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Brief communication

Identification of Human Bocavirus type 4 in a child asymptomatic for respiratory tract infection and acute gastroenteritis – Goiânia, Goiás, Brazil

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ABSTRACT

Human Bocavirus (HBoV) has been identified from feces and respiratory samples from cases of both acute gastroenteritis and respiratory illness as well as in asymptomatic individuals.

The aim of this study was to detect and characterize HBoV from fecal samples collected from hospitalized children aged less than five years old with no symptoms of respiratory tract infection (RTI) or acute gastroenteritis (AGE). The study involved 119 children and one fecal sample was collected from each participant between 2014 and 2015. HBoV was detected using Nested-PCR, and the viral type identified by genomic sequencing. HBoV-4 was identified from one sample obtained from a hospitalized child with soft tissue tumor of the submandibular region. This is the first report of HBoV-4 identification in Brazil, but we consider that this type may be circulating in the country similar to the other types and new investigations are necessary.

Introduction

Human Bocavirus (HBoV), first described in 2005,[1] belongs to the family Parvoviridae, genus Bocaparvovirus and includes four types (HBoV 1–4).[2] The viral genome is composed of linear single-stranded DNA (ssDNA) of about 5 kb[3] with three open reading frames. The first and second regions encode the non-structural proteins, NS1 and NP1, respectively, and the third encodes for VP1/VP2, which form the viral capsid.3 HBoV-1 has been linked to cases of respiratory tract infection (RTI), and types 2 and 3 are mainly detected in feces from children with acute gastroenteritis (AGE) or in asymptomatic cases for both syndromes.[4,5] HBoV-4 has been less reported, but it has been identified in cases of RTI, AGE, and in healthy individuals.[6–8] In Brazil, to our knowledge, types 1, 2, or 3 have been identified in children symptomatic for RTI or AGE.[9–12] Moreover, to

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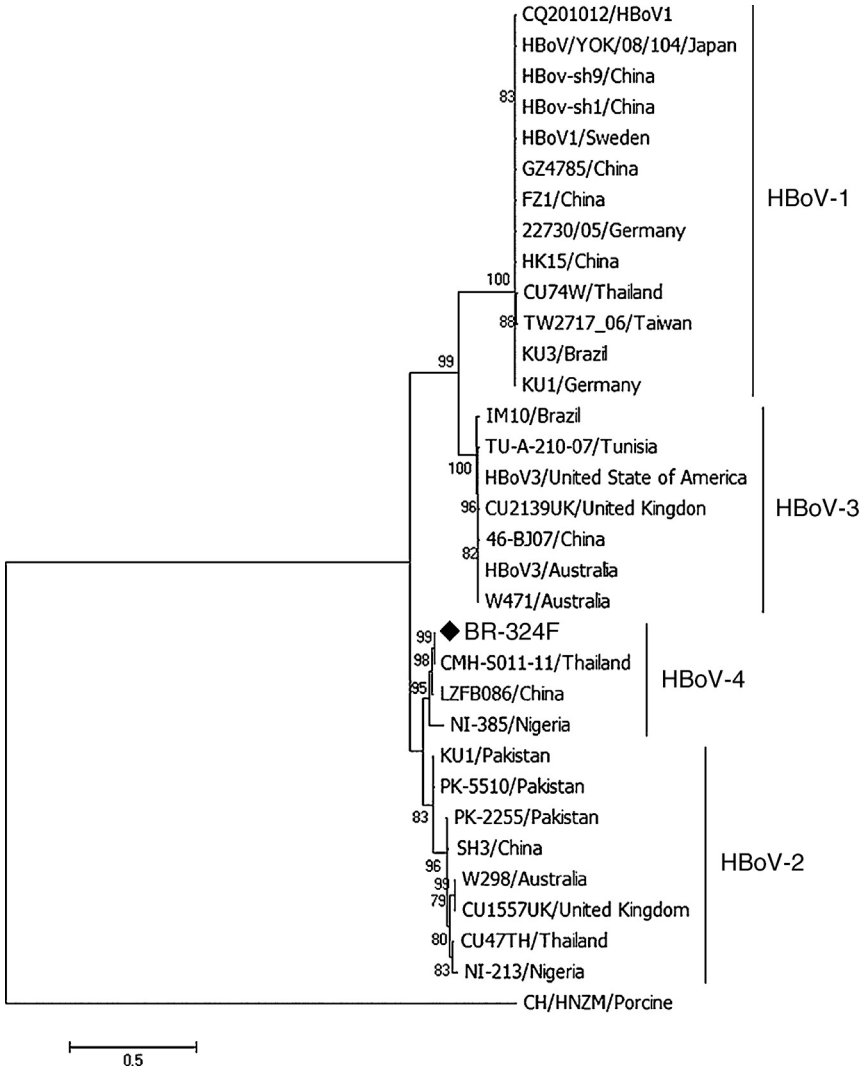

Fig. 1 – Phylogenetic analyses of the complete genome of HBoV-4 from feces of an individual asymptomatic for respiratory tract infection and acute gastroenteritis. The sample BR-324F is marked with a diamond. The *scale bar* corresponds to 0.5 nucleotide substitutions per site and the nodes have bootstrap values ≥70.

date HBoV-4 has not yet been identified in symptomatic or in healthy individuals in the country. This study aimed to detect and characterize HBoV in fecal samples from hospitalized children under five years old without RTI or AGE symptoms. This study presents the first identification of HBoV-4 in Brazil, detected in a child without symptoms of RTI or AGE who was hospitalized with tumor of the submandibular region.

Materials and methods

The study was part of a cross-sectional study in the period 2014–2015 that involved children less than five years old, who were admitted to a child care referral hospital in Goiânia, Goiás – Hospital Materno Infantil. Respiratory (nasopharyngeal swab) and fecal samples were collected from each child. The group consisted of 192 children with RTI and/or AGE and 119 who were asymptomatic for both syndromes, and were hospitalized for other reasons like malnutrition, intestinal obstruction, a variety of surgeries, diabetes, heart diseases, kidney diseases, cancer, hematological diseases, liver diseases, and convulsive crisis. Clinical samples were collected only after children's parents or guardians completed and signed the Informed Consent Form (ICF) and provided their child's personal and demographic data. The study was approved by the Research Ethics Committee at the Clinical Hospital of Federal University of Goiás (protocol: 19920013.7.0000.5078). HBoV was identified by Nested-PCR, only from the fecal samples of the asymptomatic group, where viral DNA was extracted by commercial kit QIAamp® Viral RNA Mini Kit (Qiagen, Hilden, Germany) following the manufacturer's instructions and primers specific for regions VP1 and VP2 were used as previously described.[6] The first amplification reaction was performed using a commercial PCR mixture GoTaq (GoTaq Colorless Master Mix, Promega Corporation, WI, USA) and specific primers (20 μM): AK-VP-F1 and AK-VP-R1. A second amplification (Nested-PCR) was performed with 1 μL of the amplified product and the same reaction mixture and