

Characterization of the vaginal microbiome of pregnant women undergoing preterm or full-term delivery

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Objective

To characterize the vaginal microbiome using the 16S rRNA gene in a sample of 40 pregnant Colombian women undergoing preterm or full-term delivery and its relationship with perinatal outcomes.

Methods

A pilot, prospective, exploratory, cross-sectional study was carried out, which included pregnant women undergoing preterm delivery (n = 20) and those undergoing full-term delivery (n = 20) in two-level III centres in the city of Bogotá D. C.

Results

A normal vaginal microbiome (Lactobacillus > 80%) was frequently observed in full-term pregnant women (60% vs. 25%) (p = 0.016). An intermediate microbiome (30%–80% Lactobacillus) (30% vs. 25%) (p = 0.386) and microbiome imbalance (Lactobacillus < 30%) was frequently observed in preterm pregnant women (50% vs. 10%) (p = 0.0042). Of the 11 neonates admitted to the neonatal intensive care unit (NICU), early-onset neonatal sepsis was diagnosed in 5 (45.45%), with the findings of a normal (n = 1), intermediate (n = 3), and unbalanced (n = 1) maternal microbiome. Of the neonates admitted to the NICU, L. iners was isolated in 8/11 admitted neonates and 4/5 neonates who had sepsis (p = 1,000).

Conclusion

The use of the latest generation of molecular techniques (16S rRNA gene sequencing) enables the specific analysis of the vaginal microbiome. In addition, the results of this study suggest that variations in the vaginal microbiome predispose patients to preterm delivery and may also be associated with possible neonatal complications.