JOURNAL OF
CONTEMPORARY MEDICINE

DOI:10.16899/jcm.1075112
J Contemp Med 2022;12(2):332-338

Orijinal Araştırma / Original Article

Does The COVID-19 Pandemic Have an Effect on Perioperative Intra-Abdominal Wound Culture in Patients Undergoing Appendectomy? A Retrospective Cohort Study

COVID-19 Pandemisinin Apendektomi Geçiren Hastalarda Perioperatif Karın İçi Yara Kültürüne Etkisi Var Mı? Retrospektif Bir Kohort Çalışması

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Abstract

Aim: The aim of this study is to examine the effect of the changing microbiota structure during the pandemic period on the bacterial aerobic culture profile of the wound taken from patients operated for acute appendicitis, together with clinical variables.

Material and Method: Our study included 125 patients who underwent an appendectomy in the General Surgery Clinic between 01.03.2019-01.02.2021 and whose wound culture was taken during an appendectomy. The patients were divided into two groups; group1 (pre-pandemic) and group2 (during a pandemic). Both groups were compared in terms of age, gender, clinical, laboratory and wound culture data.

Results: There was no significant difference between the groups in terms of age, clinical symptoms, surgical method, laboratory and radiological data (p>0.05). In the pre-pandemic group, there was growth of Escherichia coli in 35 (53%) patients, Klebsiella pneumoniae in 3 (4.5%) patients, and Pseudomanas aeruginosae in 2 (3) patients from Gram-negative bacteria while Streptecoccus anginosus and Strep. constellatus growth were most common from Gram-positive bacteria. In the pandemic group, there was the growth of E. coli in 29 (49.2%) patients, P. aeruginosae in 5 (8.5%) patients, K. pneumoniae in 2 (3.4%) patients from Gram-negative bacteria, Citrobacter freundii and Strep. anginosus growth were the most common from Gram-positive bacteria. E. coli is the most common bacteria in both groups.

Conclusion: Although E. coli was found to be the most frequently identified microorganism in patients with acute appendicitis, an increase in the density and resistance of Pseudomonas group bacteria were detected, possibly due to the effect of the COVID-19 pandemic.

Keywords: COVID-19 pandemic, appendectomy, wound culture, antibiotic resistance

Öz

Amaç: Yaptığımız bu çalışmada amaç pandemi döneminde değişen mikrobiyota yapısının akut apandisit nedeni ile opere edilen hastalardan alınan yara yeri bakteriyel aerobik kültür profiline olan etkisini klinik değişkenlerle birlikte incelemektir.

Gereç ve Yöntem: Çalışmamıza 01.03.2019-01.02.2021 tarihleri arasında Genel Cerrahi Kliniğinde apendektomi yapılan ve apendektomi esnasında yara yeri kültürü alınan 125 hasta dahil edildi. Hastalar iki gruba ayrıldı; grup1(pandemi öncesi) ve grup2 (pandemi süreci). Her iki grup; yaş, cinsiyet, klinik, laboratuvar ve yara yeri kültür verileri açısından karşılaştırıldı.

Bulgular: Gruplar arasında yaş, klinik semptomlar, ameliyat yöntemi, laboratuvar ve radyolojik verileriler açısından anlamlı fark yoktu(p>0,05). Pandemi sürecindeki grupta perfore apendisit, apendokolit, hastanede kalış ve antibiyotik kullanım süresi daha fazla oduğu tespit edildi(p<0,05). Pandemi öncesinde Gram negatif bakterilerden 35 (%53) hastada Escherichia coli, 3 (%4,5) hastada Klebsiella pneumoniae, 2 (%3) hastada Pseudomanas aeruginosae üremesi olurken Gram pozitif bakterilerden en çok Streptecoccus anginosus ve Strep.constellatus üremesi olmuştur. Pandemi döneminde ise Gram negative bakterilerden 29 (%49,2) hastada E. coli, 5 (%8,5) hastada P. aeruginosae, 2 (%3,4) hastada K. pneumoniae üremesi olurken Gram pozitif bakterilerden en çok Citrobacter freundii ve Strep. anginosus üremesi olmuştur. Her iki grupta da en yaygın üreyen bakteri E.coli'dir.

