

REVIEW



Human bocavirus—the first 5 years

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SUMMARY

Four species of human bocavirus (HBoV) have been recently discovered and classified in the *Bocavirus* genus (family *Parvoviridae*, subfamily *Parvovirinae*). Although detected both in respiratory and stool samples worldwide, HBoV1 is predominantly a respiratory pathogen, whereas HBoV2, HBoV3, and HBoV4 have been found mainly in stool. A variety of signs and symptoms have been described in patients with HBoV infection including rhinitis, pharyngitis, cough, dyspnea, wheezing, pneumonia, acute otitis media, fever, nausea, vomiting, and diarrhea. Many of these potential manifestations have not been systematically explored, and they have been questioned because of high HBoV co-infection rates in symptomatic subjects and high HBoV detection rates in asymptomatic subjects. However, evidence is mounting to show that HBoV1 is an important cause of lower respiratory tract illness. The best currently available diagnostic approaches are quantitative PCR and serology. This concise review summarizes the current clinical knowledge on HBoV species. Copyright © 2011 John Wiley & Sons, Ltd.

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INTRODUCTION

Human bocavirus (HBoV, lately denoted HBoV1) was discovered by Allander *et al.* in 2005 [1]. It was the first virus identified by “molecular virus screening”, a procedure based on DNase treatment of nasopharyngeal samples, random nucleic acid amplification and cloning, followed by large scale sequencing and bioinformatic analyses. After excluding human, bacterial and known viral sequences, a new parvovirus sequence was identified. Further analysis based on the deduced amino acid sequences showed that the closest relatives of the new parvovirus were bovine parvovirus and

canine minute virus of the genus *Bocavirus*. The new virus was therefore named human bocavirus. In 2009–2010, this genus was expanded by three additional species of human bocaviruses, HBoV2, HBoV3 and HBoV4 (Figure 1) [2–4]. HBoV2 can further be divided in strains A and B based on a >5% divergence in the nonstructural gene nucleotide sequences [4].

Human bocaviruses have been detected worldwide by PCR not only in respiratory (Table 1) and stool samples (Table 2) but also in serum [5–10], tonsillar [11], saliva [12], and urine samples [13,14] as well as in river [15] and sewage water [16,17]. Contrary to HBoV1, HBoV2–4 seem to occur mainly in human stool (Table 2) [2–4,18,19] but rarely also in the respiratory tract [20,21]. Relatives of HBoV have further been detected in animals [22–27]. Although HBoV1 has been encountered in individuals of all ages, its predilection has been young children with respiratory symptoms. However, with molecular diagnostics of respiratory tract secretions, HBoV1 may often be seen also in asymptomatic children raising justified concerns on causality [28–35]. Recent analyses of blood samples and advances in

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Abbreviations used

AAV2, adeno-associated virus 2; BAL, bronchoalveolar lavage; B19V, human parvovirus B19; DNA, deoxyribonucleic acid; EIA, enzyme immunoassay; HBoV, human bocavirus; Ig, immunoglobulin; ML, maximum likelihood; NP, nuclear phosphoprotein; NPA, nasopharyngeal aspirate; NS, nonstructural protein; ORF, open reading frame; PCR, polymerase chain reaction; Th, T helper; VP, viral (structural) protein; VLP, virus-like particle.

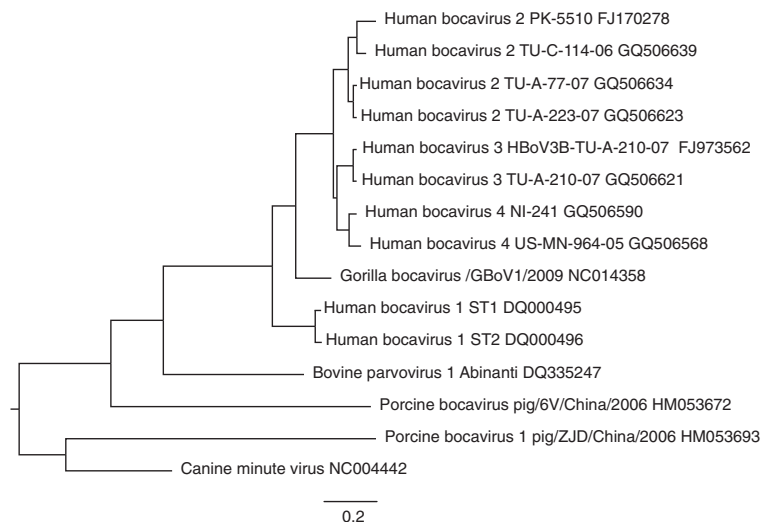


Figure 1. Maximum likelihood (ML) phylogenetic tree of representative members of the genus *Bocavirus* based on partial VP1 gene sequences (CDS 3282–3738 according to FJ170278 sequence). The alignment was constructed using Se-AL and regions that were difficult to align were removed. The final alignment was 480 nucleotides long. The ML tree was inferred using PhyML 3.0 with 5 random starting trees, the SPR (subtree pruning regrafting) and nearest NNI (neighbor interchange) search algorithms, and the GTR + G + I substitution model, which was identified as the best model by FindModel. The scale bar indicates nucleotide substitutions per site

serodiagnosis, however, have provided compelling evidence for HBoV1 being a true respiratory pathogen [10,14,36–40]. In this concise review, we update the current clinical knowledge on HBoV infections in humans.

SEARCH STRATEGY AND SELECTION CRITERIA

Since the discovery of HBoV, we have performed active research on HBoV and followed the literature. For this review, we searched the PubMed data base for articles published before 23.5.2011 with “bocavirus” as a search term (335 hits including 295 published in English). Of the latter, we include major molecular and clinical studies on HBoV.

