



UNIVERSITI PUTRA MALAYSIA

***GENETIC ANALYSIS OF BETA 2 ADRENERGIC AND DOPAMINE
RECEPTOR GENE POLYMORPHISMS IN HYPERTENSIVE SUBJECTS
AT HOSPITAL SEREMBAN, MALAYSIA***

MAKANKO KOMARA

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in the fulfillment of the requirement for the degree of Master of Science

**GENETIC ANALYSIS OF BETA 2 ADRENERGIC AND DOPAMINE
RECEPTOR GENE POLYMORPHISMS HYPERTENSIVE SUBJECTS AT
HOSPITAL SEREMBAN, MALAYSIA**

By

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Essential hypertension which is a major risk factor for cardiovascular diseases is a complex trait influenced by multiple genes and environmental factors. According to The Third National Health and Morbidity Survey in 2008, the prevalence of hypertension among Malaysian adults was 43%. The heritability of hypertension has been estimated to be 60%. β 2 adrenoceptor and Dopamine receptor genes have been known to play a major role in blood pressure regulation. This study aims to determine the association of Arg16Gly (rs1042713), Gln27Glu (rs1042714) and Thr164Ile (rs1800888) polymorphisms of β 2 adrenoceptor and A-48G (rs4532) and *Taq1A* (rs1800497) polymorphism of dopamine receptor in Malaysian hypertensive subjects. A total of 160 of each cases and control subjects were recruited. Systolic blood pressure (SBP), diastolic blood pressure (DBP) and anthropometric measurement were obtained from each subject. Biochemical analysis of lipid profile

was measured using auto analyzer. DNA samples were extracted from blood and buccal cells. Genotyping was done by PCR-Restriction Fragment length Polymorphism. SBP, DBP, BMI and biochemical analysis were significantly different between cases and controls ($p < 0.05$). Genotypes of Arg16Arg, Arg16Gly and Gly16Gly among cases were 22.5%, 70% and 7.5% respectively compared to 33.1%, 63.1% and 3.8% respectively among controls. The genotype frequencies of Gln27Gln, Gln27Glu and Glu27Glu among cases were 41.1%, 50% and 1.9% respectively compared to 77.5%, 20.6% and 1.9% respectively among controls. For Thr164Ile polymorphism, all subjects were homozygote for the wild type genotype. For the Dopamine receptor 1 gene polymorphism, the genotypes frequencies of AA, AG and GG among cases were 54.4%, 38.8% and 6.9% respectively, while the frequencies were 61.2%, 32.5% and 6.2% among control subjects. The genotype frequencies of A1A1, A1A2 and A2A2 of Dopamine receptor 2 gene among cases were 16.2%, 61.9% and 21.95 respectively compared to 14.4%, 50.6% and 35% respectively among control subjects. In this study two polymorphisms were significantly associate with hypertension; Gln27Glu and *Taq1A* polymorphisms ($p = 0.000$) and ($p = 0.033$). In ANOVA analysis, the Age, BMI, SBP, DBP and biochemical analysis results were not significantly associated with study genotypes. The analysis of Multifactor dimensionality reduction showed a significant interaction between $\beta 2$ adrenoceptor and dopamine receptor genes polymorphism ($p = 0.001$). This study suggests that Gln27Glu and *Taq1A* polymorphism of $\beta 2$ adrenoceptor and dopamine receptor genes could be a risk factor associated with hypertension among Malaysians with possible interaction between the genotypes of both genes.

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

**ANALISIS GENETIK ADRENERGIC BETA2 DAN POLIMORFISME GEN
RESEPTOR DOPAMIN DALAM SUBJEK HIPERTENSI DI HOSPITAL
SEREMBAN, MALAYSIA**

