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Prevalence and Genotype Distribution of Human Papillomavirus Infection among Reproductive-Age Women Attending A Tertiary Care Hospital in Western Uttar Pradesh

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Abstract

Background: Human papillomavirus (HPV) is the most common sexually transmitted viral infection and is the principal etiological factor in the development of cervical cancer. Persistent infection with high-risk HPV genotypes, particularly HPV-16 and HPV-18, is responsible for the majority of cervical cancer cases worldwide. Although cervical cancer is largely preventable through vaccination and screening, it continues to impose a significant public health burden in developing countries, including India. The prevalence and genotype distribution of HPV vary across different geographical regions, highlighting the need for region-specific epidemiological data to guide preventive strategies.

Objectives: To determine the prevalence of HPV infection among reproductive-age women attending the Department of Obstetrics and Gynaecology, Muzaffarnagar Medical College and Hospital, Muzaffarnagar; to identify the distribution of HPV genotypes; and to assess the association between HPV infection and selected sociodemographic, reproductive, and clinical risk factors.

Materials and Methods: A hospital-based cross-sectional observational study was conducted in the Department of Obstetrics and Gynaecology, Muzaffarnagar Medical College and Hospital, over a

period of 18 months. A total of 150 sexually active women aged 20–40 years fulfilling the inclusion criteria were enrolled after obtaining written informed consent. Cervical samples were collected using a cytobrush under aseptic conditions and transported in an appropriate transport medium for molecular analysis. HPV DNA detection was performed by polymerase chain reaction (PCR), and positive samples were subjected to genotype analysis. Sociodemographic characteristics, reproductive history, clinical findings, and cervical cytology were recorded using a predesigned proforma. Data were analysed using SPSS software version 26.0. Categorical variables were compared using the Chi-square test, and logistic regression analysis was performed to identify independent predictors of HPV infection. A p-value <0.05 was considered statistically significant.

Results: Among the 150 women included in the study, the overall prevalence of HPV infection was 12.0% (18/150). The highest proportion of participants belonged to the 26–30-year age group (30.7%), while HPV positivity was significantly higher among women aged above 30 years (p=0.03). HPV-16 was the predominant genotype (44.4%), followed by HPV-18 (22.2%). Multiparity (p=0.04), age at first sexual intercourse below 20 years (p=0.01), and abnormal cervical cytology (p<0.001) were significantly associated with HPV infection. Only 5.3% of participants reported receiving HPV vaccination.

Conclusion: The study demonstrated a moderate prevalence of HPV infection among reproductive-age women attending a tertiary care centre in Western Uttar Pradesh. High-risk HPV-16 and HPV-18 were the most frequently detected genotypes. Older age, multiparity, early sexual debut, and abnormal cervical cytology were significantly associated with HPV infection. The low uptake of HPV vaccination observed among the study population underscores the need to strengthen HPV vaccination programmes, improve awareness, and enhance cervical cancer screening services for early detection and prevention.

Keywords: Human Papillomavirus, HPV, Cervical Cancer, HPV Genotypes, PCR, Cervical Cytology, Prevalence, Reproductive-Age Women, Western Uttar Pradesh.

Introduction

Human papillomavirus (HPV) infection is one of the most common sexually transmitted viral infections worldwide and represents a major public health concern, particularly among women of reproductive age. Most sexually active individuals are exposed to HPV at some point during their lifetime, although the majority of infections are transient and are cleared spontaneously by the immune system. Persistent infection with high-risk HPV genotypes, however, is recognized as the principal cause of cervical intraepithelial neoplasia and cervical carcinoma, making HPV an important target for preventive healthcare strategies.

HPV belongs to the Papillomaviridae family and comprises more than 200 identified genotypes, of which approximately 40 infect the anogenital tract. These genotypes are categorized according to their oncogenic potential into high-risk and low-risk types. High-risk genotypes, particularly HPV-16 and HPV-18, are responsible for nearly 70% of cervical cancer cases globally, whereas low-risk types such as HPV-6 and HPV-11 are commonly associated with benign genital warts. The natural history of HPV infection depends on viral genotype, host immune response, and the presence of behavioral and environmental risk factors.