VIRUS STRUCTURE

Human bocaviruses belong to the family *Parvoviridae*, subfamily *Parvovirinae*. They are minute DNA viruses that for replication are highly dependent on cellular functions including the DNA polymerase. Their linear single-stranded genome is only ~5 kb in length with still unknown terminal sequences [41]. The genome putatively encodes two forms of the nonstructural protein NS1 and a for bocaviruses unique, nuclear phosphoprotein NP1, as well as two major structural proteins, VP1 and VP2 (Figure 2) [42–44]. These latter capsid proteins share in common

the C-terminal part except the very N-terminus of VP1, containing a phospholipase-A motif, unique (VP1u). By electron microscopy, the structure of HBoV is typical of *Parvoviridae*, that is, non-enveloped capsid of icosahedral symmetry and diameter of ~25 nm [10,39,45,46]. The 3-dimensional ultrastructure has been solved with recombinant HBoV VP2 capsids at 7.9-Å resolution, showing many characteristics in common with other parvoviruses, such as a depression at the twofold axis, a protrusion at the threefold axis and a channel at the fivefold axis surrounded by a canyon [46]. In smooth topology, the HBoV VP2 capsid resembles that of human parvovirus B19 (B19V). The fivefold channel of B19V is, however, closed, whereas that of HBoV, similarly to many other parvoviruses, may permit the VP1-N or VP2-N termini to be externalized. This might imply that VP1u in the virion could reside inside the capsid rather than on the surface. In line with this notion is our serological results showing, contrary to B19V, only minor antibody reactivity with HBoV VP1u compared with VP2 and a relative resistance of VP2 against denaturation by low concentrations of urea [36,40].

EPIDEMIOLOGY

The true prevalence of HBoV1 infection was difficult to determine until the development of serology

Table 1. Major clinical studies on human bocavirus-1 DNA etiology of respiratory illnesses by PCR^a

1st author	Study site	Study year	n	Age (years)	HBov1+, n (%)	HBov1 qPCR reported	Viruses tested	Mixed viral findings (%)	HBov1 co-infection, n (%)
Allander [1]	Sweden	03-04	540	70% pediatric	17 (3)	no	8	n/g	3 (18)
Lu [158]	Thailand	04-05	1178	n/g	39 (3)	yes	n/g	n/g	n/g
Bastien [63]	Canada	03-04	1209	<6: 290 (24%) 6-15: 149 (12%) 16-50: 444 (37%) >50: 324 (27%)	8 (3) ^b 3 (2) ^b 6 (1) ^b 1 (0.3) ^b	no	9 ^b	n/g	n/g
Choi [53]	Korea	00-05	515	<6	58 (11)	no	11	36 (7)	22 (38)
Foulongne [127]	France	03-04	589	<6	26 (4) ^b	no	9 ^b	n/g	9 (35)
Weissbrich [129]	Germany	02-05	835	<9	87 (10)	no	8 ^b	n/g	34 (39)
Manning [52]	United Kingdom	05-06 + archive	924	<5: 624 (68%) ≥5: 300 (32%)	53 (6)	yes	8 ^b	47 (5)	23 (43)
Allander [5]	Finland	00-02	259	<16	49 (19)	yes	16	89 (34)	37 (76)
Fry [6]	Thailand	04-05	1680	all ages	73 (4)	yes	14	n/g	42/53 (79%) ^d
Lau [99]	Hong Kong	04-05	400	all ages	20 (5)	no	12 ^b	n/g	26/79 (33)
Kesebir [50]	USA	04	425	<2	83 (7)	no	8	n/g	n/g
Ma [159]	Japan	02-03	318	median 1.8	22 (5)	no	4 ^c	—	—
Vicente [97]	Spain	05-06	520	<3	18 (6)	no	12	n/g	25 (63)
Monteny [160]	The Netherlands	05-06	257	<3	4 (2)	yes	14	n/g	3 (75)
Völz [133]	Germany	05-06	389	<2	11 (3)	no	10 ^b	n/g	4 (36)
Pozo [13]	Spain	04-06	917	<14	123 (13)	no	16	n/g	74 (60)
Esposito [145]	Italy	04-05	1332	<15	99 (7)	no	15	230 (17)	50 (51)
Chiochansin [101]	Thailand	06-07	302	<15	20 (7)	no	7 ^b	n/g	8 (40)
Christensen [161]	Norway	06-07	376	children	45 (12)	yes	17	103 (27)	35 (78)
Regamey [28]	Switzerland	99-04	112	<1	5 (4)	no	16	18 (16)	n/g
I.P. [162]	Hong Kong	05-06	1906	<15	95 (5)	no	8 ^b	n/g	18 (19)
Calvo [89]	Spain	05-07	710	<14	99 (14)	no	16	127 (18)	64 (65)
Garcia-Garcia [60]	Spain	04-06	908	<14	153 (17)	no	16	187 (21)	n/g
von Linstow [32]	Denmark	04-06	697	<1	57 (8)	yes	13	n/g	27 (47)
Briou [58]	France	06-07	507	<5	55 (11)	yes	9	n/g	22 (40)
Pierangeli [163]	Italy	04-07	214	children	34 (8)	no	multiple	n/g	21 (62)

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Table 1. (Continued)

