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The virus distributions in both seasons were considerably different between children and adults.

In summary, comparison of results of respiratory virus diagnostics in children and adult populations shows substantial differences, which demonstrates the need and usefulness of multiplex PCR for broad spectrum detection of respiratory viruses.

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Presence of human bocavirus 1 and other viral co-infections in hospitalized children with lower respiratory tract infection in Latvia

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Background: Acute respiratory tract infection (ARTI), especially lower respiratory tract infection (LRTI), is the common cause of illness and hospitalization in children worldwide. However, in many cases the etiological agent of disease is unknown. The viruses primarily associated with respiratory tract infections in children are respiratory syncytial viruses, influenza viruses, parainfluenza viruses, adenoviruses, coronaviruses, rhinoviruses and enteroviruses. In recent years the role of several new respiratory viruses in respiratory tract diseases have been reported, including human metapneumovirus, four coronaviruses (SARS-CoV, HCoV-NL63, HCoV-HKU1, MERS-CoV) and human bocavirus 1 (HBoV1). The aim of this study was to determine the presence of HBoV1 and 18 other respiratory viruses in nasopharyngeal aspirates (NPAs) from hospitalized children with LRTI in Latvia.

Material and methods: Forty four children (28 male and 16 female) aged one to 50 months who were hospitalized in Children’s Clinical University Hospital and fulfilled WHO LRTI criteria plus had fever (T ≥ 38°C) were enrolled in this study. In all cases the etiological agent of the disease was not revealed using standard routine clinical methods. NPAs from all patients were obtained on admission and DNA from NPAs was extracted using phenol–chloroform method. All 44 DNA samples were tested for HBoV1 and 18 other respiratory viruses (influenza viruses A, A-H1, A-H1pdm09, A-H3 and B, respiratory syncytial viruses A and B, adenovirus, enterovirus, parainfluenza viruses 1–4, metapneumovirus, rhinovirus, coronaviruses NL63, 229E and OC43) using multiplex real-time PCR method.

Results: Among 44 patients with LRTI, 29 (65.9%) were positive for HBoV1 which was the most frequently detected virus in patients. However, only HBoV1 genomic sequence without any analysed co-infection was detected in two out of 29 (6.9%) patients. Respiratory syncytial virus A was found in 23 out of 44 (52.3%) DNA samples and it was the most common co-infection. Other respiratory viruses detected were: adenovirus in 14 (31.8%), rhinovirus in 9 (20.5%), respiratory syncytial virus B in 7 (15.9%), metapneumovirus in 3 (6.8%), parainfluenza virus 3 in 2 (4.5%), coronavirus 229E in 2 (4.5%), (enterovirus in 1, influenza A virus in 1, influenza B virus in 1), coronavirus OC43 in 1 and coronavirus NL63 in 1 patient with LRTI. In 13 cases presence of more than two respiratory pathogens were found and in two cases, none of the tested respiratory viruses were detected.