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Hipertensi esensial yang merupakan faktor risiko utama untuk penyakit kardiovaskular, adalah ciri kompleks trait dipengaruhi oleh pelbagai gen dan faktor persekitaran. Menurut Kajian Kesihatan dan Morbiditi Negara Ketiga (NHMS III) pada tahun 2008, kadar prevalen hipertensi di kalangan orang dewasa Malaysia ialah 43%. Sebanyak 60% telah dianggarkan bahawa hipertensi diwariskan kepada generasi seterusnya. Gen reseptor B2 adrenoceptor dan gen reseptor Dopamine telah dikenal pasti memainkan peranan utama dalam pengawalaturan tekanan darah. Kajian ini bertujuan untuk menentukan perkaitan polimorfisme β 2 adrenoceptor Arg16Gly (rs1042713), Gln27Glu (rs1042714) dan Thr164Ile (rs1800888) serta polimorfisme reseptor dopamine A-48G (rs4532) dan Taq1A (rs1800497) dalam subjek hipertensi di Malaysia. Sebanyak 160 orang bagi setiap subjek kes dan kawalan, telah direkrut. Tekanan darah sistolik (SBP), tekanan darah diastolik (DBP) dan pengukuran antropometri telah diperolehi daripada setiap subjek. Analisis biokimia profil lipid telah dilakukan menggunakan penganalisis automatik. Sampel DNA telah diekstrak daripada darah dan sel bukal. Genotyping telah dilakukan dengan teknik Tindak Balas Rantaian Polimerase - Polimorfisme Panjang Cebisan

Pemotongan (PCR-RFLP). SBP, DBP, BMI dan analisis biokimia mempunyai perbezaan yang signifikan antara kes dan kawalan ($p < 0.05$). Genotip Arg16Arg, Arg16Gly dan Gly16Gly di kalangan kes dengan masing-masing adalah 22.5%, 70% dan 7.5% berbanding dengan 33.1%, 63.1% dan 3.8% di kalangan kawalan. Frekuensi genotip Gln27Gln, Gln27Glu dan Glu27Glu di kalangan kes-kes adalah 41.1%, 50% dan 1.9% berbanding dengan 77.5%, 20.6% dan 1.9% masing-masing di kalangan kawalan. Bagi polimorfisme Thr164Ile, semua subjek adalah homozigot untuk genotip jenis liar. Bagi polimorfisme DRD1 gen, frekuensi genotip AA, AG dan GG di kalangan kes masing-masing adalah 54.4%, 38.8% dan 6.9%, manakala frekuensi 61.2%, 32.5% dan 6.2% di kalangan subjek kawalan. Frekuensi genotip A1A1, A1A2 dan A2A2-DRD2 kalangan kes masing-masing adalah 16.2%, 61.9% dan 21.95 berbanding 14.4%, 50.6% dan 35% masing-masing di kalangan subjek kawalan. Dalam kajian ini dua polimorfisme iaitu polimorfisme Gln27Glu dan Taq1A, mempunyai signifikasi yang ketara dengan hipertensi dengan nilai $p = 0.000$ dan 0.033 . Umur, BMI, SBP, DBP dan keputusan analisis biokimia adalah tidak signifikan berbanding kajian genotip. Analisis pelbagai faktor pengurangan dimensi menunjukkan interaksi yang signifikan antara $\beta 2$ adrenoceptor dan polimorfisme gen reseptor dopamin ($p < 0.001$). Kajian ini menunjukkan bahawa polimorfisme Gln27Glu dan Taq1A $\beta 2$ gen reseptor adrenoceptor dan dopamine boleh menjadi faktor risiko yang dikaitkan dengan tekanan darah tinggi di kalangan rakyat Malaysia dengan kemungkinan interaksi antara genotip kedua-dua gen.

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LIST OF ABBREVIATIONS

ADRB2	β 2 adrenoceptor gene
Arg	Arginine
BMI	Body Mass Index
bp	Base Pair
cAMP	Cyclic Adenosine Monophosphate
CPG	Clinical Practice Guideline
CVC	Cross Validation Consistency
CVD	Cardiovascular Disease
DBP	Diastolic Blood Pressure
DNA	Deoxyribonucleic acid
DRD1	Dopamine receptor 1 gene
DRD2	Dopamine receptor 2 gene
Gln	Glutamine
Glu	Glutamic acid
GWAS	Genome Wide Association Studies
HDL	High Density Lipoprotein
Ile	Isoleucine
JNC-6	The Sixth Report of the Joint National Committee on Prevention, Detection, Evaluation, and Treatment of High Blood Pressure
JNC-7	The Sixth Report of the Joint National Committee on Prevention, Detection, Evaluation, and Treatment of High Blood Pressure
LDL	Low Density Lipoprotein
mmHg	millimeter mercury
-Na-H	Sodium /Hydrogen exchanger
Na-K	Sodium/Potassium exchanger
NCBI	National Center for Biotechnology Information
nm	nanometer
PCR-RFLP	Polymerase Chain Reaction Restriction Fragments Length Polymorphism
SBP	Systolic Blood Pressure
SNP	Single Nucleotide Polymorphism
TG	Triglyceride
Thr	Threonine
VLDL	Very Low Density Lipoprotein
WHO	World Health Organization

