Chapter 9

IMPACT OF CLIMATE CHANGE ON THE DISTRIBUTION OF BACTERIA IN THE TURKISH SEAS

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Summary

Microorganisms are the only living species in the globe that can live anywhere other creatures live, and also in environments with extreme environmental conditions. The seas are home to natural-environment bacteria that find life in ecosystem cycles with the decomposition of organic matter, as well as pathogen bacteria that enter the environment based on human-based activities. It is known that climate change forces the species to adapt, migrate, take their place or extinction. However, the interactions of microorganisms with climate change have not been much of an issue so far. In terms of the sustainability of marine ecosystems and global health, it is necessary to define not only how microorganisms affect climate change, but also how microorganisms are affected by climate change and other human activities.

This study draws attention to the microbial communities that form the biosphere's life support system, providing examples of regional changes of pathogen bacteria data from the Turkish Sea, and presented ways to respond to the global climate change of

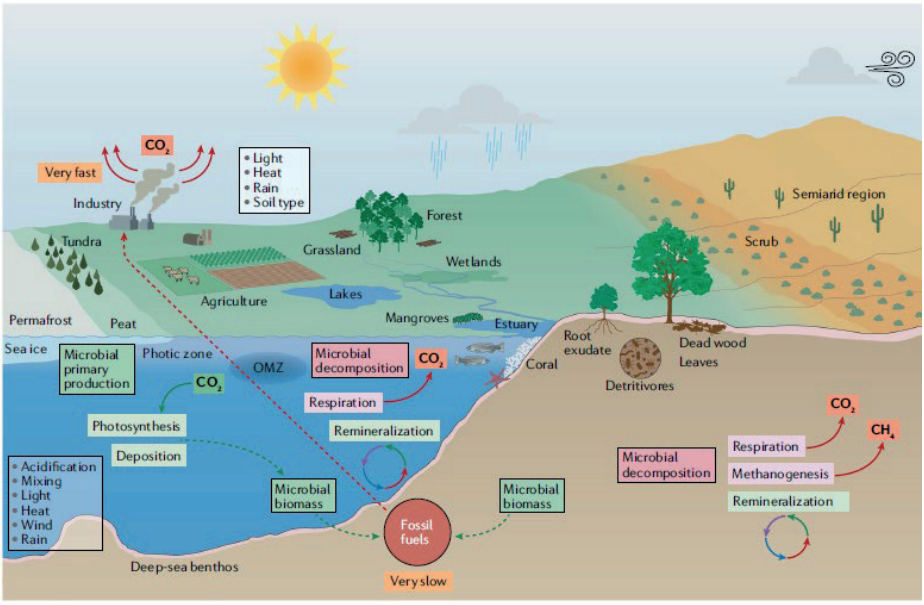
processes related to microorganisms. This study contributes to the importance of the correct evaluation of the response to the stress factors of bacteria that contribute significantly to the breathing of the seas and the circulation of many elements to create a healthy environment in the future.

Keywords: Climate change, eutrophication, pathogen bacteria, sea,Turkish

1. INTRODUCTION

Generally, microorganisms can disperse more easily than macroscopic organisms. Nevertheless, biogeographic distinctions occur for many microbial species, with dispersal, lifestyle (for example, host association) and environmental factors strongly influencing community composition and function Ocean currents and thermal and latitudinal gradients are particularly important for marine communities (Hanson et al.2012). If movement to more favourable environments is impossible, evolutionary change may be the only survival mechanism (Hoffmann and Sgrò 2011). Microorganisms, such as bacteria, archaea and microalgae, with large population sizes and rapid asexual generation times have high adaptive potential (Riebesell and Gattuso,2015). Relatively few studies have examined evolutionary adaptation to ocean acidification or other climate change-relevant environmental variables (Hutchins and Fu, 2017). Similarly, there is limited understanding of the molecular mechanisms of physiological responses and the implications of those responses for biogeochemical cycles.

