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

A Thesis Submitted by

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Dedication

Dedicated To My Family,

To my MOTHER, Nagwa.

Thank you so much for spending your life loving me and taking such good care of all my needs. You always had your own ways of making me feel so special. You are one great MOM.

To my DAD, Mohamed Selim

Thank you for a lifetime of unfailing love, loyalty and support. Allah gave me one huge blessing when he decided to give me the chance to be your number 1 SON.

To my dear and sweet WIFE, Sahar:

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To my LOVING SISTER, Menna

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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.

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