



UNIVERSITI PUTRA MALAYSIA

***IDENTIFICATION OF CANDIDATE GENES EXPRESSIONS AND
POLYMORPHISMS ASSOCIATED WITH ATHEROSCLEROSIS FROM
POSTMORTEM CASES IN HOSPITAL KUALA LUMPUR AND HOSPITAL
SERDANG, MALAYSIA***

JOAN ANAK BLIN

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**MASTER OF SCIENCE
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2013



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JOAN ANAK BLIN

By

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirements for the Degree of Master of Science**

September, 2013

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment
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POSTMORTEM CASES IN HOSPITAL KUALA LUMPUR AND HOSPITAL
SERDANG, MALAYSIA**

By

JOAN ANAK BLIN

September 2013

Chairperson: Zalinah bte Ahmad, PhD

Faculty: Medicine and Health Sciences

Atherosclerosis as presented by coronary artery disease is a slow progressing, pathological process of plaque formations within arteries. Differential expression of susceptibility genes plays important role in the pathogenesis of atherosclerosis. This study aimed to determine differential expression of 11 candidate genes and polymorphisms associated with atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang. Seventy six atherosclerotic coronary artery tissues (ACAT) (cases) and 149 non-atherosclerotic coronary artery tissues (NCAT) (healthy controls) were gathered from the Forensic Department of Hospital Kuala Lumpur and Hospital Serdang based on predetermined inclusion and exclusion criteria. Gross examination findings showed the presence of mild to severe atheroma in ACAT samples, whereas NCAT samples showed clean tissues. Microscopic findings of ACAT samples showed presence of both stable (80.3%) and unstable atheroma (19.7%) respectively, with 11.8% of the samples were superimposed with thrombosis. Six RNA samples of each ACAT and NCAT were analyzed using

GenomeLab Genetic Analysis System (GeXP). Student's *t*-test showed significant increase in expression levels of low density lipoprotein receptor (*LDLR*), tumor protein 53 (*TP53*), and matrix metalloproteinase 9 (*MMP9*) genes in ACAT samples ($p < 0.05$). No significant differences in the expression levels were obtained for the remaining eight candidate genes. Restriction fragment length polymorphism (RFLP) analysis was performed on 76 ACAT and 149 NCAT samples to investigate the variation in *LDLR* (C88S), *TP53* (*TP53* codon 72), and *MMP9* (*MMP9*-1562C>T) genotypes. Descriptive statistics were used to determine genotypes distribution of each polymorphism in both groups. The Chi-square (χ^2) test revealed significant differences in CT genotype and T allele of *MMP9*-1562C>T polymorphism when compared between the ACAT and NCAT groups (CT: $\chi^2 = 19.758$, $df = 1$, $p = 0.000$ and T allele: $\chi^2 = 21.109$, $df = 1$, $p = 0.000$). The CT genotype and the T allele were significantly higher in ACAT samples (CT: 57.9% in ACAT vs. 27.5% in NCAT and T allele: 77.9% in ACAT vs. 48.3% in NCAT). There were positive associations of CT genotype and T allele with atherosclerosis (CT: OR= 3.622, 95% CI= 2.028 – 6.470 and T allele: OR= 3.780, 95% CI= 0.2115 – 6.755). There were no significant differences of CT genotype and T allele distribution among the three major ethnicities and between genders of the healthy population. No significant associations were identified in the C88S and *TP53* codon 72 polymorphisms with regard to atherosclerosis risk. In conclusion, CT genotype and T allele of the *MMP9*-1562C>T polymorphism displayed associations with the risk of developing atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai
memenuhi keperluan untuk ijazah Master Sains

**PENGENALPASTIAN EKSPRESI CALON GEN DAN POLIMORFISME
BERKAITAN DENGAN ATEROSKLEROSIS DARIPADA KES-KES BEDAH
SIASAT DI HOSPITAL KUALA LUMPUR DAN HOSPITAL SERDANG,
MALAYSIA**