Fig 1. Microorganisms and climate change in marine and terrestrial biomes (Cavicchioli, 2019)



In marine environments, microbial primary production contributes substantially to CO_2 sequestration. Marine microorganisms also recycle nutrients for use in the marine food web and in the process release CO_2 to the atmosphere. In a broad range of terrestrial environments, microorganisms are the key decomposers of organic matter and release nutrients in the soil for plant growth as well as CO_2 and CH_4 into the atmosphere. Microbial biomass and other organic matter are converted to fossil fuels over millions of years. By contrast, burning of fossil fuels liberates greenhouse gases in a small fraction of that time. As a result, the carbon cycle is extremely out of balance, and atmospheric CO_2 levels will continue to rise as long as fossil fuels continue to be burnt. The many effects of human activities, including agriculture, industry, transport, population growth and human consumption, combined with local environmental factors, including soil type and light, greatly influence the complex network of microbial interactions that occur with other microorganisms, plants and animals. These interactions dictate how microorganisms respond to and affect climate and how climate change (for example, higher CO_2 levels, warming, and precip-

itation changes) in turn affect microbial responses. OMZ, oxygen minimum zone (Fig 1).

Climate change is profoundly altering ecosystems and the goods and services that they provide . While warming temperatures have been the central focus of studies on climate change from genes to ecosystems, increases in extreme precipitation events are also rendering fundamental changes in marine enviroment. Outbreaks of waterborne infectious diseases are ofen associated with heavy precipitation events. Marine ecosystems are hotbeds of disease transmission because pathogens can avoid desiccation, and hosts abound. Waterborne pathogens (including *Vibrio cholerae, Escherichia coli 0157:H7,Salmonella typhi*) of humans and wildlife include infectious viruses, bacteria, protozoans, and fungi. Epidemics in wildlife species can alter food webs, community composition, genetic diversity and biogeochemical cycling (Lake and Barker, 2018).

Studies we have conducted in the Turkish Seas since 2000 show the dominant presence of pathogen bacteria in coastal areas, and natural environment bacteria in the oligotrophic areas (Altuğ et al. 2012). Ocean warming, acidification, eutrophication, and habitat destruction are the effects of host-pathogenic bacteria on the spread of diseases depending on specific factors. As with the pathogenic Vibrio species that find life in the sea, in some water-borne infections, the spread toward the poles is correlated to the reduction in salinity of the water environment on the beaches due to rising rains due to global climate change. These changing conditions can improve the development of other pathogens as in Vibrio types. Similar findings are also available for Salmonella types. The pathogen bacteria are heavily affected by climate changes caused by large-scale climate events that disrupt the normal rainfall, including infectious diseases caused by many pathogen bacteria and water-borne diseases, and cause temperature changes in about two-thirds of the world every few years.

The pathogen bacteria in the sediment are exposed and multiplied by heavy rainfall. Especially those pathogens that are transmitted orally can be mixed in drinking water due to heavy rain. To better understand the spread of diseases and develop effective

control strategies, we need to be familiar with the ecology vectors of pathogens and the impact of environmental factors. While natural and experimental microbial populations are examined in terms of adaptation mechanisms and results, the adaptation of species to their environment is less researched for microorganisms compared to animals and plants.

The different stress responses developed by microorganisms based on high diversity and regional conditions make it difficult to identify their roles in the ecosystem. Revealing the geographical differences of microbiological responses is necessary to identify bacterial roles in marine ecosystems. Our studies in the Turkish Seas show the regional metabolic differences, resilience characteristics, and distributions of bacteria (Altuğ et al. 2010a, 2020). To prevent new negatives of the current bacteriological situation detected due to global climate change, it is necessary to focus on data on compositions of microbial communities, metabolic functions, regional mutations associated with eutrophication, and to make global comparisons.

