Association of XRCC1 gene polymorphisms and pancreatic cancer risk in a Chinese population

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ABSTRACT. We conducted a case-control study to assess the role of the XRCC1 Arg399Gln, Arg280His, and Arg194Trp gene polymorphisms in pancreatic cancer susceptibility in a Chinese population. A total of 152 patients diagnosed with pancreatic cancer and 264 control subjects were enrolled in this study between March 2012 and October 2014. XRCC1 Arg399Gln, Arg280His, and Arg194Trp were genotyped using the polymerase chain reaction-restriction fragment length polymorphism method. As determined by the chi-squared test, a statistically significant difference was observed between pancreatic cancer patients and control subjects in regard to the genetic distribution of XRCC1 Arg399Gln (χ² = 16.13, P < 0.001). Using an unconditional regression analysis, we found that the TT genotype of Arg399Gln was associated with a significantly increased risk of pancreatic cancer (OR = 2.33, 95%CI = 1.20-4.51), and that the CT+TT genotype also significantly increased pancreatic cancer risk (OR = 1.58, 95%CI = 1.04-2.41), compared to the wild-type genotype. In conclusion, we found that XRCC1 Arg399Gln genetic
variations are associated with pancreatic cancer development, whereas the XRCC1 Arg280His and Arg194Trp polymorphisms did not affect pancreatic cancer risk.

**Key words:** XRCC1; Arg399Gln; Arg280His; Arg194Trp; Polymorphism; Pancreatic cancer