicken/Hubei/489/2004
DQ997147	China	2003	0	A/chicken/Hubei/wn/2003
DQ997156	China	2003	7	A/chicken/Hubei/wo/2003
HM172074	China	2009	2.3.4	A/chicken/Hunan/1/2009
FJ784847	China	2007	2.3.4	A/chicken/Hunan/1793/2007
HM172112	China	2005	2.3.4	A/chicken/Hunan/21/2005
FJ784854	China	2006	2.3.4	A/chicken/Hunan/3157/2006
HM172114	China	2004	9	A/chicken/Hunan/41/2004
DQ320910	China	2005	2.3.1	A/chicken/Hunan/999/2005
DQ997396	China	2004	6	A/chicken/Hunan/fg/2004
CY090116	India	2010	2.2.2	A/chicken/India/241272/2010
CY111057	India	2008	2.2.2	A/chicken/India/81753/2008
CY111065	India	2008	2.2.2	A/chicken/India/81754/2008
CY090124	India	2008	2.2.2	A/chicken/India/81766/2008
CY111073	India	2008	2.2.2	A/chicken/India/81890/2008
CY111081	India	2008	2.2.2	A/chicken/India/82544/2008
CY111089	India	2008	2.2.2	A/chicken/India/82580/2008
CY111097	India	2008	2.2.2	A/chicken/India/82616/2008
CY111105	India	2008	2.2.2	A/chicken/India/83093/2008
CY111113	India	2008	2.2.2	A/chicken/India/85459/2008
CY111121	India	2008	2.2.2	A/chicken/India/96880/2008
GQ917223	India	2008	2.2.2	A/chicken/India/AS-NIV15983/2008
EF362418	India	2006	2.2	A/chicken/India/NIV33487/06
GQ917225	India	2008	2.2.2	A/chicken/India/WB-NIV16915/2008
GQ917227	India	2009	2.2.2	A/chicken/India/WB-NIV16924/2009
CY046070	India	2008	2.2.2	A/chicken/India/WB-NIV2653/2008
CY046077	India	2008	2.2.2	A/chicken/India/WB-NIV2656/2008
CY046079	India	2008	2.2.2	A/chicken/India/WB-NIV2664/2008
CY046081	India	2008	2.2.2	A/chicken/India/WB-NIV2665/2008
CY046083	India	2008	2.2.2	A/chicken/India/WB-NIV2670/2008

CY046085	India	2008	2.2.2	A/chicken/India/WB-NIV2800/2008
CY046089	India	2008	2.2.2	A/chicken/India/WB-NIV2806/2008
CY046091	India	2008	2.2.2	A/chicken/India/WB-NIV2807/2008
CY046095	India	2008	2.2.2	A/chicken/India/WB-NIV2812/2008
CY046097	India	2008	2.2.2	A/chicken/India/WB-NIV2813/2008
CY046107	India	2008	2.2.2	A/chicken/India/WB-NIV527/2008
CY046112	India	2008	2.2.2	A/chicken/India/WB-NIV529/2008
GQ917231	India	2009	2.2.2	A/chicken/India/WB-NIV92456/2009
GQ917229	India	2009	2.2.2	A/chicken/India/WB-NIV96526/2009
FJ010993	India	2006	2.2	A/chicken/Jalgaon/12419/2006
FJ010985	India	2006	2.2	A/chicken/Jalgaon/13732/2006
FJ010977	India	2006	2.2	A/chicken/Jalgaon/13735/2006
DQ887062	India	2006	2.2	A/chicken/Jalgaon/8824/2006
HM172092	China	2008	7.2	A/chicken/Jiangsu/18/2008
KC631943	China	2009	2.3.4	A/chicken/Jiangsu/WJ/2009
KC631942	China	2010	2.3.4	A/chicken/Jiangsu/XZ/2010
KC709803	China	2010	2.3.4	A/chicken/Jiangsu/k0101/2010
DQ997268	China	2003	0	A/chicken/Jilin/ha/2003
DQ997318	China	2003	0	A/chicken/Jilin/hj/2003
DQ997325	China	2004	0	A/chicken/Jilin/hk/2004
DQ997352	China	2003	5	A/chicken/Jilin/hn/2003
DQ997355	China	2003	5	A/chicken/Jilin/ho/2003
DQ997370	China	2003	5	A/chicken/Jilin/hq/2003
EU233691	South Korea	2006	2.2	A/chicken/Korea/CA7/2006
EU233675	South Korea	2006	2.2	A/chicken/Korea/IS/2006
EU233683	South Korea	2006	2.2	A/chicken/Korea/IS2/2006
EU233699	South Korea	2006	2.2	A/chicken/Korea/IS3/2006
EF541412	South Korea	2003	2.5	A/chicken/Korea/es/2003
HM172453	China	2005	2.2	A/chicken/Liaoning/23/2005
HM172078	China	2007	7	A/chicken/Liaoning/A-1/2007
HM172077	China	2006	7.2	A/chicken/Liaoning/A-11/2006
FJ719834	India	2007	2.2	A/chicken/Manipur/NIV9743/2007
GU454581	India	2006	2.2	A/chicken/Nandurbar/7966/2006
GU354065	India	2006	2.2	A/chicken/Nandurbar/7979/2006
DQ887061	India	2006	2.2	A/chicken/Navapur/India/7972/2006
HM172093	China	2009	2.3.4	A/chicken/shandong/A-1/2009
HM172073	China	2006	7	A/chicken/shandong/A-10/2006
HM172082	China	2006	7	A/chicken/shandong/A-5/2006
DQ767725	China	2004	0	A/chicken/shandong/K01/2004
KC709802	China	2010	2.3.4	A/chicken/shandong/K0701/2010
KC631945	China	2010	2.3.4	A/chicken/shandong/k0603/2010
DQ992779	China	2006	2.3.4	A/chicken/Shantou/1233/2006
CY028954	China	2003	9	A/chicken/Shantou/133/2003
CY028959	China	2003	2.5	A/chicken/Shantou/3744/2003
DQ992785	China	2006	2.3.4	A/chicken/Shantou/3840/2006
DQ992786	China	2006	2.3.4	A/chicken/Shantou/3923/2006
HM172069	China	2005	2.3.4	A/chicken/Sichuan/81/2005
GU354081	India	2009	2.2.2	A/chicken/Sikkim/151464/2009
CY080355	India	2009	2.2.2	A/chicken/Sikkim/151466/2009

