

KARAKTERISASI PROTEIN *POLYMERASE BASIC 2* DAN PROTEIN *NON STRUKTURAL (NS1)* VIRUS AVIAN INFLUENZA ASAL ITIK

**A.Magfira Satya Apada
11/326053/PKH/000447**

**Pembimbing Utama: Dr. drh. Michael Haryadi Wibowo, MP
Pembimbing Pendamping: Prof. drh. Widya Asmara, S.U., Ph.D**

INTISARI

Kasus avian influenza di Indonesia pertama kali terjadi pada tahun 2003, menyerang peternakan ayam ras di Jawa Barat dan Jawa Tengah. Wabah penyakit ini kemudian menjadi endemis di beberapa daerah dan menyerang hampir seluruh wilayah di Indonesia, kecuali Maluku Utara yang sampai saat ini masih dinyatakan bebas. Virus avian influenza selain dapat menyerang unggas, juga memiliki potensi untuk bisa menular pada mamalia termasuk manusia. Kemampuan penularan ini diperantarai oleh beberapa protein yang dimiliki oleh virus AI antara lain protein *Polymerase Basic 2* dan *Non Struktural (NS1)*. Dewasa ini dilaporkan matinya ratusan itik di wilayah Jawa Tengah dan Jawa Timur yang diketahui penyebabnya adalah virus avian influenza *clade 2.3.2*. Penelitian ini bertujuan untuk melakukan karakterisasi protein PB2 pada posisi 627 dan NS 1 pada posisi 92 virus avian influenza yang berasal dari isolate itik daerah Jawa Timur tahun 2013. Sampel berupa organ paru-paru dan swab kloaka dipropagasi pada telur berembrio kemudian diidentifikasi dengan uji HA/HI menggunakan antiserum spesifik H5N1. Amplifikasi gen PB2 dan NS1 dilakukan dengan *reverse transcriptase polymerase chain reaction* menggunakan primer spesifik protein PB2 dan NS 1. Hasil amplifikasi kemudian divisualisasikan dengan elektroforesis. Produk PCR dengan hasil positif disekuensing. Hasil sekuensing yang diperoleh dianalisa dengan program mega 5.0 meliputi prediksi asam amino, *multiple alignment* dan *phylogenetic tree* dengan metode *Neighbor Joining*. Hasil yang diperoleh pada pemeriksaan serologis menunjukkan isolat sampel positif H5N1. Prediksi asam amino menunjukkan posisi asam amino 627 protein PB2 isolat sampel adalah glutamat (E). Posisi asam amino 92 protein NS1 mengalami perbedaan dengan virus avian influenza yang telah beredar di Indonesia sebelumnya, dimana pada virus lama ditempati oleh aspartat (D) sedangkan pada isolat sampel ditempati oleh glutamat (E). Hasil *phylogenetic tree* protein PB2 dan NS1, keduanya menunjukkan tingkat kekerabatan yang tinggi dengan data virus *gen bank* asal Vietnam yang disolasi pada tahun 2012 dan 2013.

Kata kunci : *avian influenza*, amplifikasi, PB2, NS1

**CHARACTERIZATION OF THE POLYMERASE BASIC 2 PROTEIN
AND NON STRUCTURAL PROTEIN (NS1) OF THE AVIAN INFLUENZA
VIRUS FROM DUCKS**

**A.Magfira Satya Apada
11/326053/PKH/000447**

**Supervisor: Dr. drh. Michael Haryadi Wibowo, MP
Co-Supervisor: Prof. drh. Widya Asmara, S.U., Ph.D**

ABSTRACT

The avian influenza case in Indonesia first occurred in 2003, attacking purebred chicken farms in West Java and Central Java. This disease later became endemic in several other regions and spread through almost the entire country, except North Maluku, which until now is still declared avian influenza free. The avian influenza virus not only attacks the poultry, it also has the potential to be infectious in mammals including humans. This transmission capability is mediated by several proteins possessed by A1 viruses, among others, Polymerase Basic 2 and non structural protein (NS1). Recently, the death of hundreds of ducks in Central Java and East Java have been reported and the cause is later known to be the virus avian influenza clade 2.3.2. The aim of this research is to characterize PB2 protein at position 627 and NS1 at position 92 of avian influenza virus that come from isolate duck of East Java area in 2013. Samples of lungs and cloacal swabs are propagated in embryonated eggs and then identified by HA/HI using a specific H5N1 antiserum. Amplification of PB2 and NS1 genes was performed by reverse transcriptase polymerase chain reaction using PB2 and NS protein specific primers 1. The amplification results were then visualized by electrophoresis. PCR products with positive results are sequenced. The obtained sequencing results analyzed by MEGA 5.0 program include prediction of amino acid, multiple alignment and phylogenetic tree by Neighbor Joining method. Results obtained on serological examination showed positive H5N1 sample isolates. Amino acid prediction shows the position of amino acid 627 protein PB2 isolate sample is glutamate (E). The position of amino acid 92 NS1 protein differs from avian influenza virus that has been circulating in Indonesia before, whereas in old virus it is occupied by aspartate (D), while in sample isolate it is occupied by glutamate (E). Results of phylogenetic tree proteins PB2 and NS1 both showed a high level of kinship with data gene virus of Vietnamese banks that were insulated in 2012 and 2013.

Key words: *avian influenza*, amplifikasi, PB2, NS1