Introduction: Breast cancer is major cause of death related to cancer among women. A study in breast cancer shows that changes in serum levels of TRAIL and in expression of death receptors can be associated with the prognosis (1). Additionally, it is highlighted that CCL5, trigerring cancer microenvironment formation, take part in development and progression of cancer (2). In our study, it was aimed to evaluate serum death receptor (DR4) and CCL5 levels in patients with breast cancer.

Materials and Methods: Our study group includes 62 patients with breast cancer and 62 healthy individuals in the Department of General Surgery, Gazi University Medical Faculty Hospital. Serum levels of DR4 and CCL5 were measured at 450 nm using commercial ELISA kits. Data has been evaluated in SPSS 20.0 package program.

Results: Serum DR4 levels in breast cancer patients were found to be significantly higher than in the healthy control group ($p<0.01$). Although serum levels of CCL5 measured in patients were higher than in control, it was observed no significant change between patient and control groups ($p>0,05$). It were observed that correlation between TRAIL levels measured in previous study and CCL5 ($p<0,01$).

Conclusions: It is thought that increased DR4 levels in breast cancer patients may be associated with an induced extrinsic apoptotic pathway in the cancer pathophysiology. Relationship between CCL5 and TRAIL in our study support the thesis that increasing TRAIL levels may induce CCL5 production (3).

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P177: LACK OF ASSOCIATION BETWEEN VARIATIONS ON TOLL-LIKE RECEPTOR GENES AND BREAST CANCER IN MERSİN, SOUTHERN TURKEY

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Introduction: Breast cancer has been identified as the second type of cancer diagnosed among women worldwide. Breast cancer is a type of cancer that occurs as a result of genetic changes in cell groups that make up breast tissue. Cancer cells have distinctive features compared to normal cells. At the onset of the disease, it is believed to be the result of an accumulation of genetic damage resulting in activation of protooncogens and inactivation of tumor suppressor genes (1). The pathogenesis of breast cancer and a significant portion of breast cancer risk are thought to occur due to complex interactions and combinations between multiple environmental and genetic factors (2). Genes such as BRCA1, BRCA2, TP53 and ATM, which show a hereditary predisposition to breast cancer, have been identified. Genetic polymorphisms determined in these genes are very common in the general population (3). In recent years, the potential of genetic polymorphisms for breast cancer risk assessment has become increasingly evident and has been used as a marker (4). In the light of the available information, we aimed to investigate whether T399I and D299G polymorphisms are associated with coronary artery disease in the TLR-2 and TLR-4 genes, which is thought to be risk factors.

Material and Methods: In our study, those who applied to Mersin University Medical Faculty Hospital Oncology Department, were diagnosed with breast cancer as a result of routine examinations (n=102) and who were accepted as healthy (n=101) who were not diagnosed with breast cancer were included. The variation was determined using the Tetra-Primer ARMS PCR methodology.

Results: There was no significant difference in the polymorphisms of T>C (rs3804099) on TLR2 gene, and A>G (rs4986790) on TLR4 gene among case and control groups.

Conclusions: This study suggest that both of these polymorphisms of the TLR2 and TLR4 genes does not constitude a risk factor for susceptibility to breast cancer in a sample of Mersin population.

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