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Implications of Methylated SFN Gene and MiRNA-200c on Pathogenesis of Breast Cancer

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Arab. J. Lab. Med. 2018; 43(2): 297-310

Abstract

Background: Breast cancer is considered the most popular malignant tumor among females in the world. Stratifin (SFN) gene encodes a cell cycle check-point protein that regulates translation. MicroRNAs are endogenous regulator for protein expression.

Objectives: The purpose of this study was to estimate the diagnostic potential of methylated SFN gene and MiRNA-200c in Egyptian women with breast cancer and detect the correlation between both.

Methods: We analyzed the expression of methylated SFN gene and MiRNA-200c using quantitative Real Time-PCR (qRT-PCR) in serum of 60 breast cancer patients, 30 fibroadenoma patients and 30 healthy controls.

Results: We found that 32 (53.3%) exhibited positive methylated SFN gene and 28 (46.7%) were negative. Among breast cancer patients; the methylated SFN gene was statistically significantly higher ($p=<0.001$) whereas the MiR-200c was statistically significantly lower ($p=<0.001$) in comparison with fibroadenoma group and control group. We detect significant association between invasive ductal carcinoma and positive SFN methylation ($p = 0.026$) and significant negative correlation between MiR-200c and methylated SFN gene in the study groups($r=-0.713$, P-value <0.001).

Conclusion: Our results revealed an association between each of SFN methylation and MiR-200c and development of breast cancer in Egyptian females. Thus, methylated SFN gene and MiR-200c might be utilized as biomarkers for early detection of breast cancer among high risk women, providing potential new strategies for early screening and therapy.

Key words: SFN gene, MiRNA-200c, breast, cancer