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Bacterial community composition of five freshwater resources poured into the Gulf of Iskenderun, the northeast Mediterranean region, Turkey

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ABSTRACT

The Gulf of Iskenderun is located on the Mediterranean coast of Turkey**.** The Gulf is one of the areas under the threat of intense pollution due to the existing residential areas, industrial establishments and the resulting sea traffic. Although many studies have been carried out on the pollution of the Gulf of Iskenderun, there are very few studies on the resources poured into the Gulf. In this study, bacteria that cause microbiological contamination in the region and their antibiotic resistance have been investigated. Bacteria identified by regions are as follows. *Acinetobacter baumannii, Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, Klebsiella pneumoniae* in Akçay and Deliçay streams; *A. baumannii, E. coli, P. aeruginosa and S. aureus* in Arsuz stream; *A. baumannii, E. coli, P. aeruginosa, S. epidermidis, Enterococcus faecalis and K. pneumoniae* in Demirtaş stream and *A. baumanni, E. coli, P. aeruginosa, S. aureus, S. epidermidis, E. faecalis, Proteus vulgaris and K. pneumoniae* in Feyezan channel. Eight different bacterial species were detected in the isolates obtained from fresh water sources pouring into the Gulf of Iskenderun. The majority of these isolates were *E. coli.* When the antibiotic resistance levels of *E. coli*, one of the bacteria isolated in the study, were examined, the highest resistance was found against the antibiotic levofloxacin.

1. INTRODUCTION

Biological contamination and degradation cause changes in the quality parameters of aquatic environments which directly affect aquatic organisms. Hence, water pollution causes damage to aquatic ecosystems and extinguishes the self-cleaning capacity of waters resources (Gidirişlioğlu et al., 1998; Yılmaz et al., 2019).

It is known that water plays an important role in the transport of some infectious diseases agents such as typhoid fever, dysentery and hepatitis A and their transmission to healthy people. The physical and chemical cleanliness of the water does not always indicate that it is healthy. Therefore, the resource to be used as drinking and utility water must be pathogen-free (Akbaş, 1998).

Bacteriological analysis is based on the presence of coliform group bacteria. For example, *E. coli* among coliform bacteria is used as an indicator in bacteriological analyzes. Although *E. coli* is not a pathogenic microorganism, it is important for public health; because, its presence may also induce fecal or oral transmission of other pathogens. If sewage waters are discharged into rivers or lakes without any treatment, these water resources may be loaded with pathogens to be transmitted to humans (Unat, 1997).

Turkey's Mediterranean coast, where the Gulf of Iskenderun is located, is rich in fish species and serve as fishing area; yet, suffer from many pollution sources such as surrounded residential areas, industrial organisations and intense shipping activities. (Demirhan et al., 2020; Yılmaz et al., 2022). Also recently, marine aquaculture activities are carried out in the Gulf. All these activities increase the concentration of nutrients in water and creating suitable conditions for phytoplankton blooms (Başusta, 1997; Polat et al., 2006). Furthermore, the Gulf is under pressure of intensive domestic tourism activities, especially during the summer season. The Gulf is also an area open to all kinds of waste of Eastern Mediterranean countries with its discharge systems (Avşar, 1999; Mazlum et al., 2019).

The Mediterranean Sea, which occupies an area of 2.5 million km², is the world's largest inland sea; fed by the Atlantic Ocean via the Strait of Gibraltar and it is separated from the Red Sea by the Suez Canal. Hence, it is very important both for Turkey's economy and ecology. Although many studies have been carried out on the environmental pollution in Gulf of Iskenderun, there are very few studies dealing with the incoming water contamination through surrounding surface waters which poured into the Gulf. Considering previous studies, it is seen that the Gulf of Iskenderun, which is an important region both in terms of settlements and commercially, has been exposed to irreversible pollution over time. In this study, bacteria that cause microbiological contamination in the region and their antibiotic resistance have been investigated.

