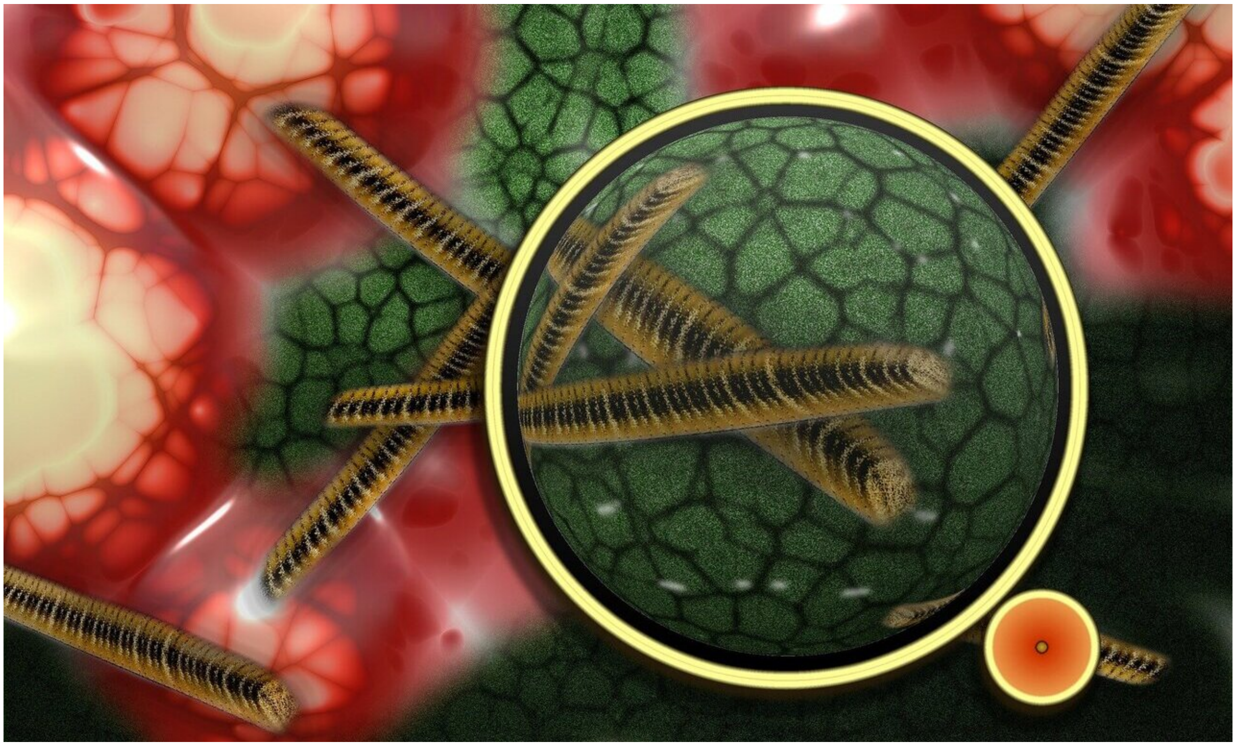
'Oral' bacteria may disrupt the balance of the vaginal microbiome

August 25 2020



Credit: CC0 Public Domain

Bacterial vaginosis (BV) is an imbalance of the vaginal microbiome that can lead to adverse health outcomes, including increased likelihood of potential pathogens colonizing the vagina, yet the mechanisms underlying these processes are poorly understood. A study published in *PLOS Biology* by Amanda Lewis at University of California, San Diego, and colleagues suggests that mutually beneficial relationships between different species of vaginal bacteria may encourage growth of potentially harmful pathogens, such as the common oral bacterium Fusobacterium nucleatum. The work challenges the belief that a suitable living environment supporting pathogen colonization is created solely by the absence of healthy bacteria, and may explain prior clinical links between oral sex and BV.

Approximately 29% of women in the United States are affected by BV, putting them at risk for adverse health outcomes such as preterm labor and amniotic fluid infections during pregnancy. To analyze interaction between bacterial communities and the ability of different bacteria to access required nutrients in an already-occupied microbiome, Lewis and colleagues conducted experiments in human vaginal specimens and in mice. The authors inoculated mice or mouse vaginal communities with F. nucleatum and found evidence of increased biochemical activities previously linked with BV, such as the enzyme sialidase. After performing models in mice, the authors conducted similar experiments in which Fusobacterium nucleatum, a bacterium found in the mouth and linked with gum disease, intrauterine infection and preterm birth, was inoculated into human vaginal microbial communities cultivated from vaginal swabs of twenty-one women. Samples incubated with Fusobacterium displayed higher levels of multiple key indicators of BV compared to the identical women's microbiomes incubated without Fusobacterium.

The experiments led to the discovery that Fusobacterium nucleatum does not act in a simple one-way relationship with other bacteria, but may engage in a mutually beneficial relationship, potentially encouraging dysbiosis (microbial imbalance) in susceptible vaginal communities. Fusobacterium was helped by bacteria in BV-like communities that produce an enzyme called sialidase, enabling Fusobacterium to consume sialic acids from mucus produced by the host. Fusobacterium also acted by unknown mechanisms to greatly benefit the growth of Gardnerella vaginalis, a sialidase producer believed to be a key player in BV.

The researchers demonstrated that mutual benefit between bacteria species may promote pathogen colonization of the vagina and encourage features of vaginal dysbiosis. However, additional studies are needed to develop modes of prevention or treatment of BV in women. Fusobacterium is widespread in human mouths and overgrows in dental plaque; the authors speculate that it may be introduced during oral sex, which has been identified in some clinical studies as a risk factor for BV.

More information: Agarwal K, Robinson LS, Aggarwal S, Foster LR, Hernandez-Leyva A, Lin H, et al. (2020) Glycan cross-feeding supports mutualism between Fusobacterium and the vaginal microbiota. *PLoS Biol* 18(8): e3000788. doi.org/10.1371/journal.pbio.3000788

Provided by Public Library of Science

Citation: 'Oral' bacteria may disrupt the balance of the vaginal microbiome (2020, August 25) retrieved 24 April 2024 from
https://medicalxpress.com/news/2020-08-oral-bacteria-disrupt-vaginal-microbiome.html