

## **High proportion of norovirus infection and predominance of GII.3 [P12] genotype among the children younger than 5 in Sabah, Malaysian Borneo**

### **ABSTRACT**

Globally, norovirus (NoV) has become one of the important causes of acute gastroenteritis (AGE) in children. It is responsible for death of children younger than 5 years in developing countries. Although there is limited information and the rate of child mortality caused by diarrhea is low in Malaysia, the burden of diarrhea is high, especially in Sabah. NoV GI, GII and GIV genogroups are known to infect humans, and GII.4 is the predominant genotype distributed worldwide. Better understanding of the etiology of NoV will help to inform policies for prevention and control. The aim of this study was to determine the burden and genotype distribution of NoV in children younger than 5 years with AGE who attended health-care facilities in Sabah, Malaysia. Diarrhea stool samples were collected from 299 children with AGE and NoV was detected by amplifying the capsid and RNAdependent RNA polymerase gene and reverse transcription-polymerase chain reaction (RT-PCR) analysis. Nucleotide sequencing of the amplicons was used for genotypes and phylogenetic analyses. NoV-positive stool samples were found in 17.7% (53/299) among which 13/53 (24.5%), 38/53 (71.7%), and 2/53 (3.8%) identified as NoV GI, GII and combination of GI and GII, respectively. The most common genotypes were GII.3 [P12] (80%) followed by GII.6 [P7] (13.3%), and GII.17 [P17] (6.7%). In the phylogenetic tree, all Sabahan NoV samples were shown to share ancestry with their respective genotype from predominantly East Asian countries and to some extent Australia and Europe. However, the Sabahan strains formed independent clusters with significant bootstrap values, indicating a clonal spread after the strains had entered Sabah.