



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

Zienab Mosaad Abdel monsif Soliman

B.Sc. of Veterinary Medicine – Cairo University (2007)

M.V.Sc. of Virology – Cairo University (2013)

Under supervision:

Prof. Dr. Mohamed Abd-El Hameed Shalaby

Prof. of Virology and immunology

Faculty of Veterinary Medicine

Cairo University

Prof. Dr. Hussein Ali Hussein

Prof. and Chairman of Virology Dept.,
Faculty of Veterinary Medicine Cairo
University

Prof. Dr. Abd El Satar Arafa

Chief Researcher

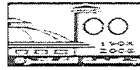
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Control on Poultry Production
Animal Health Research Institute
Dokki - Giza

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قسم الفيروسات

جامعة القاهرة



كلية الطب البيطري



Approval Sheet

This is to approve that Thesis presented by

Zienab Mosaad Abdel Monsif Soliman

For the degree of PhD. (Virology) has been approved by the examining committee

Prof. Dr. Sabry Mohamed Tammam

Sabry Tammam

Professor and Head of Department of Virology
Faculty of Veterinary Medicine
Beni-Suef University

Prof. Dr. Ahmed Abd El-Ghani El-Sanousi

Ahmed El-Sanousi

Professor of Virology
Faculty of Veterinary Medicine,
Cairo University

Prof. Dr- Abd El Satar A. Mohamed

A. Arafat

Chief Researcher in reference
Laboratory for quality control on poultry production
Animal Health Research institute
Dokki -Giza (Supervisor)

Prof. Dr. Hussein Aly Hussein

Hussein Aly Hussein

Professor and Head of Department of Virology
Faculty of Veterinary Medicine,
Cairo University (Supervisor)

Prof. Dr. Mohamed Abd El-Hamid Shalaby

Shalaby

Professor of Virology
Faculty of Veterinary Medicine,
Cairo University (Supervisor)

2017

Cairo University

Faculty of Veterinary medicine

Department of Virology

Supervision sheet

Supervisors

**Prof. Dr. Mohamed Abd-El Hameed
Shalaby**

Professor of Virology and immunology

Faculty of Veterinary Medicine

Cairo University

Prof. Dr. Hussein Ali Hussein

Professor and chairman of Virology dep.

Faculty of Veterinary Medicine

Cairo University

Prof. Dr. Abdel-Satar Arafa

Chief Researcher

Reference Laboratory for Quality Control on Poultry Production

Animal Health Research Institute

Dokki-Giza

Cairo University
Faculty of Veterinary Medicine
Department of Virology

Name	Zienab Mosaad Abdel monsif Soliman
Date of birth	3/9/1984
Place of birth	Qaliobia
Nationality	Egyptian
Degree	Philosophy of Doctor in Veterinary Medical Science
Specification	Virology
Title	Study on genetic exchange of the internal genes of local isolates of H9N2 avian Influenza viruses during 2014 - 2016 in Egypt
Supervisors :	Prof. Dr. Mohamed Abd-El Hameed Shalaby Professor of Virology and immunology, Faculty of Veterinary Medicine, Cairo University Prof. Dr. Hussein Ali Hussein Professor of Virology, Faculty of Veterinary Medicine, Cairo University Prof. Dr. Abdel-Satar Arafa Mohamed. Chief researcher, Reference laboratory of quality control on poultry production, Animal Health Research Institute

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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First of all, endless thanks and appreciation for almighty Allah for help and guidance in my whole life and my work.

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