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Characterization of human vaginal flora and dysbiosis associated with bacterial vaginosis using culturomics and metagenomics

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Statement of the Problem: Over the last decades, increased studies of the vaginal microbiota, due to the technological advances of molecular and new OMICS technics, have revealed the impact of the vaginal microbiome on reproductive health. Indeed, a recent study reported a clear relationship between bacterial vaginosis and the vagina flora. It is often associated with several obstetric and gynecologic sequels including preterm birth, miscarriage, pelvic inflammatory disease and risks for acquisition and developing sexually transmitted infections. Moreover, conventional treatments often fail with a relapse rate of 50% within the 3 months post-treatment. Although bacterial vaginosis is a common worldwide condition characterized by an abnormal loss of normal flora and an overgrowth of anaerobic bacteria, the reasons for this dysbiosis are yet unknown.

Methodology: To better understand the observed dysbiosis associated with the bacterial vaginosis in order to provide more appropriate treatments, the vaginal flora of bacterial vaginosis patients and an asymptomatic control group were comparatively characterized as using both the “Culturomics” and the metagenomics approach. All the colonies isolated by culturomics were identified using MALDI-TOF mass spectrometry and the 16S rRNA gene sequencing.

Results: We identified and isolated 654 bacteria belonging to 22 phyla including 27 putative new species with 16S rRNA sequence identity <98.7% to validly published species. Compared to healthy women, BV patients exhibited, globally, an increase of the bacterial diversity, especially of previously unknown species. Indeed, an expansion of species such as *Gardnerella vaginalis*, *Atopobium vaginae* was recorded as well as several oxygen-sensitive prokaryotes including Gram-positive anaerobic cocci, *Prevotella* spp.

Conclusion and Perspective: Using metagenomics and culturomics approaches a complex of 15 species were identified as highly associated to BV Laboratory experimentation in order to study their characteristics including the full genome sequencing can improve the current treatment of BV and prevent relapse.

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