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Experimental trials evaluating mutation evolution of local H5N1 avian influenza classical strain propagated in different avian host.

BY

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English Abstract

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English abstract	current study was tried to evaluate genetic mutation and evolution for eight segment genes of Egyptian H5N1 avian influenza classical strain clade 2.2.1.2 experimentally propagated in 10th passages at different avian host such SPF chicken and different duck species (Pekin and Muscovy), In the current study, results were found Pekin ducks show neither clinical signs, mortality nor virus shedding. In a deep genetic analysis of segment 1 (PB2). on the other hand, sequencings result of segment 2 (PB1) genes were found in the 10th passage in Muscovy ducks' substitution from K (lysine) polar basic amino acid to G (glycine) neutral nonpolar at position 57, also at position 215 substitution from K (lysine) polar basic to R (arginine) polar basic, also at position 363 substitution from K (lysine) polar basic to R (arginine) polar basic. from Genetic analysis of (HA) revealed that point and silent mutations at nucleotide sequence of 10th passage in SPF chicken.in NP analysis of 10th passage from Muscovy duck a significant substitution amino acid at position 210 from R (arginine) polar basic amino acid to Q (glutamine) polar neutral. In deep analysis sequencing of segment 6 (NA) in the Current study shows amino acids substitution at residues position 41 from (R) arginine to (G) glycine in the 10th SPF chicken passage, substitution at 228's		

position from serine (S) to asparagine (N), substitution from asparagine (N) to aspartate (D) at position 46, substitution from isoleucine (I) aliphatic AA to valine (V) aliphatic AA at position 235. NS1 genetic Analysis revealed mutation in the 10th passage from SPF chicken substitutions in C-terminal 'effector' domain at position 107 from alanine (A) is an aliphatic amino acid to threonine (T) is sulfur-containing or have amide group and at 148 position from glutamate (E) to aspartate (D). So, we concluded from this study that serial passaging of HPAI (H5N1) virus in chicken host Led to mutations in NA protein that may play a role in facilitating viral entry and release, alter replication, transmissibility, and susceptibility to antiviral especially to oseltamivir resistance. Also, mutations in NS1 protein may play a role in antagonize the induction of interferon alpha and beta produced by host cells and important role in host range and virulence in chicken, alter viral replication, transmissibility, and susceptibility to antiviral inhibitors. On the other hand, the conclusion from serial passaging of HPAI (H5N1) virus in Muscovy duck led to mutations in NP protein may affecting viral transmissibility, polymerase activity in mammalian cells, and affect replication especially at low temperatures. Also, mutations in PB1 may play role in increasing pathogenicity, virulence, and cell apoptosis.

Key words

influenza H5N1, Gene Mutations, pekin Ducks, Muscovy ducks NP, NS1, PB1, NA

Table of Contents

Acknowledgment	ii
List of tables	vii
List of figures	ix
List of Abbreviations	X
1. Introduction	1
2. Review of Literature	4
2.1 Historical Background	4
2.2 The disease in EGYPT:	6
2.3 ETIOLOGY:	7
2.4 Strain nomenclature:-	9
2.5 Physicochemical properties:-	9
2.6 Morphology and structure of avian influenza virus:	9
2.6.1 Genomic organization of influenza virus	10
2.7 Biological and antigenic properties	12
2.7.1 Surface encoding gene segments:	12
2.7.2 Polymerase encoding gene segments PB2, PB1, PA:	21
2.7.2.1 PB2 gene:	23
2.7.2.2 PB1 gene:	24
2.7.2.3 PA Gene:	26
2.7.3 Nucleoprotein encoding gene segments NP, NS1, an	
(NEP):-	27
2.7.3.1 Nucleoprotein gene:	27
2.7.3.2 Nonstructural (NS) gene:	30
2.7.4 Matrix (M) encoding gene segments:	33
2.8 Molecular diagnosis:	35
2.8.1 Polymerase chain reaction (RT-PCR):	35

