

## Quantitative Promoter Methylation Profile: Potential Molecular Marker for Head and Neck Squamous Cell Carcinoma

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Head and neck squamous cell carcinoma (HNSCC) is one of the most frequent types of cancer but the lack of early detection and high incidence of local-regional recurrence lead to high mortality. Therefore, it is important to develop new molecular markers to be used as diagnostic and prognostic indicators. An important mechanism for gene transcriptional inactivation is hypermethylation at the CpG islands within the promoter regions. The presence of hypermethylation might be useful as a molecular marker for tumor cell detection and allow early detection of tumor recurrence. The aim of this study was to evaluate promoter hypermethylation of suppressor genes via quantitative methylation-specific PCR (Q-MSP) in tumor and body fluid samples (saliva and serum) as a means to detect epigenetic alterations specific to HNSCC. Tumor samples, salivary rinse and serum were collected before and after the last curative treatment from 180 consecutive HNSCC cases. The pattern of aberrant methylation of 17 genes was analyzed and allowed the selection of a panel of 5 genes that have a specificity of 95% and a sensitivity of 38% in the detection of hypermethylation in samples of saliva. This panel may be useful in early diagnosis of HNSCC recurrence. The hypermethylation of *MGMT* in pre-treatment salivary rinse samples and *HIC1* in serum samples showed significant clinical correlation.

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