Detection of Human Bocavirus in Japanese Children with Lower Respiratory Tract Infections

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ABSTRACT

Human bocavirus (HBoV), a newly cloned human virus of the genus *Bocavirus*, was detected by PCR from nasopharyngeal swab samples collected from children with lower respiratory tract infections (8 of 318, 5.7%). HBoV may be one of the causative agents of lower respiratory tract infections in young children. (48 words)
The family Paroviridae contains two subfamilies: Parovirinae, which infects vertebrates, and Densovirinae, which infects insects. The subfamily Parovirinae consists of five genera: Parovirus, Erythrovirus, Dependovirus, Amdovirus, and Bocavirus (12). Parovirus B19, which belongs to the genus Erythrovirus, is a well-known pathogen to humans (3, 12). A new human virus of the genus Bocavirus, provisionally named human bocavirus (HBoV), was recently cloned from pooled human respiratory tract samples and is considered to be pathogenic to humans (1). In this study, nasopharyngeal swab samples obtained from children with lower respiratory tract infections were investigated for the presence of HBoV.

From October 2002 to September 2003 and from January 2005 to July 2005, a total of 318 nasopharyngeal swab samples were collected from 318 children with lower respiratory tract infections at 4 hospitals in Sapporo, Japan. All of the samples were collected after excluding the possibility of infection with hRSV or influenza A or B by rapid antigen detection tests and after excluding the possibility of infection with human metapneumovirus (hMPV) by a reverse transcription polymerase chain reaction (RT-PCR) test (6). The median age of the children was 21.3 months. The male-to-female ratio was 1.4 to 1. All samples were collected after obtaining informed consent from the children's parents. RNA and DNA were extracted from each sample
by using the method by Chomczynski’s protocol (5). RNA was used for the detection of hMPV (6) and DNA was used for the detection of HBoV as described below. The PCR primers and conditions used for detection of HBoV have been described previously (1). A forward primer with a sequence of 5’-GAGCTCTGTAAGTACTATTAC-3’ and a reverse primer with a sequence of 5’-CTCTGTGTTGACTGAATACAG-3’ were used for both PCR and sequencing. The PCR mixture consisted of 100 µmol of each deoxyribonucleotide, 1.0 U of Ampli Taq Gold, 50 mmol of potassium chloride/liter, 10 mmol of Tris·HCl (pH 8.3)/liter, 1.5 mmol of magnesium chloride/liter, 0.01% (wt/vol) gelatin, 10 pmol of each primer, and DNA in a volume of 25 µl. The PCR conditions were as follows: 94°C for 9 min, followed by 35 cycles of 94°C for 1 min, 54°C for 1 min, and 72°C for 2 min. Both sense and antisense strands of the PCR products were sequenced directly by using a BigDye terminator cycle sequencing ready reaction kit (Perkin-Elmer Applied Biosystems, Tokyo, Japan) with an ABI Prism 310 genetic analyzer (Perkin-Elmer Applied Biosystems).

DNA sequences of HBoV were detected in samples from 18 (5.7%) of the 318 patients with lower respiratory tract infections. Seventeen of the 18 HBoV-positive samples were collected during the period from January to May (one sample in January, three in February, one in March, four in April, eight in May and one in July). The ages of patients with HBoV-positive samples ranged from 7 months to 3 years (one patient of 7
to 9 months in age, five of 10 to 12 months in age, ten of 1 to 2 years in age and two of 2
to 3 years in age). Direct sequencing of PCR products of the 18 samples showed that
14 of the 18 sequences were completely identical to the published sequence of HBoV
(GenBank accession numbers DQ000495 and DQ000496) (Group 1 in Fig. 1). Three of
the 18 sequences had a single base pair substitution in the NP-1 gene, resulting in an
amino acid exchange (Group 2 in Fig. 1). One of the 18 sequences had a single base
pair substitution in the NP-1 gene without amino acid exchange (Group 3 in Fig. 1).
The sequences were deposited at GenBank (accession numbers DQ296618 to
DQ296635).

