

Novel Reassortant Avian Influenza A(H5N6) Viruses in Humans, Guangdong, China, 2015

Technical Appendix

Virus Isolation and Sequencing

On December 28, 2015, avian influenza A(H5N6) was detected in a throat swab sample from a patient (female, 26 years of age) with severe pneumonia by Shenzhen Municipal Center for Disease Control and Prevention (CDC). On December 31, 2015, another H5N6–positive case was detected in throat swab and tracheal aspirate samples from a patient (female, 40 years of age) with fever by Zhaoqing Municipal CDC. Both viruses were further confirmed to be H5N6 by full genome sequencing conducted at Guangdong Provincial CDC. Both H5N6–infected patients died; their deaths were reported to National Health and Family Planning Commission (NHFPC) of the People’s Republic of China and World Health Organization (WHO) (<http://www.who.int/csr/don/11-january-2016-avian-influenza-china/en/>) (<http://www.who.int/csr/don/4-january-2016-avian-influenza-china/en/>).

Long–term avian influenza virus (AIV) surveillance was conducted in Guangdong province. We collected pairs of cloacal and oropharyngeal swab specimens from healthy poultry in several live poultry markets. Samples were stored in viral medium at 4°C until they were transported to the laboratory and then stored at –80°C until virus isolation. A 0.22–µm filter was used to sterilize the samples, which were then used to inoculate 9-day-old SPF embryonated eggs. After incubation at 37 °C for 72 h, allantoic fluid was harvested and tested by using the hemagglutination assay. Subtypes of the viruses were determined by conventional hemagglutination

inhibition and neuraminidase inhibition assays. Nine samples that tested positive for H5 and N6 were chosen for RNA extraction and sequencing in this study.

Complete genomes of the H5N6 and H6N6 AIVs were amplified by using a Qiagen OneStep RT-PCR Kit (Qiagen, Germany). PCR products were purified and sequenced on an ABI 3730XL automatic DNA analyzer. All 8 gene segments were sequenced; the nucleotide sequences were deposited into the Global Initiative on Sharing Avian Influenza Data (GISAID) (accession numbers: EPI_ISL_205959-EPI_ISL_206569).

Data Source and Analyses

All previously published H5, H6N6, and H9N2 AIV subtype sequences were collated from GenBank and the Global Initiative on Sharing Avian Influenza Data (GISAID) on 3 January 2016. Sequences of each gene segment were aligned by using MUSCLE (1). Phylogenetic trees were constructed by using RAxML (2), and the 94 sequences (Technical Appendix Table) most closely related to the H5N6 outbreak isolates were selected for further refined analyses. Maximum likelihood phylogenies were reconstructed by using PhyML with bootstrap analysis (1,000 replicates) (3). Evolution of virus strains is shown in online Technical Appendix Figure 2. Phylogenetic trees constructed for the HA, NA, polymerase basic-2, polymerase basic-1 (PB1), polymerase acidic (PA), nucleoprotein (NP), matrix (M), and nonstructural (NS) segments are shown in online Technical Appendix Figure 1.

References

1. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 2004;32:1792–7.
<http://dx.doi.org/10.1093/nar/gkh340>

2. Stamatakis A. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics*. 2006;22:2688–90.
<http://dx.doi.org/10.1093/bioinformatics/btl446>
3. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Syst Biol*. 2010;59:307–21. <http://dx.doi.org/10.1093/sysbio/syq010>

Technical Appendix Table. Complete genomes of 94 avian influenza viruses isolated from poultry and the environment, China*