Sonuç: Akut apandisitli hastalarda en sık tanımlanan mikroorganizma E. coli olarak bulunmuş olsa da muhtemel olarak COVID-19 pandemi sürecinin etkisi ile Pseudomonas gurubu bakterilerin yoğunluğunda ve direnç durumunda artış tespit edilmiştir.

Anahtar Kelimeler: COVID-19 pandemisi, apandektomi, yara yeri kültürü, antibiyotik direnci

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Received *(Geliş Tarihi)*: 17.02.2022 **Accepted *(Kabul Tarihi)*:** 02.03.2022

INTRODUCTION

COVID-19 (SARS-CoV-2) virus, which was first seen in Turkey in March 2020, first appeared in Wuhan, China in December 2019 and was declared a pandemic by the World Health Organization on March 11, 2020, as it spread all over the world.[1] It has been determined that SARS-CoV-2 has corona virus characteristics and is a virus of the Betacoronavirus 2B family, and bats and seafood have been accused as intermediate hosts, although it is not certain.[2,3] The virus spreads between humans by droplets and close contact, with an average incubation period of 2 to 14 days. The virus affects many organs, especially respiratory system organs.[2] Although it is transmitted mainly by droplet infection, it has been reported in studies that it can also be transmitted by fecal-oral and environmental ways.[4] It has been reported that corona patients in Wuhan, China, where the virus first originated, have gastrointestinal symptoms such as diarrhea, abdominal pain and vomiting in up to 10% of patients as well as fever, fatigue, and cough complaints.[5] However, in recent studies, this rate was much higher and Tian et al. found it to be 39.9% in their study.[6]

Acute appendicitis is the most common cause of admission to the emergency department with acute abdomen in approximately 7% of adults, slightly more in males.[7] Although various causes are held responsible for its etiology, it is not known precisely.[8] While surgical treatment was used in previous years in the treatment of acute appendicitis, this has changed in recent years depending on whether the appendix is complicated or not. If it is complicated, surgery is recommended, if not, medical treatment is recommended.[9] It has been reported that taking an interoperative culture during an appendectomy in patients with acute appendicitis is important in terms of preoperative and medical treatment regulation.[10] Routine intra-abdominal culture is recommended for appropriate antibiotic therapy since many bacteria grow in wound cultures especially during complicated appendicitis.[11] Although the appendicitis microbiota is richer, it is similar to the rectum microbiota, so it has been suggested that changes in the rectum microbiota will guide the diagnosis and treatment of acute appendicitis.[12] It has been put forward that in the COVID-19 pandemic, the disease itself, the drugs and the changes in habits lead to changes in the intestinal microbiota.[13]

The gastrointestinal system flora has been affected due to the changes in eating, sleeping and travel habits during the COVID-19 pandemic. Therefore, considering that the appendix may also be affected, it was the aim of this study to determine possible changes in the treatment protocol of the appendix by examining the wound culture in acute appendicitis.

MATERIAL AND METHOD

The study included 125 patients who were admitted to Niğde Ömer Halisdemir University Faculty of Medicine Training and Research Hospital General Surgery Clinic between March 1, 2019, and March 1, 2021, taken to emergency operation with the diagnosis of acute appendicitis, who met the study criteria, and whose intraoperative wound culture was taken during an appendectomy. The study was carried out in accordance with the Declaration of Helsinki, after the approval of the ethics committee with the decision dated 22.04.2021 and numbered 2021/53.

Patients who met the research criteria and agreed to participate in the study, who underwent appendectomy and whose wound culture was taken, were included in the study. Inclusion criteria for the study were defined as patients who had an open appendectomy and had a wound culture taken during the COVID-19 pandemic period and in the previous year with the diagnosis of acute appendicitis, and being between the ages of 18-80. Exclusion criteria were defined as patients who were diagnosed with lymphoma and leukemia, who did not undergo open appendectomy, who used antibiotics during the culture period, and who received chemotherapy and radiotherapy in the last 6 months.

