Abstract

**BACKGROUND:** miRNA-181a is a member of miRNA-181 family, recent studies have reported the involvement of miR-181a in diverse cellular functions. Though some studies have shown that miR-181a expression is downregulated in several human solid tumors, others have demonstrated that upregulation of miR-181a may promote metastasis and invasion of human cancers. **AIM OF THE STUDY:** The aim of this work is to detect the level of circulating miRNA-181a in breast cancer cases at different stages and to study its role in metastasis & epithelial mesenchymal transformation through the possible association between (mRNA 181 a) and (SNAIL-1), TGF–beta and proapoptotic protein Bim. **SUBJECTS AND METHODS:** The present work included 70 female patients, with breast cancer at different stages 30 patients with metastatic disease and 40 patients with non-metastatic disease 20 healthy subjects were taken as a control group. We detected miRNA-181a expression in peripheral blood with qRt PCR, and TGF-beta, SMAD-4, SNAIL-1 and Bim expression by quantitative PCR. **RESULTS:** we found that miRNA-181a, TGF-beta, SNAIL-1 and SMAD-4 were significantly upregulated significantly in patients with metastatic breast cancer compared to patients with non-metastatic disease. While Bim is significantly downregulated in metastatic versus non-metastatic group. We also found that miRNA-181a was a prognostic marker for disease progression and overall survival. **CONCLUSION:** We suggests the signaling pathway of TGF-beta through SMAD, SNAIL transcription factors and their association between miRNA-181a which play role in tumor aggressiveness and metastasis through EMT and possibly through down-regulation of Bim, proapoptotic protein.

**Key words:**

Breast cancer - metastasis – miRNA-181a- TGF beta- SNAIL/SMAD