CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

AB	Anti-body
AGP test	Agar gel precipitation test
AI	Avian influenza
APMV-1	Avian paramyxo virus type-I
b.p.	Base pair
Ch.	Challenge
CRD	Chronic respiratory disease
ECE	Embryonated chicken egg
ELD_{50}	Embryo Lethal Dose 50
ELISA	Enzyme linked immune-sorbent assay
END	Exotic Newcastle disease
F	Phenyl-alanine
F0	Precursor of the F-protein
FAO	Food and agriculture organization
F-protein	Fusion protein
Gr.D	Greenish intestinal content (Diarrhea)
HA	Haemagglutination
HB1	Hitchner B1
Heg.	Haemmorhage
HI	Haemagglutination inhibition
HPAI	Highly pathogenic avian influenza
IB	Infectious bronchitis
IBDV	Infectious bursal disease virus
ICPI	Intracerebral pathogenicity Index
IM	Intramuscular
IVPI	Intravenous pathogenicity Index
K	Lysine
Kb	Kilo base
LoNDV	Low virulence Newcastle disease virus
LPAI	Low pathogenic Avian Influenza
mAb	Monoclonal antibody
MDT	Mean death time
n.d.	Not done
N.Obs.	Not observed
ND	Newcastle disease
NDV	Newcastle disease virus
No.	Number
NTC	No template control
OIE	Office International des Epizootics

PI	Post infection
PPMV	Pigeon paramyxovirus
R	Arginin
rRT-PCR	Real time reverse transcriptase polymerase chain reaction
RT-PCR	Reverse transcriptase polymerase chain reaction
Sh.	Shedding
SPF	Specific pathogen free
VN	Virus neutralization
vNDV	Velogenic Newcastle Disease virus

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Full sequence analysis of F gene of NDV and comparative evaluation of genotype II and VII vaccines

Abstract

The present study was conducted using samples from seven suspected Newcastle disease virus (NDV) flocks of vaccinated chickens during 2012 to 2016 from 6 governorates in Egypt. The pathogenicity of the NDV isolates has been estimated through ICPI and ranged from 1.66 to 1.73 which indicates the velogenic type of NDV isolates. Pathotyping and genotyping of these isolates were done through sequencing of full length F gene. Results indicated that the seven NDV isolates showed characteristic cleavage site motif (112RRQKRF117) for the velogenic strains of NDV. Phylogenetic analysis of the F gene clustered these isolates within group I of genotype VIId within Israeli strains NDV/IS/2015, NDV-Ch/SD883**,** and most of Middle East strains. Six out of seven sequenced isolates have 6 potential N-linked glycosylation sites. The neutralization epitope on the 5 antigenic sites of fusion are conserved in all Egyptian strains of this study except NDV-KFR-B7-2012 which has a substitution at D**170 G** in epitope A4. In this study we compare two vaccination programs one using genotype VII inactivated and live NDV vaccine and second using genotype II inactivated and live vaccine. Contact chicks were added in both groups post challenge. The results indicated that both programs can protect birds from mortalities (up to 100 %). The vaccinated group with genotype VII was significantly prevent the virus shedding at $3^{th,}$ 5^{th}, 7^{th} and 10^{th} days post challenge unlike the genotype II vaccinated group.

Key words: Fusion gene, cleavage site, Heptad Repeat domains, Virus shedding.