UNIVERSITI TEKNOLOGI MARA

DEVELOPMENT OF PCR METHOD FOR DETECTION OF GENETIC POLYMORPHISM OF CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED PROTEIN 4 (CTLA4) GENE IN TYPE 1 DIABETES MELLITUS (T1DM)

SORAYA BINTI ROSLI

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

ACKNOWLEDGEMENTS

Alhamdulillah, I am so blessed and thankful to The Almighty for the chances, strength and ability He showers me through the journey of doing this study.

I would like to express my appreciation and thankful to my supervisor, Assoc. Prof. Dr. Hamid Fauzi for giving me the chances to conduct this study besides his guidance and explanation during the practical and discussion. Special thanks to all the members of BRAIN Laboratory- Dr. Vasudevan Mani, Dr. Rakesh Kumar Mishra and post-grad students for giving me the chance to conduct this study in their lab.

I also would like to thanks my family and friends for their help, support and understanding for this whole two semesters until the completion of this study.

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ABSTRACT

Type 1 Diabetes Mellitus is a condition in which the β cells that produce insulin undergo autoimmune destruction. It is associated with susceptibility gene of *HLA* region as well as non-MHC loci for example *CTLA4* gene. A/G transition at position 49 of exon 1 of the *CTLA4* gene results in threonine to alanine substitution and was reported to have association with Type 1 Diabetes Mellitus. Objective of this study is to develop genotyping method for polymorphism detection of *CTLA4* gene with Type 1 Diabetes Mellitus. Primers were designed and conditions for PCR were manipulated to obtain the most optimized PCR condition. 1st PCR was run at annealing temperature of 55°C and the intensity of the bands is higher as compared to annealing temperature of 58°C. Both wild type and mutant type bands appeared at different densities during the 2nd PCR analysis for all the five samples. More studies on association of *CTLA4* gene with Type 1 Diabetes Mellitus are needed especially on Malaysian population as early detection is able to slow down or even stop disease progression and hence improve their quality of life.

CHAPTER 1

INTRODUCTION

1.1 Background

Diabetes mellitus (DM) is a metabolic disorder that is common nowadays due to various causes and several complications (McCowen & Smith, 2013). DM can be classified into two major categories that are Type 1 diabetes mellitus (T1DM) and Type 2 diabetes mellitus (T2DM) (Acharje et al., 2013).

Generally, hyperglycemia is either due to the inadequate insulin produce by the pancreas or cells of the body do not respond properly to the insulin produced. T1DM is immune mediated diabetes in which the insulin producing pancreatic β cells undergo autoimmune destruction (Sudagani & Hitman, 2013). T2DM is characterized by the ineffective use of insulin by the body due to insulin resistance and is also a multifactorial disease in which genetic and environmental factors are contributing to it.