

Title:	Dysregulation of miR-31 and miR-375 expression is associated with clinical outcomes in oral carcinoma
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Abstract:	<p>Objectives To identify differentially expressed miRNA between oral squamous cell carcinoma (OSCC) and non-cancer (NC) and to associate these with clinico-pathological parameters.</p> <p>Materials and methods miRNA microarray profiling was utilized to obtain the expression profile of miRNAs in four OSCC and four NC samples. The expression of miR-31 and miR-375 was further validated in 26 OSCC and three NC samples using real-time-PCR. The association between miRNA expression and clinico-pathological parameters was tested by univariate and multivariate analyses.</p> <p>Results</p>

	<p>Microarray profiling demonstrated that 15 and four miRNAs were up-regulated and down-regulated, respectively, in OSCC as compared with NC. miR-31 and miR-375 were validated as up- and down-regulated miRNAs, respectively. In univariate analyses, expression of miR-31 was significantly elevated in early stage, tumours with no metastatic nodes and those from the buccal mucosa. By contrast, low miR-375 expression was significantly associated with late stage disease, larger tumour size and the non-cohesive type of pattern of invasion in OSCC. The association between miR-31 expression with tumour staging and site and miR-375 with tumour staging remained significant in multivariate analyses.</p> <p>Conclusions</p> <p>This study has identified 19 miRNAs significantly associated with OSCC, and expressions of miR-31 and miR-375 were significantly related with clinico-pathological parameters suggesting they could be important in driving oral tumourigenesis.</p>
Keyword:	miR-31; oral squamous cell carcinoma; microRNA profiling; clinico-pathological parameters; miR-375
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