## **Real Time PCR Analysis of microRNA Expression in Oral Cancer**

## Authors : Karl Kingsley

Abstract : Many mechanisms are involved in the control of cellular differentiation and growth, which are often dysregulated in many cancers. Many distinct pathways are involved in these mechanisms of control, including deoxyribonuclease (DNA) methyltransferase and histone deacetylase (HDAC) activation that controls both genetic and epigenetic modifications and micro ribonucleic acid (RNA) expression. Less is known about the expression of DNA methyltransferase (DNMT) and HDAC in oral cancers and the effect on microRNA expression. The primary objective of this study was to evaluate the expression of DNMT and HDAC family members in oral cancer and the concomitant expression of cancer-associated microRNAs. Using commercially available oral cancers, including squamous cell carcinoma (SCC)-4, SCC-9, SCC-15, and SCC-25, RNA was extracted and screened for DNMT, HDAC, and microRNA expression using highly-specific primers and quantitative polymerase chain reaction (qPCR). These data revealed low or absent expression of DNMT-1, which is associated with cellular differentiation but increased expression of DNMT-3a and DNMT-3b in all SCC cell lines compared with normal non-cancerous cell controls. In addition, no expression of HDAC1 and HDAC2 expression was found among the normal, non-cancerous cells but was highly expressed in each of the SCC cell lines examined. Differential expression of oncogenic and cancer-associated microRNAs was also observed among the SCC cell lines, including miR-21, miR-133, miR-149, miR-155, miR-365, and miR-720. These findings also appeared to vary according to observed growth rates among these cells. These data may be the first to demonstrate the expression and association between HDAC and DNMT3 family members among oral cancers. In addition, the differential expression of these epigenetic modifiers may be associated with the expression of specific microRNAs in these cancers, which have not previously been observed to the best of the author's knowledge. In addition, some associations and relationships may exist between the expression of these biomarkers and the rates of growth and proliferation, which may suggest that these expression patterns might represent potentially useful biomarkers to determine tumor aggressiveness and other phenotypic behaviors among oral cancers.

Keywords : oral cancer, DNA methyltransferase, histone deacetylase, microRNA

Conference Title : ICSRD 2020 : International Conference on Scientific Research and Development

Conference Location : Chicago, United States

Conference Dates : December 12-13, 2020

1