



UNIVERSITI PUTRA MALAYSIA

PREVALENCE AND GENETIC ANALYSES OF SELECTED AGE-RELATED MACULAR DEGENERATION-RELATED POLYMORPHISMS AND THEIR RESPONSES TO INTRAVITREAL RANIBIZUMAB

NUR AFIQAH BINTI MOHAMAD

IPPM 2018 5



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Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in
Fulfilment of the Requirements for the Degree of Doctor of Philosophy

May 2018

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of
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NUR AFIQAH BINTI MOHAMAD

May 2018

Chair : Vasudevan Ramachandran, PhD
Faculty : Malaysian Research Institute on Ageing

Age-related macular degeneration (AMD), a leading cause of vision loss among elderly people is a progressive chronic disease of the central retina associated with environmental and genetic factors. Studies reported that gene polymorphism of various genes were analysed among AMD subjects from different populations with conflicting results. Among those, complement factor, vascular endothelial growth factor (VEGF), high temperature requirement A1 (HTRA1) and age-related maculopathy susceptibility 2 (ARMS2) genes were studied extensively among AMD subjects. In Malaysia the data on intravitreal ranibizumab drug therapy and the genetic association of gene polymorphisms among AMD remains unclear. The current study was initiated to determine the genetic association between the candidate gene polymorphisms in response to ranibizumab and also, the prevalence and changes in treatment patterns of ranibizumab and photodynamic therapy (PDT) among retinal eye disease patients from a tertiary care hospital. Upon ethical approval and consent, a total of 149 AMD and 152 controls were recruited for the prospective study. Moreover, a total number of 821 subjects were recruited for retrospective study using Electronic Medical Record database software from Hospital Selayang, Selangor. Genomic DNA and total RNA were extracted and the genotyping were analyzed using the conventional PCR and PCR-RFLP methods. The gene expression analysis was also performed for ARMS2 and HTA1 genes. The statistical analysis was performed and all the data were analysed with the level of significance was set at $P < 0.05$. The mean age of AMD subjects were 68.6 ± 8.47 and 64.8 ± 10.21 years for the controls. Males were frequent in both AMD (64%) and controls (74%) compared to females. Among AMD, Chinese (57%) were high compared to Malays (34%) and Indians (9%), whereas in controls, Malays were high (42%) compared to Chinese (41%) and Indians (17%). From the retrospective analysis, ranibizumab was the most common (30.8%) drug used as a treatment for AMD, while PDT (84.4%) or combined therapy (58.2%) were used for polypoidal choroidal vasculopathy (a subtype of AMD) patients. A significant difference ($P < 0.05$) was observed for the genotypic frequencies of VEGF +405 G/C, ARMS2 A69S, and HTA1 -625 G/A gene polymorphisms when compared between

AMD subjects and controls. However, the complement factor H (*CFH*) *Y402H*, complement component 3 (*C3*) *R102G*, *VEGF* -460 *C/T* and *VEGF* Insertion/deletion gene polymorphisms did not show any significant differences ($P>0.05$). The *ARMS2* A69S and *HTRA1* -625 G/A gene polymorphisms in response to the ranibizumab treatment among AMD subjects shows a significant association ($P<0.05$). Moreover, an over-expression of mRNA in the *HTRA1* GG genotype was also reported and could contribute to the non-responders' reaction to ranibizumab. However, no significant association ($P>0.05$) was observed in the *CFH* *Y402H* gene polymorphism with response to ranibizumab therapy based on both visual and anatomical outcome among AMD subjects. In conclusion,, *Y402H*, +405 G/C, A69S, 625 G/A polymorphisms of the *CFH*, *VEGF*, *ARMS2* and *HTRA1* genes, respectively, could be an independent risk factor and can be considered as a genetic susceptibility for the development of AMD among Malaysians.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

**PREVALENS DAN ANALISIS GENETIK TERHADAP POLIMORFISME
YANG BERKAIT DENGAN DEGENERASI MAKULA TERKAIT UMUR DAN
TINDAK BALAS TERHADAP INTRAVITREAL RANIBIZUMAB**

