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HPV Associated with the Vaginal Microecosystem in Cervical Cancer Patients

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Abstract:

Infection with HPV in women is common in developing countries. Human Papillomavirus is grouped into HR-HPV and LR-HPV based on the capability of rate of infection. Infection with HR-HPV in women causes a high chance of Cervical Cancer (C.C.). Cervical Cancer is the most common type of cancer in women worldwide. This infection can be spread from person to person, mainly via sexual intercourse with an infected person. HPV types 16 and 18 dominantly cause up to 70% of infections. They inhibit the growth of *Lactobacillus* species in the vaginal area and promote the growth of harmful bacteria. They are associated with the vaginal microecosystem and grow dominantly in the cervix and causing lesions.

Keyword:

Human Papillomavirus, Vaginal Microbiome, Cervical Cancer,

Human Papillomavirus (HPV) :

The most prevalent virus that infects the reproductive system in humans is the Human Papillomavirus (Rezqalla et al. 2021). They are a group of small double-stranded DNA viruses(Stanley, Pett, and Coleman 2007). The majority of the eight proteins encoded by the circular, roughly eight-kilobase-pair HPV genome are classified as either "early" or "late." Six proteins (E1, E2, E4, E5, E6, and E7) found in the "early" area are in charge of immune regulation and HPV genome replication. The L1 and L2 capsid proteins, which make up the "late" region, have been implicated in the virus's ability to spread(Choi et al. 2023). They are almost 55 nm in diameter(Burd 2003). HPV is known to be the most prevalent sexually transmitted virus and one of the leading causes of STDs in both males and females globally(Burd 2003). After 1 to 2 years of infection with Human Papillomavirus, around 90% of infections are cured (Lib 2021). There are more than 200 types of HPVs found (Choi et al. 2023, Burd 2003). They are further divided into 2 based on their infectious rate and association with cervical cancer in females; they are grouped into High-risk HPV (HR-HPV) and Low-risk HPV (LR-HPV). In high-risk HPV there are 18 types (16, 18, 26, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68, 69, 73, and 82) are present, and in low-risk HPV there are 8 types (6, 11, 40, 42, 44, 53, 54, and 70) are found (Choi et al. 2023, Lib 2021).

Cervical Cancer :

Cervical cancer (C.C.) is the fourth most common cancer in females globally (Y. H. Lee et al. 2020). The data represented by the Global Cancer Statistics in the 2020 report (Liu et al. 2022). Cervical cancer caused approximately 570,000 new cases and 311,000 deaths globally in 2018 (Liu et al. 2022, Buskwofie, David-West, and Clare 2020). The current death rate of C.C. patients is more than 85% in middle-income and low-income countries for women(Castanheira et al. 2021, Bedell et al. 2020, Fong Amaris et al. 2024). India accounts for over one-fifth of all cervical cancer fatalities(Karim et al. 2021). Some main factors linked to the development of C.C. are Hr-HPV infection, many sexual partners, smoking, age, childbearing, and oral contraceptive usage (Papilloma, Cancer, and Disparities 2019).

HPV and Cervical Cancer :

The most significant risk factor for cervical cancer is HPV infection (Choi et al. 2023). After the discovery of human papillomavirus (HPV) in the early 1980s, HPV infection has been linked to most incidences of cervical cancer(J. E. Lee et al. 2022). HPV infection is the primary risk factor for C.C. (Hu et al. 2024) But it is not enough to develop C.C. cases in women (Mulato-Briones et al. 2024). Genital warts and numerous benign oral cavity HPV-associated lesions are linked to low-risk HPV infection, but high-risk variants can result in HPV-related cancers. High-risk genital HPV infections are prevalent, and most people recover from them over time. However, 15% of women are unable to completely remove the virus, and the main risk factor for the emergence of anogenital cancers is the persistence of an HR-HPV infection (Stanley, Pett, and Coleman 2007). HPV types 16 and 18 account for about 70% of all instances of cervical cancer. About 20% of cervical adenocarcinomas are caused by type 18, while 50% of squamous cell carcinomas and 55.60% of all cervical malignancies are caused by type 16 (Bedell et al. 2020).

Vaginal Microbes :

There are billions of microorganisms in the vagina's vast microecosystem(Chen et al. 2021). The ability of the host to protect against the development of harmful bacteria is greatly aided by the vaginal microbiome (VMB)(Alhabardi et al. 2021). According to recent claims, almost every type of vaginal microbial community (VMC) can be recognized as normal because, even when lactobacilli are absent, symptoms are often lacking, organic acid is produced, and the VMC remains stable over the long term(Vaneechoutte 2017). Maintaining the health of the vagina and shielding the reproductive system from pathogens depends on the vaginal microbiota (VMB), particularly the presence of lactobacilli(Virtanen et al. 2019). The chronic condition known as bacterial vaginosis (BV) is characterized by a high concentration of anaerobic microorganisms and their byproducts that harm the vaginal epithelium and degrade the cervical mucosa, which protects it (Kero et al. 2017). There are often only one or a few kinds of lactobacilli types in the healthy female vaginal tract (Castanheira et al. 2021). Five community state types (CST) of the VMB were discovered after 396 women of various ethnic backgrounds had their vaginal flora examined. Low microbial diversity is found in CST I, II, III, and V, where Lactobacillus (L) crispatus, L. gasseri, L. iners, and L. jensenii predominate, respectively. On the other hand, a decrease in lactobacilli and a wide variety of bacterial vaginosis (BV)-related bacteria, which are largely anaerobic, form CST IV (Castanheira et al. 2021).

HPV Associated with Vaginal Microorganisms :

Various studies and experiments have been done on HPV-positive and HPV-negative women and the conclusion of all these studies is that HPV affects the vaginal microecosystem, it’s means that the number of *Lactobacillus spp*. decreases if diversity increases(Papamentzelopoulou and Pitiriga 2025). There is a vast diversity observed in women’s vaginal microorganisms that are associated with HPV, and the presence of non-*Lactobacillus spp.* such as *Candida, Gardnerella vaginalis, Prevotella spp.,* in high concentrations, creates a favorable environment for HPV infection(Papamentzelopoulou and Pitiriga 2025, Newton et al. 2001). In a woman's presence of Sneathia sanguinegens, Anaerococcus tetradius, and Peptostreptococcus anaerobius in high concentration, results of high chance of growth of HPV(Mitra et al. 2016).

Conclusion :

As we have shown, the result of the presence of the group a *Lactobacillus* species inhibited the growth of HPV. Infection with HR-HPV in women leads to a decrease in the species of the group *Lactobacillus* bacteria and the growth of *Candida, Gardnerella, and Prevotella* species of bacteria. HPV is associated with these microbiomes and creates a suitable environment for their growth and causing lesions in the cervix region. In many women, Infection with HPV can be cured by itself.

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