6. MATERIALS and METHODS

6.1.Sampling Areas

Seawater and sediment samples taken from diverse maritime habitats were examined for the presence of heterotrophic aerobic bacteria and the frequency of antibiotic resistance. The levels of heterotrophic aerobic bacteria and the bacterial antibiotic resistance were investigated in the coastal area of Ölüdeniz Lagoon, Gulf of Antalya, and Mediterranean Sea, Istanbul Strait, The Golden Horn Estuary, The Sea of Marmara, The Canakkale Strait, Sapanca Lake, Güllük Bay (The Aegean Sea) (Figure 1 and Table 1).

The samples were collected in a Nansen container that had been washed with acid (10 percent HCl in distilled water), disinfected with alcohol (50:50, v/v), and rinsed with sterile water. The seawater samples were then transferred to brown sterilized glass bottles and cold chained to the laboratory. Surface sediment samples were obtained from the sampling sites using an Ekman grab (HYDRO-BIOS Apparatebau GmbH, Germany, 15x 5).

Fig. 2. The locations of sample stations in Turkish marine enviroments

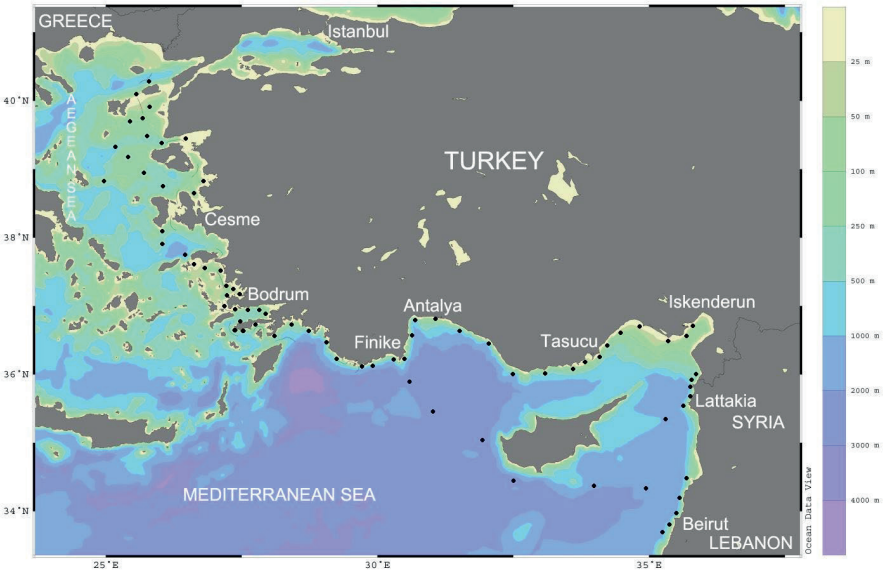


Table 1. The seawater samples taken from diverse maritime locations over various sampling times.

Sampling Areas		Type of Samples	Sampling Period	Number of Samples	References
The Aegean Sea	Ölüdeniz Lagoon	Seawater	2005-2006	20	(Altuğ 2005)
	Güllük Bay	Seawater	2011-2013	576	(Altuğ et al. 2020)
The Sea of Marmara	The Golden Horn Estuary	Seawater	2002-2003	73	(Altuğ *et al.*, 2005)
	Istanbul Strait	Seawater	2006-2007	216	(Çardak et al. 2016; Çardak, Altuğ, and Çiftçi Türetken 2015)
	The Sea of Marmara	Seawater	2011-2014	1512	(Altuğ et al. 2013)
	The Sea of Marmara	Seawater & Sediment	2011-2014	252	(Çardak et al.,2016)
	Çanakkale Strait	Seawater	2011-2012	936	(Çardak et al. 2016, 2015)
	The northern shores of the Sea of Marmara	Ballast Water	2009-2010	21	(Altuğ et al. 2012)
Mediterranean Sea	Coastal areas	Seawater	2006-2008	96	(Altuğ et al. 2010)
	Gulf of Antalya	Seawater &Sediment	2009-2010	144	(Çardak et al.2015)
		Total number of analyzed samples		3846	

6.2. Bacteriological analyses

2.1.1. Culturable Bacteria Levels Analyses

Appropriate dilutions of seawater samples taken under aseptic conditions were spread on the surface of Marine Agar (Difco) medium using the spread plate method. Petri dishes were incubated at 22 ± 0.1 °C for 72 hours. Growing colonies were counted and recorded as the level of heterotrophic mesophilic aerobic bacteria that could be cultured in 100 ml of seawater sample (Austin 1998).

