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Extended Abstract

Is mir125-a rs12976445 a significant predictor of the development of breast cancer in women?

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Abstract

Cancer is one of the main causes of mortality worldwide and the cancer deaths figure is estimated to reach 11 million by 2030 (Momenimovahed and Salehiniya, 2019). Among the cancers, breast cancer is the most common malignancy in women worldwide affecting more than 1 million women annually (Stuckey, 2011; Ghoncheh, et al., 2016). Breast cancer incidence varies widely, ranging from 27/100,0002 (Central-East Asia and Africa) to 85-94/100,0002 (Australia, North America and Western Europe) indicating that the environmental and genetic factors play significant role in incidence of breast cancer occurrence worldwide (Sancho-Garnier and Colonna, 2019). Considering the development and pathology of breast cancer, it is a highly heterogeneous cancer in its pathological characteristics, some cases showing slow growth with excellent prognosis, while others being aggressive tumors (Tao, et al., 2015). Despite many studies carried out to investigate the etiology of breast cancer, much of the etiology of this disease is unknown, however, many gene polymorphisms of breast cancer have been described as possible neoplasm etiologic factors (Bugano et al., 2008).

MicroRNAs (miRNAs) have been reported to have a pivotal role in gene regulation and the control of cancer-related mechanisms such as apoptosis and metastasis. miRNAs are short non-coding RNAs that are involved in post-transcriptional regulation of gene expression. miRNAs are transcribed by RNA polymerase II. The primary transcript is cleaved by the Drosha ribonuclease III enzyme to produce pre-miRNA, which is further cleaved by the cytoplasmic Dicer ribonuclease to generate the mature miRNA. The mature miRNA is incorporated into a RNA-induced silencing complex, which recognizes target mRNAs through imperfect base pairing with the miRNA and most commonly results in translational inhibition or destabilization of the target mRNA. Studies have shown that the miR-125 family acts as a tumor suppressor in breast cancer and inhibits ERBB2, ERBB3 and other target genes at post-

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transcriptional level. The miR-125 family has three homologues, hsa-miR-125a, hsa-miR-125b-1 and hsa-miR-125b-2 located at (19q.13.41), (11q.23) and (21q.21), respectively. Research shows ERBB2, HUR, ROCK-1, KLF13 and ARID3 genes are controlled by miR-125a. However, increased expression level of the genes is related to decreased expression of miR-125a, in breast cancer. Single nucleotide polymorphisms (SNP) of the miRNA encoding genes are believed to be involved in cancer development (Bahreini et al., 2020). Single nucleotide polymorphisms such as rs143525273, rs12975333, rs10404453 and rs12976445 are effective in miR-125a expression. Due to the increasing incidence of breast cancer and important role of miR-125a rs12976445 in the disease many studies have cited this single nucleotide polymorphism (Tang et al., 2015; Tang et al., 2019; Duna et al., 2007; Inoue et al., 2014; Deng et al., 2017; Bahreini et al., 2021).

In this study, blood samples were prepared from two groups: patients with breast cancern (approved by an oncologist) (n=51) and control healthy women (n=50) after obtaining written informed consent form. PCR-RFLP technique was used to determine miR-125a genotype. The data were analyzed using Chi-Square.

Our findings indicated that there was significant difference regarding rs12976445 genotype distribution between the control group and patients with breast cancer indicating that rs12976445 might be a predictor of the development of breast cancer in women.

Keywords: Braest cancer, miR-125a, rs12976445

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Conflict of interests

The authors declare that there are no competing interests.

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