Original Article

Molecular Characterization of Human Papilloma Virus in Carcinoma Cervix along with Screening of Risk Factors and their Regional Comparison

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ABSTRACT

Introduction: Background: The threat of cervical carcinoma is still a major public health challenge in low- and middle-income countries, including India. In this context, disparate findings about HPV genotypes are reported from different regions of India. Interestingly, although HPV-16 and HPV-18 have demonstrated global supremacy as risk factors for cervical cancer, recent observations from India indicate a rising trend of high-risk non-18 genotypes. **Aim and objectives:** To assess the prevalence, distribution of genotypes, and molecular profile of the human papillomavirus in women presenting with suspected cervical pathology in the Agra region of North India. In addition, the cytology-VIA correlation and epidemiological risk factors in the region were assessed. **Material and Methods:** In this hospital-based cross-sectional study, the data were collected over a period of 18 months from April 2023 to January 2025. A total of 500 symptomatic women between the age group of 25 and 65 years were included from a tertiary care hospital in Agra. Cervical samples were obtained for the Pap smear, VIA, and HPV DNA. Genotyping for various types of HPV was done by real-time PCR for 28 types of HPV. Sociodemographic, reproductive, and behavioral factors of the subjects were taken into consideration. **Results:** The DNA of the human papillomavirus was detected in 13% of the 500 patients. There was no association between sociodemographic and behavioral factors. Abnormal cytology was found to be highly significantly associated with the presence of the human papillomavirus. Abnormal cytology was 74.7% associated with the presence of human papillomavirus ($p < 0.001$). Pap smear was found to be 95.6% specific and 86.2% sensitive. VIA was found to be 100% sensitive but 62.8% specific. In the present study, the human papillomavirus type 16 was the most prevalent. In addition to human papillomavirus type 16, human papillomavirus type 39. **Conclusion:** This study underlines marked regional diversity in HPV genotypes at high risk other than HPV-16/18 and confirms a strong concordance between infection with high-risk human papillomavirus and cytological abnormalities. These findings raise the demand for genotype-informed surveillance of human papillomavirus infection, expanded vaccine coverage, and integrated screening to advance the effort at cervical cancer prevention in north India.

KEYWORDS: *Genotype, human papillomavirus infections, papillomavirus vaccines, polymerase chain reaction, postmenopause, uterine cervical neoplasms*

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Introduction

Cervical carcinoma is a global public health issue, with significant disease burden, especially in developing countries. In the year 2020, there were more than 600,000 newly reported cases and over 340,000 deaths due to cervical carcinoma worldwide.[1] There are more than 200 different genotypes of human papillomavirus (HPV) reported, with about 13 mucosal types designated as being of high-risk origin for the process of carcinogenesis, specifically types 16, 18, 31, 33, 45, 52, and 58 among them.[2] The E6 and E7 proteins of the virus induce the inactivation of the tumor suppressor proteins p53 and pRb, respectively, causing the net outcome of genomic instability, dysregulation of the cell cycle.

Mounting data from Indian research indicate a considerable variation in genotype distribution and a certain burden of high-risk HPV (HR-HPV) genotypes 31, 33, 35, 39, 51, 52, 56, 58, 59, 66, and 68, increasing in their prevalence in Indian cases not presently covered by commercially available bivalent, quadrivalent, or nonvalent HPV vaccine formulations.[3-5]

Hence, the assessment of cervical carcinoma should necessarily incorporate, aside from the detection of the virus's genotype, viral load, integration, and modifications in the human genome, as has been well described in the past studies.[6] In fact, the integration of such molecular information with epidemiologic and behavioral risk factor profiling, including in addition to age at sexual debut, parity, smoking, and use of contraceptive measures regional differences within a given geographic location in regard to viral genotypes would greatly help to contextualize, among others, the specific etiology of cervical carcinoma's development as noted in studies aimed at fully defining such understanding of HPV driven cervical carcinogenesis.[7]

In India, cervical cancer is one of the chief female cancers with uneven distributions of HPV genotype and absent molecular surveillance.[3,4] In the context of cervical cancer, molecular genotyping of HPV infections is critical for public health purposes as it identifies the prevalent HR-HPV types within a region not covered by the vaccine, thus better defining the vaccine's expected efficacy for the development of screening algorithms for the population.