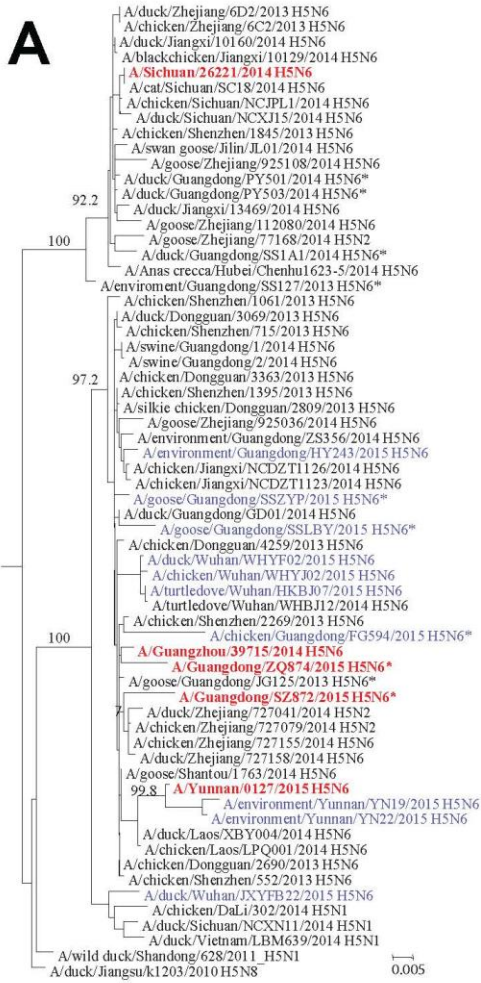
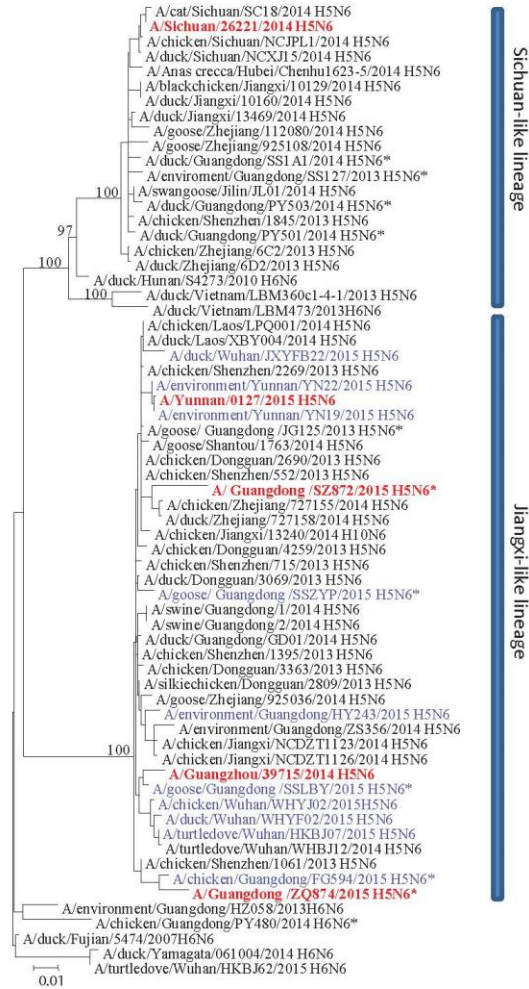
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A/cat/Sichuan/SC18/2014 (H5N6)	KM873635	KM873636	KM873637	KM873638	KM873639	KM873640	KM873641	KM873642
A/chicken/DaLi/302/2014 (H5N1)	KP732559	KP732560	KP732561	KM392379	KP732562	KP732563	KP732564	KP732565
A/chicken/Dongguan/2690/2013 (H5N6)	KP286098	KP286099	KP286100	KP286101	KP286102	KP286103	KP286104	KP286105
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A/chicken/Dongguan/3964/2013 (H9N2)	KP414642	KP414643	KP414644	KP414645	KP414646	KP414647	KP414648	KP414649
A/chicken/Dongguan/4189/2013 (H9N2)	KP414666	KP414667	KP414668	KP414669	KP414670	KP414671	KP414672	KP414673
