Clinical and Molecular Epidemiology of Human Bocavirus in Respiratory and Fecal Samples from Children in Hong Kong

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(See the editorial commentary by Mackay, on pages 968–70.)

Background. Human bocavirus (HBoV) is a recently discovered parvovirus associated with respiratory tract infections in children. We conducted the first systematic prospective clinical and molecular study using nasopharyngeal aspirates (NPAs) and fecal samples.

Methods. NPAs negative for influenza virus, parainfluenza virus, respiratory syncytial virus, adenovirus, and coronavirus and fecal samples from patients with acute gastroenteritis were included. On the basis of results from a pilot study using 400 NPAs from all age groups, a prospective 12-month study was conducted to detect HBoV in 1200 NPAs and 1435 fecal samples from patients <18 years old by polymerase chain reaction. The complete genome sequences of HBoVs from 12 NPAs and 12 fecal samples were determined.

Results. Of the 400 NPAs collected in the pilot study, 20 (5.0%) were found to contain HBoV, all from children <5 years old. In the subsequent prospective study of pediatric patients, HBoV was detected in 83 (6.9%) of 1200 NPAs. Upper and lower respiratory tract infections were equally common. HBoV was detected in 30 (2.1%) of 1435 fecal samples. Fever and watery diarrhea were the most common symptoms. The seasonality of HBoV in NPAs and fecal samples was similar. Codetection with other pathogens occurred in 33% and 56% of NPAs and fecal samples, respectively, from patients with HBoV infection. Genomes of HBoVs from NPAs and fecal samples displayed minimal sequence variations.

Conclusions. HBoV was detected in fecal specimens in children with acute gastroenteritis. A single lineage of HBoV was associated with both respiratory tract and enteric infections.

Because a substantial proportion of respiratory tract infections remain undiagnosed [1, 2], research has been conducted to identify novel causative agents. Over the past few years, several novel respiratory viruses—including human metapneumovirus (hMPV) [3], severe acute respiratory syndrome coronavirus (SARS-CoV) [4], human coronavirus NL63 (HCoV-NL63) [5, 6], and coronavirus HKU1 (CoV-HKU1) [7–10]—have been identified.

In 2005, Allander et al. [11] reported the discovery of a previously undescribed human parvovirus in respiratory secretions from children with respiratory tract disease in Sweden. Phylogenetic analysis showed that this virus belonged to the genus Bocavirus (subfamily, Parvovirinae; family, Parvoviridae) and was most closely related to bovine parvovirus (BP) and minute virus of canines (MVC). The virus was thus named

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“human bocavirus” (HBoV). By a specific polymerase chain reaction (PCR) assay, the virus was found to be present in 17 (3.1%) of 540 respiratory specimens collected from hospitalized children over a 1-year period [11].

Subsequently, HBoV has been reported in respiratory samples from children in various parts of the world (including Australia, North America, Europe, Asia, and Africa), suggesting that the virus is circulating worldwide [12–24]. Among these studies, HBoV was detected in 1.5%–18.3% of respiratory samples from individuals with acute respiratory tract illness, especially those from young children and infants. Despite these findings, the clinical spectrum of disease and a causative role for this novel virus remain to be ascertained. In a recent study, HBoV DNA was found to be frequently present in serum samples from patients with acute wheezing, suggesting that the virus may be associated with systemic infection [25]. However, it is not known whether HBoV is associated with nonrespiratory tract illness and can be detected in other clinical specimens. Moreover, few studies to date have included specimens from older children or adults.

To assess the epidemiology of HBoV infection in our population, in a pilot study we examined the prevalence of HBoV in randomly selected nasopharyngeal aspirates (NPAs) from hospitalized patients of all ages. On the basis of the results of this pilot study, a 1-year prospective study was conducted using NPAs and fecal samples from pediatric patients to determine clinical disease associations and the epidemiology of HBoV infection in children in Hong Kong. The molecular epidemiology of HBoV detected in NPAs and fecal samples was also analyzed.

