
**Abstract**

Sapoviruses (SaVs) are responsible for sporadic cases and outbreaks of acute gastroenteritis. Despite this, few studies in India have focused on the epidemiological investigation of SaV in cases of acute gastroenteritis. The aim of this study was to understand the molecular epidemiology, genetic diversity and clinical impact of SaV in diarrhoeic children from Pune, Western India. Between 2007 and 2011, a total of 985 faecal samples from diarrhoeic cases and non-diarrhoeic controls were collected and examined for the presence of SaV by nested RT-PCR. SaV was detected in 2.7% (21/778) of the cases and 1.9% (4/207) of the controls. We observed that the majority of SaV mono infections caused severe gastroenteritis (67%) with clinical manifestations of diarrhoea (100%), vomiting (73%) and dehydration (80%). All known human SaV genogroups were detected in the study. At least 8 genotypes were identified from cases and controls. Genogroups GI.V and GV, along with genotypes GI.5, GI.I.4 and GI.I.6, were discovered for the first time in India. Two GI.I.4 study strains were found to be 98.5-99% identical, having a novel intra-genogroup recombinant (GI.I/GI.I.4) recently reported from the Philippines, suggesting probable evidence of recombination. The circulation pattern of SaV genotypes varied during the study period, with GI.I.1 being predominant in 2007 and 2009, GI.V.1 in 2008, and GV.1 in 2011.


**Abstract**

Although acute gastroenteritis is a major public health problem worldwide, ~40% of the cases remain undiagnosed for any etiological agent. Human Bocavirus (HBoV) has been detected frequently in feces of diarrhoeic children suggesting its possible etiological involvement in the disease. HBoV has not
been reported in association with acute gastroenteritis from India. Fecal samples (n = 418) collected from children (age ≤5 years) hospitalized with acute gastroenteritis, between January 2009 and December 2011, from three local hospitals were examined for presence of HBoV using PCR targeting the partial VP1/VP2 capsid region (~575 bp) followed by phylogenetic analysis. HBoV was detected in 24/418 (5.7%) cases. Co-infection was observed in 5/24 (21%) cases. HBoV infections occurred in children ≤12 months of age. Peak HBoV activity was observed in monsoon and post monsoon season. All four HBoV genotypes were detected in the study region. Major clinical symptoms of HBoV mono infections included diarrhoea (100%), fever (90%), dehydration (74%), and vomiting (58%). Dehydration was observed in all of the HBoV2-4 cases and in 50% of the HBoV1 cases. Clinical severity varied with genotype (HBoV2 > HBoV1 > HBoV3 > HBoV4). HBoV2 cases recorded severe and very severe infections. The study illustrates prevalence and vast genetic diversity of HBoVs in acute gastroenteritis. It highlights the clinical features of HBoV1-4 infections and sheds light on clinical impact of HBoV genotypes in gastroenteritis.


Abstract
Acute gastroenteritis is a leading cause of mortality in children from developing countries. Recently, Salivirus has been frequently detected in acute gastroenteritis patients, suggesting its possible aetiologica role. Conflicting reports available on disease association of Salivirus have made it difficult to ascertain their causative role. The overall epidemiology and clinical features of Salivirus infections are poorly understood. The present five year study was undertaken to investigate the presence and genetic diversity of Salivirus in acute gastroenteritis cases from Pune, Western India and to determine the clinico-epidemiological features of Salivirus infections. A total of 985 faecal samples (778 acute gastroenteritis and 207 asymptomatic
controls), collected from three local hospitals (Jan2007-Dec2011) were examined for the presence of Salivirus by RT-PCR. Molecular characterization was performed by PCR amplification of the 3D and VP regions. Frequency of Salivirus detection in cases (2.6%) and controls (1.93%) was not significantly different (p = 0.57). Co-infection with other enteric viruses was seen in 50% of the cases. Comparison of clinical features between Salivirus mono and mixed infections revealed that Salivirus alone did not exacerbate gastroenteritis. The frequency of diarrhoea and overall clinical severity of mixed infections was significantly greater than mono infections (p = 0.02). Based on clinical findings, our study suggests that Salivirus does not cause severe gastroenteritis. Phylogenetic analysis indicated that study strains belonged to Salivirus A1 and formed 2 distinct clusters which shared nucleotide identities of 94.1-96.2% and 88.9-93.8% between themselves in 3D and VP regions, respectively. Interestingly, the more divergent Cluster2 strains shared a low nucleotide identity with the closest reference strain in both regions (~95% in 3D and ~92% in VP) suggesting that they could represent a variant type of Salivirus A1. The genetic diversity in strains detected from study region, emphasizes the need for Salivirus surveillance from other regions of India.


5. Lasure N, Gopalkrishna V. Contribution of Sapovirus (SaV), Human Bocavirus (HBoV) and Salivirus in outbreaks of acute gastroenteritis occurring in Solapur, Western India. Manuscript under preparation.