BioGecko Vol 12 Issue 03 2023

ISSN NO: 2230-5807

Assessment of some Biochemical Parameters among Covid-19 Patients in Al-Najaf Province

Zahraa Abdulridha Baqer AL-Phayyadh[1] and Khalida Kadhum AL-Kelaby[2]
[1]Department of biology sciences, Faculty of sciences, Kufa University, Iraq.
[2] Department of clinical and laboratory sciences, Faculty of pharmacy, Kufa University, Iraq.
Corresponding author

ABSTRACT
The coronavirus SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), which is responsible for the disease COVID-19 (coronavirus disease 2019), has infected over 9.5 million people and has caused more than 480,000 deaths globally, as of 24 June 2020.These are positive-sense single-strand RNA viruses with around 24 similar species from the family of coronaviridae. This family of coronaviridaeis further categorized as α, β, λ, and δ based on its distinct genetic features. However, among these, only alpha (α) and beta (β) coronavirus genera are pathogenic to mammalian and humans. Liver disease is a global health problem and is a primary cause of mortality and morbidity worldwide. Specifically, it accounts for approximately two million deaths per year worldwide. The common causes of mortality are the complications of liver cirrhosis, viral infection, and hepatocellular carcinoma (HCC).
Keywords: Covid-19, Liver dysfunction, Liver parameter.

INTRODUCTION TO THE STUDY

According to the genome characteristics, coronavirus is separated into four genera (α-CoV, β-CoV, γ-CoV, and δ-CoV). Novel coronavirus isolated from lower respiratory tract samples of patient with COVID-19 belongs to β-CoV. SARS-CoV-2 is the causative pathogen of COVID-19, identified as the seventh type of coronavirus to infect humans , six other kinds of coronaviruses are known to cause human disease, including Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome coronavirus (MERS-CoV) with high mortality rate. Four common human coronaviruses that cause mild to moderate upper respiratory tract illnesses, including 229E (α coronavirus), NL63 (α coronavirus), OC43 (β coronavirus), and HKU1 (β coronavirus), were first recorded in the 1960 s. Two other human coronaviruses are SARS-CoV and MERS-CoV, which lead to severe lung infections known as severe acute respiratory syndrome – SARS and the Middle East respiratory syndrome – MERS, respectively. The SARS-CoV outbreak occurred in 2002, starting in China and spreading to other countries, with a death rate of 11%. The MERS-CoV outbreak occurred in 2012, starting in Saudi Arabia and spreading to other countries, with a death rate of 37%. The new SARS 2 virus appeared for the first time in Wuhan, China, in late 2019 in December and spread quickly, which prompted the World Health Organization to declare a state of maximum health emergency in January 2020 and that the disease has become a global pandemic on 11 March 2020 , The outbreak of 2019-nCoV, which can affect both upper respiratory and lower respiratory tracts and causes unusual viral pneumonia.The first infection with SARS-COV-2 was discovered on the 24th of February in Iraq was for an infected Iranian visitor who visited Najaf Governorate. It reached its highest level in September of the same year with a weekly average of 4,500 infections, and then the number of infections began to decline gradually reaching its lowest level in mid-January 2021, with a rate of 750 confirmed infections throughout Iraq.

REVIEW OF LITERATURE

Fung *et al.*, (2020) Coronaviruses are crown shape peplomers, positive-sense ssRNA (single strand RNA) virus, which was reported with 80–160 nm size (Shang *et al*., 2020). Both SARS COV-1 and SARS COV-2, which are the new addition to the human coronavirus family, include (OC43, NL63, HKU1, and MERS) which belong to the genus β-Coronavirus, and (229E and NL63) that belong to the genus of α-Coronavirus

which contains a polycistronic genome. It encodes for the structural proteins that are included in the phenotype of the virus, along with the accessory proteins in the last third of the RNA strand. It also interferes with the manufacture of proteins that are not related to the formation of the structure of the non-structural proteins (nsp) virus near the N-end of the genome.

