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Genetic Changes of Reemerged Influenza A(H7N9) Viruses, China

To the Editor: From March 30, 2013, through April 8, 2014, a total of 401 human infections with novel avian influenza A (H7N9) virus were reported in China (1). In the initial wave from February through May 2013, cases were laboratory confirmed for 133 patients (45 died), mainly in eastern China. From June through early October 2013, only 2 laboratory-confirmed cases were reported in China. One of these, identified on August 10, 2013, was the first case of influenza A(H7N9) virus infection in Guangdong Province (strain A/Guangdong/HZ-01/2013). However, a second wave of influenza A(H7N9) virus infection began on October 14, 2013 (2). As of April 8, 2014, a total of 266 laboratory-confirmed cases had been reported, mainly in Zhejiang Province in eastern China (92 cases, 37 deaths) and Guangdong Province in southern China (99 cases, 30 deaths).

Previous sequencing studies suggested that 6 of the 8 influenza A(H7N9) virus RNA segments were acquired from influenza A(H9N2) virus. This acquisition process involved at least 2 steps of sequential reassortment; the most recent event most likely occurred in the Yangtze River Delta

area of eastern China (3–5). To date, nearly all analyses have been performed by using sequences obtained from viruses isolated during the first wave of infection; changes associated with viruses isolated during the second wave are largely unknown (6). We therefore conducted phylogenetic analyses of whole-genome sequence data for 15 influenza A(H7N9) viruses isolated from human patients in Guangdong from November 4, 2013, through January 15, 2014.

We estimated maximum-likelihood trees for all 8 RNA segments by using MEGA version 5.2 and the general time-reversible model (7). RNA segments encoding the hemagglutinin, neuraminidase, and matrix genes of A/Guangdong/H7N9 viruses isolated after November 2013 were genetically similar to those of A/Guangdong/HZ-01/2013 and H7N9 strains from the first wave of influenza (online Technical Appendix, <http://wwwnc.cdc.gov/EID/article/20/9/14-0250-Techapp1.pdf>). An additional 4 RNA segments (non-structural protein [NS], nucleocapsid protein [NP], polymerase basic proteins [PB] 1 and 2) of A/Guangdong/H7N9 influenza viruses isolated after November 2013 were clustered with A/Guangdong/HZ-01/2013 virus and were divergent from all currently sequenced subtype H7N9 viruses from the first wave in eastern China. The only exception was the NP segment of A/Guangdong/SZ-026/2014, which was found segregated into a separate cluster with subtype H9N2 viruses from Shandong Province. Moreover, analyses showed that RNA segments encoding NS, NP, PB1, and PB2 of A/Guangdong/H7N9 isolated after November 2013 were most similar to the same segments from influenza A(H9N2) viruses that had recently circulated in Guangdong (online Technical Appendix Figure, panels D–G). That is, NS, NP, PB1, and PB2 showed greater similarity to local subtype H9N2 viruses from Guangdong than to subtype H7N9 viruses from the first wave of influenza.

Notably, 2 separate clusters were observed for the phylogenetic tree of the RNA segment encoding the polymerase acidic gene (online Technical Appendix Figure, panel H). A/Guangdong/HZ-01/2013-like viruses clustered with subtype H7N9 viruses from the first wave of influenza. However, A/Guangdong/DG-02/2013-like viruses were clustered with subtype H9N2 influenza viruses circulating in Guangdong, suggesting that recent reassortment with circulating subtype H9N2 viruses occurred after the first case of infection with influenza A(H7N9) virus reported in Guangdong (online Technical Appendix Figure, panel H).

This study provides evidence that influenza A(H7N9) viruses isolated during the second wave of influenza in Guangdong differ genetically (in 5 of the 8 RNA segments) from that of influenza A(H7N9) viruses isolated during the first wave. High similarity of these 5 segments with those of locally circulating subtype H9N2 viruses suggests that rapid and continued reassortment with circulating subtype H9N2 viruses occurred during the second wave of the influenza A(H7N9) virus epidemic. Because reassortment and genetic changes can contribute to host fitness and infection capacity of reemerged influenza A(H7N9) viruses, studies of pathogenicity and transmission, to reveal the exact role of each genetic alteration, are needed.