2.8.2 Sequencing and phylogenetic analysis of the virus genome.
2.9 Responses to Avian Influenza Viruses in Ducks and Chickens.
2.9.1 Sialic Acid Receptor Distribution and Influenza Virus Tissue Tropism in Ducks and Chickens:
2.9.2 Factors Affecting Susceptibility to Disease in ducks 38
2.9.2.2 Age of Birds
2.9.2.3 Viral Strain-Dependent Differences in Infection Outcome
3. Materials & Methods
1.1 Materials
3.1.1 Virus
3.1.2 Birds
3.1.3 Samples
3.1.4 Real time-PCR and conventional PCR testing for contamination free of each passage from different avian host groups as pooled tracheal swabs
3.1.5 full genome sequencing with Next Generation Sequencing
3.1.6 isolation of avian influenza virus of each passage from different avian host groups
3.1.7 characterization of avian influenza virus by Hemagglutination (HA) test
3.1.8 Preparation of hyperimmune sera against H5N1 original virus A/chicken/Egypt/75S/2015
3.1.9 Hemagglutination inhibition test (OIE, 2018) for cross reactivity between different passages of different hosts and original virus.
3.2 Methods
3.2.1 Experimental design

	Method of Real time-PCR and conventional PCR testing for in free of each passage from different avian host groups 54
3.2.3	Method of full genome sequencing (next generation
sequencing).	
	molecular analysis of A/chicken/Egypt/S75/2015 after different avian hosts AIV genes
3.2.5	submission of the sequenced viruses to gene bank 65
3.2.6	Isolation of avian influenza virus
	Preparation of hyperimmune sera against H5N1 original cken/Egypt/75S/2015
(2018) for cr	Hemagglutination inhibition test (HI) According to OIE oss reactivity between different passages of different hosts virus
4.Results.	
4.1 viru	s passages in different hosts' experiment
passaging in SI	tamination free results of H5N1 virus propagated and PF chicken and muscovy duck hosts by real time RT-PCR al PCR from NDV, ILT, IB, H9, IBD
4.3 Gen	etic analysis of PB2 gene:72
4.4. Ger	netic analysis of PB1 gene:
4.5. Ger	netic analysis of PA gene:89
4.6 Gen	etic analysis of HA Gene
4.7 Gen	etic analysis of full NP Gene: 103
4.8 Gen	etic analysis of full NA Gene: 109
4.9 Gen	etic analysis of full M Gene:
4.10 Ge	netic analysis of full NS Gene:119
	bmission of the sequenced viruses after propagation in hosts to gene bank126
	magglutination inhibition test for cross reactivity between tes of different hosts and antiserum from original virus. 126

العربي	المستخلص	Error! Bookmark not defined.
العربي	الملخص	
6.	Conclusions	
5. Dis	Discussion	