Materials and Methods

This observational, cross-sectional study was conducted in the Gynaecology department and department of microbiology and pathology of S.N. Medical College, Agra, over a period of 18 months from April 2023 to January 2025. A total of 500 symptomatic women, aged 25–65 years, presenting to the Gynecology outpatient department with complaints suggestive of cervical pathology were enrolled. The study was conducted in accordance with the Declaration of Helsinki and was approved by the Institutional Review Board of S.N. Medical College, Agra (IEC approval no. SNMC/IEC/2023/27 Dated June 15, 2023). Written informed consent was obtained from all participants in both English and Hindi, ensuring adherence to ethical standards for human research.

Inclusion and exclusion criteria

Women presenting with postcoital or postmenopausal bleeding, irregular menstruation, persistent vaginal discharge, dyspareunia, or lower abdominal pain, or showing cervical erosion or unhealthy cervix on examination were included in the study. Women who were unmarried, pregnant, had hysterectomy, or unwilling to provide consent were excluded.

A structured questionnaire was administered to collect demographic (age), socioeconomic (education, occupation, socioeconomic status, and residence – urban/rural), reproductive (parity, age at first intercourse, number of sexual partners, contraceptive use such as condom, oral contraceptive pills, intrauterine contraceptive device (IUCD), or depot medroxyprogesterone acetate (DMPA) use, mode of delivery, and history of sexually transmitted infections), and behavioral data (smoking habits and personal hygiene practices). For women who satisfied the inclusion criteria and gave consent to participate in the study, samples for Papanicolaou smear (Pap smear) and HPV testing were taken during gynecological examination.

All data were anonymized and coded for statistical analysis. HPV genotype distribution and molecular profiles obtained from the study cohort were compared with published data from other regions of India and globally. Regional variations in genotype prevalence and molecular characteristics were analyzed to identify epidemiological patterns and their implications for HPV screening and prevention strategies.

Sample collection and laboratory procedures

All participants were examined in the Dorso lithotomy position under aseptic precautions. Following insertion of a sterile Cusco's speculum, sequential samples were obtained for HPV DNA testing, Pap smear, and Visual Inspection with Acetic Acid (VIA).

Human papillomavirus DNA sampling for polymerase chain reaction

Endocervical and ectocervical cells were collected using a sterile cytobrush by performing 4–5 gentle clockwise rotations at the transformation zone. The collected specimens were immediately transferred into

a viral transport medium and preserved at –80°C until molecular analysis.

Cervical exfoliated cells were obtained using an Ayre's wooden spatula by rotating 360° over the ectocervix and transformation zone. The cellular material was uniformly spread on pre-labeled glass slides, immediately fixed in 95% ethanol for a minimum of 30 min, and stained by the conventional Papanicolaou method. Smears were interpreted according to The Bethesda System (2001) for reporting cervical cytology and classified as negative for intraepithelial lesion or malignancy (NILM), Atypical Squamous Cells of Undetermined Significance, Low-Grade Squamous Intraepithelial Lesion, and High-Grade Squamous Intraepithelial Lesion or Carcinoma.[8]

Visual inspection with acetic acid

The cervix was inspected 1 min after application of 5% freshly prepared acetic acid. VIA positivity was defined as the appearance of distinct, dense acetowhite areas with well-demarcated margins, particularly near the squamocolumnar junction. The presence of ulcerative, nodular, or cauliflower-like lesions was considered suggestive of high-grade disease or malignancy.

