ABSTRACT

Molecular Analysis of Hepatitis A Virus from Clinic’s Sample of Acute Hepatitis Patients in East Java, 2015 - 2016

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INTRODUCTION: Acute hepatitis is an infectious disease mainly by hepatitis A virus which has 7 genotypes. Nevertheless there is no study revealing the genotype distribution of hepatitis A virus in Indonesia. It is reported that outbreak happened in 2015 in Bogor and Bondowoso. Therefore it is imperative to investigate the virus distribution to suppress infection cases of acute hepatitis patients from Bondowoso in which outbreak have taken place at late November 2015 till the beginning of 2016.

METHODS: Sera sample was carried out by the ELISA. The positive sera of anti-HAV were subjected to RT-PCR to detect HAV RNA and then direct sequencing. The HAV genotype was examined sequencing scanner in VP1/P2A region and VP3/VP1 region. Then, it analyze by phylogenetic analysis.

RESULTS: Result anti-HAV reveals 100% of samples (16 samples) are infected by hepatitis A virus. Despite that through genotype analysis only 50% (8 from 16 samples) have RNA detectable and indicate genotype 1A infection.

DISCUSSION: This study shows that HAV outbreak in Bondowoso is caused mainly by genotype 1A. It has similar subgenotype with other HAV infection in Indonesia and Japan’s case which is infected during his time in Surabaya. In spite of that there is no research yet focusing on characterization of the virus and its distribution pattern in Indonesia. Thus it is urgent to find hepatitis A vaccine to thwart this virus infection, prevent the large case and as a parameter for the rule of government.

CONCLUSION: Hepatitis A virus genotype 1A is the dominant strain responsible for infection cases in Indonesia. The epidemiological data of each case should be reported and researched.

Keyword: HAV, PCR, ELISA, outbreak, East Java, Indonesia