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Associations between three XRCC1 polymorphisms and the hepatocellular carcinoma risk: a meta-analysis of case-control studies

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Abstract

Conflicting results have been obtained regarding the association between X-ray repair cross complementation group 1 (XRCC1) and susceptibility to hepatocellular carcinoma (HCC). In this study, associations between HCC and three polymorphisms (Arg194Trp, Arg280His, and Arg399Gln) were evaluated using a meta-ananlysis approach. PubMed, Web of science, Cochrane Library, the Chinese National Knowledge Infrastructure, and the Wanfang standard database were systematically searched to identify all relevant case-control studies published through March 2018. A total of 32 case-control studies, including 13 that evaluated Arg194Trp, 14 that evaluated Arg280His, and 26 that evaluated Arg399Gln, were analyzed. In the entire study population, XRCC1 Arg399Gln was significantly associated not only with the overall risk of HCC (homozygous model, OR = 1.53, 95% CI: 1.34–1.76, P = 0.00; recessive model, OR = 1.31, 95% CI:1.15–1.49, P = 0.00), but also with the risk of HCC in Chinese patients (homozygous model, OR = 1.78, 95% CI: 1.53–2.08, P = 0.00; recessive model, OR = 1.47, 95% CI: 1.27–1.70, P = 0.00). Limiting the analysis to studies demonstrating Hardy–Weinberg equilibrium (HWE), the results were consistent and robust. Similarly, a significant association between XRCC1 Arg399Gln and HCC risk was found in healthy controls in the general population but not in hospital controls. Trial sequential analysis (TSA), the false-positive report probabilities (FPRP) and the combined genotype analysis revealed that XRCC1 Arg399Gln is mainly associated with susceptibility to liver cancer. However, there was no association between Arg194Trp or Arg280His and the risk of HCC. These results, indicating that the Arg399Gln polymorphism of XRCC1 is associated with the risk of HCC in the Chinese population, provide a basis for the development of improved detection and treatment approaches.

Attachments

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