

Sequence and phylogenetic analysis of Newcastle disease virus genotypes isolated in Malaysia between 2004 and 2005

Abstract

Sequence analysis of the fusion (F) gene of eight Malaysian NDV isolates showed that all the isolates were categorized as velogenic viruses, with the F cleavage site motif 112R-R-Q-K-R116 or 112R-R-R-K-R116 at the C-terminus of the F2 protein and phenylalanine (F) at residue 117 at the N-terminus of the F1 protein. Phylogenetic analysis revealed that all of the isolates were grouped in two distinct clusters under sub-genotype VIIId. The isolates were about 4.8–11.7% genetically distant from sub-genotypes VIIa, VIIb, VIIc and VIIe. When the nucleotide sequences of the eight Malaysian isolates were compared phylogenetically to those of the old published local isolates, it was found that genotype VIII, VII, II and I viruses exist in Malaysia and caused sporadic infections. It is suggested that genotype VII viruses were responsible for most of the outbreaks in recent years.