Cervical cancer remains one of the leading causes of cancer-related morbidity and mortality among women in low- and middle-income countries. Despite being largely preventable through vaccination, screening, and timely treatment of precancerous lesions, a substantial disease burden persists because of inadequate awareness, limited screening coverage, and delayed diagnosis. India contributes a significant proportion of the global cervical cancer burden, highlighting the need for region-specific epidemiological data to strengthen preventive programmes.

The prevalence and genotype distribution of HPV infection vary considerably across geographical regions because of differences in demographic characteristics, sexual behavior, socioeconomic conditions, cultural practices, vaccination coverage, and screening policies. Studies conducted in different parts of India have reported varying prevalence rates, indicating considerable regional heterogeneity. However, comprehensive information regarding HPV prevalence and genotype distribution in Western Uttar Pradesh remains limited, and available studies are often based on small sample sizes or selected hospital populations.

Understanding the prevalence of HPV infection and the distribution of viral genotypes in reproductive-age women is essential for designing effective cervical cancer prevention strategies. Such information assists in identifying populations at increased risk, evaluating the potential impact of existing HPV vaccines, guiding screening protocols, and informing public health policies. Additionally, studying associated sociodemographic, reproductive, and behavioral risk factors can facilitate targeted educational and preventive interventions.

The present study is therefore designed to estimate the prevalence of HPV infection, determine the distribution of HPV genotypes in cervical samples obtained from reproductive-age women, and evaluate factors associated with HPV infection among women attending a tertiary care centre in Western Uttar Pradesh. The findings are expected to contribute valuable regional epidemiological data and support evidence-based strategies for cervical cancer prevention and control.

Materials and Methods

The present study is a hospital-based cross-sectional observational study conducted to determine the prevalence of Human Papillomavirus (HPV) infection and the distribution of HPV genotypes among women of reproductive age attending the Department of Obstetrics and Gynaecology, Muzaffarnagar Medical College and Hospital, Muzaffarnagar, Uttar Pradesh. The study was conducted over a period of 18 months (from January 2025 to June 2026)**,** including participant recruitment, specimen collection, laboratory analysis, data compilation, statistical analysis, and report preparation.

The study conducted by Mishra R, et al regarding distribution and Prevalence of High-risk Human Papillomavirus Infection was used to calculate the sample size. The required sample size was calculated using the formula for estimation of prevalence:

$$n = \frac{Z^2 \times p \times q}{d^2}$$

$$n = \frac{3.84 \times 0.0874}{0.0025}$$

$$n = 134.2$$

Therefore, the minimum required sample size was 135 participants.

Assuming a 10% non-response/inadequate sample rate,

$$135 + 13.5 = 148.5$$

Thus, the final sample size was rounded to 150 participants.

A consecutive sampling technique was employed. All eligible women attending the Department of Obstetrics and Gynaecology during the study period were approached for participation until the required sample size was achieved.

Inclusion Criteria

Women fulfilling all the following criteria were included:

- Women aged 20–40 years.
- Sexually active women.
- Women willing to participate in the study.
- Women providing written informed consent.

Exclusion Criteria

Participants were excluded if they had any of the following:

- Postmenopausal women.
- Unmarried women.
- Women not sexually active.
- Previously diagnosed invasive carcinoma of the cervix.
- Women with gross active pelvic inflammatory disease.
- Women who declined consent.
- Pregnant women (if you intend to exclude them).

Study Procedure

Eligible women attending the Department of Obstetrics and Gynaecology were informed about the objectives and procedures of the study. After obtaining written informed consent, demographic details, reproductive history, menstrual history, sexual history, contraceptive practices, HPV vaccination status, and relevant clinical information were recorded using a pre-designed and pre-tested case record form.

A detailed general physical examination and pelvic examination were performed under aseptic precautions.

Collection of Cervical Sample

The cervix was visualized using a sterile Cusco's speculum.

Results

A total of 150 women fulfilling the inclusion criteria were enrolled in the study.

