MicroRNAs expression profiles as novel biomarkers for the diagnosis, prognosis of breast cancer

Fouad M Badr
Suez Canal University, Egypt

MicroRNAs (miRNAs) are short, non-coding RNA molecules of 19-25 nt, involved in a wide array of physiological and pathological processes by modulating the expression of their cognate target genes through cleaving mRNA molecules or inhibiting their translation. In cancer, microRNAs can act as oncogenes or tumor suppressor genes. Oncogenic miRNAs may be amplified, resulting in increased expression of the oncomir. Tumor-suppressive miRNAs could reside in chromosome fragile sites characterized by deletions or mutations, leading to reduced levels of these miRNAs. Some miRNAs are emerging as a novel class of potential biomarkers for early breast cancer (BC) diagnosis, prognosis, and prediction of therapeutic outcomes. MiRNAs are of interest as easily accessible, affordable, non-invasive tools for the management of patients with BC. MicroRNA expression signature appears to provide a better characterization of cancer subtypes than gene expression profiling and may represent a new classification system for breast cancer. Abnormal microRNA expression patterns are closely related to specific tumor stages, lymph node, steps of the metastasis cascade, poor survival, disease outcomes and responses to specific therapies in many types of cancer. MicroRNA profiling has been assessed to differentiate patients with BC as responding or not responding to therapies. MicroRNA deregulation in the development of BC in several tissues and lineages, have correlated miRNA profiles with mRNA subtypes. In this review, the potential value of these microRNAs as diagnostic and prognostic markers, and the possible development of microRNA-based therapies will be assessed.

fmbadr@gmail.com