Human Bocavirus, a Respiratory and Enteric Virus

Diego Vicente,* Gustavo Cilla,* Milagrosa Montes,* Eduardo G. Pérez-Yarza,* and Emilio Pérez-Trallero†

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The Study

To determine the prevalence and clinical characteristics of HBoV, we investigated the presence of this virus in children with respiratory tract illness in practically all areas of the world in which it has been investigated (2–5), an indication of its wide dissemination.

Conclusions

Of the 527 stool samples analyzed from December 2005 through March 2006, HBoV was detected in 48 (9.1%). From a second group of 520 children <3 years of age who came to the pediatric emergency unit of our hospital with an episode of acute respiratory infection during the same period, a similar frequency of HBoV detection was obtained (40/520, 7.7%) when nasopharyngeal aspirates were tested. Analysis of NP1 and VP1 partial gene sequences obtained from all fecal and respiratory HBoV-positive samples showed a similarity of >95% with previously published HBoV sequences.

Of 40 HBoV-positive respiratory samples, 25 (62.5%) showed coinfection with other viruses (respiratory syncytial virus in 13, rhinovirus in 3, influenza A in 3, coronavirus OC43 in 2, adenovirus in 1, influenza B in 1, respiratory syncytial virus and coronavirus OC43 in 1, and influenza A and rhinovirus in 1). Of the 48 HBoV-positive fecal samples, 28 (58.3%) showed coinfection with another intestinal pathogen (Salmonella enteritidis in 1, Campylobacter jejuni in 5, rotavirus in 14, norovirus in 7, and C. jejuni and norovirus in 1).

In this study, simultaneous detection of HBoV and other agents was frequent for respiratory or enteric specimens. The incidence of coinfection in respiratory illness

cDNA was obtained by using M-MuLV reverse transcriptase (Promega, Madison, WI, USA) and random primers. Aliquots of the DNA and cDNA were frozen at −40°C until PCR for HBoV detection was performed. Respiratory samples were investigated for respiratory syncytial virus, influenza viruses A and B, parainfluenza virus type 1–4, and adenovirus by cell culture and PCR. Rhinovirus, coronavirus (NL63 coronavirus included), and metapneumovirus were studied by PCR alone. Fecal specimens were examined for Shigella spp., Salmonella spp., Yersinia enterocolitica, Campylobacter spp., and enteroinvasive Escherichia coli O157 by standard culture methods. Rotavirus was investigated by enzyme immunoassay and norovirus by reverse transcriptase PCR. HBoV detection was performed by PCR with primers derived from the NP1 gene (1). Positive samples were retested and confirmed as positive by using a second PCR assay with primers derived from another location in the HBoV genome (VP1 gene) (7). Amplified NP1 and VP1 gene fragments (354 bp and 403 bp, respectively) were sequenced and analyzed by using the BLAST software (www.ncbi.nlm.nih.gov/BLAST). Each PCR run included a negative control (water) that was treated as the clinical sample throughout, and PCR was performed with the usual precautions to avoid contamination. Strain Spain001 (GenBank accession no. EF186830) was included as positive control in each PCR run.

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was similar to that observed in studies that were not limit-
ed to specimens that had already tested negative for other
microorganisms and in which a wide number of agents
were investigated (4). Adenoviruses have been associated
with infection of the colon and the gut and are a cause of
severe gastroenteritis in nonindustrialized countries. In this
study, coinfection of adenovirus and HBoV was detected
in 1 respiratory specimen but these viruses together were
not detected in any fecal sample.

HBoV and parvovirus B19 are the only 2 species of
the Parvoviridae family that have been associated with
disease in humans. To date, HBoV has only been detected
in samples from the respiratory tract and has been associ-
ated with both upper and lower respiratory tract disease in
infants and young children. The results of our study show
that HBoV is also present in the gastrointestinal tract in
children with gastroenteritis with or without symptoms of
respiratory infection. The fecal excretion adds new con-
cern about the transmission of HBoV.

To our knowledge, this report is the first to document
HBoV in human feces. The high frequency of HBoV
detection in the feces of children with gastroenteritis and
the absence of any other intestinal pathogen suggest that
this new virus species is an enteric, as well as a respira-
tory, pathogen. Further investigations to confirm this prelim-
inary hypothesis and gain greater knowledge of the
association between HBoV and enteric disease are
required.

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