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Norovirus GII.Pe genotype: tracking foodborne outbreak on a cruise ship through molecular epidemiology, Brazil, 2014

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Background: Norovirus (NoV) are recognized as the most common cause of foodborne outbreaks. In 2014, an outbreak of acute gastroenteritis occurred on a cruise ship in Brazil, and NoV became the suspected etiology. Here, we present the molecular identification of the NoV strains and the use of sequence analysis to determine modes of virus transmission.

Material/methods: Five suspected food items were taken: cream cheese, tuna salad, grilled fish, orange mousse and vegetables soup. A total of 12 specimens were obtained from patients who presented gastroenteritis symptoms at the time of collection. Food and clinical samples were analyzed by ELISA, conventional RT-PCR, qRT-PCR and sequencing.

Results: Genogroup GII NoV was identified by ELISA and conventional RT-PCR in fecal samples from 5 of 12 patients tested (41.7%), and in the orange mousse food sample by conventional RT-PCR and qRT-PCR. Two fecal GII NoV samples and the orange mousse GII NoV sample were successfully genotyped as GII.Pe (ORF 1). The IAL NoV GII.Pe stool sequences showed 98.4% similarity at nucleotide level (nt) (95.0% aa) between them; 98.0-98.8% nt (93.8-96.2% aa) when compared to the food sample; and 90.6-95.3% nt (76.5-87.6% aa) when compared to representative GII.Pe strains. In addition, the IAL NoV GII.Pe strains detected in the orange mousse and fecal samples could be discriminated in a unique cluster, phylogenetically distinct from the others. The IAL GII.Pe strains exhibited high nucleotide and amino acid identity to strains isolated in 2012 and 2013 in Europe (13L243090088, PA48, and SanSebastian132889) and Japan (Iwate and Shimane) (94.1-95.3% nt; 83.9-87.6% aa).

Conclusions: Establishing the source of a NoV outbreak can be a challenging task.). In this investigation, the genetic sequencing of the partial RNA polymerase (RdRp) gene revealed the presence of very similar NoV nucleotide sequences in the fecal specimens from the patients and the suspected complex food matrix item, the orange mousse. The results strongly suggested food-to-human transmission for NoV. Therefore, the molecular analysis of the partial RdRp NoV gene provided a powerful tool for genotyping (GII.Pe) and tracking of outbreak related samples. An overall increase in the incidence of GIIPe associated to NoV outbreaks have been occurring since 2012, and the genetic analysis conducted here revealed that NoV GIIPe strains collected in Brazil in 2014 were closest to the current pandemic GIIPe/GII.4 Sydney 2012 variant strains circulating worldwide. This is the first recorded foodborne outbreak on cruise ship in Brazil where NoV was detected from patients with gastroenteritis and the suspected food item (orange mousse). The same fast and simple extraction methods applied to clinical samples could be successfully used for complex food matrices, and have the potential to be introduced in routine laboratories for screening foods for presence of NoV.