Oleh

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Aterosklerosis yang ditunjukkan melalui penyakit arteri koronari adalah proses patologi pembentukan plak secara perlahan di dalam arteri. Pengekspresan berbeza oleh gen-gen berkaitan memainkan peranan penting dalam patogenesis aterosklerosis. Kajian ini bertujuan untuk menentukan ekspresi 11 calon gen dan polimorfisme-polimorfisme yang berkaitan dengan risiko aterosklerosis daripada kes-kes bedah siasat di Hospital Kuala Lumpur dan Hospital Serdang. Tujuh puluh enam tisu arteri koronari aterosklerotik (ACAT) (kes) dan 149 tisu arteri koronari bukan aterosklerotik (NCAT) (kawalan sihat) telah dikumpul dari Jabatan Forensik Hospital Kuala Lumpur dan Hospital Serdang berdasarkan kriteria-kriteria penglibatan dan pengecualian yang telah ditetapkan. Penemuan pemeriksaan “mata kasar” menunjukkan kehadiran ateroma daripada sederhana kepada teruk dalam sampel ACAT, sementara sampel NCAT menunjukkan tisu-tisu bersih. Penemuan mikroskopik terhadap sampel ACAT menunjukkan kehadiran kedua-dua ateroma stabil (80%) dan tidak stabil (19.7%), dengan 11.8% daripada sampel tersebut

menunjukkan thrombosis yang bertindih. Enam sampel RNA daripada setiap ACAT dan NCAT telah dianalisis menggunakan Sistem Analisis Genetik GenomeLab (GeXP). Ujian-t menunjukkan peningkatan yang signifikan dalam tahap ekspresi gen-gen reseptor lipoprotein ketumpatan rendah (*LDLR*), protein tumor 53 (*TP53*), dan metalloproteinase matriks 9 (*MMP9*) di dalam sampel ACAT ($p < 0.05$). Tiada perbezaan yang signifikan dalam tahap ekspresi yang telah diperoleh untuk kelapan-lapan baki gen lain. Analisis polimorfisme panjang serpihan penyekatan (RFLP) telah dilakukan ke atas 76 sampel ACAT dan 149 sampel NCAT untuk menyiasat variasi dalam genotip-genotip *LDLR* (C88S), *TP53* (*TP53* codon 72), dan *MMP9* (*MMP9*-1562C>T). Statistik deskriptif telah digunakan untuk menentukan taburan genotip setiap polimorfisme di dalam kedua-dua kumpulan. Ujian Chi-square (χ^2) telah menunjukkan perbezaan yang signifikan terhadap genotip CT dan alel T dalam polimorfisme *MMP9*-1562C>T semasa perbandingan di antara kumpulan ACAT dan NCAT (CT: $\chi^2 = 19.758$, $df = 1$, $p = 0.000$ dan alel T: $\chi^2 = 21.109$, $df = 1$, $p = 0.000$). Genotip CT dan alel T secara signifikan lebih tinggi di dalam sampel ACAT (CT: 57.9% di dalam ACAT vs. 27.5% di dalam NCAT dan alel T: 77.9% di dalam ACAT vs. 48.3% di dalam NCAT). Terdapat perkaitan yang positif bagi genotip CT dan alel T dengan aterosklerosis (CT: OR= 3.622, 95% CI= 2.028 – 6.470 dan alel T: OR= 3.780, 95% CI= 0.2115 – 6.755). Walau bagaimanapun, tidak terdapat perbezaan yang ketara pada taburan genotip CT dan alel T di kalangan tiga etnik utama dan antara jantina populasi yang sihat. Tiada perkaitan yang signifikan dikenalpasti di dalam polimorfisme C88S dan *TP53* codon 72 ke atas risiko aterosklerosis. Kesimpulannya, genotip CT dan alel T bagi polimorfisme *MMP9*-1562C>T telah menunjukkan perkaitan dengan risiko mendapat aterosklerosis daripada kes-kes bedah siasat di Hospital Kuala Lumpur dan Hospital Serdang.

