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Region-Specific HR-HPV Prevalence and Genotype Distribution in Karnataka, India: A Multicentre Study

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Abstract: **Aim: - To determine the prevalence of high-risk human papillomavirus infection and to describe the pattern of HR-HPV genotypes among women attending for cervical cancer screening in Karnataka, India by using a PCR based assay. The main etiologic factor of cervical cancer is persistent infection with high-risk human papillomavirus. HPV-16 and HPV-18 are the most prevalent genotypes responsible for cervical cancer globally, the distribution of HR-HPV genotypes is geographically heterogeneous. Methods: - This study was conducted at Greenarray Genomics Research and Solutions Pvt. Ltd., on cervical samples received from multiple hospitals in Karnataka, India between 2020-2026. A total of 500 clinician-collected cervical samples were screened for HR-HPV using a validated PCR-based assay. Furthermore, the genotype distribution of the positive samples was analysed. Results: Of the 500 women screened, 16 were positive for HR-HPV with the overall prevalence of 3.2%. The most detected genotype was HPV-16 (5 cases), followed by HPV-66 (4 cases). HPV-18 and HPV-33 were each found in 2 cases and HPV-31 and HPV-58 were each found in 1 case and 1 case of co-infection with HPV 16,66. Conclusions: The prevalence of HR-HPV infection in the screened population had HPV-16 as the predominant genotype followed by HPV-66. These results underscore the need for continuous regional surveillance of HR-HPV genotype distribution and support the rationale for the inclusion of extended HPV genotyping in cervical cancer screening and prevention programs. Larger multicentric studies with cytological, histopathological and longitudinal clinical follow up are warranted to better understand the epidemiology and clinical significance of HR-HPV genotypes in Indian population.**

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

1. INTRODUCTION

Human papillomavirus (HPV) is one of the most common sexually transmitted infections worldwide and is known as the main etiological factor for cervical cancer. HPV causes approximately 4.5% of all human cancers and is associated with cancers of the cervix, anus, vagina, vulva, penis and oropharynx. Among these, cervical cancer is the most important HPV-associated malignancy with an estimated 604,000 new cases and 342,000 deaths annually worldwide.

Human papillomavirus (HPV) is the main etiologic agent of cervical cancer and is a heterogenic group of more than 200 genotypes, more than 40 of which infect the anogenital tract. Of these, 14 genotypes (HPV-16, -18, -31, -33, -35, -39, -45, -51, -52, -56, -58, -59, -66 and -68) are classified as high-risk (HR-HPV) because of their strong association with cervical carcinogenesis. Although HPV infection is extremely common among sexually active women and is usually self-limiting, persistent infection with high-risk HPV genotypes is the key factor in the initiation of cervical intraepithelial neoplasia and invasive cervical cancer.[(Choi & Park, 2016)]

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.[(Arora et al., 2025; Sykes et al., 2025)]

2. METHOD AND MATERIAL

Study Design

This study was carried out at Greenarray Genomics Research and Solutions Pvt.Ltd. on cervical specimens received from multiple hospitals of Karnataka, India for high-risk human papillomavirus (HR-HPV) test during 2020 to 2026. The Gupte hospital Ethics committee approved the study- GHEC/2022-23/013.

Sample collection

The clinicians used Digene Cervical Sampler for collection of cervical swab samples (QIAGEN®). The digene Cervical Sampler from QIAGEN is a dedicated DNA collection device. The total number of collected and processed sample were 500. HR-HPV detection and genotyping was done by a validated Polymerase Chain Reaction (PCR)-based assay. The assay was used to assess the prevalence and genotype distribution of HR-HPV in the study population.

3. RESULT

500 women were screened for high-risk human papillomavirus (HR-HPV) during this study period and 16 of them were found to be positive for HR-HPV with an overall prevalence of HR-HPV of 3.2%. Genotype analysis revealed that HPV-16 was the most detected genotype, in 5 cases, followed by HPV-66 in 4 cases. HPV-18, HPV-33 and were detected in 2 cases each, while HPV-31 and HPV -58 were detected only in 1 case each, also got 1 case positive with coinfection of HPV 16,66.

Importantly, HPV-16 was the most prevalent genotype which was detected. 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.

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HR-HPV Genotype	Total Positive Samples (n)
HPV-16	**5**
HPV-66	**4**
HPV-18	**2**
HPV-33	**2**
HPV-31	**1**
HPV-58	**1**
Co-Infection 16,66	**1**

4. DISCUSSION

The present study showed a 3.2% prevalence of high-risk human papillomavirus (HR-HPV) infection in the women undergoing cervical cancer screening in centres across Karnataka, India. Other South Asian populations have reported similar genotype patterns with high prevalence of HPV-16 and HPV-66, though studies from several Asian countries have identified HPV-52 and HPV-58 as the predominant non-16/18 high-risk genotypes[(Agents, 2026)][(Chakraborty et al., 2024)]

In the current study, HPV-16 was the most detected genotype, consistent with its known role as the predominant oncogenic HPV genotype responsible for the majority of cervical cancer cases worldwide. Two cases each had HPV-18 and HPV-33 which are known high-risk genotypes implicated in cervical carcinogenesis. HPV-66 was the second most prevalent genotype with five detected cases. The prevalence of HPV-66 varies according to the geographical location but it is generally considered to have a lower carcinogenic potential than HPV-16 and HPV-18 case each of HPV-31 and HPV-58 was found and these have also been associated with the development of cervical cancer.

The observed genotype distribution highlights the importance of continued HPV surveillance to monitor regional genotype patterns and to evaluate the potential impact of vaccination and screening programs. Moreover, genotype-specific data are useful for guiding public health policies, improving cervical cancer screening strategies and evaluating the efficacy of current HPV vaccines in the local population. progression of different HR-HPV genotypes in Indian women. 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.

5. CONCLUSION

This study showed 3.2% prevalence of HR-HPV infection among women undergoing cervical cancer screening in multiple centres in Karnataka, India. The most prevalent genotype was HPV-16, followed by HPV-66,33,18 and some other high-risk genotypes and co-infections were found. These results highlight the importance of extended HR-HPV genotyping for the understanding of regional genotype distribution and for supporting cervical cancer screening and prevention strategies. Further large scale multicentric prospective studies including cytological and histopathological correlation are warranted to validate these findings and to better define the epidemiology of HR-HPV infection among Indian population.

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