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THE RELEVANCE OF RESIDENCY ON THE TUMOR SUPPRESSOR GENES MUTATION OF BREAST CANCER WOMEN AND THEIR RELATIVES

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ABSTRACT

Background

Breast cancer is characterized by various malignant tumors arise from breast tissues, Genetic factors, age, reproductive and hormonal factors, diet and environmental factors, socioeconomic factors and some types of benign breast disease are factors related to an increased risk of breast cancer. Tumor suppressor genes are genes whose loss of function results in the promotion of malignancy.

Aim of the Study

The present study was conducted to verify the relevance of residency on the tumor suppressor gene mutations in breast cancer women and their relatives

Material and Methods

Three groups of samples were included. The first consisted of 100 blocks of formalin-fixed, paraffin-embedded (FFPE) tissues of breast cancer women (group 1). The second contained blood samples of 46 breast cancer women (group 2). The third comprised blood samples of46 apparently healthy women who were relatives of the breast cancer patients of group two (group 3). The ages of patients of tissue samples were 46.78±11.5 years, while of blood samples patients were 47.34±11.18 years. The ages of the healthy relatives were 40.79±9.84 years. Five tumor suppressor gene mutations were examined. BRCA1 185delAG, BRCA1 5382insC and BRCA2 6174delT mutations were evaluated by mutagenically separated polymerase chain reaction, while CHEK2 1100delC and Tp53 exon 7 mutations were analyzed by RFLP.

Results

The amplification of *BRCA1*gene for185 delAG mutation revealed amplicons of 335 bp for the wild type and 354 bp for the mutant gene, whereas for 5382 insC mutation exhibited 2 amplicons of sizes 271 bp for the wild type and 295 bp for the mutant gene.

The analysis of *BRCA2*6174 delT mutation indicated 2 amplicons of 151 bp for the wild type and 171 bp for the mutant gene. *Tp53* exon 7 mutation analysis highlighted an amplicon of 125 bp size. Digestion of thisamplicon with the Hae III enzyme resulted in 2 fragments with sizes of 83 bp and 42 bp in the wild type. *CHEK2* 1100 delC mutation evaluation showed an amplicon of 116 bp size. Digestion of this applicant with Sca I enzyme exhibited 2 fragments with sizes of 92 bp and 24 before the wild type. Data analysis demonstrated that 27 (27%) out of the 100 enrolled breast cancer

patients of tissue samples have mutations in tumor suppressor genes, 11 (23.9%) out of 46enrolled breast cancer patients of blood samples have such mutations, while 8 (17.4%) out of 46 relatives have these mutations. Nine (9%) patients of group1 were indicated to have *BRCA1* 185delAGmutation, while 4 (8.7%) and 3 (6.5%) women from groups 2 and3 exhibited the same mutationrespectively. *BRCA1*5382insC mutation was identified in 7 (7%), 3 (6.5%) and 1 (2.2%) women of groups 1, 2 and 3 respectively. The *BRCA2* 6174delT mutation was observed in 5 (6%), 2 (4.3%) and 2 (4.3%) women of groups 1,2 and 3 respectively. Three (3%) patients of group1 and 1 (2.2%) and 1 (2.2%) women from groups 2 and 3 were found to have *CHEK2* 1100delC respectively. *Tp53*exon 7 mutation was evident in 2 (2%), 1 (2.2%) and 1 (2.2%) women of groups 1, 2 and 3 respectively. No patient had more than one mutation. Residency of breast cancer patients appeared to be independent of the distribution of tumor suppressor gene mutations.

Conclusions

About one quarter of the investigated breast cancer patients have mutations in their tumor suppressor genes and 17% of their relatives have such mutations. Residency of breast cancer patients and the relatives are independent on the tumor suppressor gene mutations.

KEYWORDS: Residency, Tumor Suppressor Genes Mutation, Breast Cancer