CHAPTER I

INTRODUCTION

Background of the Study

High blood Pressure or hypertension is defined as sustained increase of systolic blood pressure of 140 millimeter mercury (mmHg) or greater and/or diastolic blood pressure of 90 mmHg or greater. Hypertension is a major public health problem and the leading cause of death worldwide (Chockalingam, 2008). Moreover, hypertension is known as a risk factor for cardiovascular and renal diseases. It has been estimated that 82% to 95% of all hypertension cases are primary or essential hypertension with no specific cause (Carey, 2008). Secondary form of hypertension is caused by some medical conditions such as, renovascular disease, Cushing Syndrome and primary aldosteronism (Carey, 2008).

Hypertension is a complex disease controlled by multiple genes and environmental factor (Munroe *et al.*, 2000). The aggregation of hypertension in families explains the role of genes in the development of hypertension. The heritability of blood pressure has been estimated to be 0.6% (Lewis, 2007). Non genetics factors that might increase the risk of developing hypertension are obesity, high alcohol consumption, high salt intake, stress and smoking (Carretero *et al.*, 2000). There are two basic strategies for the genetic analysis of complex diseases, whole-genome scan and candidate gene analysis (Schork, 1997). The term whole-genome scan is screening for any variations that are present throughout the entire genome without prior

knowledge about the variations, while in candidate gene analysis a known gene or variation is analyzed to see whether they are associated with a disease phenotype. To date, finding the susceptibility loci for complex diseases has been less successful than the other disorders. This is due to the complicated architecture of complex diseases such as locus heterogeneity, age-dependent penetrance, gene-gene and gene-environmental interaction (Schork, 1997). Gene-gene interaction or epistasis is one of the interests of the current research in the field of human genetics. Large number of research has been conducted to investigate epistasis in human complex diseases such as cancer, diabetes and hypertension (Cordell, 2002).

The most stable variation of the genome occurs in the form of single nucleotide polymorphisms (SNPs) which make 90% of the common variations in the genome (Doris, 2002). In recent years SNPs have been postulated as the next generation for the identification of loci associated with complex diseases (Lai, 2001). SNPs association studies have revealed promising results in the genetic studies of complex diseases. Several candidate genes have been hypothesized to play a role in the development of hypertension. These genes encode proteins known to be involved in blood pressure regulation. Among these genes are the β 2 adrenoceptor and dopamine receptor genes (Agarwal *et al.*, 2005). Sympathetic nervous system plays a major role in blood pressure regulation. Therefore genes coding for major proteins of the sympathetic nervous system were proposed as candidate genes for the genetic study of hypertension. β 2 adrenoceptor is a G-protein couple receptor that upon activation by catecholamine increases the intracellular second messenger cyclic Adenosine Monophosphate (cAMP). β 2 adrenoceptor mediates vasodilatation that is important

in blood pressure control. Other blood pressure regulating effects of β_2 adrenoceptor include renal sodium handling and control of renin release (Pereira *et al.*, 2003).

Three common SNPs of β_2 adrenoceptor are functionally important. The Arginine substitute by Glycine at nucleotide 16 (Arg16Gly) (rs1042714), the Glutamine substitution by Glutamic acid at nucleotide number 27 (Gln27Glu) (rs1042714) and Threonine substitution by Isoleucine at nucleotide number 164 (Thr164Ile) (rs1800888). These genetic variations might influence the receptor function and/or gene expression and hence contribute to the pathophysiology of several diseases such as hypertension. These polymorphisms have been studied in relation to hypertension and related conditions in different populations with conflicting results (Candy *et al.*, 2000; Kotanko *et al.*, 1997; Large *et al.*, 1997; Masuo *et al.*, 2005; Sethi *et al.*, 2005).