HM172086	China	2008	2.3.4	A/chicken/Tibet/6/2008
GU083637	India	2008	2.2.2	A/chicken/West Bengal/100879/2008
GU083626	India	2008	2.2.2	A/chicken/West Bengal/106181/2008
GU354073	India	2008	2.2.2	A/chicken/West Bengal/142121/2008
GU356583	India	2009	2.2.2	A/chicken/West Bengal/148713/2009
GU271998	India	2009	2.2.2	A/chicken/West Bengal/155505/2009
CY080363	India	2009	2.2.2	A/chicken/West Bengal/155508/2009
GU083653	India	2009	2.2.2	A/chicken/West Bengal/162642/2009
GU083661	India	2009	2.2.2	A/chicken/West Bengal/170564/2009
CY080371	India	2009	2.2.2	A/chicken/West Bengal/174881/2009
GU272006	India	2009	2.2.2	A/chicken/West Bengal/193936/2009
CY061294	India	2010	2.2.2	A/chicken/West Bengal/239020/2010
CY061302	India	2010	2.2.2	A/chicken/West Bengal/239022/2010
EU871811	India	2008	2.2.2	A/chicken/West Bengal/80995/2008
EU871814	India	2008	2.2.2	A/chicken/West Bengal/81010/2008
CY080379	India	2008	2.2.2	A/chicken/West Bengal/81537/2008
GU083618	India	2008	2.2	A/chicken/West Bengal/81760/2008
CY080387	India	2008	2.2.2	A/chicken/West Bengal/82583/2008
GU083645	India	2008	2.2.2	A/chicken/West Bengal/82613/2008
CY080395	India	2008	2.2.2	A/chicken/West Bengal/83098/2008
HM172108	China	2005	7	A/chicken/Xinjiang/16/2005
HM172102	China	2005	7	A/chicken/Xinjiang/17/2005
HM172091	China	2006	7	A/chicken/Xinjiang/27/2006
HM172090	China	2006	7	A/chicken/Xinjiang/28/2006
HM172094	China	2005	7	A/chicken/Xinjiang/53/2005
HM172111	China	2005	7	A/chicken/Xinjiang/54/2005
HM172099	China	2005	7	A/chicken/Xinjiang/67/2005
HM172106	China	2005	7	A/chicken/Xinjiang/68/2005
HM172103	China	2005	7	A/chicken/Xinjiang/78/2005
AY623430	China	2004	6	A/chicken/Yichang/lung-1/04
DQ520855	China	2005	2.3.4	A/chicken/Zhejiang/24/2005
CY028960	China	2003	9	A/chukar/Shantou/4690/2003
CY036125	Hong Kong	2007	2.3.4	A/common kestrel/Hong Kong/2372/2007
DQ992843	Hong Kong	2006	2.3.4	A/common magpie/Hong Kong/2125/2006
DQ992844	Hong Kong	2006	2.3.4	A/common magpie/Hong Kong/2256/2006
DQ992839	Hong Kong	2006	2.3.4	A/common magpie/Hong Kong/645/2006
JQ966928	China	2003	1	A/condor/Guangdong/139/2003
CY036061	Hong Kong	2007	2.3.4	A/crested goshawk/Hong Kong/458/2007
DQ992838	Hong Kong	2006	2.3.4	A/crested myna/Hong Kong/540/2006
GQ478333	India	2008	2.2.2	A/crow/Assam/142119/2008
KC690156	China	2006	2.3.4	A/domestic green-winged teal/Hunan/3450/2006
EU430496	China	2005	7	A/domestic green-winged teal/Hunan/67/2005
EU430511	China	2005	7	A/domestic green-winged teal/Hunan/79/2005
CY098790	China	2009	2.3.4	A/duck feces/Hebei/5/2009
HM172115	China	2006	2.3.4	A/duck/Anhui/1/06
HM172107	China	2005	2.3.4	A/duck/Anhui/56/2005
DQ992825	China	2005	2.3.4	A/duck/Fujian/10934/2005
DQ992826	China	2005	2.3.4	A/duck/Fujian/11094/2005
DQ992827	China	2005	2.3.4	A/duck/Fujian/11311/2005