DNA extraction and human papillomavirus genotyping

DNA was extracted from a 200 µl aliquot of exfoliated suspended cell samples using the QIA amp DNA Blood Mini Kit (Qiagen) as per the manufacturer's instructions. Amplification of the human β-globin gene was performed to test sample sufficiency. To detect HPV genotypes, Polymerase chain reaction (PCR) was performed by using PGMY09/PGMY11 primers (MY11:50-GCMCAGGGWCATAAYAATGG-30; M Y09:50-CG TCCM ARRGGAWACTGATC-30–) targeting a 450-bp region of the HPV L1 gene.

Molecular detection and genotyping of HR-HPV were performed using the TRUPCR® HPV High Risk Genotyping Kit (3B Black Bio Biotech India Ltd., India), a Real-Time PCR assay designed for qualitative identification of 28 oncogenic HPV genotypes (HPV 6, 11, 16, 18, 26, 31, 33, 35, 39, 40, 42, 43, 44, 45, 51, 52, 53, 54, 56, 58, 59, 61, 66, 68, 69, 70, 73 and 82). DNA extraction, amplification, and analysis were carried out in accordance with the manufacturer's guidelines. The assay targets the L1 region of the HPV genome and includes internal controls to monitor sample integrity and PCR inhibition.

All laboratory procedures were conducted under standard biosafety conditions, and both positive and negative controls were included in each PCR run to ensure analytical validity.

Table 1: Distribution of socioeconomic and demographic characteristics

Factor	Categories	Percentage of HPV positive (total)	*P*
Age (years)	<25.00	8.57 (35)	0.854
	25.00–34.00	11.79 (195)	
	35.00–44.00	13.64 (176)	
	45.00–54.00	15.49 (71)	
	55.00–64.00	20 (15)	
	65.00+	12.5 (8)	
Education	No schooling	12.89 (194)	0.667
	1–5	17.86 (56)	
	6–9	15.87 (63)	
	10th	12.9 (62)	
	12th	14.29 (35)	
	Graduate	8.7 (69)	
	Postgraduate	4.76 (21)	
Religion	Hindu	11.78 (399)	0.148
	Muslim	17.82 (101)	
Socioeconomic status	Lower	14.16 (226)	0.571
	Middle	12.04 (274)	
Demographic	Rural	14.45 (173)	0.574
	Urban	12.23 (327)	
Marital duration (years)	<5.00	8.33 (36)	0.223
	5.00–14.00	11.29 (186)	
	15.00–24.00	12.97 (185)	
	25.00–34.00	20.9 (67)	
	35.00–44.00	5.26 (19)	
	45.00–54.00	33.33 (6)	
	55.00+	0 (1)	
Age at first coitus (years)	<15.00	20 (35)	0.224
	15.00–24.00	12.05 (415)	
	25.00–34.00	14.58 (48)	
	35.00+	50 (2)	
Parity	Nulliparous	9.52 (21)	0.352
	Primiparous	12.7 (63)	
	Multiparous	12.59 (397)	
	Grand multiparous	26.32 (19)	
Mode of delivery	NVD	13.58 (427)	0.400
	C-section	13.89 (36)	
	NVD+C-section	0 (18)	
	Not applicable	10.53 (19)	
Total		13 (500)	

NVD: Normal vaginal delivery, HPV: Human papillomavirus

Results

Out of 500 patients, 65 were positive HPV, i.e., 13% prevalence in the region. Table 1 presents $P > 0.05$, so there is no statistically significant association between the HPV positive status and the socioeconomic and demographic characteristics of the individuals.

Table 2 represents that the *P* values were more than 0.05, so there is no statistical association between these symptoms and HPV positive status. Out of the total females with irregular periods (113) 14.16% were positive HPV, whereas

out of total 387 females with regular periods, 23.77% were positive HPV.

The Pap smear findings in Table 3 reveal that the majority of the females had the problem of inflammatory smear or NILM followed by Squamous Metaplasia. 1.2% of the females were detected with cancerous cervix.

