

Full-length title: Sequencing and characterization of human bocavirus genomes from patients diagnosed in Southern France between 2017 and 2022

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Abstract

The diversity and evolution of the genomes of Human Bocavirus (HBoV), which causes respiratory diseases, have been scarcely studied. Here, we aimed to obtain and characterize HBoV genomes from patients's nasopharyngeal samples collected between 2017-2022 period (five years). Next-generation sequencing (NGS) used Illumina technology after having implemented using GEMi an in-house multiplex PCR amplification strategy. Genomes were assembled and analyzed with CLC Genomics, Mafft, BioEdit, MeV, Nextclade, MEGA, and iTol. A total of 213 genomes were obtained. Phylogeny classified them all as of Bocavirus 1 (HBoV1) species. Five HBoV1 genotypes determined by hierarchical clustering analysis of 27 variable genome positions were scattered over the study period although with differences in yearly prevalence. A total of 167 amino acid substitutions were detected. Besides, coinfection was observed for 52% of the samples, rhinoviruses then adenoviruses (HAdVs) being the most common viruses. Principal component analysis showed that HBoV1 genotype α tended to be significantly correlated with HAdV co-infection. Subsequent HAdV typing for HBoV1-positive samples and negative controls demonstrated that HAdVC species predominated but HAdVB was that significantly HBoV1-associated. Overall, we described here the first HBoV1 genomes sequenced for France. HBoV1 and HAdVB association deserves further investigation.

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