Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China

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Since March 2013, three waves of human infection with avian influenza A(H7N9) virus have been detected in China. To investigate virus transmission within and across epidemic waves, we used surveillance data and whole-genome analysis of viruses sampled in Guangdong during 2013–2015. We observed a geographic shift of human A(H7N9) infections from the second to the third waves. Live poultry market interventions were undertaken in epicenter cities; however, spatial phylogenetic analysis indicated that the third-wave outbreaks in central Guangdong most likely resulted from local virus persistence rather than introduction from elsewhere. Although the number of clinical cases in humans declined by 35% from the second to the third waves, the genetic diversity of third-wave viruses in Guangdong increased. Our results highlight the epidemic risk to a region reporting comparatively few A(H7N9) cases. Moreover, our results suggest that live-poultry market interventions cannot completely halt A(H7N9) virus persistence and dissemination.

Since its first notification on March 30, 2013 (*1*), avian influenza A(H7N9) virus caused 3 complete epidemic waves of human infection in China, comprising 670 laboratory-confirmed clinical cases and 274 deaths as of December 28, 2015 (http://www.wpro.who.int/outbreaks_emergencies/H7N9/en/). Despite the accumulating number of human cases, how this virus disseminated and transmitted across the 3 epidemic waves is not yet understood.

Direct or indirect prior exposure to live poultry or poultry-related environments is the major risk for A(H7N9) infection in humans (*2*,*3*). In response to the A(H7N9) outbreak, major efforts were undertaken to temporarily close and sanitize live poultry markets (LPMs) in epicenter cities during epidemics (*4*–*6*). These interventions are thought to temporarily decrease A(H7N9) contamination of LPM environmental samples (*4*,*6*) and to reduce the incidence of clinical infection (*3*,*6*). However, whether these viruses persist locally across epidemic waves despite current interventions has yet to be answered.

Guangdong Province in southern China accounts for ≈10% of China's domestic poultry industry and is thought to be an important epicenter of influenza A virus circulation (*7*). The province reported no clinical cases during the first wave of A(H7N9) infection but represented the epicenter of the second and third epidemic waves. We integrated epidemiologic, spatial, and genetic data to trace the temporal and spatial origins of influenza A(H7N9) in humans during 2013–2015 in Guangdong.

Materials and Methods

Ethics Statement

The institutional ethics committee of the Center for Disease Control and Prevention of Guangdong Province (Guangdong CDC) approved this study. Written consent was signed by patients or their guardian(s) when samples were collected. Patients were informed about the study before providing their written consent, and the data were anonymized for analysis.

Influenza A(H7N9)Surveillance and Sequencing

Since the first A(H7N9) case in late March 2013, an enhanced provincial surveillance program in all 21 prefecture-level cities in Guangdong has been conducted by a total of 871 clinics and 21 local centers for disease control. All specimens from persons with suspected A(H7N9) infections were tested for subtypes H5, H7, and H9 as previously described (*8*,*9*).

In April 2013, Guangdong CDC launched an environmental surveillance program to monitor avian influenza

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DOI: http://dx.doi.org/10.3201/eid2212.160450

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viruses in LPMs (*9*). Environmental samples were collected from LPMs in Guangdong Province during April 15, 2013–May 30, 2015 (*8*–*10*). Ten to 20 environmental samples per market were collected from selected markets in 21 prefecture-level cities. When A(H7N9) infection was confirmed in a person in a given location and that person had exposure to a specific LPM, at least 20 environmental samples were collected from that market within 24 hours after confirmation of human infection.

Upon reverse transcription PCR testing, H7N9- and H9N2-positive swab materials and sputum samples from patients and LPM environments were blindly passaged for 2–3 generations in 9- to 10-day-old embryonated chicken eggs for virus isolation. All 8 segments of the selected isolates were sequenced by using a next-generation sequencing strategy for influenza A virus with the Ion PGM System and PathAmpFluA Reagents (Life Technologies, Carlsbad, CA, USA). Specific primer sets were used to amplify and fill potential gaps (*8*,*9*).

Sequence Alignment and Maximum-Likelihood Phylogenetic Analysis

A total of 1,124 nt sequences were generated by this study. These sequences were combined with all publicly available complete gene sequences of influenza A viruses with known sampling dates and locations that belong to subtypes H7N9, H9N2, and other closely related subtypes. Multiple sequence alignment was performed by using ClustalW (*11*), and alignments were minimally edited by using Aliview (*12*). Maximum-likelihood trees were estimated for all 8 gene segments (hemagglutinin [HA], n = 865; neuraminidase [NA], n = 788; nucleoprotein [NP], n = 1,879; basic polymerase proteins 1 and 2 [PB1 and PB2], n = 1,773 and n = 1,826, respectively; polymerase, n = 1,839; matrix, n = 1,841; and nonstructural [NS], n = 838) in RaxML (*13*) by using the generalized time-reversible nucleotide substitution model with gamma -distribution among site rate heterogeneity (*14*). For each gene dataset, we assessed temporal accumulation of genetic divergence from the root-to-tip from maximum-likelihood midpoint-rooted phylogenies using TempEst (formerly Path-O-Gen) (*15*).

Dated Phylogenetic Analysis

To infer dated phylogenetic trees in a reasonable computational time, we reduced the size of our datasets by removing identical sequences collected in the same sampling locations on the same date. We also removed H9N2 sequences that were phylogenetically unrelated to the H7N9 sequences in our study but kept all H7N9 sequences from clinical cases in Guangdong. Bayesian Markov chain Monte Carlo (MCMC) inferences were undertaken by using BEAST, using a SRD06 nucleotide substitution model (*16*), a relaxed molecular clock model with an uncorrelated lognormal rate distribution (*17*), and a Bayesian skygrid coalescent model (*18*). Four independent MCMC runs of 1×10^8 steps were computed and ≈10%–15% burn-in was discarded, resulting in ≈3.5×10^8 total steps for each gene dataset. Parameters and trees were sampled every 35,000th and 70,000th MCMC step, respectively. Convergence of MCMC chains was inspected by using Tracer version 1.6 (http://tree.bio.ed.ac.uk). A subset of 500 trees was drawn randomly from the combined posterior distribution of trees and used as an empirical distribution for subsequent analysis (*19*).

Spatial and Temporal Origins of H7N9

We used a Bayesian discrete phylogeographic approach to investigate spatial dynamics among 9 geographic regions. Specifically, we considered viral movement across eastern China (Shanghai, Zhejiang, Jiangsu, and Shandong provinces); central China (Jiangxi and Hunan provinces); northern China (Beijing, Henan, Hebei, and Xinjiang provinces); southeastern China (Fujian Province); central Guangdong Province (Guangzhou, Huizhou, Foshan, Dongguan, Zhongshan, Shenzhen, Jiangmen, and Zhaoqing Figure 1]); eastern Guangdong Province (Meizhou, Heyuan, Chaozhou, Jieyang, Shantou, and Shanwei); western Guangdong Province (Yangjiang, Maoming, and Yunfu); and other regions (related sequences isolated from other countries before the H7N9 epidemic). To trace the origin of H7N9 infection, we considered sporadic clinical infection cases from Malaysia and Taiwan as a separate discrete location. Hong Kong adjoins central Guangdong, and most imported live poultry in Hong Kong is from central Guangdong (Zhuhai and Shenzhen). Therefore, Hong Kong and central Guangdong were considered as a single spatial unit. To provide a more realistic reconstruction that includes the directionality of virus transmission, we used an asymmetric continuous-time Markov chain model (*20*) to estimate ancestral locations and location posterior probabilities for each node in the dated phylogenies. Finally, we used TreeAnnotator to obtain maximum clade credibility trees for each gene, which were visualized by using FigTree version 1.4.2 (http://tree.bio.ed.ac.uk). Nucleotide sequences generated in this study were submitted to GISAID (Global Initiative on Sharing All Influenza Data, http://www.gisaid.org) under accession nos. EPI655863–EPI656506 and EPI654015–EPI654495.

Results

An Epicenter Shift of A(H7N9) in Humans, Guangdong, 2013–2015

As of October 14, 2015, a total of 182 laboratory-confirmed clinical cases of A(H7N9) infection in humans and

68 deaths were reported in Guangdong (Figure 1; online Technical Appendix Table 1, http://wwwnc.cdc.gov/EID/article/22/12/16-0450-Techapp1.pdf). Guangdong reported no clinical A(H7N9) cases during the first epidemic wave (March 2013–May 2013) but had the highest number of cases during the second (110 cases during June 2013–May 2014) and third (72 cases during June 2014–May 2015) epidemic waves.

Unexpectedly, the geographic distributions of A(H7N9) cases in Guangdong differed during the second and third waves (Figure 1, panels B, C). During the second wave, 110 cases were reported from 14 prefecture-level cities in Guangdong. The epicenter of the outbreak was in central Guangdong in the Pearl River Delta (PRD) region (95 [86%] cases). The highest numbers of human cases were reported from cities in Guangdong that had the most LPMs and the highest population density, such as Guangzhou, Shenzhen, and Foshan (Figure 1, panel A). Citywide LPM closures of 2 weeks' duration were implemented in Guangzhou and Shenzhen cities in February 2014, during the middle of the second wave, and were extended to all prefecture-level cities in central Guangdong in January 2015 during the middle of the third wave (Figure 1, panel B; online Technical Appendix Table 2). All live poultry were removed, and LPM were disinfected once; the markets were cleaned thoroughly with 0.05%–0.1% diluted chlorine solution after poultry removal. Short-term surveillance showed that the A(H7N9) detection rate decreased from 14.83% (112/755) before LPM closure to 1.67% (5/300) on the day when markets reopened, across 31 sampled markets during the second wave (*4*). Another study found that avian influenza virus contamination in LPMs dropped precipitously after cleaning and disinfecting (*21*). Our clinical surveillance data showed that human cases reduced by 55% (online Technical Appendix Table 1) in central Guangdong during the third wave but rose in other regions of Guangdong; eastern Guangdong became a new epicenter of the outbreak. Twenty-eight human cases occurred in eastern Guangdong during the first 2 months of 2015, compared with only 2 during the same period in 2014 (Figure 1). The geographic shift of A(H7N9) infection between the second and third waves became more apparent when incidence per capita was measured (Figure 1, panel C) because eastern Guangdong has a lower average population density than the PRD region.