Table 2: Percentage of positive responses for behavioral or clinical symptoms

Behaviour or symptom	Response	Percentage HPV positive (total)	*P*
Tobacco use	No	12.2 (410)	0.332
	Yes	16.67 (90)	
Contraceptive use	No	13.91 (345)	0.446
	Yes	10.97 (155)	
CONDOM	No	13.79 (457)	0.143
	Yes	4.65 (43)	
OCP	No	13.14 (449)	0.954
	Yes	11.76 (51)	
IUCD	No	12.97 (424)	0.965
	Yes	13.16 (76)	
DMPA	No	12.88 (497)	0.850
	Yes	33.33 (3)	
Vaginal discharge	No	6.85 (73)	0.091
	Yes	14.05 (427)	
Irregular menstruation	No	13.21 (386)	0.919
	Yes	12.28 (114)	
Pain during coitus	No	12.46 (353)	0.581
	Yes	14.29 (147)	
Postcoital bleeding	No	12.42 (451)	0.341
	Yes	18.37 (49)	

HPV: Human papillomavirus, OCP: Oral contraceptive pills, IUCD: Intrauterine contraceptive device, DMPA: Depot medroxyprogesterone acetate

Table 3: PAP findings distribution

PAP finding	Frequency (%)
Inflammatory smear	189 (37.8)
NILM	161 (32.2)
Squamous metaplasia	74 (14.8)
ASCUS	37 (7.4)
LSIL	32 (6.4)
CA cervix	6 (1.2)
Atrophic smear	1 (0.2)
Total	500 (100.0)

NILM: Negative for intraepithelial lesion or malignancy, ASCUS: Atypical squamous cells of undetermined significance, LSIL: Low-grade squamous intraepithelial lesion, CA: Carcinoma

Table 4 shows that the results from Pap smear and VIA with HPV status are significantly associated at 5% level of significance. The sensitivity of the VIA is higher than Pap smear, which is 100%, revealing that it can correctly detect all HPV-positive cases. However, the specificity is quite lower for VIA (62.8%) as compared with Pap smear method, which suggests that in 95.6% of the HPV negative cases will have negative Pap smear (i.e., normal Pap smear findings), whereas VIA method will give negative results in 62.8% of the HPV negative cases. Clearly, VIA method will give more false positives. Similarly, if we compare the Positive predictive value (PPV) and Negative predictive value (NPV) of the methods, we can see that PPV of Pap smear tells that 74.7% of the abnormal Pap smear cases will have positive HPV, whereas only 28.6% of the patients with positive VIA will have positive HPV. The NPV of both the methods is quite high and not having much difference. It tells that 100% of the negative VIA patients will have negative HPV, while 97.9% of the patients with a normal Pap smear (negative result) will have negative HPV. Overall, among the two, Pap smear has better closeness with the HPV method.

The effect of HPV and VIA on Pap smear findings is seen in Table 5. Both HPV and VIA are found to have statistically significant partial effect on the PAP findings. The results show that an HPV positive female has 8.5 times higher odds of having abnormal Pap smear finding as compared with a female with negative HPV. A female with positive VIA has nearly 28 times higher odds of reporting an abnormal Pap smear finding as compared with a female with negative VIA. Although the confidence interval for VIA is very wide, indicating a very high variability in results with varying samples.

Further, the genotypes were also studied in the patients, and it is found [Table 6] that HPV16 is the most prominent type of genotypes present in HPV positive females, followed by HPV39 and HPV51. Other genotypes were found in a relatively smaller number of HPV positive females. It is also seen that nearly 30% of the HPV positive females have multiple genotypes present.

Table 4: Association between various methods of detection of cancer with human papillomavirus, along with sensitivity, specificity, positive predictive value, and negative predictive value

Method	Result	Percentage HPV positive (total)	*P*	Sensitivity (%)	Specificity (%)	PPV (%)	NPV (%)
PAP	Normal	2.12 (425)	0.000	86.2	95.6	74.7	97.9
	Abnormal	74.67 (75)					
VIA	Negative	0 (273)	0.000	100.0	62.8	28.6	100.0
	Positive	28.63 (227)					

HPV: Human papillomavirus, PPV: Positive predictive value, NPV: Negative predictive value, VIA: Visual inspection with acetic acid

