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Sommario/riassunto	Many researchers around the world have demonstrated that the expression of miRNAs is dysregulated in different tumors. Such dysregulation is caused by multiple mechanisms, and exposure to different carcinogens causes dysregulated epigenetic changes and defects in the miRNA biogenesis machinery. Cancer cells with abnormal miRNA expression evolve the capability to sustain proliferative signaling, evade growth suppressors, resist cell death, activate invasion and metastasis, and induce angiogenesis. Genome-wide profiling demonstrates that miRNA expression signatures are associated with tumor type, tumor grade and clinical outcomes, so miRNAs could be potential candidates for diagnostic biomarkers, prognostic biomarkers, therapeutic targets and preventive screening programs. Although miRNAs have multiple targets, their function in tumorigenesis is due to their regulation of a few specific targets. After the first detection of altered miRNA in leukemia, microRNAs have been demonstrated to be constantly altered in all cancer. More recently, microRNA has been shown to be altered by exposure to environmental carcinogens, thus driving the whole process of carcinogenesis. Our aim is to provide a rigorous peer review and publish cutting-edge research on the role of microRNA in cancer prevention therapy to educate and inspire the scientific community worldwide.