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**Bocavírus humano: características clínicas e epidemiológicas em
crianças com sintomas respiratórios agudos.**

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RESUMO

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As infecções respiratórias agudas são responsáveis por elevados índices de morbi-mortalidade em todo o mundo. Enquanto o vírus sincicial respiratório (RSV) permanece como a principal causa de infecção do trato respiratório inferior (ITRI) em crianças jovens, especialmente nas menores de 12 meses, outros vírus, como o metapneumovírus humano, vírus influenza, vírus parainfluenza, adenovírus e bocavírus humano (HBoV) estão também associados. Desde sua descoberta em 2005, diversos autores relataram a presença de HBoV em pacientes, na maioria crianças, com doença respiratória aguda, com prevalência variando de 1,5% a 19% nos diferentes estudos ao redor do mundo. Durante o período de estudo (março de 2008 a setembro de 2010) foram detectadas 153 amostras positivas para HBoV (14%) de 1113 amostras coletadas, sendo sete HBoV positivos na unidade neonatal. Dentre as 926 amostras incluídas de crianças da comunidade, o HBoV ocupou a terceira posição em frequência de vírus respiratórios detectados, sendo superado apenas pelo vírus sincicial respiratório e pelo rinovírus. Além de frequente causa de hospitalização, a infecção por HBoV é potencialmente grave. Foi observado que as crianças positivas para HBoV eram significativamente mais velhas (média idade 9,7 meses), utilizaram mais antibióticos, apresentaram o diagnóstico de pneumonia com maior frequência (independente da presença de outros vírus coinfectantes) e o de bronquiolite com menor frequência do que as crianças negativas para HBoV. No total de HBoV positivos, três crianças foram a óbito. O HBoV circulou ao longo de todos os meses estudados, com maior prevalência nos meses de maio a agosto. Houve uma elevada taxa de codetecção com os demais 20 vírus respiratórios pesquisados nas amostras de crianças originadas da comunidade. Apenas 16% dos bocavírus humanos positivos não estavam associados a outros vírus. Rinovírus, adenovírus e RSV, em ordem decrescente, foram os agentes com maior frequência de codetecção. A análise filogenética das amostras positivas para HBoV, demonstrou que foram detectados apenas HBoV1 nas amostras de secreção respiratória de crianças hospitalizadas por ITRI. Esse achado contribuiu para a consolidação do bocavírus humano tipo 1 como causador de doença respiratória aguda na população pediátrica.

Palavras-chave: Vírus. Infecção respiratória. Pediatria. Epidemiologia. Biologia molecular. Diagnóstico.

ABSTRACT

Durigon GS. Human Bocavirus: Clinical and Epidemiological Characteristics in Children with Acute Respiratory Symptoms. [Ph. D. thesis (Microbiology)]. São Paulo: Instituto de Ciências Biomédicas, Universidade de São Paulo; 2015.

It is well established that respiratory viruses are an important cause of hospitalizations in young children worldwide. While respiratory syncytial virus (RSV) remains as leading cause of lower respiratory tract infection (LRTI) in young children, especially those under 12 months, other respiratory viruses, such as human metapneumovirus, influenza, parainfluenza, adenovirus and human bocavirus (HBoV) are also present. Since its discovery in 2005, many authors have reported detection of HBoV in patients with acute respiratory infection, mostly children, with prevalence varying from 1.5% to 19% throughout the world. During the study period (March 2008 to September 2010) we detected HBoV in 153 samples (14%) from 1113-screened samples; seven were from the neonatal unit. Among 926 samples included from children with community-acquired infection, HBoV was the third most frequently detected, just after RSV and rhinovirus. Not only was HBoV a frequent cause of hospitalizations, but also a potentially severe disease. Children infected with HBoV were significantly older (mean age 9.7 months), used more antibiotics, had pneumonia more frequently diagnosed (irrespective of presence of other virus coinfection), and bronchiolitis less frequently diagnosed than those negative for HBoV. In all, three children died. Seasonality of HBoV was characterized by year-round circulation with peaks in months of May through August. There was a high rate of co-detection with the other 20 respiratory viruses screened in samples from the community. Only 16% of the HBoV positives were single infections. Rhinovirus, adenovirus and RSV, in this order, were the most frequently co-detected. Phylogenetic analysis of the HBoV positive samples revealed only HBoV1. This finding contributes to consolidate human bocavirus type 1 as cause of acute respiratory infection in pediatric population.

Keywords: Virus. Respiratory infection. Pediatrics. Epidemiology. Molecular biology. Diagnostics.

1 INTRODUÇÃO

Está bem estabelecido que os vírus respiratórios são causas importantes de morbidade em lactentes de todo o mundo (1). Um grande esforço tem sido feito para melhorar os métodos diagnósticos na tentativa de identificar os agentes etiológicos responsáveis pelas principais síndrome clínicas respiratórias, como a bronquiolite e a pneumonia viral. Enquanto o vírus sincicial respiratório (RSV) permanece como a principal causa de infecção do trato respiratório inferior (ITRI) em crianças jovens, especialmente nas menores de 12 meses (2), outros vírus, como o metapneumovírus humano, vírus influenza, vírus parainfluenza, adenovírus e bocavírus humano (HBoV) estão também associados às ITRI (3).

Desde sua descoberta em 2005, diversos autores relataram a presença de HBoV em pacientes, na maioria crianças, com doença respiratória aguda, com prevalência variando de 1,5% a 19% ao redor do mundo (4).

Entretanto, as síndromes clínicas causadas pelo HBoV em crianças pequenas e a participação desse vírus como agente causador de infecção respiratória aguda grave, resultando em hospitalizações, não está totalmente esclarecida. Tampouco a importância e divergência de comportamento do HBoV em populações com alguma comorbidade, que estão cada vez mais frequentes em nosso meio.

Este estudo tem como objetivo descrever os achados clínicos e epidemiológicos do HBoV em uma vigilância prospectiva de hospitalizações de lactentes menores de dois anos por infecções respiratórias agudas em um hospital terciário na cidade de São Paulo.

7 CONCLUSÕES

Durante o período de estudo (março de 2008 a setembro de 2010) foram detectadas 153 amostras positivas para HBoV (14%) de 1113 amostras coletadas, sendo sete HBoV positivos na unidade neonatal. Dentre as 926 amostras incluídas de crianças da comunidade, o HBoV ocupou a terceira posição em frequência de vírus respiratórios detectados, sendo superado apenas pelo RSV e HRV.

Além de frequente causa de hospitalização, a infecção por HBoV é potencialmente grave. Foi observado que as crianças positivas para HBoV eram significativamente mais velhas (média idade 9,7 meses), utilizaram mais antibióticos, apresentaram o diagnóstico de pneumonia com maior frequência (independente da presença de outros vírus coinfectantes) e o de bronquiolite com menor frequência do que as crianças negativas para HBoV. No total de HBoV positivos, três crianças foram a óbito.

O HBoV circulou ao longo de todos os meses estudados , com maior prevalência nos meses de maio a agosto. Houve uma elevada taxa de codetecção com os demais 20 vírus respiratórios pesquisados nas amostras de crianças originadas da comunidade. Apenas 16% dos bocavírus humanos positivos não estavam associados a outros vírus. Rinovírus, adenovírus e RSV, em ordem decrescente, foram os agentes com maior frequência de codetecção.

A análise filogenética das amostras positivas para HBoV, demonstrou que foram detectados apenas HBoV1 nas amostras de secreção respiratória de crianças hospitalizadas por ITRI. Esse achado contribuiu para a consolidação do bocavírus humano tipo 1 como causador de doença respiratória aguda na população pediátrica.

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