Hypermethylation of Promoter Region of LATS1 - a CDK Interacting Protein in Oral Squamous Cell Carcinomas - a Pilot Study in India

Vijaya Ramakrishna Reddy¹, Thangavelu Annamalai¹, Vivek Narayanan², Arvind Ramanathan³*

Abstract

Background: Epigenetic silencing of tumor suppressor genes due to promoter hypermethylation is one of the frequent mechanisms observed in cancers. Hypermethylation of several tumor suppressor genes involved in cell cycle regulation has been reported in many types of tumors including oral squamous cell carcinomas. LATS1 (Large Tumor Suppressor, isoform 1) is a novel tumor suppressor gene that regulates cell cycle progression by forming complexes with the cyclin dependent kinase, CDK1. Promoter hypermethylation of the LATS1 gene has been observed in several carcinomas and also has been linked with prognosis. However, the methylation status of LATS1 in oral squamous cell carcinomas is not known. As oral cancer is one of the most prevalent forms of cancer in India, the present study was designed to investigate the methylation status of LATS1 promoter and associate it with histopathological findings in order to determine any associations of the genetic status with stage of differentiation.

Materials and Methods: Tumor chromosomal DNA isolated from biopsy tissues of thirteen oral squamous cell carcinoma biopsy tissues were subjected to digestion with methylation sensitive HpaII enzyme followed by amplification with primers flanking CCGG motifs in promoter region of LATS1 gene. The PCR amplicons were subsequently subjected to agarose gel electrophoresis along with undigested amplification control.

Results: HpaII enzyme based methylation sensitive PCR identified LATS1 promoter hypermethylation in seven out of thirteen oral squamous cell carcinoma samples.

Conclusions: The identification of LATS1 promoter hypermethylation in seven oral squamous cell carcinoma samples (54%), which included one sample with epithelial dysplasia, two early invasive and one moderately differentiated lesions indicates that the hypermethylation of this gene may be one of the early event during carcinogenesis. To the best of our knowledge, this is the first study to have explored and identified positive association between LATS1 promoter hypermethylation with histopathological features in oral squamous cell carcinomas.

Keywords: LATS1 expression in oral carcinoma - p53 associated protein in oral carcinoma

Introduction

Genes that act to suppress the cell division are called “tumor suppressors” because the loss of function of such genes results in uncontrolled proliferation of cells leading to tumorigenesis. One of the best known examples for tumor suppressor gene is the p53 gene (Sharma et al., 2014). In the presence of DNA damaging agents (like toxic chemicals present in tobacco and related products for example that can induce mutation) cellular tumor suppressor proteins block cyclins A, E and D (Lin et al., 2014), and cyclin dependent kinases (CDK) 2, 4 and 6 to arrest the cell cycle (Cooks et al., 2014; Gao et al., 2014). Loss of function of tumor suppressor genes due to mutation(s) or loss of expression of tumor suppressor genes due to epigenetic modification causes the cell cycle machinery to undergo uncontrolled proliferation even in the presence of DNA damaging agents resulting in carcinogenesis (Yang et al., 2010; Liu et al., 2011; Adduri et al., 2014). Several studies, both in vitro and in vivo, have clearly associated mutations and epigenetic modification in tumor suppressor genes with transformation potential, progression and metastasis (Aylon et al., 2011; Rivlin et al., 2011; Mak et al., 2014).

Promoter hypermethylation is one of the most common forms of epigenetic silencing of tumor suppressor genes and is believed to be more frequently involved in cancerous lesions than mutations (Chan et al., 2008). Hypermethylation of several tumor suppressor genes involved in cell cycle regulation such as p16^INK4a, p15^INK4b, p14^ARF, p18^ARF and p19^ARF have been observed in a variety of human cancers (Herman et al., 1995; Baylin and Helin, 2007; Herman et al., 2002).
gene promoter has been reported in elsewhere (Mehta, 2014). 250 ng of genomic DNA was digested with methylation sensitive type II restriction endonuclease, HpaII (New England Biolabs, Ipswich, MA, USA). The digestion was performed with 10U of enzyme digestion.

The gene LATS1 (Large Tumor Suppressor, isoform 1) is a novel tumor suppressor molecule, the protein product of which localizes to the mitotic apparatus of a dividing cell (Hao et al., 2009). LATS1 protein forms complexes with the cyclin dependent kinase-CDK1, essential for the cells to progress from G2 phase to mitotic phase. Binding of LATS1 with CDK1 reduces the activity of CDK1 and thus blocks the cells from entering mitosis (Bothos et al., 2005). Since LATS1 negatively regulates cell division, it is called as a tumor suppressor. Mice that lacks LATS1 gene develop soft-tissue sarcomas and ovarian stromal cell tumors besides being highly sensitivity to carcinogenic agents (Bothos et al., 2005). Hypermethylation and downregulation of LATS1 gene promoter has been reported in breast cancers (56.7%) (Takahashi et al., 2005), astrocytomas (63.6%) (Jiang et al., 2006), myxoid liposarcomas, leiomysarcomas, and malignant fibrous histiocytomas (Hisaoka et al., 2002; Visser S et al., 2010). Although oral squamous cell carcinoma (OSCC) is one of the most prevalent forms of cancer in India (Mishra et al., 2014) among all reported cancers, the methylation status of LATS1 gene promoter has not been explored. Hence, we decided to investigate the methylation status of LATS1 to understand: a) its prevalence, and b) its association with histopathological differentiation.