Oleh

NUR AFIQAH BINTI MOHAMAD

Mei 2018

Pengerusi : Vasudevan Ramachandran, PhD
Fakulti : Institut Penyelidikan Penuaan Malaysia

Degenerasi makula terkait umur (AMD), punca utama kehilangan penglihatan dalam kalangan warga tua merupakan penyakit kronik progresif pusat retina yang dikaitkan dengan faktor persekitaran dan genetik. Kajian melaporkan polimorfisme gen bagi pelbagai gen yang dianalisis dalam kalangan pesakit AMD daripada populasi berbeza memberikan hasil yang bercanggah. Antaranya adalah gen faktor komplemen, faktor pertumbuhan endotelia vaksular (VEGF), keperluan suhu tinggi A1 (HTRA1) dan kerentanan makulopati berkaitan umur 2 (ARMS2) yang dikaji secara terperinci dalam kalangan subjek AMD. Di Malaysia, data tentang kaitan antara polimorfisme gen dan tindak balasnya terhadap terapi intravitreal ranibizumab dalam kalangan AMD masih tidak jelas. Kajian ini dijalankan untuk menentukan kaitan genetik dan polimorfisme gen bagi gen tercalon serta tindak balasnya terhadap ranibizumab dan juga prevalens serta perubahan corak rawatan ranibizumab dan terapi fotodinamik (PDT) dalam kalangan pesakit retina mata di hospital penjagaan tertiar. Setelah mendapat kelulusan etika dan izin subjek, sebanyak 146 AMD dan 152 kawalan direkrut untuk kajian prospektif. Tambahan lagi, sejumlah 821 subjek direkrut untuk analisis kajian retrospektif menggunakan perisian pangkalan data Rekod Perubatan Elektronik dari Hospital Selayang, Selangor. DNA genomik dan RNA diekstrak daripada sampel darah dan analisis penggenotipan dianalisis dengan menggunakan kaedah PCR kovenisional dan analisis PCR-RFLP. Analisis pengekspresan gen juga dijalankan bagi gen ARMS2 dan HTRA1. Analisis statistik dikendalikan dan kesemua data dianalisis dengan signifikan ditetapkan pada $P < 0.05$. Purata umur bagi subjek AMD yang diambil adalah 68.6 ± 8.47 tahun dan 64.8 ± 10.21 tahun bagi kawalan. Lelaki lebih kerap dalam kedua-dua kumpulan AMD (64%) dan kawalan (74%) berbanding wanita. Dikalangan AMD, peratusan Cina (57%) lebih tinggi berbanding Melayu (34%) dan India (9%) manakala bagi peratusan kawalan, Melayu lebih tinggi (42%) berbanding Cina (41%) dan India (17%). Bagi analisis retrospektif, ranibizumab merupakan ubat paling biasa (30.8%) digunakan untuk rawatan AMD, manakala PDT (84.4%) atau rawatan campuran (58.2%) diberikan kepada pesakit vaskulopati polipoidal koroidal

(subjenis AMD). Perbezaan signifikan ($P<0.05$) dicerap bagi kekerapan genotipik faktor komplementari H (*CFH*) *Y402H*, *VEGF -460 C/T*, *VEGF +405 G/C*, *ARMS2 A69S*, dan *HTRA1 -625 G/A* polimorfisme gen apabila dibandingkan antara subjek AMD dan kawalan. Namun, komponen komplementari 3 (*C3*) *R102G* dan penyisipan/penghapusan gen polimorfisme *VEGF* tidak menunjukkan sebarang perbezaan signifikan ($P>0.05$). Gen polimorfisme *ARMS2 A69S* dan *HTRA1 -625 G/A* dan tindak balas rawatan ranibizumab terhadap subjek AMD menunjukkan perkaitan yang signifikan ($P<0.05$). Tambahan lagi, pengekspresan berlebihan mRNA di dalam genotip *HTRA1 GG* dilaporkan dan boleh menyumbang kepada tindak balas oleh kumpulan tanpa respons terhadap ranibizumab. Namun, tiada perkaitan signifikan ($P>0.05$) dicerap dalam polimorfisme gen *CFH Y402H* terhadap rawatan ranibizumab bagi kedua-dua hasil visual dan anatomikal dalam kalangan subjek AMD. Kesimpulannya, polimorfisme *Y402H*, *+405 G/C*, *A69S*, *625 G/A* bagi gen *CFH*, *VEGF*, *ARMS2* dan *HTRA1* boleh menjadi faktor risiko bebas dan boleh dianggap kerentanan genetik bagi perkembangan AMD dalam kalangan warga Malaysia.

