Evaluation of HPV E6/E7 mRNA Detection in Clinically Suspected Cases of Cervical Cancer with Abnormal Cytology: Time to Upgrade the Screening Protocols

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Keywords
► human papillomavirus
► E6/E7 mRNA
► cervical cancer

Abstract

Background Human papillomavirus (HPV) E6/E7 mRNA tests determine the onco- genetic activity of the virus and represent a good clinical biomarker for predicting the risk of cervical cancer. So, the present study was conducted to know the role of HPV E6/E7 mRNA as a predictive biomarker for cervical carcinoma.

Methodology The present study was conducted on 55 clinical samples of cervical scrapings and biopsy from the clinically suspected cases (based on signs and symptoms) of cervical cancer having abnormal PAP smear. The samples were processed in three steps—(1) HPV DNA detection, (2) HPV E6/E7 mRNA detection, and (3) histopathological analysis.

Results Out of a total of 55 patients, 16 (29.09%) were positive for both HPV E6/E7 mRNA and HPV DNA and six were positive for only HPV DNA. So, a total of 22 (40%) patients were positive for HPV DNA. Out of these 22 samples, 10 (45.5%) were of HPV-16, six (27.3%) were of HPV-18, four (18.2%) were of HPV-31, and two (9.1%) were of HPV-45. Out of total 16 patients positive for HPV E6/E7 mRNA, 10 (62.5%) were of genotype 16 and six (37.5%) were of genotype 18. The patients who were found positive for HPV 31 and 45 genotypes did not have E6/E7 mRNA expression. On colposcopic-guided biopsy, among these 16 samples, eight (50%) were diagnosed with invasive squamous cell carcinoma, six (37.5%) with cervical intraepithelial neoplasia grade 3 (CIN3), and two (12.5%) with CIN2. Out of those six patients in whom only HPV DNA was positive, five had normal biopsy findings and one had CIN1.

Conclusion The present study suggests that HPV E6/E7 mRNA detection could be more reliable than DNA testing for predicting the risk of progression of HPV-induced cervical lesions to cervical carcinoma and it can be used as a non-invasive tool for triage and patient follow-up.
Introduction

Invasive cervical cancer is the second most common cancer in women worldwide and the most common cause of cancer-related mortality among women in India. The etiology and pathogenesis of cervical cancer have been clearly linked to persistent infection with human papillomavirus (HPV). Approximately, 30 distinct HPV types preferentially infect the anogenital mucosa, resulting in lesions that range from condyloma to cervical intraepithelial neoplasia (CIN)/squamous intraepithelial lesion (SIL) and invasive carcinoma. The most common oncogenic HPV type in preinvasive and invasive cervical cancer is HPV 16 and is detectable in more than 50% of women with CIN3/cervical cancer followed by HPV 18 which accounts for 10 to 15% of cervical cancers. HPV DNA detection is one of the most important screening triage tests for cervical cancer. However, since most women have self-resolving HPV infections that will not develop into cancer, a positive HPV test result provides little actionable information and causes a psychological burden on the patient and also may cause over referral to colposcopy. Therefore, HPV DNA test generally targets the conserved L1 region and it cannot discriminate between regressive and progressive HPV infections. Polymorphisms in the HPV genome may explain why some women are more likely to develop HPV-related neoplasia than others.

Materials and Methods

The given study was conducted from 1st January 2016 to 30th June 2017. The study comprised of 55 samples of cervical scrapings from the suspected cases of carcinoma cervix, attending obstetrics and gynecology outpatient department/inpatient department of the institute. The detailed history in relation to demographic features, symptoms such as abnormal vaginal discharge, post-coital bleeding, post-menopausal bleeding, menstrual and obstetric history, personal history, contraception used, and any significant past medical/surgical history was enquired as a routine protocol and all these details were entered in a pretested form. Written informed consent was obtained from all subjects. Ethical clearance was obtained from the institute’s ethical committee with reference number IEC/GMC/Th 00134. Female patients with age more than 18 years who were sexually active with clinical signs and symptoms of carcinoma cervix along with abnormal PAP smear were included in the study. Pregnant female patients and females having a prior history of cervical carcinoma were excluded.

