Reviewer's report

Title: Clinical Features and Phylogenetic Tree of Coxsackievirus A9 in Northern Taiwan in 2011

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Reviewer: Beatrix Kapusinszky

Reviewer's report:

The paper Clinical Features and Phylogenetic Tree of Coxsackievirus A9 in Northern Taiwan in 2011 written by Yi-Chuan Huang and co-authors describes the clinical presentation of Coxsackie A9 (CV-A9) infections in order to upgrade the differential diagnosis of those infection from other diseases caused by non-polio enteroviruses and provides an inside into molecular epidemiology of CV-A9.

However, the paper needs to be improved with some major and couple minor modification to meet the journal criteria before being accepted for publication.

In general, the paper should be shortened and submitted as a brief report, including new findings about CV-A9 in both clinical and epidemiological aspects.

- Major Compulsory Revisions

1. In paper title it was mentioned that infections occurred in Taiwan in 2011, however the MATERIAL AND METHODS section was describing 100 culture proven CV-A9 infections occurring in Northern Taiwan between August 2010-August 2011 and the same results were depicted in Figures and Tables. Disagreement should be corrected.

2. Authors needs to clarify which infections are sporadic and how many of them are epidemic, if possible provide information in what type community (day-care, etc.) such outbreaks occurred?

3. In INTRODUCTION authors said that Taiwan CDC reported 3.308 non-polio HEV in 2011, and only 15% (499) was due to CV-A9, but in DISCUSSION authors described that CV-A9 was the second most common serotype in Taiwan (or Northern Taiwan?). What serotype was a first one? And what is the basis for that statement since it with disagreement with the first sentence.

4. In METHODS section please indicate the size of VP1 amplicon based on its position in the reference genome, and also indicate the size of VP1 aminoacid sequence was used for phylogenetic analysis.

5. Provide in RESULTS section the paragraph on Phylogenetic analysis of CV-A9 isolates.

6. How many isolates from current study was used to build the phylogenetic tree? Indicate which one is from 2010 and 2011.
7. Also provide the GenBank accession numbers for each sequences used for phylogenetic tree construction.
8. Indicate on phylogenetic tree isolates from sporadic cases and those belonged to the same outbreak.
9. Phylogenetic tree should include an outgroup, bootstrap values below 50% might be omitted.
10. RESULTS section. Include only results from 100 patients, additional results from other patients (n=125) with missing data are confusing.
11. GenBank Accession numbers should be provided for the stain detected near the border of Mainland China and Myanmar with the reference for indicated strain in the text.
12. Where is no clear conclusion is there any genetic difference between current CV-A9 stains and those deposited in GenBank that might influence the severity and clinical outcome of the disease.
13. Is there are any evidence on importation of CV-A9 from Mainland China and Myanmar?
14. The Figures 1, 2 might be omitted from the text because their description was clearly provided in the text.
15. Figure 5 needs to be reconstructed with comments described above.

Minor Essential Revisions:
1. The language of ABSTRACT section needs a revision by native English speaker.
2. The title should be modified with using a scientific term: … and Phylogenetic Analysis of Coxsackie A9”
3. In INTRODUCTION section correct the enterovirus classification was based on nucleotide sequence of VP1 region and it was accepted by ICTV in the mid of year 2000.
4. In METHODS section for case definition would be more correct to say: “In this study we collected data from 100 patients with laboratory confirmed CV-A9 infections…”
5. In METHODS section double check the method: Real-Time RT-PCR or just RT-PCR as it was described in the reference.
6. RESULTS section. Include only results from 100 patients, additional results from other patients (n=125) with missing data are confusing,
7. In DISCUSSION hand foot and moth disease= HFMD should be abbreviated the same all other the text.

Level of interest: An article whose findings are important to those with closely related research interests
Quality of written English: Needs some language corrections before being published

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:
I declare that I have no competing interests.