1st author	Study site	Study year	<i>n</i>	Age (years)	HBov1+, <i>n</i> (%)	HBov1 qPCR reported	Viruses tested	Mixed viral findings (%)	HBov1 co-infection, <i>n</i> (%)
Longtin [61]	Canada	02–03	225	<4, adults	31 (14)	no	5 ^b	n/g	22 (71)
Dina [87]	France	03–05	126	<15	1 (1)	no	12–16	n/g	0 (0)
Tozer [8]	Australia	03–04	828	<5	11 (1) ^c	yes	26	n/g	n/g 4 (57)
Han [20]	South Korea	08–09	448	<5	7 (2)	no	14	n/g	–4 (80)
Zeng [83]	China	06–07	96	<5	17 (18)	yes	26	n/g	4 (24)
Karalar [9]	Germany	06–07	212	<5	HBov1 0 (0)	no	14	n/g	–4 (80)
Yoshida [164]	China	06–07	351	<4	HBov2 5 (2)	no	8 ^b	n/g	3 (19)
Wang [14]	Germany	06–07	156	<16	16 (5)	yes	5 ^b	n/g	2 (13)
Franz [165]	Vietnam	07–08	958	<5	15 (10)	no	13	(12) ^e	n/g
Calvo [166]	China	06–08	817	0.5–9	(2) ^e	yes	15	103 (13%)	49 (51)
Miron [167]	Germany	06–08	404	<16	96 (12)	no	13	67 (17%)	19 (68)
Martin [35]	Spain	05–08	370	<2	28 (7)	no	16	79 (21)	28 (67)
	Israel	05–06	465	<3	42 (11)	no	8	140 (30)	28 (90)
	USA	06–08	318	0–2	31 (7)	yes	15	(24) ^e	76 (72)

n, number of samples; HBov, human bocavirus; qPCR, quantitative polymerase chain reaction; n/g, not given.

^aSelection criteria: Majority of other respiratory viruses were studied. The following studies had limited focus on specific respiratory illnesses: Choi (2006) [52], lower respiratory tract illness; Lu (2006) [158], pneumonia; Allander (2007) [5], acute wheezing; Longtin (2008) [60], adults had either chronic obstructive pulmonary disease or community-acquired pneumonia; Franz (2010) [165], acute wheezing and pneumonia; Calvo (2010) [166], bronchiolitis; and Miron (2010) [167], bronchiolitis.

^bRhinovirus PCR was not included.

^cOnly other virus negative samples were tested for HBov.

^dOnly pneumonia cases were tested for co-infections.

^eOnly percentages were given.

Table 2. Major clinical studies on human bocavirus etiology of gastrointestinal illnesses by PCR^a

1st author	Study site	Study year	n	Age (years)	HBoV type tested	HBoV+, n (%)	HBoV qPCR reported	Viruses or microbes tested	Mixed viral or bacterial findings, n (%)	HBoV co-infection, n (%)
Vicente [97]	Spain	05–06	527	<3	HBoV1	48 (9%)	no	6	n/g	28 (58%)
Lau [99]	Korea	05–06	1435	<6	HBoV1	30 (2%)	no	6	n/g	14/25 (56%)
Albuquerque [98]	Brazil	03–05	705	<15	HBoV1	14 (2%)	yes	10	n/g	3 (21%)
Lee [96]	Korea	05–06	962	<6	HBoV1	8 (1%)	no	14	45 (5%)	3 (38%)
Yu [30]	China	06–07	1216	<5	HBoV1	67 (6%)	no	5	102 (8%)	52 (78%)
Chieochansin [101]	Thailand	05–06	225	0.3–4	HBoV1	2 (1%)	no	2	n/g	1 (50%)
Cheng [31]	China	06–07	397	<5	HBoV1	14 (4%)	yes	8	n/g	9 (64%)
Campe [33]	Germany	07	307	all ages	HBoV1	14 (5%)	yes	7	n/g	8 (57%)
Arthur [2]	Australia	01	186	<17	HBoV2 HBoV3	32 (17%)	no	multiple	51 (27%)	n/g
Kapoor [3]	Pakistan United Kingdom	archive	98 699	all ages	HBoV2	5 (5%) 3 (0.4%)	no	1	—	—
Nakanishi [168]	Japan	03–05	877	<15	HBoV1	4 (0.5%)	no	6	28 (3%)	1 (25%)
Han [67]	Korea	08–09	358	<17	HBoV1 HBoV2	2 (0.5%) 13 (4%)	no	6	26 (7%)	2 (100%) 3 (23%)
Szomor [103]	Hungary	07–08	61	<5	HBoV1	2 (3%)	no	9	0 (0%)	—
Tozer [8]	Australia	03–04	136	children adults	HBoV1	13 (10%)	yes	9	3 (23%)	3 (23%)
Räsänen ^b [17]	Finland	07	50	<15	HBoV1	5 (2%)	no	5–11	32 (64%)	3 (75%)
Nadji [169]	Iran	06–08	47	<17	HBoV1	4 (8%)	no	1	—	—
Pham [170]	Japan	07–08	247	0.2–15	HBoV1	6 (3%)	no	4	3 (1%)	2 (67%)
Santos [69]	Brazil	n/g	807	all ages	HBoV1 HBoV2 HBoV3	10 (1%) 30 (21%) 5 (1%)	no	multiple	n/g	2 (0.2%) 13 (43%) 2 (0.2%)
Chow [19]	USA	07–08	479	151 children 328 adults	HBoV1 HBoV2 HBoV3	9 (2%) 6 (1%) 0 (0%)	no	3	n/g	n/g
Karalar [9]	Germany	06–07	64	<15	HBoV1	5 (8%)	yes	4	n/g	3 (60%)
Kapoor [4]	Nepal Nigeria	n/g	641	children adults	HBoV1 HBoV2A	4 (1%) 4 (1%)	no	5	n/g	—

Continues

Table 2. (Continued)

1st author	Study site	Study year	<i>n</i>	Age (years)	HBoV type tested	HBoV+, <i>n</i> (%)	HBoV qPCR reported	Viruses or microbes tested	Mixed viral or bacterial findings, <i>n</i> (%)	HBoV co-infection, <i>n</i> (%)
	Tunisia				HBoV2B	76 (12%)				
	USA				HBoV3	11 (2%)				
					HBoV4	6 (1%)				
Kantola [68]	Finland	n/g	250	33 children	HBoV1	0 (0%)	yes	8	n/g	0 (0%)
				217 adults	HBoV2	4 (2%)				2 (50%)
					HBoV3	1 (0.4%)				1 (100%)
					HBoV4	0 (0%)				0 (0%)

n, number of samples; HBoV, human bocavirus; qPCR, quantitative polymerase chain reaction; n/g, not given.