2. MATERIAL AND METHODS

In this study, a total of 75 water samples (100 milliliters each) were collected into sterile bottles from water surface of 5 different discharge points (Akçay Stream, Arsuz Creek, Deliçay Stream, Demirtaş Creek and Feyezan Channel) around the Gulf of Iskenderun (Figure 1) monthly between May 2014 and April 2015. The water samples taken were transferred to tubes containing sterile water and dilutions were made by the standard dilution method (Başbülbül, 2009). Water samples were inoculated on Blood Agar for the isolation of Gram (+) bacteria and on EMB (Eosin Methylene Blue) agar for the isolation of Gram (-) bacteria. Petri plates were incubated for at least 72 hours at 37 °C. At the same time, water samples were inoculated in Mueller-Hinton Broth medium and incubated for 72 hours at 37 °C with agar smears. When necessary, bacterial passages from Mueller-Hinton broth were made into solid media and microbial isolations were performed. Bacterial identification stage was started by applying Gram stain, catalase test, plasma coagulase test, oxidase test, sugar tests and advanced biochemical tests from the fresh and pure colonies isolated at the end of the incubation (Arda, 2000). Identified isolates were kept at -70°C in storage media containing 20% glycerol until the completion of the study.

Microbial identifications were evaluated simultaneously with conventional methods and by Vitek II (Biomerieux, France) automated culture systems. Antimicrobial susceptibility tests were performed by Vitek II (Biomerieux, France) automated culture system. Microorganism susceptibility tests were performed in accordance with CLSI (2015).

Microbiological analyzes of the water samples were made and bacterial identifications were performed. Gram (-) and Gram (+) antibiogram susceptibility tests were performed according to the type of bacterium. In this study, Gram (-) bacterial strains were tested for amikacin, levofloxacin, gentamycin, cefepime, meropenem, ciprofloxacin, imipenem, piperacillin and ceftazidim susceptibility and Gram (+) cocci strains were tested for oxacillin, clindamycin, ciprofloxacin, erythromycin, vancomycin, penicillin and rifampin susceptibility.

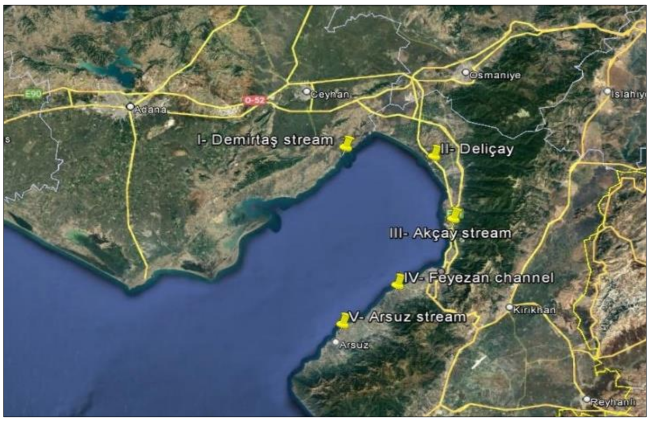

Figure 1. Sampling stations around the Gulf of Iskenderun

3. RESULTS

Bacterial identification

In this study, 8 different bacterial species (*Escherichia coli, Staphylococcus aureus, Staphylococcus epidermidis, Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterococcus faecalis, Proteus vulgaris, Acinetobacter baumannii*) were identified from water samples collected from around the Gulf of Iskenderun. The distribution of the species according to the saeson and sampling site were shown in Table 1.

