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Cervical cancer screening - comparison between molecular assay to detect Human Papilloma Virus (HPV) DNA genotype and cytology examination from LBC samples in a Reference Laboratory in East India

Jayitri Das (Jt. 1st author)[1], Swatilekha Banerjee (Jt. 1st author)[1], Sumedha Dey[1], Himadri Mondal[1], Zishan Akhter[1], Reena Nakra[2], Vandana Lal[2] and Mallika Ghosh[1*]

[1]Dr. Lal PathLabs Ltd., Kolkata Reference Lab, India
[2]Dr. Lal PathLabs Ltd., National Reference Lab, India

**Corresponding author*

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A B S T R A C T

Cervical cancer is a public health problem in developing countries like India, so much so that India alone accounts for one-quarter of the worldwide burden of cervical cancers; and Human papilloma virus (HPV) is the most common causative factor. 30 different strains of HPV is associated with high risk for cervical cancer. The premise of our descriptive prospective study is based on the above context and compares HPV genotype prevalence with cytological findings. Cervical samples were collected in Eziprep liquid based cytology vials from 1009 patients from East/ North East India. HPV DNA genotyping was done using automated platform of QiaSymphony SP and cytology smears were made using Eziprep Nanocyt machine which uses Thin prep type LBC method. Commonest genotypes detected were 16 and 52, both of which were high risk genotypes. Cases with multiple infections also had at least one high risk genotype. 17 showed epithelial abnormality and most common type was atypical squamous cell of uncertain significance (ASCUS) followed by Atypical squamous cell cannot rule out high grade lesion (ASC-H). Most common genotypes associated with epithelial abnormalities were 16 followed by 58 and 59. 3 cases were identified with HPV negative epithelial abnormality. HPV 16 was found to be most common high risk genotype. Contrary to literature, 2nd most common genotype was not found to be HPV 18. HPV 52 was overall 2nd most common genotype while 58 and 59 were 2nd most common genotypes associated with epithelial abnormality.

Introduction

Cancer is one of the leading causes of adult deaths worldwide. Every year about 14 million new cancer cases are detected, and 8 million people die of cancer (Ferlay, 2012). Cervical cancer is the fourth most common cancer in women worldwide. In 2022 660000 new cases were identified globally (World Health Organization (WHO) (n.d.). *Fact sheet on cervical cancer*). Cervical cancer is a public health problem in developing countries like India, so much so that India alone accounts for one-quarter of the worldwide burden of cervical cancers (Ferlay, 2012; Institute for Health Metrics and Evaluation, 2011). In 2022, 94% of 350000 deaths from cervical cancer occurred in low- and middle-income countries (World Health Organization (WHO) (n.d.). *Fact sheet on cervical cancer*). This regional difference in prevalence is contributed by inequality in access to vaccination, screening & treatment services, awareness, poverty and gender bias (World Health Organization (WHO) (n.d.). *Fact sheet on cervical cancer*). Cervical cancer is the second most common cancer among women in India, which contributes to one-fifth of the global burden (Bhatla *et al.,* 2021).

Human papillomavirus (HPV) is a small, non-enveloped deoxyribonucleic acid (DNA) virus that infects skin or mucosal cells. It is one of the most common sexually transmitted viral infection worldwide (Burd, 2003). Not only penetrative sexual intercourse, but even genital contact can also transmit the virus from infected to the partner. The infection ranges from benign lesions such as cutaneous warts to malignant lesions such as cervical, anal, oropharyngeal or penile cancer. HPV is highly transmissible, with peak incidence soon after the onset of sexual activity, and most people acquire infection at some time in their lives (Ferlay, 2012).

Based on DNA sequencing data more than 200 different types of HPV have been identified, most of which are harmless (Burd, 2003). Around 30 types have been identified to be transmitted sexually and 15 of which are associated with cervical cancer. The virus is classified as high risk (oncogenic) and low risk (non oncogenic) genotypes. High risk HPV genotypes include 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68, 73 & 82 which are associated with cervical cancer and precancerous lesions. 6, 11, 42, 43 and 44 are non oncogenic genotypes responsible for benign lesions, which are occasionally found in cancerous lesions as well (Walboomers, 1999). In most of the cases HPV causes transient changes in cervical mucoepithelial cells which reverts spontaneously within one to three years. There are many other factors like genetic predisposition, suppressed immune response, long time oral contraceptive usage, smoking, multigravida women which contribute significantly to progression towards cervical cancer (Okunade, 2020).

