

Molecular Characterization and Phylogenetic Analysis of Influenza a(H3N2) Virus Circulating during the 2010-2011 in Riyadh, Saudi Arabia

Authors : Ghazanfar Ali, Fahad N Almajhdi

Abstract : This study provides data on the viral diagnosis and molecular epidemiology of influenza A(H3N2) virus isolated in Riyadh, Saudi Arabia. Nasopharyngeal aspirates from 80 clinically infected patients in the peak of the 2010-2011 winter seasons were processed for viral diagnosis by RT-PCR. Sequencing of entire HA and NA genes of representative isolates and molecular epidemiological analysis were performed. A total of 06 patients were positive for influenza A, B and respiratory syncytial viruses by RT-PCR assays; out of these only one sample was positive for influenza A(H3N2) by RT-PCR. Phylogenetic analysis of the HA and NA gene sequences showed identities higher than 99-98.8 % in both genes. They were also similar to reference isolates in HA sequences (99 % identity) and in NA sequences (99 % identity). Amino acid sequences predicted for the HA gene were highly identical to reference strains. The NA amino acid substitutions identified did not include the oseltamivir-resistant H275Y substitution. Conclusion: Viral isolation and RT-PCR together were useful for diagnosis of the influenza A (H3N2) virus. Variations in HA and NA sequences are similar to those identified in worldwide reference isolates and no drug resistance was found.

Keywords : influenza A (H3N2), genetic characterization, viral isolation, RT-PCR, Saudi Arabia

Conference Title : ICSRD 2020 : International Conference on Scientific Research and Development

Conference Location : Chicago, United States

Conference Dates : December 12-13, 2020