^aSelection criteria: PubMed search using key words "bocavirus" and "gastroenteritis" or "gastrointestinal".

^bRecruited during a waterborne outbreak.

in 2007–2008 [36,47,48]. By PCR analysis of respiratory tract secretions, HBoV1 has been found worldwide in approximately 2–19% of patients with upper or lower respiratory disease (Table 1). HBoV1 DNA is mainly detectable in children aged 6–24 months, year-round, yet predominantly during the winter and spring [1,6,10,31,49–62]. HBoV1 is detectable less frequently in other age groups including adults [6,53,56,58,61,63–65]. Data are scarce on the occurrence and consequences of HBoV1 infection among the elderly.

HBoV2, HBoV3, and HBoV4 DNA occur mainly in stool [2–4,18,19,21,66–70], and HBoV2 and possibly HBoV3 are associated with gastroenteritis [2,19,67,69]. Of these enteric species, HBoV2 is the most common with incidences up to 26%, followed by HBoV3 (5%) and HBoV4 (2%). The detection rates in adults (respectively, 4%, 1%, and 1%) appear in some but not all studies to be lower than in children [2,4,19,67–69]. Of the enteric HBoVs, only HBoV2 has in two studies been detected also in nasopharyngeal samples [20,21]. Co-infections by other gastrointestinal viruses have been common (Table 2).

The seroepidemiological studies on HBoV1 are in line with the PCR data. HBoV1 infection is very common during early childhood (Table 3). Because of vertical antibody transfer, seropositivity is common in infants aged <2 months, after which it declines [47,48]. Low antibody detection rates persist up to age 6–12 months after which seropositivity increases until age 6 years, when almost all children have circulating HBoV1 antibodies [9,14,36,39,40,47,48,71,72]. The vast majority of adults seem to have antibodies to HBoV1, in line with the fact that HBoV1 infections are common [14,37,39,43,48,71,73,74]. Gender-specific differences have not been reported [9]. Most HBoV1 antibodies in human sera seem to target the viral capsid protein VP2 [36,37,39,40,48,71,75].

Serological studies have used recombinant HBoV1 capsid proteins as antigen, but have not ruled out cross-reactivity with the capsid proteins of the other three HBoV species [36,46,48,72,106]. Very recently, it has been shown that cross-reactivity with HBoV2–4 immunoglobulin (Ig) G partially accounts for the high HBoV1 seroprevalences of up to 96% that have been reported [76]. When measured after competition with HBoV2–4 virus-like particles (VLPs), only ~60% were IgG positive. Based on the competitive EIA, the prevalences of

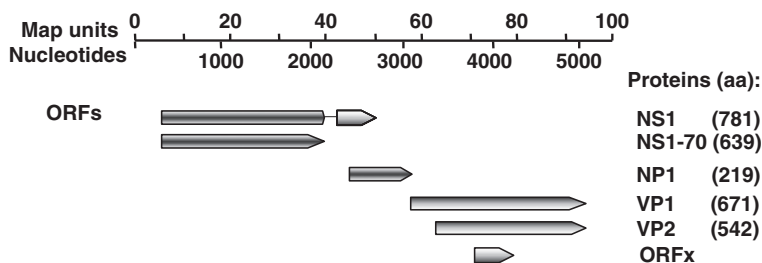


Figure 2. The genome of human bocavirus-1 with major open reading frames and proteins. The linear ssDNA genome is divided in map units and also given as nucleotides. The putative open reading frames (ORFs) are indicated as arrowed boxes, the thin line is an intron gap, and the corresponding proteins detected from transfection are shown on the right side with predicted amino acid lengths. Expression of ORFx has not been determined. Data are simplified from Dijkman *et al.* [42] and Chen *et al.* [44]. VP, viral (structural) protein; aa, aminoacids; NS, nonstructural protein; NP, nuclear phosphoprotein

HBoV infections in humans are likely to be in descending order, HBoV1, HBoV2, HBoV3, and HBoV4.

CO-INFECTIONS

HBoV DNA-positive subjects have a high co-infection rate: in respiratory samples up to 83% and in fecal samples up to 100% (Tables 1 and 2). Accordingly, HBoV1 DNA may be detectable in the nasopharynx of immunocompetent individuals for at least 6 months after infection [14,32,34,35]. Consequently, asymptomatic subjects may show high HBoV1 detection rates; in two studies up to 43–44% and in others lower 0–9% (Table 4). Approximately half of HBoV1-DNA findings have been of low copy number [5,54,77–79].

These data indicate that HBoV may exist in the respiratory or gastrointestinal tracts as a bystander without causality to the current symptoms. We observed that among wheezing children with HBoV1 detected together with other viruses by PCR in nasopharyngeal aspirate (NPA), 64% had serologically verified primary infection, whereas 36% had probably HBoV1 DNA persistence or mucosal contamination without viral replication/immunoactivation [39]. On the other hand, several PCR studies of children and/or adults including asymptomatic controls have shown an association between presence of the virus and symptomatic illness [6,10,50,58,60,62]. In many studies, a positive correlation was seen between respiratory illness and high copy numbers of HBoV1 DNA or the presence of HBoV1 mono-infection [5,10,14,40,58,77,79,80]. These multiple pieces of evidence strongly suggest that HBoV is an important respiratory pathogen in children.