In 2020 WHO launched global strategy to accelerate the elimination of cervical cancer with specific targets of vaccinating 90% of eligible girls against HPV, to screen at least 70% of eligible women twice in their life time and to treat 90% of positively screened women effectively. The present approaches to cervical cancer screening are Nucleic acid amplification tests for HPV DNA, Conventional Pap smear/ liquid based cytology testing and VIA (visual inspection with acetic acid or lugol's iodine). WHO recommends "screen and treat" approach or "screen-triage-and treat" approach for general population of women. HPV DNA detection is advised as a primary mode starting at the age of 30 years followed by other modalities if required. The screening should continue regularly every 5 to 10 years (World Health Organization, 2021).

As per National Family Health Survey (NFHS) 5 data, in India only 1.9% of women have undergone any form of cervical screening in their lifetime. West Bengal is among the lowest performing states with 0.2% participation rate along with Gujrat and Assam. Even though all the diagnostic modalities are not much technically challenging, it is clearly evident that integration of National Programme for Prevention and Control of Cardiovascular Disease, Diabetes, Cancer and Stroke (NPCDCS) program activities are deficient, and additional efforts are desired to overcome the alarming situation (Gopika, Prabhu and Thulaseedharan, 2022).

The study has been conducted to evaluate the prevalence of HPV positivity along with its genotype as well as cytological positivity. This study also compares the molecular assay and cytological categorization to identify association between HPV positivity / Cytological positivity if any. In addition, the authors have assessed the vaccination status among the study population as well as its association with screening result.

Materials and Methods

A descriptive prospective study was conducted on all submitted LBC samples for cervical screening by molecular assay to detect HPV genotype and Cytological

examination at a reference lab of Eastern India from September 2024 to December 2024.

The sample size was calculated considering a study setting of Prevalence rate 0.72 (Estimated prevalence rate in Indian population 72%) (The George Institute for Global Health India, 2023), Confidence level 0.95 (Desired confidence level 95%), Margin of error = 0.05 (Desired margin of error 5%), Z = 1.96 and using the formula (z^2 * p * (1 - p)) / (E^2). The minimum sample size calculated through r programming language 4.4.1 was found to be 310. During this study duration total 1009 cases were included, and the study variables were age, vaccination status, HPV DNA report along with its genotype if positive and cytological reporting. Any case which showed inhibition in PCR or did not meet adequacy criteria for cytology as per Bethesda criteria (2014) was excluded.

Cervical samples were collected in Eziprep liquid-based cytology vials (manufactured by VDNA laboratories) by clinician/ trained phlebotomist/ nurse. The samples were transported in refrigerated conditions. For molecular assay extraction of HPV DNA was done in automated platform of QiaSymphony SP using QiaSymphony DNA mini kit that involves silica-based purification of DNA with magnetic particle technology for automated isolation of DNA from specimens with eluted volume of 100 ul (sample volume-500ul). Master Mix was prepared for each of the 14 genotypes by mixing premix, primer-probe mix (FAM & VIC labelled) and nucleotide free water. PCR set up done with 2.5 ul of extracted DNA and positive & negative (no template) control as per table 1.

Real time PCR was done in Quant studio 5 Dx using home brew kit. The batch run is considered valid if all the PCs and NCs meet desired criteria. Amplification of housekeeping gene (PBG; Porphobilinogen) as Internal control (IC) indicates good sample quality as well as adequate extraction. The detected genotype is reported. A sample is considered Indeterminate/Inhibition detected when IC fails for 2 consecutive runs. The LOD of assay was verified up to 38 CT value.

Cytology smears were made using Eziprep Nanocyt machine which uses Thin prep type LBC method. The slides were stained using Papanicolaou stain method (Sathawane *et al.,* 2022).

