

---

# Uncovering the Evolutionary and Ecological Landscape of Vaginal *Prevotella* through Genomic Comparisons

Alice Gallot<sup>\*1,2</sup>, Jacques Ravel<sup>2</sup>, Michael France<sup>2</sup>, and Melanie Quain<sup>2</sup>

<sup>1</sup>École normale supérieure [ENS] – IBENS, Département de Biologie, École Normale Supérieure, CNRS, INSERM, Université PSL, 75005 Paris, France. – France

<sup>2</sup>Center for Advanced Microbiome Research and Innovation [CAMRI], Institute for Genome Sciences [IGS], University of Maryland Baltimore School of Medicine [UMBSOM], Baltimore MD - USA – États-Unis

## Résumé

Bacterial vaginosis (BV) is the most common vaginal infection in women of reproductive age and is linked to increased risks of severe gynecological and obstetric complications. BV is associated with a dysbiosis of the vaginal microbiome and is characterized by a lower abundance of beneficial lactobacilli and a higher abundance of a diverse array of anaerobes, including several species in the genus *Prevotella*. The *Prevotella* species, principally *P. amnii*, *P. bivia*, and *P. timonensis*, are notable due to their associations with spontaneous preterm birth, and female genital tract infections, including HIV. Despite their importance as a key member of vaginal communities, little is known about the ecology and evolution of these bacteria in the vaginal environment. We compared genomes of several vaginal *Prevotella* species to better describe their functional potential and evolution. Our analysis revealed that several *Prevotella* species (e.g., *P. amnii* and *P. bivia*) have two chromosomes, while others have one (e.g., *P. timonensis*). The multipartite structure of *Prevotella* genome is a unique opportunity to compare the chromosome architecture of species of the same genus that cohabit in the same ecological niche. Comparative metabolisms reflect *Prevotella* habitat specificity on the host and their adaptation to the human vagina. Further, the identified metabolic pathways could be leveraged to shift a community away from a dysbiotic state and towards an optimal state dominated by *Lactobacillus spp.* The ecology of *Prevotella* bacteria can also be seen through its interactions with other bacteria. We characterize the ecological synergetic interaction between co-resident *Gardnerella vaginalis* and *Prevotella spp.* isolates. We examined the genomic capacity of vaginal *Prevotella* species through a lens of ecology and evolution to better understand their function in the vaginal environment and their relationship to vaginal health.

---

\*Intervenant