DQ992829	China	2005	2.3.4	A/duck/Fujian/12032/2005
DQ992832	China	2006	2.3.4	A/duck/Fujian/668/2006
DQ992833	China	2006	2.3.4	A/duck/Fujian/671/2006
DQ992834	China	2006	2.3.4	A/duck/Fujian/720/2006
DQ320875	China	2005	9	A/duck/Fujian/897/2005
DQ992819	China	2005	2.3.4	A/duck/Fujian/9651/2005
AY737304	China	2004	9	A/duck/Guangdong/173/04
DQ320901	China	2005	9	A/duck/Guangzhou/20/2005
FJ784844	China	2006	2.3.4	A/duck/Henan/1647/2006
FJ784845	China	2006	2.3.4	A/duck/Henan/1650/2006
FJ784846	China	2006	2.3.4	A/duck/Henan/1652/2006
FJ784852	China	2007	2.3.4	A/duck/Hubei/2911/2007
DQ520856	China	2005	2.3.1	A/duck/Hubei/3/2005
HM172071	China	2005	2.3.4	A/duck/Hubei/49/2005
EU594349	China	2006	2.3.4	A/duck/Hubei/Hangmei01/2006
DQ997163	China	2003	2.5	A/duck/Hubei/wp/2003
DQ997172	China	2003	2.5	A/duck/Hubei/wq/2003
HM172088	China	2007	2.3.4	A/duck/Hunan/11/2007
DQ095630	China	2005	2.3.1	A/duck/Hunan/114/05
DQ320902	China	2005	2.3.1	A/duck/Hunan/127/2005
CY028968	China	2003	1	A/duck/Hunan/1386/2003
DQ320903	China	2005	2.3.1	A/duck/Hunan/139/2005
DQ320904	China	2005	2.3.1	A/duck/Hunan/149/2005
EF670479	China	2004	2.3.1	A/duck/Hunan/15/2004
DQ320905	China	2005	2.3.1	A/duck/Hunan/152/2005
DQ320906	China	2005	2.3.1	A/duck/Hunan/157/2005
FJ784848	China	2007	2.3.4	A/duck/Hunan/1930/2007
FJ784849	China	2007	2.3.4	A/duck/Hunan/1964/2007
FJ784850	China	2007	2.3.4	A/duck/Hunan/1994/2007
HM172097	China	2006	2.3.4	A/duck/Hunan/29/2006
CY028965	China	2003	OUTLIERS	A/duck/Hunan/300/2003
DQ992790	China	2006	2.3.4	A/duck/Hunan/324/2006
FJ784855	China	2006	2.3.4	A/duck/Hunan/3315/2006
FJ784856	China	2006	2.3.4	A/duck/Hunan/3340/2006
CY028966	China	2003	OUTLIERS	A/duck/Hunan/378/2003
CY028969	China	2004	2.3.1	A/duck/Hunan/533/2004
FJ784841	China	2006	2.3.4	A/duck/Hunan/689/2006
HM172098	China	2004	2.3.1	A/duck/Hunan/69/2004
HM172105	China	2004	2.3.1	A/duck/Hunan/70/2004
CY028970	China	2004	2.3.1	A/duck/Hunan/733/2004
CY028967	China	2003	2.1.1	A/duck/Hunan/782/2003
DQ992792	China	2006	2.3.4	A/duck/Hunan/856/2006
DQ992793	China	2006	2.3.4	A/duck/Hunan/988/2006
CY046102	India	2008	2.2.2	A/duck/India/TR-NIV4396/2008
HM172100	China	2005	2.3.4	A/duck/Jiangxi/80/2005
EU233707	South Korea	2006	2.2	A/duck/Korea/Asan5/2006
EU233715	South Korea	2006	2.2	A/duck/Korea/Asan6/2006
AY676036	South Korea	2003	2.5	A/duck/Korea/ESD1/03
JN613381	Nepal	2010	2.2.2	A/duck/Nepal/PTS58/2010

JN613382	Nepal	2010	2.2.2	A/duck/Nepal/PTS60/2010
GU596984	China	2008	2.3.4	A/duck/shandong/009/2008
AY854190	China	2004	0	A/duck/shandong/093/2004
DQ992776	China	2005	2.3.4	A/duck/Shantou/13323/2005
DQ320914	China	2003	OUTLIERS	A/duck/Shantou/4610/2003
GU252822	India	2008	2.2.2	A/duck/Tripura/103597/2008
AY676034	Hong Kong	2003	1	A/egret/Hong Kong/757.2/2003
KF888538	Bangladesh	2011	2.2.2	A/environment/Bangladesh/9675/2011
GU182230	China	2007	7.2	A/environment/Hunan/1-12/2007
GU182222	China	2007	7.2	A/environment/Hunan/1-35/2007
GU182214	China	2007	2.3.4	A/environment/Hunan/1-8/2007
GU182238	China	2007	7.2	A/environment/Hunan/2-16/2007
GU182182	China	2008	2.3.4	A/environment/Hunan/6-69/2008
EU233731	South Korea	2006	2.2	A/environment/Korea/W149/2006
EU233739	South Korea	2006	2.2	A/environment/Korea/W150/2006
FJ455820	China	2008	0	A/environment/Qinghai/1/2008
CY098838	China	2009	2.3.4	A/environment/Xinjiang/6/2009
DQ997405	China	2003	4	A/goose/Fujian/bb/2003
KC784944	China	2005	2.3.4	A/goose/Guangdong/08/2005
HM172089	China	2004	9	A/goose/Guangdong/72/2004
DQ842487	China	2006	2.3.4	A/goose/Guangzhou/471/2006
HM172070	China	2005	2.3.4	A/goose/Hubei/65/2005
DQ997276	China	2003	2.5	A/goose/Jilin/hb/2003
DQ992777	China	2005	2.3.4	A/goose/Shantou/18442/2005
DQ992781	China	2006	2.5	A/goose/Shantou/2086/2006
DQ320915	China	2005	9	A/goose/Shantou/2216/2005
DQ992778	China	2006	2.5	A/goose/Shantou/239/2006
DQ992783	China	2006	2.3.4	A/goose/Shantou/3265/2006
DQ992784	China	2006	2.3.4	A/goose/Shantou/3295/2006
GU252830	India	2008	2.2.2	A/goose/Tripura/103596/2008
HM172083	China	2006	2.2	A/great cormorant/Tibet/12/2006
CY036101	Hong Kong	2007	2.3.4	A/house crow/Hong Kong/1203/2007
CY036069	Hong Kong	2007	2.3.4	A/house crow/Hong Kong/719/2007
GU220793	China	2007	2.3.4	A/lesser kestrel/Heilongjiang/194/2007
DQ992840	Hong Kong	2006	2.3.4	A/little egret/Hong Kong/718/2006
CY036157	Hong Kong	2007	2.3.4	A/long-tailed shrike/Hong Kong/2762/2007
AB530992	Japan	2009	0	A/mallard/Hokkaido/24/2009
DQ320916	China	2005	9	A/migratory duck/Jiangxi/1653/2005
DQ320919	China	2005	2.2	A/migratory duck/Jiangxi/2136/2005
DQ320920	China	2005	2.2	A/migratory duck/Jiangxi/2295/2005
AB525191	Japan	2007	2.2	A/mountain hawk-eagle/Kumamoto/1/07
DQ992845	Hong Kong	2006	2.3.4	A/munia/Hong Kong/2454/2006
JF732739	China	2003	0	A/ostrich/Suzhou/097/2003
CY028957	China	2003	3	A/partridge/Shantou/2886/2003
AY651362	Hong Kong	2004	9	A/peregrine falcon/HK/D0028/2004
CY036269	Hong Kong	2008	2.3.4	A/peregrine falcon/Hong Kong/2142/2008
AB521159	Hong Kong	2009	2.3.4	A/peregrine falcon/Hong Kong/810/2009
CY028958	China	2003	3	A/pheasant/Shantou/3535/2003
CY028953	China	2003	1	A/pheasant/Shantou/40/2003

