

XPC Lys939Gln polymorphism, smoking and risk of sporadic colorectal cancer among Malaysians

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Author contributions: Ahmad Aizat AA, Siti Nurfatimah MS and Aminudin MM collected samples; Ahmad Aizat AA performed the research and drafted the paper; Ankathil R designed the research, corrected and revised the paper.

Supported by Fundamental Research Grant Scheme (FRGS), No. 203/PPSP/6171112

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Received: September 26, 2012 Revised: December 24, 2012

Accepted: March 8, 2013

Published online: June 21, 2013

frequencies, variant allele C was associated with a significantly increased risk of CRC (OR = 1.375; 95%CI: 1.050-1.802; $P = 0.020$). Moreover, the risk was markedly higher for those who were carriers of the Gln/Gln variant genotype and were also cigarette smokers (OR = 3.409; 95%CI: 1.061-10.949; $P = 0.032$).

CONCLUSION: The XPC Gln/Gln genotype alone and in combination with smoking increases the risk of CRC among Malaysians.

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Key words: DNA repair; Xeroderma pigmentosum group C Lys939Gln polymorphism; Cigarette smoking; Colorectal cancer; Susceptibility risk

Ahmad Aizat AA, Siti Nurfatimah MS, Aminudin MM, Ankathil R. XPC Lys939Gln polymorphism, smoking and risk of sporadic colorectal cancer among Malaysians. *World J Gastroenterol* 2013; 19(23): 3623-3628 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v19/i23/3623.htm> DOI: <http://dx.doi.org/10.3748/wjg.v19.i23.3623>

Abstract

AIM: To investigate the risk association of xeroderma pigmentosum group C (XPC) Lys939Gln polymorphism alone and in combination with cigarette smoking on colorectal cancer (CRC) predisposition.

METHODS: Peripheral blood samples of 510 study subjects (255 CRC patients, 255 controls) were collected. DNA was extracted and genotyping was performed using polymerase chain reaction-restriction fragment length polymorphism. The association between polymorphic genotype and CRC predisposition was determined using the OR and 95%CI.

RESULTS: The frequency of the homozygous variant (Gln/Gln) genotype was significantly higher in cases compared with controls (16.0% vs 10.2%, $P = 0.049$). The Gln/Gln genotype of XPC showed a significantly higher association with the risk of CRC (OR = 1.884; 95%CI: 1.082-3.277; $P = 0.025$). In the case of allele

INTRODUCTION

Colorectal cancer (CRC) is a major public health problem worldwide, being the third most common cancer and the fourth most common cancer causing death^[1]. In Malaysia, CRC has become the most common cancer among males and the second most common among females^[2]. The development of CRC is a complex, multistep process involving interaction between environmental and genetic factors. Environmental factors such as dietary and lifestyle habits, smoking, alcohol consumption, and obesity interact with host's genetic factors, especially genetic variations, and may modulate the risk of CRC^[3]. Genetic variations, such as single nucleotide polymorphisms (SNPs), may increase the sensitivity to environmental