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"BIOINFORMATICS, CANCER MIRNA'S, AND BIOMARKERS: A GOLDEN TRIANGLE"

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Mature microRNAs (miRNAs) are a class of naturally occurring, small non-coding RNA molecules, about 21–25 nucleotides in length. MicroRNAs are partially complementary to one or more messenger RNA (mRNA) molecules, and their main function is to downregulate gene expression in a variety of manner, including translational repression, mRNA cleavage, and deadenylation. During the late stages of biogenesis of miRNA, in the cytoplasm, the pre-miRNAs undergo a processing step by the RNAse III enzyme Dicer, generating the miRNA, a double-stranded RNA aproximately 22 nucleotides in length. Dicer also initiates the formation of the RNA-induced silencing complex (RISC). RISC is responsible for the gene silencing observed due to miRNA expression and RNA interference.

Growing evidence shows that miRNAs exhibit a variety of crucial regulatory functions related to cell growth, development, and differentiation, and are associated with a wide variety of human diseases. Several miRNAs have been linked to cancer and heart disease. Expression analysis studies reveal perturbed miRNA expression in tumors compared to normal tissues. MicroRNAs are deregulated in breast, lung, and colon cancer, and upregulated in Burkitt's and other human B-cell lymphomas. As a consequence, human miRNAs are likely to be highly useful as biomarkers, especially for future cancer diagnostics, and are rapidly emerging as attractive targets for disease intervention. More recently, there has been growing interest in the field of miRNAs as biomarkers of cancer risk, diagnosis and response to therapy. Understanding the associations between miRNA expression and cancer phenotypes with aid of bioinformatics tools would potentiate profiling of miRNA in clinical applications which promises to be highly rewarding in the field of cancer research.