C-1

LEMBAR
HASIL PENILAIAN SEJAWAT SEBIDANG ATAU *PEER REVIEW*
KARYA ILMIAH : JURNAL ILMIAH

Judul Artikel Ilmiah :Dietary Fat Intake and Changes in Tunica Intima-Media Thickness Internal Carotid Artery in Post Ischemic Stroke Patients

Penulis Artikel Ilmiah : **DWI PUDJONARKO**, DODIK TUGASWORO, ISNAWAN WIDYAYANTO

Status Pengusul : **Penulis pertama**/penulis anggota/penulis korespondensi

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- [✓] Jurnal Ilmiah Internasional bereputasi
- [ ] Jurnal Ilmiah Nasional Terakreditasi
- [ ] Jurnal Ilmiah Nasional tidak Terakreditasi

I. Hasil Penilaian *Peer Review* :

Komponen Yang Dinilai	Nilai Maksimal Karya Ilmiah (isikan di kolom yang sesuai)			Nilai Akhir Yang Diperoleh
	Internasional	Nasional Terakreditasi	Nasional tidak Terakreditasi	
	40			
a. Kelengkapan dan Kesesuaian unsur isi artikel (10%)	4			3.50
b. Ruang lingkup dan kedalaman pembahasan (30%)	12			10.50
c Kecukupan dan kemutahiran data/informasi dan metodologi (30%)	12			10.50
d. Kelengkapan unsur dan kualitas penerbit (30%)	12			10.50
Nilai Total = (100%)	**40**			35.00
Nilai pengusul =			**(60% x 35 =21)**	**21,00**

KOMENTAR/ULASAN PEER REVIEW

Kelengkapan dan Kesesuaian Unsur	:	Abstrak disajikan dengan baik dan informatif, Pendahuluan-metode penelitian dan hasil penelitian, diskusi dan referensi sudah sesuai kaidah ilmiah yg baik
Ruang Lingkup dan Kedalaman Pembahasan	:	Ruang lingkup keilmuan sudah sesuai bidang ilmu pengusul dan pembahasan cukup dalam dan luas dengan membandingkan hasil dg penelitian2 sebelumnya
Kecukupan & Kemutakhiran Data & Metodologi	:	Data dikumpulkan dengan menggunakan kuesioner dan alat diagnostik yang cukup akurat. Metode penelitian kohort schingga akurat dalam pengumpulan data.
Kelengkapan Unsur dan Kualitas Penerbit	:	Jurnal Internasional terindeks Scopus Q4 dg SJR 0.12

Semarang, 18 Mei 2020
Penilai 1

Prof. Dr. dr. TRI NUR KRISTINA, DMM, M.Kes.
NIP 19590527 198603 2 001
Unit kerja : Fakultas Kedokteran
Bidang Ilmu : Ilmu Kedokteran
Jabatan/Pangkat : Guru Besar

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Kategori Publikasi Jurnal Ilmiah (beri ✓ pada kategori yang tepat)	:	✓ Jurnal Ilmiah Internasional Bereputasi ☐ Jurnal Ilmiah Nasional Terakreditasi ☐ Jurnal Ilmiah Nasional tidak Terakreditasi

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		Internasional	Nasional Terakreditasi	Nasional tidak Terakreditasi	
		40			
a.	Kelengkapan dan Kesesuaian unsur isi artikel (10%)	4			3,50
b.	Ruang lingkup dan kedalaman pembahasan	12			11,00
c	Kecukupan dan kemutahiran data/informasi dan metodologi (30%)	12			10,60
d.	Kelengkapan unsur dan kualitas penerbit (30%)	12			10,50
Nilai Total = (100%)		**40**			**35,60**
Nilai pengusul =				**60% x 35,6 =**	**21,36**

KOMENTAR/ULASAN PEER REVIEW

Kelengkapan dan Kesesuaian Unsur	:	Abstract: lengkap mulai background, method, result, conclusion sampai acknowledgement ; References: 50% > 10 tahun namun mendukung penelitian
Ruang Lingkup dan Kedalaman Pembahasan	:	Sesuai dengan lingkup keilmuan, dengan kedalaman bahan cukup dalam dan bermanfaat dengan menganalisis diet lemak terhadap perubahan ketebalan
Kecukupan & Kemutakhiran Data & Metodologi	:	Studi Prospektif kohort dengan follow up 6 bulan --> data cukup akurat untuk dianalisis --> analisis bivariat dan multivariat hasil bermakna
Kelengkapan Unsur dan Kualitas Penerbit	:	Simpulan bahwa terdapat korelasi positif antara diet lemak per hari dengan ketebalan tunica intima pembuluh darah --> dapat digunakan untuk edukasi

Semarang,
Penilai 1

Prof. Dr. drg. OEDIJANI, M.S.
NIP 19490209 197901 2 001
Unit kerja : Fakultas Kedokteran
Bidang Ilmu : Kedokteran Gigi
Jabatan/Pangkat : Guru Besar

