

ABSTRACT

This study was performed to detect intra-familial transmission of HCV and to figure out the incidence of such transmission, to determine the risk of HCV transmission via intra-familial route on exposed family group compared to control group, and to ascertain the role of viremic level on the risk of HCV transmission on the exposed family.

The hypothesis of the study were (1) the presence of HCV-viraemic on family members as a source of transmission (index case), consequently the transmission of HCV will occur as shown by seroconversion of anti-HCV and or HCV-RNA positive on family members of exposed group, (2) the risk of HCV transmission on family members of exposed group is not different from the same risk on unexposed group, and (3) the risk of intra-familial HCV transmission is increased if the index cases showed higher viraemic level than the lower one.

The initial samples were 524 family members which consist of 234 family members of exposed group and 290 family members of unexposed group. At the end of this study, totally 1236 serum samples of family members were examined, comprise of 556 family members of exposed group and 680 family members of unexposed group, selected by purposive sampling.

This study is longitudinal epidemiological study using cohort design. Blood samples was drawn from both family members of exposed and unexposed group at the beginning of the study, 6 months later, and on 236 samples at 12 months after the first sampling. Serologic markers of HBV and HCV were examined on each samples. The presence of HCV-RNA were also

determined on each samples. To confirm the intrafamilial transmission of HCV, the homology of HCV-RNA sequence of index case and infected case were determined. At the end of the study, all respondents answered the questionnaire for determining the risk factors for HCV transmission. In this study, longitudinal epidemiological research was done to detect the incidence of HCV transmission and a sophisticated biology molecular technique was used to proved that the transmission occurred intrafamilialy.

The data were analysed statistically by normality test (Kolmogorov Smirnov Goodness of Fit test), homogeneity test, X^2 test, Student's t test, Relative risk, Mann Whitney test, and regression.

The results showed that the first and second hypothesis was accepted, but concerning the third hypothesis, the null hypothesis could not be rejected. On the first hypothesis, the incidence of HCV transmission on exposed family members was found very low. On the second hypothesis, the result of this study showed that the relative risk of intra-familial HCV transmission among exposed family members was not different compared to the same risk on unexposed family members. Whereas on the third hypothesis, the result of this study showed no role of HCV viraemic level on intra-familial HCV transmission. The results of this study support the epidemiology data of intra-familial HCV transmission which was very low, therefore the prevention of HCV transmission especially directed to other routes of HCV transmission.

Key words: Hepatitis C Virus (HCV)
Intra-familial transmission
Exposed and unexposed group.