Emerging Norovirus GII.17 in Taiwan

To the Editor—Human noroviruses (NoVs) are one of the most common causative agents of acute gastroenteritis (AGE) worldwide. Among them, genotype 4 of NoV genogroup II (GII.4) has been the leading cause of NoV-associated AGE [1]. In Taiwan, NoV GII.4 has caused several outbreaks of AGE in either healthcare facilities or community since 2004 [2, 3]. In contrast, NoV GII.17 is considered an uncommon genotype for human infection. This genotype was first reported from Africa and South America and recently was identified as an outbreak strain in Japan and China [4–6]. Here we report 2 cases of NoV GII.17 infection detected in Taiwan and compared their genome sequences with those collected from other regions of the world. This is the first report of GII.17 in Taiwan.
On 26 January 2015, a 5-year-old girl was admitted to Chang Gung Children’s Hospital for treatment due to sudden onset of abdominal pain, accompanied by forceful vomiting and severe dehydration. There was no travel history. The stool analysis showed the presence of occult blood, along with a positive stool NoV reverse transcription polymerase chain reaction (RT-PCR) test result. She recovered well in 3 days. One month later, on 25 February 2015, a 13-year-old girl who had acute onset of watery diarrhea, severe vomiting with bilious content, and persistent fever was admitted for treatment. The entire family had a domestic travel to Chia-Yi county in southern Taiwan. Similar gastrointestinal symptoms

Figure 1. Phylogenetic tree analyzed based on the nucleotide sequence of the partial sequence of VP1 gene (A) and the human norovirus full genome sequence (B). The samples are marked with a black circle. Scale bar indicates the number of mutations per sequence position. The numbers at the nodes represent the percentage of 1000 bootstrap resamplings. Reference sequences were selected based on previous reports [5, 8] and presented as accession numbers. GII.4 is used as the outgroup.
were also found in 4 family members, and all of them ate the same food at a night market in Fen-Chi Lake region, Chia-Yi. The stool analysis was positive for occult blood, and NoV RT-PCR testing. After hydration and medical treatment, she recovered uneventfully within 2 days. Fecal specimens were collected from these patients after obtaining informed consent (Institutional Review Board 101-3621A3) and the RNA was extracted using QIAamp Viral RNA Mini Kit (Qiagen, Venlo, Netherlands). NoV genome was amplified using RT-PCR with specific primers, the accession number of the 2 GII.17 isolates were KR154230 and KR154231 in GenBank. The phylogenetic trees based on capsid gene (VP1) and full genome sequences were constructed using MEGA software version 6.0 [7].

The VP1-based tree divided the GII.17 isolates into 2 clusters as revealed in a previous study [8]. The Taiwan isolates were exclusively included in cluster A (Figure 1A). In the same cluster there were isolates from China, Japan, Cameroon, and Kenya. The isolates in the cluster B showed much more diverse geographic sources, covering Africa, Europe, East Asia, and North and South America. There are at least 2 hypotheses for explaining the disassociation between phylogeny and isolation site. First, global travel has been increasingly common, along with which the GII.17 virus has spread worldwide. Second, GII.17 exists everywhere in the world originally, and has been gradually emerging. We are inclined to the second hypothesis, because the patients and their neighboring people in the present report do not have any travel history to Africa.

In the full genome tree, the Taiwan GII.17 isolates were still assigned into cluster A (Figure 1B). Due to paucity of the full genome sequence data, cluster B contained only 1 isolate (accession number KC597139). An interesting recombination event was detected in the United States GII.17 isolate. Although being classified to GII.17 by the VP1-based tree, the full genome-based tree showed that the United States isolate was relatively closer to GII.4. The entire NoV genome is composed by 3 genes—that is, POL, VP1, and VP2. A detailed BLAST analysis on the VP1 and VP2 genes showed that this United States isolate is a typical GII.17, whereas its POL gene has >95% nucleotide identity with GII.4. In other words, this isolate was a recombinant between typical GII.17 and GII.4; the exact breakpoint of recombination was between POL and VP1. Whether this recombination event confers special advantage to the fitness of the NoV is unknown. Nevertheless, our results suggest that to obtain accurate genotyping information, analysis based on full viral genome, rather than just sequences of the partial VP1 gene, should be considered.

In conclusion, this study reported the emergence of a novel NoV GII.17 causing AGE in Taiwan. The clinical manifestations were generally the same as those caused by GII.4. Although less widely reported, NoV GII.17 may have existed worldwide. Recombination events could occur between GII.17 and other GII genotypes. Continuous surveillance is necessary.

Notes

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