

**KARAKTERISASI GEN HEMAGLUTININ VIRUS AVIAN INFLUENZA
H5N1 PADA UNGGAS DI WILAYAH KERJA BALAI VETERINER
LAMPUNG TAHUN 2014-2017**

Arif Setiani Wahyuning Tyas

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ABSTRAK

Avian Influenza (AI) adalah penyakit infeksius yang disebabkan virus influenza tipe A, yang mengakibatkan kerugian sangat besar baik sosial ekonomi maupun kesehatan masyarakat. *Avian influenza* merupakan salah satu penyakit hewan menular strategis (PHMS) dan hama penyakit hewan karantina (HPHK) di Indonesia yang menyebar di 33 provinsi termasuk di wilayah kerja Balai Veteriner Lampung. Diantara gen-gen yang mengkode protein virus AI, gen haemagglutinin (HA) menjadi faktor utama untuk membedakan patogenitas virus AI yang memiliki kemampuan evolusi yang lebih tinggi dan sekuens dari gen ini selalu mengalami perubahan. Penelitian ini bertujuan untuk melakukan karakterisasi, patogenesitas dan kekerabatan berdasarkan perubahan molekuler virus *highly pathogenic avian influenza* (HPAI) di wilayah kerja Balai Veteriner Lampung. Dalam penelitian ini digunakan 6 sampel koleksi dari Provinsi Lampung dan Sumatera Selatan tahun 2014-2017. Identifikasi subtipe H5 dengan *real time RT-PCR* H5 dan N1 dilakukan dengan konvensional RT-PCR. Dilanjutkan dengan karakterisasi gen HA secara utuh dan sekuensing. Hasil sekuensing dianalisis menggunakan *software* Bio Edit dan MEGA 6. Dari penelitian diperoleh hasil: keenam sampel positif terhadap identifikasi subtipe H5 dan N1; susunan asam amino penyusun *cleavage site* PQRESRRKKRG, PQRERRRKKRG dan PQRERRRK-RG dengan pola konsensus sekuens asam amino *receptor binding site* GVSSA (130-134) dan NGQSG (220-224) serta ditemukan substitusi asam amino pada K189M dan S133A; sampel A/Chicken/Lampung Barat/03.0095/2014 dan A/Chicken/Muara Enim/03.0493/2015 termasuk dalam *clade* 2.1.3.2a dengan nilai homologi 93,78 – 97,30%. Sampel A/Chicken/Tanggamus/03.0872/2016, A/Quail/Oku/03.1383/2016, A/Chicken/Metro/03.0074/2017 dan A/Chicken/ Pesawaran/ 03.0042/2017 termasuk *clade* 2.3.2.1c dengan nilai homologi 96,89 – 97,89 %. Berdasarkan hasil disimpulkan: sampel penelitian adalah virus AI subtipe H5N1; berdasarkan pola asam amino pada daerah *cleavage site* merupakan HPAI; berdasarkan pola konsensus pada *receptor binding site* masih memiliki kecenderungan berikatan dengan reseptor unggas; sampel penelitian dari tahun 2014-2017 termasuk dalam sub-sub-sub *clade* 2.1.3.2a dengan nilai homologi 93,78-97,30% dan sub-sub-sub *clade* 2.3.2.1c dengan nilai homologi 96,89-97,89%. Hasil tersebut sangat penting untuk membantu program pengendalian AI.

Kata kunci: virus *avian influenza*, hemagglutinin, analisis genetik, substitusi, *clade*

CHARACTERIZATION OF HEMAGGLUTININ GENE OF H5N1 AVIAN INFLUENZA VIRUS IN POULTRY IN THE DISEASE INVESTIGATION CENTRE LAMPUNG WORKING AREAS IN 2014-2017

Arif Setiani Wahyuning Tyas

15/388334/PKH/00533

ABSTRACT

Avian Influenza (AI) is an infectious disease caused by influenza virus type A, which resulted in huge losses both socioeconomic and public health. Avian influenza is one of the strategic spreading animal diseases (PHMS) and quarantine animal pests (HPHK) in Indonesia, spreading in 33 provinces including Disease Investigation Centre Lampung working area. Hemagglutinin (HA) gene is the major factor for differentiating the pathogenicity of AI viruses that have higher evolutionary capabilities and the sequences of these genes are constantly changing among the genes encoding the AI virus proteins. This study was conducted to observe pathogenic and viral linkage of highly pathogenic avian influenza (HPAI) based of characterize molecular in the Disease Investigation Centre Lampung working area. Six samples collected from of a Disease Investigation Centre Lampung working area Lampung and South Sumatra from 2014-2017 were used in this study. Identification of H5 and N1 subtypes were done respectively using real time RT-PCR and conventional RT-PCR, and then followed by hemagglutinin (HA) gene characterization and sequencing. The sequencing results were analyzed using Bio Edit and MEGA 6 software. The results showed that all samples were positive avian influenza virus (AIV) subtypes H5 and N1. The arrangement of amino acids on the cleavage site were PQRESRRKKRG, PQRERRRKKRG and PQRERRRK-RG. The amino acids on the receptor binding site were GVSSA (130-134) and NGQSG (220-224), and there were also amino acid substitution such as K189M and S133A. Molecular characterization revealed two genetically distinct sub-sub-sub clade 2.1.3.2a and sub-sub-sub-clade 2.3.2.1c with homology values from 93.78 to 97.30%, and 96.89 to 97,89%. Based on the research result of the present study can be concluded that the virus were identified as H5N1 avian influenza virus; that could be categorized as HPAI and tend to bind to poultry receptors; and two genetically distinct sub-sub-sub clade 2.1.3.2a and sub-sub-sub-clade 2.3.2.1c with high homology values. All of these findings are very important to help in disesase control program of AIV.

Keywords: avian influenza virus, hemagglutinin, genetic analysis, substitution, clade