Phylogenetic analysis of the Egyptian equine influenza virus (A/Equine/Egypt/VRLCU/2008 (H3N8))

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Phylogenetic analysis of the Egyptian equine influenza virus
(A/Equine/Egypt/VRLCU/2008 (H3N8))

Ahmed, B.M; Hussein, H.A; and A.A, El-Sanousi
Department of Virology, Faculty of Veterinary Medicine, Cairo University

Summary:

In the present Study, nucleotide sequence analysis of 373 bp fragment of the heamagglutinin gene of an isolated Egyptian Equine influenza virus (A/Equine/Egypt/VRLCU/2008 (H3N8)) amplified Using OIE reference Primers in a modified RT-PCR assay was achieved. Sequence analysis using NCBI BLAST revealed 100 % identity with H3N8 isolates of Florida subclade1 which is predominant in North America. Both nucleotide and amino acid, rooted and unrooted phylogenetic trees constructed using neighbor joining method of MEGA4 Software revealed clustering of the isolated virus with the most recent isolates of Florida subclade1 including the isolate of NAMRU3 unit (A/equine/Egypt/6066NAMRU3-VSVRI/2008(H3N8)). There are no Change in the amino acid sequences of the BII, CII, DI, DII and DIII antigenic sites located in the amplified fragment. However one amino acid change was determined in the isolated virus compared to those belonging to the genetic lineage. This study reports the Phylogenetic analysis of the circulating H3N8 EIV associated with 2008 outbreak in Egypt. The sequence was submitted to GenBank with the accession number JF812270.