TRANSMISSION

The transmission routes of human bocaviruses are unknown. However, many parvoviruses are transmitted by inhalation or contact with infectious sputum, feces, or urine [81]. It is likely that HBoV1 is transmitted similarly, as its DNA has been detected in many human secretions. Nosocomial respiratory acquisition may be as high as 18% among hospitalized HBoV1 cases, and up to 19% of nosocomial acute respiratory tract infections have been HBoV1 positive [50,56,82–84]. Intrauterine infection is unlikely because of the high degree of immunity among pregnant mothers [73,74].

TARGET ORGANS AND PATHOGENESIS

The pathogenesis of human bocaviruses is not known because no well established *in vitro* or animal models are available [41,42,44,85]. HBoV1 has, however, been cultured in primary airway epithelial cells differentiated into pseudo-stratified human airway epithelium [42]. Based on HBoV1 DNA sequences detected in that culture and in HBoV1-positive clinical samples, a hypothesis was proposed of HBoV1 having a different replication mechanism than parvoviruses in general [41]. This will, however, need further elucidation. The mechanisms of cell entry and the *in vivo* host range are unknown [41]. Multiple clinical studies suggest that HBoV1 is mainly a respiratory pathogen (Tables 1 and 3). Studies on children with pneumonia, acute wheezing, asthma and/or bronchiolitis suggest that HBoV1 is able to infect the lower airways down to the bronchioles [5,6,36,41,50,86–92]. Some reports show HBoV1 DNA in up to 3% of adult bronchoalveolar lavage (BAL) specimens

Table 3. Clinical studies on acute human bocavirus-1 infection using serodiagnosis in patients with respiratory symptoms^a

1st author	Study site	Study year	Age (years)	Methods	NPA PCR+, <i>n</i> (%)	Serodiagnosis of NPA PCR + cases, <i>n</i> (%)	Serum PCR+, <i>n</i> (%)	Serodiagnosis of serum PCR + cases, <i>n</i> (%)	Serodiagnosis of cases with respiratory symptoms, <i>n</i> (%)
Endo [47]	Japan	06–07	0.2–6	IgGsc	8	4/4 (100)	4	4/4 (100)	n/g
Lindner [37]	Germany	n/g	0.1–10	IgM	n/g	n/g	24	10 (42)	n/g
Lin [71]	China	06 children		IgGsc	5	3 (60)	n/g	n/g	n/g
Söderlund-Venermo [39]	Finland	00–02	0.3–6.1	IgM, IgGsc	49 (any) 28 (high) 27 (low)	35 (71) 27 (96) 8 (38)	49	45 (92)	48/253 (19) ^b
Wang [14]	China	06–08	0.5–9	IgM	36 (sole) 43 (co-infected) 22 (high load)	26 (69) 18 (42) 16 (73)	21	15 (71)	44/79 (56) ^c
Don [38]	Italy	01–02	0.1–15	IgM, IgGsc	n/g	n/g	n/g	n/g	12/101 (12) ^d
Karalar [9]	Germany	06–07	0.1–15	IgM	n/g	n/g	22	16 (73) ^e	n/g

n, number of samples; NPA, nasopharyngeal aspirate; PCR, polymerase chain reaction; IgGsc, IgG seroconversion; n/g, not given.

^aSelection criteria: PubMed search using key words “bocavirus” and “serology”.

^bAcute wheezing.

^cLaryngitis 19%, bronchitis 5%, bronchiolitis 22%, bronchopneumonia 21%, asthma 21%, and other 12%.

^dPneumonia.

^eIgM positive (*n* = 10) or weakly positive (*n* = 6).

Table 4. Human bocavirus-1 detection by PCR in respiratory samples in asymptomatic subjects^a

1st author	Study site	Study year	n	Age (years)	Sample type	HBoV1+n (%)	HBoV1 qPCR done	Viruses or microbes tested	Mixed viral or bacterial findings, n (%)	HBoV1 co-infection, n (%)	Comparison between HBoV1+ symptomatic and HBoV1+ asymptomatic subjects
Kesebir [50] Fry [6]	USA	04	96	<2	respiratory	0 (0)	no	8	n/g	—	—
	Thailand	04–05	280	all ages	NPS	3 (1)	yes	14	n/g	1 (33)	HBoV1 was found more often in pneumonia cases than controls. All controls had low viral loads.
Maggi [54]	Italy	01 03	30 21	infants and school-aged	respiratory	0 (0)	no	11	n/g	—	—
Chiochansin [101]	Thailand	05–06	202	0.2–5	stool	0 (0)	no	2 ^b	n/g	—	Prevalence: NS
Longtin [61]	Canada	02–03	100	children	NPS	43 (43)	no	5 ^b	n/g	n/g	HBoV1 was found more often in asymptomatic (43%) than symptomatic (14%) cases.
García-García [60]	Spain	04–06	116	<14	NPS	8 (7)	no	16	5 (3)	4 (50)	—
Cheng [31]	China	06–07	115	<5	stool	4 (4)	yes	8 ^b	n/g	n/g	Prevalence: NS viral load: NS
von Linstow [32]	Denmark	04–06	152	<1	nasal	13 (9)	yes	13	n/g	n/g	Consecutive positive specimens contained decreasingly lower viral loads.
Brieu [58]	France	06–07	68	<5	NPS	0 (0%)	yes	9 ^b	n/g	—	—

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Table 4. (Continued)

