A Signature Disfavors T Cell-Mediated Cytolysis for Predicting Survival and Immunotherapy Effect in Head and Neck Cancer

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Objectives: The T cell-based cancer therapies provided effective treatment in several cancer patients. However, several patients with high T cells infiltration may suffer a limited response to immunotherapy. Our aim was to establish a signature that reflects the resistance of cancer cells to T cell killing for treatment decision-making and prognosis in head and neck cancer (HNC).

Methods: We used publically expression data from HNC samples from The Cancer Genome Atlas (TCGA) to stratify patients according to a signature of inducible tumor-expressed genes that disfavor T cell-mediated cytolysis (iD_CTL). Kaplan-Meier analysis was employed to explore the survival outcomes and the immune landscape in tumor microenvironment was also evaluated through Immuno-Oncology Biological Research (IOBR). We also used the IMvigor210 cohort to verify the predictive value of iD_CTL signature about immunotherapy effect.

Results: iD_CTLH represented a poorer prognosis and was validated in four HNC cohort from Gene Expression Omnibus (GEO). Enrichment analysis revealed that iD_CTLH was significant enrichment of Epithelial mesenchymal transition, TGF beta signaling, Angiogenesis. Meanwhile, iD_CTLH was significantly associated with the tumor microenvironment. iD_CTL is characterized by high TAM, MDSC, T-cell exhaustion, and T-cell regulatory, as well as high Pan_F_TBRs and PPAGs. In addition, iD_CTLH values of patients with poor immunotherapy response showed an increasing trend in the IMvigor210 cohort. And patients with higher iD_CTL scores had worse prognoses.

Conclusion(s): Our findings might contribute to further understanding of iD_CTL in the prognosis of HNC and provide novel and reliable biomarkers for immunotherapy.