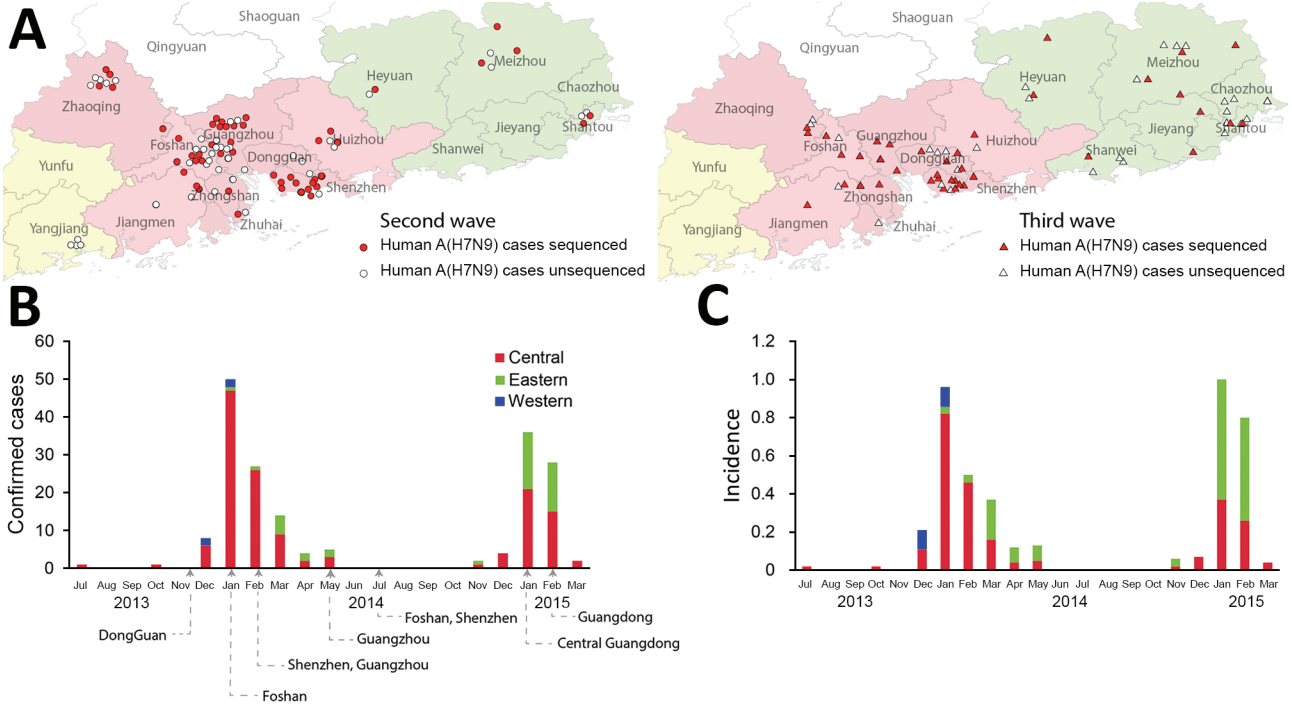

Figure 1. Avian influenza A(H7N9) infection in humans, Guangdong, China, 2013–2015. A) Geographic distribution of H7N9 in humans during the second (June 2013–May 2014) and third (June 2014–May 2015) waves. Confirmed cases in humans identified during the second wave are marked with circles and during the third wave with triangles. H7N9 isolates newly sequenced in this study are highlighted in red. Pink and green shading indicates city prefectures in central and eastern Guangdong Province, respectively. B) Numbers of human H7N9 infections in different regions of Guangdong Province during 2013–2015. Arrows indicate the dates at which live-poultry markets were closed in epicenter cities. No infections were reported during April–October. C) Incidence (human H7N9 infections/1 million population) in each region.

Epidemic Origins of Human A(H7N9) Infections in Guangdong

We undertook a phylogenetic molecular clock analysis to identify the epidemic origins and transmission dynamics of circulating avian influenza A strains during the third wave. The H7N9 sequences included in our analyses represented 55% (60/110) and 49% (35/72) of all diagnosed H7N9 cases in Guangdong during the second and third waves, respectively. H7N9 and H9N2 viruses obtained from poultry and LPM environmental samples during 2013–2015 also were sequenced, resulting in 44 complete and 79 incomplete virus genomes generated using high-throughput sequencing (*8*,*9*).

Phylogeographic analysis of 433 H7 HA genes revealed spatial patterns of A(H7N9) transmission across China (Figure 2, panel A). During the first epidemic wave, A(H7N9) virus spread from eastern China to northern, central, and southeastern China, causing a few human infections (Figure 2, panel A), consistent with previous analyses

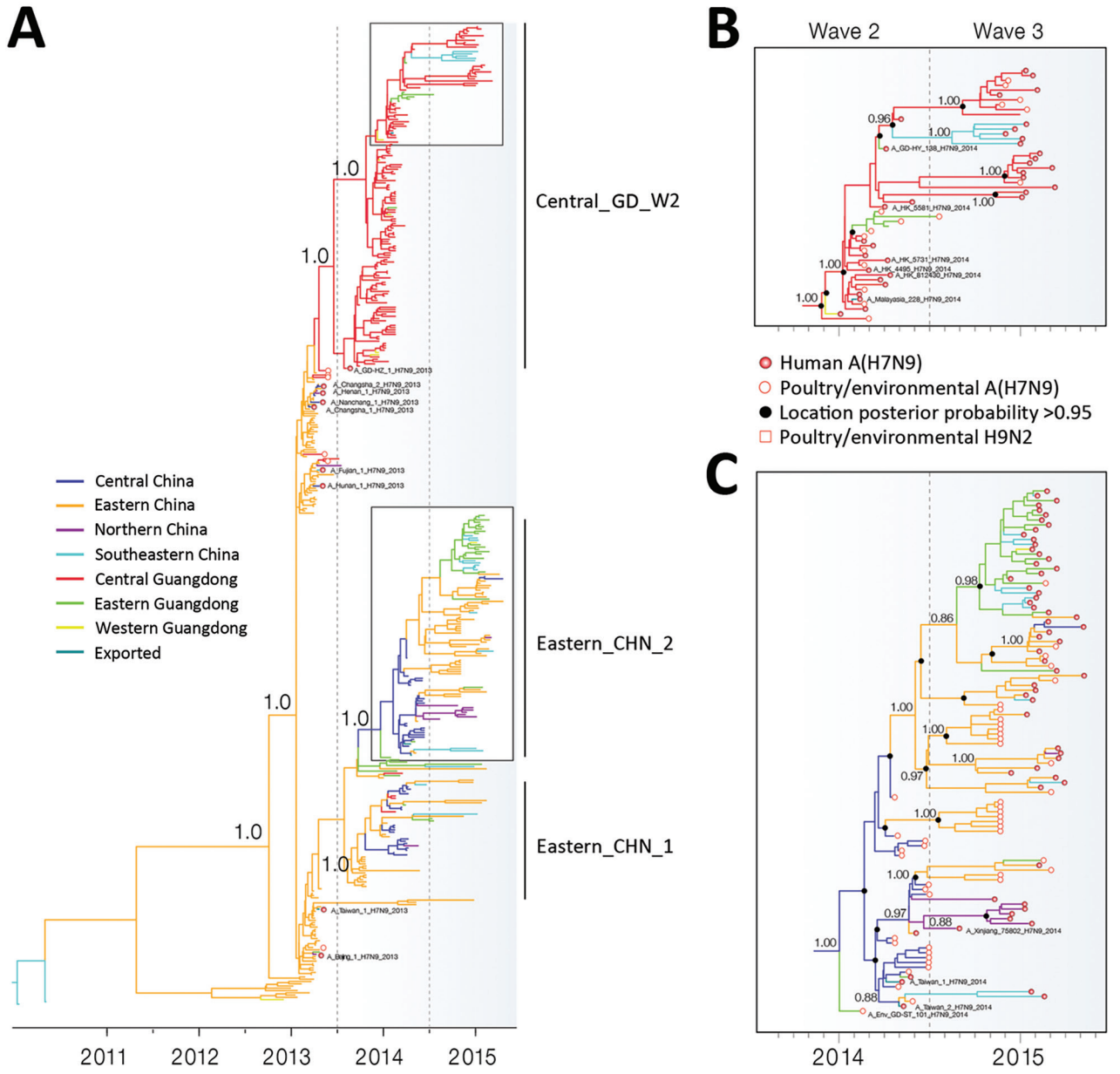

Figure 2. A) Bayesian maximum clade credibility molecular clock tree of influenza virus H7 gene sequences. Branch colors represent the most probable ancestral locations of each branch, inferred from using a spatial phylogenetic model (see Materials and Methods for details). Three major clades of avian influenza A(H7N9) virus were nominated, and phylogenetic posterior probability support is shown for selected clades. B, C) Phylogenies showing hemagglutinin, Guangdong, China, third-wave clades. Phylogenetic posterior probability support is shown for selected clades.

(*22*,*23*). All A(H7N9) viruses identified from chicken and environmental samples in Guangdong during the first wave were derived from viruses circulating in eastern China (Figure 2, panel A). These Guangdong viruses fell into 2 distinct phylogenetic clusters, indicating multiple independent introductions to the region, possibly through different poultry trade routes.

During the second epidemic wave, local transmission and proliferation of A(H7N9) virus was detected in Guangdong, particularly in central Guangdong. The HA phylogeny indicated that 94% of A(H7N9) from clinical cases and 92% of H7 subtypes from LPM environmental samples in Guangdong during the second wave clustered into 1 large clade, designated here as Central_GD_W2 (Figure 2, panel A; Figure 3). The earliest second wave case in this clade was sampled in August 2013 (A_GD-HZ_1_H7N9_2013; Figure 2, panel A). Our analysis suggested that viruses related to A_GD-HZ_1_H7N9_2013 persisted in and disseminated through central Guangdong, giving rise to a large number of A(H7N9) cases in the region during the second wave. Moreover, we found that Central_GD_W2 clade viruses also disseminated from central to eastern and western Guangdong during the second wave and caused human cases (e.g., A_GD-HY_138_2014) (Figure 2, panels A, B). Four isolates from humans in Hong Kong and 1 from a human in Malaysia during the second wave also fell within this clade (Figure 2, panel B). The phylogeny of N9 NA sequences displayed similar virus transmission patterns (online Technical Appendix Figure, panel A). Most (73%) N9 genes from A(H7N9) isolates in Guangdong during the second wave clustered within the Central_GD_W2 clade. In contrast to HA, the NA phylogeny showed that A(H7N9) isolates during the second wave in central Guangdong did not form a single cluster (online Technical Appendix Figure, panel A). However, fewer human cases (27%) were caused by these viruses, and most cases were limited to Shenzhen and Shantou cities, suggesting less transmission of viruses in this clade (online Technical Appendix Figure, panel A).

The incidence of A(H7N9) in humans in central Guangdong decreased by 55% during the third wave (Figure 1, panel B; online Technical Appendix Table 1). However, phylogenetic analysis indicated that the virus persisted in central Guangdong. The H7 phylogeny showed that all A(H7N9) viruses from central Guangdong during the third wave were descended from Central_GD_W2 clade viruses of the second wave (Figure 2, panel B). The outbreaks of A(H7N9) in humans in Fujian Province (southeastern China) during the third wave also were caused by Central_GD_W2 clade viruses, suggesting a possible transmission of A(H7N9) virus from central Guangdong to cities in southeastern China during the second wave.

A major feature during the third epidemic wave was an increase in A(H7N9) cases in humans in eastern Guangdong (Figure 1, panels B, C; online Technical Appendix Table 1). Most (94%) isolates identified in eastern Guangdong during the third wave clustered into a single subclade of Eastern_CHN_W2 clade viruses in both the H7 and N9 phylogenies (Figure 2, panel C; online Technical Appendix Figure, panel A). The Eastern_CHN_W2 clade viruses were mainly found in poultry from central China during the second wave but became predominant (among both poultry and humans) in eastern China and eastern Guangdong during the third wave (Figure 2, panel C). Moreover, these viruses formed location-specific clades during the third wave, suggesting that they have become established and enzootic to the poultry populations in each locality (Figure 2, panel C).