Patients who underwent open appendectomy and whose intraoperative wound cultures were taken were divided into two groups as before and after the COVID-19 pandemic. Patients underwent open appendectomy and their wound culture was taken; Group 1 consisted of those who underwent these interventions between 01 March 2019-28 February 2020, and Group 2 were between 01 March 2020 and 01 March 2021. Age, gender, radiological diagnosis, laboratory results (WBC, Lymphocyte, PLT neutrophil and CRP), the surgery, histopathological results, complications, length of stay in the hospital, duration of antibiotics used, bacteria grown in wound culture and antibiotic sensitivity data of all participants in the study were recorded one by one. These data were compared between the two groups. All patients in the study were diagnosed and operated on by the same physician in the same general surgery clinic. Patients were taken into operation with the diagnosis of preoperative acute appendicitis after evaluating the diagnosis of acute appendicitis physical examination, radiological (Ultrasonography and Computed Tomography) and laboratory results. Open appendectomy operation was performed in all patients. Wound cultures were taken intraoperatively in a sterile environment just after appendectomy was performed, and were then transferred to the storage medium with a sterile swab from the infected area by opening the lumen of the appendix by the general surgery specialist. The culture samples were sent to the medical microbiology laboratory within one hour at the latest. Preoperative and peroperative antibiotics were not given to the patients, and metronidazole and ampicillin + sulbactam antibiotics were given just after the operation. Ciprofloxacin was given to those allergic to ampicillin + sulbactam.

The samples sent to the medical microbiology laboratory were inoculated on 5% sheep blood agar and EMB (Eosin Methylene Blue) media and incubated at 35±1°C for 24 hours. The grown samples at the end of the incubation were pre-evaluated according to gram staining, colony morphology, and catalase and oxidase test results. Identification of the isolates and antibiotic susceptibility were performed with the Vitek 2 Compact (Biomerieux, France) device as well as by using classical microbiological methods. The susceptibility rates were interpreted by a medical microbiologist according to EUCAST (European Committee on Antimicrobial Susceptibility Testing) criteria.[14]

Data were analyzed by IBM SPSS V23. Conformity to normal distribution was evaluated by the Kolmogorov-Smirnov test. Independent samples t test and Mann Whitney U test were used to compare quantitative data according to groups. Categorical data were analyzed with the Chi-Square Test. The significance level was taken as p<0.05.

RESULTS

The median values of age did not differ between the groups (p=0.231). While the median value was 40 in Group 1, it was 33 in Group 2. Gender distributions differed between the groups (p=0.008). While the proportion of women in Group 1 was 57.6%, it was 33.9% in Group 2. Median values of hospital stay differed between the groups (p<0.001). While the median value was 4 in Group 1, it was 5 in Group 2. The median values of antibiotic duration differed between the groups (p<0.001). While the median value was 9 in Group 1, it was 10 in Group 2 (**Table 1**).

WBC average values did not differ between the groups (p=0.845). While the average value was 14 in Group 1, it was 13.9 in Group 2. Lymphocyte median values did not differ between the groups (p=0.74). While the median value was 2 in Group 1, it was 2 in Group 2. The median values of platelets did not differ between the groups (p=0.095). While the median value was 271.5 in Group 1, it was 250 in Group 2. The median values of CRP did not differ between the groups (p=0.365). While the median value was 19.5 in Group 1, it was 27 in Group 2. The median values of neutrophils did not differ between the groups (p=0.686). The median value was 11.2 in Group 1, and it was 11 in Group 2 (**Table 2**).

The presence of appendicolith differed between the groups (p=0.030). While the rate was 21.2% in group 1, it was 40.7% in group 2. While the perforation rate was 11.1% in group 1, it was 30.5% in group 2, and there was a statistical difference between them (p=0.015). Other categorical variables did not differ between the groups (p>0.05) (**Table 1**).

