

Evaluation of virulence and phylogenetic study of Newcastle disease virus isolated from broiler poultry farms in Mazandaran province

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Abstract

Newcastle disease (ND) is one of the important viral diseases of poultry that causes considerable economic loss to breeding farms. Continuous evaluation of circulating virus genotypes and pathotypes is the crucial step to control the disease prevalence. The present study aimed to study the phylogenetic and pathogenicity indices of circulating ND virus (NDV) in poultry farms located in Mazandaran province during 2018. Following the isolation of the virus from the brains of the dead chickens in five different farms, intracerebral pathogenicity index (ICPI) and the mean death time (MDT) were determined. For phylogenetic analysis, virus RNA was extracted and following RT-PCR, the sequence of the F gene was determined and compared with those presented in the gene bank. Results showed that the isolated viruses had ICPT of 1.97 and MDT of 56 hours, related to the velogenic pathotype and their virulence was close to the standard strains of challenge viruses. Also, based on the results of phylogenetic analysis, the isolated viruses were classified as genotype VII. By determination of phenotypic and genotypic identity of the isolated viruses, the clinical evidence showing the velogenic and visceral form of ND was confirmed. The present study showed that the NDV causing mortality in commercial poultry farms during 2018 had virulence near to standard challenge strains and belonged to VII genotype and VII.1.1 subgenotype of NDV. Therefore, the isolated virus, as a local virulent strain, could be used in challenge tests and evaluation of the preventive vaccination programs.

Key words: Broiler, Genotype, Newcastle disease virus, Pathogenicity index, Phylogenetic analysis, Virulence

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