Thi-Qar Medical Journal (TQMJ):Vol.(26),No.(2),2023

Web Site: https://jmed.utq.edu Email: utjmed@utq.edu.iq

ISSN (Print):1992-9218

Detection of Other Microbial Infections Among COVID-19 Patients in Thi-Qar Province/Southern Iraq

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Abstract:

Background. SARS-CoV-2 virus, a type of Coronaviridae virus that affects people, is the cause of COVID-19.This viral disease like any other diseases, the infection linked to this one might be brought on by a parasite, virus, bacteria, or other kind of microbe.

Methods. Examining the level of antibodies in the serum of patients of anti- E. histolytica IgA, IgG and IgM antibodies and anti-CMV IgG and IgM antibodies are measured by immunoassay of patient's sera by ELISA system and whole blood was withdrawn to check for bacteremia.

Results. As a result, 60 blood samples from COVID-19 patients were taken, along with 30 samples from healthy individuals, for testing to find antibodies against E. histolytica and Cytomegalovirus. The patients were clinically and radiographically proven to have the COVID-19. To screen for bacteremia, the entire blood was tested.

Conclusions. The results show a significant difference in the titration of E. histolytica-IgA antibody, IgG and IgM. COVID-19 patients with CMV-IgG antibody showed (100%) rate of infection reporting a significant differences during the current study, while CMV-IgM antibody showed (3.3%) rate of infection. Regarding bacteremia, all results of bacteria detection in blood culture of Covid-19 patients were negative and there is no relationship between the infection of COVID-19 and bacteremia.

Keywords. Entamoeba histolytica; Cytomegalovirus ; Bacteria and COVID-19.

Introduction:

SARS-CoV-2, which causes Coronavirus disease (COVID-19), is a highly contagious virus that spreads globally in a short time, prompting the World Health Organization to design it as global pandemic on 11, March, 2020(1). COVID-19 has been linked to asymptomatic or symptomatic variants of the virus, as well as acute viral pneumonia with respiratory failure, multi-organ, and systemic imbalances, sepsis, septic shock, and death. Since its breakout, COVID-19 has been linked to a multi-organ effect (2).

Many other micro-organisms have been associated as coinfection with covid-19 like parasite, bacteria, virus and fungi (2). Chronic and persistent parasite infections are frequent in surrounding countries, and chronic parasitic infections have been found to affect the clinical outcomes of other illnesses, presumably in part by direct regulation of host immune responses. Pre-existing parasite infection can have both positive and negative consequences. COVID-19 has been found to have an inverse connection with intestinal worms, schistosomiasis, and malaria infection in recent studies. (3).

There are additional viruses related to COVID-19 that cause infections, including cytomegalovirus(CMV) infection, which is extensively transmitted in the general population and has a high seroprevalence. CMV establishes lifetime latency and reactivates regularly after infection. CMV infection is frequently asymptomatic reactivation in healthy people because of active humoral and cellular immunity, which is characterized by the release of Th1-polarizing immune cytokines (Tumor necrosis factor [TNF], interferon gamma [IFN-γ], and other interleukins) (4).

The most common pathogen-related to bacterial pathogens that cause bacteraemia in COVID-19 patients are Staphylococcus aureus. SuperAg is a kind of exotoxin produced by S.aureus that binds directly to the main complex T-cell receptors (MHCII), causing widespread T-cell activation and cytokine release. This was mediated by CD4+ T cells that generated large amounts of interferon-gamma (IFN-γ) in a SuperAg-dependent way, which contributed to S.aureus bacteriuria by considerably increasing the bacterial load in the liver (5).

Methods

-Study Design and sample collection:

The total number of patients with COVID-19 that included in the present study was 60 whom entered AL-Hussein teaching hospital in Nasiriyah city, Thi-qar province during the period extended from March 2022 to June 2022. The patients were examined clinically and diagnostically by Chest X-ray, COVID-19 IgG, and COVID-19 IgM. 30 of healthy person were also included in the current study as control group. Age, Sex, Location and occupation for

all of 90 people (60 patients and 30 controls) that included in the following study were checked based on a designed questioner.

