Contribution of human rhinovirus infections among patients presenting with influenza like illnesses in Kenya

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Contribution of human rhinovirus infections among patients presenting with influenza like illnesses in Kenya

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BACKGROUND

Recently, there have been several reports of respiratory outbreaks with associated mortality due to human rhinovirus (HRV) infection (1, 2). 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% (3). From these studies, human rhinovirus has been shown as one of the most prominent respiratory viruses that co-infect patients with influenza (3). In Kenya, the ongoing Influenza surveillance has provided a platform that now allows for exploration of other respiratory viruses that cause influenza-like illnesses (ILI)(4). Currently, there is scanty information on the patterns of HRV circulation throughout the country.

OBJECTIVE

To determine the presence of Human Rhinoviruses among patients presenting with (ILI) in Kenya.

MATERIALS AND METHODS

This study utilized a retrospective cross-sectional descriptive design. It involved analyses of 517 archived samples from the ongoing country-wide influenza Surveillance protocol. The nasopharyngeal specimens had been collected from ILI patients from a population comprising persons of ≥2 months who attended outpatient clinics in the year 2008, in hospitals located in 8 different regions in Kenya (Fig. 1). Viral RNA was extracted from the samples followed by real-time RT-PCR assays with HRV-specific primers.

RESULTS

Table 1 and Fig. 2 show the positivity proportions amongst patients from the four regions of the country. A total of 131 (25%) of the samples were positive for HRV. The highest proportion (33%) was recorded from samples obtained from the Coast region of the country, followed by Western region (32%) while Eastern region had the lowest proportion (11%). Analysis of demographic data showed that 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.

CONCLUSIONS

The study has shown 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.

Fig. 1: The Kenya ILI sentinel surveillance site network

Table 1: HRV infection among ILI patients in different parts of Kenya in 2008.

<table>
<thead>
<tr>
<th>Region</th>
<th>Number +ves</th>
<th>% positive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coastal</td>
<td>43</td>
<td>33</td>
</tr>
<tr>
<td>Western</td>
<td>42</td>
<td>32</td>
</tr>
<tr>
<td>Eastern</td>
<td>14</td>
<td>11</td>
</tr>
<tr>
<td>Nairobi/central</td>
<td>32</td>
<td>24</td>
</tr>
<tr>
<td>Totals</td>
<td>131</td>
<td>100</td>
</tr>
</tbody>
</table>

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1. The funds for this study are provided by US Department of Defense through the DoD GeIS
2. The views expressed are those of the authors and should not be construed to represent the position of the Department of the Army or Department of Defense

References:
2. N. Renwick et al. A recently identified rhinovirus genotype is associated with severe respiratory tract infection in children in Germany. The journal of infectious diseases 196; 1754 (Dec 15, 2007).