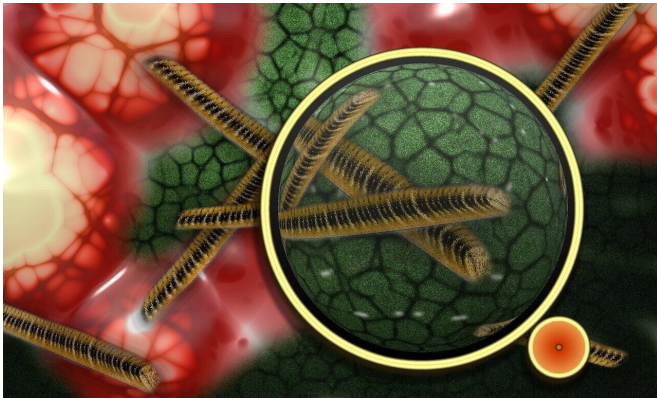


# 'Oral' bacteria may disrupt the balance of the vaginal microbiome

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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](https://doi.org/10.1371/journal.pbio.3000788)

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