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Avian Influenza A Virus (H5N1) Outbreaks, Kuwait, 2007

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Phylogenetic analysis of influenza A viruses (H5N1) isolated from Kuwait in 2007 show that (H5N1) sublineage clade 2.2 viruses continue to spread across Europe, Africa, and the Middle East. Virus isolates were most closely related to isolates from central Asia and were likely vectored by migratory birds.

Highly pathogenic avian influenza (HPAI) virus (H5N1) has been endemic in poultry in Asia since 2003 (1,2). From 2002 through 2005, influenza virus (H5N1) has also been sporadically isolated from dead wild birds in Hong Kong Special Administrative Region, People's Republic of China; however, these birds were considered dead-end hosts of viruses acquired from poultry (3,4). In April 2005, an influenza (H5N1) outbreak was detected in bar-headed geese (*Anser indicus*) at Qinghai Lake in western China (5). Following this outbreak, the Qinghai-like (clade 2.2) influenza virus (H5N1) lineage was detected in wild birds and domestic poultry in countries in central Asia, the Middle East, Europe, and Africa (6–10). The source of these introductions, while still debated, is likely through bird migration, although in some instances, the role of the poultry trade has not been ruled out (6–12).

The clade 2.2 influenza (H5N1) viruses continue to be detected throughout these regions; 69 human cases with 31 deaths were reported from Azerbaijan, Djibouti, Egypt, Iraq, Nigeria, Pakistan, and Turkey from January 2006 through December 2007 (13). Since early 2007, the Qinghai-like influenza (H5N1) lineage has continued its geographic spread and has been reported from more than 40 countries in Eurasia and Africa (6). The continued detection of these viruses in Africa, Europe, and the Middle East from mid-2006 onward suggests that the virus may now be endemic in these regions.

The Study

On February 13, 2007, the Public Authority for Agriculture and Fisheries of Kuwait reported the initial outbreak of influenza (H5N1) in poultry in the Al Wafrah farm area in southern Kuwait. Subsequently, 131 influenza virus (H5N1)-infected poultry were confirmed from 20 farms throughout the country (Figure 1, panel A). The disease resulted in high mortality rates among infected flocks, especially in the commercial broiler farms in Al-Wafrah and among poultry raised in privately owned residential homes and backyard farms. Disease control measures were implemented beginning February 18, 2007, including control of poultry movement, vaccination, disinfection of infected premises, and culling of ≈500,000 birds. The final case of subtype H5N1 was detected on April 20, 2007, and



Figure 1. A) Kuwait, with location of subtype H5N1 virus outbreaks in 2007. Circles indicate location of farms with confirmed influenza (H5N1) infections in poultry; square indicates the Al Sulaibiya area where virus isolation was conducted. B) Eurasia, with location of subtype H5N1 isolates phylogenetically related to Kuwait isolates.

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Table. Antigenic analysis of influenza viruses (H5N1) by hemagglutinin inhibition test, 2007*

Virus	Clade†	Anti-VNM/1203‡	Anti-IDN/5	Anti-CDC357	Anti-QH/1A	Anti-Anhui/1
Vietnam/1203/2004	1	160	160	40	40	40
Indonesia/5/2005	2.1	<40	640	640	40	80
Indonesia/CDC357/2006	2.1	40	1,280	1,280	80	160
BHG/Qinghai/1A/2005	2.2	80	640	320	160	640
Dk/Laos/3295/2006	2.3.4	40	320	80	40	320
Ck/Kuwait/KISR2/2007	2.2	<40	640	160	320	<40

*BHG, bar-headed goose; Dk, duck; Ck, chicken. **Boldface** numbers indicate titers to prototype viruses.

†Based on the World Health Organization (H5N1) nomenclature system (14).

‡Ferret antisera dilution started at 1:40.

H5PAI (H5N1) outbreak in wild birds in Qinghai Lake, China, in 2005 (5).

