IBMS

JOURNAL-BASED LEARNING EXERCISES

Each article's contents should be read, researched and understood, and you should then come to a decision on each question. The pass mark is 17 out of 20 questions answered correctly. JBL exercises may be completed at any time until the published deadline date. Please select your choice of correct answers and complete the exercises online at: **www.ibms.org/cpd/jbl**

DEADLINE WEDNESDAY 2 JANUARY 2019			
Genetic polymorphisms in <i>KCNJ11</i> (<i>E23K, rs5219</i>) and <i>SDF-1</i> β (<i>G801A, rs1801157</i>) genes are associated with the risk of type 2 diabetes mellitus. Rizvi S, Raza ST, Mahdi F, Singh SP, Rajput M, Rahman Q. <i>Br J Biomed Sci</i> 2018; 75 (3): 139–44. Assessment No G101018		Potential value of circulating microRNA-126 and microRNA-210 as biomarkers for type 2 diabetes with coronary artery disease. Amr KS, Abdelmawgoud H, Ali ZY, Shehata S, Raslan HM. Br J Biomed Sci 2018; 75 (2): 82–7. Assessment No C101018	
01	More than 150 distinct genetic loci, with more than 120 variants, have been identified that may be involved in the pathogenesis of diabetes.	01	The International Diabetes Federation (IDF) listed Egypt among the world's top 10 countries in the number of patients with diabetes.
02	Type 2 diabetes has a multifactorial aetiology, where genetic factors in combination with environmental factors confer risk of disease development and progression.	02	MicroRNAs are highly conserved large non-coding endogenous RNA molecules involved in the regulation of key processes such as proliferation, differentiation, apoptosis and metabolism.
03	Genetic alterations in <i>KATP</i> are associated with diabetes due to the effect of KCNJ11 channels on insulin secretion.	03	MiR-210 is abundantly expressed in endothelial cells, maintains endothelial homeostasis and vascular integrity via regulating several components of the vascular endothelial growth factor pathway.
04	Genomic DNA was extracted from peripheral blood leucocytes using the standard phenol-chloroform extraction method.	04	Plasma miRNAs are potential non-invasive biomarkers for the diagnosis and prognosis of many diseases.
05	Fasting blood sugar was measured by the glycerol phosphate oxidase–peroxidase amidopyrine method.	05	miR-126 levels are reduced in diabetes, while miR-210 levels are raised in diabetes.
06	Cases and controls were matched for age (45 and 46 years, respectively) and gender (99 males/101 females and 98 males/102 females, respectively).	06	Type 2 diabetes is a metabolic disorder characterised by insulin resistance and pancreatic α -cell dysfunction.
07	Mean creatinine level was 70 $\mu mol/L$ in healthy controls and 50 $\mu mol/L$ in cases.	07	In this study, venous blood samples for glucose determination were taken into K-EDTA tubes.
08	Polymorphisms in <i>KCNJ11</i> result in neonatal diabetes and congenital hypo-insulinaemia.	08	Plasma relative expressions of miR-126 and miR-210 were 0.38 \pm 0.03 and 5.3 \pm 0.56 in diabetes alone versus 0.08 \pm 0.03 and 21.44 \pm 0.97 in diabetes with coronary artery disease (CAD).
09	Studies have shown that the <i>rs5219</i> variant may alter the charge of the ATP-binding region and decrease channel sensitivity to ATP.	09	Quantitative real-time polymerase chain reaction (qRT-PCR) was performed using a TaqMan microRNA assay for 40 cycles in duplicate reactions containing the prepared cDNA.
10	Stromal cell derived factor-1 (SDF-1), also known as CXCL12, is a peptide chemokine that is coded for by a gene on chromosome 10q11.1.	10	Area under the curve (AUC) for plasma miR-210 in type 2 diabetic patients with CAD versus controls was 0.95.
11	Many of the published links between polymorphisms in <i>KCNJ11</i> and <i>SDF-1β</i> and diabetes consider multiple genotype models.	11	High-density lipoprotein cholesterol (HDL-c) level (mean \pm SD) in the control group was 1.0 + 0.6 mmol/L.
12	Figure 1 shows a 3% agarose gel picture of <i>Mspl</i> -digested products.	12	A total of 100 patients with type 2 diabetes and 100 controls were enrolled in the study.
13	A number of risk alleles for diabetes and mutations in several genes may add up and predispose an individual to increased risk of disease.	13	The results showed no significant difference in age and gender between the three groups studied.
14	Distribution of <i>SDF-1β</i> (<i>G801A</i> , <i>rs1801157</i>) genotypes according to dominant, recessive and additive models showed no significant differences in dominant and additive models between cases and controls.	14	In patients with diabetes alone there was a significant inverse correlation between miR-126 and fasting glucose and HbA1c.
15	Genetic factors are now regarded as the leading cause of diabetes.	15	There was a significant difference in disease duration between the diabetes group and the diabetes with CAD group (<i>P</i> <0.001).
16	ATP-sensitive potassium channels (KATP) are transmembrane proteins present on beta cells.	16	The ROC curve of miR-210 significantly discriminated between both patient groups and controls as well as between diabetes patients with and without CAD.
17	Genotyping data were compared between cases and controls using the $\chi 2$ test.	17	Low serum levels of miR-210 have been reported in rheumatoid arthritis.
18	In this study, genetic polymorphism analysis was performed by loop-mediated isothermal amplification.	18	The epigenetic effect of miR-126 is encoded within an intron of Egfl7.
19	G801A polymorphism has been studied in various diseases, including diabetes, HIV infection and cancer.	19	miR-210 promotes vascular endothelial growth factor (VEGF) signalling by suppressing two negative regulators of the VEGF pathway.
20	In this study, the frequency of AA genotype in cases was 4.5%, which was lower than reported in Iranian diabetics.	20	Ordinal logistic regression analysis revealed a significant association between groups and miR-126 and HDL-c.
REFLECTIVE LEARNING			
01	Type 2 diabetes mellitus (T2DM) is a global health problem resulting from the interaction of environmental and genetic factors. Based on the results of a literature search, what other genetic factors have been implicated in T2DM?	01	Micro-ribonucleic acids (miRNAs) are currently in the spotlight as post- transcriptional regulators of gene expression, and the field of miRNAs in cardiovascular biology and disease has expanded at an incredible pace. Discuss the implications for pathology.
02	Explain the difference between the terms dominant, recessive and additive in relation to the effects of different genotype models.	02	MicroRNAs in diabetes and diabetes-associated complications. Discuss.