Collection and Transportation of Samples

The specimen was collected by introducing a bivalve speculum into the vagina for a complete visualization of the external os and ectocervix. The samples were collected in the specimen collection tube containing phosphate-buffered saline. The specimen was sent to the microbiology laboratory for further processing. The samples were processed on the same day, and in case of delay, samples were stored at −80°C. A colposcopic-guided biopsy sample was taken for histopathological analysis.

Processing of Samples

The samples were proceeded in two—(1) HPV DNA detection and (2) HPV E6/E7 mRNA detection.

• HPV DNA detection:
  - DNA extraction
    Each sample was processed for DNA extraction according to the instruction manual given along the QiAamp DNA by Qiagen (Hilden, Germany).
  - DNA amplification
    The sequence of primers is given in Table 1. Details are provided in Supplementary Material.

Polymerase chain reaction (PCR) products, thus, obtained were subjected to gel electrophoresis for HPV detection.

• HPV E6/E7 mRNA detection
  - RNA extraction by a spin column technique
    Each sample was processed according to the instructions manual given along the RNasey mini kit by Qiagen.
  - Reverse transcription and amplification
    Both reverse transcription and amplification of cDNA occurred in a single step by Qiagen one-step reverse transcription-kit. The sequence of primer is given in Table 1. Details are provided in Supplementary Material.

Table 1 Sequence of primer GP5+ and GP6+

<table>
<thead>
<tr>
<th>HPV genotype</th>
<th>Amplicon (bp)</th>
<th>Sequence (5′-3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GP5+</td>
<td>140</td>
<td>FP- TTT GGT ACT GTG GTA GAT AC</td>
</tr>
<tr>
<td>GP6+</td>
<td>140</td>
<td>RP- GAA AAA TAA ACT GTA AAT CA</td>
</tr>
</tbody>
</table>

Abbreviation: HPV, human papillomavirus.
transcription (RT)-PCR Kit 210212. Details are given in 
Supplementary Material.

- Type-specific PCR for HPV 16, 18, 31, and 45 oncogenes 
E6 and E7 mRNA

Next PCR reactions were performed to ascertain the 
presence of E6/E7 mRNA of the following HPV types: 
16, 18, 31, and/or 45. The reaction was performed 
separately for each HPV genotype using specifically 
designed primers (~Table 2). For details of 
cycling condition, refer Supplementary Material.

- Analysis of amplified products

Amplified products were subjected to gel electropho-
resis and analyzed on a gel documentation system.

<table>
<thead>
<tr>
<th>HPV</th>
<th>Region</th>
<th>Size (pb)</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>E6</td>
<td>± 659</td>
<td>5′ TAAACAACAGGGCCGTAACGG 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ TCTATTTGCACCTCTCTCCGT 3′</td>
</tr>
<tr>
<td>16</td>
<td>E7</td>
<td>± 491</td>
<td>5′ ACTTGTCCTCTGAAAGAAGCA 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ AACCATCACATTACATCCGGT 3′</td>
</tr>
<tr>
<td>18</td>
<td>E6</td>
<td>± 608</td>
<td>5′ TAGGTGTTTGTACGTGGCCTG 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ ATACCTGTTTCTCTGCTGGG 3′</td>
</tr>
<tr>
<td>18</td>
<td>E7</td>
<td>± 358</td>
<td>5′ CGACCGAGAAGAAACAAGATAT 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ ATCGTCCCTACTGCTGGGCTAT 3′</td>
</tr>
<tr>
<td>31</td>
<td>E6</td>
<td>± 606</td>
<td>5′ AAGTCGCGAGGGAAGGAT 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ AACGAGCAGCTAGCTATCCAC 3′</td>
</tr>
<tr>
<td>31</td>
<td>E7</td>
<td>± 437</td>
<td>5′ AGGCAAGGCGAAAGGAT 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ AAAGACCGCCATACACC 3′</td>
</tr>
<tr>
<td>45</td>
<td>E6</td>
<td>± 659</td>
<td>5′ ATACAGATACAGTCAGGGTG 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ AGGCACGGCCAAAGAAGCT 3′</td>
</tr>
<tr>
<td>45</td>
<td>E7</td>
<td>± 439</td>
<td>5′ AGGCACGGCCAAAGAAGCT 3′</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5′ AAAGACCGCCATACACC 3′</td>
</tr>
</tbody>
</table>

Abbreviation: HPV, human papillomavirus.

