

# **Molecular Detection and Characterization of Human Metapneumovirus (hMPV) in Hospitalized Children Residing in Southern Palestine**

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## **ABSTRACT**

The recent discovery of Human Metapneumovirus (hMPV) by Van Den Hoogen from the Netherlands in 2001 has added a new member to the group of viruses which can cause respiratory tract infections. hMPV is a pleomorphic enveloped virus which contains single-stranded RNA with negative polarity. hMPV has been classified in the *Paramyxoviridae* family. Since its discovery, both hMPV lineages A and B and their sub-lineages have been reported in many parts of the world with a detection rate between 2-25%. Moreover, hMPV has been reported to be associated with respiratory tract illness in children less than 5 years of age.

In this study, we investigated the frequency of hMPV in 790 nasopharyngeal aspirates of Palestinian children, age one day to 13 years, hospitalized at Caritas Baby hospital between November 2005 and October 2006. Viral RNA was extracted using QIAamp RNA extraction kit (Qiagen GmbH, Hilden, Germany), and amplified for hMPV using an in-house RT-PCR assay. Moreover 1019 bp from the N gene was amplified and partially sequenced in order to perform phylogenetic analysis.

hMPV was detected in 251 (31.8%) of the patients samples analyzed. This positivity rate was one of the highest percents reported to date and might suggest that there was an outbreak of hMPV during the study period. Phylogenetic analysis of 34 (14%) positive hMPV amplified RNA of the N-gene showed that two serotypes of hMPV A lineage circulated in Southern Palestine. Indeed, one of the serotypes was not the same as that reported for the reference strains. Of the sequenced samples, 43% belonged to a novel clade of the lineage A. Upon determining the homology of the newly discovered clade, 95% homology was observed. Having this 5% difference from the 377 base pair sequences allowed to hypothesize that we are dealing with a new clade of the A lineage.

This study is the first to report and describe the epidemiology of hMPV in Southern Palestine. Moreover; it identified the genetic lineages and clades that circulated in Southern Palestine. The discovery of hMPV and its incorporation to routine diagnostic procedures has allowed us to identify the cause of a significant number of respiratory tract infections (31.8%) during the study period.