**METHODS**

**Patients and microbiological methods.** All samples were collected from hospitalized patients at 3 hospitals in Hong Kong. All NPAs were tested for influenza viruses A and B; parainfluenza viruses 1, 2, and 3; respiratory syncytial virus; and adenovirus by direct immunofluorescence. NPAs were also tested for human coronavirus 229E, human coronavirus OC43, HCoV-NL63, and CoV-HKU1 by reverse-transcription PCR (RT-PCR) [9, 10, 26]. As a pilot study to determine the age distribution of HBoV infection in our population, 200 NPAs negative for the respiratory viruses listed above (118 from pediatric patients [<18 years old] and 92 from adult patients [≥18 years old]) and 200 NPAs positive for any of these viruses (166 from pediatric patients and 34 from adult patients) sent to the microbiology laboratories were randomly selected for HBoV testing by PCR.

Because all positive samples from the pilot study were from young children, a prospective study that aimed to determine the epidemiology of HBoV infection and the clinical spectrum of disease caused by this infection was done using specimens from pediatric patients during a 12-month period (November 2004–October 2005). One hundred NPAs from pediatric patients that tested negative for the respiratory viruses listed above were randomly selected each month for HBoV testing by PCR. During the same period, fecal samples were also collected from pediatric patients with acute gastroenteritis, which was defined as the development of acute diarrhea with 3 or more loose stools per day. All fecal samples were tested for common bacterial diarrheal pathogens, rotavirus (by antigen detection [27]), and HBoV (by PCR). When HBoV was detected, the corresponding patients were identified, and their clinical features, laboratory results, and outcome were analyzed retrospectively.

**PCR for HBoV and sequencing.** DNA from NPAs and fecal samples was extracted using the QIAamp DNA Mini Kit (Qiagen), in accordance with the manufacturer’s protocol. DNA was subjected to PCR for HBoV as described elsewhere, using forward primer 5′-GAGCTCTGTAAGTACTATTAC-3′ and reverse primer 5′-CTCTGTGTTGACTGAATACAG-3′ targeted to a 354-bp fragment of the *NP1* gene; the primers were based on the corrected sequences published as a corrigendum [11]. The amplified products were detected by agarose gel electrophoresis. Both strands of all PCR products were sequenced twice with an ABI Prism 3700 DNA Analyzer (Applied Biosystems), using the PCR primers. The sequences of the PCR products were compared with the sequences of HBoV strains available in GenBank.

**Detection of hMPV and rhinovirus by RT-PCR.** There was no significant difference in the rate of detection of HBoV between NPAs that were positive and those that were negative for other respiratory viruses, which raised the possibility that concomitant respiratory viruses that were not included in our tests may also be present in the NPAs. Therefore, stored RNA from all NPAs positive for HBoV was retrieved and subjected to RT-PCR for hMPV and rhinovirus. Viral RNA was extracted from NPAs by use of the QIAamp Viral RNA Mini Kit (Qiagen). RT was performed using random hexamers and the SuperScript II Kit (Invitrogen) [7, 8]. PCR for hMPV and rhinoviruses was performed using protocols described elsewhere [28, 29].

**Complete genome sequencing and phylogenetic analysis of the NS1, NP1, and VP1/VP2 genes of HBoV.** The complete genomes of HBoVs from 12 NPAs and 12 fecal samples were amplified and sequenced using primers that have been described elsewhere [8]. Primers were designed by multiple alignment of the genomes of HBoV available in GenBank, and additional primers were designed on the basis of the results of the first and subsequent rounds of sequencing. The terminal sequences were confirmed by a modified protocol for rapid amplification of cDNA ends [11]. However, these terminal sequences may be incomplete because of their hairpin structures. The nucleotide and the deduced amino acid sequences of the NS1, NP1, and VP1/VP2 genes were compared with those of...
HBoV strains with a complete genome sequence available in GenBank. Phylogenetic trees were constructed by the neighbor-joining method with GrowTree, using Kimura’s 2-parameter correction with ClustalX 1.83 (Genetics Computer Group).

Nucleotide sequence accession numbers. The complete genome sequences of the 24 strains of HBoV identified here have been deposited in GenBank under accession numbers EF450717–EF450740.

