

METHYLATION AND EXPRESSION VALIDATION RESULTS OF *GPRC5C* GENE OBTAINED FROM EPIGENOMICS AND TRANSCRIPTOMICS DATA IN ORAL CAVITY TUMORS

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ABSTRACT

Objective: Demokan et.al identified *G/Protein/Coupled/Receptor/Class-C/Group-5/Member-C (GPRC5C)* as a candidate gene in OSCC via expression and methylation array results (logFC:0.59663; DeltaBeta: -0.130984561) from their previous unpublished data. In our study, the methylation and expression status of *GPRC5C* gene was investigated in a larger group of OSCC patients and healthy cohort for further validation. Its potential candidate biomarker was evaluated for early diagnosis of OSCC by non-invasive methods.

Materials and Methods: DNA and RNA were isolated from tissues/body fluid samples of 30 patients OSCC and 15 healthy individuals. The methylation and expression levels were analyzed by using QMSP and QRT-PCR methods, respectively. The data were compared with clinical parameters and evaluated by statistical analysis.

Results: Decreased expression levels were observed in 43% and increased expression levels were observed in 33% in the tumor tissues compared to corresponding-normal tissues of OSCC patients. Methylation-based expression loss was observed in 4 patients having the ratio between 3.4 and 12.2%. We also observed a decrease in expression in OSCC patients with observed methylation. There was statistical significance between differentiation degree and expression in OSCC.

Conclusion: It was concluded that *GPRC5C* may play a role as a potential methylation biomarker candidate of specific subgroups of the oral cavity. Other mechanisms need to be explored to understand the differences in expression levels.

Keywords: gene expression, DNA methylation, OSCC, *GPRC5C*