In Silico Analysis of Salivary miRNAs to Identify the Diagnostic Biomarkers for Oral Cancer

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Abstract : Oral squamous cell carcinoma (OSCC) is one of the most common cancers worldwide. Recent studies have highlighted the role of miRNA in disease pathology, indicating its potential use in an early diagnostic tool. miRNAs are small, double stranded, non-coding RNAs that regulate gene expression by deregulating mRNAs. miRNAs play important roles in modifying various cellular processes such as cell growth, differentiation, apoptosis, and immune response. Dis-regulated expression of miRNAs is known to affect the cell growth, and this may function as tumor suppressors or oncogenes in various cancers. Objectives: The main objectives of this study were to characterize the extracellular miRNAs involved in oral cancer (OC) to assist early detection of cancer as well as to propose a list of genes that can potentially be used as biomarkers of OC. We used gene expression data by microarrays already available in literature. Materials and Methods: In the first step, a total of 318 miRNAs involved in oral carcinoma were shortlisted followed by the prediction of their target genes. Simultaneously, the differentially expressed genes (DEGs) of oral carcinoma from all experiments were identified. The common genes between lists of DEGs of OC based on experimentally proven data and target genes of each miRNA were identified. These common genes are the targets of specific miRNA, which is involved in OC. Finally, a list of genes was generated which may be used as biomarker of OC. Results and Conclusion: In results, we included some of pathways in cancer to show the change in gene expression under the control of specific miRNA. Ingenuity pathway analysis (IPA) provided a list of major biomarkers like CDH2, CDK7 and functional enrichment analysis identified the role of miRNA in major pathways like cell adhesion molecules pathway affected by cancer. We observed that at least 25 genes are regulated by maximum number of miRNAs, and thereby, they can be used as biomarkers of OC. To better understand the role of miRNA with respect to their target genes further experiments are required, and our study provides a platform to better understand the miRNA-OC relationship at genomics level.

Keywords : biomarkers, gene expression, miRNA, oral carcinoma
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