RESULTS

Detection of HBoV in NPAs from pediatric patients. Of the 200 NPAs that were negative for influenza A and B viruses; parainfluenza viruses types 1, 2, and 3; respiratory syncytial virus; adenovirus; and the 4 human coronaviruses, 7 (3.5%) were positive for HBoV. Of the 200 NPAs that were positive for any of these respiratory viruses, 13 (6.5%) were positive for HBoV. All of the 200 NPAs that were positive for any of these respiratory viruses, 13 (6.5%) were positive for HBoV. Of the 20 HBoV-positive NPAs that were positive for HBoV, 13 (6.5%) were positive for HBoV. Of the 20 HBoV-positive NPAs that were children <5 years old. The detection rate in pediatric patients (<18 years old; 20/284 [7%]) was significantly higher than that in adults (≥18 years old; 0/126 [0%]) (P < .005, χ² test). Therefore, the subsequent prospective study was conducted in pediatric patients.

During the 12-month prospective study period, 1200 NPAs (100 per month) from pediatric patients (male to female ratio, 1.6:1; mean ± SD age, 3.8 ± 3.9 years) were subjected to PCR for HBoV. HBoV was detected in 83 NPAs. These 83 NPAs were obtained from 79 patients who were <10 years old (median age, 2 years; range, 6 months–9 years). Since 1081 of the 1200 NPAs were obtained from patients <10 years old, the 83 positive NPAs represent a 7.7% (83/1081) detection rate in this population. Of the 79 patients positive for HBoV, 46 were male, and 33 were female. HBoV was detected throughout the year, with the highest prevalence during fall and winter (figure 1).

Of the 79 patients, 36 had received a clinical diagnosis of upper respiratory tract infection (URTI), and 35 had a lower respiratory tract infection (LRTI). The remaining 8 patients did not have respiratory symptoms (table 1). Of the 35 patients with LRTI, 27 had pneumonia, 6 had acute bronchitis/bronchiolitis, and 2 had croup. One patient with pneumonia had Streptococcus pneumoniae isolated from the sputum. Although fever, cough, and rhinorrhea were the most common symptoms in patients with URTI, 2 had acute pharyngitis (with β-hemolytic group A streptococcus isolated from a throat swab in one of them), and 1 patient had acute sinusitis. Three patients with URTI and 3 with LRTI also had acute nonsuppurative otitis media. Fourteen patients experienced an asthma exacerbation, with 1 complicated by status asthmaticus. A number of patients with acute respiratory illness also had nonrespiratory symptoms or additional diagnoses. Nine had febrile convolution, and 2 others with underlying epilepsy had breakthrough seizures. Six had symptoms of gastroenteritis, and 1 had intussusception. One had pneumonia and gastroenteritis compli-
Table 1. Clinical characteristics of the patients with human bocavirus (HBoV) detected in nasopharyngeal aspirates.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patients, total no.</td>
<td>79</td>
</tr>
<tr>
<td>Male to female ratio</td>
<td>46:33</td>
</tr>
<tr>
<td>Age, median (range)</td>
<td>2 years (6 months–9 years)</td>
</tr>
<tr>
<td>Diagnosisa</td>
<td></td>
</tr>
<tr>
<td>URTI</td>
<td>36 (46)</td>
</tr>
<tr>
<td>Acute pharyngitis</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Acute sinusitis</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Acute otitis media</td>
<td>6 (9)</td>
</tr>
<tr>
<td>Acute bronchitis/bronchiolitis</td>
<td>6 (8)</td>
</tr>
<tr>
<td>Pneumonia</td>
<td>27 (34)</td>
</tr>
<tr>
<td>Croup</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Asthma exacerbation</td>
<td>14 (18)</td>
</tr>
<tr>
<td>Febrile convolution</td>
<td>9 (11)</td>
</tr>
<tr>
<td>Breakthrough seizure</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Aseptic meningitis</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Gastroenteritis</td>
<td>9 (11)</td>
</tr>
<tr>
<td>Acute hepatitis</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Intussusception</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Kawasaki disease</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Infectious mononucleosis</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Herpangina</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Herpetic gingivostomatitis</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Henoch-Schönlein purpura</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Roseola infantum</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Nephrotic syndrome</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Copathogens</td>
<td></td>
</tr>
<tr>
<td>Streptococcus pyogenes</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Streptococcus pneumoniae</td>
<td>1 (1)</td>
</tr>
<tr>
<td>Enterovirus</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Epstein-Barr virus</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Herpes simplex virus</td>
<td>2 (3)</td>
</tr>
<tr>
<td>Rhinovirus</td>
<td>14 (18)</td>
</tr>
<tr>
<td>Human metapneumovirus</td>
<td>2 (3)</td>
</tr>
</tbody>
</table>