Table 1. Bacteria isolated from water samples

Months/Region	AKÇAY	ARSUZ	DELİÇAY	DEMİRTAŞ	FEYEZAN
JANUARY	*A. baumannii* *E. coli*	*A. baumannii*	*A. baumannii* *P. aeruginosa*	*A. baumannii* *E. faecalis* *P. aeruginosa* *S. epidermidis* *E. coli* *K. pneumoniae*	*A. baumannii* *S. epidermidis* *P. aeruginosa* *E. faecalis* *E. coli* *K. pneumoniae* *P. vulgaris*
FEBRUARY	*A. baumannii* *E. coli*	*P. aeruginosa* *E. coli*	*A. baumannii*	*A. baumannii* *E. faecalis* *P. aeruginosa* *S. epidermidis* *E. coli* *K. pneumoniae*	*A. baumannii* *S. epidermidis* *P. aeruginosa* *E. faecalis* *E. coli* *K. pneumoniae* *P. vulgaris*
MARCH	*P. aeruginosa*	*E. coli*	*A. baumannii* *E. coli* *P. aeruginosa*	*A. baumannii* *Klebsiella spp.* *E. faecalis* *E. coli*	*A. baumannii* *S. epidermidis* *E. faecalis* *Proteus spp.* *E. coli* *Klebsiella spp*
APRIL	*A. baumannii* *E. coli* *S. aureus*	*A. baumannii* *S. aureus*	*A. baumannii* *E. coli* *S. aureus*	*A. baumannii* *E. faecalis* *E. coli* *P. aeruginosa* *Klebsiella spp*	*A. baumannii* *S. epidermidis* *E. coli* *P. aeruginosa* *S. aureus* *Klebsiella spp* *Proteus spp.* *E. faecalis*
MAY	-	*E. coli* *P. aeruginosa*	*A. baumannii*	*A. baumannii* *P. aeruginosa* *E. faecalis* *E. coli* *Klebsiella spp*	-
JUNE	-	*A. baumannii* *P. aeruginosa* *S. aureus* *E. coli*	*A. baumannii* *P. aeruginosa*	*A. baumannii* *E. faecalis* *E. coli* *S. epidermidis* *Klebsiella spp* *S. aureus* *P. aeruginosa*	*A. baumannii* *Proteus spp.* *E. coli* *S. epidermidis* *Klebsiella spp* *S. aureus* *E. faecalis*
JULY	-	*A. baumannii* *P. aeruginosa* *S. aureus* *E. coli*	-	*A. baumannii* *S. aureus* *E. coli* *E. faecalis* *P. aeruginosa* *S. epidermidis* *Klebsiella spp*	*A. baumannii* *E. faecalis* *Klebsiella spp* *Proteus spp.* *E. coli* *S. epidermidis* *P. aeruginosa*
AUGUST	-	*A. baumannii*	-	*E. coli* *S. epidermidis* *E. faecalis* *Klebsiella spp*	*A. baumannii* *P. aeruginosa* *S. epidermidis* *E. faecalis* *E. coli* *Klebsiella spp* *Proteus spp.*
SEPTEMBER	*P. aeruginosa* *Klebsiella spp*	*P. aeruginosa*	*E. coli*	*P. aeruginosa* *E. faecalis* *S. epidermidis* *E. coli* *Klebsiella spp*	*A. baumannii* *E. coli* *S. epidermidis* *E. faecalis* *Klebsiella spp* *Proteus spp.*
OCTOBER	*A. baumannii*	*P. aeruginosa*	-	*A. baumannii* *E. faecalis* *E. coli* *Klebsiella spp*	*A. baumannii* *E. faecalis* *S. epidermidis* *Klebsiella spp*

					E. coli
NOVEMBER	*P. aeruginosa*	*A. baumannii*	-	*A. baumannii* *P. aeruginosa* *E. faecalis* *E. coli* *Klebsiella spp*	*A. baumannii* *P. aeruginosa* *E. faecalis* *S. epidermidis* *Klebsiella spp* *Proteus spp.* *E. coli*
DECEMBER	*A .baumannii*	*E. coli*	*P. aeruginosa* *Klebsiella spp.*	*A. baumannii* *E. faecalis* *E. coli* *Klebsiella spp*	*A. baumannii* *P. aeruginosa* *S. epidermidis* *E. coli* *Klebsiella spp* *Proteus spp.* *E. faecalis*

In terms of species, the most number of species were found in the Feyezan channel. The reason for this is that the Feyezan channel has become a pollution area over time (Anonymous, 2022) and therefore it is thought to be expected that the species of bacteria will be too high (Table 1).

All of the reproductive samples were found to be pathogenic microorganisms for human health. When the distribution of these pathogenic microorganisms were examined, 16% Staphylococcus aureus, 30.7% Staphylococcus epidermidis and 56% Pseudomonas aeruginosa were detected. In addition, *Escherichia coli, Klebsiella pneumoniae, Acinetobacter baumannii, Enterococcus faecalis* and *Proteus vulgaris* were detected among intestinal bacteria (Table 2 and Table 3).

