Determination of the Physical Status (Episomal/Integral) of HPV by qPCR in Esophageal Squamous Cell Carcinoma

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Abstract

Background: In cervical cancer, the carcinogenic mechanism of human papillomavirus (HPV) occurs through the integration of viral DNA into the host genome. This process initiates with a disruption in the E2 open reading frame (ORF) of the viral genome. Disruption of E2 ORF results in an increased expression of the viral oncoproteins, E6 and E7, by removal of E2 suppression effect on their promoters. E6 and E7 interfere with the normal cell cycle by degrading the p53 and pRb tumor suppressor proteins, respectively.

Objectives: The objective of this study was to determine the physical status (episomal/integral) of HPV genome in esophageal squamous cell carcinoma (ESCC).

Materials and Methods: The rate of copy numbers of E2 and E6 genes in HPV-18 and HPV-16 positive samples were analyzed by quantitative polymerase chain reaction (qPCR) in order to assess the physical status (episomal/integral) of HPV. DNA extracts from HeLa cell line were used as the positive control.

Results: The E2 gene was detected in 1 sample, co-infected with HPV-16 and HPV-18. While, E6 gene was detected in all 11 HPV positive samples. The qPCR analysis showed the presence of integrated form of viral DNA in all HPV positive samples and only 1 mixed episomal-integrated form was detected.

Conclusion: The presence of integrated forms of high risk HPV-16 and HPV-18 genomes might reflect a crucial process towards malignant transformation of ESCC.

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Objective

The aim of this study was to determine the physical status (episomal/integral) of HPV genome in order to investigate the carcinogenic mechanism of HPV using quantitative polymerase chain reaction (qPCR) in ESCC. The study was performed on the patients from Kurdish and Kermanshah provinces of Iran.

Materials and Methods

Patients and Clinical Samples

In this study, 59 subjects from Kermanshah province and 44 subjects from Kurdistan province were participated. The patients were diagnosed with the HPV virus during 2007 to 2013. A total number of 11103 biopsies (HPV positive samples) were obtained, and then formalin fixed and paraffin embedded (FFPE). The blocks diagnosed with ESCCs were in the Kurdish population.

DNA Extraction

The samples were cut into small pieces (5 µm in thickness) and collected in sterile tubes. To avoid contamination, a new disposable microtome blade was used for each sample. DNA was extracted (QIAamp DNA FFPE Tissue Kit, Qiagen, Germany) according to the manufacturer’s instructions. DNA quality and the absence of PCR inhibitors in the extracted DNA samples were analyzed by PCR for β-globin (110bp) gene using PCO3, 5′-ACA CAA CTG TG TCA CTA GC-3′ and PCO4 5′-CAA CAT AGC TGG GCA CT-3′ primers. The PCR conditions were adjusted as follows: initial denaturation at 95°C for 5 minutes, 30 cycles (95°C for 30 seconds, 52°C for 45 seconds, 72°C for 45 seconds), extension at 72°C for 5 minutes, and final hold at 4°C.

Quantitative PCR for Detecting the Ratio of E2 and E6 Sequences

To determine the physical status (episomal/integral) of HPV genome in the infected samples with HPV, the real time PCR (qPCR) was performed. The E2 and E6 genes were amplified4 (4) using the Rotor-gene 6000 and 2x QuantiFast SYBR® Green PCR kit (Qiagen, Germany). The rate of copy numbers of E2 and E6 sequences determine the physical status. This study was a relatively comparative study in that we used DNA extracts from HeLa cell line with a mixed status and physical status (episomal-integral) as standard.

The amplification conditions were as 95°C for 5 minutes, followed by 45 cycles (2 steps) (95°C for 10 seconds and 60°C for 30 seconds). Primer sets for E2 and E6 sequences detection in HPV-18 positive samples were as follows: 5′-AGA AGC AGC ATT GTG GAC CTG CT-3′ and 5′-GGT CGC TAT GTT TTC GCA AT-3′ for E2, and 5′-TCA CAA CAT AGC TGG GCA CT-3′ and 5′-CTGTGTTT CTCTGCGTCTG-3′ for E6. The sizes of the E2 and E6 amplicons were 167 and 91 bp, respectively.16 Primer sets for E2 and E6 sequences detection in HPV-16 positive samples were as follows: 5′-AAC GAA GTA TCC TCT CCT GAA ATT AG-3 and 5′-CCA AGG CGA CGG CTT TG-3 for E2, and 5′-AGA AAC TGC AAT GTT TCA GGA CC-3 and 5′-TGT ATA GTT TGT TCG AGC TCT GTG C-3 for E6. The amplicon size for E2 was 76 bp and for E6 was 81 bp.19 DNA extracts from HeLa cell line were used as the positive control for HPV-18 which showed the mixed physical status (episomal-integral) and its curves.

