International Journal for Multidisciplinary Research (IJFMR)
E-ISSN: 2582-2160 ● Website: www.ijfmr.com ● Email: editor@ijfmr.com

Prevalence and Genotype Distribution of High-Risk Human Papillomavirus among Women Undergoing Cervical Cancer Screening in Bangalore, India

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Abstract

Aim: To find out the prevalence and distribution of genotypes of high-risk human papillomavirus (HR-HPV) among women attending for cervical cancer screening in Bangalore, India. Methods: A retrospective observational study was conducted at Greenarray Genomics Research and Solutions Pvt. Ltd. using 692 cervical samples received from Divakar's Specialty Hospital, Bangalore, India, between 2020 and 2026. Detection and genotyping of HR-HPV were performed using a validated real-time polymerase chain reaction (PCR) -based assay. Results: Out of 692 cervical samples screened, 14 were positive for HR-HPV giving overall prevalence of 2.02%. In total, 22 genotype detections were found in the positive samples indicating that some women had multiple HR-HPV infections. HPV-66 was the most common genotype (n = 7), followed by HPV-33 (n = 3). Two samples contained HPV-16, HPV-18 and HPV-59 and one sample contained HPV-35, HPV-45, HPV-51, HPV-52, HPV-56 and HPV-68. Conclusion: The present study reports low prevalence of HR-HPV infection among women screened in Bangalore. HPV-66 is the most common genotype detected whereas HPV-16/18 is relatively less common. These findings illustrate the regional variation of HR-HPV genotypes distribution and highlight the importance of extended HPV genotyping over HPV-16/18 alone. Region-specific genotype surveillance can enhance cervical cancer screening, improve risk stratification and support more effective prevention strategies in Indian populations.

Keywords: Human papillomavirus (HPV), International Agency for Research on Cancer (IARC), Polymerase Chain Reaction (PCR),HPV 16, HPV 18, HPV 66.

Introduction

Human papillomavirus (HPV) is the most common sexually transmitted infection worldwide and remains an important public health problem. It is estimated that 85–90 % of sexually active individuals will acquire HPV infection at some time in their life and women bear a disproportionately higher burden. Most HPV infections are transient and clear spontaneously; however, persistent infection with high, risk HPV

genotypes can lead to precancerous lesions and invasive cancers. The World Health Organization has declared HPV to be one of the main infectious reasons for cancer worldwide, accounting for around 5% of all cancers globally.(Baba et al., 2025; Honnavar et al., 2026)

As reported by the World Health Organization (WHO) and the International Agency for Research on Cancer (IARC), about 604,127 cases of cervical cancer occurred globally in 2020; most cases were in low, and middle, income countries. Persistent infection with high, risk human papillomavirus (HR, HPV) is one of the most prevalent causes of cervical cancer. The majority of cervical cancer cases (more than 90%) are associated with one of 14 different HPV genotypes that have been classified as high, risk (HPV,16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58 ,59, 66, and ,68), as each of these genotypes has a strong association with cervical cancer development.(Yin et al., 2025)(Massad et al., 2025)

Specifically, 70% of patients with high, grade cervical lesions and patients with invasive cervical cancer have either HPV,16 or HPV,18. Based on IARC's categorization of HPV genotypes by risk level, HPV genotyping and accurate detection of these viruses are key components of screening programs. Screening allows for the prompt and accurate identification of women at increased risk for developing cervical cancer and provides insight into appropriate clinical management options for these women.(Yin et al., 2025)(Massad et al., 2025)

HR-HPV is the primary screening method for detection of precancerous lesions (the HPV test has a high sensitivity compared to the Pap test). Cervical samples collected by the clinician are the gold-standard way of obtaining specimens for HR-HPV testing, but self-collection (of vaginal specimens) has also been shown to provide diagnostic accuracy similar to clinician-collected specimens. Self-collection provides greater acceptability and accessibility than clinician-collected specimens, which makes self-collection a useful strategy for increasing screening rates, especially among those families who are under-screened for cervical cancer.(Sykes et al., 2025)

Method and Material

Study Design

This study was carried out at Greenarray Genomics Research and Solutions Pvt.Ltd. on cervical specimens received from Divakar's Speciality Hospital, Bangalore, India, for high-risk human papillomavirus (HR-HPV) test during 2020 to 2026. The Gupte hospital and ethics committee members approved the study-GHEC/2022-23/013

Sample collection

Digene HPV self-collection kit was used for sample collection and they were clinician collected cervical samples. The total number of collected and processed were 692. HR-HPV detection and genotyping was done by a validated Polymerase Chain Reaction (PCR)-based assay according to the manufacturer's instructions. The assay was used to assess the prevalence and genotype distribution of HR-HPV in the study population.

