



Significance of miRNAs with Increasing Usage in Recent Years

Suleyman Kaleli*

Professor, Department of Medical Biology, The Faculty of Medicine, Sakarya University, Turkey

***Corresponding Author:** Suleyman Kaleli, Professor, Department of Medical Biology, The Faculty of Medicine, Sakarya University, Turkey.

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In human genome, some DNA sequences are transcribed to RNA, although their protein translation is not in progress. Some of these non-coding RNAs have been found to play a role in gene expression regulation. These molecules, that are called microRNAs (miRNAs) because of composed of 22 nucleotide short sequences, were found to be overexpressed or decreased in several tumors and diseases [1]. For example, miR-15a and miR-16a genes were found in the 13q14 region frequently deleted in chronic lymphocytic leukemia and expression of these two miRNAs was reduced in about two-thirds of the cases [2].

The majority of miRNAs (61%) are found in intronic regions of protein-coding genes but they can also be found in intergenic regions of genes or exons. More than 50% of miRNA genes are in gene regions associated with cancer or fragile sites. This indicates that miRNAs have important roles in the pathogenesis of neoplasia [3].

In order to fully understand the functional importance of miRNAs and to make use of them for diagnostic or therapeutic purposes, it is necessary to determine how they are connected to their goals and how they regulate gene expression at different levels [4,5].

It has also been shown in several studies that the importance of miRNA has increased in many acute chronic diseases such as chronic venous diseases, psychiatry, diabetes mellitus, heart disease etc. Nowadays, analysis of miRNAs in blood sample is studied in routine laboratories. It is important that miRNA can be used as diagnostic markers due to its high stability in tissues and fluids. In addition, they can be measured in very low amounts of material and highly degraded samples. This is very important to support their possible use at the clinical level as emerging biomarkers [4-6].

As seen in recent studies, miRNA is on its way to becoming a potential biomarker in acute and chronic diseases, particularly cancer.

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