

Abstract

Introduction: Human Respiratory Syncytial Virus is the leading viral cause of bronchiolitis and pneumonia in children and infants. Amongst adults, the elderly and the immuno-compromised are also at risk of severe RSV. RSV is classified into two genetically distinct groups: RSV A and RSV B. In the case of RSV A, 11 genotypes have been reported to date. Amongst these are three new variants (NA1, NA2 and ON1). Appearance of new genotypes has been accompanied by rapid spread and near replacement of existing variants. There is need to constantly re-examine the nature of genotypic changes amongst circulating viruses. **Objective:** To assess the geographic distribution and genotypic diversity of RSV A in outpatients presenting with Influenza-Like-Illness from 2007 and 2010 across Kenya. **Methods:** Nasopharyngeal (NP) swabs were obtained from subjects ≥ 2 months of age presenting with fever $\geq 38^{\circ}\text{C}$ and cough or sore throat at district hospitals under surveillance across 5 regions of Kenya. RNA was extracted from the NP samples and screened using multiplex real-time RT-PCR. A 490bp fragment of the RSVA G-gene was amplified by nested RT-PCR and nucleotide sequencing carried out using the Sanger dideoxy termination method. The sequences were analyzed using a suite of bioinformatics software. **Results:** 159 NP samples were positive for RSV A, of which, 130 were genotyped; 21 (16%) were GA5, 39 (30%) GA2, 66 (50%) NA1, 1 GA1 and 3 (2%) GA2 variants closely related to NA2. GA2 and NA1 genotypes were identified in the highlands from 2007 – 2010. In 2009, NA1 was highest in Nairobi and Coast regions (11; 17%). GA2 genotype was highest in Northeastern (8; 21%) and was most prevalent in 2009 (44%). The Western region had the highest prevalence of GA5 in 2008 (6; 29%). **Conclusion:** Five genotypes were in circulation across the country in 2007 and of these NA1 genotype increased dominance year by year and spread to all the regions by 2009. These data provide insight into the dynamics of persistence of RSV strains within a national geographical area