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A/chicken/Qingdao/013/2014 (H9N2)	KT449724	KT449704	KT449684	KT449584	KT449644	KT449624	KT449604	KT449664
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A/chicken/Shenzhen/715/2013 (H5N6)	KP286074	KP286075	KP286076	KP286077	KP286078	KP286079	KP286080	KP286081
A/chicken/Sichuan/NCJPL1/2014 (H5N6)	KM251533	KM251523	KM251513	KM251463	KM251493	KM251486	KM251473	KM251503
A/chicken/Taizhou/TZJF05/2015 (H9N2)	KU143584	KU143541	KU143498	KU143287	KU143412	KU143351	KU143326	KU143455
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A/chicken/Wuhan/WHYJ02/2015 (H5N6)	KU143578	KU143535	KU143492	KU143268	KU143403	KU143364	KU143319	KU143449
A/chicken/Zhejiang/6C2/2013 (H5N6)	KJ807774	KJ807775	KJ807776	KJ807777	KJ807778	KJ807779	KJ807780	KJ807781
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A/duck/Jiangsu/k1203/2010 (H5N8)	JQ973691	JQ973692	JQ973693	JQ973694	JQ973695	JQ973696	JQ973697	JQ973698
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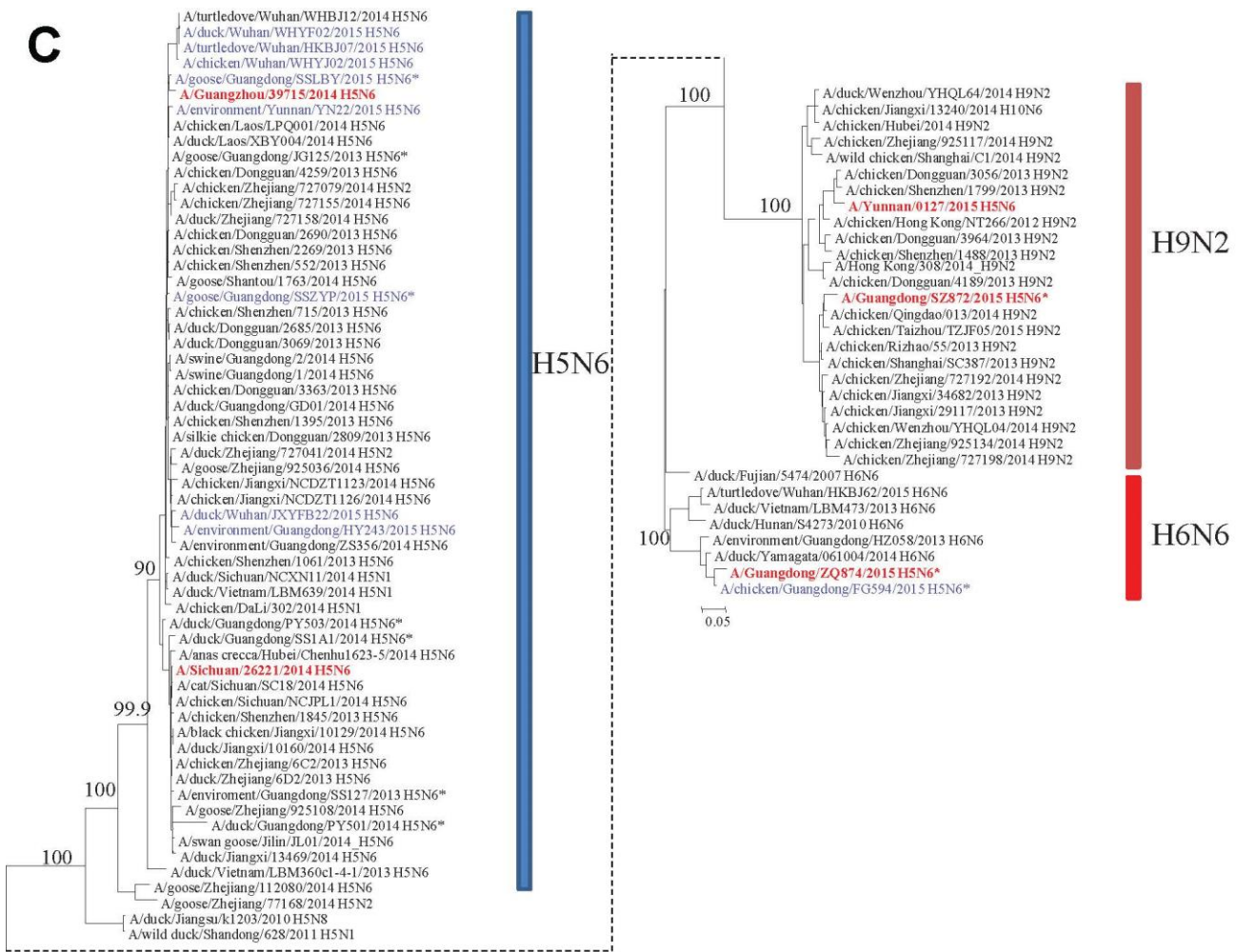
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A/Hong Kong/308/2014 (H9N2)	EPI498034	EPI498035	EPI498033	EPI498037	EPI498030	EPI498036	EPI498032	EPI498031
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Strain name	Genbank accession numbers							
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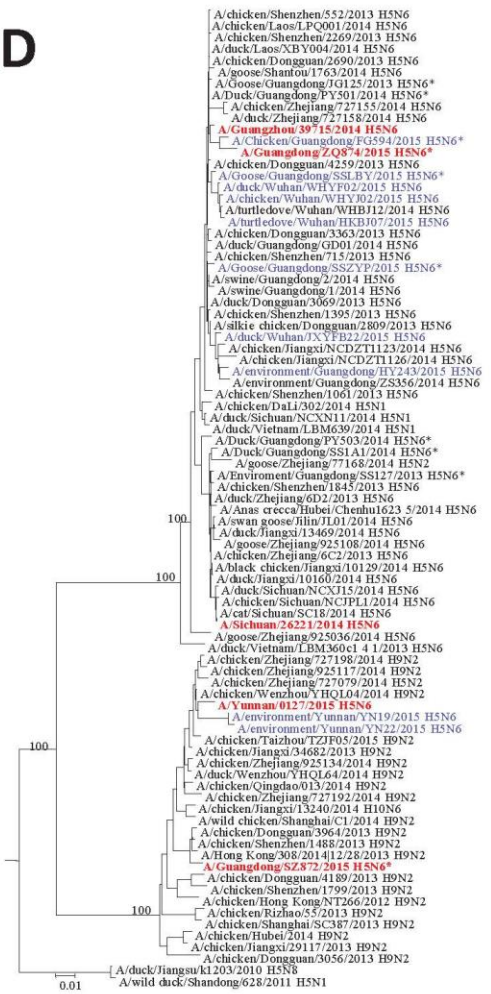
*PB, polymerase basic; PA, polymerase; HA, hemagglutinin; NP, nucleoprotein; NA, neuraminidase; M, matrix; NSP, nonstructural protein; ND, no data.