Table 5: Effect of human papillomavirus and visual inspection with acetic acid on PAP result

Method	OR (95% CI)	*P*
Intercept	0.003 (0.001–0.01)	0.000
HPV		
Negative	Reference	
Positive	8.523 (3.593–21.847)	0.000
VIA		
Negative	Reference	
Positive	28.372 (8.897–143.121)	0.000

HPV: Human papillomavirus, VIA: Visual inspection with acetic acid, OR: Odds ratio, CI: Confidence interval

Table 6: Prevalence of genotypes among human papillomavirus positive cases

Genotype	Percentage
HPV16	44.6
HPV39	18.5
HPV51	13.8
HPV31	9.2
HPV45	7.7
HPV56	6.2
HPV58	6.2
HPV66	6.2
HPV33	6.2
HPV18	6.2
HPV52	4.6
HPV59	3.1
HPV67	3.1
HPV37	1.5
Multiple genotype	29.2

HPV: Human papillomavirus

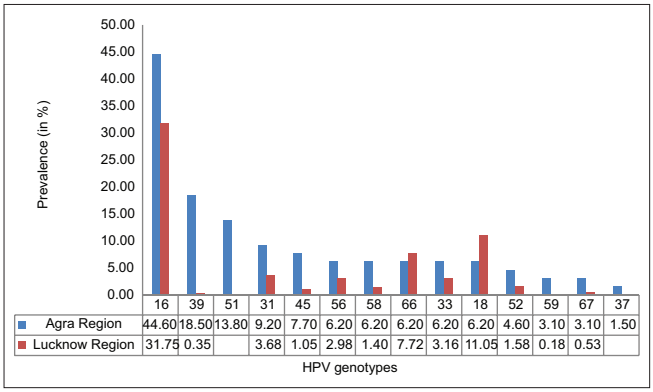

Figure 1: Comparison of prevalence of human papillomavirus strain types in Agra and Lucknow regions

The prevalence of the various genotypes among the HPV positive females in Agra and Lucknow regions is compared in Figure 1. We see that HPV16 is the most prevalent genotype in both regions. However, as compared to the Lucknow region, it is more prevalent in Agra region. In Agra, where HPV39, HPV51, and HPV 31 are more prevalent after HPV16, in Lucknow, HPV18, HPV66 are more prevalent. The prevalence of HPV 31 in Agra is 9.2%, whereas in Lucknow, it is only 3.68%.[9]

Discussion

In the current analysis, the overall HPV positivity rate was 13%, with differing rates among different sociodemographic and reproductive variables. Although most of the results did not have statistically significant associations, some epidemiologically consistent patterns emerged. The increase in HPV positivity (20%) among the age group of 55–64 years in the present population underlines the established "postmenopausal excess" of HR-HPV prevalence. This secondary peak, also noted in recent Indian epidemiological studies,[10] is due to immunosenescence, hormone-induced atrophy of the cervical epithelium, and latent infection reactivation rather than new infections. Similar findings from the study of the North Indian population showing higher persistence rates of HR-HPV in women beyond the age of 50 years,[11] our data also emphasize that persistent, rather than incident infections, contribute to oncogenic risk in older women. Early sexual initiation also had a notable trend where women who had their first sexual intercourse before the age of 15 years had a significantly higher prevalence of HPV infection (20%) than those who started their sexual life at 15–24 years (12.1%). This is supported by the fact that many studies conducted in India have confirmed that the probability of persistent infection by the HPV increases substantially if the first sexual contact takes place at a young age, when the immature Transformation Zone in the cervix is highly vulnerable to attack.[12] Grand multiparity was associated with the highest incidence of HPV infection (26.3%), as also found in large Indian studies, where parity was recognized as an important risk factor for cervical carcinogenesis.[13] Cervical trauma due to childbirth, hormonal factors, and vulnerability of metaplastic epithelium to HPV persistence have been postulated as mechanisms.[13]

