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MicroRNAs – A New Era of Cancer Therapeutics

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Abstract

In just over 20 years since the invention of the primary microRNA (miRNA), the sphere of miRNA biology has swollen significantly. Insights into the roles of miRNAs in development and sickness, significantly in cancer, have created miRNAs enticing tools and targets for novel therapeutic approaches. Useful studies have confirmed that miRNA dis regulation is causative in several cases of cancer, with miRNAs acting as neoplasm suppressors or oncogenes (oncomiRs), and miRNA mimics and molecules targeted at miRNAs (antimiRs) have shown promise in pre symptomatic development. many miRNA-targeted medicine have reached clinical development, together with a mimic of the neoplasm suppressor miRNA miR-34, that reached phase I clinical trials for treating cancer, and anti miRs targeted at miR-122, that reached clinical trial trials for treating liver disease. During this article, we tend to describe recent advances in our understanding of miRNAs in cancer and in alternative diseases and supply an outline of current miRNA medicine within the clinic. we tend to conjointly discuss the challenge of distinctive the foremost efficacious therapeutic candidates and supply a perspective on achieving safe and targeted delivery of miRNA medicine.

Background
There were 17 million new cases of cancer worldwide in 2018. The four most common cancers occurring worldwide are lung, female breast, bowel and prostate cancer. 57% of new cancer cases in 2012 occurred in less developed regions of the world that include Central America and parts of Africa and Asia; 65% of cancer deaths also occurred in these regions. The number of new cancer cases per year is expected to rise to 23.6 million by 2030. Oral cancer can affect the mouth, palate, sinuses, and pharynx. Squamous cell carcinoma is the most common type of oral cancer.

Aim
MicroRNAs (miRNAs) have been shown to be involved in a wide range of biological processes. A significant role for miRNA in cancers is to target their expression level through their respective signaling pathways. Our study analyzed gene expression profiles of a few microRNAs such as miR-21, miR-137, miR-200c and miR-205 in pathogenesis of oral squamous cell carcinoma (OSCC).

Methods
Biopsy samples from 50 patients recently diagnosed with oral cancer along with corresponding nonmalignant portions were obtained for our study. With the approval of Institutional Ethics Committee and informed written consent biopsy samples were collected for microRNA studies. Quantitative real time PCR (qRT PCR) was used to quantify the levels of miRNAs expression. The association between miRNA expression levels and clinico-pathological parameters was analyzed using MedCalc software.

Results and interpretation
This study found miRNA-21 was up-regulated (in 54% cases) whereas miR-137 (48%), miR-200c (46%), miR-205 (42% of cases) was down-regulated in OSCC. Among these four microRNAs, only miR-137 was not associated with the risk of OSCC, whereas all other microRNAs were found to be associated with OSCC. This study demonstrated an association of miR-21, miR-137, miR-200c and miR-205 in OSCC with altered gene expression, suggesting that in spite of varying expressions in miRNAs' its role in the development of oral cancer was very much evident.

Conclusion
It is suggested that these miRNAs could probably serve as biomarkers for oral cancer management and could provide targets for drug development.