Cytology reporting was done using Bethesda criteria for reporting gynecological samples, which was updated in 2014 (Nayar and Wilbur, 2015). The samples were considered adequate if minimum 5000 cells are seen except for history of post chemotherapy, radiotherapy, postmenopausal, post hysterectomy and if abnormal cells/ atrophic changes are found. In such cases the minimum cell requirement can vary. The reporting categories are divided into Negative for intraepithelial lesion and malignancy (NILM), Atypical squamous cells of uncertain significance (ASCUS), atypical squamous cells cannot exclude High grade squamous intraepithelial lesion (ASC-H), Low-grade squamous intraepithelial lesion (LSIL), High grade squamous intraepithelial lesion (HSIL), and frank malignancy for squamous cells. All non-neoplastic cases were reported as NILM. In case of presence of squamous cells with nuclei 2.5 - 3 times the size of a normal intermediate cell nucleus, and other nuclear atypical features are minimal or absent, the cases were reported as ASCUS. In ASC-H, atypical cells show HSIL like features but are scant in number. If large squamous cells with marked nuclear atypia and nuclear enlargement greater than 3 times are seen diagnosis of LSIL was given. For HSIL to be reported smaller cells than LSIL with marked nuclear atypia are necessary. If there are additional features of invasion, then the case was reported as Squamous cell carcinoma.

For glandular cells, AIS (Endocervical adenocarcinoma in situ) was used when there were many groups or clusters of cells with marked nuclear atypia. If there are features of AIS with features of invasion like tumor diathesis then a diagnosis of Adenocarcinoma was given. Any case with few glandular cells showing nuclear atypia more than reparative changes or of less quantity are reported as atypical glandular cell (AGC).

A case record form/proforma (table 2) has been used for data collection. To avoid any direct patient identifier specific lab generated Ids have been used for data collection & analysis.

The data was further analyzed to find out association if any between different genotypes and cytological categorization.

Results and Discussion

Mean age (years) of participants was 40.4± 10.2 SD and 50.3% of participants were 39 years or younger (table 3). All the participants in the present study had not been vaccinated against HPV or couldn't give history of vaccination except one.

HPV DNA was detected in 88 participants (8.72%). 72 of them had presence of single genotype (diagram 1), whereas multiple genotypes were detected in 16 participants (table 4). Commonest genotypes detected were 16 (n=33) and 52 (n=16); both are high risk genotypes.

All cases with multiple genotype positive contained high risk genotypes.

In cytological examination, 17 cases showed abnormal epithelial findings (diagram 2). Of these 17 cases, 3 were negative for HPV and remaining 14 were positive for HPV. As can be seen, majority of the cases were ASCUS (47%), followed by ASC-H (23.5%). We also found HSIL (17.6%) and a single case of LSIL and AGC each. Diagram 3 shows further categorization with HPV genotype versus epithelial abnormality subtype. Most common HPV genotype associated with epithelial abnormalities was 16 (52.9%) followed by 58 (23.5%) and 59 (11.8%). This includes both single and multiple genotype associations. Additionally, a spurious HPV 6 was also seen; however, this case also had other high risk HPV genotypes.

Diagram 4 shows the age distribution versus abnormal cytology findings. Majority of the abnormal cases were found in 30-39 range (35.3%), 40-49 range (29.4%) and 50-59 range (23.5%). ASCUS cases were seen more commonly in 30-39 range (50% of all ASCUS cases), ASC-H had even distribution between 40-49 and 50-59 ranges. HSIL had a wider age distribution with single cases seen in 20-29 range, 30-39 range and in above 60 age group. LSIL and AGC cases were seen in 30-49 range

Additionally, the single patient (39 Y) who had history of vaccination was found to be NILM category and HPV negative.

HPV prevalence in various Indian studies varies from 2.3% to 36.9%, which may be due to heterogeneity of study population (Bruni *et al.,* 2019) as studies that included predominantly symptomatic women attending health facilities showed higher prevalence (Aggarwal *et al.,* 2006; Vinodhini *et al.,* 2012; Kerkar *et al.,* 2011). One study has compiled five studies from India that selected apparently normal women from the community and used a PCR based assay to detect a large number of HPV types (Muwonge *et al.,* 2020; Datta *et al.,* 2010; Franceschi *et al.,* 2005; Sharma *et al.,* 2015; Srivastava, Gupta and Roy, 2012; Varghese, 2000). These studies also documented a wide range of HPV prevalence, from 6.1% in south India to 19.2% among tribal women from central India [18-22]. The prevalence observed in our study (8.72%) agrees with these studies as the recruited study population in our study involves both symptomatic and asymptomatic women. Across literature HPV 16 is the most common genotype which corroborates with our study with prevalence of 3.3%. The prevalence of HPV 16 varies from 2.5% in Asian population to 5.8% in North American population (Bruni *et al.,* 2010).

