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: 24 Jan 2019

Reviewer: Lize Cuypers

Reviewer's report:

I have some additional comments, all with respect to the phylogenetic analysis that has been included in the revised manuscript.

The authors report to have constructed phylogenetic trees using neighbour-joining and UPGMA methods. However, the latter implies that the tree that can be explained by minimum evolution, is the so-called 'best' tree, a statement that we know is incorrect. I would rather advise the authors to include a maximum-likelihood phylogenetic analysis, but certainly not UPGMA.

Related to the phylogenetic analysis, is the representation of the trees. The authors state that the 5'UTR region does not contain sufficient phylogenetic signal to distinguish the different HCV genotypes/subtypes, but that core and NS5B region do. I do not agree with this conclusion, as you clearly see in Figure 2 that, although the different HCV subtypes are separated, the inter-genotypic relations are not correctly represented. For instance, HCV subtypes 1a and 1b belong to the same HCV genotype, however in the tree inferred from the core region, they are not clustering together. The latter is however correctly represented in Figure 3, using nucleotide information from the NS5B region. For samples for which more than one genetic region is sequenced, the authors could consider to concatenate fragments, to increase the phylogenetic signal in the tree.

To end, I highly recommend the authors to improve their visualisation of the phylogenetic trees. The choice of colours is not the best, but more importantly I would certainly remove the genetic distances that are presented on the branches. In general, it is more appropriate to visualise the bootstrap support values, to show the correct diversification of the tree in HCV genotypes. Also, instead of having a separate legend, I would label the respective clades on the tree itself.
Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

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

Yes

Are the conclusions drawn adequately supported by the data shown?
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Yes

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I am able to assess the statistics

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