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Aims:-The aim of the present study was to characterize the endometrial microbiota in a cohort of women undergoing Assisted Reproductive Technologies (ART), focusing on examining the bacterial populations using a metabarcoding approach.

Methods:- Endometrium samples were collected from a cohort of women undergoing ART to investigate the endometrial microbiota. A comprehensive metabarcoding approach utilizing next-generation sequencing (NGS) targeted the V2-4-8 and V3-6,7-9 hypervariable regions of the 16S rRNA gene. Bioinformatic analysis was performed on the amplicon sequences for denoising and taxonomic classification, using the Greengenes database as a reference for the 16S rRNA gene.

Results:- The metabarcoding analysis revealed the presence of various genera in the endometrial microbiota, including Lactobacillus, Gardnerella, Pseudomonas, Serratia, Escherichia, and Staphylococcus. The specific proportions of these genera strongly suggest their potential influence on supporting successful pregnancies, thereby indicating their possible role in reproductive health.

Conclusions:- The study's findings shed light on the diverse bacterial populations within the endometrial microbiota of women undergoing ART. These findings set the stage for further investigations into the intricate relationship between these specific bacterial populations and their impact on the achievement of successful pregnancies. The study underscores the potential influence of the endometrial microbiota on women's reproductive health and the attainment of successful pregnancies, offering promising insights for future research in this field.

Keywords:- Endometrium, Microflora, Metagenomics, Next Generation sequencing, Infertility