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Non-coding RNAs and Their Use in Cancer Diagnosis and Treatment

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Abstract – Non-coding RNAs (ncRNAs) are non-protein-coding RNAs that are involved in important cellular processes as well as in the regulation of gene expression. In recent years, ncRNAs have been implicated in cancerization and have been found to be valuable biomarkers for cancer diagnosis and treatment. Therefore, understanding gene expression and other important cellular processes regulated by ncRNA networks can provide significant new insights into cancer biology and further lead to the development of new and effective therapeutic strategies. ncRNAs, especially microRNAs (miRNAs) and Long non-coding RNAs (lncRNAs), act as decoys to affect the binding of regulatory molecules to target genes. Therefore, these unique molecules can play a role in cancer by regulating genes involved in cell growth, apoptosis, and angiogenesis. In conclusion, ncRNAs hold great potential for cancer diagnosis and treatment. Further research into the specific functions and mechanisms of these molecules in cancer will lead to the development of more effective therapeutic and/or diagnostic approaches for cancer patients.

Keywords – Cancer, Non-coding RNAs, MicroRNAs, Long Non-coding RNAs

I. INTRODUCTION

The abnormal and uncontrolled growth of cells in the body is defined as cancer [1]. The diagnosis and treatment of cancer depends on several factors, including the type of cancer, its stage, and the patient's overall health [2]. Diagnosis is a critical component of cancer treatment and management. Accurate diagnosis plays a crucial role in cancer treatment and management. It helps patients get the ideal treatment regimen for them at the right time and with the best outcomes [3]. It is important to remember that early detection is key to improving the chances of a successful treatment outcome in cancer patients. The most appropriate treatment approach for an individual will depend on factors such as the stage of cancer, overall health, and personal preferences. It's important to note that the causes of cancer are complex and may involve multiple factors, such as age, genetics, lifestyle factors, infections, exposure to radiation, hormonal imbalances, chronic inflammation, and previous cancer treatments [4].

A. *Non-coding RNAs*

Non-coding RNAs (ncRNAs) play important regulatory roles in various cellular processes including gene expression, RNA splicing, and epigenetic modification [5]. Unlike coding RNAs, ncRNAs do not undergo translation into proteins, but instead interact with other cellular components to regulate gene expression or other cellular processes [6]. The field of non-coding RNA research has continued to expand and evolve, leading to the discovery of many new types of ncRNA with important biological functions.

1. microRNAs (miRNAs) and cancer

MicroRNAs (miRNAs), one of the best-known non-coding RNA molecules, play important roles in the cell, especially in gene expression. They are involved in post-transcriptional regulation and are involved in many biological processes such as growth, development, and disease [7]. miRNAs bind to messenger RNA molecules and inhibit protein synthesis or degrade the mRNA. By doing so, they can fine-tune gene expression and control the expression of lots of genes at once. Abnormalities in miRNA expression have been implicated in various diseases including cardiovascular diseases, neurological disorders, and cancer [8]. Thus, the levels of certain miRNAs in blood, tissue, or other biological samples are promising therapeutic targets for various diseases, and can be measured and used to diagnose or monitor cancer progression.

Studies have shown that changes in miRNA expression levels critical for development and progression of different types of cancer. In cancer, miRNAs can act as oncogenes (promoting cancer development) or tumor suppressors (inhibiting cancer development). Oncogenic miRNAs promote tumor development by inhibiting the expression of genes that regulate cell proliferation, apoptosis, and angiogenesis [9]. On the other hand, tumor suppressor miRNAs suppress the expression of oncogenic genes and promote cell death.

Some miRNAs have been identified as biomarkers for cancer diagnosis and prognosis, and some are being explored as potential therapeutic targets for cancer treatment. Thus, understanding the complex network of miRNA regulation in cancer is crucial for developing novel diagnostic and therapeutic strategies for cancer patients [10]. However, miRNA biomarker analysis is still in its early stages and more research is needed to establish its reliability and clinical utility.

