Reviewer's report

Title: The microbiome of chronic rhinosinusitis: culture, molecular diagnostics and biofilm detection

Version: 1 Date: 1 November 2012

Reviewer: Hsiu-Jung Lo

Reviewer's report:

The manuscript entitled “The microbiome of chronic rhinosinusitis: culture, molecular diagnostics and biofilm detection” by Boase et al. applied three different methods to detect bacteria and fungi from sinonasal mucosa. Even though this is not the first report, this type of study is still interesting since the pathophysiology of chronic rhinosinusitis is not well known.

The major concerns:

1. Mucus was harvested for histopathological examination, and for routine bacterial and fungal culture. In the absence of mucus, a middle meatal swab was taken for bacterial and fungal cultures.
   1.1. How many patients did not have mucus specimen?
   1.2. Were there differences (number of species, number of colony of the same species) between the culture results of mucus and swab specimens?
   1.3. Potato dextrose agar may be a better medium than Sabouraud agar for molds.

2. The BAC detection plate contains 16 PCR primer pairs that collectively survey all bacterial organisms and 16 PCR primer pairs that collectively survey nearly all pathogenic fungal species.
   2.1. It would be nice to list the sequence of those primers or provide references.

3. Did those patients have other chronic diseases, such as hypertension, or taking medicine?

4. Did hobbits of patients, such as smoking, affect the results of microbiome?

5. A total of 33 different bacterial species were identified in CRS patients by the Ibis system. In control patients, 5 different organisms were detected.
   5.1. It would be helpful to provide the species and amount of genome detected in this study.
   5.2. It would be interesting and important to list the prevalence of mixed microbes. That is, were there dominant combinations of microbes?
   5.3. Was any combination of microbes correlated with certain type of diseases?
   5.4. Was the number of genomes correlated with the number of species detected
in the same patient?

6. 12 different bacterial species were identified by conventional culture methods.
6.1. Did all culture positive organisms had positive results in ibis analysis? If not, why?
6.2. Again, it would be useful and helpful to provide all species detected in this study.
6.3. Again, it would be interesting and important to list the prevalence of mixed microbes. That is, was there a dominant combination of microbes?
6.4. Again, was the number of genomes correlated with the number of species detected in the same patient?

7. This discussion section can be more concise since parts of the content have been described in the result section.

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

Quality of written English: Acceptable

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.