An outbreak of human astrovirus lineage 1b in a middle school in Guangxi, Southern China in 2017

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To the Editor: Human astroviruses (HAstVs) are important etiologic agents of viral gastroenteritis worldwide,[1,2] especially in pediatric patients aged $\leq$5 years.[3] However, reports on HAstV outbreaks in middle schools remain limited. Here, we report a HAstV outbreak in a middle school in China. Clinical and environmental samples tested positive for HAstV, showing a 100% nucleotide identity of the 348-bp region of the capsid protein gene.

It was the part of continuous public health surveillance for a notifiable infectious disease in China and was thus exempt from institutional review board assessment. All patient information was kept anonymous to protect patient confidentiality.

On November 23, 2017, a total 125 adolescents aged 12 to 17 years were diagnosed with symptomatic acute gastroenteritis in a middle school with 1476 students in a county in Wuzhou City, Guangxi Zhuang Autonomous Region, southern China. The following common HAstV infection-associated symptoms[4] were observed: fever, 99.2% cases (124/125); abdominal pain, 40.8% (51/125); diarrhea, 35.2% (44/125); and vomiting, 6.4% (8/125). Meanwhile, the following influenza-like symptoms were also recorded: headache, 48.0% cases (60/125); cough, 16.0% (20/125); chills, 16.0% (20/125); runny nose, 8.0% (10/125); nasal obstruction, 7.2% (9/125); and pharyngalgia, 6.4% (8/125). A total of 122 patients received outpatient services; three patients were hospitalized. All patients showed good resolution.

The first case that was reported on November 7 involved a 14-year-old girl who developed fever, headache, and cough. She had not been traveling or in contact with any person showing similar symptoms 1 week before onset. Two cases were reported on the next day [Figure 1A]. The number of reported cases reached the first peak during November 9 and November 10 with 37 and 30 cases, respectively. The 10, 1, 9, and 0 cases were reported on November 11, 12, 13, and 14, respectively. The second peak began on November 15 and lasted for 4 days, with 12, 8, 11, and 4 cases were reported, respectively. After these, no other cases were reported. Based on the information that HAstV has an incubation period of 1 to 4 days and infection period of 2 to 6 days, the first wave of this outbreak was suspected to be the common exposure source while the second wave was caused by human-to-human transmission.

To identify the etiological agent, samples were collected twice. First, the outbreak was considered to be associated with upper respiratory tract infection; diarrhea-associated symptoms were neglected. Nineteen throat swabs were collected from symptomatic students on November 13 for testing genotypes of respiratory tract pathogens including influenza (A/B), human adenovirus, human parainfluenza virus (1–4), human rhinovirus (A/B/C), human respiratory syncytial viruses (A/B), human bocavirus (1–4), human coronaviruses NL63, 229E, and OC43, human viruses from the family Paramyxoviridae, and human enterovirus. Viral RNA was extracted using the viral RNA mini kit (Qiagen, Hilden, Germany); respiratory pathogens were detected using real-time reverse transcription polymerase chain reaction (RT-PCR) kits. We found that 1 and 3 samples tested positive for human adenovirus and human rhinovirus, respectively.

Following this, a survey and second sample collection were conducted on November 16. Thirty clinical specimens (including rectal swabs and throat swabs) from 16 students and 10 canteen staff and 5 environmental samples were collected to detect diarrhea-associated pathogens. All 16 students had fever and diarrhea or abdominal pain, while the 10 canteen staff denied having any symptoms. The five environmental samples included two swabs from the chopping board and one swab each from the kitchen garbage bin, vegetable freezer room, and vegetable refrigerator room. Rotavirus,

