Title: *Gut microbiota in normal pregnancy: A characterization of Senegalese women microbiota by 16S rRNA sequencing analysis*

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Abstract :

Background: Pregnancy is a critical and special period involving many physiological changes that ensure the requirements for maternal wellness and fetal development. Over the last decade, there has been a great deal of attention given to the intestinal microbiota and its shifts. However, specific microbial signatures of Senegalese pregnant women and its association with external factors remain poorly characterized.

Objective: To investigate the gut microbiota composition of Senegalese pregnant women and assess its association with women age, gestational age, the habitat, and the presence of cultivable pathogens (ESBL).

Methods: We performed 16S rRNA gene sequencing on stool samples from 131 pregnant women. Taxonomic classification was performed using the Greengenes2 database and QIIME2 pipeline. Alpha and beta diversity metrics were computed, and differential abundance analysis was performed using DESeq2.

Results: Gut microbiota of Senegalese pregnant women was dominated by two major bacterial phyla, Bacillota (accounting for 31.94% of total sequences) and Bacteroidota (12.93%). At family level, the Bacteroidaceae was mainly found with 9.06% of total sequences, followed by Lachnospiraceae (6.96%) and Ruminococcaceae (6.79%). The Faecalibacterium and Prevotella are the two major genus of the gut microbiota of pregnant women. No significant differences in α-diversity represented by Chao, Ace, Shannon and Simpson indexes were found within all age classes and within the two groups of absence/presence of ESBL bacteria ($P > 0.05$). PCoA based on Bray-Curtis distances revealed significant difference between the two groups of absence/presence of ESBL bacteria (PERMANOVA, $p = 0.029$, $r^2=0.9\%$), suggesting an influence of one or a few specific taxa in ESBL+ group.

Conclusion: Our results indicated a richness in the composition of gut microbiota of Senegalese pregnant women. These findings could lead to a better understanding of the role of the intestinal microbiota in pregnancy.