Reviewer's report

Title: A unified approach to molecular epidemiology investigations: tools and patterns in California as a case study for endemic shigellosis

Version: 1 Date: 20 May 2009

Reviewer: Norma Binsztein

Reviewer's report:

The paper requires MAJOR COMPULSORY REVISIONS regarding the following items:

a) They did not characterize “outbreak patterns”, nor give any results that could support those statement regarding a “unified approach for characterizing endemic and outbreak patterns…” (lines 77 and 78). They should review this in all the paper. Moreover they did not discuss nor give references for analyzing the comparison between endemic vs outbreak strains. This important question was not answered.

b) It is important, at least in such a paper, to show the S flexneri serotypes. I think it is not enough to include all of them as serogroup B. They should establish the frequency of the different serotypes. And this is more important because they demonstrated that S.flexneri is the predominant species, a different result from the rest of United States, so it is important to know the distribution of the different serotypes and the relation with the resistance, plasmid profiles and PFGE patterns

c) Regarding PCR analysis they should review the Fig 5: S dysenteriae was not showed in the fig 5a, in fig 5c was showed only five lines, it should be replaced for another gel with the 8 described isolates

d) PFGE: the Pulse Filed Gel Electrophoresis should be done again with the complete PulseNet protocol, as was published by CDC and with more isolates from both species

They are using the PulseNet running conditions for Shigella sonnei BUT they are not using the PulseNet protocol: they didn´t use the reference international strain Salmonella Braenderup, they are using a molecular marker and it is not suitable for the analysis.

Moreover, it is not possible to compare S flexneri with S.sonnei, the comparison should be done intra species.

For having a conclusion regarding the molecular approach for establishing the endemic Shigella situation in California, they should do the PFGE in an important and representative number of isolates from these two species, the ideal is that they do that with all the isolates included in the study.

They should also show the analysis using BioNumerics software (Applied Math), and the PFGE profiles
It is not possible to say “there is a high level of diversity…” (L 242) with the PFGE of only 13 isolates.

e) in the DATA ANALYSIS, they said that “antimicrobial resistance patterns….were evaluated with respect to …. and PFGE patterns” (L 151 and 152) BUT they didn’t do the comparison to PFGE profiles

Level of interest An article of importance in its field
Declaration of competing interests I declare that I have no competing interests