Isolation and Molecular Identification of Respiratory Syncytial Virus in Children with Acute Respiratory Infections at Kenyatta National Hospital, Nairobi, Kenya

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ABSTRACT

Respiratory syncytial virus (RSV) is the most commonly identified viral agent of acute respiratory infections of children and infants. RSV causes repeat infections throughout childhood. However, limited data are available on molecular epidemiology of RSV in Nairobi. Two major subgroups (A and B) have been identified based on antigenic differences in the attachment G protein which is one of the most unusual features of RSV. This antigenic variability is thought to contribute to the capacity of the virus to establish infections in childhood. This study aimed at isolating, identifying and sequencing the RSV inorder to determine their demographic characteristics, prevalence and also determine the RSV isolates among pediatric cases in KNH. Two hundred and eighty seven nasopharyngeal swabs were collected from children under five years old at the pediatrics ward at Kenyatta National Hospital. Both the cell culture technique and the direct immunoflourescence method were used for the study. Ribonucleic acid was extracted from the samples using the QIAMP viral RNA kits (Qiagen UK Ltd) followed by amplification using reverse transcription Polymerase Chain Reaction (RT-PCR). Nineteen (6.6%) samples were tested positive by cell culture and IF techniques. All the isolates subjected to RT-PCR belonged to sub-group A. However, according to the study findings there was no significant association between the age groups and RSV outcome. Two samples were then analysed further by sequencing of the nucleocapsid region (*N*) *gene*. The Nairobi samples were compared with other sequences producing significant alighments which had a maximum identification of between 94-97%. The phylogenetic analysis done after the sequencing of the samples showed very close similarity with other RSV isolates in Cambodia, Fiji, United Kingdom and South Africa. Kenyatta National Hospital samples had more than 94% maximum identification with samples from Cambondia, Fiji and United

Kingdom. According to the findings the RSV prevalence was 6.6% between May and September 2008. This study contributes towards the understanding of RSV infection and control. It also contributes towards the improved understanding for reasons behind RSV re infections and yearly epidemics.