The spread plate technique was used for heterotrophic aerobic bacteria analyses in sediment samples. Each sediment sample was mixed and homogenised. Then 1 g sample was taken from each and serially diluted with sterile commercial seawater. 0.1 ml samples of 10–5 dilutions were taken and spread on Marine Agar 2216 (Difco, Detroit, MI). The plates were incubated for five days at 22 ± 0.1°C. Growing colonies were evaluated as CFU g–1. Further processes related to heterotrophic bacteria (Benchi et al.,1992).

2.1.2 Bacteria Analyses

The samples, filtered through 0.45 μm pore diameter membrane filters placed aseptically in a sterile filter device (Sartorius) connected to the vacuum pump were placed in ready-made dehydrated media moistened with sterile distilled water (3 ml) without air bubbles. m.FC-NKS (Sartorius) and Endo-NKS (Sartorius) nutrient pad systems were used for fecal coliform and total coliforms. Petri dishes with filters were incubated for 24 hours at 44.5 ± 0.1 ºC for fecal coliform and 24 hours at 37 ± 0.1 ºC for total coliform and intestinal streptococcus (APHA 2000).

2.1.3.Indentification of Bacterial Isolated

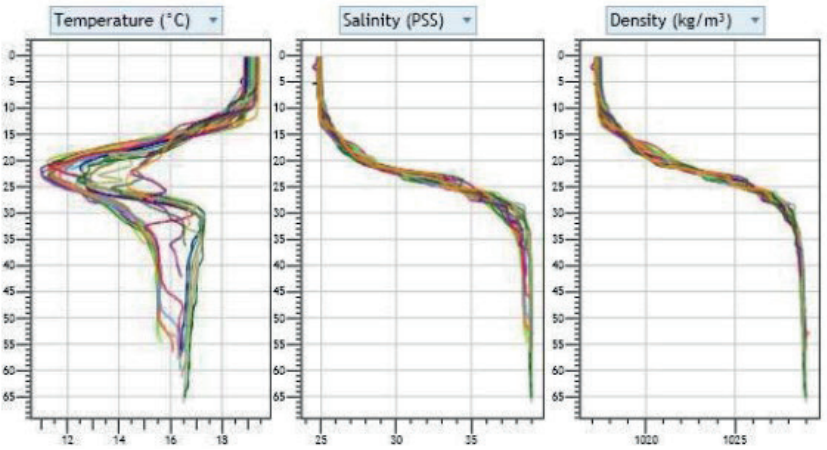
The VITEK 2 Compact 30 (bioMérieux, France) automated micro identification system was used for detecting biochemical responses of the bacterial isolates against various substrates. The pure isolates were Gram-stained and then identified using GN (Gramnegative fermenting and nonfermenting bacilli), GP (Gram-positive cocci and nonspore-forming bacilli), and BCL (Gram-positive spore-forming bacilli) cards in the automated micro identification system VITEK 2 Compact 30 (bioMerieux, France). The identification cards are based on biochemical tests (46 tests for BCL, 43 tests

for GP, 47 tests for GN) measuring carbon source utilization, enzymatic activities, inhibition, and resistance. Calculations are performed on raw data and compared to thresholds to determine reactions for each test. On the VITEK 2 Compact, test reaction results as appear in parentheses were evaluated as an indicator of weak reactions that are too close to the test threshold (Pincus 2005) .

6.3. Hydrographic Parameters.

Temperature, salinity and density values were measured in situ using the CTD (RBR Concerto) at the sampling areas.