Genetic Diversities of A(H7N9) Virus in Guangdong

During the second wave, sequences from 4 internal genes (NP, NS, PB1, PB2) of A(H7N9) isolates from central Guangdong mostly clustered into a single major clade, together with local A(H9N2) strains; these sequences were distinct from the A(H7N9) sequences from central or eastern China (Figure 4, panel A; online Technical Appendix Figure, panels B, D, F) (*8*,*22*). However, by the third wave, most A(H7N9) viruses from central Guangdong had

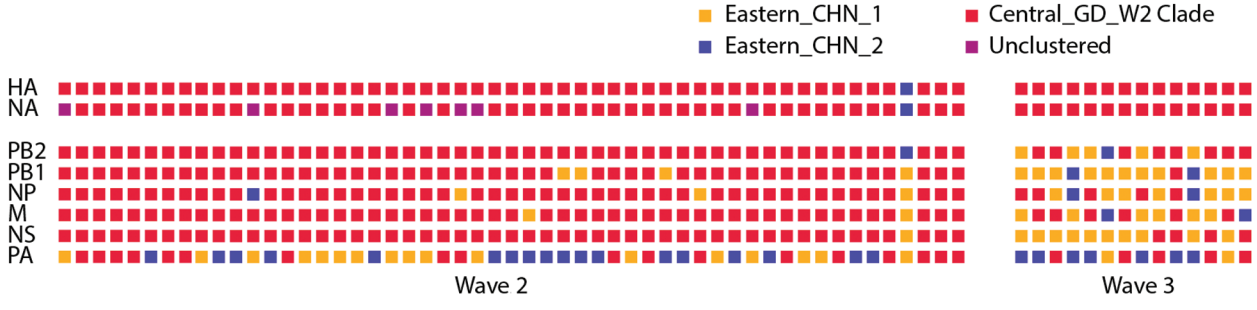

Figure 3. Genotypic analysis of influenza A(H7N9) viruses. Proposed genotypes are shown for 68 fully sequenced A(H7N9) viruses isolated from humans in central Guangdong during 2013–2015. Each square represents a gene sequence, and its color indicates the most probable clade to which that sequence belongs, as inferred from the phylogenies in Figures 2 and 4 and online Technical Appendix Figure, panels B–F (http://wwwnc.cdc.gov/EID/article/22/12/16-0450-Techapp1.pdf).

acquired some internal genes from viruses from central or eastern China. In particular, PB1, PB2, NP, and NS sequences obtained from humans with A(H7N9) infection and from H7N9/H9N2 environmental samples in central Guangdong during the third wave were distinct from those from the second wave (Figure 4, panel A; online Technical Appendix Figure, panels B, D, F). For instance, analysis of the PB2 gene revealed that 65 of 69 viruses from clinical samples clustered into the Central_GD_W2 clade during the second wave. However, during the third wave, only 8 of 32 H7N9 viruses from clinical isolates fell into this group. The remaining 24 H7N9 isolates were phylogenetically related to H7N9 or H9N2 isolates from central or eastern China. It therefore appears that >70% of third-wave H7N9 viruses from central Guangdong acquired a PB2 gene through reassortment with strains circulating elsewhere. A similar pattern also was observed for H7N9 and H9N2 isolates from LPM environments (Figure 4). These findings supported the hypothesis that H9N2 viruses previously circulating outside Guangdong were introduced into central Guangdong during the third wave and increased the diversity of internal genes of H7N9 in this place by reassortment.

We further classified all human A(H7N9) isolates from central Guangdong according to the phylogenetic placement of their genome segments. Genome segments of second-wave A(H7N9) from central Guangdong were typically co-inherited (except polymerase) and belonged to the Central_GD_W2 clade (Figure 3; Figure 4, panel A; online Technical Appendix Figure). A total of 12 different

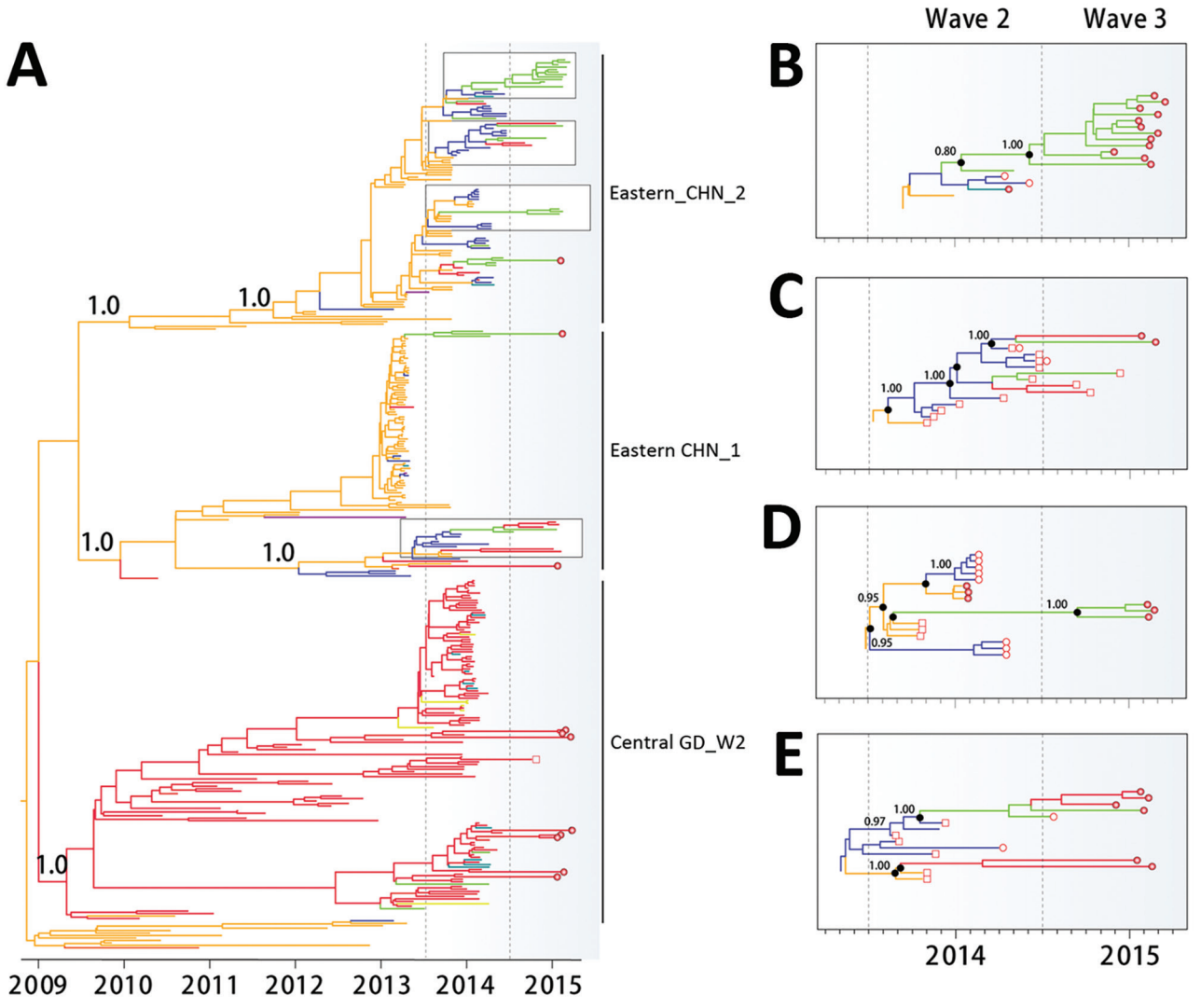

Figure 4. A) Bayesian maximum clade credibility phylogeographic tree of influenza virus polymerase protein 2 gene sequences. Branch colors represent the most probable ancestral locations of each branch, inferred from using a spatial phylogenetic model (see Materials and Methods for details). B–E) Phylogenies showing selected PB2 Guangdong third-wave clades. Empty squares indicate A(H9N2) virus sequences.

lineages were observed in 55 human A(H7N9) viruses isolated during the second wave in central Guangdong. This pattern was absent during the third wave; instead, the genomic structures of human A(H7N9) viruses were highly variable, with the exception of the HA and NA segments, which retained their association with the Central_GD_W2 clade (Figure 3).

In contrast, phylogenetic reconstruction of PB1, PB2, NP, and NS sequences indicated that most third-wave sequences seen in eastern Guangdong were genetically similar (Figure 4, panel B; online Technical Appendix Figure, panels. B–F). These sequences grouped into a single clade, whereas those sampled in central Guangdong were phylogenetically dispersed.

Discussion

We analyzed epidemiologic data pertaining to influenza A(H7N9) virus in humans and virus sequence data from 52% (95/182) of all persons in whom A(H7N9) infection was diagnosed and from LPMs environment samples during 2013–2015 to characterize the origin and transmission of A(H7N9) in humans across epidemic waves in Guangdong. The phylogeographic analyses of HA and NA indicate that the virus strain that caused third-wave outbreaks in central Guangdong descend from second-wave viruses that circulated in the same region. In other words, H7N9 circulating during the second wave probably persisted in targeted cities and/or their neighboring areas until the third epidemic wave.

In contrast, the histories of the H7N9 internal genes, which are affected by frequent reassortment with prevalent H9N2 viruses, most likely mirror the trade routes of live poultry. We found that A(H7N9) viruses from central Guangdong during the second wave possessed 5 (PB2, PB1, matrix, NP, NS) of 6 internal genes mainly from the Central_GD_W2 clade. However, in the third wave, viral internal genes were dispersed in phylogenetic trees; most strains fell into the Eastern_CHN1 or Eastern_CHN2 clades, suggesting another source for the parental viruses of these reassortants (Figure 3). This finding suggests there were changes in nature of A(H9N2) viruses that were cocirculating in central Guangdong (Figure 4, panel C; online Technical Appendix Figures B–F). Our data indicate that the genetic diversity of H7N9 or H9N2 in central Guangdong increased during the third wave, even though the number of human infections was lower in this region.

From a public health standpoint, our results underscore 3 major concerns with current A(H7N9) infections in humans in China. First, the persistence and spread of A(H7N9) have not been completely constrained. A(H7N9) circulating in central Guangdong during the second wave was persistent and caused outbreaks in humans during the third wave. For example, 5 and 3 cases, respectively, were identified in humans in March 2014 in Shenzhen and Guangzhou in Guangdong after the reopening of LPMs in February 2014 (online Technical Appendix Tables 1, 2). This finding suggests that interventions such as the temporary closure and sanitation of LPMs can reduce virus contamination in poultry and environmental samples but apparently cannot eliminate the risk for human infection (*21*). Recent long-term LPM surveillance in Guangzhou suggests that different types of poultry markets were recontaminated by A(H7N9) and other avian influenza A strains; up to 2 days after markets were reopened, detection rates of the viruses in LPM environments were as high as those before market closure (*5*).

