International Journal of Medical and Pharmaceutical Sciences
Open access peer-reviewed Journal
Volume 2, Issue 8, Page 348-350.
https://doi.org/10.5281/zenodo.21838261

Research Article

Detection and Genotypic Characterization of High-Risk Human Papillomavirus Infections Among Women: A Single-Centre Cross-Sectional Study

Sarjan Shah*[1], Urmila Sureka[2], Jagruti Karande[3], Shruti Jawale[4], Preeti Arora[5]

[1]*Director, Greenarray Genomics Research and Solutions Pvt Ltd, Pune, Maharashtra, India*
[2]*Gynaecologist, Obstetrician, Infertility Specialist, Anand Nursing Home and Healthcare, Mumbai, Maharashtra, India*
[3]*Clinical Research Coordinator, Research and Development, Research Division of ADPL, Pune, India*
[4]*Genomic Scientist, Research and Development, Research Division of ADPL, Pune, India*
[5]*Chief Genomic Scientist, Research and Development, Research Division of ADPL, Pune, India*

Persistent infection with high-risk HPV (HR-HPV) genotypes is the major etiologic factor for cervical cancer, the 5th most common cancer in women worldwide. The knowledge of regional distribution of HR-HPV genotypes is important for the optimization of screening and prevention strategies. This study analysed cervicovaginal specimens collected between 2020 and 2026 from women attending Anand Mother and Child Hospital, Mumbai, India. A total of 249 cervicovaginal swabs were collected by the clinicians and tested for HR-HPV using a validated Polymerase chain reaction-based assay. Among the 249 women screened, five tested positive for HR-HPV. The reported genotypes included HPV33, HPV31 and HPV51 and coinfections involving HPV31/66 and HPV16/31/33/56. The detection of multiple HR-HPV genotypes highlights the occurrence of coinfections and underscores the value of extended genotyping for comprehensive HPV detection. The overall prevalence of high-risk HPV infection in the study population was 2%. Despite the low HR-HPV prevalence observed in this study, the identification of multiple HR-HPV genotypes and co-infections highlights the value of extended HPV genotyping in cervical cancer screening. Extended genotyping may improve risk stratification, support timely clinical management, and generate epidemiological evidence to guide cervical cancer prevention programmes.

Keywords: HPV 31, HPV33, HPV51, International Agency for Research on Cancer, HR-HPV.

INTRODUCTION

Human papillomavirus (HPV) is a non-enveloped, double-stranded DNA virus comprising more than 200 identified genotypes. 14 genotypes are commonly included in high-risk HPV (HR-HPV) testing. According to the International Agency for Research on Cancer classification, HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 and 68 are carcinogenic to humans Although most HPV infections are transient and are cleared spontaneously by the immune system, persistent infection with oncogenic HPV types may lead to cervical intraepithelial neoplasia and, eventually, invasive cervical cancer. Persistent oncogenic HPV infection is responsible for nearly all cervical cancers, with HPV16 and HPV18 together accounting for approximately three-quarters of cases worldwide.(1);(2); (3);(4) ;(5) Cervical cancer remains a major global public-health concern. It is the fifth most commonly diagnosed cancer in women globally with around 604 000 new cases and around 280 000 deaths in 2024.(6)Nearly 94% of these deaths occurred in low- and middle-income countries, reflecting substantial inequalities in access to HPV vaccination, cervical screening, early diagnosis, and appropriate treatment. India bears a particularly high disease burden, with an estimated 127,526 new cases and 79,906 deaths reported in 2022. Despite being the

world's fifth-largest economy, India ranks fourth in cervical cancer new cases and death. Age standardized incidence contributes the highest number of cervical cancer-related deaths(4). Nevertheless, cervical cancer is largely preventable through HPV vaccination, regular screening, and timely treatment of precancerous lesions. In many resource-limited settings, screening uptake remains inadequate because of limited healthcare infrastructure, insufficient awareness, socioeconomic inequalities, and restricted access to quality healthcare services. (5);(7) The prevalence and distribution of HR-HPV genotypes vary geographically because of differences in population characteristics, sexual and behavioural factors, screening practices, and vaccination coverage. Characterising region-specific genotype patterns is therefore important for optimising cervical-cancer screening strategies, evaluating vaccine effectiveness, and monitoring changes in circulating HPV types. PCR-based HPV genotyping provides sensitive and specific detection of HR-HPV infections and enables the identification of individual and multiple genotypes, thereby supporting risk-based screening and epidemiological surveillance. (8);(9)

MATERIAL AND METHOD

Study Design

The study was carried out at Greenarray Genomics Research and Solutions Pvt.Ltd., Pune, India. This study analysed cervicovaginal specimens collected by clinicians of women attending Anand Mother and Child Hospital, Mumbai, India for high-risk human papillomavirus (HR-HPV) screening. The Gupte hospital Ethics committee approved the study-GHEC/2022-23/013.The total number of collected and processed sample were 249. HR-HPV detection and genotyping was done by a validated Polymerase Chain Reaction (PCR)-based assay.

