

Genetic analysis of H3N2 influenza A viruses isolated in 2006-2007 in Nairobi, Kenya

Abstract:

BACKGROUND: Minimal influenza surveillance has been carried out in sub-Saharan Africa to provide information on circulating influenza subtypes for the purpose of vaccine production and monitoring trends in virus spread and mutations. **OBJECTIVE:** The aim of this study was to investigate a surveillance program in Kenya to isolate and characterize influenza viruses.

RESULTS: In the 2006-2007 influenza season, nine influenza A viruses were isolated. All were of H3N2 subtype with key amino acid (aa) changes indicating that they were more closely related to recent World Health Organization recommended vaccine strains than to older vaccine strains, and mirroring the evolution of circulating influenza A globally. Hemagglutination inhibition data showed that the 2006 Kenya isolates had titers identical to the 2005-2006 H3N2 vaccine strain but two- to threefold lower titers to the 2006-2007 vaccine strain, suggesting that the isolates were antigenic variants of the 2006-2007 vaccine strains. Analysis of aa substitutions of hemagglutinin-1 (HA1) protein of the 2006 Kenyan viruses revealed unique genetic variations with several aa substitutions located at immunodominant epitopes of the HA1 protein. These mutations included the V112I change at site E, the K 173 E substitution at site D and N 278 K change at site C, mutations that may result in conformational change on the HA molecule to expose novel epitopes thus abrogating binding of pre-existing antibodies at these sites.

CONCLUSION: Characterization of these important genetic variations in influenza A viruses isolated from Kenya highlights the importance of continuing surveillance and characterization of emerging influenza drift variants in sub-Saharan Africa