Table 2. Isolation rates of Gram (+) bacteria isolated from water samples

Gram Positive Bacteria						
	Staphylococcus aureus		***Enterococcus faecalis***		***Staphylococcus epidermidis***	
	(*n*)	%	(*n*)	%	(*n*)	%
Reproductive (+)	12	16	39	52	23	30.7
Reproductive (-)	63	8 4	36	48	52	44.3

Table 3. Isolation rates of Gram (-) bacteria isolated from water samples

Gram Negative Bacteria										
	Escherichia coli (*n*)	%	***Klebsiella pneumoniae*** (*n*)	%	***Acinetobacter baumannii*** (*n*)	%	***Pseudomonas aeruginosa*** (*n*)	%	**Proteus *vulgaris*** (*n*)	%
Reproductive(+)	53	70.7	48	64	58	77.3	42	56	21	28
Reproductive(-)	22	29.3	27	36	17	22.7	33	44	54	72

Antibiotic susceptibility tests

Bacteria isolated in this study showed resistance against many of the antibiotics tested with different rates. Distribution of resistance rates in Gram (+) bacterial isolates were shown in Table 4 and in Gram (-) bacterial isolates were shown in Table 5. The highest resistant rates were observed against levofloxacin and cefepim among the Gram (-) bacterial isolates and against penicillin and clindamycin among the Gram (+) isolates.

Table 4. Distribution of resistance rates in Gram (+) bacterial isolates

Species	**(n)**	**P**	%	**O**	%	**C**	%	**E**	%	**Ci**	%	**V**	%	**R**	%
		n		***n***		***n***		***n***		***n***		***n***		***n***	
S. aureus	(12)	9	31	2	7	4	14	7	24	4	14	0	0	3	10
E. faecalis	(39)	10	37	-	-	9	33	5	19	3	11	0	0	-	-
S. epidermidis	(23)	8	30	3	11	5	19	5	19	3	11	0	0	3	11

P: Pencillin O: Oxacillin C: Clindamcin E: Erythromycin Ci: Ciprofloksasin V: Vancomycin R: Rifampin

Table 5. Distribution of resistance rates in Gram (-) bacterial isolates

Species	(n)	A	%	M	%	Ci	%	L	%	İ	%	P	%	G	%	C	%	Ce	%
		n		*n*		*n*		*n*		*n*		*n*		*n*		*n*		*n*	
E. coli	(53)	2	2.9	3	4	12	17	15	21	4	6	-	-	9	13	11	16	14	20
K. pneumoniae	(48)	3	3	3	3.1	19	20	20	21	4	4.1	-	-	11	11	20	21	17	18
A. baumannii	(58)	18	9	12	6	27	14	30	15	11	6	21	11	21	11	30	15	24	12
P. aeruginosa	(42)	6	8	5	6	5	6	6	8	6	8	11	14	12	15	16	20	12	15
P. vulgaris	(21)	1	6	0	-	3	17	3	17	1	6	-	-	2	11	5	28	3	17

A: Amikacin M: Meropenem Ci: Ciprofloksasin L: Levofloxacin I: Imipenem P: Piperacilin G: Gentamicin C: Cefepim Ce: Ceftazidime

4. DISCUSSION

In this study, water samples were collected from 5 sampling sites around the Gulf of Iskenderun, a region in Turkey's Mediterranean coast which is under intense threat of pollution due to mass human population, industrial and agricultural activities and sea traffic. Although many studies have been carried out on the pollution of the Gulf of Iskenderun (Bircan Yıldırım et. al., 2017; Matyar et. al., 2008), there are very few studies on the resources poured into the Gulf. In this study, bacteria that cause microbiological contamination in the region and their antibiotic resistance have been investigated.

As a result of the identification of the isolates isolated from the water sources pouring into the Iskenderun Bay, 8 different bacterial species were identified. When the identification results are examined, it is seen that *E. coli* constitutes the majority of all isolates. The high value of *E. coli*, known as a fecal pollution indicator in aquatic environments, can be shown as an indicator of direct or indirect contamination of aquatic environments with large amounts of sewage waste (Toroğlu, et al., Kara 2008).