Second, a geographic shift of the epicenter of human infections between the second and third waves in Guangdong suggests an epidemic of A(H7N9) infection is difficult to control solely by interfering in the epicenter of an outbreak. Some regions, once contaminated, might act as sources of infection to the wider poultry sector. Current sequence data suggest that the A(H7N9) human infections in eastern, northern, and southeastern China and eastern Guangdong during the third wave were mainly caused by viruses belonging to the Eastern_CHN_W2 clade, which were predominantly isolated from poultry populations in central China at the end of the second wave (Figure 2, panel C). In eastern Guangdong, 94% of A(H7N9) cases in humans during the third wave were caused by Eastern_CHN_W2 clade viruses.

Third, other measures complementary to LPM closures should be considered by government administration. We observed a continued reassortment of Guangdong A(H7N9) lineages with viral strains from central and eastern China since February 2014 (Figures 3, 4), suggesting that live poultry from central and eastern areas might have been introduced into central Guangdong after the local LPMs were closed. Indeed, it is plausible that official closure led to an increase in illicit trading in some markets or neighborhoods (http://gzdaily.dayoo.com/html/2015-03/18/content_2885023.htm; http://shenzhen.sina.com.cn/news/n/2015-04-20/detail-iavxeafs5854802.shtml). In this context, the closure of central LPMs without a strict ban on the live poultry trade could, at least in theory, have detrimental effects. Illicit trading has the potential to change the poultry trade and make officially monitoring and controlling it more difficult. Other less disruptive measures that have been proven to reduce risk can be considered, such as rest days and banning live poultry overnight (*24*).

One limitation of this study is a lack of long-term surveillance of live poultry in Guangdong. Such surveillance is difficult to implement because of a low infection rate and the absence of signs during A(H7N9) infection in poultry. However, most A(H7N9) infection in humans results from direct exposure to live poultry (*25*) (online Technical

Appendix Table 3). Furthermore, we used in our analyses environmental samples from LPMs, which partially reflect the circulation of avian influenza A strains in poultry. In addition, surveillance efforts in different regions might differ and could affect our interpretation on virus origin and transmission. In this study, we have analyzed most publicly available, genetically related A(H7N9) sequences out of Guangdong Province, and the regions of eastern China and central Guangdong that reported most clinical H7N9 cases represent most H7N9-related sequences. However, sampling bias cannot be excluded, especially for environmental and poultry samples. Central China is a major poultry farming area but has a limited number of A(H7N9) sequences from poultry, which could be caused by a lower prevalence of the virus in this region or by a possible limited surveillance effort in poultry population. As a result, sequences data from Eastern_CHN_W2 clade are still limited to illustrate the evolution and transmission route of this clade of A(H7N9) (Figure 2, panel C). Longer-term and larger-scale studies are necessary to provide more robust evidence about the value of interventions for controlling the epidemic at national and regional scales.

During February 5–11, 2016, twenty-eight new A(H7N9)cases were reported in humans. Clearly, the public health risk from A(H7N9) remains. Our results highlight some limitations of the current geographically restricted LPM interventions on the epidemic control of A(H7N9), which might also apply to other avian influenza viruses. To focus only on end-stage epidemic LPM interventions without including the entirety of the LPM transmission chain might, however, be of limited value. Public health organizations might wish to consider the possibility of proactively closing LPMs, and alternative measures as recently suggested (*24*), in areas potentially at-risk, although we recognize that practical, economic, and administrative considerations also contribute to decision-making processes.

Acknowledgment

We thank Tommy Lam for sequence alignments.

C.K., J.W., J. Li, X.H., M. Ko, and J.H. designed the study. J.W., X. Ze, J. Lu, Y.S., L.Z., L.Y., L.L., H.N., M. Ka, X. Zhang, G.H., and H.Z. prepared sample collection and genome sequencing. J. Lu, N.R.F., T.B., J.R., and O.P. analyzed the data. J. Lu, N.R.F., O.P., and C.K. interpreted the data. J. Lu, N.R.F., and C.K. prepared the figures. J. Lu, N.R.F., L.Y., O.P., and C.K. wrote the article.

This work was supported by grants from the Research Project of H7N9 Influenza of Guangdong [2014] (no. 1046), the Scientific, Technological Research of Prevention and Control of H7N9 Subtype Avian Influenza Virus (20140024), and China Scholarship Council (grant no. 201508440009).

Dr. Wu is a virologist in Guangdong CDC. Her primary research interest is the investigation of influenza virus epidemiology, evolution, and transmission.

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Article DOI: http://dx.doi.org/10.3201/eid2212.160450

Live Poultry Market Interventions for Influenza A (H7N9) Virus, Guangdong, China

Technical Appendix

Technical Appendix Table 1. Reported avian influenza A(H7N9) cases in humans, Guangdong Province, China, March 2013–October 2015

	Wave 2, 2013 Jun–2014 May								Wave 3, 2014 Jun–2015 May				
Prefectual cities	Jul	Oct	Dec	Jan	Feb	Mar	Apr	May	Nov	Dec	Jan	Feb	Mar
Dongguan (DG)*		1	1	1					1	2	3	2	
Foshan (FS)*			3	8	4						1	2	1
Guangzhou (GZ)*				7	14	3	1				1	4	
Huizhou (HZ)*	1			3		1					1	1	
Jiangmen (JM)*				3	2			1			0	2	1
Shenzhen (SZ)*			2	16	1	5	1			1	11	1	
Zhuhai (ZH)*					1						1		
Zhaoqing (ZQ)*				6	4					1	1	2	
Zhongshan (ZS)*				3				2			2	1	
Central Guangdong					95						43		
Chaozhou (CZ)†						1					2	3	
Heyuan (HY)†						2					2	2	
Jieyang (JY)†											2		
Meizhou (MZ)†				1	1	1		2	1		4	3	
Shantou (ST)†						1	2				1	5	
Shanwei (SW)†											4		
Eastern Guangdong					11						29		
Yangjiang (YJ)			2	2							0		
Guangdong					110						72		

* Cities in Central Guangdong.

† Cities in Eastern Guangdong.

Technical Appendix Table 2. Interventions implemented in LPMs during epidemics of avian influenza A(H7N9) virus, Guangdong Province, China*

City	Time	LPM interventions	Reference
Dongguan	2013 Nov–2014 Jan	Ten LPMs of the city were separately closed for 2 wks where human infection cases were identified	Kang, et al.†
Foshan	2014 Jan 13–2014 Jan 29	LPMs of Nanhai and Chancheng districts were closed	Wu et al.‡
Shenzhen	2014 Jan 31–2014 Feb 13	All LPMs of the city were closed; cleaning and disinfecting were conducted	Wu et al.‡
Guangzhou	2014 Feb 15–2014 Feb 28	All LPMs of the city were closed; cleaning and disinfecting were conducted	Wu, et al.‡
Guangzhou	2014 May 5–current	Four districts of Guangzhou ban the sales of live poultry, and only frozen poultry was allowed	http://www.chinadailyasia.com/news/2014-04/30/content_15132977.html
Foshan	2014 July 1–current	Chancheng district ban the sales of live poultry, and only frozen poultry was allowed	http://gzdaily.dayoo.com/html/2014-06/30/content_2674385.htm (In Chinese)
Shenzhen	2014 July 1–current	Futian district ban the sales of live poultry, and only frozen poultry was allowed	http://gzdaily.dayoo.com/html/2014-06/30/content_2674385.htm (In Chinese)
Central Guangdong	2015 Jan 15	Cities at various levels in the Pear River Delta were required to ban the sale of live poultry	http://www.wantchinatimes.com/news-subclass-cnt.aspx?id=20150126000004&cid=1201
Guangzhou	2015 Feb 13–2015 Feb 18	All LPMs of the city were closed; cleaning and disinfecting were conducted	http://www.chinanews.com/tp/2015/02-13/7063641.shtml
Guangdong Province	2015 Feb 19–2015 Feb.28	All LPMs were closed; cleaning and disinfecting were conducted	http://news.sina.com.cn/o/2015-02-15/193231524882.shtml (In Chinese)

*LPM, live-poultry market.

†Kang M, He J, Song T, Rutherford S, Wu J, Lin J, et al. Environmental sampling for avian influenza A(H7N9) in live-poultry markets in Guangdong, China. PLoS One. 2015;10:e0126335.

‡Wu P, Jiang H, Wu JT, Chen E, He J, Zhou H, et al. Poultry market closures and human infection with influenza A(H7N9) virus, China, 2013–14. Emerg Infect Dis. 2014 Nov;20:1891–4.

Technical Appendix Table 3. Epidemiologic characteristics of 182 patients with confirmed avian influenza A(H7N9)virus infection, Guangdong, China, 2013–2015

	Patients with confirmed cases	
Characteristic	Wave 2, n = 110	Wave 3, n = 72
Age, y		
Median	55.5	52
Interquartile range	3–88	0.8–83
Male sex, no. (%)	68 (61.8)	51 (70.8)
Type of residence, no. (%)		
Rural	21 (19)	13 (18)
Urban	79 (81)	59 (82)
A(H7N9) cluster	3	3*
No. deaths (%)	37 (33.6)	31 (43.1)

*A(H7N9) infection was diagnosed in 2 physicians in a respiratory unit at a hospital in Shantou city, Guangdong, with no known recent exposure to live poultry.

Technical Appendix Table 4. Global Initiative on Sharing All Influenza Data accession numbers of avian influenza A(H7N9) viruses isolated from humans in a study of the effect of live-poultry market interventions, Guangdong, China*