Fig 3.Temperature, salinity and density profiles of water column at sampling location (Altuğ et al 2019)



3. RESULTS and DISCUSSION

The mean values of total culturable heterotrophic bacteria levels in seawater and sediment samples which were taken from various m are summrine enviroments summarized in Figure 4.

The percentage of distribution of heterotrophic aerobic bacteria species belonging to 17 different families from the seawater and sediments samples were recorded as 62.72% in Enterobacterıaceae, 60.82% in Bacıllaceae, 36.01% in Staphylococcaceae, 21.92% in Pseudomonadaceae, 18% in Aeromonadaceae. 15% in Mıcrococcaceae 15% in Aeromonadaceae and 3% Neisseriacea.

Fig 4. The percentage of distribution of heterotrophic aerobic bacteria (HAB CFU/ml)

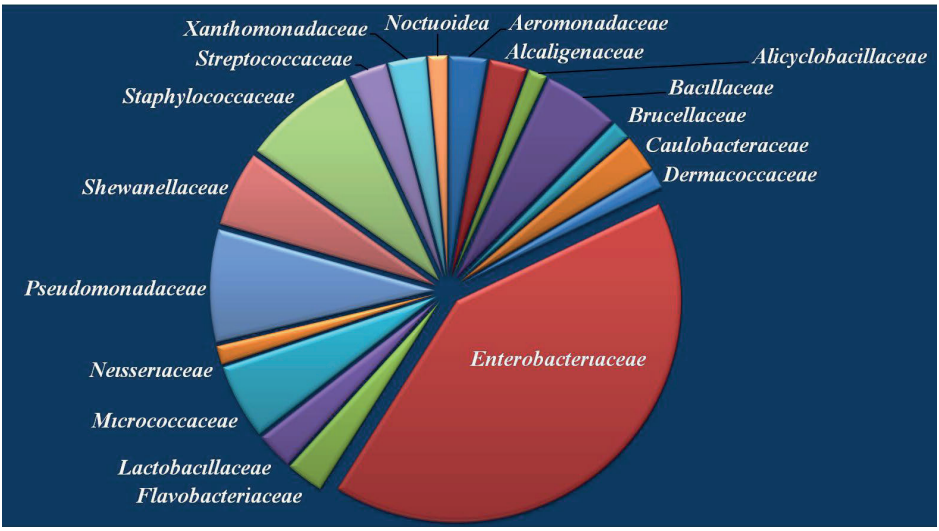
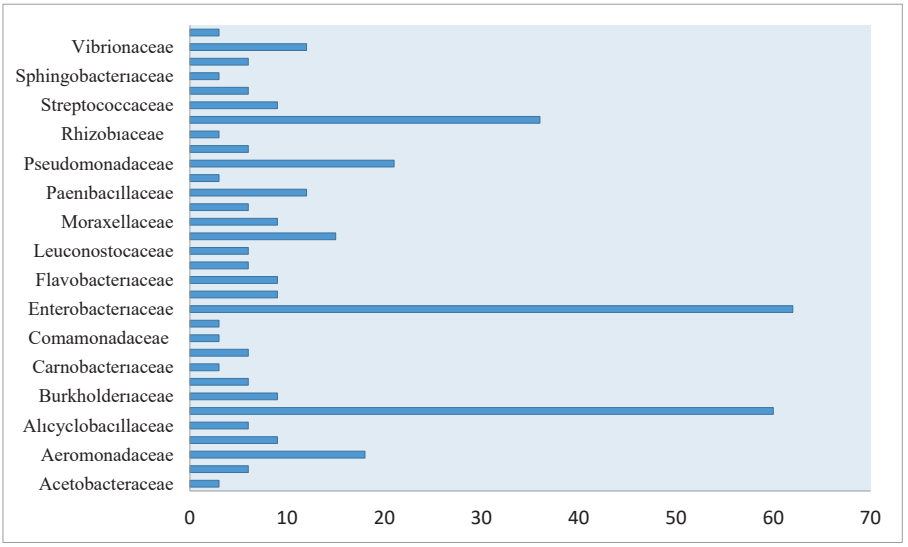