Materials and Methods

Patient samples

Thirteen patients with oral squamous cell carcinoma with confirmed histopathological diagnosis were included in the study after obtaining informed consent from patients. Biopsy tissues were collected in 2ml microfuge tubes containing 1.5ml of RNA Save reagent and transferred to the refrigerator. 24h later the samples were transferred to freezer and stored until transported to the laboratory.

DNA extraction and methylation sensitive restriction digestion

Tissues were washed once with cold 1X PBS (Phosphate Buffered Saline) to remove traces of RNA Save (Biological Industries Israel Beit-Haemek Ltd. Kibbutz Beit-Haemek, 25115, Israel) and were lysed in 500µl of lysis buffer to extract genomic DNA as described elsewhere (Mehta, 2014). 250ng of genomic DNA was digested with methylation sensitive type II restriction endonuclease, HpaII (New England Biolabs, Ipswich, MA, USA). The digestion was performed with 10U of enzyme in a 20µl reaction volume at 37°C for 4h, after which the enzyme was inactivated by incubating the reaction mix at 65°C for 20m. Methylated DNA (EpiTect Control DNA, cat # 59655, Qiagen) was included as positive control for enzyme digestion.

Methylation sensitive polymerase chain reaction (MS-PCR)

The Hpa II digested tumor DNA samples were amplified with a set of LATS1 promoter specific primers. Primers were designed flanking 500bp of promoter sequence upstream of translational start site, since this region is rich in CCGG content (Figure 1). The following set of primer sequences was used: Left primer: AAGTAAACCTCTTGTCAACC, Right primer: CAATCCCTTTCCCCATTG. PCR was performed in triplicates with the above LATS1 promoter set of primers on HpaII digested or undigested tumor samples and control DNA. Control DNA was obtained from peripheral blood of a healthy volunteer. The following conditions were used: initial denaturation at 94°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 45 seconds, primer annealing at 55°C for 45 seconds, primer extension at 72°C for 45 seconds, with a final extension at 72°C for 5 minutes.

Results

Promoter analysis and primer designing

The sequence of promoter region of LATS1 was acquired from the public database (www.ncbi.nlm.nih.gov/gene), and 1000 base pairs upstream of transcription start site was analyzed for the relative presence of CG (Cytosine and Guanine) (Figure 1). A total of fifty six CG motifs were identified, of which six were within the CCGG tetranucleotide recognition motif of HpaII, type 2 restriction enzyme. Based on the location of the CCGG motifs, forward and reverse primers were designed to encompass the first three CGG motifs upstream of the transcriptional start site.

![Image](https://example.com/dna_sequence.png)

**Figure 1. DNA Sequence of LATS1 Promoter Region (-1000bp) Upstream of Transcriptional Start Site is Shown.** All CG motifs are highlighted in bold letters. CG motifs within the HpaII enzyme recognition site CCGG is highlighted in red.
Table 1. Consolodate Data of Hypermethylation Status and Histopathological Feature of the OSCC Patients

<table>
<thead>
<tr>
<th>Total No. of Samples</th>
<th>Age and Gender</th>
<th>Location of Tumour</th>
<th>Histo-Pathological Diagnosis</th>
<th>Methylation Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>60 / Male</td>
<td>Right maxillary alveolus</td>
<td>Early invasive</td>
<td>Methylated</td>
</tr>
<tr>
<td>2</td>
<td>62 / Female</td>
<td>Left buccal vestibule</td>
<td>Epithelial dysplasia</td>
<td>Methylated</td>
</tr>
<tr>
<td>3</td>
<td>70 / Male</td>
<td>Right mandibular alveolus</td>
<td>Early invasive</td>
<td>Not methylated</td>
</tr>
<tr>
<td>4</td>
<td>55 / Male</td>
<td>Right buccal mucosa</td>
<td>Early invasive</td>
<td>Methylated</td>
</tr>
<tr>
<td>5</td>
<td>65 / Male</td>
<td>Left buccal mucosa</td>
<td>Moderately differentiated</td>
<td>Methylated</td>
</tr>
<tr>
<td>6</td>
<td>46 / Male</td>
<td>Left buccal mucosa</td>
<td>Moderately differentiated</td>
<td>Not methylated</td>
</tr>
<tr>
<td>7</td>
<td>42 / Male</td>
<td>Right maxillary alveolus</td>
<td>Moderately differentiated</td>
<td>Not methylated</td>
</tr>
<tr>
<td>8</td>
<td>65 / Female</td>
<td>Right buccal mucosa</td>
<td>Well differentiated</td>
<td>Not methylated</td>
</tr>
<tr>
<td>9</td>
<td>45 / Female</td>
<td>Right buccal mucosa</td>
<td>Well differentiated</td>
<td>Methylated</td>
</tr>
<tr>
<td>10</td>
<td>65 / Male</td>
<td>Left buccal mucosa</td>
<td>Well differentiated</td>
<td>Methylated</td>
</tr>
<tr>
<td>11</td>
<td>43 / Male</td>
<td>Right buccal mucosa</td>
<td>Well differentiated</td>
<td>Not methylated</td>
</tr>
<tr>
<td>12</td>
<td>45 / Male</td>
<td>Right buccal mucosa</td>
<td>Well differentiated</td>
<td>Not methylated</td>
</tr>
<tr>
<td>13</td>
<td>45 / Female</td>
<td>Left mandibular alveolus</td>
<td>Well differentiated</td>
<td>Methylated</td>
</tr>
</tbody>
</table>