HM172456	China	2006	2.2	A/pied magpie/Liaoning/7/2006
FJ517645	China	2005	2.3.1	A/pigeon/Zhejiang/17/2005
GQ227359	China	2007	2.2	A/pika/Qinghai/BI/2007
FJ390061	China	2007	0	A/plateau pika/Qinghai/04/2007
EU233723	South Korea	2006	2.2	A/quail/Korea/KJ4/2006
EU420038	China	2005	OUTLIERS	A/raccoon dog/shandong/sd1/2005
EU420046	China	2005	OUTLIERS	A/raccoon dog/shandong/sd2/2005
DQ992837	Hong Kong	2006	2.3.4	A/robin/Hong Kong/366/2006
DQ992835	Hong Kong	2006	2.3.4	A/robin/Hong Kong/75/2006
CY036133	Hong Kong	2007	2.3.4	A/scaly-breasted munia/Hong Kong/2433/2007
CY036149	Hong Kong	2007	2.3.4	A/scaly-breasted munia/Hong Kong/2572/2007
CY036053	Hong Kong	2007	2.3.4	A/scaly-breasted munia/Hong Kong/45/2007
HM172101	China	2006	2.3.4	A/shrike/Tibet/13/2006
CY028955	China	2003	9	A/silky chicken/Shantou/540/2003
CY036117	Hong Kong	2007	2.3.4	A/silver-eared mesia/Hong Kong/2065/2007
DQ997392	China	2004	6	A/swine/Anhui/ca/2004
DQ997076	China	2004	7	A/swine/Anhui/cb/2004
AY747609	China	2003	5	A/swine/Fujian/1/2003
DQ432045	China	2003	5	A/swine/Fujian/2003
KC683522	China	2008	7.2	A/swine/Jiangsu/1/2008
KC683523	China	2009	2.3.4	A/swine/Jiangsu/2/2009
AY646424	China	2003	0	A/swine/shandong/2/03
EU532423	China	2005	OUTLIERS	A/tiger/Shanghai/01/2005
AY741215	China	2004	6	A/tree sparrow/Henan/1/2004
AY741217	China	2004	7	A/tree sparrow/Henan/2/2004
AY741219	China	2004	6	A/tree sparrow/Henan/3/2004
AY741221	China	2004	6	A/tree sparrow/Henan/4/2004
GQ202211	China	2008	2.3.4	A/tree sparrow/Jiangsu/1/2008
CY098766	China	2009	2.3.4	A/water/Hebei/1/2009
CY098774	China	2009	2.3.4	A/water/Hebei/2/2009
CY098782	China	2009	2.3.4	A/water/Hebei/3/2009
CY098845	China	2009	2.3.4	A/water/Hunan/3/2009
CY098830	China	2009	2.3.4	A/water/Xinjiang/3/2009
CY036085	Hong Kong	2007	2.3.4	A/white-backed munia/Hong Kong/828/2007
GU186700	Mongolia	2005	2.2	A/whooper swan/Mongolia/244/2005
JX258651	South Korea	2009	0	A/wild bird/Korea/A344-2/2009
AY950235	China	2004	9	A/wild duck/Guangdong/314/2004
EU329177	China	2005	2.3.4	A/wild duck/Hunan/021/2005
EU329186	China	2005	2.3.4	A/wild duck/Hunan/211/2005
JF510041	South Korea	2009	0	A/wild duck/Korea/CSM4-12/2009
JX497768	South Korea	2009	0	A/wild duck/Korea/SNU50-5/2009
HM172084	China	2006	2.2	A/wild duck/Liaoning/8/2006
JX534549	China	2011	7.2	A/wild duck/shandong/1/2011
JX534565	China	2011	2.3.4	A/wild duck/shandong/628/2011
DQ659327	China	2005	2.2	St Jude H5N1 influenza seed virus 163222
DQ659326	Mongolia	2005	2.2	St Jude H5N1 influenza seed virus 163243
AY651358	Hong Kong	2003	2.1.1	A/Ck/HK/YU324/2003
EU243133	China	2005	7	A/chicken/Hebei/102/2005
CY090108	India	2008	2.2.2	A/chicken/India/100071/2008