List of tables

TABLE 1:INFLUENZA A VIRUS GENOME RNA SEGMENTS AND CODING ASSIGNMENTS10
TABLE 2: ANTIGENIC SITES AND THEIR AMINO ACIDS OF HA GENE:
TABLE 3: ACCESSION NUMBERS OF DIFFERENT GENES OF ORIGINAL VIRUS USED IN STUDY
TABLE 4: PRIMERS AND PROBES USED FOR REAL TIME RT-PCR IDENTIFICATION OF
VIRUSES IN SAMPLES OF THE STUDY
TABLE 5 COMPONENTS USED FOR PREPARATION OF ALSEVER'S SOLUTION
TABLE 6: SHOWS EXPERIMENTAL GROUPS DESIGN
TABLE 7 REAL TIME PCR REACTION MIX, PRIMERS, AND PROBE WERE ADJUSTED AS THE
FOLLOWING56
TABLE 8:THERMO CYCLING CONDITIONS FOR GENE-SPECIFIC PROBE AND PRIMER FOR
H5 AND H957
TABLE 9:THERMO CYCLING CONDITION FOR GENE-SPECIFIC PROBE AND PRIMER SETS
FOR NDV
TABLE 10: THERMO CYCLING CONDITION FOR GENE-SPECIFIC PROBE AND PRIMER FOR
IBV57
TABLE 11THERMO CYCLING CONDITION FOR GENE-SPECIFIC PROBE AND PRIMER FOR
IBD 57
TABLE 12: THERMO CYCLING CONDITION FOR GENE-SPECIFIC PROBE AND PRIMER FOR
ILT58
TABLE 13: MIX THE FOLLOWING COMPONENTS IN A STERILE MICROFUGE TUBE ON ICE, 59
TABLE 14 PREPARATION OF ADAPTOR LIGATED DNA
TABLE 15 PREPARE AND INSTALL THE AMPLIFICATION SOLUTION
TABLE 16 COMPONENTS OF MELT-OFF SOLUTION
TABLE 17 62
TABLE 18: RESULTS OF VIRUS PROPAGATION PASSAGES IN DIFFERENT AVIAN HOST
CONFIRMED WITH RRT-PCR68
TABLE 19 CONTAMINATION FREE RESULTS OF H5N1 VIRUS PASSAGING IN SPF CHICKEN
AND MUSCOVY DUCK HOSTS68
TABLE 20: CONCLUDED AMINO ACIDS SUBSTITUTIONS IN PB1 PROTEIN AMONG ORIGINAL
STRAINS A/CHICKEN/EGYPT/S75/2015 PB1 (ACCESSION NUMBER MN607976) IN
COMPARISON WITH 10TH PASSAGE OF DUCK (A/DUCK/EGYPT/S75-P10/PB1)
(ACCESSION NUMBER OF GENE BANK MW063640)89
TABLE 21: CONCLUDED AMINO ACIDS SUBSTITUTIONS IN NP PROTEIN AMONG ORIGINAL
STRAINS A/CHICKEN/EGYPT/S75/2015 NP (ACCESSION NUMBER MN607973) IN
COMPARISON WITH 10TH PASSAGE OF DUCK (A/DUCK/EGYPT/S75/2015 P.10/NP)
(ACCESSION NUMBER OF GENE BANK MW063638)
TABLE 22: CONCLUDED AMINO ACIDS SUBSTITUTIONS IN NA PROTEIN AMONG ORIGINAL
STRAINS A/CHICKEN/EGYPT/S75/2015 NA (ACCESSION NUMBER MN607972) IN
COMPARISON WITH 10TH PASSAGE OF CHICKEN (A/CHICKEN/EGYPT/S75-P10/NA)
(ACCESSION NUMBER OF GENE BANK MW044655)113

TABLE 23: CONCLUDED AMINO ACIDS SUBSTITUTIONS IN NS1 PROTEIN AMONG OF	RIGINAI
STRAINS A/CHICKEN/EGYPT/S75/2015 (ACCESSION NUMBER MN6079	74) IN
COMPARISON WITH 10TH PASSAGE OF CHICKEN (A/CHICKEN/EGYPT/S75-	P10/NS)
(ACCESSION NUMBER OF GENE BANK MW044661)	122
Table 24: Concluded amino acids substitutions in 10^{th} passage of Muscov	Y DUCK
IN COMPARISON WITH ORIGINAL VIRUS A/CHICKEN/EGYPT/S75/2015	124
Table 25: concluded amino acids substitutions in 10^{th} passage of SPF chi	CKEN IN
COMPARISON WITH ORIGINAL VIRUS A/CHICKEN/EGYPT/S75/2015	124
TABLE 26: CONCLUDED NUCLEOTIDE AND AMINO ACIDS SUBSTITUTIONS IN 10TH F	ASSAGE
OF SPF CHICKEN AND 10TH PASSAGE OF MUSCOVY DUCK IN COMPARISO	N WITH
ORIGINAL VIRUS A/CHICKEN/EGYPT/S75/2015	125
TABLE 27: DESIGNATION AND ACCESSION NUMBERS OF DIFFERENT GENES SEQUE	ENCE OF
THE EXAMINED VIRUSES	126
TABLE 28: SHOWN RESULTS OF CROSS REACTIVITY BETWEEN DIFFERENT P	ASSAGE
ISOLATES AGAINST ANTISERUM FROM ORIGINAL VIRUS A/CHICKEN/EGYPT/S	75/2015
	127