Table 2 Primers designed for HPV 16, 18, 31, and 45 E6/E7 mRNA detection

- Cytopathological Analysis

All samples for cytology were taken using the Thin Prep PAP 
smear cytology and were analyzed in the pathology 
lab of the institute. Cytological results were classified according to 
the revised Bethesda classification,13,14 such as ASC-US; ASC, 
cannot exclude a high-grade squamous intraepithelial lesion 
(HSIL); LSIL (CIN grade 1[CIN1]); HSIL (CIN2; CIN3; carcinoma 
in situ) and invasive squamous cell carcinoma.

- Histopathological Analysis

Colposcopic-guided biopsy samples for histopathological 
analysis were taken and were sent to the histopathological 
department of the institute, and diagnoses were made according to the CIN reporting system.15

- Statistical Analysis

Different parameters like age and parity were presented as 
mean ± standard deviation (SD). A p-value <0.05 was consid-
ered statistically significant. Fisher’s exact test was used 
when the number of observations in a cell was less than 5, 
and to compare between the continuous variables like age at 
presentation and marital age, independent t-test was used. In 
others, the chi-square test was used to study the associ-
ations between various risk factors and HPV E6/E7 mRNA 
expression. The minimum sample size was calculated as 45 
using a formula: \( n = Z^2(1 - P)/\delta^2 \), where \( n \) is the sample size, 
\( Z \) is the statistic corresponding to the level of confidence 
(taken as 95%), \( P \) is expected prevalence, and \( \delta \) is precision 
after taking the prevalence of cervical cancer as 3% in Punjab 
region.16 Data were analyzed using Microsoft Excel version 
16 (Microsoft Corp., Richmond, CA, United States), and 
statistical analysis was performed using GraphPad 
Prism V.6.0 (GraphPad Software, La Jolla, CA, United States).

Results

- Demographic details and risk factors

The mean age of the females in the given study was 
34 ± 10 years. Mean parity in the patients was 2.1 ± 0.7. 
The mean age of the patients at the time of marriage was 
25 ± 8 years. The majority (96.36%) of the patients had a 
single sexual partner, and only 3.64% gave the history of 
multiple sexual partners. Out of total 55 patients, partners 
of majority patients, i.e., 26 (54.17%) were using male 
condoms. Oral contraceptive pills (OCPs) were used by 16 
(33.33%) patients, two (4.17%) patients were using a 
copper intrauterine device, one (2.08%) practiced coitus 
interruptus, and three (6.25%) patients gave a history of 
tubectomy done in the past. Seven patients had no history 
of use of contraception since they were in the post-
menopausal state.

- Clinical signs and symptoms

Out of the 55 patients, majority (27) presented with foul-
smelling discharge per vaginum. The next common 
complaint was pain in the lower abdomen (24) followed by 
irregular bleeding per vaginum (18) and post-coital 
blooding (12). Only eight patients presented with post-
menopausal bleeding. The majority of the patients had 
multiple complaints.

On examination, the majority of them (34) had cervical 
erosions followed by hypertrophied cervix with discharge 
in 20 patients. Only 10 patients had polypoidal growth. 
Multiple findings were observed in some of the patients

- Cytopathological (PAP smear) findings

All the patients had abnormal PAP smear findings. Out of 
55 patients, 36 patients had ASC-US on their cytology, one 
had LSIL, eight had HSIL, eight had invasive squamous cell 
carcinoma, and only two patients had atypical glandular 
cells of undetermined significance.

- HPV DNA detection and its genotype

Out of the total, 22(40%) were positive and 33(60%) were 
negative for HPV DNA. Out of these 22 patients, 10 (45.5%)
were of HPV-16, six (27.3%) were of HPV-18, four (18.2%) were of HPV-31, and two (9.1%) were of HPV-45.

