Case Report

Latent infection of human bocavirus accompanied by flare of chronic cough, fatigue and episodes of viral replication in an immunocompetent adult patient, Cologne, Germany

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Introduction: The human bocavirus (HBoV) is a parvovirus and is associated with mild to life-threatening acute or persisting respiratory infections, frequently accompanied by further pathogens. So far, there is limited knowledge on the mechanisms of persistence, and no reports on chronic infections or latency have been published so far.

Case presentation: An immunocompetent male patient suffers from a chronic HBoV1 infection, i.e. viral DNA was detected in both serum and bronchoalveolar lavage (BAL) for >5 months without co-infections and with respiratory symptoms resolved spontaneously while receiving symptomatic treatment with montelukast and corticosteroids. Following the symptomatic medication of a chronic infection with HBoV1 viraemia indicating active viral replication lasting over 5 months, the patient cleared the viraemia and no further viral DNA was detectable in the BAL. However, by fluorescence in situ hybridization analyses of mucosal biopsies, it was shown that the virus genome still persisted in the absence of viral shedding but in a more compact manner possibly representing a supercoiled episomal form of this otherwise linear single-stranded DNA genome. This indicated the entry into a latency phase. Moreover, the cytokine profile and the IP-10/TARC ratio, a marker for fibrotization, seem to have been altered by HBoV1 replication. Although specific IgG antibodies were detectable during the whole observation period, they showed an apparently insufficient neutralising activity.

Conclusion: On the one hand, these findings suggest that the symptomatic medication may have led to clearance of the virus from blood and airways and, moreover, that the viral DNA persists in the tissue as an altered episomal form favoured by lacking neutralising antibodies. This appears to be important in order to reduce possible long-term effects such as lung fibrosis.

Keywords: human bocavirus; chronic persistence; chronic cough.

Introduction

In the majority of clinical studies and single cases described and observed so far, the human bocavirus (HBoV) type 1 HBoV1 was associated with mild to severe acute or persisting respiratory infections and symptoms ranging from the common cold to life-threatening pneumonia, mainly in children but occasionally also in adults (Allander, 2008; Garcia-Garcia et al., 2010).

Because no animal model is available so far due to the narrow host range of the virus, clinical cases, besides in vitro

Abbreviations: BAL, bronchoalveolar lavage; EIA, enzyme immunoassay; FISH, fluorescence in situ hybridization; HBoV, human bocavirus.
studies in cell cultures, remain the major source of information about the pathogenesis of this virus. One feature of HBoV appears to be its ability to establish a latent stage or even chronic infection (Byington et al., 2015; Kaur et al., 2014; Schildgen et al., 2013; Windisch et al., 2013; Deng et al., 2014; Manning et al., 2007; Schenk et al., 2011). Therefore, the presented case is of major importance; as for the first time, we describe an HBoV1-associated chronic respiratory infection in detail, provide evidence for clinical improvement following symptomatic treatment, gain insight into the molecular mechanisms of viral persistence and immune evasion of the virus and provide evidence that the chronic infection with HBoV can include flares of active viral replication followed by symptom free latency.

Case report

The patient was a 29-year-old never-smoker Caucasian male, who came to our out-patient clinic because of chronic cough of so far unknown origin resistant to previous antimicrobiotic treatment. When presenting first in May 2013, the patient had symptoms of a persisting pharyngitis; from this time point on, he suffered from a worsening of his cough, which became chronic and persisted until January 2015. In addition, the patient described chronic fatigue that prevents the patient from practising his profession as a percussionist.

Bronchoscopy confirmed an acute tracheobronchitis in February and June 2014. Thereby, macroscopically mucosal lesions in the hypopharynx were observed in June 2014, and a biopsy was taken in June 2014.