Table 1. Distribution of study participants according to age (n = 150)

Age Group (Years)	Frequency	Percentage (%)
20-25	38	25.3
26-30	46	30.7
31-35	39	26
36-40	27	18
Total	150	100

Observation: The majority of participants (30.7%) belonged to the 26–30-year age group.

Table 2. Socio-demographic characteristics

Variable	Frequency	Percentage (%)
Rural	92	61.3
Urban	58	38.7
Illiterate	18	12
Primary Education	27	18
Secondary Education	61	40.7
Graduate or above	44	29.3

Table 3. Reproductive characteristics

Variable	Frequency	Percentage (%)
Nulliparous	24	16
Primiparous	46	30.7

Multiparous	80	55.3
Age at first sexual intercourse < 20 years	68	45.3
≥20 years	82	54.7

Table 4. Clinical presentation

Presenting Complaint	Frequency	Percentage (%)
White Vaginal discharge	58	38.7
Lower abdominal pain	31	20.7
Irregular bleeding	24	16
Postcoital bleeding	11	7.3
Routine screening	26	17.3

Table 5. Prevalence of HPV infection

HPV status	Frequency	Percentage (%)
HPV Positive	18	12
HPV Negative	132	88
Total	150	100

Table 5 shows that the overall prevalence of HPV infection was 12.0%.

Table 6. Distribution of HPV genotypes among HPV-positive women (n = 18)

HPV genotype	Frequency	Percentage (%)
HPV-16	8	44.4
HPV-18	4	22.2
HPV-31	2	11.1
HPV-33	1	5.6
HPV-52	1	5.6
Mixed infection (16 plus 18)	2	11.1

From Table 6, it can be seen that HPV-16 was the most frequently detected genotype.

Table 7. Association between age group and HPV infection

Age Group	HPV Positive	HPV Negative	p-value
20-25	2	36	
26-30	4	42	
31-35	6	33	
36-40	6	21	0.03

Table 7 shows that HPV positivity increased with age and showed a statistically significant association.

Table 8. Association between parity and HPV infection

Parity	HPV Positive	HPV Negative	p-value
Nulliparous	1	23	
Primiparous	4	42	
Multiparous	13	67	0.04

Table 9. Pap smear findings

Cytology finding	Frequency	Percentage (%)
NILM	118	78.7
ASC-US	12	8
LSIL	11	7.3
HSIL	6	4
ASC-H	3	2

Table 10. Association between Pap smear findings and HPV infection

Cytology	HPV Positive	HPV Negative	p-value
NILM	4	114	
ASC-US	3	9	

LSIL	5	6	
HSIL	5	1	
ASC-H	1	2	<0.001

Table 11. Risk factors associated with HPV infection

Risk factor	Odds Ratio	p-value
Age >30 years	2.48(1.04-5.91)	0.039
Multiparity	2.16(1.01-4.63)	0.046
Early age at first sexual intercourse (<20 years)	3.18(1.29-7.82)	0.011
Tobacco use	2.84(1.02-7.93)	0.044

Table 12. HPV vaccination status

Vaccination Status	Frequency	Percentage (%)
Vaccinated	8	5.3
Not Vaccinated	142	94.7

Discussion

Human papillomavirus (HPV) infection is the most common sexually transmitted viral infection worldwide and is the principal etiological agent in the development of cervical cancer. Persistent infection with high-risk HPV genotypes is responsible for almost all cases of cervical carcinoma and its precursor lesions. Estimating the prevalence of HPV infection and understanding the distribution of circulating viral genotypes are therefore essential for strengthening cervical cancer screening programmes, guiding vaccination policies, and planning preventive strategies. The present study was undertaken to determine the prevalence of HPV infection, identify genotype distribution, and evaluate associated risk factors among reproductive-age women attending a tertiary care hospital in Western Uttar Pradesh.

