

Molecular and phathotyping survey of Newcastle virus isolated from migratory birds in Bushehr province

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Abstract

Migratory birds and waterfowl are know reservoirs of avian paramyxoviruses and it considered cause of the disease in poultry industry, therefore, the survey of pathotyping viruses isolated from migratory birds to prevent transmission is necessary. Samples of present research collected from wetlands of Boushehr province in south of Iran and obtained from Razi Vaccine and Serum Research Institute, Shiraz, Iran. Virus isolation and characterization of the samples were performed at the Razi institute. The biological properties and pathogenicity of five NDV isolated were studied by intracerebral pathogenicity index (ICPI), mean death time (MDT) value and reverse transcription-polymerase chain reaction (RT-PCR) methods. The PCR was used to amplify 362bp the cleavage site of all isolates. Sequencing of PCR products was performed to identify nucleotides and deduce amino acids. Aligment and phylogentic analysis of F protein (cleavage site) was performed by software Megaline5, Blast and Bioedit. MDT and ICPI method showed that all of 5 samples were detected as lentogenic strain with low virulent and so, in RT-PCR method all of the samples in the special motif were positive. The deduced amino acid sequence of the cleavage site of the fusion (F) protein confirmed that, all isolates contained the avirulent motif ¹¹² GRQGRL¹¹⁷ at the cleavage site. All isolates have high similarity with LaSota and B1 strain in gene bank. The result in this study showed that migratory birds particularly aquatic birds in Bushehr carries lentogenic NDVs and act as one the reservoirs for the virus. Therefore, ND is always a great risk for the native avian population living on the routes of migratory birds.

Key words: Newcastle virus, Migratory birds, Reverse transcription-polymerase chain reaction (RT-PCR)

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