ACKNOWLEDGEMENTS

First and foremost I would like to express my gratitude to my supervisor, Dr. Vasudevan Ramachandran for his generous guidance, encouragement and his full support in guiding me to successfully complete my project. I would also like to acknowledge my co-supervisors, Prof. Patimah, Dr. Hazlita and Prof. Paul for their kindness and assistance in making this research possible with their support.

I would like to thank all staff members of the Nutrition Lab, UPM that also help in accomplishing my project and also all the medical staffs and working doctors in both Hospital Selayang (Dr. Fariza and Dr. Shelina) and UKM Medical Centre (Dr. Hazlita and Dr. Wong) for their assistance in recruiting the subjects for this research. Not forgotten, I express my gratitude to all participants in this study. Apart from that, I would like to acknowledge my lab mates, Norshakimah and Erma Suryana for their assistance and support throughout my project.

Lastly, I would like to appreciate my parents and family for their endless encouragement, patience and sacrifices, which helped me in completing my study.

Thank you very much.

I certify that a Thesis Examination Committee has met on 2nd May 2018 to conduct the final examination of Nur Afiqah Binti Mohamad on her thesis entitled “Prevalence and Genetic Analyses of Selected Age-Related Macular Degeneration-Related Polymorphisms and Their Responses to Intravitreal Ranibizumab” 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 Doctor of Philosophy.

Members of the Thesis Examination Committee were as follows:

Y. Bhg. Tengku Aizan Binti Tengku Ab Hamid, PhD

Professor

Malaysian Research Institute on Ageing
Universiti Putra Malaysia
(Chairman)

Lai Mei I, PhD

Associate Professor

Faculty of Medicine and Health Sciences
Universiti Putra Malaysia
(Internal Examiner)

Abdah Binti Md Akim, PhD

Associate Professor

Faculty of Medicine and Health Sciences
Universiti Putra Malaysia
(Internal Examiner)

Anne C. Cunningham, PhD

Associate Professor

Pengiran Anak Puteri Rashidah Sa'adatul Bolkiah Institute of Health Science,
Universiti Brunei Darussalam,
Brunei
(External Examiner)

NOR AINI AB. SHUKOR, PhD

Professor and Deputy Dean
School of Graduate Studies
Universiti Putra Malaysia

Date: 28 June 2018

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

Vasudevan Ramachandran, PhD

Research Fellow
Malaysian Research Institute on Ageing
Universiti Putra Malaysia
(Chairman)

Patimah Ismail, PhD

Professor
Faculty of Medicine and Health Sciences
Universiti Putra Malaysia
(Member)

Hazlita Dato' Mohd Isa, MSurg (Ophthalmology) UKM

Consultant Ophthalmologist and Senior Lecturer
Department of Ophthalmology
Universiti Kebangsaan Malaysia
(Member)

Paul N Baird, PhD

Associate Professor
Centre for Eye Research Australia
Australia
(Member)

