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Abstract

Amino Acid changes at the hemagglutinin antigenic site amongst Kenyan influenza A(H1N1)pdm09 viruses in 2009-2010

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Background: Influenza viruses evolve very rapidly and mutations in the HA1 gene can lead to genetic drifts necessitating alterations in the annual vaccine formulations. It is therefore important to constantly monitor evolution of these viruses globally for timely detection and interventions to such events.

Objective: To study the changes that occurred within antigenic HA1 protein of the influenza A(H1N1)pdm09 viruses that circulated in Kenya at the height of the 2009 influenza pandemic.

Methodology: Nasopharyngeal samples from patients meeting the WHO pandemic influenza case definition were collected from consenting patients between 2009 and 2010 from across Kenya. The detection of influenza A(H1N1)pdm09 viruses was carried out using real-time RT-PCR. The positive samples were then cultured in MDCK cells and confirmed using the HAI assay. 23 isolates from this period were selected for RNA extraction followed by PCR amplification of the HA1 gene segments. Nucleotide sequencing was performed using the Sanger method followed by data analysis using a suite of bioinformatics tools.

Results: HAI assays showed that the Kenyan isolates were antigenically similar to A/California/07/2009 vaccine strain. However, at the genetic level, all Kenyan isolates had P83S, S203T and I321V parallel amino acid changes in the HA1 protein not present in the vaccine strain. The P83S change occurred in the Cb antigenic binding site. Additionally all the 2010 Kenyan isolates except isolates A/Kenya/057/2010 and A/Kenya/059/2010 had D97N, S185T and E374K amino acid changes when compared to the vaccine strain. The Kenyan isolates A/Kenyan/057/2010 and A/Kenyan/059/2010 showed K142R amino acid changes instead. There were other mutations which occurred randomly among the Kenyan individual isolates, these included changes such as N129D on (A/Kenyan/0015/2009, A/Kenya/0043/2009, and A/Kenya/0016/2009), K142R on (A/Kenyan/057/2010 and A/Kenya/059/2010) and G170R change which were present in the A/Kenya/057/2010 isolate. These other mutation occurred at Sa, Ca_2 and Ca_1 antigenic sites of the HA1 protein.

Conclusion: Our results show that although amino acid changes rapidly occurred on antibody binding sites of HA1 protein, the antigenicity of the protein was retained and that the A/California/07/2009 vaccine strain component was appropriate for Kenya.

Key words: Amino acid, hemagglutinin antigenic, Kenyan, influenza A(H1N1)pdm viruses

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