• HPV E6/E7 mRNA expression and its specific genotype
  Out of total 55 patients, 16 (29.09%) were positive and 39 (70.91%) were negative for HPV E6/E7 mRNA. Out of total 16 patients positive for HPV E6/E7 mRNA, 10 (62.5%) were of genotype 16 and 6 (37.5%) were of genotype 18. The patients who were found positive for HPV 31 and 45 genotypes did not have E6/E7 mRNA expression. So, in total, 16 patients were positive for both HPV-DNA and HPV E6/E7 mRNA, whereas six were positive for only HPV DNA (►Table 3).

• Histopathological findings
  On histopathological analysis, 38 had normal findings, eight had invasive squamous cell carcinoma, six had CIN3, two had CIN2, and one had CIN1. Out of all HPV DNA-positive cases (22), only 16 were positive for HPV E6/E7 mRNA. Among those 16, eight (50%) were diagnosed with invasive squamous cell carcinoma, six (37.5%) with CIN3, two (12.5%) with CIN2. Whereas out of those six patients in whom only HPV DNA was positive, five had normal biopsy findings and one had CIN1. Sensitivity, specificity, positive predictive value, and negative predictive value of HPV DNA and HPV E6/E7 mRNA against gold-standard histopathology method were calculated (►Table 4).

• Association between various risk factors and HPV E6/E7 mRNA expression
  The positivity rate of HPV E6/E7 mRNA between different age groups was compared along with various other risk factors (►Table 5).

Discussion

The given study highlights the role of detection of E6/E7 mRNA of HPV for predicting the risk of progression of HPV-induced cervical lesions to cervical carcinoma as all the patients in the given study showing expression of HPV E6/E7 mRNA had features of cervical cancer on histopathology. It shows that the detection of HPV E6/E7 mRNA is more specific than HPV DNA detection.

In our study, HPV infection was detected in 40% of patients which is quite less than the previous studies. The difference may be attributed to the smaller sample size taken in our study. According to the International Agency for Research on Cancer analysis, the five most common HPV genotypes with decreasing frequency are, HPV-16, -18, -45, -31, and -33, found in 82.9% of the cases. Similarly, according to one study, the most prevalent genotype was HPV 16 (87.28%) followed by HPV 18 (24.56%) and HPV 51 (3.46%). Similarly, our study depicted that among HPV DNA-positive patients, HPV 16 (45.45%) was the most prevalent type followed by

Table 3  Comparison between HPV E6/E7 mRNA and HPV DNA vis-à-vis the histopathological and cytological finding

<table>
<thead>
<tr>
<th></th>
<th>HPV DNA (n)</th>
<th>HPV E6/E7 mRNA (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive (22)</td>
<td>Negative (33)</td>
</tr>
<tr>
<td><strong>Cytology (n)</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ASCUS (36)</td>
<td>4</td>
<td>32</td>
</tr>
<tr>
<td>AGUS (2)</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>LSIL (1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>HSIL (8)</td>
<td>8</td>
<td>0</td>
</tr>
<tr>
<td>Invasive squamous cell carcinoma (8)</td>
<td>8</td>
<td>0</td>
</tr>
<tr>
<td><strong>Histopathology (n)</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Normal (38)</td>
<td>5</td>
<td>33</td>
</tr>
<tr>
<td>CIN 1 (1)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>CIN 2 (2)</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>CIN 3 (6)</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>Invasive squamous cell carcinoma (8)</td>
<td>8</td>
<td>0</td>
</tr>
</tbody>
</table>

Abbreviations: AGUS; atypical glandular cells of undetermined significance; ASCUS, atypical squamous cells of undetermined significance; CIN, cervical intraepithelial neoplasia; HSIL, high-grade squamous intraepithelial lesion; HPV, human papillomavirus; LSIL, low-grade squamous intraepithelial lesions; n, number of the patients.