HM172455	China	2004	OUTLIERS	A/chicken/Jiangxi/25/2004
AY653200	China	2004	OUTLIERS	A/chicken/Jilin/9/2004
DQ997341	China	2003	5	A/chicken/Jilin/hm/2003
DQ997361	China	2003	0	A/chicken/Jilin/hp/2003
DQ997547	China	2003	0	A/chicken/Jilin/xw/2003
DQ992787	China	2005	2.3.4	A/duck/Hunan/5106/2005
KC784947	China	2005	2.2	A/goose/Jilin/514/2005
JX013485	China	2005	9	A/parrot/Guangdong/C99/2005
AY651366	China	2004	2.3.2	A/Ph/ST/44/2004
AY737296	China	2004	2.3.2	A/chicken/Guangdong/178/04
DQ320923	Hong Kong	2004	2.3.2	A/grey_heron/Hong_Kong/728/2004
DQ320924	Hong Kong	2004	2.3.2	A/grey_heron/Hong_Kong/837/2004
CY028961	China	2004	2.3.2	A/silky_chicken/Shantou/475/2004
HM172116	China	2004	2.3.2	A/duck/Guangdong/23/2004
DQ095626	China	2005	2.3.2	A/Chicken/Shantou/810/05
DQ320925	Hong Kong	2005	2.3.2	A/Chinese_pond_heron/Hong_Kong/18/2005
DQ095627	China	2005	2.3.2	A/Quail/Shantou/911/05
EU874899	China	2005	2.3.2	A/chicken/Guangdong/1/2005
DQ992797	China	2005	2.3.2	A/duck/Yunnan/4400/2005
DQ992799	China	2005	2.3.2	A/duck/Yunnan/4589/2005
DQ992803	China	2005	2.3.2	A/duck/Yunnan/5251/2005
DQ992806	China	2005	2.3.2	A/duck/Yunnan/5820/2005
DQ992807	China	2005	2.3.2	A/duck/Yunnan/5877/2005
DQ992812	China	2005	2.3.2	A/duck/Yunnan/6607/2005
DQ992795	China	2005	2.3.2	A/goose/Yunnan/3720/2005
DQ992796	China	2005	2.3.2	A/goose/Yunnan/4129/2005
DQ992798	China	2005	2.3.2	A/goose/Yunnan/4494/2005
DQ992800	China	2005	2.3.2	A/goose/Yunnan/4804/2005
DQ992808	China	2005	2.3.2	A/goose/Yunnan/6027/2005
DQ992811	China	2005	2.3.2	A/goose/Yunnan/6368/2005
EU635874	China	2005	2.3.2	A/chicken/Yunnan/chuxiong01/2005
DQ320911	China	2005	2.3.2	A/duck/Hunan/1265/2005
DQ320912	China	2005	2.3.2	A/duck/Hunan/1608/2005
DQ320913	China	2005	2.3.2	A/duck/Hunan/1652/2005
DQ992813	China	2006	2.3.2	A/duck/Yunnan/1126/2006
CY036045	Hong Kong	2006	2.3.2	A/peregrine_falcon/Hong_Kong/5211/2006
DQ992782	China	2006	2.3.2	A/pheasant/Shantou/2239/2006
CY036181	Hong Kong	2007	2.3.2	A/Daurian_starling/Hong_Kong/1532/2007
GU182142	China	2007	2.3.2	A/chicken/Hunan/3/2007
GQ290463	China	2007	2.3.2	A/environment/Dongting_Lake/Hunan/5-41/2007
GU182198	China	2007	2.3.2	A/environment/Hunan/5-25/2007
GU182206	China	2007	2.3.2	A/environment/Hunan/5-32/2007
CY036213	Hong Kong	2007	2.3.2	A/grey_heron/Hong_Kong/3088/2007
CY036189	Hong Kong	2007	2.3.2	A/house_crow/Hong_Kong/5288/2007
CY036197	Hong Kong	2007	2.3.2	A/little_egret/Hong_Kong/8550/2007
CY036205	Hong Kong	2007	2.3.2	A/little_egret/Hong_Kong/8863/2007
CY036093	Hong Kong	2007	2.3.2	A/peregrine_falcon/Hong_Kong/1143/2007
GQ227380	China	2007	2.3.2	A/pika/Qinghai/GRL/2007
GQ227367	China	2007	2.3.2	A/pika/Qinghai/HMH/2007

