GINGIVO-BUCCAL ORAL CANCER: INFERRING PROGNOSIS FROM IMMUNE CONTEXTURES OF TUMOR AND SURROUNDING MARGIN


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Background Interactions between cancer and immune cells create a tumor-promoting or tumor-rejecting environment and correlate with prognosis for many cancers. The variability of immune contextures among oral squamous cell carcinoma of gingivobuccal region (OSCC-GB) patients and their relationship with prognosis are largely unknown.

Methods In this study we estimated the immune infiltration in the tumor, surrounding surgical negative margins and adjacent normal tissues of 43 treatment naïve OSCC-GB patients, using bulk RNA-sequencing and immunohistochemistry. Prognosis of each patient was followed-up for at least two years. Immune subtypes were inferred from gene expression data. Association of patient subtypes and disease prognosis was studied.

Results Using expressions of 544 immune related genes (IRGs) we identified a subgroup of patients with poor prognosis (high recurrences and deaths). High expression levels of three genes – CD73, ITGA3, and ITGA6 – were associated with poor overall survival and higher recurrence. Patients with good prognosis had (a) in their tumors, a high proportion of CD4+ and CD8+ T cells, B cells, NK cells, M1 macrophages, higher TCR and BCR repertoire diversity and cells positive for immune checkpoint markers, and (b) their surgical negative margins were enriched with resting memory-T and dendritic cells.

Conclusions Better prognosis in OSCC-GB is associated with appropriate immune contextures and a subgroup, with high expression of immune checkpoint genes, may further benefit from immunotherapy.


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Ethics Approval Ethical approval was obtained from the Tata Medical Institution, Kolkata, from where patients were recruited in the study.

Consent "Written informed consent was obtained from the patient for publication of this abstract and any accompanying images. A copy of the written consent is available for review by the Editor of this journal."