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I certify that a Thesis Examination Committee has met on 27th September 2013 to conduct the final examination of Joan Anak Blin on his thesis entitled " Identification of Candidate Genes Expressions and Polymorphisms Associated with Atherosclerosis from Postmortem Cases in Hospital Kuala Lumpur and Hospital Serdang, Malaysia " in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Master of Science.

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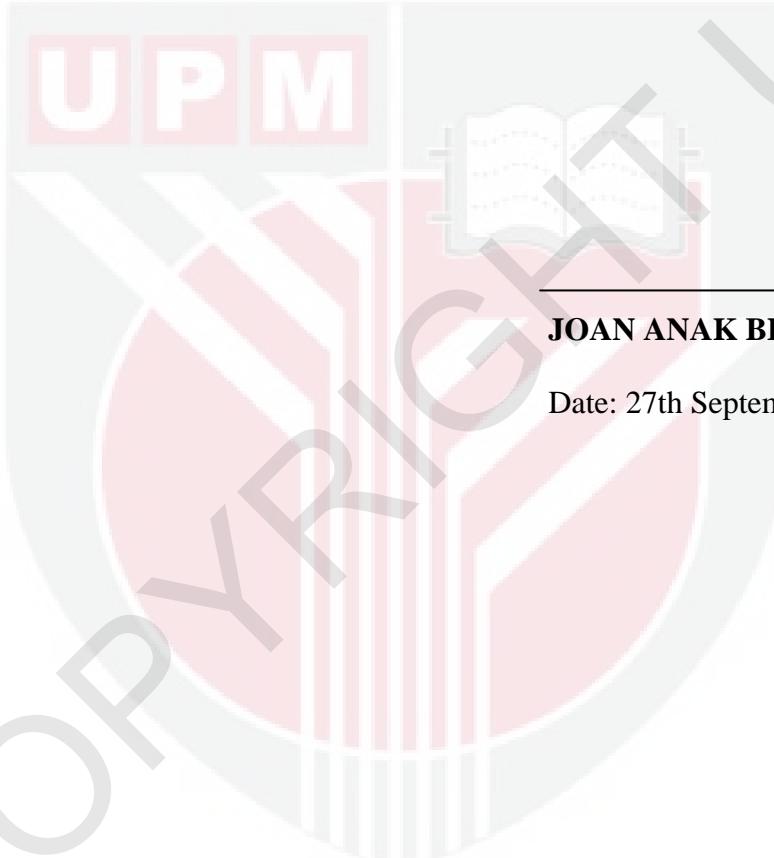
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DECLARATION

I declare that the thesis is my original work except for quotations and citations which have been duly acknowledged. I also declare that it has not been previously, and is not concurrently, submitted for any other degree at Universiti Putra Malaysia or at any other institution.



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Date: 27th September 2013

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LIST OF ABBREVIATIONS

%	Percentage
°C	Degree of Celsius
α	Alpha
β	Beta
μ	Micro
μg	Microgram
μl	Microliter
μm	Micrometre
μM	Micromolar
χ ²	Chi-square test
ABCA1	ATP-binding cassette, subfamily A, member 1
ACAT	Atherosclerotic coronary artery tissue
ALOX5AP	Arachidonate 5-lipoxygenase-activating protein
ANGPTL3	Angiopoietin-like 3
Apo A-I	Apolipoprotein A-I
APOA3	Apolipoprotein A3
APOA4	Apolipoprotein A4
APOA5	Apolipoprotein A5
APOB	Apolipoprotein B
APOB100	Apolipoprotein B-100
APOC	Apolipoprotein C
ApoE	Apolipoprotein E
ApoE ε2	Apolipoprotein E ε2 allele
ApoE ε3	Apolipoprotein E ε3 allele
ApoE ε4	Apolipoprotein E ε4 allele
ASP-PCR	Allele-specific primer polymerase chain reaction
ATP5O	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O

