Phylogenetic Analyses of Newcastle Disease Virus Isolated from Unvaccinated Chicken Flocks in Kyrgyzstan from 2015 to 2016

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Abstract : Newcastle disease virus (NDV) is a contagious viral disease of the poultry industry and other birds throughout the world. At present, very little is known about molecular epidemiological data regarding the causes of ND outbreak in commercial poultry farms in Kyrgyzstan. In the current study, the NDV isolated from the one out of three samples from the unvaccinated flock was confirmed as NDV. Phylogenetic analysis indicated that this NDV strain is clustered in the Class II subgenotype VIId, and closely related to the Chinese NDV isolate. Phylogenetic analyses revealed that the isolated NDV strain has an origin different from the 4 NDV strains previously identified in Kyrgyzstan. According to the mean death time (MDT: 61.1 h) and a multibasic amino acid (aa) sequence at the F0 proteolytic cleavage site (112 R-R-Q-K-R-F¹¹⁷), the NDV isolate was determined as mesogenic strain. Several mutations in the neutralizing epitopes (notably, 347 E \rightarrow K) and the global head were observed in the hemagglutinin-neuraminidase (HN) protein of the current isolate. The present study represents the molecular characterization of the coding gene region of NDV in Kyrgyzstan. Additionally, further study will be investigated on the antigenic characterization using monoclonal antibody.

Keywords : Kyrgyzstan, Newcastle disease, genotype, genome characterization

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