

## ABSTRACT

MOLECULAR CHARACTERIZATION AND PATHOGENICITY PROFILE OF  
H5N1 VIRUS ISOLATED FROM A LOCAL TREE SPARROW (*PASSER MONTANUS*)  
AS SOURCE NATURAL RESERVOIR IN EAST JAVA- INDONESIA

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The isolation of an H5N1 Influenza A virus from a tree sparrow (*Passer montanus*) which we captured in East Java (Sidoarjo) was reported. The analysis showed that the virus titer was  $10^{6.5}$ ELD 50 and the virus had antigenicity relationships with all the antisera panel derived from clade 2.1.3, but not with a panel of antisera derived from clade 2.1.1 that were considered representation of the virus in Indonesia.

Based on the result of phylogenetic tree and homology analysis revealed that its haemagglutinin (HA) and neuraminidase (NA) were genetically similar with the virus chicken isolated of East Java 2010 and the virus human isolated from Indonesia in 2006-2007. The sequence revealed that the HA protein cleavage site sequence was PQRESRRKKR and the sequence of receptor binding site was QSG. This showed that the virus is classified as High Pathogenic Avian Influenza H5N1, but it could not transmit among human.

In the experimental laboratories, it was reported that the pathogenicity of this virus was higher in chicken than in tree sparrow. Thus tree sparrow was more potential to spread this virus than chicken.

The finding of a tree sparrow H5N1 virus is genetically similar to the virus isolated from human, thus it is important to always monitor the existence of virus in wild birds to anticipate pandemic.

**Key words:**

H5N1, Haemagglutinin, Neuraminidase, Tree sparrow.