1.1. Dysregulation of miRNAs in Cancer

miRNA dysregulation has been linked to the development and progression of various types of cancer. In cancer, miRNA expression is altered, resulting in changes in gene expression and leading to the undesirable growth and proliferation of cancer cells. miRNA expression levels may cause them to function as oncogenes or tumor suppressors [11]. Over-expression of oncogenic miRNAs can trigger tumorigenesis by targeting anti-tumor genes and increasing cell proliferation, while downregulation of tumor suppressor miRNAs can contribute to the development of cancer by reducing the activity of genes that inhibit cell growth and survival [12]. In addition, miRNA dysregulation in cancer can affect the immune system by altering the immune response genes. This can lead to the suppression of the immune response and the development of a microenvironment that is conducive to tumor growth and survival.

It is important to note that miRNA dysregulation is not a definitive cause of cancer, but rather a contributing factor to the development and progression of the disease. Aberrant expression of miRNAs has been observed in various types of cancer, including lung, breast, and colon cancer. For example, the over-expression of oncogenic miR-21 has been related to enhanced cell proliferation and resistance to chemotherapy in various cancers [13]. Similarly, the loss of expression of tumor suppressor miR-34 has been associated with the cancer progression and drug resistance [14]. Overall, dysregulation of miRNAs has a significant impact on cancer and is being actively studied for its potential as a diagnostic and therapeutic target.

In conclusion, the dysregulation of miRNAs in cancer is a complex and multi-faceted process that can contribute to the development and progression of the disease. More research is needed to fully understand the function of these extraordinary molecules in cancer and how they can be used to develop more effective therapeutic approaches.

2. Long non-coding RNAs and cancer

Long non-coding RNAs (lncRNAs) are transcripts of RNA that are longer than 200 nucleotides in length and do not encode proteins. LncRNAs have been shown to regulate several hallmarks of cancer, including cell proliferation, apoptosis, angiogenesis, and invasion. In particular, lncRNAs have been found to regulate gene expression by binding to specific DNA regions, modifying chromatin structure, or affecting the stability of mRNA. Since lncRNAs are known to be effective on gene expression, they are predicted to play a role in the development and progression of cancer [15]. Recent studies have shown that besides gene regulation, lncRNAs play roles in critical cellular processes such as RNA metabolism and critical epigenetic modifications. Some lncRNAs have been found to be overstimulated in cancer cells and contribute to the initiation and progression of the disease by modulating gene expression, influencing chromatin structure, and regulating key signaling pathways involved in cancer [16]. In particular, lncRNAs have been found to play a significant role in the development of cancer. Therefore, it is thought that lncRNAs can be used as ideal biomarkers in the diagnosis, prognosis and therapy of cancer.

2.1. Dysregulation of lncRNAs in Cancer

Dysregulation of lncRNAs plays a significant role in cancer and holds great potential as a therapeutic target. Studies have identified several lncRNAs that are abnormally expressed in cancer, including HOTAIR, ANRIL, and MALAT1, and CCAT2 [17]. These lncRNAs have been shown to contribute to cancer by promoting cancer cell survival, suppressing tumor suppressor genes, and altering chromatin structure to facilitate the activation of oncogenes.

2.1.1. HOTAIR

HOTAIR (HOX Transcript Antisense RNA), one of the most well-known lncRNAs in cancer, is involved in gene regulation, and is overexpressed in different cancer types [18]. It functions by binding to the polycomb group proteins which are responsible for repressing gene expression. HOTAIR contributes to the development and progression of tumors by silencing tumor suppressor genes. HOTAIR is also thought to be involved in the dysregulation of cancer related cellular processes, such as cell proliferation and differentiation [19].

HOTAIR is an epigenetic modulator that can manipulate gene expression and play a role in tumorigenesis [20]. In recent years, it has been implicated in various cancer types development. It is a known regulator of gene expression, and its dysregulation has been associated with cancer progression and poor patient outcome. HOTAIR is believed to play a role in the cancer development process by altering gene expression patterns and modulating the activity of important cellular pathways, such as the Wnt, Notch, and p53 pathways [21]. These pathways are involved in regulating cell growth, division, and death, and when they are altered, they can contribute to the development of cancer. Furthermore, HOTAIR has been shown to enhance the growth and survival of cancer cells and promote their ability to migrate and invade other tissues. This can contribute to the formation of metastasis, which is a major contributor to cancer-related deaths [22]. Overall, targeting HOTAIR may provide a potential therapeutic approach for the treatment of cancer.

