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Abstract Title:- Comparative in-silico and expression analysis of noncoding RNA ZFPM2-AS1 in Oral Squamous cell carcinoma

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Aims:-Long noncoding RNAs (lncRNAs) were reported to play important roles in tumorigenesis and cancer progression. lncRNA zinc finger protein, FOG family member 2-antisense 1 (ZFPM2-AS1), located on the 8q23 chromosome and next to the zinc finger protein, FOG family member 2 (ZFPM2) gene, was shown to play a role in carcinogenesis and tumour progression in oral, hepatocellular carcinoma and gastric cancer by acting as a competing endogenous RNA (ceRNA) by binding competitively to microRNAs (miRNAs). Hence, we aimed to study the expression of lncRNA ZFPM2-AS1 and its miRNA targets in Oral Squamous Cell Cancer (OSCC).

Methods:- The insilico analysis of miRNA targets of the lncRNA were shortlisted using public databases. Quantitative real-time PCR was used to study the relative expression levels of ZFPM2-AS1 and its targets hsa-miR-148a-3p in OSCC and adjacent normal tissues. Comparative expression profiling in epithelial tumours was done using cBioportal online tool for Cancer Genomics. Statistical analyses were performed using GraphPad Prism 6 for validating miRNA/lncRNA expression.

Results:- We observed expression level of lncRNA ZFPM2-AS1 was elevated in oral tumour and adjacent normal tissues and the expression of hsa-miR-148a-3p was higher in adjacent normal compared to tumour was quantified by probe hydrolysis based relative quantification method but there was no statistical significance. Based on the analysis from TCGA, we observed over-expression of ZFPM2-AS1 in HNSC compared to other tumours. This study gives an insight about the association between the lncRNA ZFPM2-AS1 and hsa-miR-148a-3p in our sample set.

Conclusions:- The chromosome 8q23 region is a high susceptibility locus for several types of cancer and genome-wide association studies (GWAS) have identified number of cancer-associated single nucleotide polymorphisms that are adjacent to the ZFPM2-AS1 and ZFPM2 gene in this region. The miRNA hsa-miR-148a-3p has been reported as an oncogene and its overexpression in oral tumours with undifferentiated cellular pathology. It increases the proliferation, migration and invasion of human cancers of epithelial origin. We suggest assessment of expression levels of ZFPM2-AS1 and its targets in more large-scale research is required to explain the precise molecular pathways through it contributes to carcinogenesis. Exploring the lncRNA and its miRNA targets will help elucidating the oral carcinogenesis.

Keywords:- OSCC, noncoding RNA, ceRNA, biomarker