In February 2014, a mild alveolitis with increased lymphocyte subsets was confirmed in the BAL, and in both BALs from February and June 2014, HBoV1-DNA (>10^5 copies per millilitre) was detected by quantitative PCR (qPCR) in both cases accompanied by a viraemia verified by detection of viral DNA in corresponding serum samples independently in Cologne and Helsinki. The copy numbers in the BALs were analysed for facultative and obligate respiratory bacteria as well as viruses and fungi by the Respifinder Smart 22 and Meningofinder Custom Assays (i.e. the standard Meningofinder plus mumps and measles probes, Pathofinder). The Respifinder and Meningofinder assays were previously described as suitable and sensitive tools by our group and others (Kaur et al., 2014; Hardt et al., 2014; Wolffs et al., 2009; Dabisch-Ruthe et al., 2012; Raymaekers et al., 2011). In detail, the patient’s BAL was tested for influenza viruses, parainfluenza viruses 1–4, RSV, HMPV, HBoV1, coronaviruses NL63, OC43, 229E and HKU-1, adenoviruses, Mycoplasma pneumoniae, human parechoviruses, rhinoviruses and enteroviruses, Legionella pneumophila, Chlamydia pneumoniae and Bordetella pertussis by Respifinder; mumps, measles, herpes simplex 1, herpes simplex 2, varicella zoster virus, Epstein Barr virus, cytomegalovirus, enterovirus and parechovirus by Meningofinder; Pneumocystis jirovecii by PCR (Schildgen et al., 2014); and Aspergillus by ELISA (BioRad). Human herpesviruses 1–8 were also tested by qPCR as previously described (Windisch et al., 2013). In addition, qPCR for quantification of HBoV1 was performed as previously described using the Qiagen QuantiTect Sybr Green Kit (Qiagen) using primers HBoV-Ku1 and HBoV-Ku2 followed by melting curve analyses (Kaur et al., 2014; Kupfer et al., 2006). Mycobacteria were tested by the MYCO-Direct 1.7 assay (Chipron). Routine culturing, including culturing of anaerobic pathogens, was performed by a microbiology laboratory. The laboratory results for viruses were further confirmed by the University Hospital Bonn, where also an immunodeficiency was excluded and normal immune cell counts and antibody titres were confirmed.

So far, as there is limited information about the local inflammation processes during an HBoV infection in vivo, we decided to retrospectively test the two BAL fluids of which aliquots were archived at −80 °C for the presence of cytokines, and we compared them to a BAL sampled in January 2015, in which no HBoV1-DNA was detected anymore. Therefore, the Abcam Cytokine Human Membrane Antibody Array (80 Targets, ab133998) was used as previously described (Khalfaoui et al., 2016). The method detects the cytokines ENA-78, GCSF, GM-CSF, GRO, GRO-alpha, I-309, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-10, IL-12 p40/p70, IL-13, IL-15, IFN-gamma, MCP-1, MCP-2, MCP-3, M-CSF, MDC, MIG, MIP-1beta, MIP-1delta, RANTES, SCF, SDF-1, TARC, TGF-beta1, TNF-alpha, TNF-beta, EGF, IGF-I, Angiogenin, Oncostatin M, Thrombopoietin, VEGF-A, PDGF-BB, Leptin, BDNF, BLC, Ck88-1, Eotaxin, Eotaxin-2, Eotaxin-3, FGF-4, FGF-6, FGF-7, FGF-9, Fli-3 Ligand, Fractalkine, GCP-2, GDNF, HGF, IGFBP-1, IGFBP-2, IGFBP-3, IGFBP-4, IL-16, IP-10, IIF, LIGHT, MCP-4, MIF, MIP-3 alpha, NAP-2, NT-3, NT-4, Osteopontin, Osteoprotegerin, PARC, PLGF, TGF-beta2, TGF-beta3, TIMP-1 and TIMP-2, respectively.

Moreover, the hypophysyegal biopsies were tested for intracellular HBoV1-DNA by fluorescence in situ hybridization (FISH) as previously described (Schildgen et al., 2013). HBoV1-specific IgM and IgG antibodies were assayed in
serum samples obtained in February and June 2014 by competitive enzyme immunoassay (EIA) (Kantola et al., 2011). The ODs measured in this ELISA were 1.589 for HBV-1 IgG and 0.049 for HBV-1 IgM in February, followed by 1.625 HBV-1 IgG and 0.051 for HBV-1 IgM in June, both indicating a past immune reaction.