Fig 5. The percentage of distribution of heterotrophic aerobic bacteria (Altuğ et al.,2013)



Heterotrophic bacteria were isolated from 3845 different stations on Marine Agar from Turkish Seas. Approximately 81 % of the isolates were identified to genus level. The heterotrophic bacteria species which were isolated from the study area and their metabolic peculiarities are summarized in Fig 5.. Gamma Proteo-

bacteria was the most common group in terms of species number in comparison to the other taxonomic groups in the coastal areas. Table 1. The species belonging to Enterobacteriaceae family was the most common taxonomic group in the marine areas of Turkish Seas. Bacilli family was the second most common group.

The species diversity and distribution also varies in other Mediterranean regions (Sanz-Sáez et al.2020). The enzymatic versatility of these genera is well known and has been suggested as an explanation of their importance in particle turnover (Richa et al. 2017). Because their differentenzymatic activities the bacterial genera found could integrate to accomplish at the best the complete degradation of the scarce resources of such an oligotrophic ecosystem. Thus, further studies will be carried out to evaluate the role of each isolated genus in recycling bioelements, and to further characterize the Turkish Sea.

The similaries in the bacterial temporal density trends between the sampling areas is described in (Fig. 5). The biodiversity the differences among the areas due, exclusively to the bacterial abundance typical of each site, while enhancing the differences in the temporal trend. Cluster analysis indicated that the eastern and western Turkish Seas were not closely related. Furthermore, the differences among sites are more evident than those between surface and bottom for each site.

Table 2. Diversity of pathogen bacteria according to their isolated areas.

Species	Taxonomy	References
Achromobacter denitrificans	Proteobacteria/ Beta Proteobacteria	Coenye et al. 2003
Aerococcus viridans	Firmicutes/ Bacilli	Stewart et al., 1969
Aeromonas caviae	Proteobacteria/Gamma Proteobacteria	Eddy 1962,
Aeromonas hydrophila	Proteobacteria/Gamma Proteobacteria	Schubert 1964
Aeromonas sobria	Proteobacteria/Gamma Proteobacteria	Popoff and Vron 1981
Aeromonas veronii	Proteobacteria/ Gama Proteobacteria	Hickman-Brenner et al., 1987
Alcaligenes faecalis subsp. faecalis	Proteobacteria/ Beta Proteobacteria	Castellani and Chalmers 1919
Alicyclobacillus acidoterrestris	Firmicutes/ Bacilli	(Deinhard et al. 1988) Wisotzkey et al. 1992
Brevundimonas vesicularis	Proteobacteria/Alpha Proteobacteria	(Busing et al. 1953) Segers et al. 1994
Brucella melitensis	Proteobacteria/Alpha Proteobacteria	(Hughes 1893) Meyer and Shaw 1920
Chromobacter violaceum	Proteobacteria/ Beta Proteobacteria	Bergonzini 1880
Chryseobacterium indologenes	Flavobacteria	(Yabuuchi et al. 1983) Vandamme et al. 1994
Citrobacter freundii	Proteobacteria/ Gama Proteobacteria	(Braak 1928) Werkman and Gillen 1932
Citrobacter sedlakii	Proteobacteria/ Gama Proteobacteria	Brenner et al. 1993
Cronobacter dublinensis ssp lausannensis	Proteobacteria/ Gama Proteobacteria	(Iversen et al. 2008)
Dermacoccus nishinomiyaensis	Firmicutes/ Bacilli	(Deinhard et al. 1988) Wisotzkey et al. 1992
E. coli O157:H7	Proteobacteria/ Gama Proteobacteria	(Migula 1895) Castellani and Chalmers 1919
Enterobacter cloacae ssp dissolvens	Proteobacteria/ Gama Proteobacteria	Hormaeche and Edwards 1960
Enterococcus faecium	Firmicutes/ Bacilli	(Orla-Jensen 1919) Schleifer & Kilpper-Bälz 1984
Granulicatella elegans	Firmicutes/ Bacilli	(Roggenkamp et al. 1999) Collins and Lawson 2000
Klebsiella oxycota	Proteobacteria/Gamma Proteobacteria	(Flugge 1886) Lautrop 1956
Klebsiella pneumoniae ssp pneumoniae	Proteobacteria/Gamma Proteobacteria	(Schroeter 1886) Trevisan 1887
Kocuria kristinae	Actinobacteria	(Kloos et al. 1974) Nouioui et al. 2018
Lactococcus garvineae	Firmicutes/ Bacilli	Schleifer et al. 1986
Leuconostoc mesenteroides subsp. cremoris	Firmicutes/ Bacilli	(Knudsen and Sorensen 1929) Garvie 1983
Micrococcus luteus	Actinobacteria	(Schroeter 1872) Cohn 187
Ochrobactrum anthropi	Proteobacteria/Alpha Proteobacteria	(Holmes et al. 1988) Hördt et al. 2020
Pantoea spp.	Proteobacteria/ Gama Proteobacteria	
Pasteurella canis	Proteobacteria/ Gama Proteobacteria	Mutters et al. 1985

