Reviewer's report

Title: Human metapneumovirus prevalence and patterns of subgroup persistence identified through surveillance of pediatric pneumonia hospital admissions in coastal Kenya, 2007-2016

Version: 1 Date: 08 Jul 2019

Reviewer: Makoto Takeda

Reviewer's report:

Authors' Response: The strains cluster within A2c, we have highlighted the strains in the trees (Figure 1) and mention in the results (lines 187-189) and discussion (lines 295-298) sections. To our the best of our knowledge, the novel strains with the duplication have not been observed or reported in Kenya.

Reviewer's additional comment: If the new HMPV strains with 180- or 111-nucleotide duplication are clustered in the provisionally assigned A2c, it may be beneficial not using the term A2b to describe these strains in line 60-67. References 17 and 41 are seemingly the same paper. The papers describing the HMPV strains with 111-nucleotide duplication (Saikusa et al. Microbiol Immunol 2017; Saikusa et al. Jpn J Infect Dis 2019) are not referenced.

Authors' Response: There is a general but not exact agreement of genotype prevalence patterns between Kilifi and other locations. We suggest that at finer (subgroup) levels there are differences due to variation in sample size or sampling methods. Our study is based on hospital surveillance, representing only a small proportion of cases in the community, and it is likely we missed some genotypes, which may have only occurred in mild, asymptomatic cases not presenting at the hospital. We have clarified this in the revised manuscript (line 210-213).

Reviewer's additional comment: The sentence 'These patterns mirrored the global picture (line 40)' in Abstract may be still somewhat an overstatement.

Authors' Response: The authors appreciate the reviewer's concerns that the short region limits inferences compared to longer genomic regions. In order to compare our data with what is currently available from other studies, we had to trim the F gene sequences to 354 nucleotides. For the G gene data we analysed nearly complete gene fragment (640 nucleotides), which gives better inferences on evolutionary rate, genetic distance estimation or selection pressures for the different subgroups, as this genomic region is more variable.

Reviewer's additional comment: Authors may discuss the limitation of this study, regarding the analyses of evolutionary rate, genetic distance estimation, and selection pressures, due to the use of short regions.
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.

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.

Not relevant to this manuscript

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

Needs some language corrections before being published

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