Impact of Nucleic Acids in Cancer Diagnosis

Frenidse Gorge*
Department of Biotechnology, V. G. Shivdare College, Solapur, Maharashtra, India

Corresponding Author*

Frenidse Gorge
Department of Biotechnology
V. G. Shivdare College
Solapur, Maharashtra, India
E-mail: gorgef423@gmail.com

Received: February 10, 2022, Manuscript No. OCCRS-22-54093; **Editor assigned:** February 14, 2022, Pre QC No. OCCRS-22-54093 (PQ); **Reviewed:** March 01, 2022, QC No. OCCRS-22-54093; **Revised:** April 12, 2022, Manuscript No. OCCRS-22-54093 (R); **Published:** April 20, 2022, DOI: 10.4172/2471-8556.22.009

Opinion

The coding genes that make about 1-2 percent of the human genome have been the focus of cancer research. Furthermore, the focus of cancer research in coding genes has been on genetic alterations and protein activities/functions. Noncoding genomic sections and noncoding RNAs, on the other hand, have received less attention, and are typically dismissed as genetic noise or by-products. Nonetheless, most cancer-related anomalies, including genetic mutations, are discovered outside of coding genes in genomic domains. The activities of noncoding RNAs in cancer have been discovered, cancer researchers have shifted their focus from the 1–2% coding genes of the human genome to the 98–99%noncoding transcripts. As a result, in most forms of cancer, a number of noncoding RNAs and their functional processes have been found and characterized. The changes of genomic DNA and RNA also shed light on the nucleic acid's functional mechanisms in cancer. Beyond the standard gene regulatory mechanism of transcription factors, other DNA changes influence the expression of coding and noncoding genes. Furthermore, RNA alterations affect both coding and noncoding RNAs' functional activity. As a result, scientists' perceptions of DNA and RNA as protein producers and by-products have shifted. Coding genes and proteins, on the other hand, are the accessories of nucleic acids, according to the nucleic acid-centered view in the post-central dogma world.

Exosome biology and its clinical relevance in oncology have gotten a lot of interest recently. Exosomes are tiny Extracellular Vesicles (sEVs) that are produced from diverse cells when multivesicular bodies fuse with the plasma membrane. They arise from Intraluminal Vesicles (ILVs) in the endosomal system. Exosomes can be found in a variety of physiological fluids, including blood, urine, saliva, and breast milk, and carry a variety of biological components from their mother cells, such as proteins, lipids, DNA, mRNAs, and Non Coding RNAs (ncRNAs). These exosomal payloads can be transferred to recipient cells from their parental cells. The Tumour Microenvironment (TME) is remodeled by exosome-mediated interactions between cancer cells and surrounding cells, generating favorable conditions for cancer development and metastasis.

Nucleic acids are also being studied as cancer biomarkers. Circulating nucleic acids are DNA and RNA fragments found not only in cancer cells but also in extracellular settings such as the circulation and bodily fluids. As a result, some disease-specific circulating DNA or RNA fragments in cancer patients may be useful diagnostic indicators. The unique nucleic acid markers expressed in cancer and/or circulating in extracellular settings will bring huge benefits in clinical cancer detection thanks to the convenience and accuracy of nucleic acid detection. Many researchers have begun to concentrate on the function and potential of DNA and RNA as primary targets in cancer research. Finally, increasing research interest in nucleic acids has increased research interest in the functions and mechanisms of nucleic acids, including RNA-binding proteins, DNA/RNA modifications, cell-free circulating DNA/RNA, and unique RNA subtypes such as tRNA fragments and circular RNAs, as well as well-established noncoding RNAs such as microRNAs and long noncoding RNAs.

Pathologists have exploited cellular morphology to aid in cancer diagnosis. The form, size, structure, and content of the nucleus are among the morphological traits that distinguish benign from malignant cells. Furthermore, nuclear morphologies are frequently pleiotropic within a single tumour, demonstrating cancer's diverse nature. During transformation, altered nuclear morphology reflects widespread alterations in genomic location as well as epigenetic changes. Recent studies demonstrate that broad epigenetic alterations are among the most visible and prevalent hallmarks of the cancer nucleus. Interactions between DNA and nuclear structural proteins such as nuclear lamins, as well as epigenetic changes, govern chromatin arrangement. These alterations and variations in nuclear structure are important markers that distinguish cancer cells from normal cells. Modifications in genome structure and epigenetic changes can potentially be tumorigenic by creating genomic instability, which is a hallmark of cancer.

Cite this article: Gorge F. "Impact of Nucleic Acids in Cancer Diagnosis". Oncol Cancer Case Rep, 2022, 8(4), 001.