

Were the WHO-recommended Human Influenza Vaccine Formulations Appropriate for Kenya During the 2010-2011 Season? Inferences from the HA1 Gene Analysis

Abstract:

Background: The knowledge of evolutionary patterns of the HA gene of the influenza virus is important in vaccine strain selection. Objective: Genetic analysis of HA1 of influenza viruses isolated in Kenya during the 2010-2011 season with reference to WHO vaccine strains. Methods: A total of twenty seven (27) influenza A (H1N1) pdm09, Nineteen (19) influenza A (H3N2) and Sixteen (16) influenza B virus isolates were analyzed. A partial HA1 gene was amplified by RT-PCR and sequenced. Results: Phylogenetic analyses revealed that influenza B viruses were closely related to B/Brisbane/60/2008 vaccine strain while A (H1N1) pdm09 viruses were genetic variants of A/California/07/2009. The Kenyan A (H1N1) pdm09 isolates had P83S, D97N, S185T, I321V and E374K amino acid substitutions. Influenza A/H3N2 isolates showed K62E, T212A and S214I simultaneous amino acid substitutions when compared to A/Perth/10/2009. The K62E change occurred at antigenic site E. Majority of the Kenyan H3N2 isolates further had S45N and K144N amino acid substitutions at sites C and A respectively, which introduced N-glycosylation motifs absent in the vaccine strain. Conclusion: The study showed that although the WHO 2010 vaccine strains recommendations for the southern-hemisphere matched with influenza viruses which circulated in Kenya during the 2010-2011 season, the viruses had evolved genetically from the vaccine strains