



Prevalence and Genomic Distribution of Human Papillomavirus

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ABOUT THE STUDY

In this study, 1,51,564 women were recruited from four different regions of China. HPV was discovered in 5.81% of people. High-risk Human papillomavirus (HPV) infection was 31.56%, low-risk HPV infection was 7.21%, and mixed HPV infection was 4.70%. The most common four Highest Risk Human papillomavirus (HR-HPV) subtypes were HPV-52, HPV-16, HPV-58, and HPV-53, accounting for 9.49%, 7.93%, 1.54%, and 2.01% of all cases, respectively. HPV-6 was the most common LR-HPV genotype (9.17%), followed by HPV-81 (7.03%) and HPV-11 (1.27%). According to HPV genotype subgroup analysis, single-type infections were the most common (17.26%) among HPV positive people. The most common multi-infection genotype, with a frequency of 34.04%, was double infection. According to this large study, the overall prevalence of HPV in China is high, with different patterns emerging across different age groups and regions. HPV genotypes 28 and 4 were frequently detected in this population, indicating that they require immediate clinical attention.

Cervical cancer, the third most common female gynecologic malignancy and the fourth leading cause of female cancer death in 2018, is estimated to have 1,23,870 new cases and 71,000 new deaths (GLOBOCAN, 2018). The age-standardized incidence rate of cervical cancer is higher in developing countries than in developed countries (5.7 per 1,00,000 vs 6.3 per 68,000 women-years, respectively). China is responsible for roughly 14% of the world's annual cervical cancer incidence. As a result, with rising morbidity and mortality rates among young women, cervical cancer remains a relatively heavy burden of public hygiene management in China.

The primary cause of cervical cancer has been identified as the Human Papillomavirus (HPV), a sexually transmitted DNA virus

in the *Papovaviridae* family. It is believed that the majority of sexually active adults are infected with at least one HPV genotype. If the infection with high-risk HPV strains persists, it has the potential to become a well-known cause of cervical cancer. Over 200 distinct HPV genotypes have been identified to date, with approximately 15 infecting the anus and genital tract mucosal epithelium. They are classified as High-Risk HPV (carcinogenic HPV types, HR-HPV), Low-Risk HPV (non-carcinogenic HPV types, LR-HPV), and Intermediate-Risk HPV based on their carcinogenic risk or potential pathogenicity (IR-HPV).

This cancer is widely recognized as one of the most preventable cancers. Currently, HPV vaccination and HPV-based screening programs are used as part of comprehensive cervical cancer control strategies, and they have been shown to effectively eliminate the global burden of cervical cancer. Despite this, the prevalence and genotype distribution of HPV infections are heterogeneous (differences vary across nations and regions, as well as within a country), making progress toward prevention difficult. Therefore, for both the development of prophylactic vaccines based on HPV and the development of HPV-based cervical cancer screening strategies, a detailed understanding of the regional distribution patterns of HPV genotypes is essential. Large-scale data on the genotypic range of HPV infection in China have received relatively few reports. As a result, we calculated and examined the overall prevalence, age-specific prevalence, and genotype distribution of HPV in various locations using a large quantity of historical data on HPV genotype distribution in China. Future screening and prevention programs could be created with the help of this research.

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