Table 2. (Devamı) Diversity of pathogen bacteria according to their isolated areas.

Species	Taxonomy	References
Providencia alcalifaciens	Proteobacteria/ Gama Proteobacteria	(de Salles Gomes 1944) Ewing 1962
Pseudomonas aeruginosa	Proteobacteria/ Gama Proteobacteria	Schröter 1872, Migula 1900
Pseudomonas fluorescens	Proteobacteria/ Gama Proteobacteria	Migula 1895
Pseudomonas luteola	Proteobacteria/Gamma Proteobacteria	Kodama et al. 1985
Pseudomonas putida	Proteobacteria/Gamma Proteobacteria	(Trevisan 1889) Migula 1895
Pseudomonas studzeri	Proteobacteria/Gamma Proteobacteria	(Lehmann and Neumann 1896) Sijderius 1946
Raoultella ornithinolytica	Proteobacteria/Gamma Proteobacteria	(Sakazaki et al. 1989) Drancourt et al. 2001
Salmonella enterica subsp. arizonae	Proteobacteria/Gamma Proteobacteria	(Borman 1957) Le Minor and Popoff 1987
Serratia fonticola	Proteobacteria/Gamma Proteobacteria	Gavini et al. 1979 (Approved Lists 1980)
Shewanellla putrefaciens	Gamma Proteobacteria	(Lee et al. 1981) MacDonell and Colwell 1986
Sphingomonas paucimobilis	Proteobacteria/Alpha proteobacteria	(Holmes et al. 1977) Yabuuchi et al. 1990
Staphylococcus aureus	Firmicutes/ Bacilli	Rosenbach 1884
Staphylococcus hominis ssp novobiosepticus	Firmicutes/ Bacilli	Kloos et al. 1998
Staphylococcus sciuri	Firmicutes/ Bacilli	Kloos et al. 1976
Staphylococcus warneri	Firmicutes/Cocci	Kloos & Schleifer 1975
Streptococcus pneumoniae	Firmicutes/ Bacilli	(Klein 1884) Chester 1901
Vibrio alginoliticus	Proteobacteria/ Gama Proteobacteria	(Miyamoto et al. 1961) Sakazaki 1968
Vibrio fluvialis	Proteobacteria/ Gama Proteobacteria	Lee et al. 1981
Vibrio parahaemolyticus	Proteobacteria/ Gama Proteobacteria	(Fujino et al. 1951) Sakazaki et al. 1963
Vibrio vulnificus	Proteobacteria/ Gama Proteobacteria	(Reichelt et al. 1979) Farmer 1980
Virgibacillus pantothenticus	Firmicutes/ Bacilli	(Proom and Knight 1950) Heyndrickx et al. 1998

