

SPATIAL-TEMPORAL DISTRIBUTION AND SEQUENCE DIVERSITY OF GROUP A HUMAN RESPIRATORY SYNCYTIAL VIRUSES IN KENYA PRECEDING THE EMERGENCE OF ON1 GENOTYPE

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Abstract

Background: Human respiratory syncytial virus (HRSV) is a major cause of severe viral acute respiratory illness and contributes significantly to severe pneumonia cases in Africa. Little is known about its spatial-temporal distribution as defined by its genetic diversity. Methods: A retrospective study conducted utilizing archived nasopharyngeal specimens from patients attending outpatient clinics in hospitals located in five demographically and climatically distinct regions of Kenya; Coast, Western, Highlands, Eastern and Nairobi. The viral total RNA was extracted and tested using multiplex real time RT-PCR (reverse transcriptase polymerase chain reaction). A segment of the G-gene was amplified using one-step RT-PCR and sequenced by Sanger di-deoxy method. Bayesian analysis of phylogeny was utilized and subsequently median joining methods for haplotype network reconstruction. Results: Three genotypes of HRSVA were detected; GA5 (14.0%), GA2 (33.1%) and NA1 (52.9%). HRSVA prevalence varied by location from 33% to 13.2% in the Highlands and the Eastern regions respectively. The mean nucleotide diversity ($Pi(\pi)$) varied by genotype: highest of 0.018 for GA5 and lowest of 0.005 for NA1. A total of 58 haplotypes were identified (GA5 10; GA2 20; NA1 28). These haplotypes were introduced into the population locally by single haplotypes and additional subsidiary seeds amongst the GA2 and the NA1 haplotypes. Conclusions: HRSVA was found across all the regions throughout the study period and comprised three genotypes; GA5, GA2 and NA1 genotypes. The genotypes were disproportionately distributed across the regions with GA5 gradually increasing towards the Western zones and decreasing towards the Eastern zones of the country.

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