Cairo University

Faculty of Veterinary Medicine

Department of Virology

PhD Thesis

Study on genetic exchange of the internal genes of local isolates of H9N2 avian Influenza viruses during 2014 - 2016 in Egypt

Presented by

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Abstract

The LPAI H9N2 subtype is the most prevalent and the major cause of disease in domestic poultry in Egypt, since 2011 the extensive co-circulation of the LPAI H9N2 & HPAI-H5N1 viruses create great worry about virus reassortment. There is concern about the potential risk for these viruses to cross the species barriers and affect human health. In this study, The whole genome sequenced, and genetic exchange in the internal genes of field viruses of H9N2 avian Influenza circulated in Egypt between 2014 and 2016 was carried out. Phylogenetic analysis showed that Egyptian H9N2 viruses closely related to the viruses isolated from neighbouring Middle Eastern countries, and sharing the same progenitor virus of the G1-lineage. There is new distinct cluster designated as (Egy\G1-Var) carry several mutations. No reassortment was detected with H5N1 subtypes with in chicken or quail isolates under study. The evolutionary analysis gene segments (HA, NA, NS and M) belonging to cluster B, and the remaining segments belong to cluster A. Multiple mutations that favour transmission from avian to mammalian hosts are detected. The full length PB1-F2 and PA-X and other mutations related to virulence are also identified. No obvious changes in antiviral drugs resistance sit. This study indicates the progressive evolution of H9N2 viruses in Egypt and the emergence of new escape mutant that can introduce additional risk if transmitted to the commercial chicken flocks.

Key word: hemagglutinin [HA]: neuraminidase [NA], non-structural [NS], matrix [M], and polymerase basic 1 and 2 [PB1, PB2]; polymeric acid [PA], and nucleoprotein [NP], LPAI H9N2 and HPAI-H5N1

Dedication

To my

Father

Mother

Husband

Sons

(Mahmoud and Youssef)

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