Insight into the cervicovaginal microbiota profiles in Moroccan women

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Disclaimer: This data is unpublished yet however it's going through final stages of review process and most likely would be published by the time of the conference and more results will be showed.

Abstract

Background: The composition of the cervicovaginal microbiota is increasingly recognized as a factor influencing susceptibility to sexually transmitted infections (STIs), particularly Human Papillomavirus (HPV) and *Chlamydia trachomatis* (CT). Coinfection with these pathogens elevates the risk of cervical cancer development.

Objective: This study aims to characterize the cervical microbiota profile and its diversity among Moroccan women infected with HPV and/or CT.

Methods: Cervical samples (n = 120) were collected and divided into four equal groups: HPV-positive, CT-positive, HPV/CT coinfected, and healthy controls. Microbial communities were profiled using 16S rRNA gene amplicon sequencing. Downstream analysis was performed in R/RStudio included assessment of alpha and beta diversity, taxonomic composition, and community state types (CSTs) via hierarchical clustering. Differential abundance testing was conducted using the ANCOM-BC method.

Results: Healthy controls exhibited significantly greater microbial alpha diversity compared to all infected groups, suggesting an association between HPV/CT infection and reduced microbiota diversity. *Lactobacillus iners* predominated across all groups.

Conclusions: These insights may inform future development of microbiome-targeted strategies for STI prevention.

Keywords: HPV, *Chlamydia trachomatis*, coinfection, cervical microbiota, 16S rRNA sequencing, abnormal cytology.