Reviewer’s report

Title: Methylenetetrahydrofolate Reductase (MTHFR) C677T polymorphism and high plasma homocysteine in Chronic Hepatitis C (CHC) infected patients from the Northeast of Brazil.

Version: 1 Date: 25 May 2011

Reviewer: Masataka Shiraki

Reviewer’s report:

The manuscript entitled on MTHFR polymorphism and high plasma homocysteine in CHC infected patients from the Northeast Brazil was reviewed. The primary aim of the study was investigated the interaction between MTHFR genotype, plasma homocysteine (Hcy), HCV genotype and histopathology of liver, especially steatosis and fibrosis of the liver. The structure of the manuscript was so complicated, and therefore, the authors failed to show the relationship between these parameters mentioned above efficiently. The manuscript included several criticisms, which should be addressed properly.

1) The structure of the manuscript was not proper to address the inter-relationship among CHC genotype, pathological finding of liver, homocysteine concentration and MTHRF genotype. The typical missing ring was in the Table 3. Why didn’t you present plasma Hcy level between the genotypes of MTHFR? Did your population bearing T allele of MTHFR show higher level of Hcy?

2) The same non adequate presentation was seen in the Table 1. Why didn’t you present plasma Hcy level in the groups of patients infected by HCV genotype 1 and 2. Because plasma Hcy level seemed to be key substance to connect MTHFR polymorphism, HCV genotype and steatosis in liver. If plasma Hcy is higher in the patients with HCV genotype 1 and the patients bearing T allele of MTHFR than the other genotypes, the authors can say the interaction among the 4 elements plays an important role to have steatosis in the patients with HCV.

3) In page 5, the last paragraph of the introduction, the authors stated the aim of the present study, but the statement should be changed more definitely.

4) The subject’s break down was unclear, because around 20% patients were missing and 138 patients were adapted to the analysis. The remaining 36 patients were missing by the unknown reason. Please make sure whether or not the final group had selection bias.

5) The reason(s) why the patients with T allele showed higher susceptibility of Genotype non-I HCV. Please discuss more.

6) The statistical method in the Table 7 and 8 were not suitable to show the evidence, which you want to indicate. Logistic analysis only indicated the OR between two variables, however, we would like to know what element is the mostly contributed variable to have steatosis. Therefore, the authors must utilize
multi-regression analysis, in which MTHFR polymorphism, plasma Hcy level and HCV genotype as independent variables for steatosis as a dependent variable.

**Level of interest:** An article of limited interest

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**

No
No
No
No
No
No

Thus, I declare that I have no competing interest.