	subunit	
AUC	Area-under-the-curve	
bp	Base pairs	
CABG	Coronary artery bypass grafting	
CAD	Coronary artery disease	
CBS	Cystathionine-beta-synthase	
cDNA	Complementary Deoxyribonucleic acid	
CEA	Carotid endarterectomy	
CETP	Cholesteryl ester transfer protein	
CI	Confidence interval	
CRP	C-reactive protein	
CVD	Cardiovascular disease	
df	Degree of freedom	
DNA	Deoxyribonucleic acid	
DNase	Anti-Deoxyribonuclease	
EST	expression sequence tag	
FH	Familial hypercholesterolemia	
g	Centrifugation force	
GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	
GCKR	Glucokinase regulatory protein	
GeXP	GenomeLab Gene Expression Profiler	
H & E	Haematoxylin and eosin staining	
HDL	High density lipoprotein	
HMG-CoA	3-hydroxy-3-methylglutaryl coenzyme A reductase inhibitors	
IHD	Ischemic heart disease	
IRS1	Insulin receptor substrate 1	
Knar	Kanamycin gene	
LAD	Left anterior descending	

LCAT	Lecithin-cholesterol acyltransferase
LDL	Low density lipoprotein
LDL-C	Low density lipoprotein cholesterol
LDLR	Low density lipoprotein receptor
LIPG	Endothelial lipase gene
LMNA	Lamin A/C gene
Lp(a)	Lipoprotein (a)
LPL	Lipoprotein lipase
MALDI-TOF-MS	Matrix-assisted laser desorption ionization time-of-light mass spectrometry
MCP-1	Monocyte chemoattractant protein-1
mg	Milligram
MgCl ₂	Magnesium chloride
MLXIPL	MLX interacting protein-like
mM	Millimolar
MMAB	Methylmalonic aciduria (cobalamin deficiency) cblB type
MMP9	Matrix metalloproteinase 9
MMPs	Matrix metalloproteinases
mRNA	messenger Ribonucleic acid
MTHFR	5,10-methylenetetrahydrofolate reductase
MVK	Mevalonate kinase
n	Sample size
NADPH	Nicotinamide adenine dinucleotide phosphate
NCAN	Chondroitin sulfate proteoglycan 3 (neurocan)
NCAT	Non-atherosclerotic coronary artery tissue
ng	Nanogram
NO	Nitric oxide
OR	Odds ratio
<i>p</i>	Significant alpha value

p_1	Estimate exposure rate (proportion exposed) in cases
PCSK9	Proprotein convertase subtilisin/kexin type 9
p_o	Estimated exposure rate (proportion exposed) in controls
R	Relative risk
RFLPs	Restriction Fragment Length Polymorphisms
RIN	RNA integrity number
RNA	Ribonucleic acid
ROS	Reactive oxygen species
RPLP0	Ribosomal protein, large, P0
RT	Reverse transcription
RT-PCR	Reverse Transcription-Polymerase Chain Reaction
SAGE	Serial analysis of gene expression
SD	Standard deviation
SMCs	Smooth muscle cells
SNPs	Single nucleotide polymorphisms
SORT1	Sortilin 1
SPSS	Statistical Package for Social Sciences
TAFI	Thrombin-activatable fibrinolysis inhibitor
TBE	Tris-Borate-EDTA
TCEP	Tris (2-carboxyethyl) phosphine
TCFA	Thin cap fibroatheroma
TGFBR2	Transforming growth factor, beta receptor II
THBD	Thrombomodulin
TP53	Tumor protein p53
TRIB1	Tribbles homolog 1 (<i>Drosophila</i>)
VCAM-1	Vascular cell adhesion protein 1
VLDL	Very low density lipoprotein

CHAPTER 1

INTRODUCTION

1.0 Background of study

Cardiovascular disease (CVD) is a leading cause of death in Malaysia for the last 45 years and remains as a major public health problem globally (Rampal *et al.*, 2008).

Cardiac related mortality statistics have shown increasing trends in many developing countries, including India, China, Korea and other Asian countries (Cheng *et al.*, 2005). Although a lot of effort has been invested for interventions, prevention, and treatments of the disease, cardiac related mortality remains high. Unsurprisingly, this CVD burden in most Asian populations is expected to double over the next decade (Tai *et al.*, 2009).

