Reviewer’s report

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

Version: 2 Date: 5 May 2015

Reviewer: Yi-Ming Arthur Chen

Reviewer’s report:

The paper by Villano et al. entitled “Molecular epidemiology and phylogenetic analysis of Hepatitis B virus in a group of migrants in Italy” addresses the HBV genotype and phylodynamics among migrants who were HBV chronic infection in Italy. There are major issues in the results and methodology which I list as followings. Therefore, I recommended this article to be accepted pending major compulsory revision.

Major points: 1. The authors used only maximum likelihood method to construct phylogenetic tree (Supplementary Figure 2 and 3). The authors should use other methods (e.g. Bayesian inference) to confirm the tree topology.
2. In line 269, the authors described that there are 3 sequences were “unclassified”, how are unclassified sequences defined? Please describe in detail.
3. The authors described that the Moldavian sequences (17 sequences) were intermixed and most correlated with the sequences from Russian, East European and Asian countries. Why the authors did not add the reference sequences from Moldova to confirm the transmission relationship? If there the sequences from Moldova are available, I suggest that the author should add these sequences to the phylogenetic tree analysis.

Minor points:
1. The author should provide the GenBank accession numbers.
2. The author should check the spelling carefully such as in line 271 (Among) and line 345 (East-Europe).

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

Quality of written English: Needs some language corrections before being published

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.