

**CHARACTERIZATION OF GEN CODING FUSION PROTEIN OF
NEWCASTLE DISEASE VIRUS INFECTED NATIF CHICKEN (*Gallus
gallus domesticus*) IN SURABAYA**

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ABSTRACT

This study was aimed to discover the homology of nucleotide sequence, homology percentage, and those relation phylogenetic of protein Fusion (F) gene coding of Newcastle disease (ND) in domestic chicken (*Gallus gallus domesticus*) in Surabaya using some comparison isolat from GenBank. Research samples were scour of digestive organs from domestic chicken, that were collected from traditional market in Wonokromo, Surabaya. Samples were tested using RT-PCR with primer forward and reverse with target 976bp, positive sample which is continued with sequencing then homology and nucletide analyis which is done and which is translsted into amino acid. Result from RT- PCR showed chc/SBY/2018 was positive, then will be done comparison with references sequence, lasota vaccine and various isolates of ND from Indonesia. Result of homology chc/SBY/2018 sample has similarity 88% with references sequence, while with lasota vaccine has similarity 87%, and the highest result of homology was showed by the comparison with various isolates in indonesia 90-95%. Translation result from nucleotide aligment into amino acid showed shifts on amino acid structure, which is amino acid shifts could be affected by many things like nutrition, wheater, environment, etc. The conclusion was chc/SBY/2018 sample has quite high similarity with Indonesian isolates and undergo mutation on nucleotide structure on amino acid and phylogenetic analysis from isolates in this study relate to some isolates of vaccine and some isolates in Indonesia.

Keywords: *Newcastle Disease, homology, amino acid*