Atherosclerosis as presented by coronary artery disease (CAD) is one of the major contributors of CVD. Atherosclerosis is a slow progressing, pathological process of plaque formations within the intima of coronary arteries. It develops asymptotically for decades, and usually is advanced by the time symptoms occur. This phenomenon poses a big challenge for treatments of atherosclerotic vascular disease (Graham and O'Callaghan, 2003).

One of the strategies for better management of the disease is through personalized medicine approach. Personalized medicine is particularly based on the science of pharmacogenomics, a study on how individual's genetic inheritance affects the body's response to drugs. Pharmacogenomics is a combination of traditional pharmaceutical sciences with knowledge of genes, proteins, and single nucleotide polymorphisms. It is more precise and predictable and may lead us to more accurate diagnoses, safer drug prescribing, and more effective treatment. Personalized medicine approach depends mainly on a comprehensive understanding of the genes and gene variants that contribute to disease susceptibility and progression (Seo *et al.*, 2004). Thus, a better understanding on the molecular mechanisms of atherosclerosis is crucial as a fundamental initial step in this long journey.

Candidate gene association study is the most widely used to identify susceptibility genes for coronary artery disease. The approach seeks for associations between phenotype and genotype of the candidate genes (Franchini *et al.*, 2008). It is a branch of genome-wide association studies, which has been attempted to assess the role of genes that are already implicated in the pathophysiology of the disease (Lee *et al.*, 2009). Candidate genes are predetermined genes located within regions of interest and are identified based on prior knowledge of their function. These candidate genes are suspected of being involved in the expression of a trait that contributes to the disease development. In atherosclerosis, up- or down-regulation pattern of candidate genes have been thought to alter the microenvironment that may protect or worsen the lesion progression (Fortunato and Taranto, 2007). Besides, polymorphisms within susceptibility genes in lipid metabolism, inflammation, and thrombogenesis

are all responsible for atherosclerotic vascular disease susceptibility (Chen *et al.*, 2007).

Association studies are designed to compare statistical difference in genotype frequencies between case and control groups, which may offer evidence that a genotype is associated with the trait (Arnett, 2007). A problem with many published association studies is that a positive association observed in one report is often not reproducible in subsequent studies. This scenario is due to inconsistently defined phenotypes, variability in sample size, as well as different populations and ethnic groups under study. Indeed, in single nucleotide polymorphisms (SNPs) analysis, allele frequencies may differ widely in different populations (Gibbons *et al.*, 2004). Thus, data collection of genetic variation associated with the risk of developing atherosclerosis in Malaysian population which is also multiracial is very important. This baseline data could lead towards early detection of CVD risk in Malaysia.

Research concerning CAD in Malaysian population is still limited, although its molecular basis has been widely studied in the western world (Abdullah *et al.*, 2012). Without proper prevention and managements of CVD, the increasing burden of CVD will directly affect the economic status of the country. More extensive effort is required in molecular aspects so that thorough understanding of the disease is acquired. Therefore, there is an urgent need for a comprehensive study concerning the genetics basis of atherosclerotic vascular disease in Malaysia. The outcome of these fundamental efforts is hoped to facilitate the development of early detection

technique which in turn may contribute to a better prevention action of CVD in Malaysia.

1.1 Research Objectives

General Objective:

1. To study the association between the differential expression of candidate genes and polymorphisms with the risk of developing atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang, Malaysia.

Specific Objectives:

1. To determine the morphology of atherosclerotic coronary artery tissue using haematoxylin and eosin (H & E) staining.
2. To determine list of candidate genes associated with risk of developing atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang, Malaysia using GenomeLab Gene Expression Profiler (GeXP) genetic analysis system.
3. To determine the polymorphisms and distribution of genotypes and alleles frequency of candidate genes associated with risk of developing atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang, Malaysia.

1.2 Hypothesis

There are associations of differential expressions and polymorphisms of candidate genes with the risk of developing atherosclerosis from postmortem cases in Hospital Kuala Lumpur and Hospital Serdang, Malaysia.

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