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: 0 Date: 04 May 2019

Reviewer: Makoto Takeda

Reviewer's report:

Oketch et al. have conducted a molecular epidemiology study of human metapneumovirus (HMPV) in coastal Kenya between 2007 and 2016. This reviewer appreciates the authors' effort and thinks that the data is of value to understand the global transmission pattern of HMPV, when considering that the HMPV data in Africa is limited. However, this reviewer suggests significant improvement necessary for this study.

Major comments

1. No consensus has been reached on the subgrouping of HMPV strains among the researches. Each researcher uses different methods and different gene regions or length to propose new sub-clusters, such as A2c, A2b1, A2b2, or novel sub-lineage of A2b. The 'A2c' has been provisionally proposed only using the short F gene region (321-nucleotide region) and limited numbers of HMPV strains. The provisional new sub-lineage of A2b strains, including A2c strains, have been still classified into the subgroup A2b in certain studies. The variations of genotype nomenclature among researchers may confuse the situations of HMPV molecular epidemiology. First, please define clearly the nomenclature of HMPV subgroups in this study, comparing with those in other studies. This reviewer expects that subgrouping analysis is conducted systematically using as many available sequence data from database as possible (maybe in other study).

2. The authors analyzed the full-length F and G coding regions of 114 HMPV strains (line 114). If the full-length sequence data is used, is the A2c sub-clustering still evident?

3. Recently, unique A2b HMPV strains, which possess 180- or 111-nucleotide duplication in G gene, have been detected in several countries. Could the similar strains be detected in Kenya? When these strains are included in the phylogenic tree, where are they located in the tree?
4. Letters in all figures are very small, nearly unrecognizable. Certain figures do not meet the criteria or requirements of BMC journal. Additional information is necessary for Figure 5.

5. This reviewer partially disagrees with the authors' conclusion that the genotype prevalence pattern in Kilifi was similar to that of global one (lines 193-196). They show a certain similarity, but differ significantly in many points. In many years, A2a has been detected globally, but not in Kilifi. A2c has been detected every year globally. The dominance of B1 is evident in 2011 globally. Unlike in Kilifi, B1, A2c, and A2b have persisted over the 9 years globally (lines 195-196). The dominance of A2b between 2007 and 2011 and the dominance of B1 between 2012 and 2014 are less evident globally (lines 268-269).

6. If only partial short regions (345-nucleotide regions) were used for the analysis of evolutionary rate, genetic distance estimation, or selection pressures, significance of the resulting value or data in this study is quite limited.

7. The difference in methods may significantly affect the results of genotype rate data in this study (line 307-309).

Minor comments

1. Many molecular epidemiology studies have been reported to data, although the data in Africa is still limited. Line 25-26.

2. There are many unnecessary citations. For example, as many as 23 papers are cited to describe the general information of HMPV.

3. The paper (reference 31) does not use the term 'A2c' (line 66 and 269). In the same paper, HMPV strains detected between 2012 and 2014 are used. Was the A2c detected in 2007 (line 66)?

4. Dose 'few' mean almost none or several? If it is not 'none', authors may use 'a few'. (Lines 68, 72, and 74)

5. Please define 714F and 500G (line 192).
6. Was phylogenetic tree constructed using 345- or 714-nucleotide region?

7. What is 'inadequate temporal signal'?

8. The reference 56 may be changed. The reference 56 shows only data in a single city, Japan, but not the global data.

9. Are there any supportive evidence or reports to show genotype-specific herd immunity for HMPV? (Lines 272-274)

10. Why does reduction in bacterial pneumonia result in a reduction in viral pneumonia? (Lines 297-298)

11. Why do the purifying selection pressures drive virus evolution?

12. Globally persistent circulation is observed also for B1, A2b, and A2c (line 303-304).

13. No journal name is shown in the references.

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?
If not, please explain in your comments to the authors.

No
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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