GQ227391	China	2007	2.3.2	A/pika/Qinghai/QW/2007
GQ227383	China	2007	2.3.2	A/pika/Qinghai/SHK/2007
CY036165	Hong Kong	2007	2.3.2	A/red-billed_starling/Hong_Kong/4925/2007
CY036221	Hong Kong	2007	2.3.2	A/common_buzzard/Hong_Kong/9213/2007
CY036173	Hong Kong	2007	2.3.2	A/common_magpie/Hong_Kong/5052/2007
GU182150	China	2007	2.3.2	A/duck/Hunan/3/2007
CY036229	Hong Kong	2008	2.3.2	A/black-crowned_night_heron/Hong_Kong/659/2008
GU182158	China	2008	2.3.2	A/chicken/Hunan/8/2008
GQ412053	South Korea	2008	2.3.2	A/chicken/Korea/Gimje/2008
GQ412051	South Korea	2008	2.3.2	A/chicken/Korea/ISQ250/2008
GQ412055	South Korea	2008	2.3.2	A/chicken/Korea/USQ284/2008
GQ412056	South Korea	2008	2.3.2	A/chicken/Korea/YAQ173/2008
GU182190	China	2008	2.3.2	A/environment/Hunan/6-45/2008
GU182174	China	2008	2.3.2	A/environment/Hunan/7-73/2008
CY036237	Hong Kong	2008	2.3.2	A/great_egret/Hong_Kong/807/2008
CY036245	Hong Kong	2008	2.3.2	A/grey_heron/Hong_Kong/1046/2008
AB517661	Hong Kong	2008	2.3.2	A/house_crow/Hong_Kong/7677/2008
CY036253	Hong Kong	2008	2.3.2	A/magpie_robin/Hong_Kong/1097/2008
CY036261	Hong Kong	2008	2.3.2	A/magpie_robin/Hong_Kong/1897/2008
AB436736	Japan	2008	2.3.2	A/whooper_swan/Akita/1/2008
AB458239	Japan	2008	2.3.2	A/whooper_swan/Aomori/1/2008
AB458247	Japan	2008	2.3.2	A/whooper_swan/Aomori/2/2008
AB436902	Japan	2008	2.3.2	A/whooper_swan/Hokkaido/2/2008
GU182166	China	2008	2.3.2	A/duck/Hunan/8/2008
GQ412052	South Korea	2008	2.3.2	A/duck/Korea/JEQ149/2008
GQ412054	South Korea	2008	2.3.2	A/duck/Korea/NSQ263/2008
AB521999	Mongolia	2009	2.3.2	A/bar-headed_goose/Mongolia/X25/2009
HM006730	Mongolia	2009	2.3.2	A/bar-headed_goose/Mongolia/X53/2009
AB523366	Mongolia	2009	2.3.2	A/bar-headed_goose/Mongolia/X54/2009
HQ020367	China	2009	2.3.2	A/brown-headed_gull/Qinghai/1/2009
HQ020368	China	2009	2.3.2	A/brown-headed_gull/Qinghai/2/2009
JN543373	China	2009	2.3.2	A/environment/Chang_Sha/1/2009
JN543374	China	2009	2.3.2	A/environment/Chang_Sha/2/2009
JN543378	China	2009	2.3.2	A/environment/Chang_Sha/25/2009
JN543375	China	2009	2.3.2	A/environment/Chang_Sha/3/2009
AB557629	Hong Kong	2009	2.3.2	A/feral_pigeon/Hong_Kong/3409/2009
HQ020369	China	2009	2.3.2	A/great_black-headed_gull/1/2009
HQ020370	China	2009	2.3.2	A/great_black-headed_gull/Qinghai/2/2009
HQ020371	China	2009	2.3.2	A/great_black-headed_gull/Qinghai/3/2009
HQ020372	China	2009	2.3.2	A/great_black-headed_gull/Qinghai/4/2009
HQ020373	China	2009	2.3.2	A/great_black-headed_gull/Qinghai/5/2009
HQ020374	China	2009	2.3.2	A/great_black-headed_gull/Qinghai/6/2009
HQ020375	China	2009	2.3.2	A/great_cormorant/Qinghai/1/2009
CY063318	China	2009	2.3.2	A/great_crested-grebe/Qinghai/1/2009
AB517663	Hong Kong	2009	2.3.2	A/grey_heron/Hong_Kong/779/2009
CY098291	Mongolia	2009	2.3.2	A/herring_gull/Mongolia/833T/2009
AB521161	Hong Kong	2009	2.3.2	A/large_billed_crow/Hong_Kong/885/2009
AB557633	Hong Kong	2009	2.3.2	A/oriental_magpie_robin/Hong_Kong/9298/2009
CY098293	Mongolia	2009	2.3.2	A/ruddy_shelduck/Mongolia/911T/2009

HM006736	Mongolia	2009	2.3.2	A/ruddy_shelduck/Mongolia/X42/2009
AB523368	Mongolia	2009	2.3.2	A/ruddy_shelduck/Mongolia/X63/2009
JF975561	China	2009	2.3.2	A/swan/Shanghai/10/2009
CY098853	China	2009	2.3.2	A/water/Hunan/7/2009
AB517665	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/2/2009
HM006741	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/4/2009
HM006742	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/5/2009
HM006743	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/6/2009
HM006745	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/7/2009
HM006746	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/8/2009
HM006747	Mongolia	2009	2.3.2	A/whooper_swan/Mongolia/9/2009
AB522001	Mongolia	2009	2.3.2	A/common_goldeneye/Mongolia/X59/2009
HM006733	Mongolia	2009	2.3.2	A/common_goldeneye/Mongolia/X60/2009
AB521163	Hong Kong	2009	2.3.2	A/crested_myna/Hong_Kong/1178/2009
HQ636461	Hong Kong	2010	2.3.2	A/Hong_Kong/6841/2010
CY098758	China	2010	2.3.2	A/Hubei/1/2010
JN807976	South Korea	2010	2.3.2	A/baikal_teal/Korea/Q524/2010
HQ020364	China	2010	2.3.2	A/bar-headed_goose/Qinghai/1/2010
JN807979	South Korea	2010	2.3.2	A/chicken/Korea/Iksan/2010
JN613388	Nepal	2010	2.3.2	A/chicken/Nepal/105/2010
JN613387	Nepal	2010	2.3.2	A/chicken/Nepal/111/2010
JN613386	Nepal	2010	2.3.2	A/chicken/Nepal/115/2010
JN613390	Nepal	2010	2.3.2	A/chicken/Nepal/2-53/2010
JN613389	Nepal	2010	2.3.2	A/chicken/Nepal/5-1cl/2010
JN613385	Nepal	2010	2.3.2	A/chicken/Nepal/81/2010
JN613383	Nepal	2010	2.3.2	A/chicken/Nepal/A135/2010
JN613384	Nepal	2010	2.3.2	A/chicken/Nepal/A136/2010
HQ020376	China	2010	2.3.2	A/great_crested_grebe/Qinghai/1/2010
AB677931	Japan	2010	2.3.2	A/hooded_crane/Kagoshima/4612J008/2010
HQ695910	South Korea	2010	2.3.2	A/mallard/Korea/1195/2010
JF699672	South Korea	2010	2.3.2	A/mandarin_duck/Korea/K10-480/2010
JF699673	South Korea	2010	2.3.2	A/mandarin_duck/Korea/K10-483/2010
JF699674	South Korea	2010	2.3.2	A/mandarin_duck/Korea/K10-485/2010
JN807993	South Korea	2010	2.3.2	A/mandarin_duck/Korea/Q525/2010
CY098292	Mongolia	2010	2.3.2	A/tundra_swan/Mongolia/1T/2010
AB677923	Japan	2010	2.3.2	A/tundra_swan/Tottori/12-002/2010
AB569348	Mongolia	2010	2.3.2	A/whooper_swan/Mongolia/1/2010
AB569607	Mongolia	2010	2.3.2	A/whooper_swan/Mongolia/11/2010
AB569609	Mongolia	2010	2.3.2	A/whooper_swan/Mongolia/21/2010
AB569353	Mongolia	2010	2.3.2	A/whooper_swan/Mongolia/7/2010
AB612909	Japan	2010	2.3.2	A/duck/Hokkaido/WZ101/2010
AB612901	Japan	2010	2.3.2	A/duck/Hokkaido/WZ83/2010
JN807985	South Korea	2010	2.3.2	A/duck/Korea/Cheonan/2010
JN613379	Nepal	2010	2.3.2	A/duck/Nepal/DTS22/2010
JN613380	Nepal	2010	2.3.2	A/duck/Nepal/DTS24/2010
JN202558	South Korea	2011	2.3.2	A/Mallard_duck/Korea/W401/2011
JN202559	South Korea	2011	2.3.2	A/Mallard_duck/Korea/W404/2011
JN807975	South Korea	2011	2.3.2	A/baikal_teal/Korea/Q34/2011
AB675740	Japan	2011	2.3.2	A/chicken/Aichi/T1/2011

