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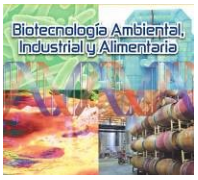


# Development of a tool for the study of the reproductive microbiome and its relationship with endometrial receptivity and functionality in infertility patients

Gómez Morano, Rosa (1); Díaz López, Claudia (1); Martínez Lara, Antonio (1); Pérez Sánchez, Marta (1); Cotán, David (1).

(1)SINAE S.L. Scientifc Consulting, Parque empresarial Arte Sacro y Afines de Sevilla, Avenida de la ingeniería, 9, Nave 34. 41015, Sevilla (Spain).

Tutor académico: Daniel Moreno Fernández-Ayala

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## ABSTRACT

**Motivation:** The uterine cavity has been considered a sterile niche until few years ago; however, recent studies have shown a characteristic and functional microbiota resides over the endometrial tissue [1]. Thanks to the next generation sequencing (NGS) of the gene encoding the rRNA 16S of prokaryotic ribosomes, microorganisms present in the endometrium were identified; among those predominantly species of the genus Lactobacillus [2]. Bacteria of this genus are classified as acid-lactic bacteria, so they are able to secrete lactic acid, hydrogen peroxide and bacteriocins in order to generate a suitable environment with other microorganisms and avoid the proliferation of potential pathogens [3]. Despite the high percentage of lactobacilli in the endometrium of most women, the microbial composition of each one is highly individualized and the microbial profile can change due to different causes appearing episodes of dysbiosis, that can affect reproductive health, causing embryonic implantation failures, spontaneous miscarriage, premature deliveries and infectious diseases such as chronic endometritis.

The main objective of this project is to develop a new tool to analyze the composition of endometrial microbiota of women with infertility problems using microfluidic techniques and studying its relationship with endometrial receptivity and functionality.

**Methods:** In order to analyze the endometrial microbiota, a bibliographical research of the main microorganisms that reside in this tissue, as well as differential genes of these species was carried out. With these sequences, we designed specific primers for the genes of the microorganisms we identify, and they have will be associated with TaqMan probes. After a correct verification of primers and probes, we perform a DNA extraction from endometrial biopsies using a commercial extraction kit and the DNA obtained was pre-amplified by PCR. Finally, thanks to current microfluidic techniques, it was possible to make a single analysis with 96 samples of patients and the primers previously synthesized, to study the microbiological profile of each woman by qPCR.

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