ABSTRACT

DNA methylation is a key epigenetic mechanism that regulates gene expression and has been implicated in cancer development. The Epidermal Growth Factor Receptor (*EGFR*) is a critical gene involved in controlling cell proliferation, differentiation, and survival. Aberrant methylation of the *EGFR* promoter may contribute to tumorigenesis. This study aimed to evaluate the methylation status of the *EGFR* gene promoter in oral cancer patients using Methylation-Specific PCR (MS-PCR). A total of 101 unrelated patients with clinically diagnosed oral squamous cell carcinoma (OSCC), and 101 healthy controls were included. Genomic DNA was extracted from peripheral blood samples, followed by bisulfite modification. Methylation-specific primers targeting the *EGFR* promoter region were used to assess methylation patterns. Correlation analysis like multinomial logistic regression and chi-square was performed to evaluate the relationship of methylation status with clinicopathological variables such as age, gender, and tumor location. The study found no significant association between *EGFR* promoter methylation and patient age or gender, consistent with previously published research. Comparative analysis between patients and controls revealed methylation in 7.93% of OSCC cases, partial methylation in 78.21%, and unmethylation in 12.87%, whereas controls showed 8.91% methylation, 52.46% partial methylation, and 3.96% unmethylation. These findings suggest that *EGFR* promoter methylation is not significantly linked to oral cancer development in this population. The high frequency of partial methylation in both groups emphasizes the need for further research on larger sample sizes and additional gene targets to clarify the potential role of *EGFR* methylation in oral cancer pathogenesis and its utility as a biomarker.

Keywords: *EGFR*, DNA methylation, oral cancer, epigenetic biomarker, OSCC, promoter methylation