Clinical and laboratory features of the 18 HBoV-positive patients are shown in Table 1.
All of the 18 patients suffered from fever, cough, and various degrees of respiratory
distress. Maximum temperature ranged from 37.5 to 40.2°C. The duration of fever
(temperature of > 37.5°C) ranged from 1 to 8 days. Eight of the 18 patients showed
abnormal findings on a chest x-ray (4 patients with lung infiltration, 3 patients with
peribronchial infiltration, and one patient with hyperinflation). The clinical
diagnoses of the HBoV-positive patients were pneumonia (6 patients), wheezy
bronchitis (6 patients), bronchitis (2 patients), bronchiolitis (2 patients), asthma attack
(1 patient), and laryngotracheitis (1 patient). Sixteen of the 18 patients were
admitted to hospital for 3 to 9 days.
Bovine parvovirus (BPV) and canine minute virus (MVC) are members of the 

*Parvoviridae* family, subfamily *Parvovirinae*, genus *Bocavirus*. BPV caused mild diarrhea in calves when inoculated *per os*, and it caused diarrhea and mild respiratory symptoms when inoculated intranasally (11). MVC was first described as an isolate from a healthy dog in the U.S.A (2). Although it is likely that most infections with MVC are subclinical, diseases associated with virus infection include fetal infections leading to reproductive failure and neonatal respiratory disease (4, 7, 8). The virus may also be associated with some cases of enteritis in puppies or older dogs (2). HBoV was first cloned from pooled human respiratory tract samples collected in Sweden and was provisionally classified into the genus *Bocavirus* from resemblance of the sequences (1). HBoV has recently been found in Australian children with respiratory tract infection (10). HBoV was detected from samples collected during the period from winter to spring (1, 10). The detection rate of HBoV in respiratory tract infections has been reported to be 3.1% to 5.6% (1, 10), which is consistent with our data (5.7%). It should be noted that the possibility of infection with other viruses (parainfluenza viruses, rhinoviruses and coronaviruses) in our bocavirus positive specimens could not be excluded and that the possibility of influenza virus infection could not be totally excluded because of the limited sensitivity (60-80%) of rapid antigen tests for influenza
virus infection (9). The sequences of the amplified NP-1 region showed limited variation (1), as our data also showed (Table 1). The HBoV genome has been detected in samples from patients aged between 5 and 17 months (1) and aged between 6 month and 2 years (10). In our study, the ages of HBoV-positive patients ranged from 9 months to 2 years and 7 months (Table 1). The antibody against HBoV derived from the mother might protect infants under 5 months of age from HBoV infection, and primary HBoV infection might occur early in life. Serological study is needed to validate this hypothesis. Clinical findings in HBoV-positive patients are indistinguishable from those caused by other respiratory viruses. Our study showed that pneumonia and wheezy bronchitis were the major diagnoses in HBoV-positive patients. Carefully controlled studies are needed to clarify the full spectrum of diseases associated with HBoV. Five nasopharyngeal samples from five patients were inoculated on LLC-MK2 cells. However, the HBoV genome was not detected in DNA extracted from cells after a 3-week culture period (data not shown), suggesting that LLC-MK2 cells might not be appropriate for initial isolation of HBoV.

To our knowledge, this is the first report of detection of HBoV in patients with lower respiratory tract infections in Asia. This study suggests that HBoV may be widespread throughout the world and that it is one of the causative agents of lower respiratory tract infections in young children. To clarify the clinical impact of HBoV,
further surveillance in various age groups and various clinical groups is needed.

