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DIFFERENTIAL GENE EXPRESSION OF PERIPHERAL ARTERIAL DISEASE IN TYPE 2 DIABETES MELLITUS AMONG THE FILIPINO POPULATION

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OBJECTIVE

The study aims to identify differentially expressed genes in Filipinos with peripheral arterial disease (PAD) and type 2 diabetes mellitus (T2DM) as possible biomarkers.

METHODOLOGY

A total of 100 Filipinos participated in this 1:2 unmatched case-control comparing participants of T2DM with PAD, and persons without diabetes. Gene expression profiling of participant's peripheral blood mononuclear cells was done via multiple microarray platforms [Illumina's Whole-Genome Gene Expression Direct Hybridization and Affymetrix Human Clariom S (human) Assays] covering over 18,000 possible genes. Differentially expressed genes were determined using the limma package to perform for Bayes t-statistics, and fold change to compute for varying gene expression between groups.

RESULTS AND DISCUSSION

There are 427 significant genes (*p-value* of <0.001) differentially expressed in PAD in T2DM compared with persons without diabetes. Majority of these genes identified are related to metabolic processes, cellular organization/differentiation, endothelial cell proliferation, and immune responses. These processes are implicated in PAD and may be contributory to its vascular pathology. Genes involved in endothelial cell proliferation are amongst the top in significance: *FGFBP1* (fibroblast growth factor-binding protein 1) (*p-value* 3.90×10^{-6}), *FGF2* (fibroblast growth factor) (*p-value* 4.92×10^{-6}), *AKT3* (AKT serine/threonine kinase 3) (*p-value* 6.78×10^{-5}), *GHSR* (growth hormone secretagogue receptor) (*p-value* 2.72×10^{-4}), *THBS4* (thrombospondin 4) (p-value 4.74×10^{-4}), *PDCL3* (phosducin like 3) (*p-value* 5.77×10^{-4}), and *MDK* (midkine) (*p-value* 9.39×10^{-4}).

CONCLUSION

The study's results identified multiple genes that may contribute to the development of PAD in T2DM which can aid in future molecular-based approaches after validation studies.

KEY WORDS

diabetes mellitus type 2, gene expression, peripheral arterial disease

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GLYCAEMIC CONTROL OF TYPE 2 DIABETIC PATIENTS WITH SELF-MONITORING OF BLOOD GLUCOSE DURING RAMADAN FASTING IN JAKARTA INDONESIA

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INTRODUCTION

Ramadan is a month in the Islamic calendar when Moslems fast every day. According to demographic study in 2010, Islam believers in Indonesia equal to 87,18% of its total population. The purpose of this study was to evaluate glucose reading provided by self-monitoring of blood glucose (SMBG) in type 2 Diabetes (T2D) patients during Ramadan fasting.

METHODOLOGY

This is an observational study that recruited T2D patients who practiced fasting during the month of Ramadan. Patients were advised to monitor their blood sugar on the last day of each week of Ramadan including before and after *suhoor*, in the morning, at noon, in the afternoon, also before and after *iftar*. Patients were educated before Ramadan about diet, medication and SMBG by glucose reading meters. We evaluated glycaemic control of patients and the rates of hypoglycaemia and hyperglycaemia

RESULTS AND CONCLUSION
Twenty-five patients fulfilled SMBG record with a total of 458 readings by glucose meters. Mean of blood glucose levels during fasting is 164.34±72.661 mg/dL, with minimum 72 mg/dL and maximum 443 mg/dL. After *iftar* evidently has the highest mean blood glucose level (214,1 mg/dL) between other times. There are only two patients who reported symptomatic hypoglycaemia, but no one categorized as biochemical hypoglycaemia that should be recommended to break the fast at the day. The rate of hyperglycaemia is 7.6% of SMBG readings among all the results.

KEY WORDS
glycemic control, type 2 diabetes, ramadan fasting, self-monitoring of blood glucose

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POLYMORPHISM IN MTNR1B VARIANT GENE IS PROTECTIVE AGAINST GESTATIONAL DIABETES MELLITUS AMONG FILIPINO PREGNANT WOMEN

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INTRODUCTION
This study aimed to determine the association of rs10830963 polymorphism on the MTNR1B gene with insulin resistance (IR), insulin sensitivity (IS), and the risk of developing gestational diabetes mellitus (GDM) among Filipino pregnant women.

METHODOLOGY
A cross-sectional study was conducted involving 232 Filipino pregnant women, 72 GDM cases and 160 non-GDM women. DNA samples were extracted using a commercially available kit with slight modifications. Rs10830963 was genotyped using *taqman* allelic discrimination assay. Mann-Whitney U-test was used to determine the significant difference of various phenotypic characteristics between pregnant women with and without GDM. Person's chi-square was used to determine the association of the said polymorphism with GDM. Lastly, odds ratio computation was used to determine the likelihood of developing GDM depending on the pregnant women's genotypic and allelic characteristics.

CONCLUSION
The occurrence of rs10830963 polymorphism in MTNR1B gene is protective against the development of GDM among Filipino pregnant women but is not associated with insulin resistance nor insulin sensitivity

KEY WORDS
gestational diabetes mellitus, gene polymorphism, MTNR1B gene