

Summary of the DVSc thesis No: 5016 Faculty of Veterinary Medicine, Urmia University.

The academic year: 2022-2023

Author: Seyed Sajjad Babaeimarzangou

Title of thesis:

Molecular Characterization and Phylogenetic Study of the Haemagglutinin-neuraminidase Gene of Newcastle Disease Viruses Isolated from Broiler Farms of Iran

Newcastle disease virus (NDV) is considered one of the most important avian viral pathogenic agents, causing a devastating economic burden to the poultry industry worldwide. The current study was conducted to gain deep insights into the molecular and phylogenetic analyses of the complete hemagglutinin-neuraminidase (HN) coding region among NDV isolates. Five hundred and forty samples from thirty-six vaccinated broiler farms located in eighteen provinces of Iran were collected between July 2017 to February 2020. Thirty collected samples, obtained from different parts of Iran (West Azerbaijan, Golestan, East Azerbaijan, Mazandaran, Kerman, Gilan), were submitted to HA, HI, and RT-PCR tests and used for phylogenetic analysis during this study. The results confirmed VII.1.1, which was previously known as subgenotype VIII, as the predominant subgenotype circulating in commercial broiler farms in Iran. Identification of (a) an additional N-glycosylation site at position 144 (NIS); (b) mutations S315P and I369V related to increasing the viral thermostability; (c) cysteine residues at positions 123; (d) amino acid substitutions in the HN antigenic sites, especially the mutations I514V and E347Q, as well as the other mutant within HN binding sites of the VII.1.1 subgenotype, seems to suggest the idea that this new subgenotype of NDV may possess a high level of pathogenicity and virulence among other NDV subgenotypes. In conclusion, the results demonstrate an additional N-glycosylation site at position 144 (NIS), which may alter the virulence of the isolates. Besides, finding the thermostable mutations (S315P and I369V) and the other amino acid substitutions among the VII.1.1 subgenotype isolates may influence the vaccine immunity against this new NDV subgenotype. In addition, using homolog vaccines with stricter biosecurity measures in Iran might also help us to implement better vaccination strategies in the future.

Keywords: Amino acid substitutions, Hemagglutinin-Neuraminidase, NDV, phylogenetic analyses, subgenotype VII.1.1.