The comparison of the bacterial species identified in the freshwater sources in the study with the previous studies is shown in Table 6. In terms of species diversity, the bacteria identified in Table 6 are similar to in this study.

Table 6. Studies on bacteriological pollution

WORKING REGION	DEFINED TYPES	REFERENCE
A river in Yugoslavia	*Enterobacteriaceae*	**Kryalikovya et al. (1984)**
Lake Terkos and its streams (İstanbul)	*E. coli*	**Samastı et al. (1989)**
River waters contaminated by sewage waters (Brezilian)	*Pseudomonas aeruginosa, C. velchii, Staphylococcus aureus, Fecal streptococci*	**Martin et al. (1991)**
Surface waters of the Gulf of Mexico	*E. coli*	**Parveen et al. (1997)**
Uluabat Lake (Bursa)	*E. coli*	**Alkan et al. (1999)**
Arga River (Spain)	*Aeromonas sp., Enterobacteriaceae sp.*	**Go-Ni-Urriza et al. (2000)**
Wastewater irrigated land (Germany)	*E. coli*	**Thimm et al. (2001)**
Mersin Coastline	*E. coli*	**Karayakar et al. (2004)**
Sarıçay River (Çanakkale)	*Pseudomonas sp., Staphylococcus sp., Enterococcus sp., Enterobacteriaceae*	**Çolakoğlu and Çakır (2004)**
Some streams in Trabzon	*Enterobacteriaceae*	**Sevim (2005)**
Dicle River (Diyarbakır)	*E. coli, S. aureus, Vibrio parahaemolyticus, Vibrio cholerae, Yersinia enterocolitica, Enterobacteriaceae*	**Erkan and Vural (2006)**
Various fresh waters (Priştina)	*Klebsiella spp., Proteus spp., E. coli*	**Lima-Bittencourt et al. (2007)**
Seyhan Dam Lake (Adana)	*E. coli, Klebsiella sp.*	**Balcı (2007)**
The Gulf of Iskenderun	*Pseudomonas spp., Aeromonas spp.*	**Matyar et al. (2009)**
The Gulf of Iskenderun coastline	*E. faecalis*	**Matyar and Dinçer (2010)**
Agyatan Lagoon (Adana)	*Enterobacter cloacae, Staphylococcus intermedius, Staphylococcus vitilinus, Achromobacter xylosoxisans, Oligella ureolytica, Pasteurella canis, Sphingomonos paucimobilis, Bordetella trematum, Moraxella grup, V. parahaemolyticus, Vibrio alginolyticus, Pseudomonas stutzeri, Aeromonas salmonicida*	**Gholami and Dinçer (2012)**
Salarha Basin Rivers (Rize)	*E. coli*	**Verep (2015)**
Akçay Stream	*A. baumannii, E. coli, P. aeruginosa, S. aureus, Klebsiella pneumoniae*	**This study**
Arsuz Stream	*A. baumannii, E. coli, P. aeruginosa, S. aureus*	**This study**
Deliçay Stream	*A. baumannii, E. coli, P. aeruginosa, S. aureus, K. pneumoniae*	**This study**
Demirtaş Stream	*A. baumannii, E. coli, P, aeruginosa, Staphylococcus epidermidis, Enterococcus faecalis, K. pneumoniae*	**This study**
Feyezan Channel	*A. baumannii, E. coli, P. aeruginosa, S. aureus, S. epidermidis, E. faecalis, Proteus vulgaris, K. pneumoniae*	**This study**

Considering the months, the most number of species were detected in the Feyezan Channel in April. The differences between the months were evaluated as a pollution that may be caused by human-animal interests and total coliforms due to contamination. Point pollution sources disrupt the ecological balance of the environment due to uninterrupted waste inputs and therefore continuously change the competitive environment between microorganisms. In a study conducted by Kimiran in 1999 in the Marmara Sea, the relationship between indicator bacteria and environmental parameters was examined and it was seen that there was no significant relationship between sea water temperature, dissolved oxygen content, salinity and pH. It was stated that besides heavy metal concentration, other oceanographic and atmospheric conditions may also be effective in this situation. According to Clark (1989), there is no expected change from environmental factors in the regions where point pollution sources are located. In a study from Bilbao, Spain, (Garcia-Barcina et al., 2006), the relationship between the environmental parameters and the fecal coliform number was investigated between 1993-2003 and the effect of monitored environmental parameters on fecal coliform was found to be less significant. They attributed this to point pollution caused by industrial waste discharged into the river.