RESULT

A total of 249 women were screened for high-risk human papillomavirus (HR-HPV), of whom 5(2 %) tested positive. 3 single-genotype infections one each with HPV33 HPV31 and HPV51 and two multiple-genotype infections involving HPV31/66 and HPV16/31/33/56, respectively were observed.

DISCUSSION

HR-HPV was detected in five of the 249 women screened (2 %), including two women with multiple-genotype infections. These findings underscore the value of extended HPV genotyping for the comprehensive detection and characterisation of HR-HPV infections. Although the number of positive cases was small and limits broader epidemiological interpretation, the detection of HR-HPV coinfections is noteworthy. Persistent infection with oncogenic HPV is the principal cause of cervical cancer; however, the presence of multiple genotypes alone does not necessarily indicate persistence or disease progression. Longitudinal follow-up is required to determine whether these infections persist and are associated with cervical abnormalities (10). In addition to HPV16, the detection of HPV33, HPV31, HPV51, and HPV66 demonstrates the circulation of oncogenic and potentially oncogenic HPV types beyond HPV16 and HPV18 in the study population. Although HPV16 and HPV18 account for most cervical cancers globally, several other genotypes contribute substantially to the remaining disease burden (11) These findings support the use of extended HPV-genotyping assays in regional screening and surveillance programmes to characterise genotype distribution, detect multiple infections, monitor changes in circulating HPV types, and inform evidence-based HPV vaccination strategies tailored to regional genotype patterns.

CONCLUSION

The detection of non-16/18 genotypes and multiple-genotype infections demonstrates the value of extended HRHPV genotyping for characterising local HRHPV types. In conclusion, extended HPV genotyping provides valuable information beyond the detection of HPV-16 and HPV-18 by identifying the regional distribution of other high-risk genotypes and multiple infections. Its integration into cervical cancer screening and surveillance programmes may improve risk stratification, support timely clinical management, monitor circulating HPV types, and inform region-specific HPV vaccination strategies and prevention policies.

REFERENCES

1. Gupte S, Parthasarathy S, Arora P, Ozalkar S, Jangam S, Rajwade K. A Rapid, Sensitive and Type - Specific Detection of High - Risk HPV - 16 and HPV - 18. J Obstet Gynecol India. 2023;73(5):440–4. https://doi.org/10.1007/s13224-023-01751-1.
2. Duran MN, Ilgin SK. Distribution of HPV genotypes and comparison of cervico- vaginal cytologies in PCR- detected HPV-positive patients: a retrospective observational study. 2026;(February).
3. Numminen E, Leino A, Karhula Q, Fonagy V, Seiskari T. Genotype and age shape the risk of persistent high-risk human papillomavirus infections. Am J Obstet Gynecol 2026;235(1):114–22. https://doi.org/10.1016/j.ajog.2026.02.038.
4. IARC. International Agency of Research on Cancer. 2022; Available from: https://www.iarc.who.int/cancer-type/cervical-cancer/
5. WHO. International agency for research on cancer. 2019. Available from: https://www.iarc.who.int/cancer-type/cervical-cancer/
6. WHO. World health organisation. 2024. WHO. Available from: https://www.who.int/news-room/fact-sheets/detail/cervical-cancer
7. Anand K V, Mishra GA, Suryawanshi VB, Pimple SA, Kulkarni VY. Experiences with HPV self-sampling in India: advancing cervical cancer prevention and screening. 2026.
8. Hossein S, Habibnia S, Rokni M. Prevalence and genotype distribution of human papillomavirus (HPV) in an at-risk and suspected population in Iran. 2026;5.
9. Deshmukh VN, Patil S, Hinge DD. The Burden and Prevention of Human Papillomavirus (HPV) Infections and Cervical Cancer in India: A Literature Review. 2024;16(10).
10. Schiffman, M., Castle, P. E., Jeronimo, J., Rodriguez, A. C., & Wacholder S. Human papillomavirus and cervical cancer. Lancet (London, England). 2007.
11. Bosch FX, Broker TR, Forman D et al. Comprehensive control of human papillomavirus infections and related diseases. Vaccine. 2013.

Cite: Sarjan Shah*, Urmila Sureka, Jagruti Karande, Shruti Jawale, Preeti Arora, Detection and Genotypic Characterization of High-Risk Human Papillomavirus Infections Among Women: A Single-Centre Cross-Sectional Study, Int. J. Med. Pharm. Sci., 2026, 2 (8), 348-350. https://doi.org/10.5281/zenodo.21838261