A(H7N9) clinical strains†	HA	NA	PB2	PB1	PA	NP	M	NS
A/GD-10/2014/H7N9/2014-01-03	EPI655870	EPI655869	EPI655867	EPI655868	EPI655866	EPI655863	EPI655865	EPI655864
A/GD-12/2014/H7N9/2014-01-03	EPI655878	EPI655877	EPI655875	EPI655876	EPI655874	EPI655871	EPI655873	EPI655872
A/GD-13/2014/H7N9/2014-01-03	EPI655886	EPI655885	EPI655883	EPI655884	EPI655882	EPI655879	EPI655881	EPI655880
A/GD-18/2014/H7N9/2014-01-07	EPI655894	EPI655893	EPI655891	EPI655892	EPI655890	EPI655887	EPI655889	EPI655888
A/GD-19/2014/H7N9/2014-01-07	EPI655902	EPI655901	EPI655899	EPI655900	EPI655898	EPI655895	EPI655897	EPI655896
A/GD-24/2014/H7N9/2014-01-10	EPI655910	EPI655909	EPI655907	EPI655908	EPI655906	EPI655903	EPI655905	EPI655904
A/GD-26/2014/H7N9/2014-01-10	EPI655918	EPI655917	EPI655915	EPI655916	EPI655914	EPI655911	EPI655913	EPI655912
A/GD-29/2014/H7N9/2014-01-11	EPI655926	EPI655925	EPI655923	EPI655924	EPI655922	EPI655919	EPI655921	EPI655920
A/GD-31/2014/H7N9/2014-01-11	EPI655934	EPI655933	EPI655931	EPI655932	EPI655930	EPI655927	EPI655929	EPI655928
A/GD-33/2014/H7N9/2014-01-12	EPI655942	EPI655941	EPI655939	EPI655940	EPI655938	EPI655935	EPI655937	EPI655936
A/GD-34/2014/H7N9/2014-01-12	EPI655950	EPI655949	EPI655947	EPI655948	EPI655946	EPI655943	EPI655945	EPI655944
A/GD-36/2014/H7N9/2014-01-12	EPI655958	EPI655957	EPI655955	EPI655956	EPI655954	EPI655951	EPI655953	EPI655952
A/GD-35/2014/H7N9/2014-01-12	EPI655966	EPI655965	EPI655963	EPI655964	EPI655962	EPI655959	EPI655961	EPI655960
A/GD-43/2014/H7N9/2014-01-15	EPI655974	EPI655973	EPI655971	EPI655972	EPI655970	EPI655967	EPI655969	EPI655968
A/GD-46/2014/H7N9/2014-01-16	EPI655982	EPI655981	EPI655979	EPI655980	EPI655978	EPI655975	EPI655977	EPI655976
A/GD-48/2014/H7N9/2014-01-19	EPI655990	EPI655989	EPI655987	EPI655988	EPI655986	EPI655983	EPI655985	EPI655984
A/GD-62/2014/H7N9/2014-01-27	EPI655998	EPI655997	EPI655995	EPI655996	EPI655994	EPI655991	EPI655993	EPI655992
A/GD-65/2014/H7N9/2014-01-29	EPI656006	EPI656005	EPI656003	EPI656004	EPI656002	EPI655999	EPI656001	EPI656000
A/GD-66/2014/H7N9/2014-01-29	EPI656014	EPI656013	EPI656011	EPI656012	EPI656010	EPI656007	EPI656009	EPI656008
A/GD-69/2014/H7N9/2014-01-30	EPI656022	EPI656021	EPI656019	EPI656020	EPI656018	EPI656015	EPI656017	EPI656016
A/GD-81/2014/H7N9/2014-01-30	EPI656030	EPI656029	EPI656027	EPI656028	EPI656026	EPI656023	EPI656025	EPI656024
A/GD-71/2014/H7N9/2014-01-30	EPI656038	EPI656037	EPI656035	EPI656036	EPI656034	EPI656031	EPI656033	EPI656032
A/GD-75/2014/H7N9/2014-01-31	EPI656046	EPI656045	EPI656043	EPI656044	EPI656042	EPI656039	EPI656041	EPI656040
A/GD-74/2014/H7N9/2014-01-31	EPI656054	EPI656053	EPI656051	EPI656052	EPI656050	EPI656047	EPI656049	EPI656048
A/GD-82/2014/H7N9/2014-02-02	EPI656062	EPI656061	EPI656059	EPI656060	EPI656058	EPI656055	EPI656057	EPI656056

A(H7N9) clinical strains†	HA	NA	PB2	PB1	PA	NP	M	NS
A/GD-98/2014/H7N9/2014-02-06	EPI656070	EPI656069	EPI656067	EPI656068	EPI656066	EPI656063	EPI656065	EPI656064
A/GD-101/2014/H7N9/2014-02-07	EPI656078	EPI656077	EPI656075	EPI656076	EPI656074	EPI656071	EPI656073	EPI656072
A/GD-103/2014/H7N9/2014-02-10	EPI656086	EPI656085	EPI656083	EPI656084	EPI656082	EPI656079	EPI656081	EPI656080
A/GD-104/2014/H7N9/2014-02-11	EPI656094	EPI656093	EPI656091	EPI656092	EPI656090	EPI656087	EPI656089	EPI656088
A/GD-105/2014/H7N9/2014-02-11	EPI656102	EPI656101	EPI656099	EPI656100	EPI656098	EPI656095	EPI656097	EPI656096
A/GD-109/2014/H7N9/2014-02-13			EPI656107	EPI656108	EPI656106	EPI656103	EPI656104	EPI656105
A/GD-110/2014/H7N9/2014-02-13	EPI656116	EPI656115	EPI656113	EPI656114	EPI656112	EPI656109	EPI656111	EPI656110
A/GD-112/2014/H7N9/2014-02-18	EPI656124	EPI656123	EPI656121	EPI656122	EPI656120	EPI656117	EPI656119	EPI656118
A/GD-114/2014/H7N9/2014-02-18	EPI656132	EPI656131	EPI656129	EPI656130	EPI656128	EPI656125	EPI656127	EPI656126
A/GD-119/2014/H7N9/2014-02-19	EPI656140	EPI656139	EPI656137	EPI656138	EPI656136	EPI656133	EPI656135	EPI656134
A/GD-120/2014/H7N9/2014-02-19	EPI656148	EPI656147	EPI656145	EPI656146	EPI656144	EPI656141	EPI656143	EPI656142
A/GD-121/2014/H7N9/2014-02-19	EPI656156	EPI656155	EPI656153	EPI656154	EPI656152	EPI656149	EPI656151	EPI656150
A/GD-116/2014/H7N9/2014-02-22		EPI656163	EPI656161	EPI656162	EPI656160	EPI656157	EPI656159	EPI656158
A/GD-117/2014/H7N9/2014-02-22	EPI656171	EPI656170	EPI656168	EPI656169	EPI656167	EPI656164	EPI656166	EPI656165
A/GD-123/2014/H7N9/2014-03-01	EPI656179	EPI656178	EPI656176	EPI656177	EPI656175	EPI656172	EPI656174	EPI656173
A/GD-124/2014/H7N9/2014-03-06	EPI656187	EPI656186	EPI656184	EPI656185	EPI656183	EPI656180	EPI656182	EPI656181
A/GD-125/2014/H7N9/2014-03-09	EPI656195	EPI656194	EPI656192	EPI656193	EPI656191	EPI656188	EPI656190	EPI656189
A/GD-126/2014/H7N9/2014-03-10	EPI656203	EPI656202	EPI656200	EPI656201	EPI656199	EPI656196	EPI656198	EPI656197
A/GD-136/2014/H7N9/2014-03-29	EPI656211	EPI656210	EPI656208	EPI656209	EPI656207	EPI656204	EPI656206	EPI656205
A/GD-138/2014/H7N9/2014-04-05	EPI656219	EPI656218	EPI656216	EPI656217	EPI656215	EPI656212	EPI656214	EPI656213
A/GD-139/2014/H7N9/2014-04-06	EPI656226	EPI656221	EPI656223	EPI656224	EPI656222	EPI656225	EPI656220	
A/GD-151/2014/H7N9/2014-05-06	EPI656234	EPI656233	EPI656231	EPI656232	EPI656230	EPI656227	EPI656229	EPI656228
A/GD-153/2014/H7N9/2014-05-08	EPI656242	EPI656241	EPI656239	EPI656240	EPI656238	EPI656235	EPI656237	EPI656236
A/GD-154/2014/H7N9/2014-05-28	EPI656250	EPI656249	EPI656247	EPI656248	EPI656246	EPI656243	EPI656245	EPI656244
A/GD-155/2014/H7N9/2014-11-19	EPI656258	EPI656257	EPI656255	EPI656256	EPI656254	EPI656251	EPI656253	EPI656252
A/GD-156/2014/H7N9/2014-11-25	EPI656266	EPI656265	EPI656263	EPI656264	EPI656262	EPI656259	EPI656261	EPI656260
A/GD-1/2015/H7N9/2015-01-03	EPI656274	EPI656273	EPI656271	EPI656272	EPI656270	EPI656267	EPI656269	EPI656268

A(H7N9) clinical strains†	HA	NA	PB2	PB1	PA	NP	M	NS
A/GD-2/2015/H7N9/2015-01-06	EPI656282	EPI656281	EPI656279	EPI656280	EPI656278	EPI656275	EPI656277	EPI656276
A/GD-10/2015/H7N9/2015-01-06	EPI656290	EPI656289	EPI656287	EPI656288	EPI656286	EPI656283	EPI656285	EPI656284
A/GD-18/2015/H7N9/2015-01-11	EPI656298	EPI656297	EPI656295	EPI656296	EPI656294	EPI656291	EPI656293	EPI656292
A/GD-17/2015/H7N9/2015-01-11	EPI656306	EPI656305	EPI656303	EPI656304	EPI656302	EPI656299	EPI656301	EPI656300
A/GD-20/2015/H7N9/2015-01-15	EPI656314	EPI656313	EPI656311	EPI656312	EPI656310	EPI656307	EPI656309	EPI656308
A/GD-21/2015/H7N9/2015-01-16	EPI656322	EPI656321	EPI656319	EPI656320	EPI656318	EPI656315	EPI656317	EPI656316
A/GD-44/2015/H7N9/2015-01-19	EPI656330	EPI656329	EPI656327	EPI656328	EPI656326	EPI656323	EPI656325	EPI656324
A/GD-27/2015/H7N9/2015-01-21	EPI656338	EPI656337	EPI656335	EPI656336	EPI656334	EPI656331	EPI656333	EPI656332
A/GD-43/2015/H7N9/2015-01-22	EPI656346	EPI656345	EPI656343	EPI656344	EPI656342	EPI656339	EPI656341	EPI656340
A/GD-30/2015/H7N9/2015-01-22	EPI656354	EPI656353	EPI656351	EPI656352	EPI656350	EPI656347	EPI656349	EPI656348
A/GD-42/2015/H7N9/2015-01-25	EPI656362	EPI656361	EPI656359	EPI656360	EPI656358	EPI656355	EPI656357	EPI656356
A/GD-45/2015/H7N9/2015-01-26	EPI656370	EPI656369	EPI656367	EPI656368	EPI656366	EPI656363	EPI656365	EPI656364
A/GD-54/2015/H7N9/2015-01-27	EPI656378	EPI656377	EPI656375	EPI656376	EPI656374	EPI656371	EPI656373	EPI656372
A/GD-55/2015/H7N9/2015-01-27	EPI656386	EPI656385	EPI656383	EPI656384	EPI656382	EPI656379	EPI656381	EPI656380
A/GD-50/2015/H7N9/2015-01-27	EPI656394	EPI656393	EPI656391	EPI656392	EPI656390	EPI656387	EPI656389	EPI656388
A/GD-51/2015/H7N9/2015-01-30	EPI656402	EPI656401	EPI656399	EPI656400	EPI656398	EPI656395	EPI656397	EPI656396
A/GD-53/2015/H7N9/2015-02-03	EPI656410	EPI656409	EPI656407	EPI656408	EPI656406	EPI656403	EPI656405	EPI656404
A/GD-57/2015/H7N9/2015-02-03	EPI656418	EPI656417	EPI656415	EPI656416	EPI656414	EPI656411	EPI656413	EPI656412
A/GD-69/2015/H7N9/2015-02-04	EPI656426	EPI656425	EPI656423	EPI656424	EPI656422	EPI656419	EPI656421	EPI656420
A/GD-72/2015/H7N9/2015-02-07	EPI656434	EPI656433	EPI656431	EPI656432	EPI656430	EPI656427	EPI656429	EPI656428
A/GD-68/2015/H7N9/2015-02-08	EPI656442	EPI656441	EPI656439	EPI656440	EPI656438	EPI656435	EPI656437	EPI656436
A/GD-80/2015/H7N9/2015-02-10	EPI656450	EPI656449	EPI656447	EPI656448	EPI656446	EPI656443	EPI656445	EPI656444
A/GD-81/2015/H7N9/2015-02-10	EPI656458	EPI656457	EPI656455	EPI656456	EPI656454	EPI656451	EPI656453	EPI656452
A/GD-76/2015/H7N9/2015-02-10	EPI656466	EPI656465	EPI656463	EPI656464	EPI656462	EPI656459	EPI656461	EPI656460
A/GD-92/2015/H7N9/2015-02-26	EPI656474	EPI656473	EPI656471	EPI656472	EPI656470	EPI656467	EPI656469	EPI656468
A/GD-91/2015/H7N9/2015-02-26	EPI656482	EPI656481	EPI656479	EPI656480	EPI656478	EPI656475	EPI656477	EPI656476
A/GD-124/2015/H7N9/2015-02-26	EPI656490	EPI656489	EPI656487	EPI656488	EPI656486	EPI656483	EPI656485	EPI656484