Table 1. Comparison of categorical data according to groups

	Group 1 (n=66) (Non-pandemic)	Group (n=59) (Pandemic)	Total (n=125)	p
Age*	38.2±14.1/40 (47.25)	36.8±16.8/33 (43)		0.231^{b}
Gender, n (%)				0.008^{a}
Male	28 (42.4)	39 (66.1)	67 (53.6)	
Female	38 (57.6)	20 (33.9)	58 (46.4)	
ASA**, n (%)				0.486^{a}
I	17 (25.8)	21 (35.6)	38 (30.4)	
II	38 (57.6)	29 (49.2)	67 (53.6)	
III	11 (16.7)	9 (15.3)	20 (16)	
Surgery (Open appendectomy), n (%)	66 (100)	59 (100)	125 (100)	
Appendicolith (yes), n (%)	14 (21.2)	24 (40.7)	38 (30.4)	0.030^{a}
Perforation (no), n (%)	8 (11.1)	18 (30.5)	26 (20.8)	0.015^{a}
Residential, n (%)				0.199^{a}
Intraperitoneal	60 (90.9)	43 (81.1)	66 (55.5)	
Retrocecal	6 (9.1)	10 (18.9)	53 (44.5)	
Post-Op Complication, n (%)				0.234^{a}
No	53 (80.3)	41 (69.5)	94 (75.2)	
Yes	13 (19.7)	18 (30.5)	31 (24.8)	
Ileus	4 (30.8)	4 (22.2)	8 (25.8)	
Ileus+Reoperation	0 (0)	1 (5.6)	1 (3.2)	
Ileus+Wound Inf.	0 (0)	1 (5.6)	1 (3.2)	
Diarrhea	2 (15.4)	2 (11.1)	4 (12.9)	
Wound Inf.	6 (46.2)	6 (33.3)	12 (38.7)	
Wound Inf.+ Hernia	0 (0)	2 (11.1)	2 (6.5)	
Wound Inf+Diarrhea	1 (7.7)	2 (11.1)	3 (9.7)	
Pathology, n (%)				0.067^{a}
Acute Appendicitis	47 (73.4)	32 (54.2)	79 (64.2)	
Acute Suppurative Appendicitis	3 (4.7)	6 (10.2)	9 (7.3)	
Appendix Mucocele (L)	1 (1.6)	1 (1.7)	2 (1.6)	
Gangrenous Appendicitis	5 (7.8)	2 (3.4)	7 (5.7)	
Perforated Appendicitis	8 (12.5)	18 (30.5)	26 (21.1)	
Hospital Stay *	4.5±1.9/4 (5)	6.3±3.3/5 (8)		$<0.00^{b}$
Antibiotic Duration *	9.4±1.6/9 (10)	11.4±3.2/10 (13)		$<0.00^{b}$

aChi-Square test, n (%), bMann Whitney U test, * average±standard deviation/median,**American Society of Anesthesiologists

Table 2. Laboratory and radiological data according to groups

	Group 1 (n=66) Non-pandemic (IQR)	Group 2 (n=59) Pandemic (IQR)	p
WBC*	14±4.8/14 (17)	13.9±3.8/14 (17)	0.845[a]
Lymphocyte *	1.9±0.9/2 (2)	2.2±1.4/2 (2)	0.740[b]
Platelets *	274.6±71.4/271.5(302.75)	249.2±65.5/250 (300)	0.095[b]
CRP*	47.2±67.5/19.5 (59)	62.3±76.4/27 (101)	0.365[b]
Neutrophil *	11.2±4.7/11.5 (14)	11±3.8/11 (13)	0.686[a]
USG, n (%)			0.775[c]
Acute Appendicitis	17 (77.3)	7 (77.8)	
Appendix Mucocele	1 (4.5)	0 (0)	
Intra-abdominal Abscess	3 (13.6)	2 (22.2)	
Perforated Appendicitis	1 (4.5)	0 (0)	
BT, n (%)			0.500[c]
Acute Appendicitis	52 (88.1)	52 (91.2)	
Appendix Mucocele	1 (1.7)	0 (0)	
Intra-abdominal Abscess	0 (0)	1 (1.8)	
Perforated Appendicitis	6 (10.2)	4 (7)	

[a]Independent samples t-test, [b]Mann Whitney U test, [c]Chi-square test, * average±standard deviation / median (min-max), IQR: the interquartile range