†The complete genomes of these viruses were deposited in the Global Initiative on Sharing Avian Influenza Data (GISAID) EpiFlu database (<http://platform.gisaid.org>).

A**B**



D

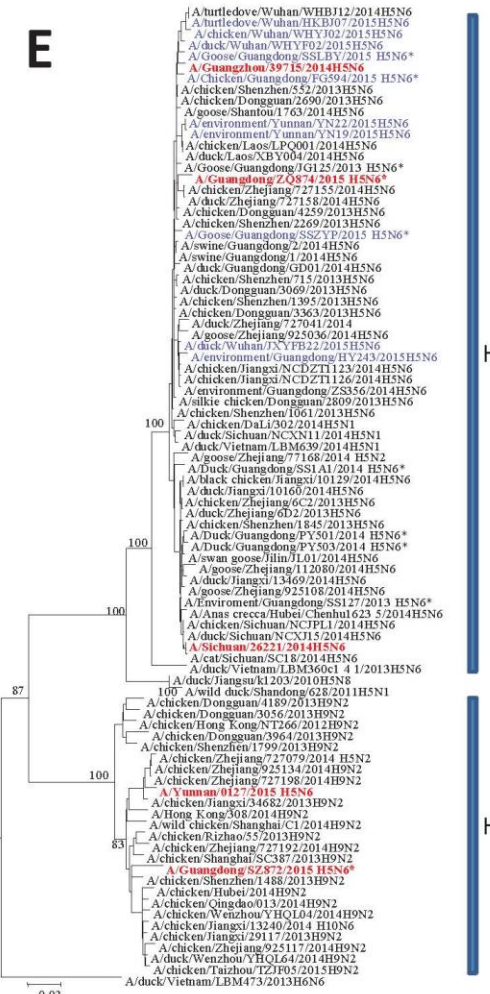


H5N6

H9N2

H5N6

E

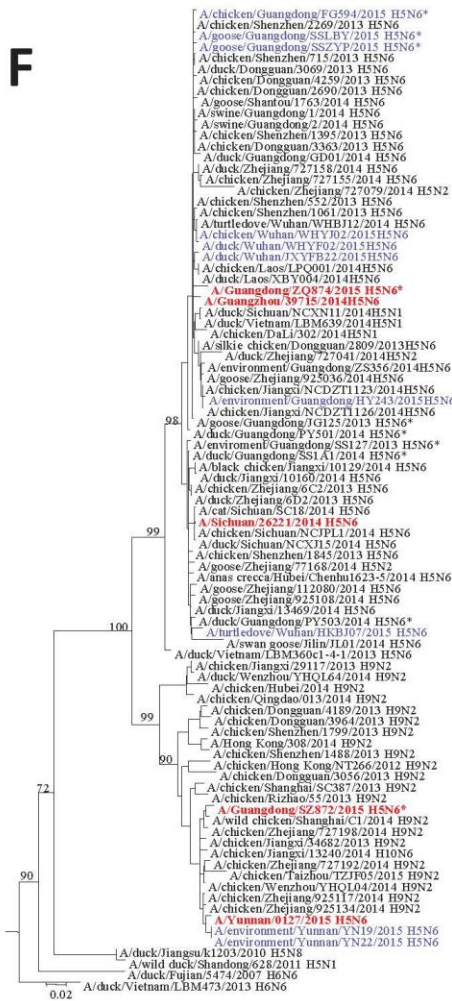


H5N6

H9N2

H5N6

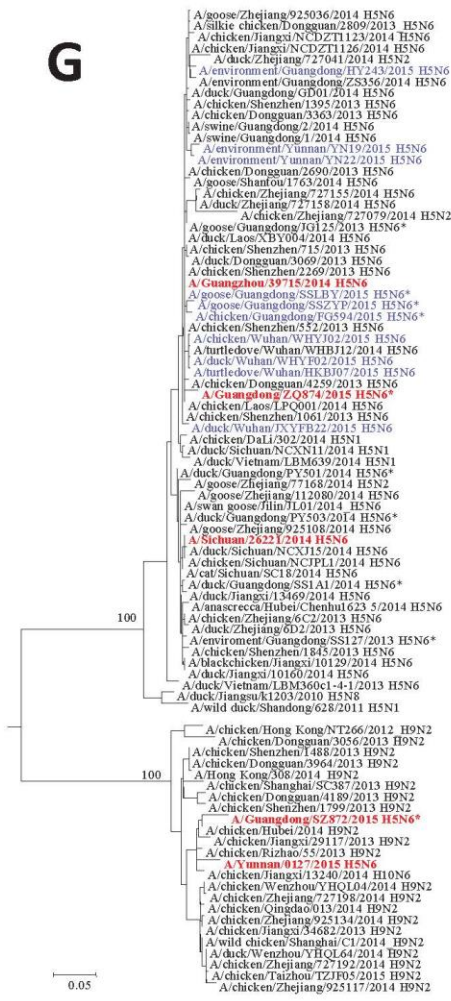
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H5N6