It has been reported that the presence of *Pseudomonas aeruginosa* in aquatic environments poses a risk to human health (Mena and Gerba, 2009). This opportunistic pathogen is an important nosocomial infection that can develop resistance against various antibiotics (Çetin, et al., 1999; Hanberger et al., 1999). The isolation of this bacterium is important in terms of its ability to spread between aquatic ecosystems, humans and animals, and its high antibiotic resistance potential. *P. aeruginosa* strains are resistant to many antibiotics, and in some cases, their susceptibility may change even during treatment (Rossolini et. al., 2005; Azık et. al., 2007). Therefore, one of the most important problems of many hospitals is the difficulty of treating P. aeruginosa strains due to the increasing resistance rates (Vitkauskien et. al., 2010).

Since *Klebsiella pneumoniae*, a bacterium that can be found widely in nature, is a bacterium found in the upper respiratory tract and fecal flora of humans, its pathogenicity is revealed as an opportunistic pathogen under unsuitable conditions. Therefore, it is a bacterium responsible for hospital infections (Çetinkaya, et al., 2005). The isolation of *K. pneumoniae* from the water sources studied is important in terms of showing that sewerage and hospital wastewater are contaminated with these sources. Antibiotic-resistant bacteria emitted from hospital wastewater can be included in human life from the receiving water environments they reach, such as agriculture and animal husbandry (İçgen, 2019).

Acinetobacter baumannii is the most isolated species from clinical specimens in hospital-acquired infections. Infections due to *A. baumannii* are an important problem due to the long-term survival of the bacteria in the external environment, easy transmission, and rapid and multi-drug resistance to many antibiotics, especially carbapenems (Koneman et al., 1992; Hoban et. al., 2015; Şahin et. al., 2019). Detection of *A. baumannii* in isolates is thought to be contaminated with hospital wastes into the water resources pouring into the Gulf, revealing the extent of the pathogenic hazard.

Proteus vulgaris is found as a member of the normal flora of the human feces and therefore it is frequently found in sewage waters. It can cause infections in human under appropriate conditions. It is especially seen in urinary tract and wound infections with hospital infections (Çopur et al., 2013). Detection of *Proteus vulgaris* in the isolates in the study is important in terms of showing that sewage water is contaminated with the water resources pouring into the Gulf.

Enterococcus faecalis, one of the bacteria isolated in the study, is found at a higher rate in feces than other enterococci species. Morinigo et al. (1990) studied on the isolation of *E. faecalis* in water samples taken from sea coasts and residential areas of rivers. As a result of their study, they isolated *E. faecalis* at a level that could pose a risk to human health, especially in areas of the sea coast where there is a risk of contamination with fecal wastes. In their studies of rivers in urban settlements, they isolated a significant level of *E. faecalis* from the rivers. The reason for the detection of *E. faecalis* in our study is thought to be the contamination of fecal wastes into the waters pouring into the gulf.

Although Staphylococcus epidermidis is generally less pathogenic, it is a major risk for immunocompromised patients and patients with permanent catheterization associated with hospital infections. *S. epidermidis* is the most common cause of catheter infections and can often be treated with antibiotics without the need to remove the catheter (Dündar et. al., 2008). Since it is a part of the human normal flora, it has developed resistance to many common antibiotics such as methicillin, novobiocin, clindamycin, and benzyl penicillin (Nilsson et al. 1998). In the study, the antibiotic that *S. epidermidis* showed the highest resistance was determined as Penicillin.

