IDENTIFICATION OF GENE EXPRESSION PROFILES ASSOCIATED WITH PATHOLOGICAL AND CLINICAL PARAMETERS IN HNSCC

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Head and Neck Squamous Cell Carcinomas (HNSCC) are associated tobacco and alcohol exposure and represents 5% of malignant tumor worldwide. Despite its common histology and presentation, HNSCC presents a wide variety of clinical behavior and treatment leads, frequently, to severe damage to organs involved in speech and eating. Therefore, gene expression profile could contribute to the identification of new markers and therapeutic targets, as well as to understand the complex transformation process. Using microarray technology, we examined seventy frozen tumors from patients with HNSCC of various anatomical sites, treated with surgery or surgery followed by radiotherapy. Clinical and pathological parameters were collected and used as categories for comparisons of gene expression profile using Student's t-test followed by bootstrap and a False Discovery Rate threshold of 5%. These analyses revealed altered expression of several genes. Aldoketo reductase AKR1C2, SCAMP3 and TMEM16A were up-regulated among tobacco+alcohol consumers. Genes related to the inflammatory process, such as IL1F9 and I?B-Zeta, were increased in tobacco+alcohol versus tobacco consumers. Patients pN=0 with no recurrence showed down-regulation of SERPINA3. MMP9 and CyclinB2 were up-regulated in colonizing versus non-colonizing tumors. Lymph node positive patients and metastazing tumors had increased MMP12 and uPA, respectively. Our data suggest that gene expression analysis of HNSCC has the potential to identify new biomarkers and treatment targets.