Bacteria grown in bacterial culture according to groups are summarized in **Table 4**. Gram-negative bacteria grew more intensely than gram-positive bacteria in both groups. Escherichia coli was most frequent in 35 (53) patients, Klebsiella pneumoniae in 3 (4.5) patients, Pseudomanas aeruginosae in 2 (3) patients from Gram-negative bacteria in Group-1, Streptecoccus anginosus and Strep.constellatus were the most common growth among Gram-positive bacteria. While E. coli in 29 (49.2) patients, P. aeruginosae in 5 (8.5) patients, K. pneumoniae in 2 (3.4) patients from Gram-negative bacteria in Group-2, Citrobacter freundii and Strep. anginosus were the most common among Gram-positive bacteria. While the most growth rate from Gram positive bacteria was Strep. spp. (21.2%) in Group 1, Staphylococcus spp. (15.3%) growth was more in Group 2. The most commonly grown bacteria in both groups was E. coli (**Table 3**).

Table 3. Bacteria isolated from wound culture according to groups.

	Group 1 (Non-pandemic)	Group 2 (Pandemic)	Total
Culture			
Acinetobacter spp.	1 (1,5)	0 (0)	1 (0,8)
Citrobacter braakii	2 (3)	0 (0)	2 (1,6)
Citrobacter freundii	3 (4,5)	4 (6,8)	7 (5,6)
E. coli	35 (53)	29 (49,2)	64 (51,2)
Enterococcus avium	0 (0)	1 (1,7)	1 (0,8)
Klebsiella oxytoca	0 (0)	1 (1,7)	1 (0,8)
Klebsiella pneuoniae	3 (4,5)	2 (3,4)	5 (4)
Lactobacillus spp.	2 (3)	0 (0)	2 (1,6)
Pseudomons aeruginosa	2 (3)	5 (8,5)	7 (5,6)
Staph. lentus	0 (0)	1 (1,7)	1 (0,8)
Staph. cohnii	0 (0)	1 (1,7)	1 (0,8)
Staph. hominis	2 (3)	4 (6,8)	6 (4,8)
Staph. lugdinensis	2 (3)	3 (5,1)	5 (4)
Strep. anginosus	5 (7,6)	4 (6,8)	9 (7,2)
Strep. constellatus	5 (7,6)	0 (0)	5 (4)
Strep. intermedius	2 (3)	4 (6,8)	6 (4,8)
Strep. mitis	2 (3)	0 (0)	2 (1,6)

Table 4. Antibiotic susceptibility of bacteria isolated from wound culture according to groups

	Group 1 (Non-pandemic)		Group 2 (Pandemic)		Total		p1
	R	S	R	S	R	S	
AMC	14 (46,7)	16 (53,3)	14 (48,3)	15 (51,7)	28 (47,5)	31 (52,5)	1,000
ETP	1 (5,6)	17 (94,4)	0 (0)	31 (100)	1 (2)	48 (98)	0,367
GN	3 (8,1)	34 (91,9)	3 (8,3)	33 (91,7)	6 (8,2)	67 (91,8)	1,000
CEF	8 (36,4)	14 (63,6)	5 (13,9)	31 (86,1)	13 (22,4)	45 (77,6)	0,059
CFM	3 (12,5)	21 (87,5)	0 (0)	5 (100)	3 (10,3)	26 (89,7)	1,000
CRO	8 (33,3)	16 (66,7)	6 (20)	24 (80)	14 (25,9)	40 (74,1)	0,425
LEV	1 (50)	1 (50)	1 (16,7)	5 (83,3)	2 (25)	6 (75)	0,464
CIP	9 (24,3)	28 (75,7)	9 (25)	27 (75)	18 (24,7)	55 (75,3)	1,000
AZT	---	2 (100)	---	5 (100)	---	7 (100)	---
AMP	22 (66,7)	11 (33,3)	17 (53,1)	15 (46,9)	39 (60)	26 (40)	0,389
AK	1 (4,8)	20 (95,3)	0 (0)	36 (100)	1 (1,8)	56 (98,2)	0,368
TGC	---	10 (100)	---	31 (100)	---	41 (100)	---
SXT	17 (43,6)	22 (56,4)	11 (35,5)	20 (64,5)	28 (40)	42 (60)	0,658
IMP	---	11 (100)	---	14 (100)	---	24 (100)	---
PIP	2 (66,7)	1 (33,3)	4 (66,7)	2 (33,3)	6 (66,7)	3 (33,3)	1,000
TZP	5 (23,8)	16 (76,2)	0 (0)	37 (100)	5 (8,6)	53 (91,4)	0,004
MEM	0 (0)	15 (100)	1 (2,7)	36 (97,3)	1 (1,9)	51 (98,1)	1,000
TOB	---	1 (100)	---	6 (100)	7 (100)	---	---
NET	1 (50)	1 (50)	1 (20)	4 (80)	2 (28,6)	5 (71,4)	1,000
F	---	10 (100)	---	---	---	10 (100)	---
FOS	---	18 (100)	---	---	---	18 (100)	---
CAZ	7 (43,8)	9 (56,3)	7 (20)	28 (80)	14 (27,5)	37 (72,5)	0,099
CXM	9 (69,2)	4 (30,8)	7 (21,9)	25 (78,1)	16 (35,6)	29 (64,5)	0,005
CZ	7 (77,8)	2 (22,2)	7 (22,6)	24 (77,4)	14 (35)	26 (65)	0,004
FOX	1 (10)	9 (90)	2 (7,4)	25 (92,6)	3 (8,1)	34 (91,9)	1,000
VA	---	8 (100)	---	9 (100)	---	17 (100)	---
ESBL*	---	---	---	2 (100)	---	2 (100)	---