A(H7N9) clinical strains†	HA	NA	PB2	PB1	PA	NP	M	NS
A/GD-95/2015/H7N9/2015-03-05	EPI656498	EPI656497	EPI656495	EPI656496	EPI656494	EPI656491	EPI656493	EPI656492
A/GD-120/2015/H7N9/2015-03-10	EPI656506	EPI656505	EPI656503	EPI656504	EPI656502	EPI656499	EPI656501	EPI656500

*HA, hemagglutinin; M, matrix; NA, neuraminidase; NP, nucleoprotein; NS, nonstructural; PA, polymerase; PB, polymerase protein.

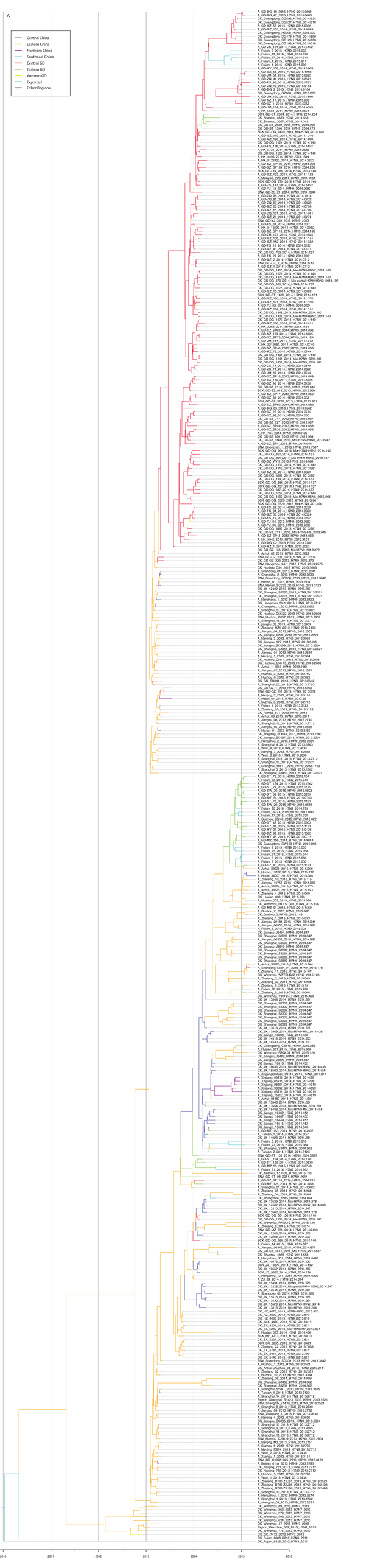
†Accession number for H7N9 and H9N2 strains from live-poultry market environment are EPI654015–EPI654495.

Technical Appendix Table 5. Geographic distribution of avian influenza A(H7N9) viruses sequences used in phylogeographic analyses*

Gene	China				Guangdong				Other	Exported
segments	Central	Eastern	Southeastern	Northern	Central	Eastern	Western	Hong Kong	countries	regions
HA	42	163	24	13	135	36	7	9	–	4
NA	42	129	23	15	116	35	15	12	5	4
PB2	47	130	2	3	109	34	8	35	–	3
PB1	39	107	2	7	104	33	7	19	3	3
PA	32	127	2	9	125	29	10	27	9	4
M	49	149	2	6	132	38	13	22	6	4
NP	54	128	3	11	121	33	11	15	7	3
NS	37	104	1	8	118	33	10	21	11	3

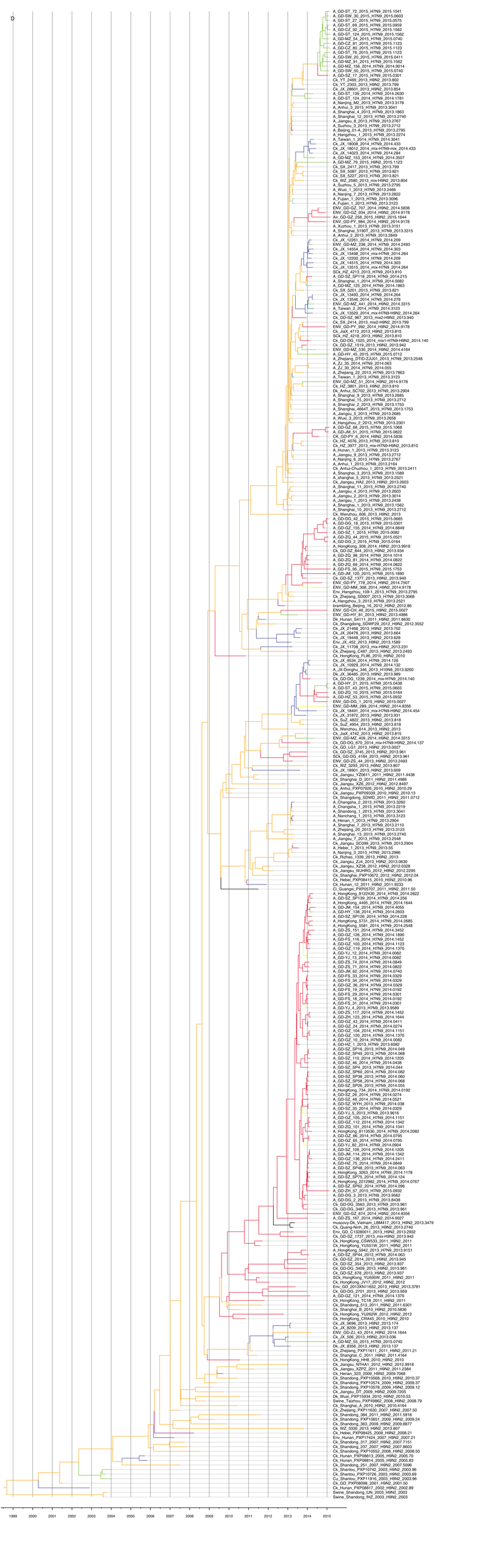
*HA, hemagglutinin; M, matrix; NA, neuraminidase; NP, nucleoprotein; NS, nonstructural; PA, polymerase; PB, polymerase protein.

Technical Appendix Figure (following pages). Bayesian maximum clade credibility phylogeographic tree of the neuraminidase (A), polymerase protein 1 (B), polymerase (C), matrix (D), nucleoprotein (E), and nonstructural (F) gene sequences. Branch colors represent the most probable ancestral locations inferred from geo-referenced sequence data through a spatial phylogenetic model (see Materials and Methods in the article main text for details). Colors and legend details are identical to those in Figure 2 and 3 in the main text.


A
Central China
Eastern China
Northern China
Southeast China
Central GD
Eastern GD
Western GD
Exported
Other Regions
2010
2011
2012
2013
2014
2015

