

## MOLECULAR DETECTION AND GENOTYPING OF HUMAN RESPIRATORY SYNCYTIAL VIRUS IN DIYALA PROVINCE

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(Received 11 October 2019, Revised 9 January 2020, Accepted 26 January 2020)

**ABSTRACT :** Globally, respiratory viral infections are an important cause of morbidity and mortality affecting peoples of all ages. human respiratory syncytial virus is one of the most common viruses infect children and increasingly recognized as an important pathogen in adults, causing upper and lower respiratory infection, that may progress to pneumonia and death. Molecular detection and genotyping of human respiratory syncytial virus in Diyala province and exploring its association with clinical picture. This cross-sectional study was conducted in the Diyala province, throughout two seasons; from January to May and from November to December/2018. A total of 323 patients who suspected as having RTIs of different ages were enrolled. Data of participants including socio-demographic and clinical observations were collected by using a questionnaire specially designed for this purpose. Three types of respiratory samples were collected including throat, nasal and nasopharyngeal swabs. In this study, real-time RT-PCR hybridization-fluorescence amplification was used to multiplex detected and identified of specific nucleic acid fragments for the seven RNA/DNA viruses, HRSV and HMPV among them, set of primers and probes were used in Real-Time PCR assay for Fusion (F) genes for determined the antigenic subgroups of Human Respiratory Syncytial virus and another set of primers used in the conventional PCR amplification for Attachment (G) gene for determined genotype of HRSV. Human privacy was respected by obtaining a verbal consent. Statistical analysis of data was carried out using the statistical package (SPSS- version 25). Statistical significance was considered whenever the P value was equal or less than 0.05. The results found that the HRSV detection rate was 4.6% with significantly higher in season one versus season two (93.3% versus 6.7%,  $P = 0.004$ ). The 5 years old children had insignificant higher rate of infection compared to other age groups (53.3%,  $P = 0.099$ ). Among the total of 15 HRSV positive swabs, 8 (53.3%) were throat swabs which was significantly higher compared to other types of swabs ( $P = 0.003$ ). the HRSV positivity rate in male was insignificantly higher than female (60% vs 40%,  $P = 0.679$ ); genotyping analysis showed circulate of the HRSV B subgroup in this study area. Study concluded that Human respiratory syncytial virus subgroup B is one of most frequently detected pathogen causing wide range of clinical illnesses particularly among children around 5 years of age.

**Key words :** Human respiratory syncytial virus, viral respiratory tract infections, Diyala.

### INTRODUCTION

Globally, respiratory viral infections (RVIs) are an important cause of morbidity and mortality affecting peoples of all ages particularly, infants, young children, the elderly, as well as immunocompromised individuals (Hijano *et al*, 2018; Li *et al*, 2019). Upper respiratory tract (URT) and lower respiratory tract (LRT) are frequently caused by a wide spectrum of viruses causing various clinical syndromes with variable outcomes ranging from common colds, pharyngitis, croup (Laryngotracheo bronchitis), otitis media, bronchiolitis, and viral pneumonia (Das *et al*, 2018; Gottlieb, 2019).

The most important RVIs are influenza viruses type A and B, Human respiratory syncytial virus (HRSV), Human Parainfluenza Viruses (HPIVs) and Human adenoviruses (HADVs), plus newly discovered human respiratory viruses including human Metapneumovirus (HMPV), Severe Acute Respiratory Syndrome Coronavirue (SARS), Middle East Respiratory Coronaviruses (MER-CoV), human bocavirus and Human Rhinovirus (Hasan *et al*, 2018; Tambyah *et al*, 2019; Bradley and Bryan, 2019). Worldwide, the rate of RVIs is very high since viruses were identified as causes of the pediatric acute respiratory tract infections (ARIs) in up to (95%) of cases (Linden *et al*, 2019).