P-159 - SOCIAL INTERACTIONS BETWEEN LACTOBACILLUS INERS AND GARDNERELLA VAGINALIS BIOFILMS: AN UNEXPECTED FRIENDSHIP IN THE BACTERIAL VAGINOSIS ECOSYSTEM

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Background

Worldwide, bacterial vaginosis (BV) is the leading dysbiosis of the vaginal microbiome. BV is a complex polymicrobial condition characterized by a disruption of the vaginal econiche, normally resulting in a reduction of beneficial lactobacilli and an overgrowth of anaerobes. It is noteworthy that a hallmark feature of BV is the presence of a highly structured polymicrobial biofilm, primarily consisting of *Gardnerella vaginalis,* strongly adhered to the vaginal epithelium, and a variety of other bacteria.
There are some observational studies that described the rapid fluctuation over time of the vaginal microflora, showing that *Lactobacillus iners* is a dominant part of the vaginal flora in a transitional stage between abnormal and normal flora. Compared to other *Lactobacillus* species, *L. iners* has more complex nutritional requirements, a Gram-variable morphology and an unusually small genome, indicative of a symbiotic or parasitic lifestyle. However, till date, the role of *L. iners* in the development of a BV-associated biofilm remains unclear.

Method

This study aimed to unravel the interactions between *G. vaginalis* and *L. iners,* both isolated from BV cases, using an *in vitro* dual-species biofilm assembly. Bacterial coaggregation ability was determined for single- or between dual- species community. Furthermore, the total biofilm biomass was also determined by the crystal violet method. Next, we discriminated the dual-species populations in the biofilm by using Peptide Nucleic Acid Fluorescence *in situ* Hybridization method. Additionally, biofilm structure was evaluated using a confocal laser scanning microscopy analysis. Finally, the transcripts levels of *G. vaginalis* virulence genes, in a dual-species consortium, were determined by quantitative PCR.

Results & Conclusions

This study pointed out that *L. iners* seems to be well adapted to BV dysbiosis. We observed that *L. iners* was able to incorporate a pre-established *G. vaginalis* biofilm. Confocal microscopy analysis revealed that both species can live in close proximity, forming clusters from the bottom to the biofilm top layer. Curiously, *L. iners* did not affect *G. vaginalis* virulence, as determined by the transcription levels of key virulence genes. Remarkably, one could argue that *L. iners* is capable of surviving and adapting to a metabolic stress-related conditions found in BV.

References & Acknowledgments

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