



سومین کنگره پزشکی مولکولی کشور

۲۵ و ۲۶ آذر ماه ۱۳۹۵

دانشگاه علوم پزشکی اصفهان



## MICRORNAs IN BREAST CANCER

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MicroRNAs (miRs) are a category of naturally noncoding, single-stranded short (18-22 nucleotides) RNA molecules. Experimental evidence indicates that miRNAs play an important role in many cellular functions and regulation of gene expression by targeting mRNAs and triggering either translation repression or RNA degradation. More than 50% of annotated human miRNA genes are located in fragile chromosomal regions that are susceptible to amplification, deletion, or translocation during the course of tumor development. Moreover, recent evidence indicates that some miRNAs can function either as oncogenes or tumour suppressors. Also, expression profiling analyses have revealed characteristic miRNAs signatures in certain human cancers. This review has focused on the potential role of miRNAs in breast cancer management. *HER2* gene amplification is as an indicator in early breast cancer. MiR-205 as a new oncosuppressor gene, able to interfere with the proliferative pathway mediated by HER receptor family. MiR-21, an increased biomarker, would correlate with the presence and extent of breast cancer. Hypermethylation of a CpG island upstream (-700 bp) of the miR-196a-2 precursor was associated with reduced breast cancer risk. MiR-335 and miR-126 are identified as metastasis suppressor microRNAs. MiR-155, miR-9 and miR-10b were found to be markedly upregulated in breast cancer cells. Also, studies have shown that Mir-125b, Mir-145 significantly deregulated in breast cancer tissues. In conclusion, this results show that specific miRNAs expression can be associated with specific stages of malignant progression with the hope that such associations might provide insights into the causal mechanisms of cancer and use as prognostic tools.

**Key Words:** miRNAs, breast cancer, prognostic, management