

Phylogenetic Analysis of Partial Surface Protein Gene Sequence of Avian Influenza A Subtype H9N2 in Layer in East Java

ABSTRACT

Avian influenza virus subtype H9N2 has become established in domestic poultry in Asia and Africa. Ninety-nine cases were observed in various provinces in Indonesia. Clinical sign, pathologic lesions and egg production were recorded. The aim of this study is to find out the homology of nucleotide sequence of surface Protein H9N2 influenza virus isolate from Chickens Layer in east Java. Confirmation was made using virus isolation, reverse transcriptase PCR (RT-PCR), and sequencing. To construct hemagglutinin (HA) phylogeny, the secondary data of Eurasian lineages were downloaded from GenBank. For Neuraminidase (NA), sequences with the highest similarities with data sequences from GenBank found in this study. Phylogenetic was inferred using neighbor-joining method in Mega 7.0 package. Homology analysis of nucleotide sequences and amino acid sequences was performed on the BLAST program at NCBI. The result showed that the nucleotide sequence of the HA-encoding gene identified in this study shared 96.96% sequence identity with that of A/duck/Hongkong/Y280/1997, while its neuraminidase-encoding gene sequences shared 94.37% identities with that A/duck/Hongkong/Y280/1997. The phylogeny shows that the HA of AIV-H9N2 found in this study forms distinct cluster with some vietnam and China's sequence data. We conclude that AIV-H9N2 widespread in districts in east java.

Key word : *Avian Influenza*, Jawa Timur, H9N2.