Results

The ratios of E2/E6 genes in 11 HPV-16 or HPV-18 positive samples were analyzed by qPCR in order to assess the integration status of HPV genomes. The presence of E2 gene associated with E6 gene was only observed in one HPV-16 and HPV-18 co-infected sample with well differentiated grade tumor, whose ratio of E2/E6 (0.31) showed mixed (episomal-integral) status (Figure 1). While, E6 gene was detected in the rest of HPV positive samples without E2 gene, which indicated the presence of integrated form of viral DNA in the entire HPV positive samples (Table 1).

Discussion

In this study, we examined the physical status of the virus genome and found mostly integrated status of HPV sequences in the infected samples.

In our previous study, the association of HPV-16 and HPV-18 with ESCC was shown in Kurdish population of the west of Iran (4), where the incidence of the disease is low (7 and 8.1 in 100 000 in Kurdistan18 and Kermanshah provinces, respectively) in comparison with an incidence of 1/1000 in some populations of Iran such as high-risk Turkmen population in the north of Iran.22

Using real-time PCR, we examined the presence of HPV-18 and HPV-16 and also the integration status of the virus, since HPV integration is considered to result in the deletion of E2 gene.8,10 Disruption of E2 causes an increased expression of the viral oncopogenic proteins, E6 and E7, by removal of E2 suppression effect on their promoters.12,13 E6 and E7 proteins interfere with the normal cell cycle by degrading the p53 and pRb tumor suppressor proteins, respectively.16

We determined the physical status of HPV genome in

![Figure 1](https://example.com/figure1.png)
In this study, the integration of HPV was detected in all HPV positive samples which show integration is strongly associated with the neoplastic process. In other studies, similar to ours, it was shown that viral genome integration is restricted to the neoplastic and the transforming efficacy of dysplastic tissue and is not observed in normal epithelium; so, no consequence has been detected in the field cancerization in HPV-positive tumors. This useful method is a sensitive technique to evaluate the physical status of HPV genome and is suitable to predict the progression of disease.

In conclusion, the results found in this study support the statement that the genome integration of high risk HPV16 and HPV-18 might reflect a crucial process towards malignant transformation in dysplastic esophageal lesions and may be an indicator of the risk of ESCC, at least for patients in the Kurdistan and Kermanshah provinces of Iran.

Abbreviations: ESCC, esophageal squamous cell carcinoma; HPV, Human papillomavirus; PCR, polymerase chain reaction.

### References

11. Thierry F. Transcriptional regulation of the papillomavirus oncogenes by cellular and viral transcription factors in the host cells on the basis of the E2 and E6 ratio. In the present study, the integrated form of HPV was detected in all the HPV-positive specimens when the lack of HPV E2 genome was considered the integration of HPV genome into the host genome. While, the presence of both episomal and integrated form was detected in only one sample, where E2 and E6 were both detected by qPCR and this ratio was larger than zero and smaller than unity. When the E2/E6 ratio was equal to or higher than one, all the HPV genome was considered to be in an episomal form which was not detected in none of the samples.

### Authors’ Contributions

Study concept and design: FS; Acquisition of data: FS and BN; Analysis and interpretation of data: FS, BN, and MK; Drafting of the manuscript: FS, MK; Study supervision: FS, MK and BN.

### Conflict of Interest Disclosures

The authors have declared that no conflict of interests exists.

### Ethical Approval

The approval of ethics committee of Kurdistan University of Medical Science was also obtained. Informed oral consent was obtained from all the patients.

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### Acknowledgments

We also acknowledge the Department of Virology, Tehran University of Medical Sciences, for providing us with the HPV positive control.

### Table 1. Detection of Copy Numbers of HPV E2 and E6 Genes in High Risk HPV Positive samples of ESCC Using Real-Time PCR

<table>
<thead>
<tr>
<th>Sample No.</th>
<th>Province Name</th>
<th>HPV Genotype</th>
<th>E6 Sequence</th>
<th>E2 Sequence</th>
<th>HPV Genome Status</th>
<th>Degree of Tumor</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Kermanshah</td>
<td>16</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Well differentiated</td>
</tr>
<tr>
<td>2</td>
<td>Kermanshah</td>
<td>16</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>3</td>
<td>Kermanshah</td>
<td>18</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Moderate differentiated</td>
</tr>
<tr>
<td>4</td>
<td>Kermanshah</td>
<td>16</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>5</td>
<td>Kermanshah</td>
<td>18</td>
<td>Positive</td>
<td>Positive</td>
<td>Episomal/integrated</td>
<td>Well differentiated</td>
</tr>
<tr>
<td>6</td>
<td>Kermanshah</td>
<td>16</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Moderate differentiated</td>
</tr>
<tr>
<td>7</td>
<td>Kermanshah</td>
<td>18</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>8</td>
<td>Kurdistan</td>
<td>18</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>9</td>
<td>Kurdistan</td>
<td>18</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Well differentiated</td>
</tr>
<tr>
<td>10</td>
<td>Kurdistan</td>
<td>18</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>11</td>
<td>Kurdistan</td>
<td>16</td>
<td>Positive</td>
<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
</tbody>
</table>

Abbreviations: ESCC, esophageal squamous cell carcinoma; HPV, Human papillomavirus; PCR, polymerase chain reaction.