Globally, HPV 18 is the second most common high-risk HPV type. But according to a meta-analysis of normal women (Bruni *et al.,* 2010; Bao, Smith and Qiao, 2008) and the previously mentioned 5 studies conducted in Asia using PCR assay (Datta *et al.,* 2010; Franceschi *et al.,* 2005; Sharma *et al.,* 2015; Srivastava, Gupta and Roy, 2012; Varghese, 2000), either of 18, 31, 33, 51, 52, 56 and 58 can be in second or third position. In our study the second most prevalent genotype was 52. As most of the CE IVD approved PCR kits use only 16 and 18 genes as separate high risk genotype targets, the other genotype detection can be missed which can erroneously make 18 to be the second most common genotype (Chen, X. *et al.,* 2017; Liu, F. *et al.,* 2021). In our study 93.1% of single genotype positive cases were high risk and 6.9% were only low risk. All multiple genotype positive cases contained high risk genotypes. This can be due to the variable occurrence of spontaneous clearance of HPV according to genotypes. In a study documented by Louvanto *et al.,* which covered 252 women in a prospective follow-up of 6 years, the lowest clearance frequency was recorded for HPV16 and multiple-type infections, of which only 51.6% and 50.5% were cleared, respectively (Louvanto *et al.,* 2010). In Kaplan-Meier analysis, HPV16 clearance was almost 20% less than that of all other genotypes. In other studies, 80.7%, 69%, and 51.9% of HR HPV infections cleared at between 14 and 19 months of FU (Goodman *et al.,* 2008; Rosa *et al.,* 2008; Sellors *et al.,* 2003). Of LR HPV types, 81% were shown to clear within 12 months FU (Goodman *et al.,* 2008), and the majority of type-specific clearance occurred in 2 years (Richardson *et al.,* 2003).

In 2010 a nationwide study by Pillai RM was done to assess region wise distribution of High risk HPV in cervical cancer. The study showed that the viral prevalence across India was not different with 92.1% cases showing HPV detection.

Table.1 PCR set up

16,18								PC16,18	NC16,18
31,33								PC31,33	NC31,33
35,39								PC35,39	NC35,39
45,51								PC45,51	NC45,51
52,56								PC52,56	NC52,56
58,59								PC58,59	NC58,59
6, IC								PC6, IC	NC6, IC
11								PC11	NC11