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Partners

Sharjeelisonline2002@yahoo.com

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ORIGINAL ARTICLE

Cytomegalovirus Infection and Glutamic Acid Decarboxylase Antibodies in Type 2 Diabetic patients

RANATALIB AI-NAFAKH[1], SAIFJABBARYASIR[2] , SHAYMAA ABDUL LTEEF AL-FADHUL[2] , EKHLAS SABAH HASSAN [3]
[1]*Lecture, Department of Medical Microbiology, Faculty of Medicine, University of Kufa, Najaf , Iraq.*
[2]*Assistant Professor, Department of Medical Microbiology, Faculty of Medicine, University of Kufa, Najaf , Iraq.*
[3]*Assistant Professor, Specialist in Internal Medicine, Department of Pharmacology and Therapeutics, Faculty of Medicine, University of Kufa, Najaf , Iraq.*
Correspondence to Dr. Ekhlas Sabah Hassan, E- mail: ekhlass.khazaal@uokufa.edu.iq, Phone: 009647803012849

ABSTRACT

Background: At present, whether human cytomegalovirus (HCMV) infection is associated with type 2 diabetes mellitus (T2DM) is debatable.
Aim: To obtain information about the prevalence of CMV IgG antibodies among type 2 diabetic patients and to identify age, gender, and laboratory differences.
Methods: This cross-sectional study was carried out among DM type2. Seven hundred eighty-three sera type 2 diabetic patients were tested for the presence of HCMV-IgM&IgG antibodies, GAD, and cytomegalovirus DNA by PCR.Chi-square test (χ2-test) was applied for testing the significant association between different variables.
Results: The study included 783 diagnosed cases of type 2 diabetic mellitus**,** 261 of them (33%) were HCMV-IgG positive. Further investigations of HCMV-IgG seropositive samples revealed that 121(46%) tested positive to HCMV-IgM with a significant statistical differences of HCMV IgM within gender (P=0.02) and age groups (P<0.001).PCR test for diagnosis of HCMV showed that 81(31%) of samples were positive. Searching for presence of GAD antibodies in all HCMV IgG positive samples revealed that 100(38%) of patients were tested positive, however, statistically there was no significant association between positive anti-GAD antibodies with age groups and gender (P>0.05)**.**
Conclusion: Our study determined that the higher prevalence of HCMV IgG in DM2 patients, depending on the results of IgM & PCR testes, more than one-third of HCMV IgG seropositive were having recent HCMV infection, about one-third of type two diabetic patient were tested positive to anti-GAD antibodies.
Keywords: HCMV, type 2 DM, anti-GAD antibodies,

INTRODUCTION

he worldwide prevalence of type 2 diabetes mellitus (T2DM) is estimated to have multiplied over the past decades and now includes rapidly increasing numbers of younger age groups. The condition is considerably more complex with much earlier onset, since there is a higher overall risk of life-time complications [1]. T2DM prevalence has risen faster in low and middle-income countries than in high-income countries[2]. Cytomegalovirus (CMV)is a virus found around the world.Itis a ubiquitous beta-herpes virus and herpesviridae that infects the majority of humans[3]. It is a common virus that infects people of all ages.CMV infection iscommonly asymptomatic in healthy individual,but can cause severe disease in immunocompromised children or adultsand in newborn. A person can also be re-infected with a different strain (variety) of the virus[4].Active CMV infection or reactivation from a latent state is considered potentially a cofactor for inflammatory disease [5].CMV may accelerate immune responses by prompting the accumulation of late-differentiated CD8+ and CD4+ T-cells which produce pro-inflammatory cytokines and thereby create a more pro-inflammatory background that might be causing T2DMonset[6].A Glutamic Acid Decarboxylase(GAD)is an enzyme that present in the pancreas and the nervous system,its aids the body produce a specific neurotransmitter called gamma-aminobutyric acid (GABA), which is an amino acid that decreases the extent of communication to and from the nerves.GAD can also trigger the immune system to produce autoantibodies against healthy cells[7]. GAD antibodies test is helping to discover whether someone has either Latent Autoimmune Diabetes of Adulthood (LADA) or type 1 diabetes. The test is done to define which type of diabetes someone has.It is particularly useful for adults more than 30 years who get diabetes where diagnosis of T2DM is uncertain[8].This research aims toobtain information about the prevalence of CMV IgG antibodies among type 2 diabetic patientsand to identify age, gender, and laboratory differences.

MATERIALS AND METHOD

This was a cross-sectional study that conducted in diabetes and endocrine gland center in AL-Sader teaching hospital in Al-Najaf Province during the period from January to July2019.The caseswereascertained as type 2 DM andchecked throughtheir hospitalrecords. All type 2 diabetic patients attendedthediabetic outpatientclinic during the period of the study were included.

