

MICRORNA-31 AS A POTENTIAL THERAPEUTIC BIOMARKER FOR ORAL SQUAMOUS CELL CARCINOMA: CURRENT EVIDENCE AND FUTURE PROSPECTS

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Dear Editor,

Cancer is a foremost death cause in each country and a substantial hindrance to improving life expectancy, accounting for more than 10 million fatalities in 2020, or around one in every six fatalities [1]. Oral cancer is among the leading causes of cancer-related mortality in developing countries. Oral squamous cell carcinoma (OSCC) is a widespread type of malignancy associated with tobacco usage and human papilloma virus infection. The majority of people are diagnosed with cancer at an advanced stage, the 5-year survival rate for OSCC patients is only around 50%. Despite biological and technological advances, in recent decades, the prognosis for OSCC has not improved, and its occurrence has increased. Identification of biomarkers that can be utilized to establish an early diagnosis or predict tumor growth is enabled by determining which molecular pathways are disrupted [2].

MicroRNAs, which can serve as both oncogenes and tumor-inhibiting factors, are misaligned in a wide range of cancers [3]. These are short, noncoding RNAs that affect protein expression following transcription at the post-transcriptional level. MicroRNAs play a vital role in proliferation, differentiation, apoptosis, immune response, and angiogenesis, among other things in the pathogenesis of cancer. Multiple researchers have documented that specific microRNAs are frequently down regulated in cancers, implying that they operate as tumor suppressors by targeting many oncogenes. According to research conducted by O'Brien *et al*,

altering levels of microRNAs expression can improve chemotherapeutic efficacy [4]. In recent decades, several researches have linked metastasis, survival, and recurrence of OSCC patients to miRNA expression [5].

MicroRNA-31, a gene on chromosome 9p21.3, was one of the first mammalian microRNAs discovered. Several studies have been conducted to evaluate the functions of miR-31 in carcinogenesis and the progression of OSCC. A prior clinical investigation conducted by Liu *et al*. [6] revealed that miR-31 levels in plasma were considerably increased in patients with OSCC when compared to age and gender-matched control participants. Several studies show that miR-31 performs a role in cancer etiology and aggressiveness via altering target genes. According to reports, miR-31 regulates a number of genes, including fibronectin type III domain containing 5, special AT-rich sequence-binding protein-2, large tumor suppressor kinase 2 (LATS2), tensin 1, AT-rich interaction domain 1A, and hypoxia-inducible factor-1 [7]. The concentration of miR-31 expression in serum, urine, saliva and organ tissue can be utilized as a diagnostic and predictive biomarker for a variety of malignancies [8].

A recent investigation by Chou *et al*. [9] found that miR-31 levels were significantly raised in OSCC cells and tumor tissues, and that the miR-31 gene locus was necessary to initiate oncogenesis in OSCC. Upregulation of miR-31 contributes to the formation of OSCC by interacting with certain genes and signaling pathways that impact cancer cell cycle, epithelial-mesenchymal transition and cell proliferation. miR-31 forms a complex network with direct target genes (such as *RHOA*, *FIH*, *ACO1*, *VEGF*, *SIRT3*, *LATS2*, *KANK1*, and *NUMB*) and initiates several signaling pathways including the ERK-

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Abbreviation used: OSCC – oral squamous cell carcinoma.

MMP9 cascade, the Hippo pathway, Wnt signaling, and the MCT1/MCT4 regulatory cascade [10]. MiR-31 interacts with a number of proteins and pathways that are crucial in OSCC and it is overexpressed in plasma, saliva, and OSCC tumor tissue. However, more research is needed to fully comprehend the molecular mechanisms by which miR-31 drives OSCC malignancy, paving the way for the development of miR-31 based diagnostic, prognostic, and predictive biomarkers for OSCC.

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