ROBIAH BINTI YUNUS, PhD

Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

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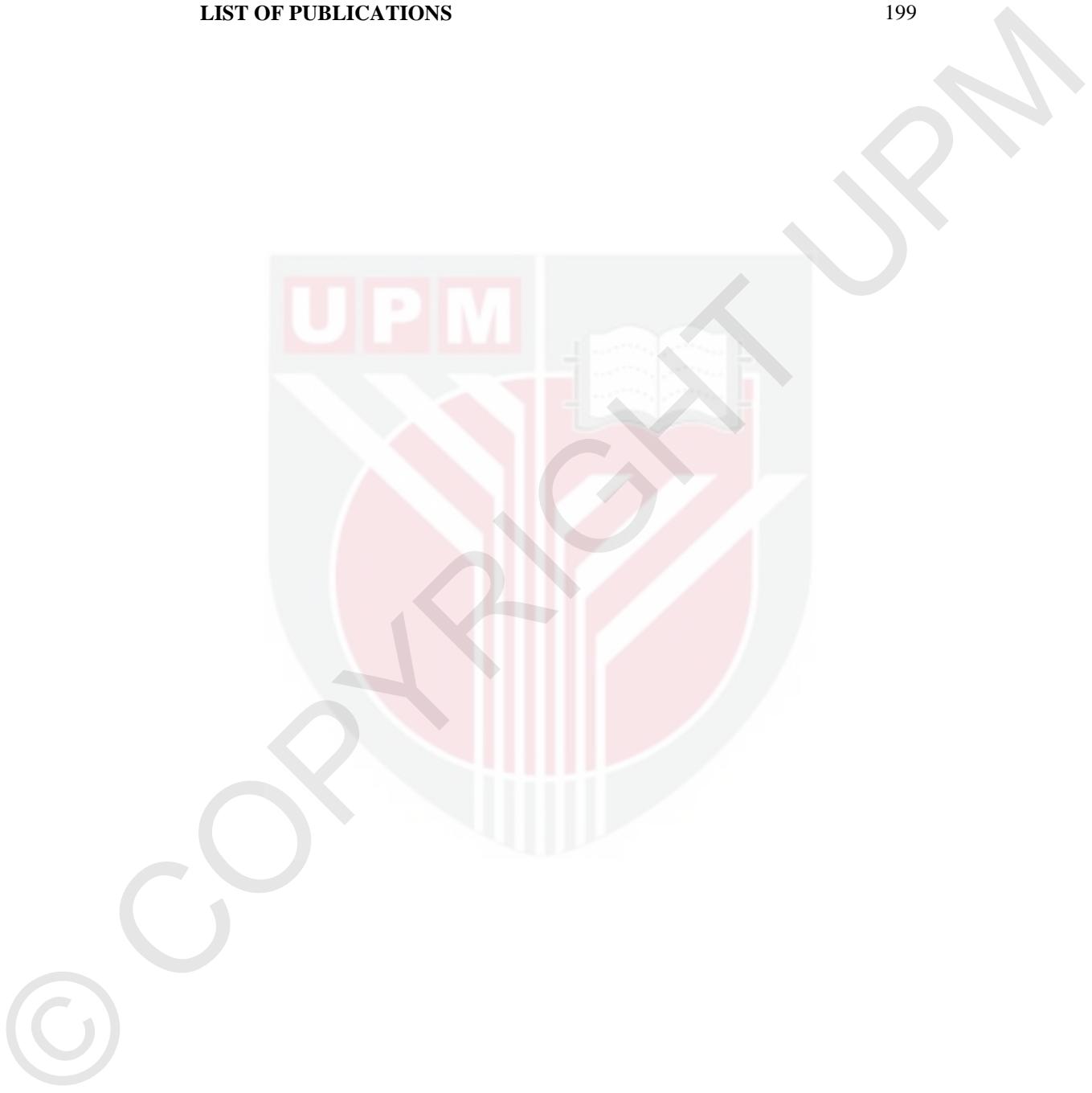
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CHAPTER 1

INTRODUCTION

Background of the Study

Age-related macular degeneration (AMD) refers to degenerative changes in the retina that have a deep impact on quality of life and independence of affected individuals (Cheung and Eaton 2013). Affected individuals are unlikely to become totally blind, but may become unable to read, write, or drive (Lim *et al.*, 2012). In particular, AMD adversely affects the quality of life in elderly sufferers, increasing the risk of falls and fractures and limiting their ability to drive safely. Rising prevalence rates of this disease are expected as the number and proportion of the aging population grows (Bird 2003). In the Malaysian population, the percentage of people aged 65 years and above is expected to rise from 5.0% in 2010 to 14.5% by 2040; Malaysia is expected to become an aging population, with 7.2% of people defined as elderly (65 years and above) by 2020 (Department of Statistic, Malaysia). An Asian meta-analysis has also shown that the age-specific prevalence of late AMD in Asians is largely similar to that seen in white people (Kawasaki *et al.*, 2010).