1st author	Study site	Study year	n	Age (years)	Sample type	HBov1+n (%)	HBov1 qPCR done	Viruses or microbes tested	Mixed viral or bacterial findings, n (%)	HBov1 co-infection, n (%)	Comparison between HBov1+ symptomatic and HBov1+ asymptomatic subjects
Arthur [2]	Australia	01	186	<17	stool	15 (8%)	no	multiple	15 (8%)	n/g	HBov1 was not associated with acute gastroenteritis. Prevalence: NS
Martin [12]	USA	07-08	56	2-4	saliva	5 (9)	yes	0	n/g	n/g	
Martin [35]	USA	06-08	45	0-2	nasal	20 (44)	yes	15	n/g	n/g	Prevalence: NS
Christensen [10]	Norway	07-09	162	children	NPS	27 (17)	yes	18	n/g	25 (93)	qPCR: NS HBov1 monoinfections were more prevalent in patients (29%) than controls (7%) but an adjusted analysis found no association to symptoms.

n, number of samples; HBov1, human bocavirus; n/g, not given; NPS, nasopharyngeal secretion; NS, non-significant.

^aSelection criteria: PubMed search using key words "bocavirus" and "asymptomatic", or "bocavirus" and "control".

^bRhinovirus PCR was not included.

[54,64,65,93,94]. In follow-up of adult lung transplant recipients, BAL HBoV1-positive cases seem to be symptomatic (mainly pneumonia or acute respiratory insufficiency), with no difference in HBoV1 prevalence between immunocompetent and immunocompromised patients, whereas non-symptomatic surveillance samples seem to be HBoV1-DNA negative [64,95]. This would further indicate that HBoV1 is not a bystander but rather a real but rare, causative agent of adult respiratory symptoms.

HBoV1 infection appears to be systemic as suggested by the occurrence of its DNA in serum [5,9,10,14,36,39]. Although HBoV1 viremia/DNAemia has been linked closely to acute primary infection and moderate-to-severe illness [10,36,39], more detailed clinical correlates of HBoV1 dissemination are hitherto unknown.

Human bocaviruses have been detected in fecal samples without evidence of replication in the gastrointestinal epithelium. On the contrary, passive spread of HBoV1 from the respiratory to the gastrointestinal tract is likely because the levels of HBoV1 DNA in stool have been low, the detection rates between subjects with and without gastrointestinal symptoms have been similar, and the detection rates (of up to 100% in stool samples) of co-pathogens (gastrointestinal viruses and bacteria) have been high (Table 2) [2,4,19,30,31,33,68,69,96–102]. On the other hand, HBoV1 has been detected in stool also when the corresponding respiratory samples have been negative or there have been no symptoms other than gastroenteritis [97,103]. However, the more recently discovered HBoV species 2–4 may be true enteropathogens with detection rates in stool (especially for HBoV2) generally higher than HBoV1, and with predominant appearances in stool [2,4,68]. The notion that HBoV1, but not HBoV2, may spread from the respiratory to the gastrointestinal tract, is also supported by a study comparing stool samples of symptomatic patients and age-matched controls, with a difference in detection rate only for HBoV2 [2].

Aside of circulating antibodies, knowledge of other host defense mechanisms against HBoV is just beginning to emerge. Three studies have investigated cytokine responses either in NPA samples or in cultures of peripheral blood mononuclear cells stimulated by recombinant HBoV1 VP2 VLPs [104–106]. Because HBoV is difficult to cultivate [42,44], recombinant technology has been needed

to engineer the antigens of interest. *In vitro*, HBoV1 VP2 VLPs have induced IL-13, interferon-gamma and IL-10 responses in CD4+ T cells [105,106]. HBoV1 DNA-positive NPAs of children with bronchiolitis relative to those of asymptomatic controls have shown increased levels of the T helper (Th) 1 and Th2 cell cytokines interferon-gamma, IL-2 and IL-4 [104]. However, the levels of IL-10 and TNF-alpha were lower in children with HBoV1-induced than RSV-induced bronchiolitis. These findings suggest that HBoV1 can elicit typical virus-induced immune responses involving both Th1 and Th2 cells.

PERSISTENCE

An interesting feature with HBoV1 is that its presence in the mucosa may be rather long-lasting; however, no in-depth studies regarding the mechanism are available [34,35,58,107]. Prolonged shedding or presence of virus in the airways could explain the high co-infection rate observed in numerous studies [34,35,58,107,108].

With HBoV1, unlike with other parvoviruses such as parvovirus B19V and the adeno-associated virus 2 (AAV2) [109–112], the available data speak against a disseminated genomic long-term tissue persistence in the human body [113,114]. HBoV1 might, however, have a more narrow tissue tropism for its persistence; in one study, high HBoV1 detection rates (up to 32%) were encountered among tonsillectomy patients suggesting that lymphatic tissue might be a persistence site [11]. Of note, a rather high detection rate (18%) of HBoV1 has been reported also in tissue samples of chronic sinusitis [115].

HBoV3 DNA has been detected in an episomal form in the ileum of a child with gastrointestinal symptoms [116]. Whether this episome is a storage form or a replicative intermediate in an alternative replication model [41,116], needs to be elucidated. Episomal genomes have been detected also in AAV2 *in vivo* persistence [111], even though genomic integration was common in cell culture [117]. It is further unknown, whether persistent HBoV, like AAV2, can establish latency and whether co-infection by other viruses in that case can be “helper viruses” and reactivate the dormant HBoV genomes, which also would contribute to the prevalent co-detections.

Another possible research topic is to assess whether proteins are produced without virus replication as observed for adenovirus, another DNA virus, in patients with chronic lung conditions

[118–121]. Contrary to many other parvoviruses, however, bocaviruses seem to cause apoptosis only if replicating, and the genome itself is needed to cause a cell-cycle arrest at the G₂/M phase, whereas mere protein expression is not enough [122].

