Reviewer's report

Title: Molecular epidemiology and phylogenetic analysis of Hepatitis B virus in a group of migrants in Italy.

Version: 2
Date: 7 May 2015

Reviewer: Yu-Ching Lan

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Major Compulsory Revisions

There are two major problems about the phylogenetic analysis which might effect the whole conclusion in this research:

1. In Figure 1, does the scale at the bottom of the tree represent the time in years with 0 indicating present year? If yes, these sequences seems sampling from the same year for their branch end at the same time point (year 0). But, the name of viral sequences represent the viruses sampling from different year. This problem might cause by the year setting process in the BEAST analysis. If the year setting of each sequences had some problem, this would effect the interpretation.

2. About the maximum likelihood phylogenetic analysis in the supplementary figure 2, why the genotype D1 didn’t shown as the monophyletic clade? How do the author recognized these were all belong to D1 if they were not clustering together? This tree might had problem for making any conclusion.

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

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

Declaration of competing interests:

I declare that I have no competing interests.