ORIGINAL ARTICLE

SIGNIFICANCE OF PROMOTER HYPERMETHYLATION OF *p16* GENE FOR MARGIN ASSESSMENT IN CARCINOMA TONGUE

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Abstract: *Background.* Loss of *p16* expression by promoter hypermethylation has been reported as an early event in the development of oral cancer. The aim of our study was to explore the prognostic implications of presence of promoter hypermethylation of *p16* gene in surgical margins in carcinoma tongue.

Methods. A prospective analysis of 38 patients with resectable carcinoma tongue was carried out. DNA from tumor and the surgical margins was assessed by methylation-specific polymerase chain reaction. Follow-up duration was 17 to 37 months.

Results. About 86.8% of tumors showed promoter hypermethylation of *p16* gene. Out of 30 patients with histologically free margins, 43.3% showed positivity on molecular assessment. Patients with positive molecular margins had a 6.3-fold increased risk of having local recurrence as compared to patients with negative margins.

Conclusion. Promoter hypermethylation of *p16* gene may serve as a useful molecular marker for predicting local recurrence in carcinoma tongue. © 2009 Wiley Periodicals, Inc. *Head Neck* **31:** 1423–1430, 2009

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Surgery in squamous cell carcinoma (SCC) of the oral tongue is undertaken with a curative intent. The primary goal of surgery is to obtain tumor free margins while sparing as much normal tissue as possible. The histopathologic status of resected margins is one of the potential indicators of tumor recurrence; however, a high rate of treatment failure of about 30% to 50% in patients with histologically free margins raises concern about the inadequacy of histologic assessment.[1,2]

On the basis of the original tenet of "field cancerization" by Slaughter,[3] studies have revealed that the phenotypically normal epithelial cells of the upper aerodigestive tract mucosa acquire distinct genetic alterations on prolonged exposure to mutagens. These genetically altered cells undergo clonal expansion and can progress in a stepwise fashion to invasive SCC. Thus, the paradigm currently is shifting toward molecular assessment of margins and whether it has a better potential to detect the malignant transformed cells as compared with the conventional techniques.