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TELOMERASE POLYMORPHISM AND BREAST CANCER

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Introduction: Breast Cancer is the most common type of cancer in women around the world. Recent numbers show an estimative of 252.710 new cases in the United States, which will be responsible for 40.610 deaths in 2017. Considering the importance of this data, we search in the literature factors that could contribute to the genesis of this type of tumor. Several studies have reported that the length of telomeres in solid tumor tissues may be a potential marker of prognosis. In addition, telomere shortening is associated to several prognostic factors in Breast Cancer. Telomeres cap the ends of linear chromosomes and play a role in maintaining genomic stability. They prevent chromosomes from shortening during DNA replication, by precluding chromosome ends from being recognized as double strand breaks that are targeted for repair, resulting in the improper joining of chromosome ends. The minimum essential components of telomerase are the catalytic subunit, telomerase reverse transcriptase (TERT), and a non-coding RNA (TERC); TERT reverse transcribes telomere DNA using TERC as the template. It was revealed that telomerase is activated in malignant cells, and that telomerase activation in cancers is closely related to acquired expression of TERT. Given the fundamental role of TERT in oncogenesis, polymorphisms of genes related to telomerase may influence the expression levels of this enzyme, influencing the host's susceptibility to tumor progression and metastasis. We aim to analyze the telomerase polymorphism in breast cancer patients and to test the correlation of such data with the prognosis and diverse clinical variables. **Methodology:** Experimental clinical study, in which the study population consisted of breast cancer patients who accepted to participate in the study, attended from March 2015 to September 2016 at Hospital Universitário de Brasília (HUB) and Cancer Center of Brasília (CETTRO). Standard extraction was performed by dehydration and precipitation with saturated NaCl solution, according to Miller, Dykes & Polesky (47) methodology. After extraction, DNA was diluted in ultrapure water (chromatographic grade). DNA concentration and purity were determined by spectrophotometry using the NanoDrop One equipment (Thermo Scientific, Madison, USA). DNA samples were aliquoted and frozen at -80°C. The Strategy was sequencing of the rs2736100 polymorphism region in the human hTERT gene after conventional PCR amplification. The primer sequences were: F: 5'-ATG CGA CAG TTC GTG GCT CA-3 'and R: 5'-ATC CCC TGG CAC TGG ACG TA-3' (Sigma Aldrich, Canada, 0.025 μmol). GraphPad Prism software version 7.02 was used for all analyzes. In addition, $p<0.05$ was considered statistically significant. **Results and Conclusion:** A total of 103 patients were selected for DNA analysis. All of them had the C allelic with the frequency of 0.79, and only 27 cases of T allelic with 0.21 of frequency. After the execution of analyzes, we found 41 cases of CC genotype, 23 cases of CT genotype and 3 cases of TT genotype. We also studied the polymorphism 92 (CC) and found that the CT polymorphism is related to a higher tumor grade, in this case grade 3 with p-value >0.0285. This relation shows that this polymorphism may be related to more aggressive tumors. Therefore, we found one among many crosses of telomerase polymorphisms with tumor characteristics.