[1] Chi-square test, n (%), *Extended-Spectrum Beta Lactamases
(AMP: Ampicillin, AMC: Amoxicillin + clavulanic acid, AK: Amikacin, AZT: Aztreonam, CAZ: Ceftazidime, CEF: Cefepime, CFM: Cefixime, CRO: Ceftriaxone, FOX: Cefoxitin, CIP: Ciprofloxacin, CXM: Cefuroxime, CZ: Cefazolin, ETP: Ertapenem, FOS: Fosfomycin, GN: Gentamicin, IPM: Imipenem, LEV: Levofloxacin, MEM: Meropenem, F: Nitrofurantoin, NET: Netilmicin, PIP: Piperacillin, SXT: Trimethoprim / sulfamethoxazole, TZP: Piperacillin + tazobactam, VA: Vancomycin, TGC: Tigecyclin, TOB: Tobramycin)

The antibiotic resistance profiles of the isolated bacteria are summarized in **Table 4** in general according to the groups. In group-1 patients, resistance was found to be 77.8% for cefazolin, 69.2% for cefuroxime, 10% for cefoxitin, 33.3% for ceftriaxone, 24.3% for ciprofloxacin, 50% for levofloxacin. In Group-2, resistance was found to be 22.6% for cefazolin, 21.9% for cefuroxime, 7.4% for cefoxitin, 20% for ceftriaxone, 25% for ciprofloxacin, and 16% for levofloxacin. While the susceptibility and resistance statuses of Piperacillin/Tazobactam, cefuroxime and cefazolin differed statistically according to the groups, the sensitivity and resistance against the others did not differ (**Table 4**). The resistance to antibiotics of the two most common bacteria is summarized in **Figure 1**.

