

Complete Genome Analysis of Human Bocavirus Isolate from Iran

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Background & Objectives: Human Bocavirus (HBoV) was firstly detected in 2005. This virus was first discovered in children with respiratory tract illness but also has been detected in stool samples from children with gastroenteritis. The complete genome has a length of approximately 4,000 to 6,000 nucleotides.

Methods: To amplify the complete genome of Human Bocavirus we used two specific designed primers with a 4750 bp PCR product. For direct sequencing of amplified genome (Chain termination Methods) we used 7 pairs of primers for primer walk procedure.

Results: All NS1, NP1, VP1 partial gene sequences and nearly full-length genome sequences of HBoV were submitted to GenBank and accession numbers were obtained.

Conclusion: This study was the first investigation of Human Bocavirus complete genome among Iranian population. The submitted sequences of Iranian strain of Human Bocavirus in GenBank could be applied for further investigation and molecular epidemiology studies.

Keywords: Human Bocavirus; Iran; Full Genome Analysis