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Carbapenem-Resistant *Enterobacter cloacae* Isolates Producing KPC-3, North Dakota, USA

To the Editor: Carbapenem-resistant *Enterobacteriaceae* (CRE) continue to emerge as a serious public health threat throughout the world (1). CRE infections in the United States are often mediated by acquisition of *Klebsiella pneumoniae* carbapenemase (KPC) expressed by *Klebsiella* spp., although KPC is also found in other genera (2). The spread of KPC-producing, gram-negative bacteria in hospitals has been linked to severity of illness, co-existing medical conditions, exposure to antimicrobial drugs, and need for chronic care (3).

After reporting of CRE infections to the North Dakota Department of Health became mandatory in 2011, a total of 20 CRE cases were noted in 12 of 53 counties (2.9 cases/100,000 population [4]). Most cases involved infection with *Enterobacter cloacae* and occurred in Cass County, where the state's largest city, Fargo, is located. We describe an outbreak of clonal carbapenem-resistant *E. cloacae* in a health care system in Fargo.

Sanford Health is a 583-bed, acute-care facility, representing ≈70% of acute-care beds in Fargo. The hospital handles ≥27,000 admissions/year and serves as a referral center for a large area of the state, and the only long-term acute-care (LTAC) facility in the eastern half of the state operates on its campus. During December 2011–December 2012, all isolates of *Enterobacteriaceae* with reduced susceptibility to ertapenem (MIC ≥1 μg/mL) identified at the hospital's clinical microbiology laboratory were screened for carbapenemase production by using the modified Hodge test (mHT), according to Clinical and Laboratory Standards Institute

recommendations (5). Identification and susceptibility testing were done with the MicroScan system (Siemens Healthcare Diagnostics, Tarrytown, NY, USA); MICs of carbapenems were confirmed with Etest (bioMérieux, Durham, NC, USA). Three carbapenem-resistant *E. cloacae* isolates from documented cases of CRE infection at the hospital during 2010 were analyzed for comparison.

To characterize carbapenem-resistant and mHT-positive isolates, we used PCR to amplify and sequence the carbapenemase genes *bla*_{IMP}, *bla*_{NDM}, *bla*_{VIM}, and *bla*_{KPC} by using established methods (6). The upstream sequence of *bla*_{KPC}-positive strains was analyzed to determine the isoform of the transposon Tn4401 that harbored *bla*_{KPC} (7). We investigated genetic similarity among isolates by repetitive sequence-based PCR; isolates with >95% similarity were considered clonal (6). We also sequenced the highly conserved *hsp60* gene (8) and attempted conjugative transfer of the *bla*_{KPC} gene by growing KPC-producing *E. cloacae* along with sodium azide-resistant *Escherichia coli* J-53. As part of the study, we examined records of patients from whom carbapenem-resistant *E. cloacae* was isolated. The study was approved by the Institutional Review Board at Sanford Health.

During December 2011–December 2012, a total of 19 single-patient *E. cloacae* isolates and 1 *E. aerogenes* isolate had positive mHT results. *bla*_{KPC} was detected in 17 of the 19 *E. cloacae* isolates and in the 3 carbapenem-resistant *E. cloacae* isolates from 2010. For all 20 of those isolates, sequencing revealed *bla*_{KPC-3} in association with isoform d of the transposon Tn4401, and all isolates were clonally related (Figure). All 20 isolates also had an identical *hsp60* sequence belonging to cluster VI in the Hoffman and Roggenkamp scheme (8). Conjugation of a *bla*_{KPC}-containing plasmid into *E. coli* J-53 was successful for 1 strain.