NOTE. Data are no. (%) of patients, unless otherwise indicated. URTI, upper respiratory tract infection. *Percentages sum to >100% because some patients had >1 diagnosis.

cated by nephrotic syndrome. Two others with pneumonia had primary Epstein-Barr virus infection. One patient with URTI had herpangina, 2 had herpetic gingivostomatitis, and another had Henoch-Schönlein purpura. Of the 8 patients without respiratory symptoms, 3 had gastroenteritis, 2 of whom had rotavirus antigen detected in their fecal samples. Two had Kawasaki disease. One had aseptic meningitis due to enterovirus. One had acute hepatitis of unknown etiology. One had roseola infantum. Interestingly, HBoV was persistently detected in a 2-year-old boy in 5 separate NPAs collected over a 1-month period. Apart from the HBoV infection in this patient, who had URTI complicated by recurrent wheezing during his prolonged hospitalization for short gut syndrome, all cases were community acquired. All 79 patients survived.

Detection of HBoV in fecal samples from pediatric patients with acute gastroenteritis. During the 12-month period, 1435 fecal samples from pediatric patients with acute gastroenteritis (male to female ratio, 1.6:1; mean ± SD age, 2.7 ± 3.4 years) were subjected to PCR for HBoV. HBoV was detected in 30 samples (2.1%) from 25 patients (tables 2 and 3). The median age of these patients was 17 months (range, 2 months–3 years). Eighteen were male and seven were female. As with the results for NPAs, HBoV was mainly detected in fecal samples during the fall and winter months, with all cases occurring from September to February. Diarrhea lasted for 1–4 days, and the frequency of stool passage ranged from 3–20 times per day. Blood was present in the stool of 4 patients and in the mucus of 2. Eight experienced vomiting, and 17 had fever. Coryzal symptoms occurred in 14 patients. Seven had LRTI, with pneumonia in 3 and acute bronchiolitis in 4. One also had urinary tract infection. Two had febrile convulsions, and 1 with underlying epilepsy had recurrent seizures. Diarrheal pathogens were frequently found in fecal samples, with rotavirus identified in 9, serogroup B Salmonella species in 2, Campylobacter species in 1, and Staphylococcus aureus in 1. HBoV was repeatedly detected in separate fecal samples from 3 patients. In particular, HBoV

Table 2. Summary of characteristics of the patients with human bocavirus detected in fecal samples.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patients, total no.</td>
<td>25</td>
</tr>
<tr>
<td>Male to female ratio</td>
<td>18:7</td>
</tr>
<tr>
<td>Age, median (range)</td>
<td>17 months (2 months–3 years)</td>
</tr>
<tr>
<td>Clinical manifestations/other diagnosesa</td>
<td></td>
</tr>
<tr>
<td>Presence of blood in stool</td>
<td>4 (16)</td>
</tr>
<tr>
<td>Presence of mucus in stool</td>
<td>2 (8)</td>
</tr>
<tr>
<td>Vomiting</td>
<td>8 (32)</td>
</tr>
<tr>
<td>Fever</td>
<td>17 (68)</td>
</tr>
<tr>
<td>Coryzal symptoms</td>
<td>14 (56)</td>
</tr>
<tr>
<td>Acute bronchiolitis</td>
<td>4 (16)</td>
</tr>
<tr>
<td>Pneumonia</td>
<td>3 (12)</td>
</tr>
<tr>
<td>Febrile convolution</td>
<td>2 (8)</td>
</tr>
<tr>
<td>Breakthrough seizure</td>
<td>1 (4)</td>
</tr>
<tr>
<td>Urinary tract infection</td>
<td>1 (4)</td>
</tr>
<tr>
<td>Copathogens</td>
<td></td>
</tr>
<tr>
<td>Rotavirus</td>
<td>9 (36)</td>
</tr>
<tr>
<td>Salmonella species</td>
<td>2 (8)</td>
</tr>
<tr>
<td>Campylobacter species</td>
<td>1 (4)</td>
</tr>
<tr>
<td>Staphylococcus aureus</td>
<td>1 (4)</td>
</tr>
<tr>
<td>Clostridium difficile</td>
<td>1 (4)</td>
</tr>
</tbody>
</table>

NOTE. Data are no. (%) of patients, unless otherwise indicated. *Percentages sum to >100% because some patients had >1 diagnosis.
was persistently found in 4 samples collected over 5 weeks from a 3-year-old boy (patient 17 in table 3) with multiple congenital malformations who developed persistent diarrhea due to *Clostridium difficile* during hospitalization. Apart from the HBoV infection in this patient, all cases were community acquired. All patients survived.

