Microbial interactions in bacterial vaginosis

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Bacterial vaginosis (BV) is the most common vaginal infection in women of childbearing age but its aetiology is not yet fully understood, with controversial theories being raised over the years. What is generally accepted is that BV is often characterized by a shift in the composition of the normal vaginal microbiota, changing from a Lactobacillus species dominated microbiota to a mixture of anaerobic and facultative anaerobic bacteria. During BV, a polymicrobial biofilm develops in the vaginal microenvironment, being mainly composed of Gardnerella species. Considering current knowledge of BV, it is not possible to determine if the presence of multispecies biofilms is the cause or simply a consequence of BV. Nevertheless, the interactions between vaginal microorganisms are thought to play a pivotal role in the shift from health to disease and might also increase the risk of sexually transmitted infections acquisition.

In recent years, my research team has been working on elucidating how different bacterial species associated with BV might interact synergistically and enhance the polymicrobial biofilm observed in vivo, during BV development. Based on our previous observations that Gardnerella, but not other relevant BV-associated species, could displace pre-adhered Lactobacillus from HeLa cells, we developed an in vitro model to test the hypothesis that Gardnerella acts as the early colonizer, forming an early biofilm that serves as a scaffold for other bacterial species to incorporate resulting in the typical multispecies consortia. Using this model, we first characterized several dual-species BV-associated biofilms, where we highlighted significant synergistic interactions that included the induction of key Gardnerella genes associated with increased virulence. More recently, we described the first in vitro triple-species biofilms, highlighting that some unique interactions occurred only in the triple-species biofilms, as compared with dual or single-species biofilms. This evidence suggests that microbial relationships between co-infecting bacteria can influence the multispecies biofilm, a hallmark of BV. Our ongoing work is now revealing how interactions in triple-species biofilms can result in increased tolerance to antibiotic therapy, as compared to single-species biofilms, which can explain the high recurrence rates observed during clinical treatment of BV patients.