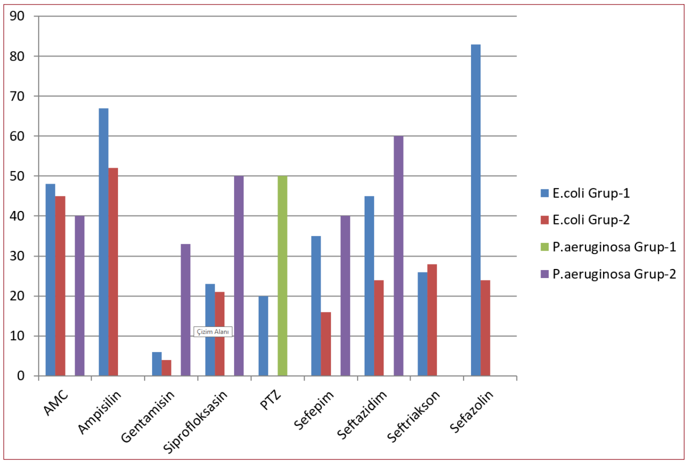

Figure 1. The resistance to antibiotics of the two most common bacteria

DISCUSSION

Gastrointestinal microbiota is generally described as a postpartum organ that can affect both systemic and intestinal physiology, and whose composition and activity is composed of a wide variety of bacteria.[15] The microbiota promotes the maturation of immune cells and the development of immune system functions in disease and health conditions.[16] While the mutualistic relationship between the host and intestinal bacteria is called symbiosis, the imbalance in the gut microbiota or decrease in diversity is called dysbiosis. Microbiota is associated with various pathologies such as constipation, obesity, inflammatory bowel disease, depression, diabetes, colon cancer, coronary artery diseases.[17-19] Although the normal GIS microbiota is composed of bacteria belonging to the Bacteroides and Firmicutes phyla intensely, a very small portion of them is potentially pathogenic bacteria such as the Proteobacteria phylum.[20]

Some studies have reported a bidirectionally functioning axis called the 'gut-lung axis'.[21] In other words, just like respiratory infections can affect the gut microbiota, the gut microbiota can affect the lung immunity and microbiota by affecting the immune system. In a study on the influenza virus, it was reported that as a result of therapy regulating the gut microbiota, the replication of viruses in the pulmonary epithelium decreased, thus the severity of the disease reduced. It was thought that this situation may also be valid for COVID-19 patients.[22] SARS-CoV-2 can change the commensal microorganism composition in the gut and lead to gut dysbiosis; and dysbiosis can cause increased cytokine levels, systemic inflammation, and exaggerated immune responses.[23] Although studies on COVID-19 and microbiota are limited, it has been reported that opportunistic pathogens (Peptostreptococcaceae, Enterobacteriaceae, Staphylococcaceae, etc.) increase and beneficial bacteria (Faecalibacterium, etc.) decrease.[22,24] In addition, Angiotensin Converting Enzyme 2 (ACE2) receptors, which are the main receptors of SARS-CoV-2, are highly present both in the respiratory tract and in the GIS.[25] In this case, it is thought that the COVID-19 virus may affect the gastrointestinal system and microbiota. In this study, the effect of the changing microbiota structure during the pandemic period on the bacterial aerobic culture profile of the wound taken from the patients who were operated on for acute appendicitis was examined together with the clinical variables.

Appendicitis is thought to be the result of bacterial overgrowth as a consequence of an obstruction of the appendix lumen for various reasons.[26] Anaerobic species such as Bacteriodes fragilis and Fusobacterium nucleatum have been reported to be the most common bacterial agents in appendicitis. E. coli has been reported as the most common bacteria detected by aerobic culture method; however, bacteria such as K. pneumoniae, Strep. spp., Enterococcus spp. and P. aeruginosa have also been shown to be a factor.[27,28] Our study was found to be compatible with the literature in this respect. It is difficult to explain the effects of these agents on infection, since the species identified in appendicitis were found to be compatible with the gastrointestinal microbiota, according to studies conducted with both new generation sequencing and culture methods.[28] In addition, microbiota profiles vary from person to person. Although factors such as diet, geography, medicines (antibiotics, etc.), surgeries, chronic diseases and genetic structure affect the microbiota structure, Peeters et al. and Arlt et al. have shown that there is a significant decrease in microbial richness and diversity in inflamed appendix tissue in two different studies.[29,30] The COVID-19 pandemic, which is thought to be one of the factors affecting these changes in the microbiota structure, is also the main subject of this study.

While E.coli (53%), K.pneumoniae (4.5%) and P.aeruginosae (3%) from gram-negative bacteria were the most common, respectively in cultures made before the pandemic, it was observed in the pandemic period that the growth of E.coli (49.2%), P.aeruginosae (8.5%) and K.pneumoniae (3%), respectively were the most common. It is noteworthy that the rate of P.aeruginosa increased during the pandemic period compared to the pre-pandemic period. Because P.aeruginosa is resistant to physical environments, antiseptics and antibiotics, and is fond of humid environments, and even grows in disinfectants, this microorganism can easily live in outdoor environments and especially in hospital environments. P.aeruginosa, which progresses with high mortality and morbidity, ranks the first among the factors of nosocomial infections.[31,32] It made us think that the reason for this change in P.aeruginosae may be the drugs used during the pandemic process and the prolongation of hospital stay.

