

Extended Abstract

Predicting Death in Patients with Squamous Cell Carcinoma of the Tongue [†]

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Tongue squamous cell carcinoma (TSCC) accounts for 40% of all squamous cell carcinoma involving the mucosal surface of the oral cavity. TSCC is highly invasive and aggressive and, nowadays, TNM staging system is considered the gold standard in predicting patients' outcomes. Nevertheless, patients with tumors classified under the same TNM stage, can undergo different outcomes, with differences in behavior, aggressiveness and therapy response. This panorama calls for new biomarkers which could be used in clinical practice in a precision medicine point of view [1]. TCGA Database [2] offers wide genome sequencing analysis, including mRNA expression of whole genome. We included patients with TSCC and we downloaded data of mRNA expression per patient and survival outcome [3]. We performed a differential expression analysis and ranking according to the outcome. This bioinformatics approach led to the detection of 12 promising genes which resulted to be able to predict patients' prognosis. Poor is known about the detected genes and future studies are needed to test this gene panel in order to assess the accuracy in predicting death in an external cohort of patients. In addition, since these genes could be linked to a higher risk of patient's death, they could be actor in some pathological pathways, which characterize the tumor biology, for example in chemotherapy resistance, metastasis or tumor growth [4].

Conflicts of Interest: The authors declare no conflict of interest.

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