Fung *et al.,* (2020) It is a non segmented and RNA virus ranging from 26 to 32 kb, which is the largest known genome for an RNA virus . The SARS COV-2 genome consists of 29,903 nucleotides containing 16 open reading frames (Kim *et al.,* 2020). all coronaviruses share the same genome organization and expression pattern, with two large overlapping reading frames (ORF1a/b). The role of (ORF1a) (ORF1b) is to encode multiple proteins (pp1a) and (pp1b), both of which work through the mechanism of changing the ribosomal frame shift on the cleavage of the virus protease into 16 regions named non-structural protein (nsp) followed by ORFS for four major structural proteins:-spike (S), envelope (E), membrane (M), and nucleocapsid (N) (ORF1a) Wang *et al.,* (2020) encoded from 1 to 11(nsp) and (ORF1b) encoded from 12 to 16 nsp.Among the main combinations, there are a series of accessory genes (ORFs 3a, 3b, 6, 7a, 7b, 8b, 9b, and 16) which encode the accessory proteins that regulate infection and evade immunity but which do not incorporate with SARS COV-2 genome.Liu *et.al*., (2020) Spike protein plays an essential role in binding to receptors and is critical for determining host tropism and transmission capacity. It is functionally divided into S1 domain and S2 domain, responsible for receptor binding and cell membrane fusion respectively. The receptor binding domain of β-CoV is commonly located in the C-terminal domain of S1. SARS-CoV-2 spike protein has 10 to 20- fold higher binding affinity to human angiotensin-converting enzyme 2 (ACE2) than SARS-CoV does (Risku *et al* ., 2010). Phylogenetic analysis showed that SARS-CoV-2 shared a closer sequence homology toward the genomes of SARS-CoV than to that of MERS-CoV.

OBJECTIVES OF THE STUDY

Primary objective:

To study the effect of Covid-19 on the levels of some biomarker such as liver enzyme include aminotransferase (AST), alanine aminotransferase (ALT), albumin, lactate dehydrogenase (LDH) concentration

SCOPE OF THE STUDY:

The study aimed to analyze the association between liver biomarker with liver damage in patients with covid-19.

RESEARCH METHODOLOGY

Patients group

During the period from (10 December 2021 to 1Jon 2022) 150 (93 male & 57 female) sample are collected from covid-19 infected patients all of them (who have positive result to RT-PCR nasopharyngeal swab for SARS-2). Who attended to (Al-Najaf AL-Ashraf National center for COVID-19 screening). The patients were divided into two groups ,the first group included patients with covid-19 infection as well as liver dysfunction (26 patient). The second group represents covid-19 only infection without liver dysfunction (124 patient).

Control group

Fifty healthy individuals where included in this study as control group. The age was year ranging between (25) years to (82) year Clinical specimens.

Collection of samples

A-5 ml of fresh venous blood samples were collected from COVID-19 infected patients by sterile syringes which divided into (3 ml) of blood was saved in EDTA tubes for study gene polymorphism that stored at-20°C.

Two ml of blood put in gel tubes , left for 10-15 minutes to clot at room temperature and then they were centrifuged for 5 minutes at 3000 (rpm) to obtain pure serum. the separated sera sample have been divided into small 100-200 µl numerated and kept at -20 °C until used for chemical parameter.

RESULTS

During the period from (10 December 2021 to 1Jon 2022) 150 patients were diagnosed as COVID-19 according to the guidelines for diagnosis and management of COVID-19, In total, the median age was 50 years ranging between (25-83) years, all patients were nasopharyngeal swabs positive for covid-19 virus, in addition to 50 healthy persons as control, revealed in the following results:

Age distribution in patients and control subjects

In the current study the covid-19 patients ages ranged between (25-82) years. The age characteristic disease in that is illustrated in Table (4-1) showed that the highest frequency was among adult patients particularly in the age group >60 years and 51-60 year, 53 (35%) and 39 (26%), respectively, followed by age group 41-51 which was 33 (22%), the least was in age group 25-41 year which was 25 (16%), while the ages of control groups ranged between (25-80) years as shown in the table (4-1).

Table (4-1): The distribution of patients according to age groups

Age groups		Study groups	
		Control NO. (%)	Patients NO. (%)
A1	25-41 years	5 (10%)	25 (16%)
A2	41-51 years	5 (10%)	33 (22%)
A3	51-60 years	20 (40%)	39 (26%)
A4	>60	20 (40%)	53 (35%)
Total		50 (100%)	150 (100%)
Chi Square P- value		0.043[S]	

S= Significant, NO= Number

In the present study, 150 patients were diagnosed by chemical test to estimated liver enzyme dysfunction. From the results, it had been shown that the 26 (17%) case had different degrees of liver enzyme dysfunction on admission, while 124 (82%) case had normal liver enzyme function, as shown in the table (4-3).

Table (4-3). Findings for patients with covid-19 with and without liver impairment.