Dopamine is a precursor of noradrenalin and adrenaline. It is an endogenous neurotransmitter which modulates behavior, ion transport, vascular tone and blood pressure (Fang *et al.*, 2005). Dopamine receptor genes polymorphisms have been hypothesized to be involved in pathogenesis of essential hypertension (Agarwal *et al.*, 2005). Dopamine receptor D1 is found on the smooth muscle of renal arteries, juxtaglomerular apparatus and on renal tubules, whereas D2 receptor is present in intimal layer of renal vasculature, glomeruli, sympathetic nerve terminal and renal tubule (Fang *et al.*, 2005; Hussain & Lokhandwala, 2003). A study revealed alteration of renal sodium handling associated with certain polymorphisms of *DRD1* gene (Sato *et al.*, 2000). These polymorphisms might impair the receptor or function which will disrupt the sodium excretion and hence increase in blood pressure in certain individuals. In this study the *DRD1* and *DRD2* polymorphisms A48G

(rs4532) and *Taq1 A* (re1800497) will be analyzed respectively. Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) is a simple laboratory technique for the detection of genetic variants. It is easy, cost-effective accurate and commonly used for SNPs detection (Barnes, 2010). In PCR-RFLP, a segment of nucleic acid (in which the mutation is detected) is amplified then digested into different segment using the restriction enzyme, and then the product will be separated on agarose gel electrophoresis for mutation analysis. This case-control study aims to compare allele frequencies between cases and control subjects. Cases are individuals diagnosed with the disease (hypertension) and controls are healthy individuals. Both groups will be selected randomly based on specific inclusion and exclusion criteria. The increase in the frequency of the SNP allele in the cases compared to the controls will indicate that the SNP could be a risk factor for the hypertension among Malaysians.

Problem Statement

According to The Third National Health and Morbidity Survey of 2006, the prevalence of hypertension among Malaysian adults who are 39 years old or above is 43% (CPG, 2008). This rapid increase in the prevalence of hypertension will eventually lead to increase in the cardiovascular events associated with hypertension. According to the Information and Documentation Unit of the Ministry of Health of Malaysia, cardiovascular diseases are the major cause of 23-26% of death in government hospitals from 1994 to 2001 (Zambahari, 2004). Despite the high prevalence of hypertension in Malaysia, there is still lack of sufficient information on the most susceptible loci with hypertension among Malaysians.

Few years back there has been an increasing interest in genetic association studies of human hypertension. Several genes that involve in hypertension modulation such as β 2 adrenoceptor and dopamine receptor have been screened for possible variation that can contribute to the pathology of hypertension in different population (Large *et al.*, 1997; Sato *et al.*, 2000; Thomas *et al.*, 2001). However, there is controversy in the results obtained from those studies and majority of these studies did not evaluate any possible interaction between different candidate genes. Hence, more studies using different population are needed in order to provide more information on genetic susceptibility of hypertension. Furthermore, to our knowledge there are no published work on the association analysis of β 2 and dopamine receptor genes polymorphism and interactions between these genes in relation to hypertension among Malaysians.

Study Hypothesis

β 2 adrenoceptor and dopamine receptor gene polymorphisms are associated with Malaysian hypertensive subjects

Study Objectives:

Main Objectives

To determine the association between β 2 adrenoceptor and dopamine receptor gene polymorphisms in Malaysian hypertensive subjects

Specific Objectives

1. To determine the association and allelic frequency of $\beta 2$ adrenoceptor gene (*ADRB2*) Arg16Gly, Gln27Glu and Thr164Ile polymorphisms with hypertension in Malaysian subjects
2. To determine the association and allelic frequency of A48G and *Taq1* A polymorphism of *DRD1* and *DRD2* respectively polymorphisms with hypertension in Malaysian subjects
3. To correlate $\beta 2$ adrenoceptor and dopamine receptor gene polymorphisms with risk factors for hypertension
4. To examine possible interaction between polymorphisms of $\beta 2$ adrenoceptor gene and Dopamine gene.

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