**Detection of hMPV and rhinovirus in NPAs.** Available RNA from 93 NPAs positive for HBoV was subject to RT-PCR for hMPV and rhinovirus. Of these 93 samples, 14 were positive for rhinovirus, and 2 were positive for hMPV. Rhinovirus was detected in 6 with LRTI and 8 with URTI. Ten of these 14 patients with rhinovirus infection had asthma exacerbations, and 2 had febrile convulsions. hMPV was detected in 1 patient with LRTI and in 1 patient with URTI and gastroenteritis.

**Complete genome sequencing and phylogenetic analysis of the NS1, NP1, and VP1/VP2 genes of HBoV.** The complete genomes of HBoVs from 12 NPAs and 12 fecal samples were amplified and sequenced. The 24 HBoV genomes (size, 5.2 kb) had G+C content of 42%. The genomic organization was the same as that of the 2 prototype HBoV strains, ST1 and ST2, and of other known bocaviruses, BPV and MVC. There were 3 open reading frames (ORFs), with the gene order NS1, NP1, and VP1/VP2. Sequence analysis showed that the 24 strains of HBoV displayed limited sequence variations among themselves as well as in relation to the available sequences of previously described HBoV strains in all 3 genes (figure 2). The NS1 gene was the most conserved gene among the 3, with only minor nucleotide polymorphisms. The predicted amino acid sequences of the 24 HBoV strains were identical among themselves and in relation to NS1 sequences of HBoVs from GenBank, except for a strain from China (HBoV_WLL-1) that had 1 amino acid substitution (His→Arg) resulting from a mutation at nucleotide position 1328. The greatest sequence variations occurred in the VP1/VP2 gene, although the overall nucleotide and amino acid differences among different strains were <2% and <1%, respectively.

**DISCUSSION**

Although the results of this study of NPAs are similar to those of previous studies, the present report is the first to document the presence of HBoV in fecal specimens. In this 1-year pro-
Figure 2. Phylogenetic trees of complete NS1, NP1, and VP1/VP2 gene sequences of 12 human bocavirus (HBoV) strains from nasopharyngeal aspirates (NPAs) and 12 HBoV strains from fecal samples. The trees were inferred from NS1 (A), NP1 (B), and VP1/VP2 (C) gene data by the neighbor-joining method, using bootstrap values calculated from 1000 trees. The trees were rooted using the NS1, NP1, and VP1/VP2 gene sequences of minute virus of canine; 1920 nucleotide positions in each NS1 gene, 660 nucleotide positions in each NP1 gene, and 2016 nucleotide positions in each VP1/VP2 gene were included in the analysis. The scale bar indicates the estimated no. of substitutions per 500 bases by Kimura’s 2-parameter model. HBoV strains ST1 and ST2, from Sweden, were the 2 prototype strains. Strains WLL-1 and CZ643 are from China, and strain CRD2 is from the United States.
mostly examined the partial conserved. Similar to the findings of previous studies, which
samples. Among the 3 genes, NS1 (a nonstructural protein), NP1
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protein). Phylogenetic analysis of these 3 ORFs in all 24 HBoV
contains 3 ORFs encoding NS1 (a nonstructural protein), NP1
which have different genotypes, possibly as a result of a high
infections in humans. This is in contrast to coronaviruses,
whether HBoV plays a causative role in these coinfections or
reported that the frequency of HBoV infection was even
asymptomatic control children at a primary care center. Because
it was not indicated whether any of the HBoV-positive speci-
ments were nasal washes, it is difficult to conclude whether the
observed difference was genuine or due to discrepancies in
sampling. Nevertheless, in another study, HBoV also appeared
to be more common among individuals with respiratory tract
disease than among those without symptoms [15]. Although
the association between HBoV and respiratory tract disease may
support a role for the virus in pathogenesis, it does not prove
causality, which is often difficult to ascertain in the case of
respiratory viruses [35].