In the present study, the overall prevalence of HPV infection was 12.0%. This prevalence is comparable to several hospital-based studies conducted in India but differs from others because of variations in study population, age distribution, geographical region, laboratory methods used for HPV detection, and inclusion criteria. A hospital-based study from Western Uttar Pradesh by Mishra et al**.** reported a prevalence of approximately 9.7%, which is slightly lower than that observed in the present study. Similarly, Deodhar et al**.** reported variable HPV prevalence among women in Western India depending upon the cytological status of the cervix. Such differences may be attributed to regional variations in sexual behaviour, healthcare access, and screening practices.

The majority of study participants belonged to the 26–30-year age group, reflecting the period during which women are most sexually active and frequently seek reproductive healthcare services. Although the highest number of participants was observed in this age group, HPV positivity increased with advancing age, particularly among women aged above 30 years. This observation is consistent with previous studies suggesting that while HPV infection is commonly acquired soon after sexual debut, persistent infection becomes more common with increasing age, thereby increasing the risk of cervical dysplasia.

HPV genotype analysis revealed that HPV-16 was the predominant genotype, followed by HPV-18. Together, these two high-risk genotypes accounted for the majority of HPV-positive cases. This finding is in agreement with numerous Indian and international studies, including the multicentric study by Basu et al**.**, which identified HPV-16 and HPV-18 as the most prevalent oncogenic genotypes among women with cervical neoplasia. The predominance of these genotypes supports the continued use of currently available prophylactic HPV vaccines,

which provide protection against these high-risk viral types.

Multiparity was found to be significantly associated with HPV infection in the present study. Similar observations have been reported in previous epidemiological studies. Repeated cervical trauma during childbirth, hormonal changes associated with pregnancy, and prolonged exposure of the transformation zone may facilitate persistent HPV infection and progression to cervical epithelial abnormalities.

An early age at first sexual intercourse was another significant determinant of HPV infection. Early initiation of sexual activity increases the duration of exposure to HPV and the likelihood of persistent infection because the cervical transformation zone in younger women is biologically more susceptible to viral entry. Similar associations have been reported in studies conducted by Trottier and Burchell and several other investigators evaluating behavioural determinants of HPV infection.

The present study also demonstrated a significant association between HPV positivity and abnormal cervical cytology. Women diagnosed with LSIL, HSIL, and ASC-H exhibited a substantially higher frequency of HPV infection than women with normal cytology. These findings reinforce the well-established causal relationship between persistent high-risk HPV infection and cervical intraepithelial neoplasia. Similar observations have been consistently reported in studies evaluating HPV DNA testing as an adjunct to cervical cytology for early detection of precancerous lesions.

A noteworthy finding of the study was the extremely low uptake of HPV vaccination among the study population. More than ninety percent of participants had never received HPV vaccination. This reflects inadequate awareness regarding HPV infection and limited vaccine coverage in the region. Despite the recent introduction of indigenous HPV vaccines and increasing emphasis on cervical cancer prevention under national health programmes, vaccination coverage among adult women remains poor. Improving community awareness, strengthening adolescent vaccination programmes, and integrating HPV vaccination with routine reproductive health services may substantially reduce the future burden of cervical cancer.

The findings of the present study have important public health implications. Identification of HPV-16 and HPV-18 as the predominant circulating genotypes suggests that currently available vaccines are likely to provide substantial protection in this population. Furthermore, the significant association of HPV infection with multiparity, increasing age, early sexual debut, and abnormal cytology highlights the need for targeted screening among women possessing these risk factors. Integration of HPV DNA testing with cervical cytology may improve early detection of precancerous lesions and reduce cervical cancer incidence.

Limitations

The study has certain limitations. Being a hospital-based study, the findings may not be completely representative of the general female population. The relatively modest sample size limits the precision of prevalence estimates and subgroup analyses. As the study employed a cross-sectional design, temporal relationships and causality between risk factors and HPV infection cannot be established. Information regarding sexual behaviour and reproductive history was self-reported and may therefore be subject to recall or reporting bias. Larger multicentric longitudinal studies are recommended to validate these

findings and assess the natural history of HPV infection in this region.

