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MOLECULAR GENETICS AND BREAST CANCER TREATMENT-A REVIEW

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Abstract:

In this review article, the databases Medline, Cochrane, Science Direct, and Google Scholar were thoroughly searched to identify the Molecular genetics and breast cancer treatment. In this review, the papers published until early January 2017, that was conducted to study the relationship between the Molecular genetics and breast cancer treatment were selected.

Key words: *cancer, breast cancer, and colorectal cancer*

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INTRODUCTION:

According to published statistics by the World Health Organization in 2011, cancer is the second leading cause of death after cardiovascular diseases throughout the world. The American Cancer Society announced in its latest report that out of every eight women, one is diagnosed with breast cancer [1]. The rate of cancer in developed countries is increasing from 1 to 0.2% and in developing countries about 0.5% annually. According to a report by the World Health Organization in 2011, cancer in Iran was reported to be 12% widespread and was recognized as the third most common cause of death [2]. Gastric cancer, breast cancer, and colorectal cancer are the three common cancers in Iran respectively. Breast cancer is the first place cancer widespread among women [3]. The average age of breast cancer diagnosis in the Western countries is 56 years and in Iran 45 years. New developments in the patients care with breast cancer have increased the overall survival rate of the patients in recent years. This increase in survival has doubled the importance of predictive factors of local recurrence and distant metastases of the disease [4]. In addition, it should be noted that the progression or regression of some diseases are not constant over time, as in the stages of recovery or worsening of the disease, the occurrence of some consequences changes the course of the disease, and the disease progress declines and this risk begins to decrease in the 2-5 years after treatment, which make the recovery process speed [5].

METHODS:

In this review article, the databases Medline, Cochrane, Science Direct, and Google Scholar were thoroughly searched to identify the Molecular genetics and breast cancer treatment. In this review, the papers published until early January 2017 that were conducted to study the relationship between the Molecular genetics and breast cancer treatment were selected.

FINDINGS:

Breast cancer is a heterogeneous disease. It has been believed for many years that tumors with different biological characteristics have different clinical results and therapeutic outcomes [6]. At present, the prognosis as well as the treatment selection for breast cancer is based on determining the status of growth hormone receptors [ER, PR, HER2] in the tumor. Four functional groups of tumor can be determined by using these indicators:

1. Positive hormone receptor and negative HER2
2. Negative hormone receptor and negative HER2 [triple negative tumor]
3. Tumors with too much HER2 or those lacking hormone receptor

Cell proliferation is an important feature of cancer and Ki67 Non-histone nuclear proteins are proper indicators for this process [7]. Ki67 staining can be used both as a durable indicator of proliferation and as an appropriate treatment indicator through various measurements on continuous tissue samples during the treatment process [8]. Some researchers have managed to classify different kinds of breast cancer to subcategories with different prognosis by using cDNA microarrays. These studies have applied hierarchical clustering analysis to identify subcategories having different gene expression patterns [9]. The differences existing in gene expression patterns of these subcategories indicate the fundamental differences in the cellular biology of these tumors that show itself through the clinical findings of these tumors. Clinical specialists consider the process method of these cellular subcategories as distinct diseases [10].

DISCUSSION AND CONCLUSION

Breast cancer tumors include heterogeneous groups of cells a small part of which is formed by the stem cells. Given their capabilities of proliferation and self-renewal, these cells effective in tumor creation process. The loss of self-renewal process regulation leads to the increase of stem cells and this is likely to affect the early stages of cancer formation [11]. The capability of miRNAs in the simultaneous regulation of several target genes have made them a good candidate for regulating the renewal process of stem cells and making decision about the fate of the cells [12]. There are numerous evidences that indicate special miRNAs are expressed differently in the stem cells. Destroying dicer, an important enzyme in the mRNA production process, is fatal for the embryos of mice and results in the destruction of stem cells population [13]. Moreover, in stem cells lacking dicer proliferation and distinction are disturbed. Furthermore, miRNAs are necessary in order to have the capability to dominate G1-S control point and conduct self-renewal. The identification and manipulation of these miRNAs can facilitate the population regulation of the stem cells affecting the formation of cancer. Discovering the role of miRNAs in the creation and development of human malignancies has made it possible to improve the current strategies of diagnosing and treating patients suffering from cancer [14]. The identification of new miRNAs, determining their target mRNA, and defining their functional effect will improve our awareness about the role of these indicators in the creation of different kinds of cancer including breast cancer and will provide new possibilities for the medical interventions needed.

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