'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* and *Gardnerella vaginalis*.

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.


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