Author’s response to reviews

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

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Author’s response to reviews:

Dear Editor,

We wish to submit the revised version of the manuscript entitled ‘Human metapneumovirus prevalence and patterns of subgroup persistence identified through surveillance of pediatric pneumonia hospital admissions in coastal Kenya, 2007-2016’ for consideration for publication in BMC Infectious diseases.

We thank the reviewers for their valuable contributions, which we believe have resulted in considerable improvement of the manuscript.

We have provided a point-by-point response to the comments from the reviewers together with this resubmission.

We look forward to your consideration.

Yours sincerely,

Corresponding author,
OUR RESPONSES TO REVIEWER COMMENTS

REVIEWER #1

1. 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 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.

Our Response: The authors agree with the reviewer’s concern its beneficial not to use A2b to refer to the strains with the duplication. We have pointed out in the discussion section the need for proper nomenclature of the HMPV strains (lines, 295-299). We have modified the sentence to refer to the major subgroup A2 (line 65).

The two papers that describe HMPV strains with 111-nucleotide duplication have been referenced (references 19-20), lines 65-66. Reference 41 has been dropped.

2. 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.

Our Response: The sentence has been dropped in the revised manuscript (line 40).

3. 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.

Our Response: We have discussed limitations of the use of short regions in the discussions section, lines 336 -343.