Five ml of blood was taken from each individual; it was drawn by vein-puncture using 5 ml disposable plastic syringes under sterile conditions. Blood was collected in the EDTA tube (for blood culture) and Gel tube (for immunological tests) that left until clotted at room temperature for one hour. After blood clotting, it was centrifuged at 4000 rpm for 10 minutes, and then the serum was divides into two equal parts in Eppendorf tubes for immunological tests (COVID-19 IgG, COVID-19 IgM, E. histolytica-IgA/IgG and IgM antibodies and anti-CMV-IgG/IgM antibodies) and whole blood was withdrawn to check for bacteraemia), the sera stored in -20◦C. Each part of sera was used once to avoid repeated thawing and freezing. All materials (i.e. reagents and sera) were allowed to stand at room temperature before use (6,7).

-Detection of E. histolytica antibodies, CMV antibodies and Bacteraemia:

The E. histolytica-IgA/IgG and IgM antibodies and CMV-IgG/IgM antibodies EIA Test Kits is a solid phase enzyme immunoassay based on indirect principle for the qualitative and quantitative detection of IgG/IgM antibodies to E. histolytica-IgA/IgG and IgM and CMV-IgG/IgM in human serum or plasma.

-Statistical Analysis

Statistical analysis were tested the samples by a continuous variables as means and SDs, medians, and interquartile ranges for categorical variables as well as frequency rates and percentages for categorical variables (IQRs). Using the $\chi 2$ test, proportions for categorical variables were compared by SPSS.

Results

The current study was target patient with Covid-19 to explain the presence of E.histolytica, Cytomegalovirus Co-infection associated with Covid-19 as well as bacteremia.

The present study did not show a significant differences in the titration of E. histolytica-IgA antibody ($P>0.05$) among COVID-19 patients compared with control group, as shown in table (1).

Table (1): COVID-19 patients with Entamoeba histolytica (IgA)

EHS Iga	Case	No.(%)	Mean
Patient	**Positive**	**Zero**	----------
	Negative	**60(100)**	**0.31** ± 0.01
Control	**Negative**	**30(100)**	**0.14** ± 0.11
Total NO. Of Patients = 60			

T test - 0.042 df = 88 P-value = 0.96

N.S: Non-Significant differences P>0.05

IgG titration of E. histolytica antibody had been showing no significant difference (P>0.05) in both COVID-19 patients and control (0.42 ± 0.41), (0.47 ± 0.45), as in table (2)

Table (2): COVID-19 patients with Entamoeba histolytica (IgG)

EHS Igg	Case	No.(%)	Mean
Patient	**Positive**	**Zero**	----------
	Negative	**60(100)**	**0.42** ± 0.41
Control	**Negative**	**30(100)**	**0.47** ± 0.45
Total NO. Of Patients = 60			

T test 0.30 df = 88 P-value = 0.56

N.S: Non-Significant differences P>0.05

Statistical analysis showed a significant differences between Covid-19 patients and E.histolytica (IgM) as listed in table (3) for the results of the current study where E.histolytica (IgM) constitute (3.3%) among Covid-19 patients.

Table (3): COVID-19 patients with Entamoeba histolytica (IgM)

EHS Igm	No.(%)	Mean
Patient	**2(3.3)**	**1.13** ± 0.06
Control	**30(100)**	**0.15** ± 0.11
Total NO. Of Patients = 60		

χ^2 = 0.52 df = 1.0 P-value = 0.001

S: significant differences P≤ 0.05

There was no significant differences correlation between all parameters in E. histolytica infection (IgA, IgG and IgM) and age groups of COVID-19 patients, as shown in table (4).

Table (4): Age of COVID-19 patients with E. histolytica (IgA, IgG and IgM).

Age(Y.)	Case	No.(%) (Iga)	Mean	No.(%) (Igg)	Mean	No.(%) (Igm)	Mean
10-20	Positive	Zero	-------	Zero	-----	Zero	-----
	Negative	6(10)	0.11±0.09	6(10)	0.08±0.07	6(10)	0.09±0.06
21-30	Positive	Zero	-------	Zero	-----	Zero	-----
	Negative	13(21.7)	0.09±0.07	13(21.7)	0.06±0.05	13(21.7)	0.10±0.08
31-40	Positive	Zero	-------	Zero	-----	Zero	-----
	Negative	13(21.7)	0.10±0.08	13(21.7)	0.08±0.06	13(21.7)	0.16±0.14
41-50	Positive	Zero	-------	Zero	-----	2(3.3)	1.12±0.07
	Negative	12(20)	0.34±0.30	12(20)	0.46±0.42	10(16.7)	0.15±0.12
51-60	Positive	Zero	-------	Zero	-----	Zero	-----
	Negative	8(13.3)	0.11±0.09	8(13.3)	0.10±0.07	8(13.3)	0.09±0.07
61-70	Positive	Zero	-------	Zero	-----	Zero	-----
	Negative	8(13.3)	0.18±0.14	8(13.3)	0.08±0.05	8(13.3)	0.07±0.05
Total NO Of Patients = 60 , Control =30							

