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## The association between miR-499a polymorphism and oral squamous cell carcinoma progression.

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#### Abstract

**OBJECTIVE:** To investigate the **association** of **miR-499a** genetic **polymorphism** with the risk of **oral** leukoplakia, **oral** submucous fibrosis (OSF), **oral squamous cell carcinoma** (OSCC), and clinicopathological outcomes of OSCC.

**METHODS:** The genotyping of **miR-499a** T>C (rs3746444) using TagMan assay was conducted in two case-control studies of 1549 subjects. **miR-499a-5p** and **miR-499a-3p** were assayed using stem-loop RT-PCR for 63 paired OSCC and adjacent normal tissues.

**RESULTS:** T/C+C/C genotypes [adjusted odds ratio (AOR) 1.84, P = 0.032] and C allelic type (AOR 1.91, P = 0.007) at **miR-499a** T>C were associated with an increased risk of BQ-related OSF as compared to those with T/T genotype or T allelic type, respectively. Conversely, T/C+C/C genotypes and C allelic type decreased the risk of OSCC, especially for non-BQ-related OSCC (for genotype: AOR 0.49, P = 0.010; for allelic type: AOR 0.50, P = 0.007). Additionally, downregulation of **miR-499a-5p** was found in OSCC tissues (P = 0.001) and correlated with the TT genotype (P = 0.001).

**CONCLUSION:** The T/C+C/C genotypes of **MiR-499a** may contribute to an increased risk of BQ-related OSF, but a decreased risk of OSCC. **miR-499a** T>C influences the expression levels of **miR-499a-5p** during the tumorigenesis of OSCC.

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**KEYWORDS:** **miR-499a**; microRNA; **oral** cancer; **oral** submucous fibrosis; **polymorphism**; **progression**

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