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# Role of glutathione S-transferase omega gene polymorphisms in breast-cancer risk

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ABSTRACT

**Background/aims.** Genetically influenced variations in the levels of activity and/or expression of some members of the glutathione S-transferase (GST) family have been identified as risk factors for cancer. One, GST omega (GSTO), has been found in a very limited number of studies. The aim of the present study was to investigate the influence of *GSTO1* and *GSTO2* polymorphisms on breast cancer risk.

**Methods.** DNA isolated from the blood of 101 patients with breast cancer and 151 healthy controls was investigated for *GSTO1* and *GSTO2* polymorphisms by polymerase chain reaction-restriction-fragment length polymorphism.

**Results.** Univariate and multivariate analyses showed no association between *GSTO1* and *GSTO2* genotypes and the risk of breast cancer. A higher prevalence of wild-type *GSTO1* (A140/A140) was significantly correlated with advanced-stage breast cancer (OR = 0.1, 95% CI, 0.01-0.77), but the presence of the genotype did not correlate with patient age at diagnosis, menopausal status, tumor size, lymph node metastasis, or estrogen-receptor status. No association was found between *GSTO2* genotype and clinicopathological features.

**Conclusions.** The results of the study suggest that *GSTO1* and *GSTO2* variants are not associated with breast cancer risk, but that wild-type *GSTO1* (A140/A140) is likely among cases at an advanced stage.

***Key words:*** breast cancer, gene polymorphism, glutathione S-transferase.

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