Liver biochemistry enzyme		
Patients	Number	Percentage(%)
Covid-19 with LD	26	17%
Covid-19 without LD	124	82%

Total	150	100%

Among 26 patients, 100% (26/26), 73% (19/26), 57% (15/26), 57% (15/26), 26% (7/26), 100% (26/26) and 30% (8/26) were abnormal in serum alanine Aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin (TB), albumin, gamma-glutamyl transferase (GGT), lactate dehydrogenase (LDH), and alkaline phosphate (ALP) respectively, as shown in the table (4-4).

Table (4-4). Findings for patients with covid-19 and liver impairment.

Liver biochemistry enzyme		
Covid-19 with LD		
Parameters	Covid-19 with LD NO.	Percentage (%)
ALT	26	(100%)
AST	19	(73%)
TB	15	(57%)
Albumin	15	(57%)
GGT	7	(26%)
LDH	26	(100%)
ALP	8	(30%)
Total	26	(100%)

ALT= Alanine Aminotransferase, AST= Aspartate Aminotransferase, TB= Total Bilirubin, GGT= Gamma Glutamyl Transferase, LDH= Lactate Dehydrogenase, ALP= Alkaline Phosphate, LD= Liver Dysfunction,.

REFERENCE

Adnan, M. S.; Khan, S.; Kazmi, A.; Bashir, N.; and Siddique, R. (2020). The Department of Cerebrovascular Diseases, The Second Affiliated Hospital of Zhengzhou University, Zhengzhou, PR China b State Key Laboratory of Virology, College of Life Sciences, Wuhan University, Wuhan, PR China c College of Life Sciences, Wuhan University, Wuhan, PR China.

Afzal, M.,I., Ali, M.,A., Nazir, U. (2021). IL-27, akey cytokine in disease pathogenesis: Linking inflammation autoimmunity, and cancer with viral infection. Cytokine and growth factor reviews, 57,63-74. Dio:10.1016lj.cytogfr.2021.02.004.

Agrati, C., Castilletti ,C., Goletti, D., Meschi, S., Sacchi ,A., Olivetti, M., Lapa, D., D., Santis, M., Petrosillo N, Marchioni L, Nicastri E, Di Caro A, Capobianchi MR, Piacentini M, Zumla A, Ippolito G. (2021). IL-7 receptor blockade blunts antigen-specific memory T cell responses and reduces severe respiratory illness in a large animal model of SARS-CoV-2. EBioMedicine. ID 33745934.

Aizarani, N.; Saviano, A.; Sagar, Mailly, L.; Durand ,S. and Herman, JS. (2019). A human liver cell atlas reveals heterogeneity and epithelial progenitors. Nature 2019;572:199-204.

Akdis, M.; Burgler, S.; Crameri, R.; Eiwegger, T.; Fujita, H.; Gomez, E.; Klunker, S.; Meyer, N.; O'Mahony, L.; Palomares, O.; Rhyner, C.; Ouaked, N.; Quaked, N.; Schaffartzik ,A.; Van, De .; Veen,

W,; Zeller, S.; Zimmermann, M. and Akdis, CA. (2011). Interleukins, from 1 to 37, and interferon-γ: receptors, functions, and roles in diseases. J Allergy Clin Immunol. 2011 Mar;127(3):701-21.e1-70.

Alfaro-Acha, A., Coto, E., Muñoz-Fernández, S., Sánchez-Corona, J., Blanco-González, E., Martín-Cortázar, C., García-Martínez, J., Cordero, E., López-Larrea, C. (2021). The IL-7 rs6897932 polymorphism is not associated with COVID-19 susceptibility or disease severity in a Spanish cohort. Journal of Clinical Virology. ID 33640898.

Alsaad, K. O.; Hajeer, A.H.; Al Balwi, M.; Al Moaiqel, M.; Al Oudah, N. and Al Ajlan, A. (2018). Histopathology of Middle East respiratory syndrome coronovirus (MERS-CoV) infection – Clinicopathological and ultrastructural study. Histopathology;72:516-524.

Alsaad, KO.; Hajeer, AH.; Al Balwi, M.; Al Moaiqel, M.; Al Oudah, N, and Al Ajlan, A. (2018). Histopathology of Middle East respiratory syndromecoronovirus (MERS-CoV)infection - Clinicopathologicaland ultrastructural study. Histopathology;72:516-524.

Alsaadi, E.A.J.; and Jones, I.M. (2019). Membrane Binding Proteins of Coronaviruses, vol. 14, pp. 275–286.