Reviewer's report

Title: Neisseria meningitidis porA, fetA and fHbp gene distribution in Western Australia 2000 to 2011.

Version: 3 Date: 10 September 2014

Reviewer: Georgina Tzanakaki

Reviewer's report:

Major Compulsory Revision
Comments to the authors:

Title: Neisseria meningitidis porA, fetA and fHbp gene distribution in Western Australia 2000 to 2011.

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By: Boan et al

Comments to the Editor

In this work, by Boan et al describes the epidemiology of the 3 antigen encoding genes in addition to FHbp for meningococcal typing.

General comments
The manuscript offers some interesting epidemiological data from Western Australia adding up to the existing knowledge. However, those data are not complete as the authors have already acknowledged in the discussion section.

It is well known that porA, fetA and fHbp gene typing give additional epidemiological information of the circulating clones in a region/country. However, MLST typing is essential for more precise genetic information in order the authors to be able to compare the characteristics of the isolates with the worldwide meningococcal epidemiology. May the authors would like to consider carrying out MLST typing.

In order to conclude that “FHbp modular groups of the multicomponent 4CMenB vaccine make up 8.26 and 47.7% respectively of the examined serogroup B isolates” another methodological approach should be carried out. The genetic data presented have insufficient discriminatory power for vaccine coverage estimation. May the authors would consider of employing other methodologies such as MATS ELISA in order to enable them to draw such conclusions. Therefore, the study, as it stands, does not provide full information for predicting the likelihood of meningococcal B vaccine efficacy in their region.

Another point which is that the origin of the strains under study are not properly
identified. Were there all from sporadic cases?

Another point which should be taken to the consideration is the annual incidence; it would be much interesting to show the annual IMD incidence amongst the aboriginal vs regional population rather than male vs female ratio or the age compared with the presence of the genes since the results have shown that none of the variables were independently associated with age and origin.

The incidence should also include the cases which were diagnosed by non cultural methods. Additionally, age vs serogroup should be shown in relation to aboriginal/non aboriginal population.

Specific comments

Methods
Line 19. The authors are advised to add the number of the non-culture IMD cases.

RESULTS
1st paragraph, line 8, page 11: the serogroups annually should be presented in a table along with the annual incidence. It would be also interesting to add the aboriginal/non aboriginal origin

2nd paragraph, line 4 page 12: In order to facilitate the readers, another table could be made showing the porA, FHbp fetA results

Supplementary tables 5,6,7 are very detailed and not needed.

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:

I declare that I have no competing interests