## UNIVERSITI TEKNOLOGI MARA

# POTENTIAL ROLE OF LDLR IN FAMILIAL HYPERCHOLESTEROLEMIA

## CANNILIA ANAK KERINE

Dissertation submitted in partial fulfillment of the requirements for the degree of Bachelor of Pharmacy (Hons.)

## **ACKNOWLEDGEMENT**

Firstly, I would like to express my deep gratitude to my supervisor, Dr John Shia Kwong Siew for his advice and guidance throughout this thesis. I would also like to thank the Head of Pharmacogenomics Centre (PROMISE), Prof. Dr Mohd Zaki Salleh, Prof. Dr Tay Lay Kek and Mdm Siti Nooraishah Hussin for their advice and assistance in the preparing my research study. My special thanks is extended to the staff and post-graduate students of PROMISE especially Miss Ismanura'in Binti Ibrahim, Miss Irma Syakina Binti Mohd Zaki, Miss Ili Nursafra Binti Tedin Ng and Miss Nur Jalinna Binti Abdul Jalil for their cooperation and kindness in assisting as well as guiding me throughout the entire process of completing my research. Lastly, I would like to thank my family and friends for their utmost support.

# TABLE OF CONTENT

		Page
TIT	LE PAGE	
API	PROVAL SHEET	
AC	KNOWLEDGEMENT	ii
LIS	T OF TABLES	v
LIS	T OF FIGURES	vi
LIST OF ABBREVIATIONS		vii
ABS	STRACT	viii
CH	APTER 1: INTRODUCTION	
1.1	Background of study	1
1.2	Problem Statement.	2
1.3	Hypothesis	3
1.4	Objectives	3
1.5	Significance of studies	3
СН	APTER TWO : LITERATURE REVIEW	
2.1	Cholesterol and Lipoproteins	5
2.2	High Density Lipoprotein and Low Density Lipoprotein	5
2.3	Hypercholesterolemia	7
2.4	Obesity.	10
2.5	Familial Hypercholesterolemia.	12

### **ABSTRACT**

Familial hypercholesterolemia (FH) is an autosomal dominant inherited disease characterized by elevated cholesterol levels. Studies have shown that polymorphism in the LDLR gene is one of the contributor of FH. Two polymorphisms were detected in exon 10 in this study done in twelve subjects. 29209G>A SNP was detected in 50% of the samples. A probable novel SNP 29326A>G was detected in only 8% of the samples. SNPs 29209G>A and 29326A>G were both synonymous with no change in amino acid. For future plan, allele specific polymerase chain reaction (AS-PCR) can be done to validate the SNPs. Further studies need to be done to increase the understanding of genetic factors that contributes to hypercholesterolemia among the Malaysians.

#### CHAPTER 1

## INTRODUCTION

## 1.1 Background of study

Familial Hypercholesterolemia (FH) is an autosomal dominant inherited diseases which is characterised by elevated cholesterol level (Michael S. Brown, Hobbs, & Goldstein, 2001). It is associated with the presence of xanthomas and early development of coronary heart diseases (CHD). FH can be classified into heterozygous FH and homozygous FH (Austin, Hutter, Zimmern, & Humphries, 2004). Homozygous FH expresses more severe phenotype compared to heterozygous FH. It has more incidence of xanthomas and much early occurrence of CHD (Michael S. Brown et al., 2001). Although more severe phenotype expressions such as much higher cholesterol levels is usually present in homozygous FH, they rarely occur usually one in every million (Goldberg et al., 2011). Heterozygous FH is more common with prevalence of one in every 500 individuals (Michael S. Brown et al., 2001). Although many studies have been done about FH, most of them were done in the Western population, there are not many studies done among the Asian population especially among Malaysians (Livy & Lye, 2011).

FH is commonly associated with the occurrence of CHD. An estimated number of 200,000 people with FH died due to CHD (Civeira, 2004). This is due to an increase rate of atherosclerosis that would eventually lead to CHD (Junyent et al., 2010). FH