List of figures

FIGURE 1 STRUCTURE OF AVIAN INFLUENZA VIRUS	
FIGURE 2:PB1, PB2 PA AND NP COMPLEX	22
FIGURE 3:SCHEMATIC REPRESENTATION OF THE INFLUENZA A VIRUS NUC	LEOPROTEIN
(NP)	29
FIGURE 4:TOPOLOGY DIAGRAM (A) AND HYPOTHETICAL MODEL (B) OF THE	C-TERMINUS
MONOMER OF THE NS1A PROTEIN	31
FIGURE 5: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN BY RRT-PC	R TO INSURE
IT IS H5N1.	69
FIGURE 6: RESULT OF H5N1 VIRUS PASSAGING IN MUSCOVY DUCK BY RRT-PC	CR TO INSURE
IT IS H5N1	69
FIGURE 7: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN AND MUS	SCOVY DUCK
HOSTS BY REAL TIME RT-PCR THAT FREE FROM IB VIRUS	70
FIGURE 8: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN AND MUS	SCOVY DUCK
HOSTS BY CONVENTIONAL PCR THAT FREE FROM IBD VIRUS	70
FIGURE 9: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN AND MUS	SCOVY DUCK
HOSTS BY RRT-PCR THAT FREE FROM ILT VIRUS	71
FIGURE 10: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN AND MU	SCOVY DUCK
HOSTS BY REAL TIME RT-PCR THAT FREE FROM NDV	71
FIGURE 11: RESULT OF H5N1 VIRUS PASSAGING IN SPF CHICKEN AND MU	SCOVY DUCK
HOSTS BY REAL TIME RT-PCR THAT FREE FROM H9N2	72
FIGURE 12 NUCLEOTIDE SEQUENCE ALIGNMENT OF PB2 GENE	78
FIGURE 13 AMINO ACID SEQUENCE ALIGNMENT OF PB2 PROTEIN	80
FIGURE 14 NUCLEOTIDE SEQUENCE ALIGNMENT OF PB1 GENE	86
FIGURE 15 AMINO ACID SEQUENCE ALIGNMENT OF PB1 PROTEIN	88
FIGURE 16 NUCLEOTIDE SEQUENCE ALIGNMENT OF PA GENE	
FIGURE 17 AMINO ACID SEQUENCE ALIGNMENT OF PA PROTEIN	96
FIGURE 18 NUCLEOTIDE SEQUENCE ALIGNMENT OF HA GENE	100
FIGURE 19 AMINO ACID SEQUENCE ALIGNMENT OF HA PROTEIN	102
FIGURE 20 NUCLEOTIDE SEQUENCE ALIGNMENT OF NP GENE	106
FIGURE 21: AMINO ACID SEQUENCE ALIGNMENT OF NP PROTEIN	108
FIGURE 22: NUCLEOTIDE SEQUENCE ALIGNMENT OF NA GENE	112
FIGURE 23: AMINO ACID SEQUENCE ALIGNMENT OF FULL NA GENE	113
FIGURE 24 NUCLEOTIDE SEQUENCE ALIGNMENT OF M1 GENE	116
FIGURE 25 AMINO ACIDS SEQUENCE ALIGNMENT OF M1 PROTEIN	117
FIGURE 26: NUCLEOTIDE SEQUENCE ALIGNMENT OF FULL M2 GENE	117
FIGURE 27: AMINO ACIDS SEQUENCE ALIGNMENT OF M2 PROTEIN	118
FIGURE 28: NUCLEOTIDE ALIGNMENT ANALYSIS OF FULL NS1 GENE	121
FIGURE 29: AMINO ACID ALIGNMENT ANALYSIS OF FULL NS1 PROTEIN	121
FIGURE 30: NUCLEOTIDE SEQUENCE ALIGNMENT OF NS2 PROTEIN	
FIGURE 31: AMINO ACIDS SEQUENCE ALIGNMENT OF NS2 PROTEIN	123