χ^2 = 8.27 df = 5.0 P-value = 0.14

N.S: Non-Significant differences P>0.05

There was no a significant differences(P > 0.05 , χ^2 = 2.36) based on the sex of COVID-19 patients and co-infection with E.histolytica (IgG, IgM and IgA) where the results revealed (3.3%) rate of infection among male having Covid-19 patients with E.histolytica (IgM) in comparison to female of COVID-19 patients and control group. Table (5) explains the previous statistical analysis.

χ^2 = 2.36 df = 1.0 P-value = 0.124

N.S: Non-Significant differences P>0.05

The results did not show a significant difference between the geographic distribution of COVID-19 patient and E.histloytica (IgM, IgG, IgA) and the statistical analysis were explained at the following table.

Table (5): Sex of COVID-19 patients with Entamoeba histolytica (IgA IgG and IgM)

Sex	Case	No.(%) (IgA)	Mean	No.(%) (IgG)	Mean	No.(%) (IgM)	Mean
Male	Positive	Zero	-----	zero	-----	2(3.3)	1.13 ± 0.06
	Negative	28(46.7)	0.32 ± 0.3	28(46.7)	0.41 ± 0.13	26(43.4)	0.17 ± 0.13
Female	Positive	Zero	----	zero	-----	zero	-------
	Negative	32(53.3)	0.17 ±0.15	32(53.3)	0.16 ± 0.15	32(53.3)	0.14 ± 0.12
Total NO of patients = 60 , control =30							

Table (6): Geographic distribution of COVID-19 patients with Entamoeba histolytica (IgA, IgG and IgM).

Location	Case	No. (%) (Iga)	Mean	No. (%) (Igg)	Mean	No. (%) (Igm)	Mean
Urban	Positive	Zero	------	Zero	-------	2(3.3)	1.13 ± 1.1
	Negative	39(65%)	0.31 ± 0.3	39(65)	0.42 ± 0.4	37(61.7)	0.15 ± 0.14
Rural	Positive	Zero	-------	Zero	------	Zero	-----
	Negative	21(35%)	0.12 ± 0.1	21(35)	0.11 ± 0.01	21(35)	0.14± 0.11
Total NO. Of Patients = 60 , Control =30							

χ^2 = 1.14 df = 1.0 P-value = 0.29

N.S: Non-Significant differences P>0.05

2: The relationship between the infection with COVID-19 and Cytomegalovirus.

Statistical analysis showed a significant difference (P<0.05) between the titration of CMV-IgG antibody among COVID-19 patients (**94.2** ± 69.8), and control group (**8.4** ± 5.0), as shown in table (7).

Table (7): COVID-19 patients with CMV (IgG) .

CMV Igg	Case	No.(%)	Mean
Patient	**Positive**	**60(100)**	**94.2 ± 69.8**
	Negative	**Zero**	**----------**
Control	**Negative**	**30(100)**	**8.4 ± 5.0**
Total NO. Of Patients = 60			

T test = 62.73 df = 88 P-value = 0.001

S: significant differences P≤ 0.05

COVID-19 patients with CMV (IgM) showed (3.3%) rate of infection reporting a significant differences during the current study the statistical analysis is shown in table (8).

Table (8): COVID-19 patients with CMV (IgM).

CMV Igm	Case	No.(%)	Mean
Patient	**Positive**	**2(3.3)**	**2.77 ± 1.0**
	Negative	**58(96.7)**	**0.50 ± 0.49**
Control	**Negative**	**30(100)**	**0.46 ± 0.45**
Total NO. Of Patients = 60			

χ^2 = 52.26 df = 1.0 P-value = 0.001

S: significant differences P≤ 0.05

The results did not detect a significant differences in IgG and IgM titration of Cytomegalovirus (CMV) among patients with COVID-19 in comparison with control group for each of age groups, as shown in table (9).