Table 4  Sensitivity, specificity, positive predictive value, and negative predictive value of HPV DNA and HPV E6/E7 mRNA against histopathology

<table>
<thead>
<tr>
<th></th>
<th>Sensitivity (95% CI)</th>
<th>Specificity (95% CI)</th>
<th>Positive predictive value (95% CI)</th>
<th>Negative predictive value (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPV DNA</td>
<td>100 (80.5–100)</td>
<td>86.84 (71.9–95.6)</td>
<td>19.03 (9.4–34.7)</td>
<td>100</td>
</tr>
<tr>
<td>HPV E6/E7 mRNA</td>
<td>94.12 (71.3–99.8)</td>
<td>100 (90.7–100)</td>
<td>100</td>
<td>99.82 (98.8–99.8)</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; HPV, human papillomavirus.
HPV 18(27.27%), HPV 31(18.18%), and HPV 45(9.10%). The present study showed that the positivity of HPV E6/E7 mRNA in women with abnormal PAP smear was 29.09%. Origoni et al., Ho et al., and Molden et al demonstrated the positivity of HPV E6/E7 mRNA among women with abnormal cytology as 26, 21, and 22.8%, respectively. However, in a recent study by Dabeski et al high-risk HPV E6/E7 mRNA infection was detected in 60.94% of patients with squamous cell abnormalities of the cervix. These differences could be due to different sample sizes in different studies along with different methodologies used. In a study by Cuschieri and Wentzensen HPV E6/E7 mRNA was found to be significantly associated with the severity of cervical lesions. The similar fact was proven by a study of Liu et al which found that 25.7% of LSIL cases and 71.9% of HSIL+ cases had positive E6/E7 mRNA tests, and as the severity of cervical lesions increased, the positive rate of HPV E6/E7 mRNA also increased. The findings were similar in our study also as in the patients who have normal biopsy findings, HPV E6/E7 mRNA is negative and as the severity of cervical lesions increases on biopsy, positivity of HPV E6/E7 mRNA also increases and all the patients who had HSIL+ lesions had HPV E6/E7 mRNA expression also. A study by Salimović-Bešić et al on 105 women with abnormal cervical cytological findings showed low HPV E6/E7 mRNA positivity in women with cytological findings of ASC-US on the PAP test. In our study, 36 patients had ASC-US cytological findings on PAP smear, but none of them showed HPV E6/E7 mRNA expression and also these patients had normal biopsy findings. A recent study done by Zhang et al showed that HPV DNA, mRNA, increased with the severity of histopathology diagnosis, from 25.5%, 19.1%, in normal to 100.0% in squamous cell carcinoma, respectively. In our study HPV E6/E7 mRNA has higher specificity (100%) and positive predictive value (100%) as compared with HPV DNA. Previous literature also showed that HPV E6/E7 mRNA testing has higher specificity and positive predictive than HPV DNA testing.22,27 In our study, out of the total patients who had normal biopsy findings (38), five had HPV DNA positive and none of them had the expression of HPV E6/E7 mRNA showing that E6/E7 mRNA expression is more specific for cervical carcinogenesis as compared with the presence of only HPV DNA. Yao et al also concluded in their study that the HPV E6/E7 mRNA test were highly concordant with cytology test results, and both the diagnostic modalities resulted in similar sensitivity, specificity, PPV, and NPV while identifying HSIL+ lesions.28 Various studies showed that HPV E6/E7 mRNA expression can reflect the stage of HPV infections, and its positive pattern can predict the development direction of CINs, so guiding the accurate treatment protocols for these patients.29,30 Nowadays various studies are being done on the detection of HPV E6/E7 mRNA expression by different methods including both quantitative and qualitative. A study

