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# Ecology and evolution of the vaginal microbiota

Samuel Alizon\*<sup>1</sup>

<sup>1</sup>Centre interdisciplinaire de recherche en biologie – CNRS – 11 place Marcellin Berthelot 75005 Paris,  
France

## Résumé

The vaginal microbiota is a key component of women's health. It has demonstrated associations with fertility, with the risk of acquiring some infections, and with general well-being. It is also an ideal study system from a scientific point of view because it can readily be clustered into five main community state types (CST). First, I will introduce a community ecology model tailored to capture the dynamics of two competing populations representing an "optimal" CST1 (dominated by *Lactobacillus crispatus*) and a "non-optimal" CST4 (dominated by *Gardnerella*, *Fannyhessea*, and/or *Prevotella* bacteria). Our findings elucidate that the prevalence of CST4 bacteria is intricately linked to their exclusive access to specific nutritional resources. Moving to the epidemiological level, I will present the results of a hierarchical Bayesian Markov model applied to a unique longitudinal dataset from the PAPCLEAR cohort. Thanks to the metabarcoding of more than 2,000 samples from 125 women, we estimate the probabilities for women to transition from one CST to another and identify potential risk factors associated with these transitions. Our analyses also show there is a relatively canalised pathway leading to the deterioration of vaginal microbiota communities, whereas the routes to recovery can be highly individualised among women. This work paves the way for an improved mechanistic understanding of microbial dynamics within the vaginal environment and the development of novel preventative and therapeutic strategies to improve vaginal health.

**Mots-Clés:** vaginal microbiota

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\*Intervenant