Later, 3 other HBov were identified in stool sequences. Analysis of the recovered gene through input sequencing methods specifically

tions.4 It occurs year-round, but most commonly in the winter. HBovV1 is more frequently detected in young children (<2 years of age) than in older children or adults. Limited knowledge of transmission, persistence, establishment of latency, reinfections and reactivations cause uncertainties regarding the epidemiology of HBovV1. Of the enteric bocavirus types, HBov2 is the most prevalent with detection rates of up to 26% in stool samples from children, and 4% from adults.2,3 DNA of HBov3 and HBov4 has been detected in ≤5% of stool samples.

Seroepidemiologic studies have documented that most children have IgG antibodies against HBovV1 by school age.5,6 Differentiation between seroresponses against HBov types 1 to 4 is, however, difficult because of cross-reactivity.7

CLINICAL MANIFESTATIONS

Many studies have reported an association between a respiratory tract infection and HBovV1 detected by PCR in the nasopharynx. Clinical manifestations have ranged from mild upper respiratory tract infections to severe pneumonia. However, because of insufficient diagnostic methods, selected patient populations and lack of control groups, the majority of studies are of limited value. The pathogenetic role of HBovV1 has been challenged by documentation of other viruses in the same samples (up to 90%) and detection of bocavirus also in asymptomatic children. However, there is no documented evidence of establishment of a persistent, latent state by the HBovV1.

EPIDEMIOLOGY

Globally the prevalence of HBovV1 DNA in young children with respiratory tract infections is around 10%, in some studies up to 33%.4 It has been detected predominantly in stool, but the host cell types are not known.2,3 DNA of HBov3 and HBov4 has been detected in ≤5% of stool samples. Seroepidemiologic studies have documented that most children have IgG antibodies against HBovV1 by school age.5,6 Differentiation between seroresponses against HBov types 1 to 4 is, however, difficult because of cross-reactivity.7

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DIAGNOSIS

HBovV1 infections cannot be clinically differentiated from other viral respiratory infections. Bocavirus isolation in tissue culture is not available for diagnostic use. HBov can be readily detected by PCR targeting NS, NP or VP genes, and it is included in several commercially available multiplex respiratory virus PCR panels. Type-specific primers or non-specific primers followed by sequencing of the PCR product can be used for the differentiation between HBov types. Quantitative PCR may be useful for judging the clinical...
significance of bocavirus DNA detection, as higher viral loads correlate with acute infections, fewer coinfections and increased disease severity. Serological methods have been developed to detect bocavirus specific IgM and IgG antibodies by utilizing recombinant capsid antigens or viral-like particles. Past-immunity antibodies toward HBov2 to 4 cross-react with HBov1, this should be corrected by depletion of HBov2–4 reactive antibodies.

Acute HBov1 infection is most reliably diagnosed by detection of DNA in serum by PCR and in respiratory tract samples by quantitative PCR, simultaneously with detection of IgM or a diagnostic IgG response in paired serum samples. The value of a mere positive PCR result in nasopharyngeal sample is questionable, but very high viral copy numbers (>10⁴ HBov1 genomes/mL of nasopharyngeal aspirate) may indicate current illness. HBov2–4 viruses can be detected by PCR in stool and by serology, but correlation of virus detection with illness has not been established.

TREATMENT AND PREVENTION

No specific antiviral treatment or prevention by immunization has been reported. Currently, treatment is supportive and directed by the clinical manifestations. Standard precautions should be applied to limit the transmission of HBov1 by respiratory secretions.

CONCLUSIONS

HBov1 is, according to currently available information, an important causative agent of respiratory tract infections in young children. However, the disease burden caused by HBov1 is not known yet. Diagnosis of HBov1 infections needs critical approach and desirable combination of PCR and serological methods.

REFERENCES