B

c


D
A_GD-ST_72_2015_H7N9_2015.1041
A_GD-SW_30_2015_H7N9_2015.0603
A_GD-ST_27_2015_H7N9_2015.0575
A_GD-ST_69_2015_H7N9_2015.0959
A_GD-GZ_92_2015_H7N9_2015.1562
A_GD-ST_124_2015_H7N9_2015.1562
A_GD-MZ_54_2015_H7N9_2015.0740
A_GD-CZ_81_2015_H7N9_2015.1123
A_GD-CZ_80_2015_H7N9_2015.1123
A_GD-ST_76_2015_H7N9_2015.1123
A_GD-SW_20_2015_H7N9_2015.0411
A_GD-MZ_91_2015_H7N9_2015.1562
A_GD-MZ_156_2014_H7N9_2014.9014
A_GD-SW_50_2015_H7N9_2015.0740
A_GD-SZ_17_2015_H7N9_2015.0301
Ck_YT_2469_2013_H9N2_2013.802
Ck_YT_2303_2013_H9N2_2013.799
Ck_JX_28601_2013_H9N2_2013.854
A_GD-ST_139_2014_H7N9_2014.2630
A_GD-ST_124_2014_H7N9_2014.1781
A_Nanjing_M2_2013_H7N9_2013.3178
A_Anhui_3_2013_H7N9_2013.3041
A_Shanghai_4_2013_H7N9_2013.1863
A_Shanghai_12_2013_H7N9_2013.2740
A_Jiangsu_8_2013_H7N9_2013.2767
A_Suzhou_3_2013_H7N9_2013.2712
A_Beijing_01-A_2013_H7N9_2013.2795
A_Hangzhou_1_2013_H7N9_2013.3274
A_Taiwan_1_2014_H7N9_2014.3041
Ck_JX_18008_2014_H7N9_2014.433
Ck_JX_18012_2014_mix-H7N9-mix_2014.433
Ck_JX_14023_2014_H7N9_2014.2842
A_GD-MZ_153_2014_H7N9_2014.3507
A_GD-MZ_79_2015_H9N2_2015.1123
Ck_SX_2417_2013_H7N9_2013.799
Ck_SX_5087_2013_H7N9_2013.821
Ck_SX_5227_2013_H7N9_2013.821
Ck_WZ_2580_2013_mix-H9N2_2013.804
A_Suzhou_5_2013_H7N9_2013.2795
A_Wuxi_1_2013_H7N9_2013.2466
A_Nanjing_7_2013_H7N9_2013.2822
A_Fujian_1_2013_H7N9_2013.3096
A_Fujian_1_2013_H7N9_2013.3123
ENV_GD-GZ_707_2014_H9N2_2014.5836
ENV_GD-GZ_934_2014_H9N2_2014.9178
Air_GD-GZ_258_2015_H9N2_2015.1644
ENV_GD-PY_984_2014_H9N2_2014.9178
A_Xuzhou_1_2013_H7N9_2013.3151
A_Shanghai_51907_2013_H7N9_2013.3315
A_Anhui_2_2013_H7N9_2013.2849
Ck_JX_12261_2014_H7N9_2014.209
ENV_GD-MZ_238_2014_H7N9_2014.2493
Ck_JX_14554_2014_H7N9_2014.303
Ck_JX_13498_2014_mix-H7N9_2014.264
Ck_JX_12200_2014_H7N9_2014.209
Ck_JX_14515_2014_H7N9_2014.303
Ck_JX_13515_2014_mix-H7N9_2014.264
SCk_HZ_4213_2013_H7N9_2013.810
A_GD-SZ_SP118_2014_H7N9_2014.215
A_Shanghai_1_2014_H7N9_2014.0062
A_GD-MZ_125_2014_H7N9_2014.1863
Ck_SX_5201_2013_H7N9_2013.821
Ck_JX_13493_2014_H7N9_2014.264
Ck_JX_13546_2014_H7N9_2014.278
ENV_GD-MZ_441_2014_H9N2_2014.3315
A_Taiwan_2_2014_H7N9_2014.3123
Ck_JX_13520_2014_mix-H7N9-H9N2_2014.264
Ck_GD-SZ_967_2013_mix2-H9N2_2013.940
Ck_SX_2414_2013_mix2-H9N2_2013.799
ENV_GD-PY_992_2014_H9N2_2014.9178
Ck_JiaX_4713_2013_H9N2_2013.815
SCk_HZ_4218_2013_H9N2_2013.810
Ck_GD-DG_1525_2014_mix1-H7N9-H9N2_2014.140
Ck_GD-SZ_1519_2013_H9N2_2013.942
ENV_GD-MZ_530_2014_H9N2_2014.4164
A_GD-HY_45_2015_H7N9_2015.0712
A_Zhejiang_DTID-ZJU01_2013_H7N9_2013.2548
A_ZJ_35_2014_H7N9_2014.063
A_ZJ_30_2014_H7N9_2014.055
A_Zhejiang_22_2013_H7N9_2013.7863
A_Taiwan_1_2013_H7N9_2013.3123
ENV_GD-MZ_51_2014_H9N2_2014.9178
Ck_HZ_3801_2013_H9N2_2013.810
Dk_Anhui_SC702_2013_H7N9_2013.2904
A_Shanghai_9_2013_H7N9_2013.2685
A_Shanghai_15_2013_H7N9_2013.2712
A_Shanghai_2_2013_H7N9_2013.1753
A_Shanghai_4664T_2013_H7N9_2013.1753
A_Jiangsu_5_2013_H7N9_2013.2685
A_Wuxi_3_2013_H7N9_2013.2658
A_Hangzhou_2_2013_H7N9_2013.2301
A_GD-GZ_68_2015_H7N9_2015.1068
A_GD-JM_51_2015_H7N9_2015.0822
CK_GD-PY_6_2014_H9N2_2014.5836
Ck_HZ_4076_2013_H7N9_2013.810
Ck_HZ_3977_2013_mix-H7N9-H9N2_2013.810
A_Hunan_1_2013_H7N9_2013.3123
A_Jiangsu_9_2013_H7N9_2013.2712
A_Nanjing_6_2013_H7N9_2013.2767
A_Anhui_1_2013_H7N9_2013.2164
Ck_Anhui-Chuzhou_1_2013_H7N9_2013.2411
A_Shanghai_3_2013_H7N9_2013.1589
A_shanghai_5_2013_H7N9_2013.2521
Ck_Jiangsu_HA2_2013_H9N2_2013.2603
A_Shanghai_11_2013_H7N9_2013.2740
A_Jiangsu_4_2013_H7N9_2013.2603
A_Jiangsu_2_2013_H7N9_2013.3014
A_Jiangsu_1_2013_H7N9_2013.2438
A_Shanghai_1_2013_H7N9_2013.1562
A_Shanghai_10_2013_H7N9_2013.2712
Ck_Wenzhou_606_2013_H9N2_2013
A_GD-DG_42_2015_H7N9_2015.0685
A_GD-DG_18_2015_H7N9_2015.0301
A_GD-GZ_155_2014_H7N9_2014.8849
A_GD-SZ_1_2015_H7N9_2015.0082
A_GD-ZQ_44_2015_H7N9_2015.0521
A_GD-DG_2_2015_H7N9_2015.0164
A_HongKong_308_2014_H9N2_2013.9918
Ck_GD-SZ_844_2013_H9N2_2013.934
A_GD-ZQ_98_2014_H7N9_2014.1014
A_GD-ZQ_81_2014_H7N9_2014.0822
A_GD-ZQ_69_2014_H7N9_2014.0822
A_GD-FS_95_2015_H7N9_2015.1753
A_GD-JM_120_2015_H7N9_2015.1890
Ck_GD-SZ_1377_2013_H9N2_2013.940
ENV_GD-PY_778_2014_H9N2_2014.7507
ENV_GD-MM_308_2014_H9N2_2014.9178
Env_Hangzhou_109-1_2013_H7N9_2013.2795
Ck_Zhejiang_SD007_2013_H7N9_2013.3068
A_Hangzhou_3_2013_H7N9_2013.2521
brambling_Beijing_16_2012_H9N2_2012.86
ENV_GD-CH_46_2015_H9N2_2015.0027
ENV_GD-HY_81_2013_H9N2_2013.4986
Dk_Hunan_S4111_2011_H9N2_2011.8630
Ck_Shangdong_SDWF29_2012_H9N2_2012.3552
Ck_JX_21468_2013_H9N2_2013.702
Ck_JX_20478_2013_H9N2_2013.664
Ck_JX_19448_2013_H9N2_2013.628
Env_JX_452_2013_H9N2_2013.1589
Ck_JX_11708_2013_mix-H9N2_2013.231
Ck_Zhejiang_C487_2013_H9N2_2013.2493
Ck_HongKong_FL96_2010_H9N2_2010
Ck_JX_9534_2014_H7N9_2014.126
Ck_JX_10929_2014_H7N9_2014.132
A_JX-Donghu_346_2013_H10N8_2013.9260
Dk_JX_36485_2013_H9N2_2013.989
Ck_GD-DG_1239_2014_mix-H7N9_2014.140
A_GD-HY_21_2015_H7N9_2015.0438
A_GD-ST_43_2015_H7N9_2015.0603
A_GD-ZQ_10_2015_H7N9_2015.0164
A_GD-HZ_53_2015_H7N9_2015.0932
ENV_GD-DG_1_2015_H9N2_2015.0027
ENV_GD-MM_289_2014_H9N2_2014.8356
Ck_JX_18491_2014_mix-H7N9-H9N2_2014.454
Ck_JX_31872_2013_H9N2_2013.931
Ck_SuZ_4822_2013_H9N2_2013.818
Ck_SuZ_4954_2013_H9N2_2013.818
Ck_Wenzhou_614_2013_H9N2_2013
Ck_JiaX_4742_2013_H9N2_2013.815
ENV_GD-MZ_409_2014_H9N2_2014.3315
Ck_GD-DG_670_2014_mix-H7N9-H9N2_2014.137
Ck_GD_LG1_2013_H9N2_2013.0027
Ck_GD-SZ_3745_2013_H9N2_2013.961
SCk_GD-DG_4184_2013_H9N2_2013.961
ENV_GD-ZS_44_2013_H9N2_2013.2493
Ck_WZ_3393_2013_H9N2_2013.807
Ck_JX_18901_2013_H9N2_2013.609
Ck_Jiangsu_YZ0611_2011_H9N2_2011.4438