In both BAL samples from February and June 2014, all tested pathogens that could have contributed to the clinical symptoms were repeatedly excluded except HBV1, whose DNA was repeatedly detected by the Respifinder. The corresponding sera were tested positive at the analytic borderline of both the qPCR and the Respifinder assay performed in Cologne and below the limit of detection in the qPCR performed in Helsinki. Furthermore, the patient had medium EIA absorbances (1.639 and 1.264) of HBV-1-specific IgG antibodies with high avidity at both serum-collection points but was negative for IgM, indicating past immunity.

So far, it was shown by Kapoor et al. and our group that the HBV-DNA can occur not only as a single-stranded DNA molecule but also as a covalently closed circular DNA (Kapoor et al., 2011; Lusebrink et al., 2011). Thereby, the Right-End-Hairpin sequence represents the ‘head’-sequence while the Left-End-Hairpin represents the ‘tail’-sequence (Schildgen et al., 2012).

Besides the exclusive detection of HBV-DNA in BAL and serum in February and June 2014, viral episomes were detected in the hypopharyngeal biopsy from June 2014 (Fig. 1a). These episomal structures were still present in the second biopsy from January 2015 (Fig. 1b), although the viraemia was cleared and the macroscopic inflammation signs were no longer present at that moment; thus, in January 2015, an objective improvement was clinically measurable, although the virus still persisted in the mucosal biopsies. Surprisingly, the HBV FISH signals in the biopsy from January had a different shape compared to the first biopsy taken in June 2014. In June 2014, both the head (green) and the tail (red) signals were adjacent to each other but clearly divided, whereas in January 2015, the head and tail signals show an overlay and appear as yellow signals (Fig. 1b). Additionally, in some cases, single red signals occur. The most likely structural explanation for the FISH result is shown in Fig. 1c, which shows a scheme how the red and green FISH signals are localized on the viral genomic DNA in its putative forms (Fig. 1c).

Simultaneously with the disappearance of HBV1-DNA from BAL and serum, the majority of cytokines was downregulated in the BAL, such as RANTES, IL-3, IL-8, IL-10, NAP-2, TIMP-1 and IP-10 (Fig. 2), while expressions of RANTES, NAP-2, Eotaxin-2, TIMP-1, TNF-α and TNF-β remain at the same level in the HBV-negative compared to the HBV-positive serum. Moreover, the TARC/IP-10 increased during the HBV infection in BAL (BAL_{Feb14} : 0.28; BAL_{Jun14} : 0.34; BAL_{Jan15} : 0.85) as well as in the serum (SER_{Jun14} : 0.23; SER_{Jan15} : 0.92), even when the viral DNA disappeared in BAL and serum. Altogether, the cytokine profiles observed in the stage of active replication followed by vanishing of the virus resemble the cytokine profile for chronic HBV infections we previously described for a patient cohort and infected CuFi-8 cell cultures (Khalfaoui et al., 2016).

**Diagnosis**

The sole pathogen detected was the HBV as described in the case presentation.

**Treatment**

The patient was treated with montelukast and inhalative budesonide for 6 months (from July 2014 to January 2015) (Cai et al., 2012) and subsequently controlled in January 2015. In this control check, the macroscopic mucosal lesions were not observed anymore, the patient displayed no objective signs of an airway infection or inflammation of respiratory epithelia, no pathogens were detected anymore in the BAL and the patient’s serum tested negative for HBV1-DNA. This check-up was accompanied by sampling of a follow-up hypopharyngeal-bronchial biopsy also showing a recurrent finding.

**Outcome and follow-up**

At the end of the observation period of our hospital, the patient appeared in increasing clinical condition before he changed to another ambulant care.

