# UNIVERSITI SAINS MALAYSIA GERAN PENYELIDIKAN UNIVERSITI PENYELIDIKAN LAPORAN AKHIR

## IDENTIFICATION PREDISPOSITION GENOTYPES THAT CONTRIBUTE TO COLORECTAL CANCER SUSCEPTIBILITY IN MALAYSIA

## **PENYELIDIK**

PROF. DR. RAVINDRAN ANKATHIL

### PENYELIDIK BERSAMA

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PROFESOR DR. ZILFALIL ALWI
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SITI NURFATIMAH SHAHPUDIN
AHMAD AIZAT ABDUL AZIZ



## **FINAL REPORT FUNDAMENTAL RESEARCH GRANT SCHEME (FRGS)**

Laporan Akhir Skim Geran Penyelidikan Asas (FRGS) IPT Pindaan 1/2009

RESEARCH TITLE Tajuk Penyelidikan

: IDENTIFICATION OF PREDISPOSITION GENOTYPES THAT CONTRIBUTE TO COLORECTAL CANCER SUSCEPTIBILITY IN MALAYSIA

PROJECT LEADER : PROF. DR RAVINDRAN ANKATHIL

Ketua Projek

(including GRA) Ahli Projek

PROJECT MEMBERS: 1. Prof Biswa Mohan Biswal

2. Dr Muhammad Radzi Abu Hassan

3. Assoc.Prof Gurjeet Kaur

4. Dr Venkatesh Naik

5. Prof Dr Zilfalil Alwi

6. Dr Hoh Boon Peng

7. Dr Ahmad Shanwani Mohd Sidek

8. Dr Zaidi Zakaria

9. Siti Nurfatimah Shahpudin (MSc student)

10. Ahmad Aizat B Abdul Aziz (Msc student)



### PROJECT INCESTIGATIONS PROJECT PROJECT

В

HIEVEMENT PER	CENTAGE	
0 - 50%	51 - 75%	76 - 100%
		X
	0 - 50%	

## RESEARCH FINDINGS

5 ernational	7 National
rnational	National
	Ivational
5	6
	5

#### **HUMAN CAPITAL DEVELOPMENT**

Human Canital	Nu	mber	Others (Plance specific):
Human Capital	On-going	Graduated	Others (Please specify):
PhD Student			
Masters Student		2	
Undergraduate Students			
Temporary Research Officer	•		
Temporary Research Assistant		•	
Total			

# Daffallinual Personem

C Budget Approved (Peruntukan diluluskan) : RM 149,500.00 Amount Spent (Jumlah Perbelanjaan) : RM 149,499.77

Balance (Baki) : RM 0.23
Percentage of Amount Spent : 99.99 %

(Peratusan Belanja)

reilla	tional_	B.C. (Mana) 37			
	Activity	Date (Month, Year)	Organizer		
onfere	ence:				
Human Genome Meeting,     Pan Arab Human Genetics     Conference		14-17 March 2011, Dubai	Human Genome Organization		
2.	International Conference on Advancement in Science and Technology, 2010	26-29 November 2010, Vistana Hotel, Pahang.			
3.	Asia Pacific Digestive Week 2010	9-22 September 2010, Kuala Lumpur Convention Centre, Malaysia	WILEY-BLACKWELL and Journal Gastroenterology and Hepatology Foundation		
4.	Asia Pacific Conference on Human Genetics	30th Nov- 3rd Dec 2010, Hong Kong	Hong Kong Academy of Medicine		
5.	3rd Regional Conference on Molecular Medicine	2-4 May 2009, Kota Bharu, Kelantan, Malaysia.	USM, INFORMM, UITM & MSAP		
lation	al				
	Activity	Date (Month, Year)	Organizer		
onfer	ence:		<del>'</del>		
1.	1st National Postgraduate Conference in Molecular Medicine, 2011	13-14 April 2011,Kota Bharu, Kelantan	USM, INFORMM & UMBI		
2.	16th National Conference on Medical and Health Sciences	22-23 June 2011, USM, Health Campus, Kelantan	School of Medical Sciences		
3.	2 <sup>nd</sup> National Conference on Environment and Health 2010	17-18 March 2010 (Renaissance Hotel, Kota Bharu, Kelantan)	School of Health Sciences and PERSALA, USM		
4.	15 <sup>th</sup> National Conference on Medical and Health Sciences	21-22 July 2010 ( Grand Riverview Hotel, Kota Bharu, Kelantan)	School of Health Sciences, USM		
5.	8th Malaysia Genetics Congress, 2009	4-6 August 2009, Awana Genting, Pahang	Persatuan Genetik Malaysia, UKM UPM and MOSTI		

Ε

Although this is the first comprehensive study on the association of SNP in xenobiotic metabolizing and DNA damage repair genes in Malaysian population, the study has been limited by the small sample size due to short time period and budget. Because of this, large number of samples could not be included. For the same reason, the frequency of variant allele observed for certain SNPs were too small or sometimes nil which must have resulted in inadequate in statistical power.

