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TRANSCRIPTION EXPRESSION OF IL-6 AND IL-1β GENES AND ITS RELATION WITH THE EFFICACY OF CHEMOTHERAPY IN WOMEN WITH BREAST CANCER

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Objective: Investigate differences in transcriptional levels of inflammatory markers in women with breast cancer (BC) submitted to chemotherapy (CT) or not, in order to identify possible biomarkers related to treatment efficacy. **Methodology:** This study was carried out in a university hospital with women who presented a positive biopsy result for BC. Women with BC were divided in two groups: patients not submitted to any antineoplastic treatment referred for elective breast surgery (n=21) and patients submitted to CT (n=24). Peripheral blood was collected at the surgical center prior to surgery, or during CT, before infusion of chemotherapy agents, and stored at -4oC until transcriptional processing and analysis. After extracting total RNA from blood samples and obtaining cDNA, the relative transcriptional quantifications of the target genes interleukin-1β (IL-1β), interleukin-6 (IL-6), interleukin-10 (IL-10) and tumor necrosis factor (TNFα) in relation to the endogenous gene β-2- microglobulin (B2M), were analyzed by real-time PCR (qPCR). Clinical and therapeutic data, such as histological tumor type and tumor receptors immunohistochemistry, were obtained from the analysis of the reports of anatomopathological exams. The model of generalized estimation equations (GEE) was used to verify the variation of IL-1β transcriptional levels regarding to tumor molecular phenotypes. **Results:** A significantly higher transcriptional expression of IL-6 in the BC group without CT was identified (p=0.05), suggesting the possible removal of tumor cells in the BC group with CT, since these cells have the ability to produce and release IL-6, by reducing the number of these cells, because CT reduces the levels of circulating IL-6. Significantly higher expression of IL-1β in BC group with CT (p=0.003) was also evidenced, indicating a possible association of this marker with the cytotoxicity promoted by chemotherapeutic agents. In addition, by analyzing the association graph of mean IL-1β transcriptional levels with the corresponding tumor molecular subtype, a change in IL-1β expression was identified according to the molecular phenotype variation and for BC group without CT was observed higher transcriptional means with the most aggressive molecular phenotype. **Conclusion:** We suggest a possible association between IL-6 and IL-1β expression level with CT efficacy, indicating the potential of these interleukins as therapeutic biomarkers.