Diagram.1 Distribution of single genotype detected cases as per risk category

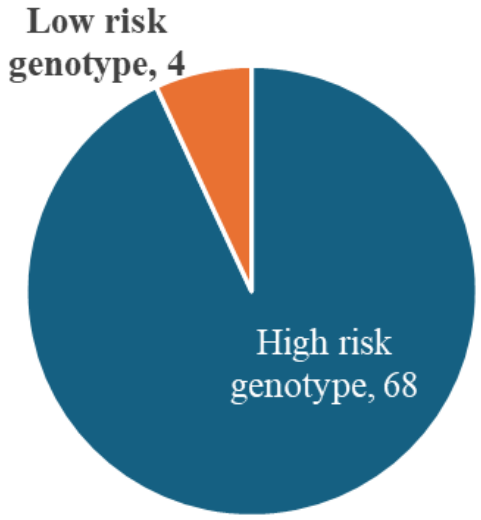


Diagram.2 HPV versus Abnormal cytology findings

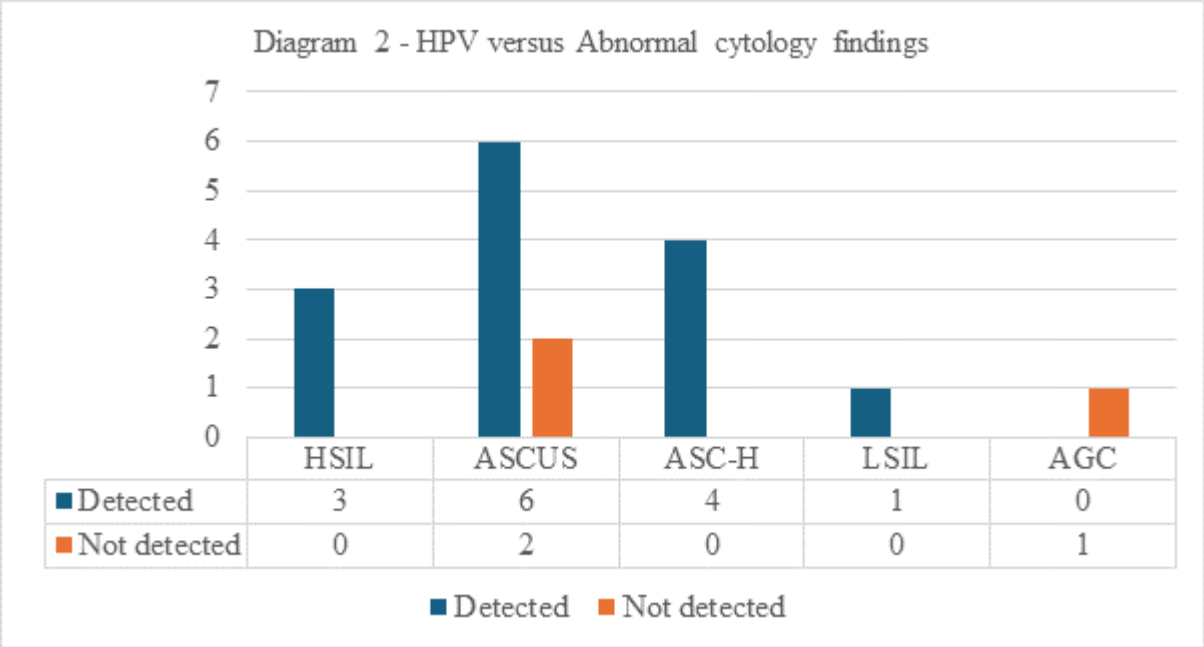
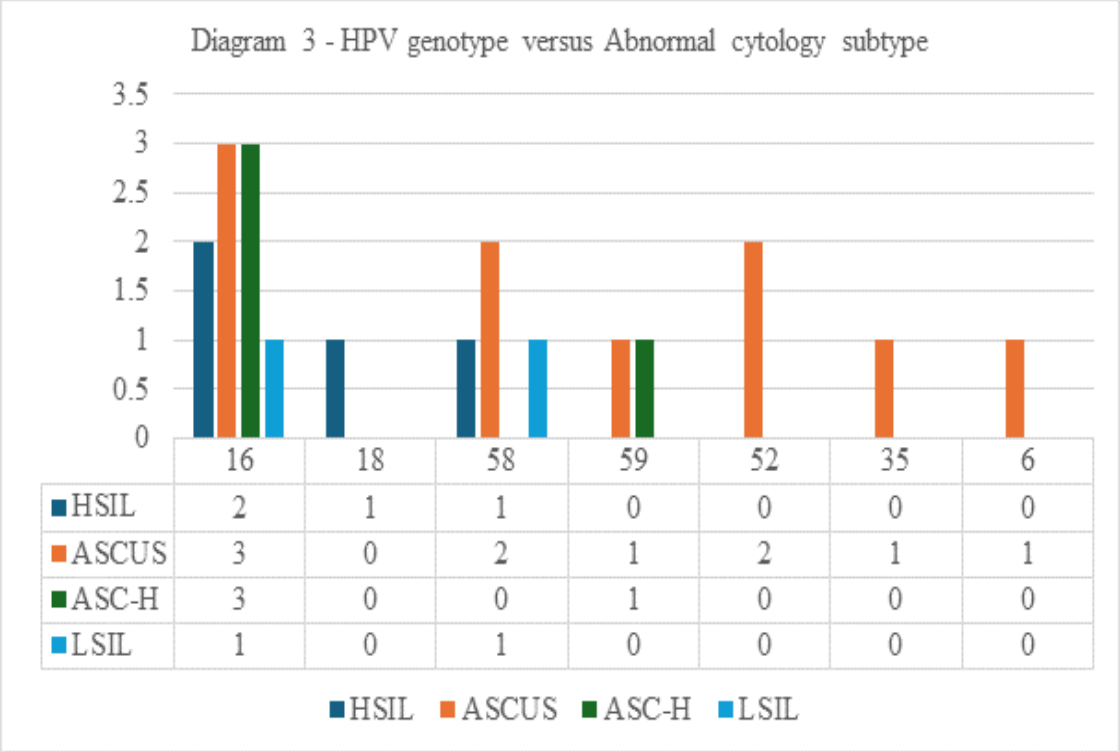
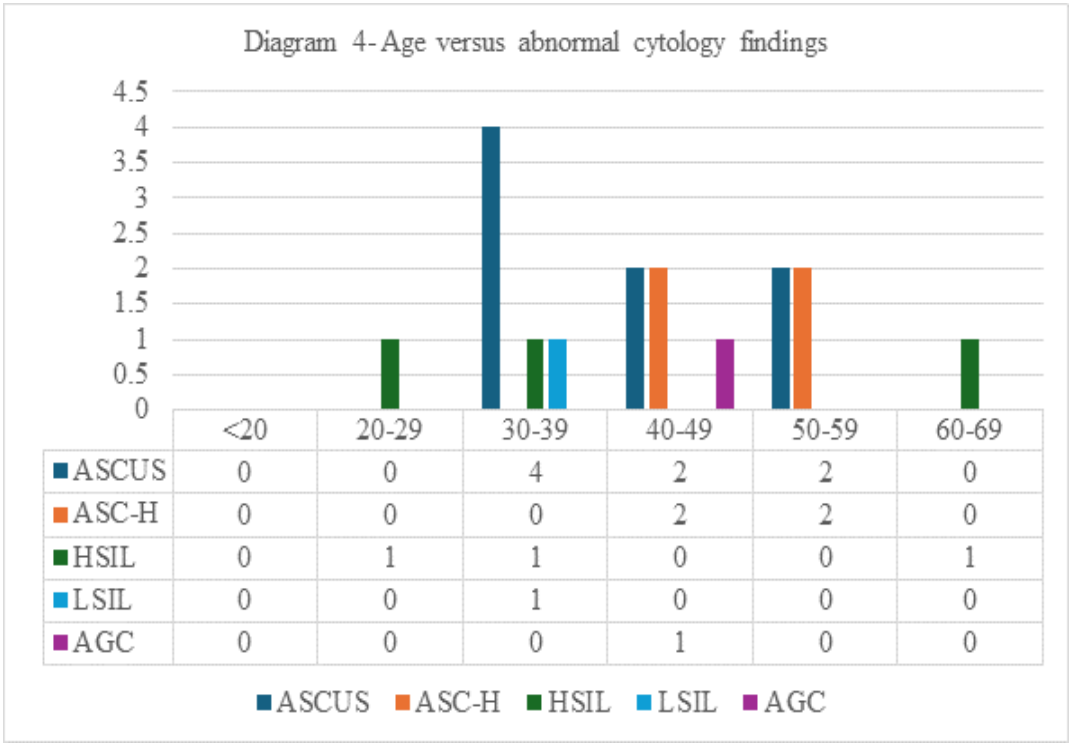