Table (9): Age of COVID-19 patients with CMV (IgG and IgM)

Age (Y.)	Case	No.(%) (Igg)	Mean	No.(%) (Igm)	Mean
10-20	Positive	6 (10)	74.16±21.3	Zero	-----
	Negative	Zero	-----	6(10)	0.52±0.32
21-30	Positive	13 (21.7)	75.0±18.2	1(1.7)	-----
	Negative	Zero	-----	12(20)	0.25±0.23
31-40	Positive	13 (21.7)	94.0±70.2	1(1.7)	------
	Negative	Zero	-----	12(20)	0.30±0.25
41-50	Positive	12 (20)	93.02±49.0	Zero	-----
	Negative	Zero	-----	12(20)	0.41±0.38
51-60	Positive	8(13.3)	78.2±23.8	Zero	-----
	Negative	Zero	-----	8(13.3)	0.16±0.14
61-70	Positive	8(13.3)	93.2±23.0	Zero	-----
	Negative	Zero	-----	8(13.3)	0.58±0.42
Total NO Of Patients = 60 , Control =30					

χ^2 = 2.70 df = 5.0 P-value = 0.74

N.S: Non-Significant differences P>0.05

The titration of CMV-IgG antibody was 93.22 ± 48.76 in serum of male patients compared with 94.12 ± 69.66 in female. The number of positive sample with CMV-IgM antibody was two only. There was no a significant difference between the sex of covid-19 patients with CMV-IgG antibody and the control group for each of males and females, as shown in table (10).

Table (10): Sex of COVID-19 patients with CMV (IgG and IgM)

Sex	Case	No.(%)(Igg)	Mean	No.(%)(Igm)	Mean
Male	Positive	28(46.7)	93.22 ± 48.76	1(1.7)	------
	Negative	Zero	-----	27(45)	0.54 ± 0.47
Female	Positive	32(53.3)	94.12 ± 69.66	1(1.7)	------
	Negative	Zero	-----	31(51.6)	0.45 ± 0.43
Total NO Of Patients = 60 , Control =30					

χ^2 = 0.009 df = 1.0 P-value = 0.92

N.S: Non-Significant differences P>0.05

The geographic distribution of COVID-19 patients who have co-infection with CMV(IgM, IgG) showed 65% rate of infection with CMV(IgG) among Covid-19 patients who lived in urban cities compared to (35%) for those who lived in rural cities. The results did not reveal a significant difference during the current study based on table (11).

Table (11): Geographic distribution of COVID-19 patients with CMV (IgG and IgM).

Location	Case	No.(%)(Igg)	Mean	No.(%)(Igm)	Mean
Urban	Positive	39 (65)	82.5 ± 58.0	2 (3.3)	2.76± 0.65
	Negative	Zero	-------	37 (61.7)	0.50 ± 0.49
Rural	Positive	21(35)	104.2 ± 59.7	Zero	-------
	Negative	Zero	--------	21(35)	0.37 ± 0.35
Total NO. Of Patients = 60 , Control =30					

χ^2 = 1.11 df = 1.0 P-value = 0.29

N.S: Non-Significant differences P>0.05

Discussion

E. histolytica is the second parasite that was investigated among COVID-19 patients by using E. histolytica (IgM, IgA and IgG) during the current study and it is found 3.3% of COVID-19 patients with E. histolytica (IgM). The age of COVID-19 patients who have infection with E. histolytica (IgM) ranged between (41-50) year old sex is male and they lived in urban cities.

Amebiasis is caused by the protozoan parasite E. histolytica, which is still a major cause of morbidity and mortality around the world. E. histolytica destroys tissue, resulting in clinical manifestations (8).

According to a study (9) although the prevalence of parasites suggests that COVID-19 does not create weakness in the battle against intestinal parasitic disorders, parasitic infections may occur with a similar frequency in societies without access to laboratories. During the pandemic, parasites were found in 529 of the 2.233 samples examined for parasites. During the lock-down stage, parasites were found in 58 of the 178 samples and 471 of the 2.055 samples during the gradual normalization period. During the pandemic and progressive normalization phases, the prevalence of E. histolytica increased (37, 39 , 40).

In HIV/AIDS patients with or without diarrhea, enteric parasite infections are prevalent (10). The antibody titers for E. histolytica in ELISA and IFA were significantly associated, and the results from these procedures were highly consistent (11).

