World Journal of Gastroenterology

Online Submissions: http://www.wjgnet.com/1007-9327office
wjg@wjgnet.com
doi:10.3748/wjg.v18.i21.2668

World J Gastroenterol 2012 June 7; 18(21): 2668-2673
ISSN 1007-9327 (print) ISSN 2219-2840 (online)

BRIEF ARTICLE

Risk modification of colorectal cancer susceptibility by interleukin-8 -251T>A polymorphism in Malaysians

Mohd Aminudin Mustapha, Siti Nurfatimah Mohd Shahpudin, Ahmad Aizat Abdul Aziz, Ravindran Ankathil

Mohd Aminudin Mustapha, Siti Nurfatimah Mohd Shahpudin, Ahmad Aizat Abdul Aziz, Ravindran Ankathil, Human Genome Centre, School of Medical Sciences, Universiti Sains Malaysia Health Campus, Kubang Kerian, Kelantan 16150, Malaysia

Author contributions: Mustapha MA, Mohd Shahpudin SN and Abdul Aziz AA collected samples; Mustapha MA performed research and drafted the paper; Ankathil R designed the research, and corrected and revised the paper.

Supported by USM Research University Grant, No. 1001/PPSP/812032

Correspondence to: Dr. Ravindran Ankathil, Professor, Human Genome Centre, School of Medical Sciences, Universiti Sains Malaysia Health Campus, Kubang Kerian, Kelantan 16150, Malaysia. rankathil@hotmail.com
Telephone: +60-9-7676968 Fax: +60-9-7658914

Received: August 10, 2011 Revised: September 22, 2011
Accepted: February 27, 2012
Published online: June 7, 2012

Abstract

AIM: To investigate the allele and genotype frequencies and associated risk of interleukin (*IL*)-8 -251T>A polymorphism on colorectal cancer (CRC) susceptibility risk.

METHODS: Peripheral blood samples of 255 normal controls and 255 clinically and histopathologically confirmed CRC patients were genotyped for *IL-8* -251T>A polymorphism employing allele-specific polymerase chain reaction. The relative association of variant allele and genotypes with CRC susceptibility risk was determined by calculating the odds ratios (ORs). Corresponding χ^2 tests on the CRC patients and controls were carried out and 95% confidence intervals (CIs) were determined using Fisher's exact test. The allele frequencies and its risk association were calculated using FAMHAP, haplotype association analysis software.

RESULTS: On comparing the frequencies of genotypes of patients and controls, the homozygous variant AA was significantly higher in CRC patients (P = 0.002) compared to controls. Investigation on the association of the polymorphic genotypes with CRC susceptibility risk, showed that the homozygous variant *IL-8* -251AA had a significantly increased risk with OR 3.600 (95% CI: 1.550-8.481, P = 0.001). In the case of allele frequencies, variant allele A of *IL-8* -251 showed a significantly increased risk of CRC predisposition with OR 1.32 (95% CI: 1.03-1.69, P = 0.003).

CONCLUSION: Variant allele and genotype of *IL-8* (-251 T>A) was significantly associated with CRC susceptibility risk and could be considered as a high-risk variant for CRC predisposition.

Key words: Interleukin-8 -251T>A; Polymorphism; Colorectal cancer; Malaysians

Peer reviewer: Francesco Feo, Professor, Department of Biomedical Sciences, Section of Experimental Pathology and Oncology, University of Sassari, Via P Manzella 4, 07100 Sassari, Italy

Mustapha MA, Mohd Shahpudin SN, Abdul Aziz AA, Ankathil R. Risk modification of colorectal cancer susceptibility by interleukin-8 -251T>A polymorphism in Malaysians. *World J Gastroenterol* 2012; 18(21): 2668-2673 Available from: URL: http://www.wjgnet.com/1007-9327/full/v18/i21/2668.htm DOI: http://dx.doi.org/10.3748/wjg.v18.i21.2668

INTRODUCTION

Colorectal cancer (CRC), the incidence of which has been increasing worldwide for the past few years, represents a significant cause of morbidity and mortality. CRC develops as a result of progressive accumulation of genetic and epigenetic alterations that lead to a series of histo-