Although a lack of proof of causality by Koch’s postulates
does not exclude the possibility that HBov is a pathogen, its
exceptionally high frequency of codetection with other respir-
atory viruses, a phenomenon that was not observed for known
respiratory viruses, has led to reservations concerning its role
in human disease. The frequency of codetection in HBoV-pos-
itive respiratory samples has ranged from 33% to 80%, de-
pending on how intensively other respiratory viruses were
sought, the sensitivities of the methods used, and the sampling
size [12, 16–21]. The highest codetection rate—observed in a
Swiss study in which 4 of 5 HBoV-positive nasal samples from
infants contained other respiratory viruses—may have been due
to the inclusion of a comprehensive panel of respiratory viruses
that included rhinovirus and coronaviruses [16]. In the present
study, although many common respiratory viruses were initially
excluded from the NPAs selected for HBoV testing, 33% of the
patients with NPAs positive for HBoV were subsequently found
to have coinfections with another pathogen. As for fecal sam-
ple, a high rate of coinfection (56%) was also observed. It has
been reported that the frequency of HBoV infection was even
higher when another virus was present [15]. In the present
study, a higher prevalence was also observed in NPAs positive
for common respiratory viruses (6.5%) than in those that were
negative (3.5%). Further studies are required to determine
whether HBoV plays a causative role in these coinfections or
acts as an exacerbating factor that simply increases the severity
of infections caused by other pathogens.

The low genetic diversity of HBoV suggested that a single
lineage was responsible for both respiratory tract and enteric
infections in humans. This is in contrast to coronaviruses,
which have different genotypes, possibly as a result of a high
frequency of recombination [36]. The 5.2-kb genome of HBoV
contains 3 ORFs encoding NS1 (a nonstructural protein), NP1
(a protein of unknown function), and VP1/VP2 (viral capsid
protein). Phylogenetic analysis of these 3 ORFs in all 24 HBoV
strains from NPAs and fecal samples did not reveal a genotypic
difference between the strains from NPAs and those from fecal
samples. Among the 3 genes, NS1 appeared to be the most
conserved. Similar to the findings of previous studies, which
mostly examined the partial NP1 gene, minor nucleotide sub-
stitutions were observed in NP1, with occasional amino acid
substitutions. When HBoV was first described, it was found
that most nucleotide polymorphisms occurred in VP1/VP2
[11]. Only 2 subsequent studies have analyzed partial se-
quences of VP1/VP2. In one study, which involved the se-
quencing of a 1-kb fragment of the VP2 gene, 97.5%–100%
nucleotide sequence identity was observed between their HBoV
strains and the prototype strains, suggesting a unique lineage
of HBoV [18]. In another study, which analyzed the 3′ 819-bp
fragment of VP1/VP2, the authors suggested that 2 distinct
genotypes were observed, with ST1 being in one cluster and
ST2 in another [14]. In the present study, comparison of the
complete VP1/VP2 gene sequences from our 24 HBoV strains
and strains from other countries showed only minor variations.
Although phylogenetic analysis of this gene showed that there
may be clustering among some strains, the existence of distinct
genotypes cannot be concluded. In fact, our present results
suggest that humans are infected by a single lineage of HBoV,
which was detected in both respiratory tract and enteric
samples.

The lack of variation in the surface protein of HBoV suggests
that HBoV infection may happen only once, with the subse-
quent development of life-long immunity via neutralizing an-
tibody. This is consistent with the fact that HBoV infection
occurs primarily in infants and young children. The develop-
ment of immunity against HBoV and the clearance of HBoV
may depend on the integrity of one’s immune system. In the
Swiss study [16], HBoV was detected in follow-up samples from
only 1 of the 5 infants, suggesting that HBoV is rapidly cleared
in most cases. In the present study, persistent HBoV shedding
for >1 month was observed in both respiratory tract and fec-
al specimens from patients with significant underlying dis-
eases, which may represent prolonged infections as a result of
underlying immunosuppression. However, routine follow-up
was not done in our patients, because our clinical data were
mainly collected retrospectively after HBoV PCR results had
become available, by which time most patients had been dis-
charged. Larger longitudinal studies should be conducted to
examine the duration of HBoV shedding and the mechanism
of immunity.

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