Mayra Muné, J Antivir Antiretrovir 2014, 6:2
http://dx.doi.org/10.4172/1948-5964.S1.022

Newly emerging C-105 enterovirus genotype in acute respiratory disease in Cuba

Mayra Muné
IRAN

Human enteroviruses (HEVs) are small non-enveloped positive strand RNA virus that belongs to the genus of Enterovirus of the Picornaviridae family. The genome encodes a single polyprotein that is cleaved into four structural protein (VP1-VP4) and seven non-structural (2A-2C, 3A-3D) proteins They are associated with a wide range of clinical manifestations, ranging from mild respiratory illness to aseptic meningitis or even flaccid paralysis. Most EVs were discovered in 1947- 1957, after cell culture methods were introduced. At that time EVs were classified based on pathogenic properties for mice and serology properties in the infectivity neutralization test . The development of molecular detection methods in the 1990 s yields multiple novel EV types. Novel enterovirus types are currently defined, almost exclusively by genomic criteria, over 100 HEV types are classified into four species, HEV-A to HEV-D. Human enterovirus (105) was first reported in 2012 in a respiratory sample from children in Peru and a fecal sample from a case of fatal acute flaccid paralysis in Congo. We report on the identification of a novel HEV-C105 strain in an adult pregnant women patient from Cuba with a lower respiratory infection (pneumonia). RNA was extracted from clinical specimen using QIAamp Viral RNA Mini Kit (Qiagen), and then Multiplex RT-PCR and Semi-Nested PCR from a partial VP2-VP4 region were performed. (Coiras et al 2004). Partial nucleotide sequencing of VP4/VP2 protein gene capsid coding region was performed (Kit DTCS Quick Start Master Mix) Sequence analysis was done by using MEGA 5.1 software Phylogenetic tree was generated by using the neighbor-joining method, with maximum-composite likelihood as a substitution model. Similarity was calculated by using MEGA 5.1 software. Sequence alignment and phylogenetic analysis revealed that our isolate belongs to a group of recently identified HEV-C 105 virus. This is the first report of this novel enterovirus in Cuba and the Caribbean region. With this report the authors hope to increase awareness in laboratories to these newly emerging enterovirus, further studies are needed to clarify the actual prevalence and clinical importance of these novel enterovirus in our country.

mgholami.sums@gmail.com