Abstract: Breast cancer, a prevalent malignancy among women across the globe, poses a significant public health challenge on a worldwide scale. It is noteworthy that breast cancer constitutes one of the most frequently occurring solid tumor cancers. It is most important to recognize that this disease ranks second highest in terms of cancer-related fatalities amongst women. Fatty acid binding proteins (*FABPs*), intracellular lipid-binding entities, are implicated in a multitude of biological cellular mechanisms, including tumorigenesis. The primary function of *FABPs* resides in the regulation of fatty acid uptake and intracellular trafficking. Within the context of cellular biological processes, lipid-binding intracellular proteins, known as fatty acid transfer proteins, play a pivotal role in tumorigenesis. Acting as lipid chaperones, *FABPs* bind to both long-chain saturated and unsaturated fatty acids, as well as other hydrophobic ligands, such as eicosanoids, endocannabinoids, and monoacylglycerols. *FABP3* actively partakes in cell growth, proliferation, lipid transport, storage, and metabolism. In addition to binding long-chain fatty acids, *FABP4* exhibits the capacity to bind a diverse array of hydrophobic compounds, including cycloxygenases and oxidative derivatives of fatty acids. It is also involved in both glucose and lipid metabolism, and plays a role in signal transduction, cellular proliferation, and apoptotic processes. *FABP7*, a constituent of the expansive hydrophobic ligand-binding protein family, exerts its influence on transcription by interacting with nuclear receptors. Notably, this protein fosters the cellular uptake and transportation of fatty acids, while concurrently governing metabolic pathways, gene expression, and cellular growth. Consequently, it is apparent that PPARs also exert an impact on the development of various human diseases, such as diabetes and cancers. Pertaining to the *PPAR* family of nuclear hormone receptors, peroxisome proliferator-activated receptor-β/δ (*PPARβ/δ*) regulates an array of biological processes, including cell differentiation, cell proliferation, lipid accumulation, as well as glucose and fatty acid metabolism. *VEGF-A*, an extracellular glioprotein associated with cysteine dimer, serves as a pivotal modulator of vascular proliferation within mature tissues, including the mammary gland. The overexpression of *VEGF-A* by malignant cells fosters angiogenesis, thereby facilitating the sustenance of neoplastic expansion. In this study, the first objective is investigate the relative expression pattern of *FABP3*, *FABP4*, *FABP7*, *PPARβ/δ* and *VEGF-A* genes in the breast tissue of patients with breast cancer compared to the control

group (tumor peripheral tissue). The second objective is evaluate the expression of *FABP3*, *FABP4*, *FABP7*, *PPARβ/δ* and *VEGF-A* genes in the breast tissue of patients with breast cancer.

Materials and Methods: Within this investigation, we analyzed the expression pattern of genes *FABP3*, *FABP4*, *FABP7*, *PPARβ/δ* and *VEGF-A* within a statistical population of 50 individuals. This population consisted of 50 biopsy tissue samples obtained from patients with breast cancer (designated as cases). Additionally, 50 non-cancerous tissue samples adjacent to the tumor were procured from the same individuals (designated as controls). The employed methodology involved the application of quantitative Real-time Polymerase Chain Reaction (Real-time qPCR), utilizing the SYBR Green substance.

Results: *FABP4* and *VEGF-A* genes in Breast cancer patients had higher expression than the control group, but the *FABP3*, *FABP7*, *PPARβ/δ* gene had decreased expression in patients. A significant positive correlation was seen between *FABP3* with *FABP7* and *PPARβ/δ* genes But *FABP4* and *VEGF-A* genes don't have a significant correlation with three other genes. *FABP7* and *PPARβ/δ* genes don't have a significant correlation together. *FABP4* and *VEGF-A* genes don't have a significant correlation together.

Conclusion: increased *FABP4*, *FABP7* and *VEGF-A* genes expression and reduction of *PPARβ/δ* and FABP3 genes expression is effective in the progression and development of breast cancer malignancy. However, confirmation or rejection of this theory requires further studies.

Keywords: Breast Cancer, Gene Expression, PPARβ/δ, FABP3, FABP4, FABP7.