Int J Colorectal Dis (2007) 22:1185–1194
DOI 10.1007/s00384-007-0308-9

ORIGINAL ARTICLE

Microsomal glutathione S-transferase gene polymorphisms and colorectal cancer risk in a Han Chinese population

Hao Zhang · Ling-Hong Liao · Shuk-Ming Liu · Kwok-Wai Lau · Albert Kai-Cheong Lai · Jin-Hui Zhang · Qi Wang · Xiao-Qian Chen · Wei Wei · Hua Liu · Jian-Hua Cai · Maria Li Lung · Susan S. W. Tai · Madeline Wu

Accepted: 15 March 2007 / Published online: 5 May 2007

Abstract
Background and aims Glutathione S-transferases (GSTs) are phase II detoxification enzymes. Human GSTs have been classified into cytosolic, mitochondrial, and microsomal families. Several studies reported the association of colorectal cancer (CRC) risk with the genetic polymorphisms of cytosolic GSTs. The microsomal GSTs are structurally distinct but functionally similar to cytosolic GSTs; their association with CRC has not been reported. In this report, we summarized the result of a case-control study aimed at investigating the association of *MGST1* gene locus polymorphisms with CRC risk among Han Chinese.
Patient/methods Three hundred and seventy-two healthy controls and 238 sporadic CRC patients participated in this study. DNA resequencing was conducted for the 3.4 kb genomic DNA region containing the promoter, exons, exon–intron junctions, and the 5′ and 3′ untranslated regions.
Results We detected 13 single nucleotide polymorphisms (SNPs) including four novel SNPs not reported in database/literature. The gene shows a much higher nucleotide diversity than most human genes. The linkage and recombination analysis revealed 24 common haplotypes (13%≥freq≥1%) and identified extensive intragenic recombination throughout the *MGST1* locus (R=81.8). Significant CRC association (P <=0.005) was not detected for each individual SNP. However, SNPs 102G>A and 16416G>A reached a marginal level of statistical significance with P values of 0.016 and 0.078, respectively. A combined genotype analysis detected

H. Zhang (✉) · L.-H. Liao · S.-M. Liu · M. L. Lung · M. Wu
Department of Biology,
Hong Kong University of Science and Technology,
Clear Water Bay,
Kowloon, Hong Kong SAR,
People's Republic of China
e-mail: bollh@ust.hk

K.-W. Lau · A. K.-C. Lai
Department of Surgery, Tuen Mun Hospital,
Hong Kong SAR, People's Republic of China

J.-H. Zhang · Q. Wang
Department of Respiratory,
the Second Hospital affiliated to Dalian Medical University,
Dalian, People's Republic of China

X.-Q. Chen
Department of Pathophysiology,
Tongji Medical College,
Huazhong University of Science and Technology,
Wuhan, People's Republic of China

W. Wei
Mammary Gland Surgical Department,
Peking University Shenzhen Hospital,
Shenzhen, People's Republic of China

H. Liu
Ankang Hospital,
Jinin, People's Republic of China

J.-H. Cai
Institute of Genetics, Fudan University,
Shanghai, People's Republic of China

M. L. Lung · M. Wu
Center for Cancer Research,
Hong Kong University of Science and Technology,
Hong Kong, People's Republic of China

S. S. W. Tai
Mochtar Riady Institute for Nanotechnology,
Jl. Boulevard Jend. Sudirman,
Lippo Karawaci Tangerang, Indonesia 15811