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Targeting drug metabolic gene expression in breast cancer

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Background & Aim: Breast cancer is one of the highest mortality rates and highest metastatic cancer of gynecological malignancies. Improving the results of chemotherapy has been slow and novel approaches to systemic treatment are needed. Each cancer cell from a given patient expresses a different array of drug-resistance genes. The aim of this study to evaluate the changes of some drug-resistance gene expression levels in patients with breast cancer.

Materials & Method: 44 patients with breast cancer, who underwent surgery, were divided into groups based on *TOP2A, ERCC1, TUBB3, TYMS, RRM1, STMN1,* hENT1 expression levels.

Result: Among women with breast cancer, 52.94% were patients with Epirupicin, Doxorubicin-resistant tumors, 24.44% were patients with 5FU, Capectabin, pemetrexed resistant tumors, 16.13% were patients with taxol, Docetaxol, Vinorelbin-resistant tumors, 6.0611.36% were patients with Gemistabine-resistant tumors, 11.11% were patients with platinum-based drug-resistant tumors. Furthermore, patients diagnosed with same breast cancer were affected to different chemotherapy combinations.

Conclusion: This suggests that gene expression analysis would be provided as a decision-making tool in the personalized and precision chemotherapy in every patient with breast cancer.

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