

Abstract

Respiratory Adenovirus Species Circulating In Kenya from 2007-2010

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Background: Human adenoviruses [HAdvs] are causative agents of several diseases including acute respiratory disease (ARD), keratoconjunctivitis, gastroenteritis, acute hemorrhagic cystitis, opportunistic infection in immuno-compromised patients and severe and potentially fatal pneumonia. Adenoviruses have been shown to affect mainly pediatric populations, military recruits and congested institutions such as hospitals and schools where they are a major cause of morbidity and mortality. In this study we examined respiratory adenovirus species and types associated with respiratory infection circulating at eight study sites in Kenya from 2007-2010.

Methods: Nasopharyngeal swab samples collected in viral transport media were transported to the National Influenza Centre in dry shippers while maintaining the cold chain. Samples originated from patients with Influenza like Illness (ILI) participating in the United States Army Medical Research unit in Kenya (USAMRU-K) sentinel surveillance network across the country. The samples were inoculated into Hep2 cells and incubated at 37 °C with 5% CO₂ for 14 days or until cytopathic effect was observed. Presence of HAdv in the supernatants was determined by immunofluorescence assays. To begin to analyze these Kenyan HAdvs, 10% were molecularly genotyped using HAdv type-specific primers followed by nucleotide sequencing and analysis using a suite of bioinformatics software. This work received ethical approval under the KEMRI ERC-approved protocol SSC#981.

Results: A total of 12,959 samples were screened during the period. 385 (3%) of these were positive for HAdv by cell culture. Molecular characterization of ~10% of the viruses using PCR yielded 20 (45%) HAdvs of the B species and 24 (55%) HAdvs species C. We did not detect any HAdv species E during the period. Analysis of the nucleotide sequences differentiated the species into types B3 [n=5], B7 [n=15], C1 [n=6], C2 [n=13] and C5 [n=4].

Although cell culture is not the most sensitive method for screening respiratory viruses, our results showed that respiratory HAdvs contributed at least 3% of the respiratory disease burden in Kenya during this period. Furthermore, the results showed that type B7 was the most prevalent HAdv followed by type C2. HAdv type B7 has been associated with the most severe forms of respiratory infections and fatalities globally, and our results showed that a substantial burden of serious respiratory disease was due to this HAdv type. These results suggest that if a respiratory HAdv vaccine were to be introduced in Kenya, it ought to contain the HAdv types B7 and C2 components.

Conclusion: We have for the first time molecularly characterized HAdv types isolated from the respiratory tract of humans in Kenya and showed that overall, types B7 and C2 substantially contribute to severe respiratory disease in Kenya. The Kenyan Ministry of Health should consider introducing a vaccine containing these two components to mitigate against respiratory illness.

Key words: Respiratory adenovirus, Kenya

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