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REFERENCES


Figure Legend

Sequences of PCR products of HBoV-positive samples. A of the ATG initiator methionine codon of NP-1 protein is denoted as nucleotide +1. The sequences of the 18 samples were divided into three groups and compared with that of the published sequence of HBoV (GenBank accession number DQ000495) as a reference. Group 1 (JPBS03-112, JPBS03-217, JPBS03-219, JPBS03-261, JPBS03-298, JPBS05-7, JPBS05-18, JPBS05-28, JPBS05-29, JPBT03-5, JPBT03-12, JPBT03-43, JPBT05-46, and JPBT05-52) was completely identical to the reference. Group 2 (JPBS03-182, JPBS03-207, and JPBS03-208) had a single base pair substitution (176G to A) in the NP-1 gene, resulting in an amino acid exchange (Ser to Asn). Group 3 (JPBS03-98) had a single base pair substitution (201G to A) in the NP-1 gene without amino acid exchange.
<table>
<thead>
<tr>
<th>Case</th>
<th>Sample</th>
<th>Sex</th>
<th>Age</th>
<th>Diagnosis</th>
<th>Max. Temp (°C)</th>
<th>Duration of Fever &gt;37.5°C (days)</th>
<th>Cough</th>
<th>Wheezing</th>
<th>Chest x-ray</th>
<th>Max. WBC (/µl)</th>
<th>Max. CRP (mg/dl)</th>
<th>Days hospitalized</th>
</tr>
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<td>1</td>
<td>JPBS03-98</td>
<td>F</td>
<td>1yr 6mo</td>
<td>Bronchitis</td>
<td>39.4</td>
<td>8</td>
<td>+</td>
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<td>14,300</td>
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<td>10mo</td>
<td>Bronchiolitis</td>
<td>37.9</td>
<td>3</td>
<td>+</td>
<td>+</td>
<td>Peribronchial infiltration</td>
<td>6,400</td>
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</tr>
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<td>JPBS03-182</td>
<td>M</td>
<td>1yr 3mo</td>
<td>Pneumonia</td>
<td>40.2</td>
<td>2</td>
<td>+</td>
<td>+</td>
<td>Bilateral lung infiltration</td>
<td>21,900</td>
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</tr>
<tr>
<td>4</td>
<td>JPBS03-207</td>
<td>M</td>
<td>1yr 10mo</td>
<td>Wheezy Bronchitis</td>
<td>39.1</td>
<td>2</td>
<td>+</td>
<td>+</td>
<td>No abnormality</td>
<td>13,980</td>
<td>0.20</td>
<td>5</td>
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<td>5</td>
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<td>Pneumonia</td>
<td>40.0</td>
<td>4</td>
<td>+</td>
<td>+</td>
<td>Right lung infiltration</td>
<td>11,800</td>
<td>1.58</td>
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<tr>
<td>6</td>
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<td>1yr 3mo</td>
<td>Wheezy Bronchitis</td>
<td>38.8</td>
<td>3</td>
<td>+</td>
<td>+</td>
<td>No abnormality</td>
<td>21,980</td>
<td>2.40</td>
<td>5</td>
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<td>7</td>
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<td>10mo</td>
<td>Pneumonia</td>
<td>40.0</td>
<td>6</td>
<td>+</td>
<td>-</td>
<td>Peribronchial infiltration</td>
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<td>8</td>
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<td>1yr 1mo</td>
<td>Wheezy Bronchitis</td>
<td>38.0</td>
<td>3</td>
<td>+</td>
<td>+</td>
<td>No abnormality</td>
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<td>1</td>
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<td>+</td>
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<td>15,190</td>
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<tr>
<td>10</td>
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<td>9mo</td>
<td>Bronchiolitis</td>
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<td>3</td>
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<td>+</td>
<td>Hyperinflation</td>
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<td>Laryngotracheitis</td>
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<td>+</td>
<td>-</td>
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<td>Pneumonia</td>
<td>38.8</td>
<td>3</td>
<td>+</td>
<td>-</td>
<td>Right lung infiltration</td>
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<td>11mo</td>
<td>Pneumonia</td>
<td>37.7</td>
<td>3</td>
<td>+</td>
<td>-</td>
<td>Right lung infiltration</td>
<td>10,220</td>
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<td>JPBT03-5</td>
<td>M</td>
<td>2yr 7mo</td>
<td>Asthma attack</td>
<td>37.5</td>
<td>1</td>
<td>+</td>
<td>+</td>
<td>No abnormality</td>
<td>15,000</td>
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<td>3</td>
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<td>M</td>
<td>2yr 4mo</td>
<td>Pneumonia</td>
<td>39.0</td>
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<td>+</td>
<td>+</td>
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<td>+</td>
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<td>3</td>
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<td>+</td>
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<td>+</td>
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