DIAGNOSIS

The diagnoses of HBoV infections reported in clinical association studies have been based almost exclusively on PCR. However, PCR is not an optimal diagnostic method because of prolonged positivity both in respiratory and gastrointestinal tracts especially in low copy numbers as discussed earlier, leading to high detection rates in asymptomatic subjects.

Primary infections diagnosed serologically or by the presence of HBoV1 DNA in serum have been linked to respiratory symptoms (Table 3) [5,9,10,14,36,39]. In one study, 94% of wheezing children with HBoV1 serodiagnosis were viremic, and 92% of viremic children showed a serodiagnosis [39]. In another study, 61% of viremic children had HBoV1-specific IgM [9]. The study also showed that 10% of patients with respiratory disease had HBoV1 viremia (upper respiratory tract disease 5%; lower respiratory tract illness 15%; pneumonia 10%), as had 8% of the patients with gastrointestinal disease. The diagnostic sensitivity of HBoV DNA detection in serum has, however, not yet been determined, nor has the precise duration of viremia/DNAemia in connection with primary infection. Serum PCR may necessitate precise timing of the sample collection.

Another question of importance is whether, or to what extent, DNA quantitation does improve HBoV diagnosis. Studies employing patient DNA stratification based on HBoV1 load in the nasopharynx have shown a correlation between load height and fewer co-infections as well as increased illness severity [5,10,58,77,79,80]. Especially very high viral loads in NPA ($>2 \times 10^8$ genomes/ml) were linked with respiratory symptoms [10]. In a study on wheezing children, 96% of those with a high load ($>10^4$ genomes/ml) of HBoV1 DNA in nasopharynx (100% with high load and sole HBoV1 infection) had in serum HBoV1 IgM or an IgG increase [39] compared with only 38% of those with a low DNA load. As some other studies failed to show an association between symptoms and HBoV copy numbers, further work is needed on

the diagnostic utility of HBoV DNA quantification in the respiratory tract [9,35,79].

Serologic studies on children with acute respiratory symptoms have shown that the mere presence of HBoV1 DNA in the respiratory tract is not reliable proof of acute primary HBoV1 infection (Table 3). Even among a clinically selected cohort did only 71% of NPA HBoV1 PCR-positive children (and 6% of the PCR-negative) exhibit a serodiagnosis [39]. Although the clinical significance of HBoV1 in co-detection with other viruses in NPA has been questioned, over half of the NPA PCR-positive wheezing children co-infected with another virus did have an acute primary HBoV infection [39].

IgG avidity EIA has been set up for even more accurate diagnosis of HBoV1 infection [40]. By measuring IgG avidity that increases along the maturation of B cells, it is possible with a single serum sample to distinguish between acute and past infections, or between primary and secondary infections or immunoactivations. The latter were observed in large numbers among adults over several years of follow-up [40]. However, the contribution to past-immunity findings like these of antigenic cross-reactivity between the four bocaviruses must be kept in mind [76].

Serology and/or HBoV1-DNA detection in serum is essential for the verification of acute HBoV1 infection-induced illness. Application of these stringent diagnostic methods will be crucial for further studies on the impact of HBoV1.

CLINICAL FEATURES

Although a causal link between HBoV1 and respiratory disease has been reported in a number of studies [5,10,14,38,39], the exact clinical pictures await determination. A vast number of papers have reported HBoV1 in the context of acute respiratory illnesses including common cold, asthma, acute wheezing, bronchiolitis, pneumonia, acute otitis media, and even plastic bronchitis [5–7,13,14,34,49–53,55,61,62,83,86,87,123–138]. It is not possible to clinically differentiate between respiratory tract infections caused by different viruses such as rhinovirus, RSV, human metapneumovirus, influenza virus and HBoV1, or even bacteria [139]. Some distinct clinical features have, however, been reported: hypoxia and neutrophilia were more severe in HBoV1-positive than RSV-positive children with lower respiratory tract illness [62]. In a recent review, the prevalences of respiratory manifestations in NPA

HBoV1 PCR-positive children included cough 79%, fever 67%, rhinorrhea 66%, oxygen therapy or hypoxia 40%, tachypnea 35%, wheeze 27%, pharyngitis 13% and other respiratory symptoms 48% (includes respiratory distress, increased work of breathing, cyanosis, apnea, rales and shortness of breath) [107]. However, because most studies are based on samples drawn for diagnostic purposes from children seeking hospital care for acute respiratory tract infection, these numbers to a large extent reflect the symptoms of the entire study population. In addition, most studies behind these numbers lack stringent criteria for HBoV1 laboratory diagnosis. In a study combining serum PCR and serodiagnostics in children, with various infectious and non-infectious diseases, only lower respiratory tract symptoms correlated with HBoV1 [9]. Among children with acute otitis media, HBoV1 DNA has been found in the nasopharyngeal aspirates in 6% and in the middle ear fluids in 3–4% of cases [140–142].

