Author’s response to reviews

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

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Version: 3 Date: 30 Jul 2019

Author’s response to reviews:

Sir,

Would you please consider the submission of our revised manuscript, “Comparison of Sanger sequencing for Hepatitis C Virus Genotyping with a Commercial Line Probe Assay in a tertiary hospital” (INFD-D-18-01576). We responded to the requests of the reviewer as specified in the attached document.

We feel this paper should now be acceptable for publication in BMC Infectious Diseases.

Yours sincerely

Sylvie Goletti
Reviewers comments to the author:

Reviewer’s comment: C

Author’s response: R

C : I suggest the authors to extend their figure legends by including details on the colouring of the outer circle encompassing the phylogenetic tree as well as the colouring of the branches. Additionally, mention in the legend which support values you have visualised, personally I would only visualise support values (aLRT) for the main branches, not for all the nodes embedded deep in the tree.

R: We agree with the reviewer’s comments and we extend the legends as follow (see Manuscript - Figure titles and legends section – Legends Figure 1, 2 and 3 Line 1 to 20, page 14). However, we did not limit the display of support values to the main branches, as this would require additional work. We believe that the values are readable as presented above. Moreover, they do not have a high added value for the interpretation of the comparison of the 3 phylogenetic trees of genotyping of HCV based on 3 genes.

“Figure 1: Maximum likelihood phylogenetic tree (ML) of the 5’UTR gene sequences from 47 reference sequences and 45 sample sequences. The tree branches, including the outer circle, are coloured according to the HCV types and subtypes 1a and 1b. The tree scale refers to the number of nucleotide substitutions per site. ML tree showed that genotyping based on 5’UTR sequencing was the least discriminating showing erroneous clustering mainly with respect to G1a (in green in the figure), G1b (in blue) and G6 (in brown). We can also observe that G4 (in light blue) is divided into 2 groups.

Figure 2: Maximum Likelihood (ML) phylogenetic tree of the Core gene sequences from 47 reference sequences and 50 sample sequences. The tree branches, including the outer circle, are colored according to the HCV types and subtypes 1a and 1b. The tree scale refers to the number of nucleotide substitutions per site. The ML tree of the Core region showed a very good grouping of the different genotypes, for reference and sample sequences.
Figure 3: Maximum Likelihood (ML) phylogenetic tree of the NS5B gene sequences from 47 reference sequences and 35 sample sequences. The tree branches, including the outer circle, are colored according to the HCV types and subtypes 1a and 1b. The tree scale refers to the number of nucleotide substitutions per site. The ML tree of the NS5B region showed the best grouping of the different genotypes, for reference and sample sequences. This discrimination even extended to the subtype for instance for G4 in light blue in the Figure.”