First Sapovirus Outbreak of Gastroenteritis in Taiwan
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Background: We report a first outbreak of sapovirus (SaV) in Taiwan. In May 2007, an outbreak of gastroenteritis occurred at a university in northern Taiwan. A total of 55 students reported symptoms associated with acute gastroenteritis and stool specimens were collected for laboratory testing from eight patients.

Methods: Stool suspension (10% w/v) was prepared in phosphate buffer and clarified by centrifugation. The precipitated specimen was mixed with 2% phosphotungstic acid and examined for the presence of viral particles with the transmission electron microscope. RNA was purified from stool suspension and reverse transcribed using SuperScript III RNaseH (−) reverse transcriptase according to the manufacture’s instructions. PCR was carried out using primers directed against the conserved N-terminal capsid region. Nucleotide sequences were prepared with the terminase directed cycle sequence kit and determined with the ABI 3130 Avant sequencer. Nucleotide sequences were aligned using Clustal X and the distances were calculated by Kimura’s two-parameter method.

Results: Only one of the eight specimens was discovered to have the presence of viral particles resembling the characteristic of “Star of David” morphology with sizes of 35—40 microns. Seven of 8 specimens were positive by RT-PCR for SaV. Phylogenetic analysis of the capsid region suggests it belongs to a SaV GI/2 species. Further determination of the complete subgenomic region reveals that Taiwan 2007 strain is closely related to the isolate discovered in Japan 2004.

Conclusion: This is the first report of a SaV-associated outbreak of gastroenteritis in Taiwan. Many of earlier SaV outbreak reports described GI/1 infection, which was a different genotype to the one in this study (GI/2). SaV symptoms are though to be milder than norovirus infection, this outbreak highlighting the need to increase in SaV surveillance and further study on the ‘silent’ transmission route via asymptomatic carrier.

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Cholera Outbreaks in India Due to Hybrid Vibrios
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Background: Vibrio cholerae O1 strains that are hybrids between the classical and El Tor biotypes were first described in Matlab, Bangladesh in 2002 and then during two consecutive years (2004—2005) from diarrheal patients in Mozambique. Such hybrid strains carry genes of classical type in CTX prophage but have phenotypic features in between classical and El Tor. Recently in our area in north India, seven clusters of cholera occurred in areas where cholera outbreaks had not been reported since 1994. Six deaths were also reported. These strains were analysed for