



biofarma

ANNUAL SCIENTIFIC MEETING INDONESIAN ASSOCIATION OF CLINICAL MICROBIOLOGY 2010

August 6th - 7th, 2010 - PT. Bio-Farma, Bandung

*Current Development on Prevention,
Diagnostic and Treatment
Infectious Diseases / Tropical Medicine*

PROGRAM BOOK

Indonesian Association Of Clinical Microbiology 2010
In Collaboration With

PT. Bio Farma and Faculty of Medicine Universitas Padjadjaran Bandung

POSTER

Analysis of Hepatitis C Virus Subtype from Patient with Hepatitis Symptoms in Mengwi District, Badung Regency, Bali

MADE AGUS HENDRAYANA¹, RETNO HANDAJANI¹,
MARIA INGE LUSIDA², SOETJIPTO¹

*Department of Clinical Microbiology Faculty of Medicine Udayana
University, Bali¹
Institute of Tropical Disease Airlangga University, Surabaya²*

Hepatitis C virus (HCV) infection is known to be a major contribution to chronic liver diseases. Bali is a world tourism destination, so a contagious infectious disease has become a serious problem. Since the last decade, Mengwi has become a developed region with the rapid growth of social economic, demographic and dynamic inhabitants. This condition can contribute the varieties of HCV genotype. The aim of this study was to analyze the genetic variety of HCV subtype among the patients with hepatitis symptoms in Mengwi district. 75 patients with hepatitis symptoms from Mengwi area were included in this study. HCV isolates obtained from anti-HCV antibody-positive patients. HCV RNA was detected by repeat analysis by reverse transcription-polymerase chain reaction (RT-PCR) for a portion of the NS5B region. HCV genotyping was performed on the HCV RNA-positive samples by phylogenetic analysis. The portion of NS5B region sequence of 4 HCV RNA positive samples were aligned with published sequences of various HCV genotypes. HCV isolates showing sequence similarities of more than 88% at the nucleotide level to any of the published subtype sequences were assigned to the corresponding subtype. Antibodies to HCV (anti HCV positive) were detected in 4 of the 75 (5.3%) blood samples. HCV RNA was detected in all blood samples with anti HCV positive. Subtype analysis revealed that 2 samples (50%) belonged to HCV subtype 1b, 1 sample (25%) belonged to subtype 1c and 1 sample (25%) belonged to subtype 3a. The HCV genotypes in these samples were subtypes 1b, 1c, and 3a. HCV subtype 1b was dominant in anti HCV positive samples.

Keywords: HCV subtype, Mengwi area, hepatitis symptoms

