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Human metapneumovirus in Jordan: Prevalence and clinical symptoms in hospitalized pediatric patients and molecular virus characterization

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Respiratory viral infections account for significant morbidity and mortality especially in young children worldwide. Human metapneumovirus (hMPV) encompassing illnesses ranging from mild respiratory problems to bronchiolitis and severe pneumonia. From January to December 2007, Two hundred and twenty nasopharyngeal aspirates (NPA) were collected from children younger than or equal 13 years old hospitalized with lower respiratory tract infection to detect hMPV by RT-PCR, and to clone and sequence the hMPV positive samples. Human metapneumovirus was detected in 28 (12.7%) specimens with a median age of 7 months ranging from 1.3-24 months. Human metapneumovirus type A and type B were detected in 26(93%) and 8(28.6%) of specimens, respectively. Co-infection with hMPV type A and type B were detected in 6(21.4%) specimens positive for hMPV. The major clinical diagnosis of hMPV positive patients was bronchiolitis (75%). Human metapneumovirus and hMPV type B, were found significantly associated with bronchiolitis ($p= 0.03$ and 0.01 respectively). Human metapneumovirus and hMPV type A were found significantly associated with pneumonia ($p= 0.004$ and 0.002 respectively). The main symptoms in patients infected with hMPV were cough (92.9%), fever (82.1%), and wheezing (78.6%) with a significant association of hMPV type A with fever ($p= 0.018$). Human metapneumovirus was seasonally distributed; most infections with hMPV were reported in the late winter and early spring. The peak of hMPV incidence was in February (10/28; 35.7%). Sequencing of purified plasmid DNA was performed in forward and reverse direction to confirm the results of hMPV positive samples which scored 97% identities to hMPV type A genome isolate NL/17/00 and showing C-T variation that had no effect on the amino acid sequence; F(Phe)-F(Phe).

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