

## **ANALYSIS OF EXPRESSION AND METHYLATION OF MOLECULAR MARKERS FOR HEAD AND NECK TUMORS**

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Head and neck cancer is a major public health problem worldwide. This work has the aim of investigating the methylation profile of CpG islands in head and neck tumors and to identify biomarker candidates for diagnosis and prognosis of these tumors. The techniques of RaSH and cDNA microarray were used to identify and select 24 genes in four cell lines treated and not treated with the DNA methylation inhibitor 5-aza-2'-deoxycytidine. The gene expression was validated by Real Time PCR. The results confirmed those gotten by the RASH and microarray in 11 genes for the cell line UM-SCC-14A, 8 for UM-SCC-17A, 8 for FaDu and none for UM-SCC-38. After, an analysis of methylation of the genes CDK7, CRABP2 and CLTC was made by the dissociation curve of Real Time PCR and promoter region sequencing of these genes. The gene CRABP2 presented a difference of methylation between FaDu treated and not treated. These data suggest a methylation standard of this gene and consequent silencing in the FaDu cell line. Its analysis in primary head and neck tumors and in other types of neoplasia, as well as in pre-malignant lesions and in different types of normal tissues can result in its inclusion in panels of hypermethylated markers in cancer and increase the sensitivity and specificity of diagnostic tests.

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