

ABSTRACT

Oral cancer is one of the most common cancers that occur worldwide, with high mortality rates. Aberrant epigenetic modifications like DNA methylation play a significant role in the pathogenesis of oral cancer. The tumor suppressor gene *p21* (CDKN1A), known for its regulation of cell cycle arrest, is frequently affected by epigenetic changes, especially DNA methylation, which can lead to its silencing and contribute to uncontrolled cell proliferation. This study aims to predict the DNA methylation profile of the *p21* gene in oral cancer patients compared to healthy controls. Using techniques such as methylation-specific PCR and bisulfite-conversion, the methylation status of CpG islands within the *p21* promoter region was analyzed. Further this methylation status was correlated with clinicopathological factors of oral cancer patients. Our findings indicate that hyper-methylation of the *p21* promoter is significantly associated with its reduced expression in oral cancer patients, suggesting its methylation could serve as a potential biomarker for early detection and a therapeutic target. This study contributes to a deeper understanding of the epigenetic mechanisms driving oral cancer and underscores the importance of DNA methylation as a regulator of tumor suppressor gene expression in cancer progression.