AMD is commonly classified into two clinical forms, dry AMD and neovascular/exudative/wet AMD. Most vision loss results from neovascular AMD, which is characterized by the incursion of blood vessels into the sub-retinal spaces (Lim *et al.*, 2012). Although advancing age is the greatest risk factor associated with AMD development, environmental and lifestyle factors may also significantly affect individuals' risk (Chen *et al.*, 2010). Modifiable environmental factors include cigarette smoking, and cardiovascular risk factors such as hypertension and diabetes are also significantly associated with AMD in various populations (Seddon *et al.*, 2005; Chakravarthy *et al.*, 2010; Chen *et al.*, 2010). In addition, genetic variations can also act as risk factors for AMD and are likely to influence differential responses to AMD treatments (Francis 2011; Abedi *et al.*, 2013). Genetic susceptibility can be modified by environmental factors; thus, together, these factors are highly predictive of onset and progression (Seddon *et al.*, 2011).

Polymorphism, a particular genetic variation, occurs when a variation is seen at a specific locus with a frequency of >1% of the population; mutation occurs less frequently (Keats and Sherman 2013). Single nucleotide polymorphisms (SNPs) are the most common genetic polymorphism comprising 90% of human variation. This is defined as a variation in a single base pair of a DNA sequence (Kruglyak and Nickerson 2001). Genetic variants are important because they serve as genetic markers and help determine those genes which confer increased or decreased risk of several diseases, including AMD, within individuals (Leveziel *et al.*, 2011).

The discovery of susceptibility genes for AMD would shed light on the critical biological processes involved in AMD development and progression. SNPs in genes such as *complement factor H* (*CFH*), *complement component 3* (*C3*), and *vascular endothelial growth factor* (*VEGF*) have all been found to predispose individuals to the development of AMD (Janik-Papis *et al.*, 2009; Chen *et al.*, 2010). Such as, *CFH* is a negative regulator of the alternative pathway of the complement system, and thus could play a central role in AMD pathogenesis; multiple SNPs that alter *CFH* function might thus contribute to the development of AMD (Gangnon *et al.*, 2012). Other candidate genes studied in association with AMD include *High-Temperature Requirement A1* (*HTRA1*) and *Age-related maculopathy susceptibility 2* (*ARMS2*) genes, which have been examined in various population with conflicting results (Kanda *et al.*, 2007; Francis *et al.*, 2008; Kanda *et al.*, 2010; Abbas and Azzazy 2013).

A decade ago, AMD was largely untreatable. However, new pharmaceuticals based on suppression of *VEGF* have substantially changed the management of the disease (Brown *et al.*, 2006; Rosenfeld *et al.*, 2006). The recognition of the key role that *VEGF* plays in choroidal neovascularisation (CNV) pathogenesis led to the development of *VEGF* inhibitors (ranibizumab, bevacizumab, and afibercept), which are typically given via intravitreal injection (Cook *et al.*, 2008; Stewart 2012). Anti-*VEGF* helps to slow severe vision loss by reducing the growth of abnormal blood vessels and slowing their leakage; in some cases, this could also improve vision (Bird 2003). Retrospective studies have been conducted to further investigate and survey compliance with and outcomes of anti-*VEGF* treatments and to investigate responses in AMD patient (Cohen *et al.*, 2013; Korb *et al.*, 2013). Anti-*VEGF* therapy is also prescribed for other eye diseases such as polypoidal choroidal vasculopathy (PCV) (Kim *et al.*, 2015), diabetic macular oedema (Karadzic *et al.*, 2015), and diabetic retinopathy (Vaziri *et al.*, 2015).

