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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