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VAGINAL MICROBIOME AND HPV INTERPLAY

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The vaginal microbiome is a dynamic ecosystem that maintains a balance between protective *Lactobacillus species* and potentially pathogenic microorganisms, thereby playing a crucial role in vaginal health. Emerging evidence suggests that the composition of the vaginal microbiome influences the acquisition, persistence, and pathogenicity of human papillomavirus (HPV), as well as the development and progression of cervical intraepithelial lesions. *Lactobacilli* contribute to vaginal homeostasis through lactic acid production, which lowers vaginal pH, enhances the antimicrobial activity of hydrogen peroxide and bacteriocins, and inhibits opportunistic infections, including HPV. The D-lactic acid isomer further increases cervicovaginal mucus viscosity, providing additional protection against urogenital infections and facilitating the degradation of HPV viral particles.

An increased abundance of strict anaerobes associated with bacterial vaginosis has been frequently observed in women with cervical dysplasia. These microorganisms may compromise the epithelial barrier through enzymatic activity, thereby facilitating HPV entry. In HPV-positive women with cervical intraepithelial lesions, *Lactobacillus iners* often predominates, although its functional role remains controversial. A vaginal pH greater than 5 is associated with a 10–20% increased risk of HPV positivity in premenopausal women, possibly due to the sensitivity of the HPV E5 oncoprotein to acidic conditions.

Despite reported associations between HPV infection, vaginal dysbiosis, and cervical pathology, existing data remain inconsistent due to diagnostic limitations and the heterogeneous nature of bacterial vaginosis. Further research is required to elucidate the complex interactions between host factors, vaginal microbiota, and cervical carcinogenesis. Clarifying these relationships may enable the development of microbiome-targeted preventive and therapeutic strategies.

Keywords: Human papillomavirus, vaginal microbiome, dysbiosis