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NOVEL EPIGENETIC BIOMARKER DETERMINATION FOR OSCC BY ARRAY-BASED EPIGENOMIC AND TRANSCRIPTOMIC TECHNIQUES

Semra DEMOKAN[1], Sena ŞEN[1], Önder ERYILMAZ[1], Sevde CÖMERT[1], Murat ULUSAN[2], Nejat DALAY[1]

[1] Istanbul University, Oncology Institute, Department of Basic Oncology, Istanbul, Turkiye
[2] Istanbul University, Istanbul Faculty of Medicine, Department of Otorhinolaryngology, Istanbul, Turkiye

ABSTRACT

Objectives: Oral squamous cell carcinoma (OSCC) has a high morbidity and mortality rates, but there are no reliable biomarkers to define patients in early phases of disease. In our study (TUBITAK-SBAG-114S497), we aimed to investigate the potential epigenetic biomarker candidate genes observed methylation-dependent expression loss via methylation and expression array methods in OSCC patients.
Material and Methods: Methylation and expression profiling in tumor and conjugate-normal tissue samples of 6 OSCC patients were analyzed by "IlluminaHumanMethylation450 chips" and "Illumina iScan", respectively. Methylation/expression array data were analyzed and interpreted by R(v3.5.1) environment using ChAMP and limma/lumi packages, and then the significant decreased expression changes due to hypermethylation of the candidate gene was detected. The selected candidate gene was validated in tumor and matched-normal tissues and body fluids (serum and saliva) of 20 OSCC patients by QRT-PCR/QMSP methods.
Results: According to the array results, it was determined that the expression levels of the candidate gene were decreased due to methylation (DiffScore:13.18826; FoldChange:-1.08345). This candidate gene (unpublished data), which plays an important role in ubiquitin-ligase activity, was found to be methylated in 45% tumor, 40% matched-normal tissue, 10% serum and 30% saliva samples. 50% of the patients observed methylation in the tumor tissue showed the differentially decreased expression levels.
Conclusion: It is thought that this candidate gene, whose expression level decreased due to methylation, will be a candidate epigenetic biomarker for the early diagnosis of the subtypes of OSCC. Further validation of this candidate gene will be needed in the larger OSCC cohorts.
Keywords: Oral Squamous Cell Carcinoma, Methylation, Expression, Biomarker