The Relationship Between the PPAR δ -87T>C Polymorphism and Colorectal Cancer Risk in a Chinese Han Population

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Abstract

Background

Peroxisome proliferator-activated receptor- β/δ (PPAR β/δ) is a transcription factor that has the potential to be associated with the development of colorectal cancer (CRC). However, the exact role of PPAR δ in the context of CRC development remains to be clarified. This present study was thus designed to understand the association between CRC risk and the PPAR δ -87T>C single nucleotide polymorphism (SNP) in a western Chinese Han population.

Methods

The PPAR δ -87T>C (rs2016520) polymorphism was analyzed via the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) approach in 410 CRC patients and 496 frequency-matched healthy controls via a case-control study design. Relationships between PPAR δ -87T>C polymorphisms and clinicopathological parameters were assessed using Pearson chi-squared tests or Fisher's exact test. Odds ratios (ORs) and 95% confidence intervals (CIs) were used to evaluate the association between the PPAR δ -87T>C SNP and CRC risk. Results

We observed significant differences in genotypic frequencies when comparing CRC patients (TT 62%, TC 32%, and CC 6.1%) and controls (TT 65.5%, TC 32.3%, and CC 22%). In addition, PPAR δ -87T>C genotype was associated with tumor differentiation ($P=0.033$), but was unrelated to clinicopathological parameters in CRC patients. An unconditioned logistic regression model analysis revealed that individuals harboring the homozygous CC genotype exhibited an elevated CRC risk relative to those harboring the TT genotype (OR=2.931, 95% CI =1.41- 6.08; $P=0.004$).

Conclusions

Our findings indicate that the homozygous PPAR δ -87T>C CC genotype is associated with an elevated CRC risk as compared to the homozygous TT genotype, indicating that PPAR δ -87T>C polymorphisms have the potential to serve as a marker for CRC risk. Keywords PPAR δ , Colorectal cancer (CRC), Single nucleotide polymorphism (SNP), Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP)

Full Text

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Tables

Due to technical limitations, table 1 to 4 is only available as a download in the Supplemental Files section.

Figures

Lane M, 2000 bp marker ladder; lanes 1-3, TT genotype (bands at 239 bp); lanes 4-5, TC genotype (bands at 239-, 201- and 38 -bp); and lanes 6s CC genotype (bands at 201- and 38-bp).

Figure 1

Genotyping of the PPAR δ -87T>C polymorphism.

(A) wild-type homozygous TT genotype; (B) heterozygous TC genotype; (C) mutant homozygous CC genotype

Figure 2

A partial PPAR δ -87T>C polymorphism nucleotide sequence.

Supplementary Files

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