It has been reported to prolong the hospital stay and duration of antibiotic use of the patients and the number of non-perforated acute appendicitis decreased significantly while the number of perforated acute appendicitis increased during the pandemic period.[33-35] Our study was found to be compatible with the literature in this respect. This situation makes us think that the increase in the incidence of hospital-acquired infectious agents in public due to prolonging of hospital stay may be a result of the pandemic.

On the other hand, while Strep. spp. (21.2%) and Staph. spp. (%6) were the most prevalent in Gram-positive bacteria before the pandemic, the balances changed during the pandemic period; and it was observed that the growth of Staph. spp. (15.3%) and Strep. spp. (13.6%) were the most. In our study, similar to the studies conducted before the pandemic, it has been observed that the growth of Strep. spp. type bacteria was more than Gram-positive bacteria.[11,36,37] The reason for this change in Gram-positive bacteria can be interpreted as an effect of the pandemic period, just like in P.aeruginosa, but more studies are needed for this.

In some studies, only the place of antibiotic therapy in patients with non-perforated appendicitis was studied. In one of these studies, appendectomy and antibiotic groups were compared in the seven-year follow-up of 423 patients. According to this study, there was no difference in satisfaction compared to appendectomy in patients who received only antibiotic treatment, and in seven years, 39 percent of those in the antibiotic group required appendectomy.[38] For non-perforated appendicitis, international authors recommend appendectomy in adults.[39,40] Our study is compatible with the literature in this respect. The aim of prophylactic antibiotic therapy is to prevent wound infection and complications such as intra-abdominal abscesses that may occur following an appendectomy. The treatment to be given should be a group of antibiotics that affect gram-negative aerobes and anaerobes.[41] While the antibiotics chosen for the recommended antibiotic treatment for non-perforated appendicitis are the first and second-generation antibiotics such as cefoxitin, cefotetan, cefazolin and metronidazole, it is clindamycin, ciprofloxacin, levofloxacin, gentamicin or aztreonam for those allergic to the cephalosporin group.[42] In patients with perforated appendicitis, antibiotic therapy should be therapeutic rather than prophylactic, and should consist of broad-spectrum therapy. Antibiotic treatment should be rearranged according to the culture results after the first empirical treatment. In empirical treatment, second and third-generation cephalosporins such as cefuroxime, ceftriaxone, and cefotaxime, ciprofloxacin or levofloxacin are mostly used, each of them in combination with metronidazole.[43]

There are also some limitations to our study. First, although only aerobic bacteria were identified and interpreted in our study, anaerobic bacteria, which constitute the majority of gut bacteria, could not be identified because our laboratory conditions were not suitable. Another limitation is that the study was conducted only within a single geographical region. Since geography is one of the factors affecting the gut microbial structure, larger-scale multicenter studies are needed to generalize the results. The strength of our study is that it is the first wound culture study to compare the pre-pandemic and during a pandemic.

CONCLUSION

As a result, although the most frequently identified microorganism in patients with acute appendicitis was E. coli, an increase in the density and resistance of Pseudomonas group bacteria was detected, possibly due to the effect of the COVID-19 pandemic. Therefore, these changes should be considered in the empirical treatment to be selected. Additional studies are needed to better understand the changes caused by the pandemic process to the microbiota and its effect on the acute appendicitis process.

ETHICAL DECLARATIONS

Ethics Committee Approval: Approval was obtained with the decision of the Ethics Committee of Niğde Ömer Halisdemir University, dated 22.04.2021 and numbered 2021/47.

Informed Consent: Because the study was designed retrospectively, no written informed consent form was obtained from patients.

Referee Evaluation Process: Externally peer-reviewed.

Conflict of Interest Statement: The authors have no conflicts of interest to declare.

Financial Disclosure: The authors declared that this study has received no financial support.

Author Contributions: All of the authors declare that they have all participated in the design, execution, and analysis of the paper, and that they have approved the final version.

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