Result

692 women were screened for high-risk human papillomavirus (HR-HPV) during this study period and 14 of them were found to be positive for HR-HPV and there was total 22 genotype detected, with an overall prevalence of HR-HPV of 2.02%. Genotype analysis revealed that HPV-66 was the most detected genotype, in 7 cases, followed by HPV-33 in 3 cases. HPV-16, HPV-18 and HPV-59 were detected in 2

cases each, while HPV-35, HPV-45, HPV-51, HPV-52, HPV-56 and HPV-68 were detected only in 1 case each.

Multiple HR-HPV genotypes were detected in some women; therefore, the total number of genotype detections exceeded the number of HR-HPV-positive cases. Overall, HR-HPV prevalence was low in this screened population. Importantly, HPV-66 was the most prevalent genotype, while the globally predominant oncogenic genotypes HPV-16 and HPV-18 were detected less frequently. These findings highlight the need for regional surveillance of HR-HPV genotypes and support the use of extended genotyping to inform cervical cancer screening, triage and prevention strategies.

HR-HPV Genotype	Number of Positive Samples (n)
HPV-66	7
HPV-33	3
HPV-16	2
HPV-18	2
HPV-59	2
HPV-35	1
HPV-45	1
HPV-51	1
HPV-52	1
HPV-56	1
HPV-68	1
Total	14

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Discussion:

The present study showed a low prevalence of high-risk human papillomavirus (HR-HPV) infection among women undergoing cervical cancer screening in Bangalore, India. Among the HR-HPV-positive cases, HPV-66 was the most frequently detected genotype, followed by HPV-33, whereas HPV-16 and HPV-18 were detected less commonly. This genotype pattern differs from many global and Indian reports in which HPV-16 and HPV-18 are usually predominant, but it is consistent with the established understanding that HPV genotype distribution can vary according to geography, population characteristics, screening practices, and regional epidemiology.

This study contributes region-specific evidence from Karnataka on the prevalence and distribution of HR-HPV genotypes in a screened population. The key finding is the relatively higher detection of non-16/18 HR-HPV genotypes, particularly HPV-66 and HPV-33, compared with HPV-16 and HPV-18 in this cohort. Similar observations from other low- and middle-income settings suggest that non-16/18 HR-HPV types may contribute substantially to the overall burden of HPV infection and may be missed or underestimated if screening strategies focus only on HPV-16 and HPV-18.

These findings support the importance of extended HPV genotyping in cervical cancer screening programs. Detection of a broader panel of HR-HPV types can provide better epidemiological information, improve risk stratification, and help guide appropriate clinical follow-up. Regional surveillance is therefore essential for understanding local HPV genotype patterns and for developing screening, triage, and prevention strategies that are relevant to the Indian population. However, the findings should be

interpreted with caution because this was a retrospective, single-centre study with a small number of HR-HPV-positive cases. In addition, clinical correlation with cytology, colposcopy, histopathology, vaccination status, and follow-up outcomes was not available. Larger multicentric studies with longitudinal clinical follow-up are required to validate these observations and to determine the true clinical significance of non-16/18 HR-HPV genotypes in cervical cancer prevention.

Conclusion:

In the present study, out of 692 women screened for cervical cancer in Bangalore, India, 14 were tested positive for HR-HPV infection indicating low prevalence of HR-HPV infection in the population. The most frequent genotype was HPV-66, followed by HPV-33, and HPV-16 and HPV-18 were detected less frequently in this cohort. The presence of several non-16/18 HPV genotypes, including co-infections in some women, highlights the importance of extended HPV genotyping in routine screening programs. These findings suggest that HR-HPV genotype distribution may vary across regions and populations, and that reliance on HPV-16/18 detection alone may not fully capture the genotype spectrum present in all screened populations. Region-specific HPV surveillance can provide useful epidemiological data for risk assessment, screening policy, and cervical cancer prevention strategies. However, because this was a single-centre retrospective study with a small number of HPV-positive cases, the findings should be interpreted cautiously and validated through larger, multicentric studies with clinical correlation, cytology/histopathology data, and longitudinal follow-up. There is a further need of large scale, multicentric studies to better characterize HR-HPV genotype distribution and its implications for the cervical cancer control in Indian population.

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6. *Table 1 Distribution of HR-HPV genotypes detected among HPV -positive cervical samples.*