Reviewer’s report

Title: Comparison of Sanger sequencing for Hepatitis C Virus Genotyping with a Commercial Line Probe Assay in a tertiary hospital

Version: 1 Date: 27 Jan 2019

Reviewer: Emmanouil Magiorkinis

Reviewer's report:

The paper has been substantially improved since the authors have answered most of the comments suggested by the reviewers. However there are some minor issues which need to be resolved before its final acceptance:

(a) The authors have performed phylogenetic analysis using NJ and UPGMA. As far as NJ is concerned, the authors do not describe which model has been employed to calculate distances (Kimura 2P, Tamura Nei?). Moreover, the UPGMA method is obsolete and not applicable in phylogenetic tree construction of HCV sequences. Authors should use an alternative method either maximum likelihood or Bayesian inference of phylogeny.

(b) There is no statistical validation for the groups in the phylogenetic tree. Authors should perform bootstrapping (at least 1000 replicates) and present the significant results (i.e. results more than 75%).

(c) Authors should present distance weighted phylogenetic trees and not UPGMA trees. Bootstrap values should appear on trees so as to assess the significance of various groupings.

(d) Based on Table 4, there are many samples with discordant genotyping between various HCV regions; for example sample HCV004 classifies as genotype 1b in 5’ UTR region and genotype 6 in core region. How the authors explain those discordant results? Recombination? Mixed genotype infection?

(e) Sample HCV075 has been assigned to three different genotypes ie 1/3/6 whereas on 5’UTR tree seems to be classified as genotype 1b. Authors should check again the table and correct errors if any.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

No

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Unable to assess

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

Quality of written English
Please indicate the quality of language in the manuscript:

Acceptable

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