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Molecular analysis of human parainfluenza viruses (HPIV) associated with acute respiratory infections (ARI) among children in AL-Muthanna/ Iraq

Mohsen A Alrodhan[2] and **Abrar A Kadim**[1]
[1]Al-Muthanna University, Iraq
[2]Al-Qadisiyah University, Iraq

Human parainfluenza viruses are important cause of respiratory tract diseases including lower respiratory infections which is a leading cause of deaths in infants and young children worldwide. This study was conducted among children in Iraq to evaluate the unclear epidemiological features of human parainfluenza viruses (HPIVs) and their role in acute respiratory infections (ARIs). Three hundred nasopharyngeal samples were collected from hospitalized pediatric patients in Al-Muthanna/Iraq at the period from January to March/2015 and screened for HPIVs by reverse transcription real time-polymerase chain reaction (RT-PCR), specific forward, reverse primer F- ACTGGAAGCACGGAAAGAAG, R-TTGTTGGTGAGCTTGTTGCC and TaqMan prob 5-FAM-TGAGCTGGAGACATCCACAGCCA-BHQ1-3 were used for detection of HPIV nucleoprotein (NP) gene. The total percentage of positive results was (45.38%). While the HPIV-1 virus was the predominate (32.17%) as compare with (13.21%) of HPIV-3 virus. Conventional end point PCR by using specific forward primer F-GCCCGAGTGTGACAGATGAT and R- GTGTCTCCCGTGAAGACCAG was applied. Ten randomly selected PCR products were purified, sequenced for GenBank submission, these our clones were recorded in GenBank with accession numbers (KT763053, KT763054, KT763055, KT763056, KT763057, KT763058, KT763060, KT763052, KT763059 and KT763061). The result of sequence alignment of our HPIV clones by using ClustalW2 with global reference strains showed high homology phylogenetic analysis with MEGA V6.0 showed that the clones of HPIV-3 (KT763052, KT763059, KT763061) were located in the same branch with (EU346887.1, M14552.1, X04612.1) isolated in Lithuania, Chile, India respectively, and has identity with other global strains isolated in USA, China and While our HPIV-1 (KT763053, KT763054, KT763055, KT763056, KT763057, KT763058, KT763060) located in the same branch with (JQ901971.1, EU346886.1, M62850.1, M62850.1, M62850.1, M62850.1, M62850.1) isolated in USA, Lithuania. And related to other strains isolated in USA, Thailand, and Japan real time RT-PCR is beneficial for epidemiologic studies as well as genotyping of the virus, the results indicate that HPIV is one of the important causative agents of ARI in infants and young children in Al-Muthanna. This is the first study in Iraq to detect HPIV clones and confirm homology and to generate sequence data that may help in understanding virus diversity and evolution.

abrarabdulla053@gmail.com
moh.alrodhan@gmail.com