Reviewer's report

Title: Sentinel surveillance for human enterovirus 71 in Sarawak, Malaysia: Lessons from the first 7 years.

Version: 1 Date: 24 March 2006

Reviewer: Katsumi MIZUTA

Reviewer's report:

General
This manuscript describes a sentinel surveillance of HEV71 over 7 years in a community of Sarawak, Malaysia, including virological, epidemiological and clinical data. Longitudinal epidemiological studies in the communities, which have rarely been reported, are necessary to control HEV71 infections. The data is interesting and should have some usefulness in either epidemiology or clinical virology. However, the significance and the originality of the article is not clear, especially in the conclusions, maybe because there are too many information in virological, epidemiological and clinical point of views to follow. As my first impression, focusing on some of them makes the article more impressive. For example, I was interested in the observation that 3 outbreaks occurred every three years due to genogroup B, which were genetically distinct from each other. Then, if I am the author, I emphasize this data as the main topic of this article.

Major Compulsory Revisions (that the author must respond to before a decision on publication can be reached)
1. The authors suggested that genogroups B viruses are evolving within Borneo and these viruses spread to other countries of Asia-Pacific region (Discussion). However, it is difficult to accept this idea, because changing of genogroup B viruses among outbreaks is the only reason shown by the authors. The distribution of genogroups B4 (Reference 24) does not support this idea. Furthermore, if HEV71 evolves in Borneo, how the authors explain the reason why genogroup C viruses do not. Borneo could be one of the epicenter of HEV71. However, I think that more epidemiological data from different countries should be necessary to identify the real epidemiology of HEV71 in this region.
2. The authors used RD cell lines and isolated HEV71, CVA16, CVA2, CVA4, CVA5, CVA10, CVA12, CVB3 and CVB5 efficiently. However, to my knowledge, RD cell lines have no sensitivity to CVB viruses (Diagnostic Procedures for Viral, Rickettsial, and Chlamydial Infections, 7th Ed, American Public Health Association, Washington p284: Growth in cell culture). It should be clarify what kind of viruses RD cell lines used in the study are able to isolate.
3. Basically serotype should be identified by neutralization test with immunized animal antisera. Why the authors did not use this traditional method? With neutralization test, we can avoid the problems of misidentification of CVA16 as HEV71 as authors described in P6, can’t we?

Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)
1. The authors use both of subgenogroup (P11 and P16) and genogroups, which should be unified.

Discretionary Revisions (which the author can choose to ignore)
1. Fig. 2. is essential? It has been almost established as the standard method of genotyping to analyze the complete sequence of the VP1 region (Reference 10, 27, and Saunders SA et al: Molecular epidemiology of enterovirus 71 over two decades in an Australian urban community. Arch Virol. 2005 Dec 22; [Epub ahead of print])
2. Fig. 4. is essential? The main outbreak due to B5, which was preceded by C1, is almost shown in the bottom panel of the Fig. 1.
3. I think some of the conclusions in the text should be put in the discussion (for example d and e).

What next?: Unable to decide on acceptance or rejection until the authors have responded to the major compulsory revisions

Level of interest: An article whose findings are important to those with closely related research interests

Quality of written English: Acceptable

Statistical review: No

Declaration of competing interests:

I declare that I have no competing interests.