

HOMOLOGY AND PHYLOGENETIC ANALYSIS OF FUSION (F) PROTEIN CODING GENE 4660 – 4988 BP OF NEWCASTLE DISEASE VIRUS FROM NATIVE CHICKEN IN SURABAYA

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ABSTRACT

Newcastle disease virus is contagious disease affecting many avian species especially poultry industries. It can be affected to domestic poultry due to high susceptibility and endemic disease in Indonesia. The program of vaccination hasn't run perfectly. This happen because the dissimilarity between vaccine strains and local strain. There are need to analysis of Newcastle disease virus for data recording to give more information about score of homology and phylogenetic virus to find the original strain and for better vaccination program to protection of poultry industries. Thirty – six NDV species samples isolated from native chicken (*Gallus gallus domesticus*), sparrow, and pigeons in Surabaya, Indonesia were analyzed for its homology with other isolates based on F protein. Three (KT, KTW, RSH) out of thirty-six showed high HA titres and HI titres of $\geq 2^6$. The partiaf F gene of 329bp of samples were amplified using One Step RT-PCR and visualized using agar gel electrophoresis. Then the products were purified using ClustaIW Alignment in Bioedit version 7.0.5.3. The only sample KTW (native chicken) was score of each homology were then analyzed using Neddleman-Wunsch Algorithm via NCBI, and show similarity 48%, and for phylogenetic was analyzed using MEGA 6.0.6, and show distant relationship between the sample and reference sequence.

Key words: Amino Acid Sequence, Homology, Phylogenetic, F, Lentogenic, ND.