Recombination of Human Coxsackievirus B5 in Hand, Foot, and Mouth Disease Patients, China

To the Editor: Hand, foot, and mouth disease (HFMD) is an acute viral infectious disease in infants and young children. However, since 2008, HFMD has emerged as a major public health problem in the People’s Republic of China, resulting in millions of infections with hundreds of deaths (1). Human enteroviruses (HEVs), including HEV71, echoviruses, and coxsackieviruses A and B (C AV16), are the major pathogens of HFMD (2). In mainland China, HEV71 and C AV16 have been recognized as the dominant causative agents for HFMD.

During a recent HFMD outbreak in Changchun during 2010, three of 16 throat swab samples tested positive for HEV but negative for HEV71 and C AV16 by reverse transcription PCR. All 3 isolates were then placed into human rhabdomyosarcoma cells, and typical cytopathic effects were observed 3–4 days later. All the isolates were finally characterized as CBV5 by using serologic and molecular technology and designated as CBV5 by using serologic and molecular technology and designated as CBV5 isolates have 85% identity with COXB5/Henan/2010, highly homologous with the recent Henan isolate, COXB5/Henan/2010, with a nucleotide identity of 88.1%. These results indicated that CBV5 might have been circulating in China for many years and represented an independent evolution tendency.

Homology and BLAST analysis (http://blast.ncbi.nlm.nih.gov/BLASTcgi) based on the complete genome sequence showed that these newly isolated CBV5 isolates have 85% identity with some human CBV3 strains. Because RNA recombination is a well-known phenomenon for HEVs during viral evolution and reemergence (3–8), recombination analysis between newly isolated CBV5 and other HEVs was performed by using SimPlot software. Similarity scanning analysis (online Technical Appendix Figure 1, wwwwnc.cdc.gov/EID/pdfs/11-1524-Techapp.pdf) by using CBV5/CC10/10 as query sequence showed that the 5′ half (nt 1–4481) of the genome had high similarity (>93%) to CBV5 strain COXB5/Henan/2010, and the 3′ half (nt 4661–7402) showed high similarity (>97%) to CBV3 strain Beijing0811. Then, bootscanning
LETTERS

Letters to the Editor

Figure. Phylogenetic analysis of selected human coxsackievirus B (CBV) strains from different origins based on the viral protein 1 gene sequences. The neighbor-joining tree was generated by using MEGA4 software (www.megasoftware.net), and the prototype strain of coxsackievirus A (CAV) 16 was used as outgroup. The Changchun strains isolated in this study are indicated by triangles and other Chinese CBV5 strains are indicated by squares. Scale bars indicate nucleotide substitutions per site.

This study was supported in part by the Major Special Program of National Science and Technology of China (no. 2009ZX10004-204), the National Natural Science Foundation of China (no. 81000721), and Beijing Natural Science Foundation (no. 7112108). C.F.Q. was supported by Beijing Nova Program of Science and Technology (no. 2010B041).

Jian-Feng Han, Tao Jiang, Xing-Liang Fan, Li-Ming Yang, Man Yu, Rui-Yuan Cao, Jun-Zhi Wang, E-De Qin, and Cheng-Feng Qin

Author affiliations: State Key Laboratory of Pathogen and Biosecurity, Beijing, People’s Republic of China (J.-F. Han, T. Jiang, L.-M. Yang, M. Yu, R.-Y. Cao, E.-D. Qin, C.-F. Qin); Beijing Institute of Microbiology and Epidemiology, Beijing, People’s Republic of China (J.-F. Han, T. Jiang, L.-M. Yang, M. Yu, R.-Y. Cao, E.-D. Qin, C.-F. Qin); and National Institutes for Food and Drug Control, Beijing (X.-L. Fan, J.-Z. Wang).

DOI: http://dx.doi.org/10.3201/eid1802.111524

References


Address for correspondence: Cheng-Feng Qin, Department of Virology, State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing 100071, People’s Republic of China; email: qincf@bmi.ac.cn

**Nontuberculous Mycobacteria in Tap Water**

To the Editor: A recently published study by Falkinham (1) showed that 17 (46%) of 37 households were contaminated with nontuberculous mycobacteria (NTM) of the same species as those found in patients with lung disease and that 7 (41%) of 17 had the same DNA fingerprint as the patient. One participant’s isolate from sputum matched the isolate found in the shower water. Therefore, the patient’s lung disease was likely acquired by inhalation of aerosols while showering. An isolate from another patient matched the isolate found in tap water. If the patient drank the contaminated water, *Mycobacterium avium* may have reached the lungs by aspiration because 26% of patients with NTM lung disease have been found to experience gastroesophageal reflux disease (GERD) (2). Even if none of these scenarios was present, however, NTM patient contamination of samples is still likely. Six of the 7 matching households had water heater temperatures ≤125°C, indicating a negative correlation between NTM growth and temperature. Most *M. avium* and *M. intracellulare* are killed in ≤5 seconds (3) when exposed to 70°C; thus, all NTM species would likely be killed a few seconds after water reached the boiling point.

In a recent study, we have shown that Canadian-born persons from ethnic groups from eastern and Southeast Asia were less likely to be colonized with *M. avium* complex than were other ethnic groups (4). We hypothesized that boiling water before consumption, a common practice in persons from Asia, may have partially protected them against pulmonary colonization. Another protective factor is the low prevalence of GERD in persons from Asia (<7%) (5), compared with 19.8% in white persons from Olmstead County, Minnesota, USA. Future studies like that of Falkinham are needed to determine routes of transmission. Factors to investigate in such studies include the ethnicity of participants and associated predisposing disorders, particularly GERD; culturing of gastric washings; handwashing frequency; and water consumption habits (whether drinking from the bottle, from the tap, or after boiling).

**Eduardo Hernández-Garduño** and **Kevin Elwood**

Author affiliations: British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada

DOI: http://dx.doi.org/10.3201/eid1802.110455

**References**


Address for correspondence: Eduardo Hernández-Garduño, British Columbia Centre for Disease Control, TB Control, 1063-655 W 12th Ave, Vancouver, British Columbia V5Z 4R4, Canada; email: investigador.tuberculosis@gmail.com

Use of trade names is for identification only and does not imply endorsement by the Public Health Service or by the US Department of Health and Human Services.