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Association between *IL-10* genetic variations and cervical cancer susceptibility in a Chinese population

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ABSTRACT. We conducted an investigation into the role of the *IL-10* polymorphisms -592A/C (rs1800872), -819C/T (rs1800871), and -1082A/G (rs1800896) in cervical cancer risk in a Chinese population. A case-control study was carried out, including 165 newly diagnosed cervical cancer patients and 165 control subjects. The polymerase chain reaction-restriction fragment length polymorphism method was used to genotype the three *IL-10* variant loci. Using conditional logistic regression analysis, we observed that homozygous *IL-10* -819C/T TT carriers were at significantly increased risk of cervical cancer compared to homozygous CC individuals, with an adjusted odds ratio (OR) of 2.23 and a 95% confidence interval (CI) of 1.16-4.30. Moreover, the CT+TT genotype was significantly associated with cervical cancer in comparison to the wild-type variant (OR = 1.69, 95%CI = 1.04-2.76; P = 0.03). In conclusion, our study suggests that the *IL-10* -819C/T

genetic variation may contribute to cervical cancer risk in the Chinese population examined.

Key words: Interleukin-10; Polymorphism; Cervical cancer