Staphylococcus auerus is found extensively in the feces of humans and animals. *S. aureus* is a highly virulent microorganism that is frequently encountered as a disease agent in humans. It gained resistance to many antibiotics since the 1950s, and in 1961, the problem of multi-antibiotic resistance emerged in methicillin-resistant S. aureus strains, and staphylococci became one of the "problematic" microorganisms (Tambic, et al., 1997; Günaydın, et al., 2002). Penicillin resistance has gradually increased in staphylococci since 1944, and in the 1950s, resistance to antibiotics such as erythromycin, tetracycline, and streptomycin developed in addition to penicillin (Haznedaroğlu, 2008). In a study conducted by Demirel (2013) against various antibiotics, it was found that this microorganism showed the highest antibiotic resistance rate against penicillin (81%), while no resistance against vancomycin was detected. Similar results were found in this study, and the highest antibiotic resistance rate of *S. aureus* was found against penicillin, and no resistance was found against vancomycin. Besides being human pathpogens, various staphylococci species caused infections in diverse aquatic environments of Turkey (Çanak 2018; Çanak and Timur, 2020). Among the staphylococci isolated in this study, *S. epidermidis* was recovered from pathologies of cultured rainbow trout *Oncorhynchus mykiss* (Timur and Akayli, 2003), gilthead seabream *Sparus aurata* (Kubilay and Uluköy, 2004) and European sea bass *Dicentrarchus labrax* (Timur et al., 2008; Çanak and Timur, 2020) and *S. aureus* was recovered from pathologies of cultured rainbow trout *Oncorhynchus mykiss* (Timur and Akayli, 2003), gilthead seabream *Sparus aurata* (Çanak and Timur, 2020) and aquarium reared yellowfin hind *Cephalopholis hemistiktos* (Çolak and Çanak, 2017).

In 2000, Goñi-Urriza et al. found that urban pollution increases the rate of antibiotic resistance in bacterial populations of rivers. Most of the researches on antibiotic resistance in aquatic environments are the bacteria with faecal origin which are both pollution indicator and related to infectious diseases.

Matyar and Dinçer (2010) investigated the resistance of 158 *Enterococcus faecalis* isolates from the Mediterranean Sea (along the coast of the Gulf of Iskenderun) against 15 different antibiotics. They concluded that the Eastern Mediterranean harbored *Enterococcus faecalis* with significant antibiotic resistance, which posed a potential risk to public health.

In recent years, the emergence of antibiotic resistance among pathogenic bacteria in clinical environments has initiated serious problems around the world. In addition, the microbial community members in the natural environment that determine genetic resistance can constitute these antibiotic resistance reservoirs of human and ecological health. In terms of global public health, it is thought that an average of 700 thousand individuals die every year due to antibiotic resistance. In addition, if the resistance rate continues to increase at this rate, it is predicted that 10 million individuals will die every year due to antibiotic resistance developed by bacteria in 2050 (Frieri et al., 2017; Lee Ventola, 2015; Yunusoğlu, et al., 2020). In the statistical studies, it is seen that Turkey is among the countries where antimicrobial resistance is observed at a high rate in the world. These results show that antibiotic resistance has become an important threat for Turkey (Yunusoğlu et al., 2020).

5. CONCLUSION

Measures to protect and improve the microbiological quality of rivers and lakes are key to maintaining the quality and quantity of water resources for the future. Sewage water should not be discharged into rivers and lakes to avoid contamination of the water supply.

It can be thought that the emergence of antibiotic resistance is caused by the intense and unconscious use of antibiotics and the inclusion of resistant bacteria in the wastes into aquatic environments through city sewers without any treatment. Since domestic wastewater is the most important source of pathogenic bacteria and antibiotic resistance development, excessive and incorrect use of antibiotics should be avoided by applying a rational antibiotic use policy.

The irreversible pollution the Gulf of Iskenderun, which is exposed to wastewater discharges with very different contents, is extremely important for both Turkish economy, ecology and the world's ecology.

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Compliance with Ethical Standards

Author Contributions

Authors contributed equally to this paper.

Conflict of Interest

The authors do not have any conflicts of interest to declare.

Ethical Approval

For this type of study, formal consent is not required.

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