



University of Sadat City
Faculty of Veterinary Medicine
Department of Bird and Rabbit Medicine



Studies on Highly Pathogenic Avian Influenza (H5N8) disease in chickens

A Thesis Submitted
By

Mohamed Tarek Taher
(B.V.Sc., Cairo University, 2012)
(M.V.Sc., Cairo University, 2017)

Under Supervision Of

Dr. Hesham Abd El-Rahman Sultan
Professor of Bird and Rabbit Medicine Department,
Faculty of Veterinary Medicine,
University of Sadat City

Dr. Abdel-Sattar Arafa Mohamed
Chief Researcher and Head of
Reference Laboratory for Veterinary Quality
Control on Poultry Production, Animal Health Research Institute Dokki- Giza

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Name: Mohamed Tarek Taher.

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Under Supervision of:

<p>Dr. Hesham A. Sultan Prof. of Birds and Rabbit Med. Faculty of Vet. Med. Sadat City University.</p>	<p>Dr. Abd El Satar Arafa Chief researcher - Head of Reference Laboratory for Quality Control on Poultry Production Animal Health Research Institute Dokki - Giza</p>
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Abstract

In the current study, 74 field samples were collected from Egyptian farms during 2017 to 2019 demonstrating Highly Pathogenic Avian Influenza. Viruses were detected and characterized as HPAI H5N8. Full HA and NA genes of detected viruses were sequenced followed by phylogenetic analysis of 11 selected viruses. The obtained phylogenetic tree revealed that H5N8 field viruses were clustered in clade 2.3.4.4b, with amino acids identity ranged from 96.8% - 99.3% between them, whereas the amino acids identity between H5N8 field viruses and the currently used H5N1 vaccines ranged from 88.1% - 91.3%. Notably, the phylogenetic trees of both HA and NA genes showed that Egyptian HPAIVs H5N8 of this study is closely related to H5N8 viruses recently isolated in Europe in 2020. Sera collected from chicken immunized by one commonly used commercial vaccine and two experimentally prepared vaccines from local H5N8 strains were evaluated for their cross reaction against the antigens of H5N8 field isolates using cross HI test. The obtained results indicate no significant difference between the H5N8 isolates each other whereas results of cross HI with antigens of the three vaccines, showed high cross reactivity toward the Egyptian strains. Similarly, the study showed high antigenic relatedness between the H5N8 isolates each other and the three vaccines which ranged from 63.2% to 94.2% that indicate no subtype difference or a minor subtype difference. In the present study, we investigated the pathobiology of two H5N8 HPAI isolates, belonging to the clade 2.3.4.4, with different origins (chickens and Ducks). Mortality, clinical signs, viral shedding levels and histopathological changes were recorded following intranasal inoculation of the virus in 4-week-old commercial chickens. Inoculation with chickens' origin virus (Russian like) resulted in 100% with 2.47 pathogenicity index, while ducks' origin virus (Europe like) resulted in 90% mortality with 2.05 PI. Accordingly, Both HPAIVs were highly virulent, but chickens' origin HPAIV produced a higher pathogenicity index and mortality rate in chickens than ducks' origin HPAIV, as well as a shorter Death time. Our results concluded that HPAI H5N8 is the predominant currently circulating Avian Influenza within Egyptian poultry flocks and the viruses circulating in Europe in late 2020 shares common ancestor with the Egyptian viruses 2019. Pathobiology experimental study of HPAI H5N8 isolates showed high severity. Vaccines of clade 2.3.4.4 is recommended to replace other used commercial vaccines of different clades, which give higher protection against H5N8 viruses as mentioned in previous studies. Additionally, Further studies are required to clarify the unusual patterns of mortality caused by H5N8 HPAI viruses.

Keywords: HPAI H5N8, HPAI H5N8 genetic characterization, HPAI H5N8 antigenic relatedness, HPAI H5N8 pathobiology.

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