Ck_Shanghai_D_2011_H9N2_2011.4986
Ck_Jiangsu_KZ8_2012_H9N2_2012.8497
Ck_Anhui_PXP07026_2010_H9N2_2010.29
Ck_Jiangsu_PXP09339_2010_H9N2_2010.13
Ck_Shangdong_SDWD_2011_H9N2_2011.0712
A_Changsha_2_2013_H7N9_2013.3260
A_Changsha_1_2013_H7N9_2013.2219
A_Shandong_1_2013_H7N9_2013.3041
A_Nanchang_1_2013_H7N9_2013.3123
A_Henan_1_2013_H7N9_2013.2904
A_Shanghai_7_2013_H7N9_2013.2110
A_Zhejiang_20_2013_H7N9_2013.3123
A_Shanghai_13_2013_H7N9_2013.2740
A_Jiangsu_7_2013_H7N9_2013.2548
Ck_Jiangsu_SC099_2013_H7N9_2013.2904
A_Hebei_1_2013_H7N9_2013.55
A_Nanjing_3_2013_H7N9_2013.2986
Ck_Rizhao_1339_2013_H9N2_2013
Ck_Jiangsu_ZJ4_2013_H9N2_2013.0630
Ck_Jiangsu_KZ38_2012_H9N2_2012.0328
Ck_Jiangsu_WJHRG_2012_H9N2_2012.2295
Ck_Shanghai_PXP10672_2012_H9N2_2012.04
Ck_Hebei_PXP08415_2010_H5N2_2010.96
Ck_Hunan_12_2011_H9N2_2011.9233
Ci_Guangxi_PXP05707_2011_H9N2_2011.50
A_HongKong_8122430_2014_H7N9_2014.2822
A_GD-SZ_SP139_2014_H7N9_2014.256
A_HongKong_4495_2014_H7N9_2014.1644
A_GD-JM_154_2014_H7N9_2014.4055
A_GD-HY_138_2014_H7N9_2014.2603
A_GD-SZ_SP126_2014_H7N9_2014.228
A_HongKong_5731_2014_H7N9_2014.2685
A_HongKong_5581_2014_H7N9_2014.2548
A_GD-ZS_151_2014_H7N9_2014.3452
A_GD-GZ_126_2014_H7N9_2014.1890
A_GD-FS_116_2014_H7N9_2014.1452
A_GD-GZ_103_2014_H7N9_2014.1123
A_GD-GZ_119_2014_H7N9_2014.1370
A_GD-YJ_12_2014_H7N9_2014.0082
A_GD-YJ_13_2014_H7N9_2014.0082
A_GD-ZS_74_2014_H7N9_2014.0949
A_GD-ZS_71_2014_H7N9_2014.0822
A_GD-JM_62_2014_H7N9_2014.0740
A_GD-FS_33_2014_H7N9_2014.0329
A_GD-FS_34_2014_H7N9_2014.0329
A_GD-GZ_36_2014_H7N9_2014.0329
A_GD-FS_19_2014_H7N9_2014.0192
A_GD-FS_29_2014_H7N9_2014.0301
A_GD-FS_18_2014_H7N9_2014.0192
A_GD-FS_31_2014_H7N9_2014.0301
A_GD-YJ_4_2013_H7N9_2013.9589
A_GD-ZS_117_2014_H7N9_2014.1452
A_GD-ZH_123_2014_H7N9_2014.1644
A_GD-GZ_43_2014_H7N9_2014.0411
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A_GD-GZ_10_2014_H7N9_2014.0082
A_GD-HZ_1_2013_H7N9_2013.6082
A_GD-SZ_SP16_2013_H7N9_2014.049
A_GD-SZ_SP49_2013_H7N9_2014.068
A_GD-SZ_110_2014_H7N9_2014.1205
A_GD-SZ_46_2014_H7N9_2014.0438
A_GD-SZ_SP4_2013_H7N9_2014.044
A_GD-SZ_SP60_2014_H7N9_2014.082
A_GD-SZ_SP38_2013_H7N9_2014.060
A_GD-SZ_SP58_2014_H7N9_2014.068
A_GD-SZ_SP26_2013_H7N9_2014.055
A_HongKong_734_2014_H7N9_2014.0192
A_GD-SZ_25_2014_H7N9_2014.0274
A_GD-SZ_48_2014_H7N9_2014.0521
A_GD-SZ_WYH_2013_H7N9_2014.038
A_GD-SZ_35_2014_H7N9_2014.0329
A_GD-YJ_5_2013_H7N9_2013.9616
A_GD-GZ_105_2014_H7N9_2014.1151
A_GD-GZ_112_2014_H7N9_2014.1342
A_GD-ZQ_101_2014_H7N9_2014.1041
A_HongKong_8113530_2014_H7N9_2014.2082
A_GD-SZ_66_2014_H7N9_2014.0795
A_GD-SZ_65_2014_H7N9_2014.0795
A_GD-YJ_62_2014_H7N9_2014.0904
A_GD-SZ_109_2014_H7N9_2014.1205
A_GD-JM_114_2014_H7N9_2014.1342
A_GD-GZ_136_2014_H7N9_2014.2411
A_GD-HZ_75_2014_H7N9_2014.0849
A_GD-SZ_SP48_2013_H7N9_2014.063
A_HongKong_3263_2014_H7N9_2014.1178
A_GD-SZ_SP75_2014_H7N9_2014.124
A_HongKong_2212982_2014_H7N9_2014.0767
A_GD-SZ_SP62_2014_H7N9_2014.096
A_GD-ZH_57_2015_H7N9_2015.0932
A_GD-DG_3_2013_H7N9_2013.9562
A_GD-DG_2_2013_H7N9_2013.8438
Ck_GD-DG_3563_2013_H7N9_2013.961
Ck_GD-DG_3487_2013_H7N9_2013.961
ENV_GD-GZ_874_2014_H9N2_2014.8356
A_GD-ZS_167_2014_H9N2_2014.0027
muscovy-Dk_Vietnam_LBM417_2013_H9N2_2013.3479
Ck_Quang-Ninh_26_2013_H9N2_2013.2740
Env_GD_C13280011_2013_H9N2_2013.2932
Ck_GD-SZ_1737_2013_mix-H9N2_2013.942
Ck_HongKong_CSW533_2011_H9N2_2011
Ck_HongKong_YU551W_2011_H9N2_2011
A_HongKong_5942_2013_H7N9_2013.9151
A_GD-SZ_SP44_2013_H7N9_2014.063
Ck_GD-SZ_2014_2013_H9N2_2013.945
Ck_GD-SZ_354_2013_H9N2_2013.937
Ck_GD-DG_3409_2013_H9N2_2013.961
Ck_GD-SZ_678_2013_H9N2_2013.937
SCk_HongKong_YU505W_2011_H9N2_2011
Ck_HongKong_JV17_2012_H9N2_2012
Env_GD_20130N1652_2013_H9N2_2013.3781
Ck_GD-DG_2701_2013_H9N2_2013.959
A_GD-GZ_121_2014_H7N9_2014.1370
Ck_HongKong_TC18_2011_H9N2_2011
Ck_Shandong_513_2011_H9N2_2011.6301
Ck_Shanghai_B_2010_H9N2_2010.5836
Ck_HongKong_YU262W_2012_H9N2_2012
Ck_HongKong_CRA45_2010_H9N2_2010
Ck_JX_9696_2013_H9N2_2013.174
Ck_JX_8209_2013_H9N2_2013.137
ENV_GD-ZJ_43_2014_H9N2_2014.1644
Ck_JX_506_2013_H9N2_2013.036
A_GD-MZ_55_2015_H7N9_2015.0740
Dk_JX_8358_2013_H9N2_2013.137
Ck_Zhejiang_PXP11611_2011_H9N2_2011.21
Ck_Shanghai_C_2011_H9N2_2011.4164
Ck_HongKong_HN8_2010_H9N2_2010
Ck_Jiangsu_NTHA1_2012_H9N2_2012.9918
Ck_Jiangsu_KZ9Z_2011_H9N2_2011.2384
Ck_Henan_323_2009_H9N2_2009.7068
Ck_Shandong_PXP10568_2010_H9N2_2010.37
Ck_Shandong_PXP10574_2009_H9N2_2009.37
Ck_Shandong_PXP10578_2009_H9N2_2009.12
Ck_Jiangsu_DT_2009_H9N2_2009.7205
Dk_Wuxi_PXP15934_2010_H9N2_2010.53
Swine_Taizhou_PXP49862_2008_H9N2_2008.79
Ck_Shanghai_A_2010_H9N2_2010.4164
Ck_Zhejiang_PXP11630_2007_H9N2_2007.50
Ck_Shandong_384_2011_H9N2_2011.5918
Ck_Shandong_PXP10651_2009_H9N2_2009.24
Ck_Shandong_363_2009_H9N2_2009.8877
Ck_WZ_3330_2013_H9N2_2013.807
Ck_Hebei_PXP08425_2008_H9N2_2008.21
Env_Hunan_PXP17424_2007_H9N2_2007.21
Ck_Shandong_317_2007_H9N2_2007.7151
Ck_Shandong_237_2007_H9N2_2007.8603
Ck_Shandong_PXP10552_2008_H9N2_2008.50
Ck_Hunan_PXP08813_2005_H9N2_2005.70
Ck_Hunan_PXP08814_2005_H9N2_2005.83
Ck_Shandong_251_2007_H9N2_2007.5096
Ck_Shantou_PXP10742_2003_H9N2_2003.96
Ck_Shantou_PXP10726_2003_H9N2_2003.69
Gu_Shantou_PXP11916_2003_H9N2_2003.96
Ck_GD_PXP08098_2001_H9N2_2001.50
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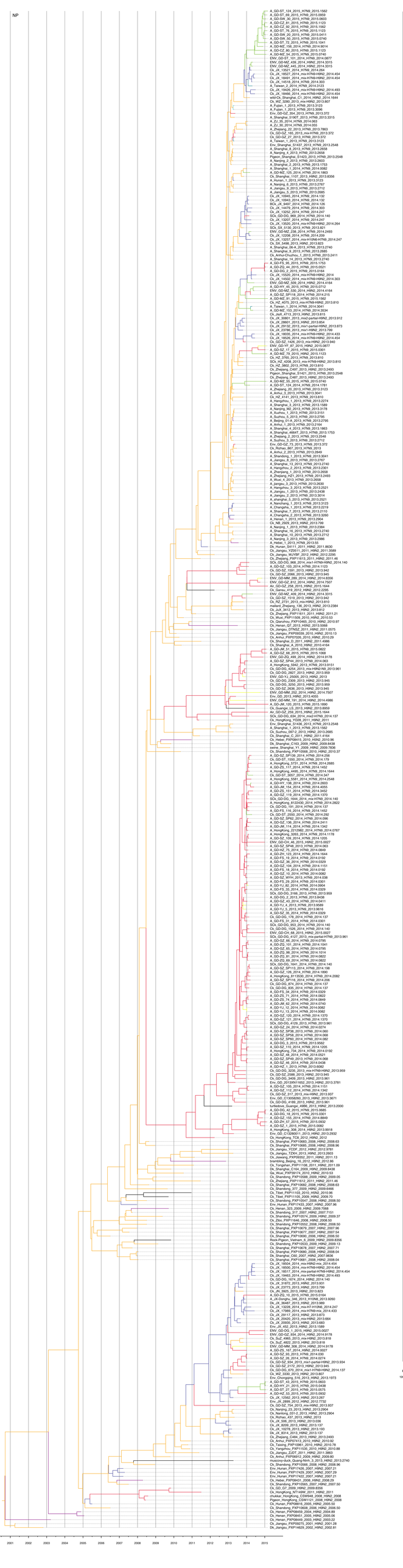
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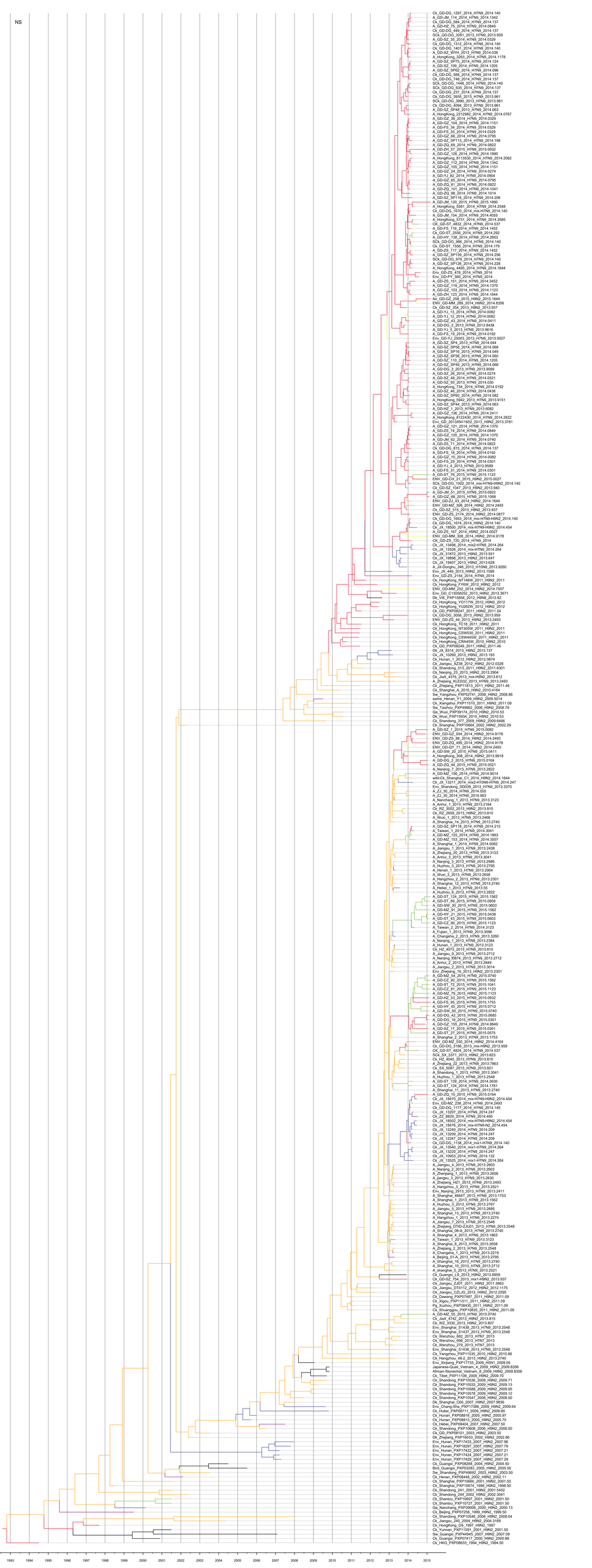
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Ck_HKG_FXP08833_1994_H9N2_1994.50
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