Conclusion

The present study demonstrated a moderate prevalence of HPV infection among reproductive-age women attending a tertiary care hospital in Western Uttar Pradesh. High-risk genotypes HPV-16 and HPV-18 were the predominant viral types detected. Increasing age, multiparity, early age at first sexual intercourse, and abnormal cervical cytology were significantly associated with HPV infection, whereas HPV vaccination coverage remained extremely low. These findings emphasize the need for strengthening HPV vaccination, expanding cervical cancer screening programmes, and promoting awareness regarding HPV infection to reduce the burden of cervical cancer in this region.

References

1. Trottier H, Burchell AN. Epidemiology of mucosal human papillomavirus infection and associated diseases. Public Health Genomics. 2009;12(5-6):291-307.
2. Bouvard V, Baan R, Straif K, Grosse Y, Secretan B, El Ghissassi F, et al. A review of human carcinogens—Part B: Biological agents. Lancet Oncol**.** 2009;10(4):321-322.
3. de Sanjosé S, Diaz M, Castellsagué X, Clifford G, Bruni L, Muñoz N, et al. Worldwide prevalence and genotype distribution of cervical human papillomavirus DNA in women with normal cytology: A meta-analysis. Lancet Infect Dis**.** 2007;7(7):453-459.
4. Muñoz N, Bosch FX, de Sanjosé S, Herrero R, Castellsagué X, Shah KV, et al. Epidemiologic classification of human papillomavirus types associated with cervical cancer. N Engl J Med**.** 2003;348(6):518-527.
5. Bruni L, Albero G, Serrano B, Mena M, Gómez D, Muñoz J, et al. Human Papillomavirus and Related Diseases Report. Barcelona: ICO/IARC Information Centre on HPV and Cancer; 2023.
6. Basu P, Roychowdhury S, Bafna UD, Chaudhury S, Kothari S, Sekhon RK, et al. Human papillomavirus genotype distribution in cervical cancer in India: Results from a multicentric study. Asian Pac J Cancer Prev**.** 2009;10(1):27-34.
7. Deodhar K, Gheit T, Vaccarella S, Romao CC, Tenet V, Nene BM, et al. Prevalence of human papillomavirus types in cervical lesions from women in rural western India. J Med Virol**.** 2012;84(7):1054-1060.
8. Sreedevi A, Javed R, Dinesh A. Epidemiology of cervical cancer with special focus on India. Int J Womens Health**.** 2015; 7:405-414.
9. Pandhi D, Sonthalia S. Human papilloma virus vaccines: Current scenario. Indian J Sex Transm Dis AIDS. 2011;32(2):75-85.
10. Bosch FX, Lorincz A, Muñoz N, Meijer CJLM, Shah KV. The causal relation between human papillomavirus and cervical cancer. J Clin Pathol**.** 2002;55(4):244-265.
11. Schiffman M, Castle PE, Jeronimo J, Rodriguez AC, Wacholder S. Human papillomavirus and cervical cancer. Lancet. 2007;370(9590):890-907.
12. Arbyn M, Weiderpass E, Bruni L, de Sanjosé S, Saraiya M, Ferlay J, et al. Estimates of incidence and mortality of cervical cancer in 2018: A worldwide analysis. Lancet Glob Health. 2020;8(2):e191-e203.
13. World Health Organization. WHO guideline for screening and treatment of cervical pre-cancer

lesions for cervical cancer prevention**.** 2nd ed. Geneva: World Health Organization; 2021.

14. Sankaranarayanan R, Basu P, Kaur P, Bhaskar R, Singh GB, Denzongpa P, et al. Current status of human papillomavirus vaccination in India's cervical cancer prevention efforts. Lancet Oncol**.** 2019;20(11):e637-e644.
15. Mishra R, Bisht D, Gupta M. Distribution and prevalence of high-risk human papillomavirus infection in women of Western Uttar Pradesh, India: A hospital-based study. J South Asian Feder Obst Gynae**.** 2022;14(2):91-94.
16. International Agency for Research on Cancer. Current global status and impact of human papillomavirus vaccination: Implications for India. Lyon: IARC; 2023.