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Stem Cell Research 2017-Long Noncoding RNAs and Human Osteosarcoma- Arshad Ali- Northwestern Polytechnical University

Arshad Ali [1,2,3], Lifang Hu [1,2,3], Airong Qian [1,2,3],Chu Chen [4] and Tuanmin Yang [4 1] Laboratory for Bone Metabolism, Key Laboratory for Space Bioscience and Biotechnology, School of Life Sciences, Northwestern Polytechnical University, Xi'an, Shaanxi 710072, P. R. China [2] Research Center for Special Medicine and Health Systems Engineering, School of Life Sciences, Northwestern Polytechnical University, Xi'an, Shaanxi 710072, China [3] NPU-UAB Joint Laboratory for Bone Metabolism, School of Life Sciences, Northwestern Polytechnical University Xi'an, Shaanxi 710072, China [4] Hong-Hui Hospital, Xi'an Jiaotong University College of Medicine, Xi'an, Shaanxi, China*

Abstract:

Osteosarcoma is the most frequently diagnosed malignant tumor in children and adolescents, characterized pathologically by spindle cells and the formation of deviant osteoids. Although significant evidence of therapeutic strategies has been obtained, the conclusion is still unclear for critical metastatic or persistent osteosarcoma. Therefore, it is essential to develop new and effective biomarkers or therapeutic targets for the diagnosis of osteosarcoma. Long non-coding RNA (nncRNA), as a new class of non-coding RNA, are composed of transcripts of more than 200 nucleotides and play an essential role in the development and progression of various cancers, including osteosarcoma. The nCRNAs are mainly involved in various biological processes such as cell growth, transcription, translation, epigenetic regulation, splicing, chromosomal dosage compensation, printing, nuclear, cytoplasmic traffic and cycle control. cellular. CncRNAs can act as oncogenic or tumor suppressants that can modulate the pathogenesis of osteosarcoma, including cell growth, migration, proliferation, metastases, invasion and cell apoptosis. In this review, we summarize the current knowledge on cRNAs and its critical role in the progression of osteosarcoma. It will be useful for researchers to assess the functional role of the cRNAs in the development of osteosarcoma and to improve the effectiveness of therapeutic treatment modalities.

Along the coding genes, a large number of transcripts of cRNA exist in the human genome. CncRNAs are precisely transcribed during cell development, differentiation, progression of cancer and other diseases [10-12]. Non-coding RNAs (cncRNAs) are endogenous RNA molecules without the ability to code proteins. Depending on the size of the nucleotides, the cRNAs can be classified as small non-coding RNAs (cRNAs, 200 nt). Small cRNAs such as microRNAs (miRNAs), transfer RNAs, small interfering RNAs (siRNAs), certain ribosomal RNAs and RNAs interacting with piou, have been studied to function in tumorigenesis, metastases and chemoresistance. The large catalog of lncRNAs is initially observed during functional studies of the human genome. The cRNAs are considered to have chromatin signatures equivalent to the coding genes. More and more recent research has revealed differences in the existence of specific histone letters [14-16] and the splicing capacity between the cRNAs and the coding genes, as well as with other cncRNAs according to the structure of chromatin. A large number of cRNAs have been identified in various types of species as well as in tissues. Some of the CNRNAs are essential for the development of the organism and the progression of cancer. CncRNAs are essential for certain biological processes such as transcription, translation, epigenetic regulation, splicing, chromosomal assay compensation, printing, nuclear and cytoplasmic traffic and cell cycle control. Research and advanced research significantly reveal the role of cRNAs in the prognosis and pathogenesis of various human diseases such as osteoarthritis [25] and osteosarcoma. Li et al. reported the expression profile of cncRNAs in osteosarcoma and showed that approximately 25,733 cRNAs consist of 789 downregulated and 403 upregulated. Further study showed that 32 lanes were downregulated transcripts and 34 lanes were upregulated transcripts. Recent studies have implied that abnormal expressions of the cRNAs are directly involved in certain diseases, including the progression, invasion and metastasis of cancers. In this review, based on the characteristics and function of the cRNAs, we have summarized recent knowledge of its pathological role in the pathogenesis of osteosarcoma. This article provides an overview of

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future research and helps scientists further elevate the therapeutic roles of cRNAs in the progression of osteosarcoma to develop innovative diagnostics / prognostic biomarkers for the treatment of osteosarcoma.

Characteristics of lncRNAs

Long non-coding RNAs (nncRNA) are known as a larger class of non-coding RNA constituting a long transcript size of 200nt-100kb without an open reading frame. Its transcription processes are mainly carried out by RNA polymerase II and regulated by the transcriptional activators of chromatin remodelers known as defective / non-fermentation sucrose switching (SWI / SNF). The nncRNAs can be classified into several large groups such as the sense nRNAs, the antisense nRNAs, the intronic nRNAs, the bidirectional nncRNAs, the intergenic nRNAs, the nrNAs associated with the untranslated region (UTR) and the nncRNAs associated with the promoter. The cRNAs are mainly spliced, styled and polyadenylated in the same way as the mRNA molecules. The cRNAs are characterized as an important and very heterogeneous set of cRNAs. The expression of the cRNAs generally depends on the cellular and tissue context]. After the discovery of H19 and XIST nRNAs in the 1990s, nncRNAs were considered to be transcription noise with almost nonexistent or extremely light functions. The cRNAs can exist in all cellular contexts, in particular with a high proportion identified in the cytoplasm and the nucleus. The secondary structure of the cncRNAs includes rod loops and hairpins, produced by post-transcriptional modifications, which allow their association with chromatin and other proteins as well as essential for the broad group of functions of the cRNAs.

Biological Function of lncRNAs

The key function of cncRNAs has been assigned to regulate the expression of coding genes by manipulating its adjacent genes (in cis) or by modifying separate genes on other chromosomes (in trans). At different levels of gene function, including transcription, translation and protein function, cRNAs can regulate individual genes or the process of gene expression by altering the basic transcription mechanism or through the epigenetic mechanism. Unambiguously, the functions of the cRNAs are as follows: (1) The cRNAs located in the upstream promoter region can alter gene expression in the downstream promoter region by chromatin remodeling and histone modification. (2) cRNAs can regulate gene expression using microRNAs or siRNAs and serve as a precursor for small RNAs. (3) The cRNAs have a closed association with special proteins and adjust the activity of the proteins (4) The cRNAs constitute a diverse product due to alternative splicing. In addition, the cRNAs are associated with the main cellular pathways regulating the differentiation, proliferation and apoptosis which are involved in the pathogenesis of various human cancers. During the transcriptional or post-transcriptional stages, the cRNAs control various genes, including oncogenes and tumor suppressor genes, and also affect cellular processes such as cell proliferation, angiogenesis, apoptosis, migration, invasion and metastases (Figure 1).

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drarshadhassan@yahoo.com

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