**Discussion**

The present case is indeed important as it is a further confirmation of the hypothesis that HBV is able to persist, also in otherwise healthy patients; beyond this, the present case report allows the conclusion that the virus not only can enter a phase of latency but also can actively replicate, the latter phase being accompanied by clinical symptoms. Here, not only the virus was shed for an unusual long time in the airways as already described by others (Martin et al., 2010; Martin et al., 2015; Byington et al., 2015) but also the otherwise short-lived viraemia lasted here over 5 months. Additionally, FISH staining revealed most likely an episomal DNA structure in the respiratory mucosa, which could display a persisting form of the virus. The DNA occurred in different shapes that may be compatible with the replication stage. In June 2014, both the head signal and the tail signal were adjacent to each other but clearly divided, indicating a relaxed form of the circular DNA, maybe due to active viral replication, whereas in January 2015, the signals show an overlay and appear as yellow signals possibly indicating a supercoiled form that is not actively replicating. Some single red signals were also detected, which presumably represent deletion forms of the viral genome. The FISH results are consistent with the fact that, in January 2015, both the viraemia and the BAL were cleared, while the previous investigations were both tested positive for HBV1-DNA.
Although the detected viraemia was weak, there is a high likelihood that HBoV contributed to the clinical symptoms as the virus was the single respiratory pathogen detected in the patient. One can assume that HBoV1 replication took place topical in the mucosal tissue where the viral DNA persisted, what is supported by the fact that HBoV also replicates in foci in cell culture (Dijkman et al., 2009). This would also explain the low-level DNA amounts in asymptomatic blood donors, in whom viral DNA could circulate in low amounts as long as the virus persists and infected cells would be released to the blood stream (Bonvicini et al., 2011).

Moreover, the patient displayed the persistent viraemia despite the presence of specific antibodies. Although the corticosteroids therapy could have transiently affected the immune system, it must be taken into account that it may be possible that, HBoV1 does not induce neutralising antibodies during the infection or triggers a so far unknown immune-escape mechanism.

Besides, it is worth noting that the patient had a leaky gut syndrome as well as a history of a myocarditis from which he recovered because, in previous HBoV cases, we have detected HBoV-DNA post-mortem also in the myocardic tissue in patients that died from idiopathic lung fibrosis (Windisch et al., 2013); thus, a causal link is possible and requires further attention.

As previously discussed, the Th2 response in the lung is accompanied by increased expression levels of IL-4, IL-5, IL-10 and IL-13 and is followed by increased levels of, among others, TARC and RANTES (Berin et al., 2001; Culley et al., 2006). Also in the present case, an increased expression of RANTES and IL-10 besides IL-3, IL-8 and IL-16 was observed in the acute replication period. In contrast, the comparison of sera and BALs reveals a delayed tissue specific increase of Leptin, EGF, VEGF, TNF-α and TNF-β, which are directly or indirectly involved in fibrosing processes. Moreover, the HBoV-specific cytokine profile in the BAL is characterized by an imbalanced TARC/IP-10 ratio leading to the hypothesis that HBoV influences the

![Fig. 1. This figure shows the FISH analysis of biopsies of respiratory mucosa sampled in June 2014 (a) during the phase of active HBoV replication and in January 2015 (b) when blood and BAL were HBoV-DNA negative. Red signals show the HBoV genome’s tail, and green signals show the genome’s head. The arrows indicate the signals. It is obvious that, in June 2014, the signals were nearby each other, indicating an episomal form of the viral genome as described earlier by Kapoor et al. and our group (Kapoor et al., 2011; Lusebrink et al., 2011) but even more condensed in January 2015 when no viral shedding was observed anymore, thus maybe indicating a phase of latency. Panel (c) shows the putative DNA structures and the localization of the FISH signals in the cccDNA/episomal DNA, the condensed/supercoiled form and the relaxed single-stranded genome. The cccDNA thereby corresponds to panel A where active replication was observed, while the supercoiled form corresponds to panel B where no active replication was observed.](image-url)
Th1/Th2 response within the lung. Furthermore, an imbalanced TARC/IP-10 ratio seems to be associated with fibrotic lung diseases and it is worth to mention that the neutralization of TARC leads to a reduction of fibrosis in the animal (Keane, 2008; Belperio et al., 2004). Despite the growing number of hints, more HBoV-positive follow-up cases have to be analysed to confirm HBoV-specific immune response modulation leading to chronic lung diseases.

However, the patient was successfully treated, and although not having lost the virus from the mucosal biopsies, he objectively recovered from the clinical symptoms and, as a matter of evidence-based speculation, the virus replaced active replication with a latency phase, as indicated by the conformational change observed in the FISH analysis.

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References