JQ409048	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-16/2011
JQ409049	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-17/2011
JQ409050	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-18/2011
JQ409051	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-19/2011
JQ409052	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-22/2011
JQ409056	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-33/2011
JN795925	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-34/2011
JQ409057	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-40/2011
JQ409058	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-43/2011
JQ409059	Bangladesh	2011	2.3.2	A/chicken/Bangladesh/11rs1984-45/2011
CY089472	India	2011	2.3.2	A/chicken/India/CA0301/2011
CY089474	India	2011	2.3.2	A/chicken/India/CA0302/2011
CY089468	India	2011	2.3.2	A/chicken/India/CA0303/2011
CY089470	India	2011	2.3.2	A/chicken/India/CL03485/2011
CY089476	India	2011	2.3.2	A/chicken/India/TR0383/2011
JN807977	South Korea	2011	2.3.2	A/chicken/Korea/Asan90/2011
JN807978	South Korea	2011	2.3.2	A/chicken/Korea/IC546/2011
JN807980	South Korea	2011	2.3.2	A/chicken/Korea/PT412/2011
JN807981	South Korea	2011	2.3.2	A/chicken/Korea/SJ378/2011
JN807982	South Korea	2011	2.3.2	A/chicken/Korea/YS171/2011
AB675741	Japan	2011	2.3.2	A/chicken/Mie/1/2011
AB675739	Japan	2011	2.3.2	A/chicken/Miyazaki/M6/2011
JN646713	China	2011	2.3.2	A/duck/Zhejiang/213/2011
JN646714	China	2011	2.3.2	A/duck/Zhejiang/224/2011
JN646715	China	2011	2.3.2	A/duck/Zhejiang/2242/2011
JN646716	China	2011	2.3.2	A/duck/Zhejiang/2243/2011
JN646717	China	2011	2.3.2	A/duck/Zhejiang/2244/2011
JN646718	China	2011	2.3.2	A/duck/Zhejiang/2245/2011
JN646719	China	2011	2.3.2	A/duck/Zhejiang/2248/2011
JN807989	South Korea	2011	2.3.2	A/eurasian_eagle_owl/Korea/Q133/2011
JN807973	South Korea	2011	2.3.2	A/eurasian_eagle_owl/Korea/Q178/2011
JN807974	South Korea	2011	2.3.2	A/eurasian_eagle_owl/Korea/Q182/2011
JN807990	South Korea	2011	2.3.2	A/eurasian_eagle_owl/Korea/Q196/2011
JN807991	South Korea	2011	2.3.2	A/eurasian_sparrowhawk/Korea/Q94/2011
AB676810	Japan	2011	2.3.2	A/goshawk/Tochigi/64/2011
AB677899	Japan	2011	2.3.2	A/great_drested_grebe/Hyogo/2802E082/2011
AB621349	Japan	2011	2.3.2	A/greater_scaup/Hokkaido/2/2011
AB629702	Japan	2011	2.3.2	A/greater_scaup/Hokkaido/28/2011
AB677891	Japan	2011	2.3.2	A/mandarin_duck/Kochi/3901C005/2011
JF699675	South Korea	2011	2.3.2	A/mandarin_duck/Korea/K10-515/2011
JN807992	South Korea	2011	2.3.2	A/mandarin_duck/Korea/Q2/2011
AB677875	Japan	2011	2.3.2	A/mandarin_duck/Miyazaki/22M807-1/2011
AB677867	Japan	2011	2.3.2	A/mandarin_duck/Nagasaki/4202A023/2011
AB677859	Japan	2011	2.3.2	A/mandarin_duck/Oita/4402B056/2011
AB677883	Japan	2011	2.3.2	A/owl/Tokushima/3602A023/2011
AB677915	Japan	2011	2.3.2	A/peregrine_falcon/Aichi/2302O017/2011
AB629713	Japan	2011	2.3.2	A/peregrine_falcon/Aomori/7/2011
AB677907	Japan	2011	2.3.2	A/peregrine_falcon/Kyoto/2602A009/2011
AB617579	Japan	2011	2.3.2	A/peregrine_falcon/Tochigi/15/2011

