



Proceedings

Prague Congress Centre Czech Republic



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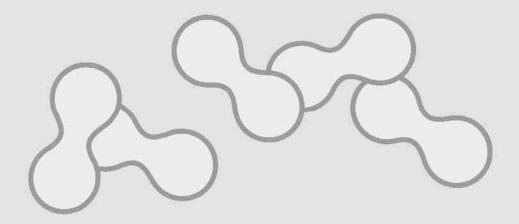
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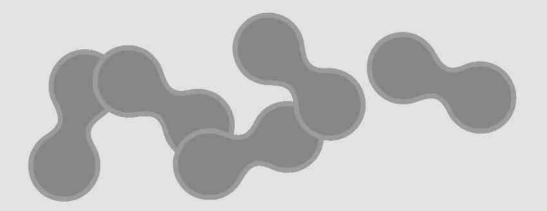
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Poster Presentations





MATERNAL AND VAGINAL HEALTH

P 31 - Recurrent Vulvovaginal Candidiasis Associates to Vaginal Microbiota **Dysbiosis**

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Introduction

The healthy vaginal microbiota is relatively non-diverse and consists mainly of Lactobacillus species, which produce lactic acid to maintain low vaginal pH and bacteriocins to kill potential pathogenic invaders. The fluctuation of microbiota and mycobiota composition in women is influenced by hormonal changes, age, sexual practices, and antimicrobial drug usage. The microbial dysbiosis in the vagina includes to overgrowth of opportunistic pathogens and contributes to the onset of disease. This work sought to determine if Women who suffer from recurrent vulvovaginal candidiasis have a profile of altered vaginal microbiota that could make them more susceptible to this infection.

Methods

We performed a cross-sectional study characterizing the vaginal microbiota diversity of Mexican women. The vaginal exudate was sampled from women during gynecologist visits obtaining 38 cases with white discharge and 26 control. The DNA extraction was performed using the GeneAll ExgeneTM Stool SV Kit (GeneAll), qPCR detection of V5-V6 loci from the 18S ribosomal gene was made to detect the presence of Candida albicans or C. glabrata DNA in the samples. The characterization of the bacterial diversity was achieved by semiconductor high-throughput sequencing of V3-16S rRNA gene libraries and subsequently analyzed using Qiime2 and R.

Results

We found the presence of candida yeast in all samples. The most abundant in cases was C. glabrata, while in controls it was C. albicans. In the alpha diversity analysis, we do not observe statistically significant (p≤0.5) in the following measures, Observed, Shannon, Simpson, and Fisher. The weighted beta diversity we performed showed similitude in the samples (R=-0.09, P=1). Regarding abundance at genera level in the samples, the Absolute Abundance shows that the most abundant was the Lactobacillus in cases than in controls. While the Relative Abundance shows more abundance of Lactobacillus in controls than in cases. For differential abundance analysis, the negative binomial distribution (DESeq2) indicates the presence of Prevotella, Phascolarctobaterium A, Lactobacillus, Escherichia 710834, and Dialister only in cases. With the Linear regression framework for differential abundance analysis (LinDA); we found Lactobacillus was more abundant in cases, and Escherichia 710834, Dialister, and Cutibacterium more abundant in cases and controls. When using ANOVA-Like Differential Expression (ALDEx); Phascolarctobacterium A, Lactobacillus, and Escherichia 710834 were only found in cases.

In our study, we found the presence of Prevotella and Lactobacillus in cases in disagreement with a previous report, showing Prevotella is prevalent in a healthy vaginal environment; In the same study, it was shown Lactobacillus can colonize women with and without microbial vaginal dysbiosis, but in our study, Lactobacillus is only present in cases. In contrast, a 2013 report shows the prevalence of E. coli in cases, while the microbiota in a 2022 study shows abundant Dialister in cases and controls.

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18 - 20 June 2024 Prague, Czechia

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IPC 2024 CONFERENCE ORGANISERS HEREBY CERTIFY THAT

Noemi Del Socorro Lazaro Perez

HELD A POSTER PRESENTATION ENTITLED

Recurrent Vulvovaginal Candidiasis Associates to Vaginal Microbiota Dysbiosis

AT THE 17TH INTERNATIONAL SCIENTIFIC CONFERENCE ON PROBIOTICS, PREBIOTICS, GUT MICROBIOTA AND HEALTH, HELD IN PRAGUE, CZECH REPUBLIC, 18-20 JUNE 2024.



Arthur Ouwehand

President of IPC 2024, Chairman of the Scientific Committee







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