Analysis of the PCR product showed amplification in 7 out of 13 (54%) tumor DNA samples, which indicated hypermethylation of the promoter region (Figure 2, top panel, lanes 2, 4, 6, 8, 10, 11) in these samples. The specificity of LATS1 promoter amplification was confirmed by migration of the DNA bands in agarose gel with reference to positive control. Undigested OSCC samples were amplified along with positive control DNA under similar condition as control for the presence of DNA in all the samples, which showed amplification in all tumor DNA samples (Figure 2, bottom panel). Similar data was obtained in the rest of triplicate PCR amplifications (data not shown).

**Discussion**

In the present study, we have used methylation sensitive restriction enzyme digestion to determine the methylation profile of the promoter region of LATS1, a tumor suppressor gene, in oral squamous cell carcinomas. Our data demonstrates promoter hypermethylation in a significant proportion of cases (54%, n=7 out of 13 OSCCs). No association between the location of OSCC lesion, age and gender of patients and LATS1 hypermethylation could be made due to smaller size of the samples that were analyzed. The sample size...
was intentionally chosen to include only a few cases in each of the three categories—early invasive, moderately differentiated and well differentiated OSCCs, so as to first explore the occurrence of \textit{LATSI} hypermethylation in OSCC lesions as no prior data on this gene was available in OSCCs. Although bisulfite modification based methylation-specific PCR (MSP) is widely used to determine the hypermethylation status of genes, the assay is difficult to optimize for all loci and requires column based purification procedures and primers for both modified and unmodified DNA. The methylation sensitive restriction enzyme technique, on the other hand, is fast and equally sensitive in detecting the methylation status of genes. This method is also proven to be sensitive in several studies including OSCCs and hence was used in the present study (Bhatia et al., 2014). Besides, the methylation sensitive PCR on HpaII digested DNA was performed in triplicates with similar end results, based on which we believe that the technique is unlikely to have influenced the higher detection of \textit{LATSI} hypermethylation in the present study.

The observation of hypermethylation in one lesion with epithelial dysplasia, two early invasive, and one moderately differentiated OSCC samples suggests that the loss of expression of \textit{LATSI} may be one of the early events during carcinogenesis. This may be considered as significant as only thirteen OSCC samples were tested altogether. This percent occurrence of \textit{LATSI} hypermethylation is similar to the prevalence pattern observed in breast cancers (56.7%) (Takahashi et al., 2005) and astrocytomas (63.6%) (Jiang et al., 2006). The lack of promoter hypermethylation in the rest of the samples indicates that the hypermethylation may not be a targeted event in OSCCs. Such heterogeneity in promoter hypermethylation has also been observed in several genes in several cancers including OSCCs. For example, the cell cycle regulators p15 and p16 are known to be hypermethylated in 23% of OSCCs, mismatch repair genes-\textit{hMLH1} and \textit{MGMT} are hypermethylated in 8% and 41% of OSCCs respectively, while the homotypic cell-cell adhesion gene-\textit{E-Cadherin} is hypermethylated in 35% of OSCCs (Marcinkiewicz et al., 2014). The above percent occurrence may be considered as a relevant indicator for heterogeneity of hypermethylation observed in the present study as the authors in the earlier study had analyzed OSCC samples obtained from patients who belonged to the southern region of India from where the samples used in the present study were also collected.

\textbf{Positive association between promoter hypermethylation and lymph node involvement and metastasis has been observed in other cancers (Peters et al., 2014). In addition, decrease in the levels of \textit{LATSI} has also been associated with poor prognosis in breast cancers (Takahashi et al., 2005). This association of \textit{LATSI} expression with clinical outcome adds significance to our finding of more frequent hypermethylation in early invasive and moderately differentiated OSCCs than well differentiated OSCCs, as it opens up the possibility of \textit{LATSI} methylation status being used as a prognostic indicator and diagnostic biomarker. However, this requires systematic evaluation in a statistically significant number of OSCCs that have been staged and graded. Taken together, the present explorative study has identified for the first time hypermethylation of \textit{LATSI} promoter region in histopathologically defined OSCCs.}

\section*{References}


