121. Investigating the Relationship between the cervical microbiome and HPV Status in HIV-Infected women in Meru County, Kenya.

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Abstract

Cervical cancer, caused by high-risk Human Papillomavirus (HPV), is a global burden affecting women. The cervical microbiome is associated with female health regulation. Immuno-compromised HIV-infected women are susceptible to persistent HPV infections. The aim of this study was to characterize the cervical bacterial communities in HIV-infected women and to investigate their relationship with an individual's HPV status. A cross-sectional study was conducted involving 38 HIV-infected women, with 52.63% being HPV-positive and 47.36% HPV-negative. The study was carried out at the Meru Teaching and Referral Hospital (MeTRH). The dry Evalyn brush was utilized for self-sample collection. DNA extraction and amplification was carried out at the Centre for Molecular Biosciences and Genomics. Microbiome characterization was done by 16S rRNA sequencing on an MGI DNBSEQ-G99 platform. The Bioconductor R package was used to perform sequence analysis. Ten bacterial phyla were identified with Firmicutes and Actinobacteria being the most abundant with relative abundances of 48% and 26% respectively. Proteobacteria (2.4%) and Spirochaetes (0.4%) were selectively enriched in HPV-positive women. Gardnerella, Lactobacillus, Prevotella and Sneathia were the most abundant genera. Three STI-associated genera were identified including Mycoplasma, Ureaplasma and Treponema. Alpha and beta diversity analyses rsevealed no significant differences in the microbiome composition between HPV-positive and HPV-negative women. The median Shannon diversity index was 5.733, and the median Simpson index was 0.9940. PERMANOVA on Bray-Curtis distances generated a p-value of 0.328. A t-test, p=0.4484 and Wilcoxon, p=1 was used to evaluate Shannon and Simpson. These indicated a high microbial diversity and dysbiosis. In conclusion, HIV infection is associated with a more diverse cervical microbiota. However, the overall composition between HPV-positive and HPV-negative women is similar. This could be attributed to HIV infection having already distorted the diversity of the microbial species. The findings thus highlight the need for targeted interventions to curb HR-HPV infections in HIV-infected women.

Keywords: *Cervical microbiome, dysplasia, Human Papillomavirus, dysbiosis, high-risk HPV, low-risk HPV.*