SUB GROUP PREVALENCE AND GENOTYPE CHARACTERIZATION OF RESPIRATORY SYNCYTIAL VIRUS AMONG KILIFI HOSPITALIZED INFANTS DURING TWO SUCCESSIVE EPIDEMICS

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ABSTRACT

Background

Respiratory Syncytial virus is the leading cause of severe respiratory illnesses in infants and young children world wide. Two major antigenic groups of RSV (A and B) exist. Viruses from both subgroups can co circulate during epidemics; however, their frequencies might differ between seasons.

Method

Sub group prevalence and genotype distribution patterns of RSV were investigated among 335 patients who were admitted to Kilifi District hospital and whose respiratory specimens had tested positive or equivocal by initial antigen test (IFAT) during two successive RSV epidemics that occurred within November 2006 and March 2008. Samples were analyzed by pcr to sub group them to either RSVA or B and genotyped by RFLP.

Results

From the results it was clear that RSV A dominated the first epidemic while RSV B took over the dominance in the second epidemic. There were multiple genotypes co circulating during these two epidemics with the emergence of new types that have not been characterized before. There was over 90% agreement between antigen test and the multiplex RT pcr used.

Conclusion.

The results from this study support the hypothesis that different subgroup dominate in a particular epidemic with their decline in the next epidemic possibly due to partial herd immunity that is developed by the community during an epidemic. Multiplex TR pcr can be accurately used to characterize RSV sub groups and to detect co infections.