Background: In humans, the inability to provide lasting protection against influenza B virus infection is due, in part, to the rapid evolution of the viral surface glycoprotein, haemagglutinin (HA), which leads to a change in its antigenic nature. Therefore, the evolution of the haemagglutinin (HA) an important influenza antigen has and continues to be a subject of intensive research. In this study, we analyzed the evolution occurring in the haemagglutinin of influenza B viruses from Kenya since virological surveillance began in 2005.

Methods: Thirty (30) influenza B haemagglutinin sequences of viruses isolated from different parts of the country between 2005-2009 at the NIC were analyzed. Nucleotide sequences, prediction of amino acid sequences, alignments, and phylogenetic tree construction were completed using BioEdit and MEGA® software

Results: During the five year study period, the two influenza B lineages B/Yamagata and B/Victoria have co-circulated in two years (2005 and 2007) while B/Yamagata viruses exclusively circulated in 2008 and B/Victoria viruses in 2006 and 2009. The nucleotide sequence identity ranged from 92.9% – 97.0% among the B/Yamagata lineage viruses and 90.6% – 98.5% among the B/Victoria lineage viruses. There was generally noted more amino acid substitutions among the B/Yamagata lineage than the B/Victoria lineage. Substitutions were observed in all the epitope regions among B/Yamagata viruses compared to three epitopes in the B/Victoria viruses. Both lineages showed substitutions at position HA1 165.

Conclusions: These results demonstrate that distinct viruses within the two lineages have been co-circulating in the country every year and that there has been a greater evolution of the B/Yamagata viruses. At the same time it is noted that like elsewhere, influenza B viruses in the country have continually been evolving by antigenic drift. In-order to understand whether reassortments have occurred, the study suggests periodic complete genomic sequencing of select.