19TH CONGRESS OF IFCPC PARIS 2026

4 › 6 JUNE 2026
VERSAILLES - FRANCE
PALAIS DES CONGRÈS

WORLD CONGRESS OF THE INTERNATIONAL FEDERATION FOR CERVICAL PATHOLOGY AND COLPOSCOPY

HPV
INFECTION AND CERVICOVAGINAL MICROBIOME COMPOSITION IN PREGNANT WOMEN LIVING WITH HIV

YARA LUCIA FURTADO[1,2] LAURA OLIVEIRA MILLER DE MOURA[2] ROBERTA F. S. R. NOVAIS[3] LETICIA LINTOMEN[2] MARCELO A. SOARES[1,2] JULIANA D. SIQUEIRA[2] LIVIA R. GOES[2,4]

[1]UNIVERSIDADE FEDERAL DO RIO DE JANEIRO, RIO DE JANEIRO, BRASIL
[2]PROGRAMA DE GENÉTICA E VIROLOGIA TUMORAL, INSTITUTO NACIONAL DE CÂNCER, RIO DE JANEIRO, BRASIL
[3]UNIVERSIDADE FEDERAL FLUMINENSE, RIO DE JANEIRO, BRASIL
[4]DEPARTAMENTO DE GENÉTICA E BIOLOGIA MOLECULAR, UNIVERSIDADE FEDERAL DO ESTADO RIO DE JANEIRO, RIO DE JANEIRO, BRASIL.

INTRODUCTION

HPV infection drives nearly all cases of cervical cancer, a leading malignancy among women of reproductive age. Pregnancy induces profound hormonal, immunological, and cervicovaginal microbiome changes that can favor viral persistence. In women living with HIV, these alterations are compounded by immunosuppression, markedly increasing the risk of persistent HPV infection and accelerations progression to cervical lesions and cancer.

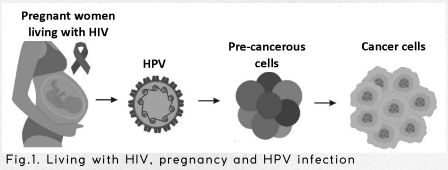

Fig.1. Living with HIV, pregnancy and HPV infection

This study aims to characterize the prevalence and diversity of cervical HPV infection and its association with the cervicovaginal microbiome in pregnant women living with HIV followed up at the Gaffrée and Guinle University Hospital (HUGG), in Rio de Janeiro, Brazil.

METHODS

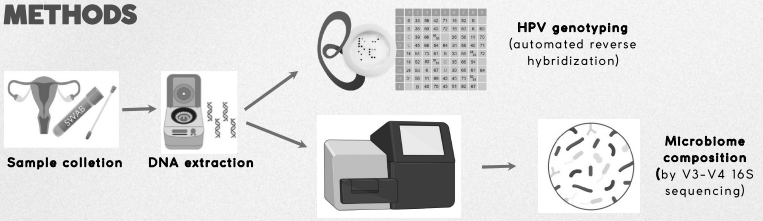

Fig.2. Study methodology

RESULTS

Sixty one samples have been collected and analyzed. HPV was found in 39 samples.The most prevalent type of HPV were genotypes 44/55 (18%) and 16 (15%). HPV types 16 and 18 were identified in 6 and 4 samples, respectively. Coinfection with more than one type of HPV was observed in 22 samples.

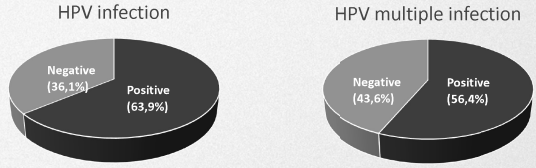

Fig.3. HPV prevalence and multiple infection.

Preliminary analysis of the cervicovaginal microbiome demonstrated a predominance of *Lactobacillus iners*, *Gardnerella vaginalis* and *Bifidobacterium scardovii* across the study population. The alpha and beta diversity analyses are being calculated.

This study stands out as one of the few to describe the microbiome profile of pregnant women living with HIV, exploring its relationship with HPV infection. Additionally, it emphasizes the importance of studying the vaginal microbiome in the context of various obstetric conditions, included the outcome of deliveries.

None of authors declare a conflicts of interest