

Phylogenetic analysis and molecular characterisation of Newcastle Disease virus genotype VII in Malaysia

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ABSTRACT

Introduction: Newcastle disease (ND) outbreaks in Malaysia cause serious economic losses to the poultry industry. The Newcastle Disease Virus (NDV) genotype VII has caused fatal infections in susceptible birds and is thought to be responsible for the fourth major ND panzootic worldwide. Analysis of GVII subtypes in birds revealed that they are highly divergent with different levels of virulence. **Objective:** The study aims to identify distinct subgroups of NDV genotype VII and to determine the pathogenicity of isolates based on fusion gene molecular motif bases from samples sent to the Veterinary Research Institute (VRI) between 2015 and 2021. **Materials and methods:** Randomly sample positive ND subgenotype VII were selected and phylogenetic analyses was conducted to identify distinct NDV subgenotype of GVII. Virulence of positive local isolates was determined based on the cleavage sites of the fusion gene. **Results and conclusion:** All twelve isolates in this study were clustered in subgenotype VII 1.2 NDV's based on partial sequencing of the hypervariable region of the fusion gene. Among isolates, five isolates were grouped in subgenotype VIIi and seven isolates in subgenotype VIIh. Besides that, five isolates subgenotype VIIi revealed the amino acid motif at the F cleavage site of 112RRQKRF117 whereas eight isolates subgenotype VIIh showed 112RRRKRF117. Based on both amino acid motifs, all isolates were virulence NDV. Furthermore, sequencing and phylogenetic analysis of all the study isolates indicated that they were all related to previous outbreaks in Southeast Asia. All of the isolates were identified as virulent strains of NDV and classified into subgenotype VIIi and subgenotype VIIh. Therefore, the current study offers essential information on the epidemiology, characteristics and prevalence of ND which is important for disease control in Malaysia.