During risk analysis of combination of genotypes, the infrequent presence or rarity of at-risk genotype or allele, for some of the combination SNPs studied resulted in deriving risk association values with high ORs values, but with extremely wide range of 95% confidence intervals. Such combinations genotypes were not considered as high risk predisposition genotypes despite the high ORs obtained.

Malaysian population comprises 3 major ethnic groups; Malay, Chinese and Indian with a ratio of approximately 60:30:10, respectively. Different the ethnic races have different genetic background. The difference in genetic background of the study subjects which comprised these 3 ethnic races was not taken into account and this was another limitation. A stratified analysis based on ethnicity with equal number of the study subjects in each ethnic group, could have given better results with adequate power.

The study subjects in this study were recruited from differing collaborating hospitals in Malaysia. From some of the hospitals, it was difficult and unable to get many of the epidemiological and clinicopathological details of the case subjects. So the interaction of confounding factors like lifestyle habits (smoking, alcohol consumption), dietary habits etc with the SNP included in the study could not be examined.

Even though the incidence of CRC is increasing in Malaysia, there is paucity of information on the nature of genetic predisposition factors that contribute to susceptibility to CRC in Malaysian patients, as no previous studies have been undertaken in Malaysia. Moreover, report on the association of SNPs in Xenobiotic metabolizing and DNA repair genes as genetic predisposition factors for CRC susceptibility from other population are inconsistent. To the best of knowledge, this is first study from Malaysia on this aspect. From this study, few Xenobiotic metabolizing and DNA repair SNPs and combination SNPs associated with CRC susceptibility risk in Malaysian population have been identified.

In future, advances in SNP mapping utilizing high throughout genotyping methods could facilitate the analysis of multiple polymorphisms within DNA repair genes and also the analysis of multiple gene within DNA repair pathways. This may lead to the advancement of knowledge on genetic predisposing factors related to CRC susceptibility in Malaysian population. This, in turn, may help to identify the high risk individuals with CRC susceptibility risk genotype in the population and devise appropriate preventive screening strategies for them. Regular, frequent and effective screening for CRC is not currently available at the population level. The public perception of genetic determinism is that, if the polymorphic at risk, genotype status of an individual is known, the cancer predisposition status of that individual can be predicted and appropriate surveillance programs can be initiated by allowing more effective prevention strategies. By this, morbidity and mortality of CRC can be reduced at the population level.

Furthemore, the detection of protective nature of few SNPs, is an interesting observation which may have a great impact in evaluating the treatment response of CRC patients carrying the specific genotypes. So it would be ideal to associate the genotype pattern with the treatment response and survival of these CRC patients.

The incidence of sporadic colorectal cancer (CRC) is increasing in Asian countries, including Malaysia. Although several factors have been implicated in CRC etiology, CRC develops as a result of interaction between environmental factors and genetic predisposition. Exposure to environmental carcinogens through dietary components and cigarette smoke are associated with an increased risk of CRC. However, the genetic predisposition factors associated with CRC development remains still undetermined. It was hypothesized that genetic variations such as single nucleotide polymorphisms (SNPs) in xenobiotic metabolism and DNA damage repair genes could have effects on the sensitivity of individuals to environmental genotoxins and may influence CRC susceptibility. In order to clarify the role of xenobiotic metabolizing and DNA repair genes in colorectal carcinogenesis, a case-control study was designed and undertaken to investigate the genotype frequencies of 10 polymorphisms from 6 genes encoding enzymes involved in xenobiotic metabolism (GSTT1, GSTM1, GSTP1 Ile105Val, CYP1A2 G3860A, CYP1A2 T739G, CYP1A2 C729T, NAT1 C1095A, NAT2 G191A, NAT2 A803G, NAT2 G857A) and 4 polymorphisms in genes involved in DNA damage repair (XRCC1 Arg399Gln, XRCC3 Thr241Met, XPD/ERCC2 Lys751Gln and P53 Arg72Pro) and to determine their influence, either singly or as combination genotypes, in CRC susceptibility risk. After getting informed consent, peripheral blood of all study subjects were collected, DNA extracted and genotyping carried out using PCR- RFLP and multiplex PCR methods. Genotypes were categorized into homozygous major, heterozygous variant and homozygous variant. The risks of CRC associated with these polymorphisms were estimated by calculating Odds Ratios (ORs) and 95% confidence intervals using unconditional logistic regression. For the risk association of xenobiotic metabolism genes and CRC susceptibility, CYP1A2 A3860A, CYP1A2 T739G, GSTP1 val/val genotypes and GSTT1 null showed significant risk association with CRC predisposition. When analyzed in 2 way combinations, remarkably increased risk was observed for carriers of CYP1A2 A3860A/T739T, GSTT1 (-/-)/ GSTM1(-/-), (GSTT1 (-/-)/ GSTP1 Ile/Ile), (GSTT1 (-/-)/ GSTP1 Ile/Val) genotype combinations. In triple genotype combination analysis, the GSTM1 (-/-)/GSTT1 (-/-)/ GSTP1 Ile/Ile) genotype combination emerged as high risk predisposition genotype associated with CRC susceptibility risk. In case of DNA damage repair genes and CRC susceptibility risk, homozygous variant P53 Pro72Pro showed significantly higher risk

