LncRNA as a Therapeutic Target for Angiogenesis

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Abstract:

Background: Out of 3 billion base pairs in human genome only ~2% code for proteins; and out of 180,000 transcripts in human cells, about 20,000 code for protein, remaining 160,000 are non-coding transcripts. Most of these transcripts are more than 200 base pairs and constitute a group of long non-coding RNA (lncRNA). Many of the lncRNA have its own promoter, and are well conserved in mammals. Accumulating evidence indicates that lncRNAs act as molecular switches in cellular differentiation, movement, apoptosis, and in the reprogramming of cell states by altering gene expression patterns. However, the role of this important group of molecules in angiogenesis is not well understood. Angiogenesis is a complex process and depends on precise regulation of gene expression.

Conclusion: Dysregulation of transcription during this process may lead to several diseases including various cancers. As angiogenesis is an important process in cancer pathogenesis and treatment, lncRNA may be playing an important role in angiogenesis. In support of this, lncRNA microvascular invasion in hepatocellular carcinoma (MVIH) has been shown to activate angiogenesis. Furthermore, lncRNA-Meg3-knockout mouse showed increased expression of vascular endothelial growth factor pathway genes and increased cortical microvessel density. Overall, there is strong evidence that lncRNA is an important class of regulatory molecule, and a number of studies have demonstrated that these can be targeted to change cellular physiology and functions. In this review, we have attempted to summarize these studies and elucidate the potential of this novel regulatory molecule as a therapeutic target.

Keywords: Epigenetic regulation, gene expression, intervening noncoding RNA, LncRNA, Linc-MD1