

The seasonal frequency of human rhinoviruses and enteroviruses in respiratory secretions of patients with respiratory infections in AhvazAmir Pouremamali^{1,2} and Farhad Pouremamali³¹Ahvaz Jundishapur University of Medical Sciences, Iran²Tabriz Educational Regional Blood Center, Iran³Tabriz University of Medical Sciences, Iran

Background: Human rhinoviruses (HRVs) and Human enteroviruses (HEVs) are causes of respiratory infections (RIs). HRVs and EVs are a group of Picornaviridae family. They are positive sense-stranded RNA (ssRNA) viruses with a 7200 bp. Many studies have now present that HRVs & HEVs infections can lead to an influenza-like illness, such as lower respiratory tract infections, chronic infections and secondary bacterial infections.

Methods: This study was a cross-sectional study which was conducted on 100 nasopharyngeal swab specimens in patients with RIs which were admitted to hospital in Ahvaz. Patients had symptoms such as fever, headache and cough. Semi-Nested PCR was done on samples for detection of HRVs and HEVs.

Results: It was shown in this study that from of 100 cases of RIs 19 patients (19%) were Rhino positive and 3 patients (3%) were HEV positive. Most positive cases of Rhino positive were in the autumn and most positive cases of HEV positive were equal in spring, summer and autumn.

Conclusion: HRV/HEVs are common pathogens in patients with RIs, similar to influenza viruses. Most positive cases of HRV positive were seen in the autumn by 31 to 45 years old age range and the rate of this virus among women is three times more than men. HEV positive rate among men is two-fold female.

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Development of a method for the sequencing of the HCV polymerase gene (*NS5B gene*) in order to determine antiviral drug resistance in hepatitis C virus (HCV)

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New antiviral drugs that inhibit the HCV polymerase enzyme are beginning to be used in the treatment of hepatitis C virus infection, particularly in the hard to treat non-genotype 2 and 3 infected patients. The efficacy of these new antivirals is limited by the presence of those mutations that give rise to amino-acid substitutions within the targeted protein and affect the viral sensitivity to these compounds. The continued emergence of HCV antiviral resistance to polymerase inhibitors reinforces the urgent requirement for development of novel amplification (PCR) and sequencing method for *NS5B* gene which is responsible for replication of HCV. This project developed a method for amplifying and sequencing the HCV polymerase gene in order to determine antiviral drug resistance in different isolates of genotype 1 hepatitis C infected patients. The sensitivity of one step and two-step reverse transcriptase polymerase chain reactions was compared in order to optimize amplification of genotype 1 HCV *NS5B* region. Higher sensitivity was observed in the two-step RT-PCR using random hexamers than the one step RT-PCR using *NS5B* gene-specific primers. Moreover, a combination of four In-House designed primers was compared with published sets of primers for amplification of HCV genotype 1a and 1a variants, using the same optimized protocol and PCR conditions. After optimization of the whole assay a total of 20 sera specimens were tested and we found that the two-step RT-PCR is more sensitive than the one step reaction. In addition, the sensitivity of the In-House primers was significantly higher than the published primers using the two step-RT-PCR method. Overall, 19 samples were sequenced and analyzed for determination of resistance mutations to different nucleoside and non-nucleoside inhibitors. After the analysis, C316N and V499A which are natural polymorphisms in the HCV genotype 1 *NS5B* region and may be associated with antiviral resistance were found in 5.25% and 84.2% of the sequenced samples, respectively.

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