As knowledge of AMD increases, association studies have increasingly been used to study drug responses and susceptibility to adverse drug reactions, resulting in the identification of some novel pharmacogenetic associations (Lee *et al.*, 2009; Hagstrom *et al.*, 2013; Kitchens *et al.*, 2013). Several studies have been conducted on genetic polymorphisms in response to anti-*VEGF* agents, with conflicting results in various populations (Francis 2011; Kang *et al.*, 2012; Kitchens *et al.*, 2013; Lotery *et al.*, 2013). This study thus mainly focuses on determining the association between genetic polymorphism of susceptibility genes and predispositions to AMD, together with an investigation of variable anti-*VEGF* treatment responses among AMD subjects.

Problem Statement

AMD is the most common cause of blindness in developed countries and accounts for 8.7% of all blindness worldwide, especially among those aged 60 years and above. The prevalence of AMD is thus likely to increase proportionally to the expected exponential population aging (Kawasaki *et al.*, 2010; Klein and Klein 2013). In Malaysia, the “4th Report of The National Eye Database”, reported that an increase in AMD prevalence was expected based on the increasing aging population in Malaysia (Salowi and Goh 2012). Recent findings on the global prevalence of AMD suggest that the largest projected number of AMD cases will be observed among Asians, despite Asians having

a lower AMD prevalence in earlier studies; this is expected to increase more rapidly than in other world regions, as Asians account for more than 60% of the world population (Wong *et al.*, 2014).

Treatments for AMD have begun to emerge since the introduction of intravitreal anti-VEGF therapy that can slow vision loss in AMD patients and improve their quality of life. However, variable treatment responses have been observed and since then, researchers are keen in identifying the causes of this disease to prevent it and delay its progression. It is well known that apart from environmental factors, genetic factors also play a role in susceptibility of AMD. Therefore, several studies have been carried out to determine the candidate genes in predisposition to AMD in various populations with conflicting results (Almeida *et al.*, 2009; Lim *et al.*, 2012; Ratnapriya and Chew, 2013). Most reported data concern polymorphisms in the complement factor, vascular endothelial growth factor A (VEGFA), high temperature requirement A1 (HTRA1) and age-related maculopathy susceptibility 2 (ARMS2) susceptibility genes in association with AMD development. The basis for determining the genetic factor of AMD is to improve the preventive efforts, diagnosis, and treatment through a better understanding of the underlying disease mechanisms, and ultimately to enhance the quality of life of elderly people.

Unfortunately, some individuals do not benefit from treatment for AMD and continue to lose vision, particularly on anti-VEGF therapy. The genetic profile of patients is thought to bring about this variability in therapeutic responsiveness. To date, a few studies with limited candidate genetic variants have been performed to investigate the association with response to intravitreal anti-VEGF agents in patients with neovascular AMD. A high possible relationship between polymorphisms of the *CFH*, *HTRA1* and *ARMS2* gene with the variable response to ranibizumab treatment has been reported in various populations; However, there is still a lack of data available in Malaysia on the genetic and pharmacogenetic associations with AMD. The current study thus provides an opportunity to explore different profiles of genetic variants in relation to their response to AMD treatment compared to the other populations along with ethnic diversity in AMD-associated polymorphisms.

Study Significance

The aim of conducting research is often to examine the association between possible risk factors for a disease and occurrence of the disease. A retrospective cohort study is a type of study that can provide information on the relationship between risk factors and disease. Furthermore, such data can be used to compare prevalences between different populations and also to examine trends or severity over time. The present retrospective study aims to observe patterns of treatment among retinal disease patients and thus determine possible risk factors related to patients receiving these treatments. While many treatment pattern studies have been reported in various countries (Ergun *et al.*, 2004; Curtis *et al.*, 2012; Lad *et al.*, 2014; Parikh *et al.*, 2016), the majority of these have focused on patients of European descent, with fewer studies investigating treatment trends in Asian populations (Koh *et al.*, 2011; Ng *et al.*, 2014; Teo *et al.*, 2014), but it must be recognised that trends in Asia might be different due to heterogeneity; additionally, this heterogeneity might result in a different prevalence of

retinal diseases such as AMD, which in turn would support different treatment trends. Conflicting results have been reported in terms of treatments in Asia, and there is a general lack of information available on treatment patterns of ranibizumab and photodynamic therapy (PDT), especially in Malaysia.

