

CHARACTERIZATION OF VAGINAL AND ENDOMETRIAL MICROBIOME IN PATIENTS WITH CHRONIC ENDOMETRITIS: A PILOT STUDY.

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September 16, 2020

Abstract

Comparative study of CD138 immunostain and microbiome of the female reproductive tract (vaginal and endometrial) in the diagnosis of chronic endometritis. A pilot study from May 2017 to May 2019. Instituto Bernabeu fertility clinic. Cohort study with sixty patients undergoing assisted reproductive treatment. The vaginal and endometrial microbiome was analyzed by mass sequencing of the V3V4 region of 16S rRNA. Bioinformatics analysis was performed using QIIME2 and MicrobiomeAnalyst packages. Alpha, beta diversity and taxonomic characterization were compared with positive and negative CD138 groups for chronic endometritis. Different bacterial communities were detected when vaginal and endometrial samples were analyzed in patients with and without endometritis diagnosed with CD138 immunohistochemistry. In patients with endometritis, a higher alpha diversity index tendency was found in vaginal samples ($p=0.15$) and significant differences in endometrial samples ($p=0.01$). In the beta diversity analysis, no significant differences were observed between the groups established as per the diagnosis of endometritis. Vaginal and endometrial samples from women with endometritis showed a microbiome pattern not dominated by *Lactobacillus* spp. Relative abundance analysis identified genera *Ralstonia* and *Gardnerella* in endometrial sample, and genera *Streptococcus* and *Ureaplasma* in vaginal sample of CE patients diagnosed with CD138. Our results demonstrate the existence of a characteristic vaginal and endometrial microbiota in endometritis patients. Different genera and species have been identified in patients with and without endometritis depending on whether the sample is endometrial or vaginal. There is a relationship between vaginal microbiome alteration and chronic endometritis.

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