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.

Keywords: Episomal, integrated, Human papilloma virus (HPV), Esophageal squamous cell carcinoma (ESCC)

Background

Human papillomaviruses (HPVs) located in the viral family, papillomaviridae, are DNA containing tumor viruses with small nonenveloped icosahedral capsids. HPVs infect epithelial cells of skin and mucosa and generally produce benign hyper proliferative lesions which have the potential to undergo malignant transformation.1 High risk HPV types are ethologic cause of cervical cancer.2 Recent studies have reported HPV DNA detection in extragenital cancers as well; even though the etiologic association of HPV in those malignancies is still contentious.3

One of the main procedures of HPV which induce carcinogenesis is the integration of its genome into the host DNA.4,5 However, the physical status (episomal/integral) of HPV genome is not absolute for the carcinogenesis and confirmation of insertional mutagenesis.6

The mechanisms of carcinogenesis for HPV in the cervical cancer, which involves DNA integration into the host genome, is attributed to a disruption of the viral genome in the E2 open reading frame (ORF).7,8 The papillomavirus E2 gene is translated into sequence-specific DNA binding proteins which regulate viral genes expression.9 The disruption of E2 gene results in the overexpression of viral oncogenic early proteins (E6 and E7) by the exclusion of E2 suppression effect on their promoters.10,11 The cellular p53 tumor suppressor protein is the target for HPV E6 oncoprotein. Binding of this oncoprotein to p53 stimulates its degradation through ubiquitin-dependent mechanism.12 E7 protein is recognized for its interaction and decay of the cellular pRb protein.13 Therefore E6 and E7 oncoproteins intervene in the normal cell cycle via degrading the p53 and pRb tumor suppressor proteins, respectively.14

Some studies have found HPV infection in extra-genital tumors including esophageal squamous cell carcinoma (ESCC),15 although the etiologic contribution of the HPV in these malignancies is still argued.
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 TGT TCA CTA GC-3’ and PCO4 5’-CAA CTT CAT CCA CGT TCA CC-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), with 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 (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 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’-CTTGTTGTTT CCTTGCCTGCT-3’ for E6. The sizes of the E2 and E6 amplicons were 167 and 91 bp, respectively.8 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 TGTC AAT GGT TCA GGA CC-3 and 5-TGT ATA GTT TTC AGC CGC CTT G-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),1 where the incidence of the disease is low (7 and 8.1 in 100 000 in Kurdistan 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.9,10 Disruption of E2 causes an increased expression of the viral oncogenic 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 the infected samples.
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>
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<td>Negative</td>
<td>Integrated</td>
<td>Moderate differentiated</td>
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<td>7</td>
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<td>Negative</td>
<td>Integrated</td>
<td>Poor differentiated</td>
</tr>
<tr>
<td>8</td>
<td>Kurdistan</td>
<td>18</td>
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<td>Negative</td>
<td>Integrated</td>
<td>Moderate differentiated</td>
</tr>
<tr>
<td>9</td>
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<td>Negative</td>
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</tr>
<tr>
<td>10</td>
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<td>Negative</td>
<td>Integrated</td>
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</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.

In conclusion, the results found in this study support the statement that the genome integration of high risk HPV's (HPV-16 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.

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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