MicroRNA profiles of oral squamous cell carcinoma (OSCC) using formalin-fixed, paraffin embedded (FFPE) tissue

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Content:

Introduction: MicroRNAs (miRNAs) have previously found to be highly tissue- or disease-specific biomarkers with clinical applicability. However, the role of miRNAs in OSCC progression has yet to be well-studied. Here, we demonstrated the use of FFPE specimens in microarray profiling and quantitative real-time PCR (qPCR) approaches to identify miRNAs that are differentially expressed in OSCC compared with non-tumour tissues.**Materials and methods**: Four OSCC and four non-tumour FFPE tissues were obtained from the Malaysian Oral Cancer Database and Tumour System (MOCDTBS), coordinated by OCRCC-UM and profiled using Agilent 8 × 15 k mammalian miRNA microarray. Based on microarray results, TaqMan miRNA Assay (qPCR) is underway to validate the selected differentially expressed miR-31, miR-7, miR-375 and miR-151-3p with an endogeneous control RNU-44 using an independent set of FFPE tissue (seven OSCC and three non-tumuor tissues). Biological functions of targeted miRNAs were analyzed using GeneGO Pathway software.**Results**: Analysis of profiling identified 19 significantly up-regulated miRNAs (2-fold change) and four significantly down-regulated miRNAs (2-fold change). The targeted miR-31, miR-7 and miR-151-3p were up-regulated whilst miR-375 was down-regulated in OSCC compared with non-tumour tissues. These initial microarray profiling results had been subsequently confirmed in qPCR validation except miR-151-3p, which was validated as down-regulated miRNA.**Discussion**: Interestingly, we have identified miRNA targets that can potentially be exploited to differentiate between betel-quid exposure OSCC with no risk habit related OSCC. These miRNA targets were found to interact with protein BuBRl in regulation of cellular component organization (p0.05, GeneGo Pathway software). BuBR1 can be modified by arecoline in betel nut leads to abnormal cell cycle progression. Further analyses with larger sample set are on-going to validate the preliminary result and examine if the betel-quid exposures related with OSCC carcinogenesis may be acting through a specific miRNA alterations to lead to a malignant phenotypes. This better understanding of the contribution of miRNA to OSCC may aid in earlier diagnosis, improved prognosis, and novel targets for therapeutic intervention.

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