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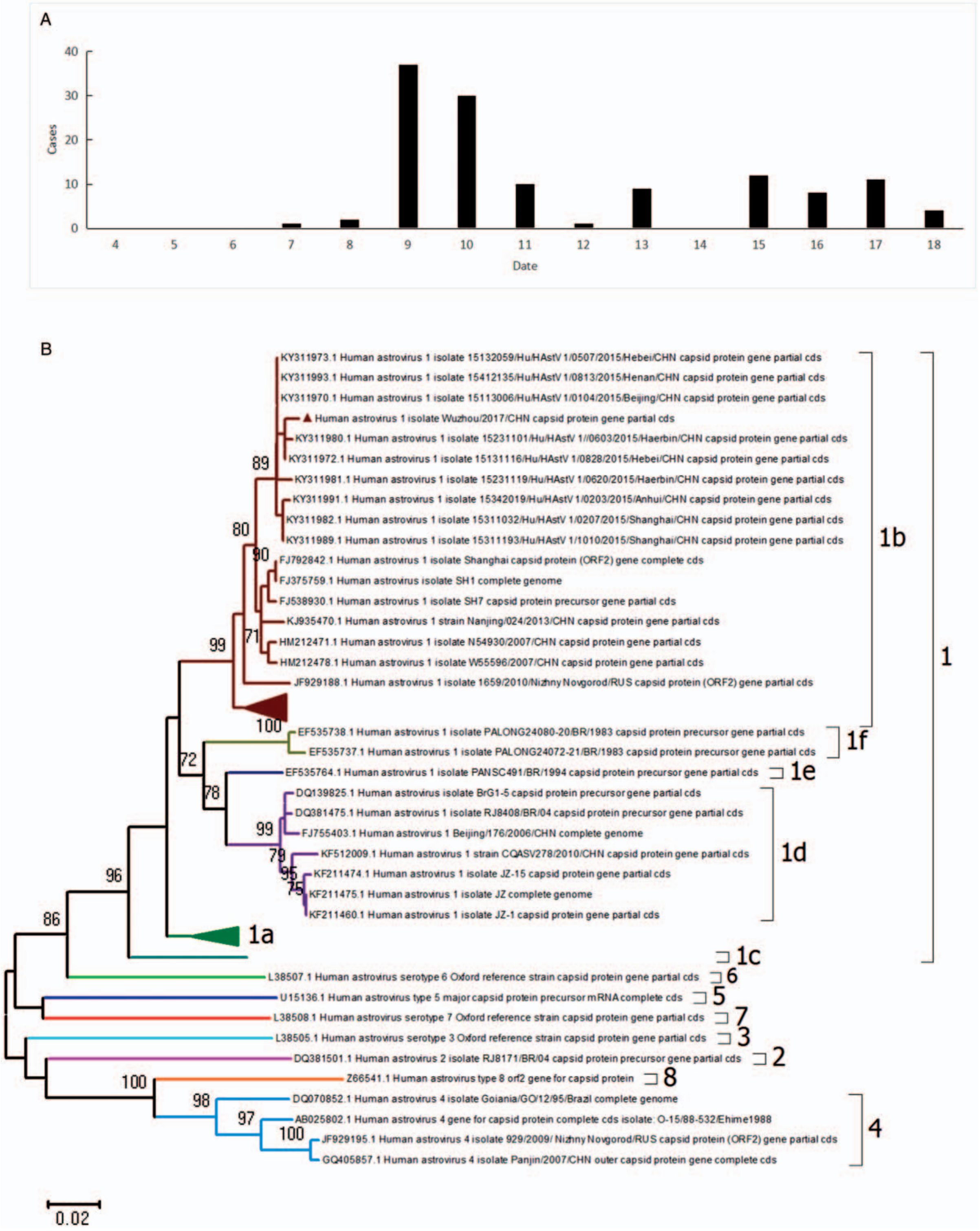

Figure 1: (A) Date of illness onset in cases associated with a human astrovirus outbreak in Guangxi, China, 2017. (B) Neighbor-joining phylogenetic tree of the capsid precursor-encoding a 348-bp region of ORF2 from the human astrovirus isolate 0631/Wuzhou/Guangxi/2017.

HAstV, adenovirus, and norovirus were examined using real-time RT-PCR kits (Jiangshu Shuoshi Biological Technology Co., Ltd, Taizhou, China). All specimens tested negative for rotavirus and adenovirus. Only one specimen from the canteen staff tested positive for norovirus. Thirteen specimens tested positive for HAstV, including specimens from six students and six canteen staff members and one swab from the chopping board.

Then, a 449-bp region of the capsid protein gene in these 13 samples was amplified using Mon269/Mon270 primers.[1] The amplified products were sent to Sangon Biotech Co., Ltd (Shanghai, China) for Sanger sequencing.

Twelve nucleotide sequences of the HAstV capsid protein gene were obtained; these sequences were found to be 100% identical to each other. Finally, this isolate was named 0631/Wuzhou/Guangxi/2017; the sequence was submitted to GenBank (GenBank accession MH643741). The Evolutionary history was inferred using the neighbor-joining method and the software program MEGA7. A phylogenetic tree was constructed based on capsid protein gene sequences (348 bp) of the HAstV 1 to 8 subtypes isolated in the present study and the respective representative strains. HAstV-1 is classified into 6 lineages (HAstV-1 a-f),[5] and the isolate in this study belonged to the HAstV 1b lineage [Figure 1B]. Generally, HAstV strains of 1b lineage from the mainland of China can be divided into 2 groups: isolated before 2015 and isolated after 2015, based on the capsid protein gene sequence (348 bp). The current isolate was closely related to Hu/HAstV1/0603/2015/Haerbin/CHN and was clustered with strains circulating in the mainland of China after 2015.

One limitation of this study was that no asymptomatic controls were included; therefore, HAstV-1b was solely predicted to be one of the causative agents of the acute gastroenteritis outbreak. Another limitation was that an insufficient number of clinical and environmental samples were collected for detection of bacterial pathogens. Our data highlight the possibility that HAstV infections not only include viral gastroenteritis-like symptoms but also influenza-like symptoms. Overall, the importance of HAstV infections occurring in middle school should not be neglected and hygiene-related conditions in middle schools should be improved to prevent HAstV outbreaks.

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Conflicts of Interest

None.

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