A significant level of pro-inflammatory cytokines and chemokines was found in lactating mothers with asymptomatic E.histolytica infection (8). COVID-19 severity appears to be linked to co-infection with E. histolytica. The findings imply that parasite-driven immunomodulatory responses could reduce COVID-19-related hyper-inflammation (12, 37).

Endemism of parasitic infections like E.histolytica, accessible antiparasitic therapies, the importance of arthropods as reservoir hosts, and the likelihood of endosymbiosis may all play a part in COVID-19, either as a protective factor or as a cause of morbidity (13).

A research project was conducted during 6-years in Iraq's Thi-Qar Province showed that males and females made up 49.6% and 50.4 % of the 38,004 cases, respectively. The age group of 5-14 years made up the largest proportion of E.histolytica infection cases (27.3%), while the 1-year age group made up the lowest proportion (9.0%), and the infection prevalence dropped with increasing age. The bulk of E.histolytica-infected individuals (69.4%) lived in rural areas, while only 30.6 percent lived in urban areas (14).

Males (55.2 %) had a greater prevalence rate of E.histolytica than females (44.8 %), according to a study in Iraq's Kerbala district. The age group (6-10) years had the highest

frequency of infection (37.1%), and the highest rate of infection (39.7%) in Al-Hurr compared to Kerbala center (28.6%) and Al-Hindiyah (32%) (15).

The prevalence rate of E. histolytica was (7.4%) in a research conducted in Erbil province, Iraq, based on morphological traits. Females had much higher infection rates than men, and low-income people had significantly higher infection rates than moderate-income people (16).

Another study in Thi-Qar showed that there was no significant difference between males (59%) and females (41%), and the highest prevalence of E. histolytica infection (23%) was found in the first age group (one year) and the lowest prevalence of infection (10%) in the second age group (2-3 years). The highest prevalence of E. histolytica infection (9%) was discovered in the second age group, while the lowest prevalence (3%) was reported in the fifth age group (4–5 years old) (17).

The E.histolytica infection was shown to be most prevalent in youngsters around (4–5 years old), according to a study conducted in Nigeria. Males (56.5%) were also more contaminated than females (43.5%) according to the findings. However, there is no statistical difference in infection rates between the sexes and age groups of the patients. Factors such as unsanitary sewage disposal, a poor drainage system, and a lack of personal cleanliness all contributed significantly to the spread and multiplication of E. histolytica (18).

Cytomegalovirus (IgG, IgM) were checked among COVID-19 patients reporting (100%) and (3.3%) rates of infection respectively with a significant differences. Infection with CMV was reported among the all of the age groups of covid-19 patients during the current study. Male and female made up (46.7%) and (53.3%) rate of infection with CMV (IgG) respectively while rate of infection with CMV (IgM) constitute (1.7%) for each of male and female with covid-19. (65%) of covid-19 patient who were infected with CMV (IgG) were urban while covid-19 patient who lived in rural cities constitute (35%) of CMV (IgG) infection.

In affluent countries, around (30%) of young adults are infected with CMV, rising to more than (60%) among the elderly. In low- and middle-income countries, (100 %) of young adults are seropositive. CMV infection increases attrition of the naive T cell pool, which is essential for producing adaptive immunological responses against a new virus such as SARS-CoV-2 by around 20 years (19).The seroprevalence of CMV antibodies among COVID-19 cases is high when compared to findings in cases without SARSCoV-2 (20).

Seropositivity to CMV is linked to a nearly twofold increased risk of hospitalization due to severe SARS-CoV-2 infection. In the absence of substantial CMV replication in the upper respiratory tract, immune profiling of blood and CMV DNA quantitative PCR in a subgroup of patients with respiratory tract samples indicated altered T-cell activation profiles. The

finding of study (21) showed that CMV-driven immunological perturbations may play a role in influencing the fate of SARS-CoV-2 infection and may have implications for COVID-19 severity differences between human populations.

CMV blood reactivation is common in COVID-19 critically unwell individuals and is dependent on the severity of illness and the presence of additional bacterial infections, but not on steroids or cytokine blocking medications. Patients with CMV reactivation had a longer hospital stay and a greater mortality rate than patients without reactivation (22).

