

A transcriptomic analysis on long non-coding RNA role in oral cancer inhibition

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ABSTRACT

Long non-coding RNAs or lncRNAs, are non-protein coding transcripts longer than 200 nucleotides, distinguishing them from small regulatory RNAs such as microRNAs (miRNAs), short interfering RNAs (siRNAs) and other short RNAs. LncRNAs have begun to gain widespread attention in recent years; as a result, the need to identify them as well as determine their functions has gained precedence. Over the years some lncRNAs have been found to be involved in numerous fundamental processes of gene regulation. For example: Chromatin modification, DNA methylation, etc. Having a variety of functions, it is expected that lncRNAs are also involved in the development of diseases. LncRNAs are quite often found to be differentially expressed, which play a significant role in carcinogenesis. Presently oral cancers are considered as two of the most prevalent cancers affecting the human population. LncRNAs suffer an alteration in its expression due to its involvement in the HPV infection. Therefore, the need to study about the mechanism and functions of the lncRNAs involved in the cancer affected by HPV infection reaches significant priority. Identification of long non coding RNAs as well as lncRNAs which are speculated to play a role in the mechanism and formation of various forms of cancer. For identification and analysis of lncRNAs, comparison between the expression of lncRNAs in normal and affected tissues will confirm the involvement of lncRNAs in the disease or the lack thereof. Similarly, the dysregulated lncRNAs will help us understand their relevance in tumor growth.

Keywords: Oral cancer, Long non coding RNA, Epigenetics