Although our study could neither find any statistically significant association of HPV infection with education level, socioeconomic status, or rural/urban place of residence, a slight increase in low-educated and rural women could still be seen. There is evidence at a national level, for instance, through an analysis made by Muthuramalingam and Muraleedharan based on National Family Health Survey-5, that a large gap in accessing screenings for cervical cancer persists along with a higher level of under-screening of rural and poor women for this malignancy.[14] Religious background also revealed a trend but no significant difference, with increased

positivity rates found amongst Muslim women (17.8%) than Hindu women (11.8%). Though there have been varying findings reported in the literature, there have been documented cultural and health-seeking practices-related differences observed within regional research, which can impact screening rates and early presentation rates, as opposed to biological risk factors *per se*.[15] Marital duration revealed descriptive highs for positivity rates amongst women married for 25–34 years (20.9%), and women married for 45–54 years (33.3%), but sample sizes were underpowered for analysis. Older age, long duration of marriage, and high parity, as in our study, were also found to be predictors of HPV infection in a 2024 hospital-based cohort from Bihar,[13] reinforcing the epidemiologic validity of our findings.

None of the behavioral and clinical variables, tobacco, contraceptive practices (condoms, oral contraceptive pill (OCP), IUCD, and DMPA), vaginal discharge, painful intercourse, and post-coital bleeding, were found to be significantly associated with HPV positivity among the current subjects. The results were consistent with Indian cross-sectional research, which revealed nonsignificant correlations between individual behavioral variables and the identification of HPV, adjusted for confounding variables.[16,17] The increased HPV positivity rates among DMPA-consumers in our series are to be understood in the light of the larger trends reported in Indian studies, where DMPA use has not been found to have a significant individual association with the prevalence of HR-HPV infection, even after adjustment for potential confounding factors.[18] By the same token, the non-association between the studied HPV positives and symptoms such as vaginal discharge and/or dyspareunia also falls in line with trends observed in a similar study published recently by Sontakke *et al*., where the authors concluded that there is poor correlation between the symptoms and the detection of HPV infection in the screened clinic attendees in India, and suggested that the correlation between the two is very weak.[19] While irregular menses depicts a numerical variation in our findings, the non-significant association also supports the claim that irregular menses is not a proven predictor for HPV infection in screening studies in India.[19]

The current study establishes a definite link between HPV positivity and abnormalities identified via both cytological and visual screening techniques.[10] The significantly higher proportion of HPV positivity among women with abnormal Pap smear tests (74.7%) than those with regular cytology (2.12%) establishes the already proven fact that HR-HPV is identified as the major causal agent responsible for both cervical intraepithelial neoplasia (CIN) and cervix carcinoma. Such findings have also been established in recent studies conducted within India, where HPV was found to be present among 60%–80% of women with abnormal cytology, thereby re-establishing a high degree of agreement between HPV and cytological abnormalities.[20,21]

The Pap smear in this current study showed a high level of sensitivity (86.2%) and specificity (95.6%) for identifying HPV-related lesions. The results agree with another similar study by Thomas *et al*. that reported a level of sensitivity of 84% and specificity of 92% for Pap cytology among South Indians.[22] Though not sensitive for low-grade lesions, traditional cytology is still a valid modality for making a diagnosis, especially in resource-poor countries when combined with HPV testing. This performance of VIA in our study, though appreciable, has a sensitivity of 100%, but when it came to specificity, it was relatively lower, that is, 62.8%. Its high sensitivity values are in accordance with the larger VIA-based screenings in India, where sensitivity values varied between 82% and 96%.[23,24] Our study's lower specificity value also matches previously described data that VIA has a tendency to overestimate, thereby increasing the false-positive values, particularly in the case of perimenopausal women. VIA's PPVs in our study were modest, which matches previously described patterns in similar studies, where Sharma *et al*. described PPV values of 20%–33% according to the investigators experience and subjects' demographic backgrounds.[25] Its NPV of 100% indicates that this test may still be a good rule-out test in developing countries.

