Gardnerella vaginalis Does Not Always Cause Bacterial Vaginosis

TO THE EDITOR—Schwebke et al [1] present a conceptual model arguing the case for Gardnerella vaginalis as the primary etiological agent of bacterial vaginosis (BV). The model posits that G. vaginalis is a sexually acquired pathogen that elicits BV via the establishment of a bacterial biofilm on the vaginal epithelium, aided by synergistic associations with vaginal anaerobes and competitive interactions with vaginal lactobacilli. The authors claim to demonstrate fulfillment of Koch’s postulates and recommend that G. vaginalis be specifically targeted in future prevention and treatment strategies. We encourage a critical analysis of these claims in light of a large body of confounding data the authors failed to take into account in the development of their model.

A major assertion of the model is that G. vaginalis is not a member of “normal” vaginal microbiota because if it were, then “one would anticipate that it would be present in all women and present in pubertal girls as well” [1]. However, there is no reason to expect any single species to be present in all healthy individuals. Numerous cultivation-independent studies have identified multiple types of vaginal microbiota among healthy, asymptomatic women [2–5], and G. vaginalis has been found in at least a quarter of healthy subjects in these studies. Schwebke et al cite similar studies but claim they were “not rigorous” in their definition of “normal or optimal flora.” Yet even in a recent study by Schwebke, Flynn, and Rivers [6], the authors detected G. vaginalis in 38.5% of women with a predominance of lactobacilli and a Nugent score of 0–3, the hallmark conditions of “normal and healthy.” The authors emphasize they were unable to detect G. vaginalis in the other 61.5% of subjects, but this hardly supports the broader assertion that G. vaginalis is absent from the vaginal microbiota of healthy women. Furthermore, several studies indicate that G. vaginalis is almost as common in both sexually inexperienced and active adolescent females [7–11]. Muzny and Schwebke acknowledged 2 of these studies [7,8] in a recent review article [12] but discounted the findings by casting doubt on whether the young participants truthfully reported their virginal status. We think a more plausible scenario is that G. vaginalis (or at least some strains) may well be a member of the normal vaginal microbiota in a significant proportion of women and that transmissibility through sexual activity does not preclude it from also being a member of healthy vaginal microbiota in both girls and women.

The omission of key evidence conveniently makes way for the assertion that “in the case of [G. vaginalis] as the causative agent for BV, [Koch’s] postulates have been fulfilled.” We have already pointed to several studies demonstrating that the first postulate is not met because G. vaginalis is commonly found in healthy individuals. In support of the third and fourth postulates (ie, the organism should elicit symptoms and be reisolated from a naive host, respectively), the authors reference a 1969 study in which 29 healthy pregnant women were inoculated vaginally with pure cultures of G. vaginalis (then classified as Haemophilus vaginalis) and monitored for clinical and laboratory signs of “H. vaginalis vaginitis” [13]. We hasten to point out that only 7 of those 29 women developed clinical signs of BV. In similar earlier studies by Gardner and Dukes, 11 of 15 women inoculated with vaginal secretions from affected individuals developed symptoms, whereas the same was true for only 1 of 13 women inoculated with pure cultures of G. vaginalis [14]. It seems clear even from these early studies that so-called nonspecific vaginitis, or BV, is almost certainly polymicrobial in nature and, thus, not easily confirmed within the framework of Koch’s postulates.
We acknowledge the association between *G. vaginalis* and BV and agree that it warrants further investigation, but we emphasize that correlation does not necessarily imply causation. Recent work indicates that multiple different bacterial species are associated with symptoms of BV, but no single species appears to be present in all cases [15]. We concur with the authors that there are likely to be strain-dependent differences in the virulence potential of *G. vaginalis*, as well as potentially important synergistic symbioses with other bacteria.

A few alternative hypotheses to the authors’ conceptual model might include the following: (1) within-species genetic differences result in strains of *G. vaginalis* that can elicit 1 or more symptoms of BV, whereas others are benign commensal strains found in healthy individuals; (2) all strains of *G. vaginalis* encode virulence determinants that are conditionally expressed under specificiotic or abiotic conditions in the vagina; and (3) all strains of *G. vaginalis* express virulence determinants in the vaginal environment, but only some individuals are susceptible or respond to these factors. These might not be mutually exclusive alternatives. Clearly there is still much work to be done in understanding the complex etiology of BV, and as we move forward it is important to recognize that our understanding of “normal and healthy” with respect to the vaginal microbiome remains incomplete.

**Notes**

**Financial support.** This work was supported by the University of Idaho Bioinformatics and Computational Biology Graduate Program, in partnership with the Institute for Bioinformatics and Evolutionary Studies (fellowship to R. J. H); the National Institute of General Medical Sciences, National Institutes of Health (NIH; grant P30 RR033376 to L. J. F.); and the National Institute of Allergies and Infectious Diseases, NIH (grant U19 AI084044 to L. J. F.).

**Potential conflicts of interest.** All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

---

**References**


Received 29 April 2014; accepted 16 May 2014; electronically published 22 May 2014.

Correspondence: Larry J. Forney, PhD, Department of Biological Sciences, University of Idaho, 875 Perimeter Dr, MS 3051, Moscow, ID 83844 (lforney@uidaho.edu).

The Journal of Infectious Diseases® 2014;210:1682–3

© The Author 2014. Published by Oxford University Press on behalf of the Infectious Diseases Society of America. All rights reserved. For Permissions, please e-mail: journals.permissions@oup.com.

DOI: 10.1093/infdis/jiu303