

Burden of Human Rhinovirus Infections in Influenza like Illnesses in Kenya

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Abstract

Background: There have been several recent reports of respiratory outbreaks with associated mortality due to human rhinovirus (HRV) infection. Studies on viral etiologies of Influenza-like illness have shown that many patients are infected with more than one viral agent with frequencies of co-infection being as high as 20%. From these studies, human rhinovirus has been shown as one of the most prominent respiratory viruses that co-infect patients with influenza. In Kenya, the ongoing Influenza surveillance has provided data that now allows for exploration of other respiratory viruses that cause influenza-like illnesses. Currently, there is scanty information on the patterns of HRV circulation throughout the country.

Methods & Materials: This study utilized a retrospective cross-sectional descriptive design. It involved the use of 517 archived samples from the ongoing country-wide influenza Surveillance protocol. The archived nasopharyngeal specimens were collected from a study population comprising persons from two months of age onwards who attended outpatient clinics in the year 2008, in hospitals located in 8 different regions in Kenya presenting with influenza like illnesses. Viral RNA was extracted from the samples followed by real-time RT-PCR assays with HRV-specific primers for screening for HRV.

Results: A total of 131 (25%) of the samples were positive for HRV. The highest prevalence (33%) was recorded from samples obtained from the Coast region of the country, followed by Western region (32.7%) while Eastern region had the lowest prevalence (11%). Children aged between 2 months -7 years were mostly infected while the age group ≥ 60 years was least affected. There was no significant difference in HRV infection in relation to gender.

Conclusion: The study notes that HRV infection is a significant viral etiology of morbidity throughout the country. However, disparities were observed between different regions. The more humid regions in the country (Western and Coast) had the highest HRV prevalence. At the same time, children below 7 years were at a greater risk of HRV infection. Determination of the molecular characteristics of the

rhinovirus strains to enable specific identification of the species and the evolutionary relationships is ongoing.