Multivariate analysis also strengthens the independent association of both HPV and VIA with cytological results. HR-HPV-positive women in our study had 8.5 times higher odds of presenting with abnormal pap smear results, which is expected given the meta-analysis range of OR values from 7.8 to 12.1 for HR-HPV positivity predicting cytological abnormalities.[26] For VIA, the odds ratio was considerably higher at 28.3 times, but the confidence interval is wide and has been observed because of variability related to individual skill, which has been identified as a limitation in studies using VIA-based screening.[24,25]

Taken together, these results support the complementary role of HPV testing, Pap cytology, and VIA in cervical cancer screening. At the same time, HPV is the most sensitive molecular marker, while the benefits of its simplicity are provided by VIA, and the advantage of the histological diagnosis is given by cytology. The evidence provided by recent cervical cancer screening

projects in India suggests the need for a blended strategy, especially in areas where the burden is high, with the utilization of molecular testing allied with immediate triage instruments to help enhance the early diagnosis and subsequent reduction in mortality caused by cervical cancer, especially in low-resourced areas.[23,27]

Lastly, the fact that all cervical carcinoma patients were infected with HPV-16 is highly likely to reflect a finding of many Indian molecular epidemiology studies, according to which HPV-16 is the most dominant HPV genotype, comprising about 65%–75% of invasive cancer cases in India.[10]

The overall analysis in the current research identified HPV-16 as the most common type in both the Agra and Lucknow areas although the incidence of the virus was significantly higher in the Agra region (44.6%) than the Lucknow region (31.8%). This is consistent with the recent trends of the incidence of HPV in India, for which the predominant type has always been HPV-16 and the most common high-risk genotype, for which the incidence has remained unabated for many years, according to various research conducted in India and its surrounding areas.[10,28] The predominant type has remained HPV-16 in Central India[11] and South India[28] and among the rural population of the northern part of the country.[9]

Although the prevalence of HPV-16 remained the highest genotype common to both regions, significant regional variation existed with respect to the distribution of other high-risk types. After the prevalence of the predominant HPV-16, the prevalence order for Agra consisted of the HPV-39, HPV-51, and HPV-31 types, whereas in Lucknow, it comprised the HPV-18 and HPV-66 types. A comparable pattern with higher HPV-18 representation has previously been reported in a rural Lucknow-based cohort.[10] The difference observed in the prevalence of the different types, with the prevalence of the HPV-31 type being approximately three-fold higher in Agra than Lucknow, indicates the regional variation noted in recent studies conducted on the Indian population regarding the prevalence of the non-16/18 high-risk types like the types mentioned above: HPV-31, 33, 39, 51, 52, and 58.[29,30]

Recent work in the Indian literature has highlighted the rising frequencies of non-16/18 HR-HPV types and the role of multiple infections in the spread of diversity.[16,19] These findings underscore the value of broad-spectrum HPV type analysis over HPV type 16/18 specific analyses. The current diversity has several significant implications for screening and vaccines. For example, the notable prevalence of genotypes covered by the nonvalent vaccine (types 31, 33, 45, 52, and 58) implies that more broadly protective vaccines may be beneficial in contexts where diversity is high.[16,30]

These differences may be affected by some methodologies, such as patterns of sampling, population demographics, sexual behavior related to sexual health, and specific genomic panels for each assay. It has also been reported in some previous studies from India that changes may exist in some proportional distributions of less common high-risk types when employing disparate PCR-based assays.[28-30] Despite these factors, the regional differences found in our study reinforce the need for population-based HPV surveillance employing a precise and sensitive assay for HPV genotyping.

Conclusion

From a public health perspective, these findings emphasize the urgent need to strengthen HPV vaccination and cervical screening programs in northern India. The regional molecular distribution of HR-HPV genotypes and associated risk factors supports population-specific surveillance and evidence-based, genotype-informed preventive strategies to enhance cervical cancer prevention and control.

Limitation

The relatively limited sample size represents an inherent constraint of this study, which may have adversely affected statistical robustness and constrained the generalizability of the results to wider populations.

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Conflicts of interest

There are no conflicts of interest.

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