

LETTER TO THE EDITOR

## p53 gene mutations in surgical margins and primary tumor tissues of patients with squamous cell carcinoma of the head and neck

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Dear Editor,

We read with interest this study by Tunca *et al.*<sup>1</sup> about p53 gene mutations in surgical margins and primary tumor tissues of patients with squamous cell carcinoma of the head and neck. The authors concluded that there was no statistically significant association between the presence of p53 mutations in the primary tumor and the outcome of head and neck squamous cell carcinoma. In addition, they concluded that the presence of p53 mutations in the surgical margins may not increase the risk of local-regional recurrence<sup>1</sup>. Although no statistical significance was demonstrated in this study, the conclusions fail to take into account a number of important parameters. This study was conducted on heterogeneous tumor tissue specimens that contain functionally diverse groups of cells. The clinical relevance of this is not fully understood<sup>2</sup> and hence the effect on the results is not known. DNA assays that perform well in laboratory dilutions may not be as reliable in clinical samples in which various contaminants, necrosis of the tumor, and degradation of DNA may introduce significant confounders on the data<sup>3</sup>. Finally, the effects of the host immune response are not taken into account in the discussion.

### References

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### IN REPLY

In our study we evaluated the presence of p53 mutations in surgical margins and primary tumor tissues of patients with squamous cell carcinoma of the head and neck. Of the 34 patients, 28 had laryngeal cancer, 2 had hypopharyngeal cancer, 2 had oropharyngeal cancer, and 2 had oral cavity cancer. Most of the tumors were thus located in the larynx. All tumors were identified as squamous cell carcinoma by histopathological analysis. At the time of surgery, both primary tumor and surgical margin samples were taken by the surgeon from areas macroscopically without necrosis, and this was confirmed by histopathological evaluation. Contaminated tissue samples as determined by the histopathological method were removed from our genetic study group. However, some heterogeneity of tumor specimens could not be ruled out, but this is a common problem in human tumor tissue sampling.

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