association with CRC susceptibility. When analyzed in 2 way combinations, the genotype combinations of XRCC3 Thr/Thr+P53 Pro/Pro emerged as high risk combination genotypes associated with CRC susceptibility. It is reasonable to suggest that SNPs studied in xenobiotic metabolism genes might be promoting CRC susceptibility through their capability of increased activation of chemical carcinogens and/or decreased ability of cells to detoxify carcinogens. So also, whereas SNPs in DNA amage repair might be promoting colorectal carcinogenesis by altering the respective DNA repair gene expression and modulating the DNA repair function and thereby enhancing the CRC susceptibility risk. In conclusion, the SNPs in xenobiotic metabolism and DNA damage repair genes, showing significant risk association with CRC predisposition, either singly or in combination, may be considered as candidate genetic predisposition factors associated with CRC susceptibility risk in Malaysian population. PROF. (DR) RAVINDRAN ANKATHIL Project Leader's Signature Professor Date 15-04-2012. Tandatangan Ketua Projekchool of Medical Science Tarikh Health Campus Universiti Sains Malayı 18150 Kubang Kerlan, Kelantan, Majayela COMMENTS, IF ANY/ENDORSEMENT BY RESEARCH MANAGEMENT CENTER (RMC) (Komen, sekiranya ada/ Pengesahan oleh Pusat Pengurusan Penyelidikan) Signature: Name: Tandatangan: Nama:

Date: Tarikh:

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#### JABATAN BENDAHARI KUMPULAN WANG PENYELIDIKAN FUNDAMENTAL PENYATA PERBELANJAAN SEHINGGA 31 JUL 2011

Jumlah Geran

RM149,500.00

Ketua Projek

PROF. RAVINDRAN ANKATHIL

Peruntukan (Tahun 1) RM49,400.00

Okt 07-Okt 08

Tajuk Projek

**IDENTIFICATION OF PREDISPOSITION** 

GENOTYPES THAT CONTRIBUTE TO COLORECTAL

CANCER SUSCEPTIBILITY IN MALAYSIA

Peruntukan (Tahun 2) RM57,000.00

Okt 08-Okt 09

Tempoh

42 BULAN (15/10/2007-15/04/2011)

Peruntukan (Tahun 3) RM43,100.00

Okt 09-Okt; 10

No. Akaun

203/PPSP/6171112

Kwgan	Akaun	PTJ	Projek	Peruntukan Projek	Perbelanjaan Terkumpul	Peruntukan Semasa	Tanggungan Semasa	Bayaran Tahun	Belanja Tahun	Baki Projek	
				•		sehingga Tahun lalu			Semasa	Semasa	•
203	11000 I	PSP	6171112	36,000.00	45,627.45	(9,627.45)	-	5,345.10	5,345.10	(14,972.55)	
203	14000 F	PSP	6171112	1	-	-	-		-	-	
203	15000 F	PSP	6171112	•	1,000.00	(1,000.00)	-		•	(1,000.00)	
. 203	21000 F	PPSP	6171112	3,800.00	5,331.30	(1,531.30)	-		-	(1,531.30)	
203	22000 T	<b>P</b> SP	6171112	2,100.00	•	2,100.00	•	-	•	2,100.00	
203	23000 F	PSP ·	6171112	1,400.00	410.85	989.15	-	52,76	52.76	936.39	
203	24000 F	PSP	6171112		80.00	(80.00)	. •		•	(80.00)	
203	26000 I	PSP	6171112	.1	(	-	-	•	-	-	
203	27000 F	PSP	6171112	88,300.00	52,030.00	36,270.00		885.06	885.06	35,384.94	
. 203	28000 I	PSP	6171112	900.00	-	900.00		•	-	900.00	
203	29000 F	PSP	6171112	17,000.00	35,682.30	(18,682.30)		3,054.95	3,054.95	(21,737.25)	
203	35000 F	PSP	6171112	-	-	-	-	-	-	-	
203	A11559 F	PSP	6171112	-	-	_		-	-	-	
203	. A11102 F	PSP	6171112	_	-	į -		•	•	-	
				149,500.00	140,161.90	9 338.10	-	9,337.87	9,337.87	0.23	