According to the findings of one study (23) in Mosul City, Iraq, IgG-CMV was found in 12% of males and 24% of females, respectively. Males have a prevalence of 2.5%, while females have a prevalence of 1% and 1.5%, respectively. CMV infection was found in 34% of males and 66% of females in the overall sample. In comparison to other nations, CMV seroprevalence in Mosul city/Iraq is relatively high, according to this study. CMV has a significant seroprevalence in older people (40-80 years old), while according to the results of another study (24) in Mosul City/ Iraq, the greatest titers of CMV IgG in females were (14.3I/ml), whereas the highest titters in males were (10.9 IU/ml).

As showed in a study in Konya city/Turkey (25), the CMV-IgG seropositivity rate was found to be 100 % in pregnant women, while the CMV-IgM seropositivity rate was found to be 0.2 %.

Based on a study in Poland (26), the total prevalence of anti-CMV IgG was 81.9% rising from 74.3% in those under 30 to 94.3% in people 45 year and older. The lowest incidence was found at the age of 15(3.8%) and the greatest was found at the age of 34(8.95%).

A take a look at a study in USA (27) pregnant women aged between (15-59) years, were either white (54.7%) or black (39.2%), CMV seropositivity became notably more common amongst non-Hispanic white women than among minority women. Also the study identified a cluster in which women had expanded odds of CMV seropositivity within the city. The CMV IgG seroprevalence extended from 50% amongst teens to more than 80% amongst women older than 40 years, while another research(28) in USA conducted between 2011 and 2015, 91 individuals aged 65 got a kidney transplant; CMV reactivation was substantially more common in the older group (71.4%).

Bacterial species were not reported among COVID-19 patients who were targeted in the present study for studying other microbial infections that are associated with COVID-19.

The overall proportion of COVID-19 patients with bacterial coinfection is lower than in prior influenza pandemics, according to a study (29). This was a descriptive research in which 985 samples were handled at the Mohammed VI University Hospital in Marrakech after requests for cyto-bacteriological investigation of urine and blood cultures were received (29).

Bacterial co-infection is relatively uncommon in hospitalized COVID-19 patients, according to study (30). A secondary infection could be one of the causes of death in these patients,

according to the findings of this study. Blood culture was used in a cross-sectional investigation (BC). Standard microbiological methods were used to confirm the bacterial isolates. The disk diffusion method was used to detect antibiotic resistance. A total of 43 (12.46 %) of the 340 individuals with COVID-19 experienced subsequent bacterial infections (30).

A study (31) showed that the patients with COVID-19 had a (1.2 %) greater rate of bacteraemia than patients without COVID-19. Nosocomial bacteraemia was more common in COVID-19 patients (95.5%) than in non-COVID-19 patients (30.5%). And the study findings revealed that, in comparison to earlier years, less blood cultures were taken during the COVID-19 period.

Blood cultures were collected from 21.451 samples during the study (32) showed that 10.000 samples were taken prior to the pandemic COVID-19 and 11.450 sample after it began. The study's criteria resulted in 605 out of 21,451 (2.8%) blood culture tests being positive; however, blood culture contamination rates were noticeably higher during the COVID-19 pandemic: 197 out of 10,001 (1.9%) versus 408 out of 11,450(3.5%).

Another study (33) study included 158 blood cultures from 1578 COVID-19 patients revealed (9.4%) of them were positive. (67%) of patients required intensive care in the ICU. Blood infections are uncommon in COVID-19 patients, according to this study.

A study(34) concluded that the occurrence of clinically relevant bacteraemia in COVID-19 patients amounted to (1.0%), which was statistically significantly lower compared to influenza A patients (4.0%) and influenza B patients (3.0%).

Furthermore, the study (35) showed no difference in rates of bacteraemia which was detected among EBOV-positive vs. EBOV-negative patients – 3.8% and 3.9%, respectively.

According to results shown in study (36), a total of 107 COVID-19 patients with a mean age 62.2 ± 10.6 years were included and showed a nosocomial bacteraemia (31%).

Conclusions.

The results did not show a significant difference in the titration of E. histolytica- IgA antibody, IgG and IgM. COVID-19 patients with CMV-IgG antibody showed (100%) rate of infection reporting a significant differences during the current study, while CMV-IgM antibody showed (3.3%) rate of infection. Regarding bacteremia, all results of bacteria detection in blood culture of Covid-19 patients were negative and there is no relationship between the infection of COVID-19 and bacteremia.

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