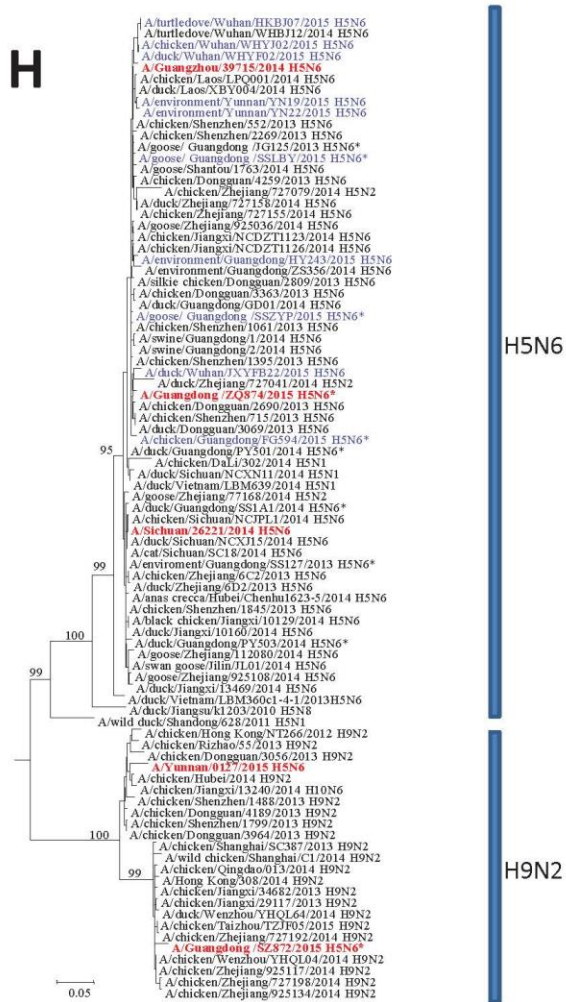
H9N2

G

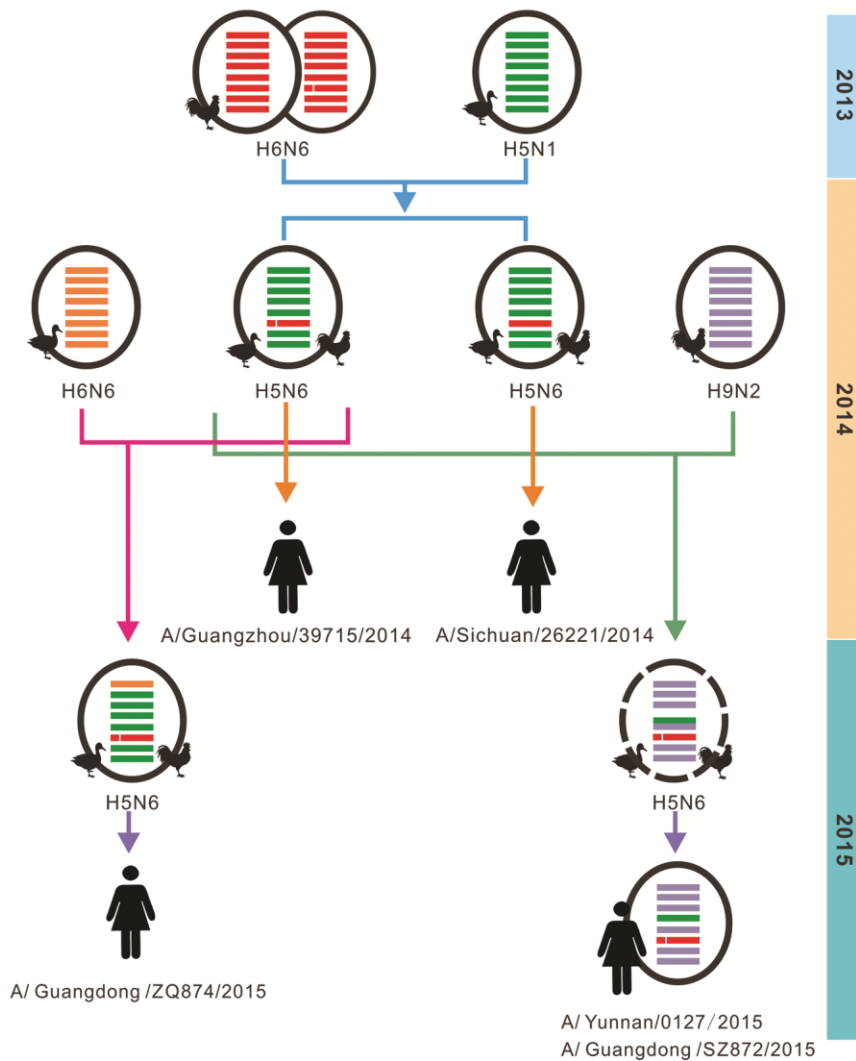


H5N6

H9N2



Technical Appendix Figure 1. Phylogenetic relationships of H5N6 influenza viruses. A) hemagglutinin (HA); B) neuraminidase (NA); C) polymerase basic-2 (PB2); D) polymerase basic-1 (PB1); E) polymerase acidic (PA); F) nucleoprotein (NP); G) matrix (M); H) non-structural (NS). Maximum-likelihood trees were constructed using PhyML. Bootstrap values were calculated on 1,000 replicates. Viruses that infect humans are indicated in red. H5N6 viruses isolated in 2015 are indicated in blue; viruses sequenced in this study were marked with *.



Technical Appendix Figure 2. Hypothetical lineage for the origin of the novel reassortant avian influenza A(H5N6) viruses in humans, Guangdong, China, 2015. Virus particles are represented by ovals containing horizontal bars that represent the 8 gene segments (from top to bottom: polymerase basic 2, polymerase basic 1, polymerase acidic protein, hemagglutinin, nucleocapsid protein, neuraminidase, matrix protein, and nonstructural protein). A broken bar representing neuraminidase (segment 6) indicates an 11 aa deletion in the stalk region. Virus indicated by a broken oval represents a hypothetical reassortant. Source viruses for a reassortant virus are adjacent to the arrow tails; arrow heads point to the resulting reassortant viruses. Colored bars indicate poultry source and year of original isolation: red: chicken, 2013; green: duck, 2013; orange: duck, 2014; purple: chicken, 2014.