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Congress Abstract

Association Between the Cervicovaginal Microbiota and Tumor Characteristics in Cervical Cancer

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Introduction: Persistent infection with high-risk human papillomavirus is a necessary step in cervical carcinogenesis; however, the development of neoplasia is also determined by the state of the local microbial and immune microenvironment. Lactobacillus deficiency, anaerobic dysbiosis, and inter-kingdom biofilms can sustain inflammation, damage to the epithelial barrier, and persistence of viral infection.

Objective: To study the cervicovaginal microbiota in cervical cancer and to determine its association with histological type and characteristics of the tumor process.

Materials and Methods: The study had an analytical case-control design with cross-sectional and prospective-analytical components and included two research arms of 100 women each: a clinical screening cohort without verified invasive cervical cancer and a cohort of patients with morphologically confirmed invasive cancer. Cervicovaginal biocenosis was investigated by quantitative real-time polymerase chain reaction using the "Femoflor-16" panel. Genotyping of 14 types of high-risk human papillomavirus, cytological assessment, and histological verification were performed. Statistical analysis included the Mann–Whitney U test, chi-square or Fisher's exact test, univariate and multivariate logistic regression, interaction analysis, and clustering of microbiome profiles.

Results: In the clinical screening cohort, high-risk human papillomavirus was detected in 72% of women, microbial community type IV in 20%, cervical intraepithelial neoplasia grade 2 or higher in 27%, Candida fungi in 56%, Gardnerella vaginalis in 59%, and their co-colonization in 30%. The combined detection of Candida fungi and Gardnerella vaginalis had the most pronounced association with cervical intraepithelial neoplasia grade 2 or higher: odds ratio 4.84; 95% confidence interval 2.41–9.70; $p < 0.001$. In invasive cancer, microbial community type IV was detected in 86% of patients. Squamous cell carcinoma predominantly corresponded to a profile dominated by bacteria of the genera Fusobacterium and Sneathia, while the glandular phenotype corresponded to a cluster dominated by bacteria of the genera Prevotella and Gardnerella. Belonging to the latter cluster retained an independent association with adenocarcinoma and adenosquamous carcinoma after accounting for human papillomavirus genotype 18 and tumor stage: adjusted odds ratio 8.76; 95% confidence interval 2.72–28.20; $p < 0.001$.

Conclusions: The cervicovaginal microbiota represents an additional biological level of human papillomavirus-associated carcinogenesis. Co-colonization with Candida fungi and Gardnerella vaginalis is most pronouncedly associated with cervical intraepithelial neoplasia grade 2 or higher, while microbial community type IV predominates in invasive cancer. Histotype-specific profiles justify further development and external validation of a microbiome-viral risk stratification model.

Keywords: Cervical Neoplasms; Papillomavirus Infections; Vaginal Microbiome; Microbiota; Candida; Gardnerella Vaginalis