Signs of pneumonia, that is, patchy or interstitial infiltrates in chest radiography, and lung hyperinflation, peribronchial cuffing, or atelectasis appear

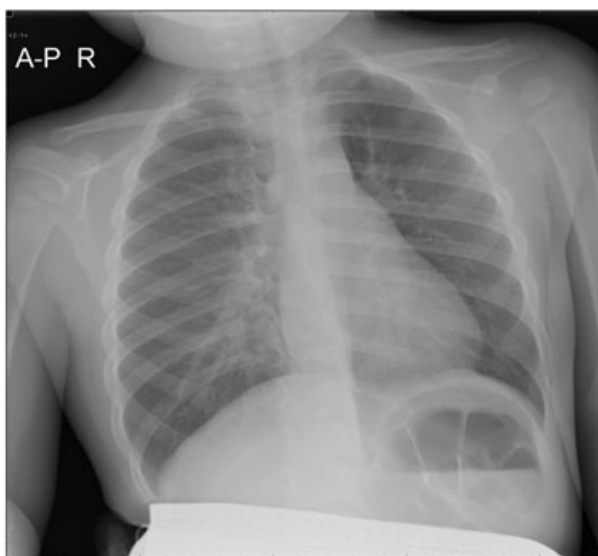


Figure 3. Radiograph of pneumonia and interstitial infiltrates in a 1.7-year old girl. Sole HBoV1-infection was serologically confirmed (16 respiratory viruses and four respiratory bacteria were searched by PCR from induced sputum samples, and *Mycoplasma* serology was performed). White blood cell count was $11.6 \times 10^9/L$, and serum C-reactive protein was 16 mg/L. Duration of respiratory symptoms was 6 days before hospitalization; during hospitalization, symptoms included fever, cough, and dyspnoea. The radiograph was kindly provided by Dr. Elina Lahti from the Department of Pediatrics, Turku University Hospital, Turku, Finland

to occur commonly (up to 43–83%) in association with pediatric HBoV1 infection, whereas lobar infiltrates or pleural effusion occur rarely (Figure 3) [1,38,50,83,127,133,138,143,144]. No radiographic sign, however, is pathognomonic for HBoV1. In one study, 18% of induced sputum samples from children with pneumonia contained HBoV1 DNA [146]. The problems discussed earlier associated with diagnosing HBoV1 infections by PCR in respiratory tract secretions must be taken into account when interpreting such data. Don *et al.* (2010) found serologically confirmed acute HBoV1 infection in 12% of children with pneumonia [38]. In all, the only symptoms that have been statistically associated with HBoV1 or confirmed by serodiagnosis are lower respiratory tract symptoms, in particular wheezing and pneumonia [5,6,10,38,39]. No study has so far provided statistical evidence for an association between HBoV1 and gastrointestinal disease, whereas one study indicated that HBoV2 is associated with gastroenteritis [2]. Other symptoms such as rash or exanthema, thrombopenia, clinical sepsis or life-threatening events have been rare in HBoV1-affected patients [50,137,145]. Blood counts and C-reactive protein levels are usually normal [49,50,125,133], whereas increased neutrophilia has been noted [62].

In one study, 31% of 16 children with Kawasaki disease harbored HBoV1 DNA in serum, cerebrospinal fluid or stool compared with 5.5% of 579 controls [146]. This association was not confirmed in a more recent study in which HBoV1 infections were diagnosed serologically; comparable seroprevalences of HBoV1-specific IgG and IgA were found between the Kawasaki cases and controls [147]. Similarly, another study using HBoV1 PCR on serum samples showed no positive findings in 12 Kawasaki patients [20].

RISK FACTORS

HBoV infection seems to produce a long-lasting, high-avidity IgG antibody response [39,40]. Thus, a lack of protecting B-cell immunity might increase the risk of HBoV infection. Risk factors for severe HBoV1-associated illness have been considered to be similar to those for common respiratory viral infections: underlying chronic medical conditions such as cardiac disease (congenital heart lesions or heart failure) or pulmonary disease (asthma or chronic obstructive pulmonary disease), prematurity with chronic lung disease and immunosuppression

[1,8,49,50,54,56,61,64,65,69,92,93,133,148–155]. In immunocompromised subjects, the detection of HBoV1 DNA in respiratory samples has been associated with fever, lower respiratory symptoms, seizures, hepatitis and gastrointestinal symptoms [149,151,155]. However, the extent of risk is not clear because the detection rates of HBoV1 in immunocompromised subjects have also been similar to those in immunocompetent subjects, and in most studies, the infections have not been confirmed by serum PCR or serodiagnostics. Young age can also be considered a risk factor because HBoV1 viremia occurs most commonly in children <2 years [10]. Among infants, risk factors for HBoV1-associated respiratory illness have included maternal smoking, winter birth time, and asthma predisposition [32,153]. Large day care groups increase the risk of HBoV infection because they likely are a main reservoir of HBoV. Maternal antibodies apparently protect young infants [47,48]. Atopy (i.e. allergen-specific sensitization) was not associated with HBoV1 infection among wheezing children [156]. Finally, contact with sewage or river water may also increase HBoV infection frequency [15–17].

TREATMENT

No comparative studies exist of antiviral agents for treatment of HBoV infection. Prednisolone was found not to be effective in a *post hoc* analysis of a randomized controlled trial on wheezing children with serologically confirmed HBoV1 infection [157]. Supportive care is the current treatment of choice. Although HBoV1 has been associated with lower respiratory symptoms, the course of HBoV disease

is often self-limiting and uncomplicated. Moreover, no specific preventive measures are available.

CONCLUSIONS

Overall, a great deal of data is available on HBoV1, whereas little is known about the other human bocavirus species. Although most studies have been based on PCR detection of HBoV1 in respiratory tract secretions, only a few have confirmed the HBoV1 diagnosis by serology or PCR in serum, the diagnostic procedures of choice. If HBoV serology or serum samples for PCR are not available, the probably next best option is quantitative PCR with a cutoff of $>10^4$ HBoV1 genomes/ml of nasopharyngeal aspirate. Diagnosis should not be based on qualitative PCR in respiratory or gastrointestinal samples because of the persistence or recurrence of HBoV1 DNA. Despite these diagnostic challenges, it is becoming increasingly evident that HBoV1 is an important respiratory pathogen. Application of stringent diagnostic methods and criteria will be crucial not only for clinics but also for further research on HBoV.

CONFLICT OF INTEREST

The authors have no competing interest.

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