We tested seven hundred eighty-three sera from type 2 diabetic patients aged from 20 to 70 years, two hundred sixty-one of them were founding Gpositive for HCMV .IgGsero positive samples were collected to determine glutamic acid decarboxylase (GAD) antibodies and HCMVIgM antibodies. Anti-GAD antibody and specific anti-cytomegalovirus antibody (IgG and IgM) were detected by the ELISA test kit. (BioCheck,Inc.). Wholly blood samples with EDTA were detecting cytomegalovirus DNA. DNA extraction kit and PCR amplification kit are (DNA –Sorb-B)where supplied by Sacaca Biotechnology, Italy. DNA isolation and PCR amplification and thermocycling

ORIGINAL ARTICLE

Protein Expression of Human Brain Microvascular Endothelial Cells in Response to Meningitic C. Sakazakii: in Vitro and in Silico Analyses

HAYAT ALI ALZAHRANI
Department of Medical Laboratory Technology, Faculty of Applied Medical Sciences, Northern Border University, Arar, Saudi Arabia
Correspondence to Dr. Hayat Ali Alzahrani, Email: dr.hayatalzahrani@hotmail.com , Tel: +966146615753

ABSTRACT

Background: Despite the confirmed association between infant meningitis and necrotizing enterocolitis and C. sakazakii lettile known about the pathogenic interaction of C. sakazakii with host cells.
Aim: To characterize functional and regulatory proteins that are differentially expressed in Human brain microvascular endothelial cells (HBMEC) in response to meningitic *C. Sakazakii*
Method: Liquid Chromatography with tandem Mass Spectrometry (LC-MS/MS) analysis was performed to the protein extracted from HBMEC in response to meningitic *C. Sakazakii* in serial time course. Bioinformatics analysis was carried out using SCIEX OneOmics cloud processing software and Advaita's iPathway**.**
Results: In response to the exposure, the LC-MS/MS analysis indicated different changes in 57 proteins: nucleic acid binding proteins, transporter proteins and structural molecule activity proteins. 1, 9 and 29 pathways were significantly affected after 60, 90 and 120 minutes, respectively. In addition, 179, 242 and 490 gene ontology components were found to be significantly enriched. Interestingly, the tight junction pathway , which is most important component regulating to brain damage, was triggered at 120 minutes post-infection with the C. sakazakii meningitic strain.
Conclusion: We conclude that the data presented in this study may facilitate a better understanding of this bacterium, which can cause irreparable damage to a new-born baby's brain. This study open up many new avenues into the research concerning this pathogenicity.
Keywords: Proteomic; HBMEC cells; C. sakazakii; Meningitis

INTRODUCTION

Cronobacter is an emerging pathogen of concern that is associated with severe and often fatal cases of infant meningitis and necrotising enterocolitis. Although a great deal of research has been conducted over the past decade to shed light on the virulence of *Cronobacter spp.* and elucidate their mechanisms of pathogenicity, survival and genetics, there are still many hidden traits to be revealed[1]. Therefore, *in vitro* studies have continued to investigate these phenomena and can potentially lead to better control of this pathogen and minimise its infections in infants, as well as the elderly and other immunocompromised people[1].

Measurement of protein expression has been detected in *Cronobacter spp.* using proteomic tools to explain the adaptation mechanisms of osmotically stressed cells[2]. Virulence of *C. turicensis was investigated by focusing on* proteins characterisation and leading to conclude the involved molecular mechanisms[3].

Likewise, another study by histopathological analysis the potential virulence factors at the proteomic level detected[4]. All of the proteomics studies so far have successfully evaluated *Cronobacter spp.* at the protein level; however, the protein expression of infected host cells is a controversial topic that needs to be studied more[5]. Understanding how cells behave in the presence of a pathogen may provide key answers such as signaling during adhesion or a variety of other stressful responses during conditions[6]. Hence, the identification of pathogenic mechanisms is mainly based on the neat description of molecular process and the detailed protein expression profile .Thus, our study aims to investigate the protein expression modifications by proteomic analysis of HBMEC cells' response to meningitic C. sakazakii strain 767 to generate new insight into its pathogenetic mechanism. We opt to determine whole protein profiles of infected HBMEC cells with C. sakazakii strain 767 by comparing them to whole protein profiles of uninfected cells and evaluating whether the important proteins are up or down regulated over the exposure time. Further, differentially expressed proteins were classified based on the protein ontology to help us to analyse and understand functional and biological information about the identified proteins.

MATERIAL AND METHODS

Bacterial strain , cell culture and strain exposure: Convenient laboratory practices were monitored for microbes, chemicals, cell culture and operating laboratory devices. The strain was isolated from an eruption of *Cronobacter* meningitis infection[7]. Clinical isolate was selected based on the phenotype analysis and virulence assays of these strains and whole genome sequence availability[8].
Cell culture: *sakazakii* strain 767 was added to confluent monolayers of HBMEC cells ($1x10^6$) and incubated for 60, 90 or 120 minutes. Cell lysis, centrifugation, alkylation and reduction and trypsinisation were performed.
Liquid chromatography with tandem mass spectrometry (LC-MS/MS): Samples were concentrated to dryness in a Speed Vac set for aqueous solution evaporation (approximately 30–40 minutes). The samples were re-suspended and moved into a new LC vial (suspension solution: 20 µL acetonitrile 5% and formic acid 0.1%). Samples were chromatographically separated based on their affinity to a 20 cm C18 column using an