determined by using the RACE System (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol. Each amplicon was sequenced 4 times by using the Sanger method, and the forward and reverse sequences agreed well. Sequences were assembled by using DNAStar software (Lasergene, Madison, WI, USA) and deposited in GenBank (accession no. KP240936). The genome of Beijing-R0132 was 7,334 nt long, including 699 nt in 5′-untranslated regions (5′-UTRs), 6,567 nt in open reading frame (ORF), and 68 nt in 3′-UTR. Beijing-R0132 shared 96% nt sequence identity with the virus circulating in the United States in 2014, US/CO/14-60. In contrast to the prototype EV-D68 (Fermon strain, AY426531), deletions of the CTCAAAACCTCCAGTACATAACA sequence in the 5′-UTR and TTATTTATAACA sequence in the front of the ORF of Beijing-R0132 were observed, corresponding with nt 682–704, and nt 721–732 of the Fermon strain, which were similar to those identified in the United States in 2014.

We then used MEGA software version 6.06 (http://www.megasoftware.net) to analyze the phylogeny of the whole genome and the VP1 gene with EV-D68 sequences available in GenBank (Figure). Beijing-R0132 was clustered with most of the EV-D68 strains that circulated throughout the United States during 2014. The strains identified from Beijing in 2008, represented by BCH895A/2008, belong to another distinct lineage according to genome phylogeny (Figure, panel A). Similar relationships were observed in the phylogenic tree of the VP1 gene (Figure, panel B). Beijing-R0132 and some EV-D68 strains from China identified in 2011 grouped with most of the strains obtained from the United States in 2014. These findings demonstrate that the EV-D68 strain circulating in Beijing was closely related to strains circulating in the United States.

The origin of the 2014 EV-D68 outbreaks in the United States is unclear. This Beijing-R0132 genome sequence provides information for tracking EV-D68 as it spreads throughout the world and for evaluating the sequence diversity in circulating EV-D68 strains. In contrast to EV-D68 detection during the outbreaks in the United States, positive detection of EV-D68 in this study was limited, although the circulating virus strains were closely related. The reason for this disparity warrants further investigation. However, the severe pneumonia caused by EV-D68 reported here underlies the need for intensive attention to surveillance and control of EV-D68 in vulnerable populations, such as young children. In addition, for a megacity with very high population density and mobility, such as Beijing, the citywide implementation of the Respiratory Virus Surveillance System is critical for monitoring the epidemic or potential outbreaks of EV-D68 and other respiratory viruses and for enabling early warning.

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The Continuing Medical Education quizzes for 2 articles were inadvertently omitted from the April issue. The quizzes are printed at the back of this issue, and the complete articles and quizzes are available online (http://wwwnc.cdc.gov/eid/article/21/4/14-1479_intro and http://wwwnc.cdc.gov/eid/article/21/4/14-1033_intro).