Reviewer’s report

Title: Vaginal flora in women from Greenland assessed by microscopy and quantitative PCR

Version: 1 Date: 27 August 2013

Reviewer: Rita Verhelst

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There is an urgent need for the development of new tools for the accurate diagnosis of bacterial vaginosis. It is difficult to develop such tools, mostly because the pathogenesis of bacterial vaginosis is unclear and because there is no single causative agent. Nevertheless, nucleic acid amplification methods are gaining ground in bacterial vaginosis diagnosis. Datcu and colleagues evaluated both qualitative and quantitative molecular detection of bacterial vaginosis using Nugent’s classification as a reference. The authors introduced threshold quantification in order to optimize molecular diagnosis. They report that their quantitative molecular method targeting both A. vaginae and Prevotella spp. had a specificity of 99% and a sensitivity of 90%, while A. vaginae or Prevotella spp. gave optimal sensitivity (100%) but a specificity of 89%, when compared with the Nugent Gram stain classification of bacterial vaginosis. Datcu and colleagues found that combining Prevotella spp and/or A. vaginae resulted in a molecular diagnostic tool that allows to diagnose bacterial vaginosis with extremely high accuracy and hereby provide us with an excellent tool for novel trials studying treatment and management of bacterial vaginosis.

Furthermore, bacterial vaginosis is associated with adverse pregnancy outcomes and enhances the acquisition and transmission of sexually transmitted infections, especially genital herpes and HIV. This makes it important to uncover the reasons why some populations have very high bacterial vaginosis prevalences and others not. Bacterial vaginosis prevalences have been found to vary considerably between ethnic groups in North America, South America, Europe, the Middle East and Asia. Although, in general, bacterial vaginosis prevalence is low in Europe, some European populations have high rates. Datcu and colleagues report that the prevalence of bacterial vaginosis in women from Greenland is very high (45%).

Major Compulsory Revisions

This paper presents a well executed study that sheds additional light on the microbiology of the vaginal ecosystem by applying quantitative PCR assays to vaginal specimens and comparing the results to Gram stain interpretation of vaginal smears. The paper is easy to follow, uses appropriate methods and reaches interesting findings. Also, the authors freely admit one short coming in their study, namely, the use of an extraction method that did not allow quantifying lactobacilli other than L. iners. I have no major comments.
Minor Essential Revisions

1. Comment on the use of the term ‘flora’

The authors use the term ‘flora’ to refer to the bacteria present in the vagina. I would suggest to consistently use the term ‘microbiota’ or ‘microbiome’ to refer to the collection of microorganisms inhabiting a certain site of the human body.

Indeed, in medical microbiology, the term ‘flora’ has long been used to refer to the collective bacteria and other microorganisms in an ecosystem or the human body. However, the term ‘flora’ may lead to confusion with the Plant Kingdom. For the same reason, also the common term ‘microflora’ is technically a misnomer.

2. Line 309 states: ‘Linearity and limit of detection for the real-time PCR assays are shown in Table S1’.

This line should state ‘Table A1’ instead of ‘Table S1’. Also, linearity is not presented in the table.

3. Table 3: Check the value for G. vaginalis 95%CI in qualitative detection (‘95-1’).

Level of interest: An article of outstanding merit and interest in its field

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