JN807994	South Korea	2011	2.3.2	A/pheasant/Korea/PT411/2011
AB621345	Japan	2011	2.3.2	A/pintail/Hokkaido/1/2011
JN807995	South Korea	2011	2.3.2	A/quail/Korea/GC395/2011
AB629698	Japan	2011	2.3.2	A/tufted_duck/Fukushima/16/2011
AB615237	Japan	2011	2.3.2	A/tufted_duck/Fukushima/2/2011
AB675503	Japan	2011	2.3.2	A/tufted_duck/Fukushima/4/2011
AB675536	Japan	2011	2.3.2	A/tufted_duck/Fukushima/5/2011
AB675544	Japan	2011	2.3.2	A/tufted_duck/Fukushima/7/2011
AB677851	Japan	2011	2.3.2	A/tufted_duck/Yamaguchi/3502B007/2011
AB629700	Japan	2011	2.3.2	A/tundra_swan/Fukushima/207/2011
JN807996	South Korea	2011	2.3.2	A/turkey/Korea/DDC518/2011
CY110738	Japan	2011	2.3.2	A/whooper_swan/Hamanaka/2011
AB629708	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/13-21/2011
AB629704	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/13-27/2011
AB620022	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/3/2011
AB610972	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/4/2011
AB621347	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/6/2011
AB629706	Japan	2011	2.3.2	A/whooper_swan/Hokkaido/A13/2011
JN807998	South Korea	2011	2.3.2	A/whooper_swan/Korea/Q28/2011
JN807999	South Korea	2011	2.3.2	A/wild_bird/Korea/IS18/2011
JN807983	South Korea	2011	2.3.2	A/common_Ketrel/Korea/Q197/2011
AB677843	Japan	2011	2.3.2	A/common_pochard/Shimane/5502B024/2011
JN795913	Bangladesh	2011	2.3.2	A/crow/Bangladesh/11rs1984-11/2011
JN795914	Bangladesh	2011	2.3.2	A/crow/Bangladesh/11rs1984-12/2011
JN795915	Bangladesh	2011	2.3.2	A/crow/Bangladesh/11rs1984-13/2011
JN795916	Bangladesh	2011	2.3.2	A/crow/Bangladesh/11rs1984-14/2011
JN795917	Bangladesh	2011	2.3.2	A/crow/Bangladesh/11rs1984-15/2011
CY089413	India	2011	2.3.2	A/duck/India/02AF1/2011
CY089421	India	2011	2.3.2	A/duck/India/02CA10/2011
JN807984	South Korea	2011	2.3.2	A/duck/Korea/AS117/2011
JN807986	South Korea	2011	2.3.2	A/duck/Korea/IC360/2011
JN807987	South Korea	2011	2.3.2	A/duck/Korea/NJ83/2011
JN807988	South Korea	2011	2.3.2	A/duck/Korea/YA54/2011

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Table S8. Statistically supported migration rates of H5N1 viruses

Gene	Area-A	Area-B	Rate	Test†	BF*
HA	MO	NEA	0.78(0.002-2.01)	0.96	33.48
	QH	MO	2.45(0.42-5.18)	1.00	>100
	MO	SA	1.11(0.02-2.83)	1.00	9.34
	SC	SEA	1.26(0.14-2.72)	1.00	>100
NA	MO	NEA	1.31 (0.03-3.14)	1.00	>100
	SC	SEA	1.63 (0.19-3.63)	1.00	>100
	SA	SEA	1.21 (0.01-3.12)	0.60	14.45
MP	SC	SEA	1.56 (0.11-3.64)	1.00	>100
NP	SC	SEA	1.55 (0.11-3.58)	1.00	>100
	SC	NEA	0.56 (0.002-1.66)	0.84	5.41
	NEA	MO	0.88 (0.005-2.68)	0.90	5.20
NS	SC	SEA	1.10 (0.07-2.80)	1.00	>100
	SC	NEA	0.62 (0.002-2.06)	0.52	3.30
PA	SC	SEA	1.04 (0.04-2.65)	1.00	>100
	MO	NEA	1.12 (0.003-2.91)	0.62	7.79
PB1	SC	SEA	1.30 (0.05-3.18)	1.00	>100
	MO	NEA	1.23 (0.001-3.14)	0.76	7.79
PB2	SC	SEA	1.54 (0.13-3.61)	1.00	>100
	MO	NEA	1.14 (0.002-2.97)	0.70	5.79

MO, Mongolia; NEA, northeast Asian, i.e., Japan and Korea; QH, Qinghai; SA, South Asia; SC, southern China; SEA, Southeast Asia.

Rate: viral migration rate. BSSVS was used to reduce the number of parameters to those with significantly non-zero transition rates. Areas A and B were the locations connected by non-zero rates.*BF > 100 indicates decisive support for migration between locations; $30 \leq \text{BF} \leq 100$ indicates very strong support; $10 \leq \text{BF} \leq 30$ indicates strong support; and $6 \leq \text{BF} \leq 10$ indicates substantial support. Only statistically supported migrations with indicator values > 0.50 are shown.

†A sensitivity test was used to calculate the probability of statistically supported migration paths in random datasets with increasingly larger random subsets of isolates (from 50%, 60%, 70%, 80%, to 90% of the original dataset) throughout the BSSVS procedure, with 50 replicates for each gene.

HA, hemagglutinin; NA, neuraminidase; MP, matrix proteins; NP, nucleoprotein; NS, nonstructural gene; PA, PB1, and PB2, RNA polymerases.