Diagram.3 HPV genotype versus Abnormal cytology subtype



	16	18	58	59	52	35	6
HSIL	2	1	1	0	0	0	0
ASCUS	3	0	2	1	2	1	1
ASC-H	3	0	0	1	0	0	0
LSIL	1	0	1	0	0	0	0

Diagram.4 Age versus abnormal cytology findings



	<20	20-29	30-39	40-49	50-59	60-69
ASCUS	0	0	4	2	2	0
ASC-H	0	0	0	2	2	0
HSIL	0	1	1	0	0	1
LSIL	0	0	1	0	0	0
AGC	0	0	0	1	0	0

Table.2 Case record proforma

Sl No	Date	Lab ID/ Unique specimen ID*	Age	Vaccination status	HPV DNA (Detected/ Not Detected)	Genotype if detected	Cytology

Table.3 Age distribution of participants in the present study (N=1009)-

Age (y)	n (%)	Mean ± SD
<20	2(0.02)	40.4± 10.2
20-29	120(11.89)	
30-39	382(37.86)	
40-49	338(33.50)	
50-59	115(11.39)	
60-69	37(3.67)	
70-79	12(1.19)	
80-89	3(0.29)	

Table.4 Distribution of genotypes in positive cases

Cases with single genotype		Cases with more than one genotype	
Genotype	n	Genotypes	n
6	3	16,18	1
11	1	16,18,39,52,58	1
16	24	16,35	1
18	2	16,45,58	1
31	1	16,52	1
33	3	16,52,59	1
35	2	16,58	1
45	4	16,59	1
51	2	18,58	1
52	10	33,56	1
56	5	35,51,52	1
58	9	35,52	1
59	6	56,58,59	1
-	-	6,16,59	2
-	-	6,52,56,58	1

Single infection was most common. The most common HPV detected was HPV 16, followed by HPV-18, -45, -73, -31, -56, -52, -58, -59, -33, -68, -51, -35, -26, and -39. Similarly in our study single infection was more common and HPV 16, 58 and 59 were the most common genotypes detected in cytologically abnormal cases (Pillai *et al.,* 2010).