Conclusions

The results of this study confirm that clade 2.2 H5PAI (H5N1) viruses were responsible for the poultry outbreaks recorded in Kuwait in early 2007. Notably, the viruses from Kuwait are most closely related to other 2007 subtype H5N1 isolates from Germany and Russia, but not to other 2007 isolates from Egypt, England, Ghana, and Hungary for which data are available (Figure 2). Furthermore, none of the current isolates from Europe or the Middle East has a close phylogenetic relationship with clade 2.2 isolates from China in 2005, although data on recent subtype H5N1 isolates from northern China are lacking (5,12). These relationships, along with reemergence of genetically similar viruses in widely distant geographic locations such as Germany, Krasnodar, and Kuwait (Figure 1, panel B), indicate that clade 2.2 influenza (H5N1) viruses may have become endemic in wild birds in central or eastern Asia (including Siberian Russia), from where they have been repeatedly introduced to Europe and the Middle East. Although it remains unclear in which hosts these viruses are maintained, the geographic distribution of closely related viruses suggests that migratory bird species are likely acting as vectors. Also, continued endemicity of clade 2.2 viruses in parts of Eurasia may result in the diversification of the virus in different geographic areas, as has been seen for subtype H5N1 lineages in eastern and Southeast Asia (11). Therefore, systematic surveillance in poultry and wild bird populations will be an important tool for tracking the evolution of clade 2.2 influenza (H5N1) viruses in this region.

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Mr AL-Azemi has been a research associate at the Kuwait Institute for Scientific Research since 2006. His primary research interests include foodborne pathogens and molecular methods of detecting emerging pathogens.

References

- Li KS, Guan Y, Wang J, Smith GJD, Xu KM, Duan L, et al. Genesis of a highly pathogenic and potentially pandemic H5N1 influenza virus in eastern Asia. *Nature*. 2004;430:209–13.
- World Health Organization Global Influenza Program Surveillance Network. Evolution of H5N1 avian influenza viruses in Asia. *Emerg Infect Dis*. 2005;11:1515–21.
- Ellis TM, Bousfield RB, Bissett LA, Dyrting KC, Luk GSM, Tsim ST, et al. Investigation of outbreaks of highly pathogenic H5N1 avian influenza in waterfowl and wild birds in Hong Kong in late 2002. *Avian Pathol*. 2004;33:492–505.
- Guan Y, Poon LLM, Cheung CY, Ellis TM, Lim W, Lipatov AS, et al. H5N1 influenza: a protean pandemic threat. *Proc Natl Acad Sci U S A*. 2004;101:8156–61.
- Chen H, Smith GJD, Zhang SY, Qin K, Wang J, Li KS, et al. H5N1 virus outbreak in migratory waterfowl. *Nature*. 2005;436:191–2.
- Food and Agricultural Organization of the United Nations. Avian Influenza Disease Emergency Bulletin. Issue 46. 2007 [cited 2008 Jan 10]. Available from <http://www.fao.org/avianflu/en/AIDEnews.html>
- Ducatez MF, Olinger CM, Owoade AA, De Landtsheer S, Ammerlaan W, Niesters HG, et al. Avian flu: multiple introductions of H5N1 in Nigeria. *Nature*. 2006;442:37.
- Lipatov AS, Evseenko VA, Yen HL, Zaykovskaya AV, Durimanov AG, Zolotykh SI, et al. Influenza (H5N1) viruses in poultry, Russian Federation, 2005–2006. *Emerg Infect Dis*. 2007;13:539–46.
- Salzberg SL, Kingsford C, Cattoli G, Spiro DJ, Janies DA, Aly MM, et al. Genome analysis linking recent European and African influenza (H5N1) viruses. *Emerg Infect Dis*. 2007;13:713–8.
- Weber S, Harder T, Starick E, Beer M, Werner O, Hoffmann B, et al. Molecular analysis of highly pathogenic avian influenza virus of subtype H5N1 isolated from wild birds and mammals in northern Germany. *J Gen Virol*. 2007;88:554–8.
- Chen H, Smith GJD, Li KS, Wang J, Fan XF, Rayner JM, et al. Establishment of multiple sub-lineages of H5N1 influenza virus in Asia—implications for pandemic control. *Proc Natl Acad Sci U S A*. 2006;103:2845–50.
- Starick E, Beer M, Hoffmann B, Staubach C, Werner O, Globig A, et al. Phylogenetic analyses of highly pathogenic avian influenza virus isolates from Germany in 2006 and 2007 suggest at least three separate introductions of H5N1 virus. *Vet Microbiol*. 2008 [cited 2008 Apr 21]. Available from <http://dx.doi.org/10.1016/j.vetmic.2007.10.012>

13. World Health Organization. Cumulative number of confirmed human cases of avian influenza A/(H5N1) reported to WHO. 2008 [cited 2008 Jan 10]. Available from http://www.who.int/csr/disease/avian_influenza/country/en/
14. World Health Organization. Towards a unified nomenclature system for the highly pathogenic H5N1 avian influenza viruses. 2007. [cited 2007 Oct 10]. Available from http://www.who.int/csr/disease/avian_influenza/guidelines/nomenclature/en/

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