<table>
<thead>
<tr>
<th>Demographic/Risk factors (total number)</th>
<th>HPV E6/E7 mRNA positive (16)</th>
<th>HPV E6/E7 mRNA negative (39)</th>
<th>p-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Age at the time of presentation, in years (n)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>18–30 (23)</td>
<td>9</td>
<td>14</td>
<td>0.0023</td>
</tr>
<tr>
<td>31–40 (22)</td>
<td>1</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>&gt; 40 (10)</td>
<td>6</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td><strong>Age at the time of marriage, in years (n)</strong></td>
<td></td>
<td></td>
<td>&lt; 0.05</td>
</tr>
<tr>
<td>18–25 (30)</td>
<td>13</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>26–30 (20)</td>
<td>3</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>31–35 (5)</td>
<td>0</td>
<td>5</td>
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</tr>
<tr>
<td><strong>Parity (n)</strong></td>
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<td>0.0046</td>
</tr>
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<td>Para 1 (10)</td>
<td>1</td>
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<td></td>
</tr>
<tr>
<td>Para 2 (28)</td>
<td>5</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>Para 3 (17)</td>
<td>10</td>
<td>7</td>
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</tr>
<tr>
<td><strong>Number of sexual partners (n)</strong></td>
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</tr>
<tr>
<td>Single (53)</td>
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<td>39</td>
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<tr>
<td>Multiple (2)</td>
<td>2</td>
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<td></td>
</tr>
<tr>
<td><strong>Contraceptives used (n)</strong></td>
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<tr>
<td>Male condom (26)</td>
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<td>25</td>
<td></td>
</tr>
<tr>
<td>OCPs (16)</td>
<td>12</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Tubectomy (3)</td>
<td>1</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>Cu-T (2)</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Coitus interruptus (1)</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: Cu-T, copper intrauterine device; HPV, human papillomavirus; n, number of the patients; OCPs, oral contraceptive pills. Note: p = 0.0001, statistically significant.
done by Wang et al.\textsuperscript{31} evaluated the performance of the Optimygene HR-HPV RT-qDx assay, which is an HPV E6/E7 mRNA-based assay, to detect 16 HR-HPV subtypes, concluded that the higher specificity and positive predictive value of this assay are valuable for predicting insignificant HPV DNA infections among patients with a borderline cytological diagnosis. Recently, a study done by Liu et al.\textsuperscript{32} on quantitative HPV E6/E7 mRNA assay using QuantiVirus HPV E6/E7 mRNA assay (Kodia, Henan, China) to compare the expression levels of HPV E6/E7 mRNA in HSIL and LSIL showed that the median E6/E7 mRNA copy number in HSIL (median, 14,684 copies/mL) was far higher than that in LSIL (median, 936.00 copies/mL) ($p < 0.001$). In our study, when we compared the positivity of HPV E6/E7 mRNA with various risk factors, it has been seen that out of 16 patients positive for HPV E6/E7 mRNA, 56.3% patients were of <30 years of age, 81.2% had marriage in the age of 18 to 25 years, 62.5% were of para 3, and 75% were using OCPs making them all as risk factors for cervical cancer, as shown by previous studies also.\textsuperscript{33–36} Recently, the American Cancer Society recommends cervical cancer screening for females from age of 25 to 65 years with an HPV-DNA test alone every 5 years. If HPV testing alone is not available, females can get screened with an HPV/Pap co-test every 5 years or a Pap test every 3 years.\textsuperscript{37} Our data suggest that HPV E6/E7 mRNA detection may be a useful non-invasive tool for the screening of HPV-induced cervical neoplasia. The smaller sample size was the major limitation of our study. Hence, further studies on HPV-E6/E7 mRNA with a large sample size are needed for establishing this diagnostic modality as a routine screening test for ruling out cervical cancer in patients with borderline cytology. The smaller sample size was the major limitation of our study, and also the patients in which only HPV DNA was present without the expression of HPV E6/E7 mRNA were not followed-up further.

**Conclusion**

The present study suggests that HPV E6/E7 mRNA detection could be more reliable than DNA testing for predicting the risk of progression of HPV-induced cervical lesions to cervical carcinoma as the former had 100% specificity as compared with latter (86.8%). Hence, it can be used as a non-invasive tool for triage and patient follow-up. However, large-scale studies with proper cost factor analysis are further needed to substantiate the findings of our study for better management of this growing menace of cervical carcinoma.

**Note**

Ethical clearance was taken from institute’s ethical committee.

**Funding**

None.

**Conflict of Interest**

None declared.

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