Studies have shown that HOTAIR is overexpressed in various types of cancer, including breast, lung, prostate, and ovarian cancer. Its elevated levels in these cancers have been linked to increased tumor invasiveness, reduced patient survival rates, and the development of resistance to chemotherapy. Therefore, the measurement of HOTAIR levels in cancer tissues has emerged as a promising diagnostic tool [23]. High levels of HOTAIR expression can indicate the presence of cancer and its aggressiveness, which can help guide treatment decisions. Additionally, the measurement of HOTAIR levels can also be used to monitor the effectiveness of cancer treatments and to predict patient outcomes.

Overall, HOTAIR has shown great potential in the field of cancer diagnosis and prognosis, and ongoing research is exploring its full potential for the management of cancer patients.

2.1.2. ANRIL

ANRIL (Antisense Noncoding RNA in the INK4 Locus) is a lncRNA molecule located in chromosome 9. Studies have shown that ANRIL plays a crucial role in the regulation of gene expression and is involved in various biological processes, including angiogenesis, cell proliferation, apoptosis, and cell migration, and has been linked to several diseases, including cancer [24]. ANRIL is known to interact with other noncoding RNA molecules and regulatory proteins, altering the expression of genes that are critical for cell growth, proliferation, and differentiation. Moreover, it is involved in the regulation of chromatin modification and has been shown to influence the expression of tumor suppressor genes. ANRIL is overexpressed in several types of cancer, and is related with poor prognosis and treatment resistance [25]. Additionally, ANRIL has been shown to regulate key oncogenes and tumor suppressor genes, making it a promising target for the development of cancer therapies.

In recent years, there has been growing evidence to suggest that ANRIL may be a useful biomarker for cancer diagnosis [26]. For example, studies have found that ANRIL expression levels are often altered in cancer cells compared to normal tissue, making it a promising target for diagnostic testing. Additionally, ANRIL has been shown to have prognostic value in cancer patients, as high levels of ANRIL expression have been associated with more aggressive disease and poorer outcomes [27]. In conclusion, ANRIL holds potential as a diagnostic biomarker in cancer due to its involvement in cancer-related gene regulation and its potential prognostic value. Further studies are needed to determine the specific role of ANRIL in different types of cancer and to assess its diagnostic potential in the clinic. Further research is needed to understand the mechanisms by which ANRIL functions and its implications for disease.

2.1.3. MALAT1

MALAT1 (metastasis-associated lung adenocarcinoma transcript 1) is another important lncRNA involved in various cancer types. Studies have shown that high levels of MALAT1 are associated with a more aggressive form of cancer, increased tumor growth, and a poorer prognosis for patients. It is thought that MALAT1 promotes tumor progression by regulating gene expression and signaling pathways involved in cancer invasion and migration [28].

Previous studies showed that its expression increased in several types of cancer, has been shown to play a role in the development of drug resistance by regulating the expression of drug-resistance genes [29]. By regulating the expression of genes involved in drug resistance, MALAT1 can contribute to the development of tumors that are less responsive to chemotherapy and other forms of treatment [30]. Overall, the presence of MALAT1 in cancer cells is considered a negative prognostic factor and a potential target for the development of new cancer therapies.

2.1.4. CCAT2

CCAT2 stands for Cyclin A2-associated transcript 2. It is a lncRNA that has been implicated in the development and progression of various types of cancer [31]. CCAT2 has been shown to act as an oncogene, promoting tumor growth and invasion by regulating the expression of genes involved in cell proliferation, migration, and angiogenesis [32]. Additionally, CCAT2 has been implicated in drug resistance and metastasis in some cancer types [33]. Despite this, further research is needed to realize the exact function of CCAT2 in cancer and how it may be targeted for therapy.

II. CONCLUSION

In conclusion, non-coding RNAs, including miRNAs and lncRNAs, have been shown to play crucial roles in the development of cancer and are emerging as important targets for cancer therapy. Further research into the mechanisms by which ncRNAs regulate cancer development will provide new insights into the disease and may lead to the development of novel therapeutic strategies.

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