

ABSTRACT

Oral cancer is the malignant dysplastic lesion which appears on the lip or oral cavity squamous epithelium. It has become the sixth most common malignancy worldwide. The present study was aimed to investigate the differentially expressed miRNA in oral metastasis, expression analysis of *CDKN1A* and *CCND1* in oral cancer patients and it's with oral cancer patients. The differentially expressed miRNAs and their targets were identified from previously analyzed dataset "GSE168227" with different bioinformatics tools such as "DIANA Tool-mir path v.3", STRING database, Cytoscape version 3.6.0 and Enrichr tool. The binding sites of potential miRNA of target genes mRNA were also predicted by several bioinformatics tools such as "TargetScan Human 7.2 database (www.targetscan.org), miRwalk (<http://mirwalk.umm.uni-heidelberg.de/>) and miRDB (http://www.mirdb.org/cgi-bin/search_custom.cgi)". For expression analysis the oral cancer patients samples of blood (n=25) were recruited from Shaukat Khanum Cancer Hospital and Research Center (SKMCH&RC) and Mayo Hospital (MH), Lahore. The recruited samples were used for RNA extraction by trizol method followed by cDNA synthesis and qPCR analysis. We selected the differentially expressed microRNA "hsa-miR-17" and its target *CDKN1A* and *CCND1*. The database analysis indicated that miR-17 has the potential binding sites for the *CDKN1A* and *CCND1* mRNA at 3'-UTR. The mRNA expression showed that *CDKN1A* and *CCND1* was upregulated in treatment naïve group of oral cancer patients as compared to other groups undergoing treatment. It was found that both the *CDKN1A* and *CCND1* has oncogenic role in oral cancer patients. Our study shows that miR-17 is the potential target of *CDKN1A* and *CCND1* and both of them are involved in the development of oral cancer. Thus, *CDKN1A* and *CCND1* may serve as significant biomarkers for the early detection of oral cancer.

Keywords: Oral cancer; miR-17; *CDKN1A*; *CCND1*; Proliferation