

Molecular Analysis of Surgical Margins in Head and Neck Squamous Cell Carcinoma Patients and Correlation with Locoregional Recurrence

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Head and Neck Squamous Cell Carcinoma (HNSCC) is a high incidence and mortality disease. Despite significant improvements in therapeutic strategies, the overall survival rate in 5 years is around 50%. The presence of microscopic tumor in surgical margins is associated with treatment failure causing an increase of locoregional recurrence and reduction of overall survival. The surgical resection extension is determined during the surgery through a low sensitivity histological exam of frozen tissue stained with Hematoxylin & Eosin. Since genetic alterations precede histological modifications, molecular markers may be useful to identify cells that have already started malignant transformation without having developed a histological phenotype that could be detected through conventional histopathological techniques. This study aimed to evaluate the gene expression pattern of specific markers in HNSCC and the utility of these markers in detecting the presence of tumor cells in surgical margins. A panel of three genes was evaluated and these analyses showed high specificity of *MMP9*, *PTHLH* and *TACSTD1* (93%, 93% and 73%, respectively) and sensibility (100%, 79% and 49%, respectively). Over-expression of at least one of these genes in surgical margins could be detected in 42% (14/33) of the cases analyzed. Next, we will try to correlate clinic-pathological characteristics of these patients (mainly, recurrence) with the molecular data and demonstrate that this kind of analysis could be useful for early recurrence diagnosis.

Supported by: FAPESP