In addition, identifying the susceptibility genes for AMD could also help further understanding of the pathophysiology of the disease. The potential impact of genomic information in terms of selecting suitable treatments for AMD may also aid in recognising those at higher risk of developing the disease and lead to new preventive approaches. This study attempts to determine the frequency of genetic variations in candidate genes that may be associated with the pathogenesis of AMD and variable treatment response to anti-VEGF therapy. Association analyses are performed by comparing cases and controls to study the candidate genes underlying the disease. Possible candidate genes associated with AMD might also influence the variable anti-VEGF treatment response among patients; hence, pharmacogenetic analysis is also performed in this study. Although age, diet, lifestyle, environment, and body condition can influence an individual's response to treatment, knowledge of their genetic makeup might also play a role in providing treatments with greater safety and efficacy, leading to an overall decrease in the cost of health care. Furthermore, pharmacogenetic findings may enable doctors to prescribe the best treatments from the beginning simply by analysing the genetic profile of the individual in question, potentially reducing recovery time.

Conflicting findings are very common in genetic studies, which could be due to confounding factors such as ethnic diversity or different genetic backgrounds in different populations which influence genetic makeup. Regardless of these confounding factors, however, candidate gene analysis provides a better approach for identifying the genotype-phenotype correlations of various populations. Gene expression analysis is also conducted by comparing the expression levels, to further clarify the biological function of the candidate genes. This also provides a better understanding of differential gene expression between normal biology and disease physiology. The expected outcome of the current study could be beneficial in terms of contributing to genetic databases on AMD development in the Malaysian population, while the findings on variable treatment responses to anti-VEGF therapy could also be useful in the future management of the disease. In the future, identifying genetic codes will allow individuals to make environmental and lifestyle changes at an early age to avoid or lessen the severity of developing AMD. The findings in this study could also provide useful information to enable thorough monitoring and appropriate treatments being prescribed to AMD patients, maximising therapy efficacy.

Hypotheses

1. Significant changes occurred in treatment patterns for ranibizumab and PDT between 2010 and 2014 in Malaysia.
2. The environmental risk factors and gene polymorphisms of selected genes highly influence the development of neovascular AMD.
3. There are certain genetic predispositions to treatment responses to anti-VEGF agents among neovascular AMD subjects.

4. Genes are differentially expressed between genotypes of selected gene polymorphisms.

Main Objective

To identify the patterns of treatment of various eye disorders and to identify the environmental and genetic risk factors (gene polymorphisms of the selected genes) for neovascular AMD, in response to anti-VEGF therapy.

Specific Objectives

1. To examine the trends in the use of ranibizumab and PDT in Malaysia.
2. To determine the demographic and environmental risk factors for neovascular AMD subjects.
3. To determine the genotypic and allelic frequencies of the selected gene polymorphisms, *C3* (*R102G*) and *VEGF* (-460 *C/T* +405 *G/C* and insertion/deletion (*I/D*)) in neovascular AMD subjects.
4. To determine the association of genetic variants of *C3* (*R102G*) and *VEGF* (-460 *C/T* +405 *G/C* and *I/D*) genes in neovascular AMD and control subjects.
5. To determine the association of *CFH* (*Y402H*) gene polymorphism on responses to ranibizumab therapy among neovascular AMD subjects.
6. To determine the association of *HTRA1* (-625 *G/A*) and *ARMS2* (*A69S*) gene polymorphism and gene expression pattern on responses to ranibizumab therapy in neovascular AMD subjects.

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