A study by Senapati R *et al.,* done amongst women with and without cervical cancer in Odisha, showed that 93.8% of invasive cancer, 54.3% of inflammatory smear and 19.1% of normal cervical cytology had positive HPV detection of which the most common genotype was HPV 16 followed by HPV 18 and HPV 51. This study also had more single detection cases over multiple ones,

and this is in concordance with our study as well (Senapati *et al.,* 2017).

Srivastava *et al.,* (Srivastava *et al.,* 2014) performed a chi square test to see the association of different risk factors with HPV infection in various grades of cervical lesion. They found 10 different genotypes with HPV 16 being most common as is seen in our study. They concurred with positive association of HPV with cervical lesions. These findings show HPV as a direct cause of cervical cancer suggesting urgent need of screening programs and HPV vaccination in women with low socio-economic status and those residing in rural areas. In another study in Uttar Pradesh the authors found 9.9% of the clinically asymptomatic women to be infected with HPV comprising of 26 different genotypes. Among HPV-positive women, 80.8% showed single infection, while 15.4% harbored multiple infections. HPV-16 (63.7%) was the most prevalent, followed by HPV-31 (6.7%), HPV-6 (5.4%), HPV-81 (4.6%) and HPV-33 (4.2%) (Srivastava *et al.,* 2014).

Munjal k *et al.,*'s study from Madhya Pradesh found 93.3% of invasive cervical cancers having HPV detection with HPV 16 being more common amongst less than 40yr age group. Our study showed similar findings (Munjal *et al.,* 2014).

15-20% of cervical glandular lesions are HPV negative and usually present at more advanced stage (Giannella *et al.,* 2022). This is corroborated by Molijn Anco *et al.,* in China whose study also showed overall 75% HPV-positivity in cervical adenocarcinomas (33-100% for different histological types) (Molijn *et al.,* 2016). Our study had one AGC case with negative HPV detection.

In conclusion, there is significant high risk HPV PCR positivity (8.22 %) among different age groups which points towards the importance of screening of women for cervical cancer. 83.13% of high-risk HPV PCR positive cases, are cytology negative, which indicates cytology alone can miss out on a significant portion of the high-risk group. 82.35 % of total abnormal cytology and 100% HISL cases are high risk genotype positive. The findings support the use of HPV PCR as a primary screening method, with cytology serving as an effective triage tool for stratifying lesion severity. This combined approach enhances the detection of precancerous lesions and improves cervical cancer prevention strategies. HPV high risk genotypes, especially 16, are associated with positive epithelial abnormalities identified on PAP smear. Single infection and infection by multiple genotypes are both found in vulnerable populations and need proper elicitation. While HPV 18 is the second most common genotype in most other studies, we found 52 to be the 2nd most common genotype and 58 and 59 to be more commonly associated with abnormal cytology. Maximum kits use 16 and 18 as only gene targets and this finding of ours points towards the necessity of individual genotype detection. In almost all cases, vaccination history was negative which indicates lack of awareness which, if addressed will help in reducing HPV infection which will ultimately lead to reduction in Cervical cancer prevalence.

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Author Contributions

Jayitri Das (Joint 1st author): Designed the model, Cytology reporting, data collection and analysis, original draft preparation. Swatilekha Banerjee (Joint 1st author): Designed the model, Molecular reporting, data collection and analysis, original draft preparation. Sumedha Dey: Conceptualized, Cytology reporting. Himadri Mondal: Molecular reporting. Zishan Akhter: Cytology reporting. Reena Nakra: Conceptualized, Review and editing of manuscript. Vandana Lal: Conceptualized, Review and editing of manuscript. Mallika Ghosh: Conceptualized, designed the model, data analysis, original draft preparation, Review and editing of manuscript, Administration

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

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