

A subtype of human bocavirus detected in *Rattus norvegicus* feces in China

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Abstract

Background Bocavirus is a typical zoonotic pathogen with a wide range of hosts. Here, we report the epidemiology of human bocavirus (HBoV) detected in *Rattus norvegicus*. Methods Between May 2015 and May 2017, 357 *R. norvegicus* were captured in four Chinese provinces. Polymerase chain reaction was used to investigate the prevalence of HBoV in fecal samples. Phylogenetic analysis and sequencing of the entire viral genome were undertaken. Results HBoV was detected in 0.84% (3/357) of samples. Phylogenetic analysis based on the partial VP1 region and near-full-sequence regions showed that HBoV obtained in *R. norvegicus* was genetically closely related to HBoV-2. One near-full-length HBoV genome (named “GZ533”) was acquired, and phylogenetic analysis of the three positive sequences revealed that they shared very high identity in nucleotides and amino acids in the VP1 region (96.0%–99.1%). Comparison of GZ533 and other HBoVs revealed ~100% identity of amino acids in the VP1 region, whereas only 37.5% identity of amino acids when compared with *R. norvegicus* bocavirus. Conclusion HBoV-2 was detected in *R. norvegicus* in China. *R. norvegicus* may be a carrier of HBoV infection, and its impact on public health merits attention.

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