HHS Public Access

Author manuscript

Am J Obstet Gynecol. Author manuscript; available in PMC 2021 July 20.

Published in final edited form as:

Am J Obstet Gynecol. 2019 August ; 221(2): 171–172. doi:10.1016/j.ajog.2019.05.016.

Bacterial vaginosis and the risk of human papillomavirus and cervical cancer

Makella Coudray, **Sandra Kiplagat**

Department of Epidemiology, Robert Stempel College of Public Health and Social Work Florida International University, Miami, FL

TO THE EDITORS: In response to the article titled "Vaginal dysbiosis and the risk of human papillomavirus and cervical cancer: systematic review and metaanalysis," we the authors believe that the findings of Brusselaers et al[1] potentially could support the theory that there is a causal link between vaginal dysbiosis and cervical cancer. However, before this theory can be fully supported, issues of ambiguity that were identified in this systematic review should be addressed. Brusselaers et al aimed to assess the association between vaginal dysbiosis and cervical cancer. Concerns arise with respect to the definition of vaginal dysbiosis that was used and the study selection criteria.

First, vaginal dysbiosis was defined as a deviation from a *Lactobacillus*-dominant microbiota. However, a definitive cut off point for *Lactobacillus* dominance was never identified, and this may vary from study to study. Further confusion occurs because the definition that was used by Brusselaers et al uses microscopy-based assessment of *Lactobacillus* dominance, but the authors included studies that used Amsel's criteria. Amsel's criteria does not directly assess *Lactobacillus* dominance, rather it assesses the presence or absence of clue cells via microscopy.[2] Additionally, the presence of clue cells is not required for the diagnosis of vaginal dysbiosis. Three of the 4 Amsel's criteria are required to be diagnosed with vaginal dysbiosis, of which presence of clue cells is only 1.[2] This may have resulted in an overestimation of results because of misclassification. It should also be noted that it is possible to have a *Lactobacillus*-dominant vaginal microbiota and be classified as unhealthy or exhibit characteristics that are similar to that of a vaginal microbiota that has deviated from *Lactobacillus* dominance.[3]

Second, we are concerned that Brusselaers et al[1] acknowledge that vaginal dysbiosis commonly is also referred to as bacterial vaginosis; however, this term was not included in the search strategy. Furthermore, although the authors used MESH and Emtree terms, CINAHL headings were not included in the search strategy for the CINAHL database. Further clarity is also needed with respect to the inclusion of grey literature. Conference abstracts were cross checked for relevant full text papers; the time frame and conferences that were searched were not included. We acknowledge the efforts of Brusselaers et al to assess bias; however, a customized tool was used for assessment of risk of bias, and the validity of the tool could not be verified. It was not expressed clearly whether this tool was

mcoud001@fiu.edu.

The authors report no conflict of interest.

validated or piloted before its use. Additionally, the authors failed to assess publication bias. Funnel plots could have been used to assess publication bias graphically. Brusselaers et al amply highlight the need for further investigation into the association between vaginal dysbiosis and the risk of human papillomavirus and cervical cancer.

REFERENCES

1. Brusselaers N, Shrestha S, van de Wijgert J, Verstraelen H. Vaginal dysbiosis and the risk of human papillomavirus and cervical cancer: systematic review and meta-analysis. Am J Obstet Gynecol 2019;221: 9–18.e8. [PubMed: 30550767]
2. Onderdonk AB, Delaney ML, Fichorova RN. The human microbiome during bacterial vaginosis. Clin Microbiol Rev 2016;29:223–38. [PubMed: 26864580]
3. Petrova MI, Reid G, Vaneechoutte M, Lebeer S. Lactobacillus iners: friend or foe? Trends Microbiol 2017;25:182–91. [PubMed: 27914761]