Reviewer’s report

Title: Hepatitis C virus prevalence and genetic diversity among pregnant women in Gabon, central Africa

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Reviewer: Hidenori Toyoda

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The manuscript by Ndong Atome et al. reported the prevalence and genetic diversity of HCV infection in pregnant women in Gabon. Although the study design is simple and the results is not surprising, the study is of value for publication because the data on pregnant women in Gabon with large study population (947 samples) would be difficult to obtain. There are some points that should be improved.

Major Comments

1. The authors studied a total of 947 pregnant women from five institutions in Gabon between January and March of 2005. Were the 947 patients all pregnant women at five institutions in Gabon between January and March of 2005 or selected one?

2. p-5, the first paragraph of the Result section, “The prevalence differed significantly by region, …” The authors should provide with some reasons (some speculations) for the difference in the prevalence of HCV infection between regions. Are there differences in the ethnicity between regions? Are there another differences between regions that can account for the difference in the prevalence of HCV infection?

3. Also, the authors should provide with some reasons (some speculations) for the difference in the genotype of HCV between randomly selected Gabonese subjects (genotype 4c of 4d) and Gabonese pregnant women (genotype 4e or 4c).

Minor points

1. Background, p-3,l-3, “such as” should be “including”, because chronic liver disease is not always liver cirrhosis or hepatocellular carcinoma.

2. p-6,l-4, “HCV RNA targeting 5’-UTR was found in 13 of 20 positive samples, …” This means that HCV RNA was not detected by PCR in 7 of 20 samples. How was the detail of these samples? Was HCV not present in these 7 individuals (only the memory of HCV infection)? Or HCV RNA failed to be detected simply because of the detection method despite the presence of HCV? Please clarify.

3. p-6,ll-11~13, “three strains were selected for amplification and sequencing of
the NS5B region. Two new positive samples obtained from routinely screened pregnant women were also included in the phylogenetic analysis.” Why the authors selected only 3 strains from 13 samples in which HCV RNA was positive for phylogenetic analysis, instead that they sequenced all samples? And why two new positive samples were included? How and where did the authors obtain these two samples? These points should be clarified. These two samples were from 947 pregnant women that were study population? If not, these samples should be excluded.

4. P-7,ll-9~10, “continuous exposure to infection during life (age effect) might explain the observed increasing prevalence with age.” This reviewer cannot understand this. What does the phrase “continuous exposure to infection during life” mean? HCV is a parenterally transmitted virus. What is the “continuous exposure to HCV”? Does the authors consider that the risk of parenteral transmission increase with age?

5. P-7,ll-10~11, “We cannot, however, exclude sexual transmission, as the duration of sexual activity increases with age.” As well as comment #4, this is also difficult to understand. Does the authors consider that the number of sex partners increases with age? If not, the increase in the duration of sexual activity never increases the risk of HCV infection.

6. In the “Conclusion” part of the text, the conclusion of the study is not described but the future perspective is described.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.