Cairo University
Faculty of Veterinary medicine
Department of Virology

Isolation and characterization of Avian Influenza viruses type H5N1 years 2015 to 2016 in Egypt.

A Thesis Submitted

by

Osama Mahmoud El shazly

(*B.V.Scs. Fac. Vet. Med., Cairo Univ., 2009*)

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Under supervision of

Prof. Dr. Hussein Aly Hussein
Prof. and head of Virology department
Faculty of Veterinary Medicine
Cairo University

Prof. Dr. Ismail reda

Prof. of Virology
Faculty of Veterinary Medicine
Cairo University

Prof. Dr.Abdel Satar M.Arafa

chief Researcher in Reference Lab.
for Quality Control on Poultry Production
Animal Health Research Institute

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قسم الفيروسات
كلية الطب البيطرى

Approval Sheet

This is to approve that Thesis presented by

Osama Mahmoud El Shazly

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

Prof. Dr. Gabr Fekry EL- Bagoury
Professor of Virology
Faculty of Veterinary Medicine
Moshtohour, Banha University.

Prof. Dr- Ayman Hanea El-Deeb
Ass. Prof. of Virology
Faculty of Veterinary Medicine
Cairo University

Prof. Dr- Abd El Satar A.Mohamed
Chief Researcher in reference
Laboratory for quality control on poultry production
Animal Health Research institute
Dokki -Giza (Supervisor)

Prof. Dr- Hussein Aly Hussein
Professor and Head of Department of Virology
Faculty of Veterinary Medicine
Cairo University (Supervisor)

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العنوان: كلية الطب البيطرى- الجيزة- مصر
تليفون: 37510309- 3571305
الرمز البريدى: 12211
فاكس: 35725240

Cairo University

Faculty of Veterinary Medicine

Department of Virology

Supervision sheet

Supervisors

Prof. Dr. Hussein Aly Hussein

Prof. and head of Virology department

Faculty of Veterinary Medicine

Cairo University

Prof. Dr. Ismail reda

Prof. of Virology

Faculty of Veterinary Medicine

Cairo University

Prof. Dr.Abdel Satar M.Arafa

Chief Researcher in Reference Laboratory for Quality Control of Poultry Production

Animal Health Research Institute

Dokki -Giza

Faculty of Veterinary Medicine
Department of Virology
Cairo University

Name : Osama Mahmoud El shazly

Nationality : Egyptian

Date of birth : 29/ 9 / 1987

Place of birth : Behira

Specification : Virology

Thesis title : Isolation and characterization of Avian Influenza viruses type H5N1 years 2015 to 2016 in Egypt.

Supervisors **: Prof. Dr. Hussein Aly Hussein**

Prof. Dr. Ismail reda

Prof.Dr. Abdel-Satar Arafa Mohamed.

Abstract

Highly pathogenic avian influenza (HPAI) viruses of the H5N1 subtype are widely distributed within poultry populations in Egypt and have great signifiqence on human public health otherwise great economic importance.. In this study six samples from five governorates; three from farms, three from backyard are submitted to RLQP during 2105 ,2016, and they are examined by real time PCR for M and H5 genes of AI and the results revealed all samples were positive for M and H5, genes. Sequencing of H5 gene of isolates revealed that all isolates are highly pathogenic contain multiple basic amino acids in cleavage site (PQGEKRRKKRGLF) and belong to clade 2.2.1.2. The samples under test show identity with A/Goose/Guangdong/1/96 ranged from 91% to 92% while show identity with (A-chicken-Egypt-06459-3-NLQP-2006) (which consider one of the first isolates in Egypt in 2006) ranged 96 to 97% and show identity 97 to 100% between each other, AIVs continue to circulate in backyard between different species and mutate leading to antigenic drift and Periodical surveillance of AI in backyard is very important for detection of the virus and monitoring of its mutations

Key words : highly pathogenic Avian Influenza(HPAI) ,H5N1, HA ,RT-PCR, Sequence

Dedication

Dedicated to my family

….. Father,

….. Mother

…….. My Brothers

…….. my sisters

……my precious wife

……my son (Qusai)

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Avian influenza (AI) is acute, highly contagious viral disease with predilection for the respiratory , digestive and nervous system of a variety of both domestic & wild bird species(***Swayne, D.E. et al 2000, Suarez D.L. 2000***).this important concern of AI due to the specific epidemiological features of it include the large number of possible virus strain, the presence of wild bird virus reservoir which represent constant ,un controllable source of infection, the inherent ability of the virus to convert to high virulent strain once it is transmitted to other host as result of mutation or reassortment so the infection of AI produces variable clinical manifestation (***Suarez D.L . et al ., 2000***).

Avian influenza virus is caused by various serotypes of influenza A virus of the Orthomyxoviridae family, that includes Influenza virus A-C,D Thogotovirus and Isavirus. Influenza A virus is known to infect birds. Avian influenza virus type A viruses can be classified into multiple subtypes 17 subtypes of HA (H1–17) and 10 subtypes of NA (N1–10) have been found to circulate in avian and/or mammalian hosts Based on the antigenic properties of the two surface glycoproteins, hemagglutinin (HA) and neuraminidase (NA) ***(Xueyong et al., 2013)***. The recent discovery of influenza viruses of a new H18N11, in a flat-faced fruit bat from Peru ***(Tong et al., 2013)***.The natural reservoir for subtypes of influenza A viruses is wild aquatic birds, primarily ducks, gulls and shorebirds