Gram-negative fermentative bacteria corresponding to Photobacterium angustum and Vibrio were more abundant in the ground whole flesh than in the sea water. It has been reported by several authors that there is a relationship between the microbiota associated with the surrounding sea water. The results of the present study agree to some extent with the mentioned studies. In fact, the culturable aerobic hetetrophic bacterial population associated with Turkish Seas is dominated, during the warmer months, by fac-

ultative anaerobic halophilic bacteria from GammaProteobacteria (i.e. Vibrionaceae, Aeromonadaceae). These bacteria were not able to thrive on anaerobic conditions by fermenting carbohydrates, but they could also use nitrate as alternative electron acceptor of their oxidative metabolism, being thus beter adapted to anaerobic microniches. During the cold season, gram-negative oxidative bacterial groups corresponding to yet undescribed AlphaProteobacteria dominated in the sea water samples.

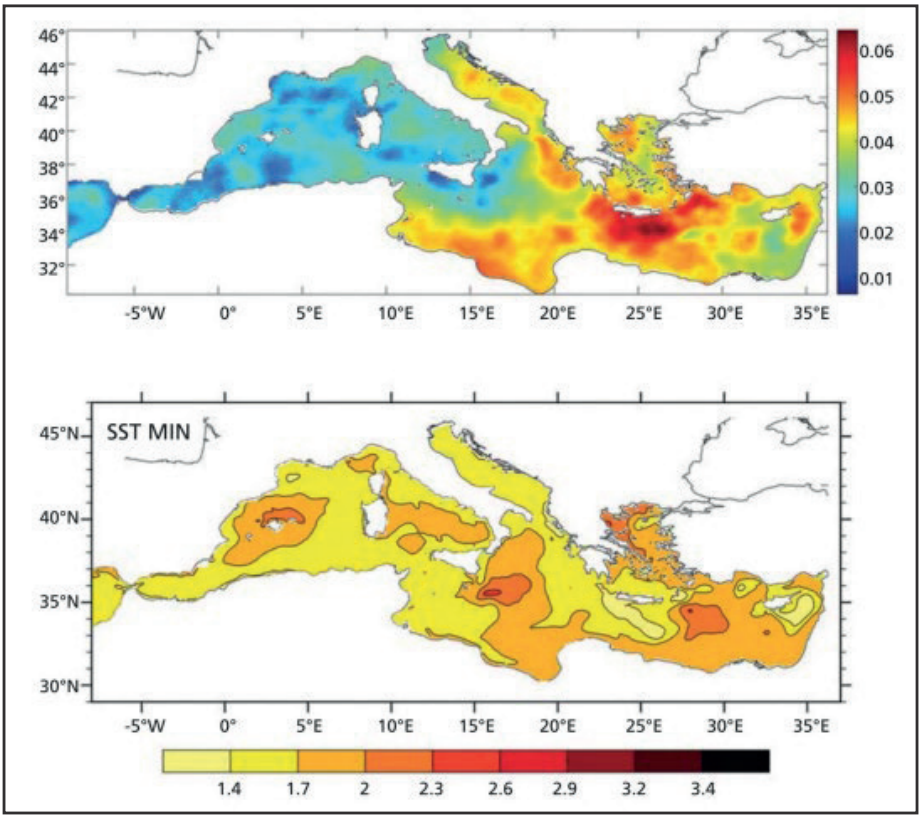
The taxonomy of bacteria species which were isolated from the various marine enviroments water samples were shown in Table 1. Many of the isolated strains are clinically significant in systemic infections such as bacteremia and endocarditis. Furthermore, many of them can cause nosocomial infections. The fact that pathogenic bacteria such as *E. coli O157:H7*, Brucella melitensis, *Aeromoas hydrophila*, and *K. pneumoniae* have been isolated shows that ballast waters pose a threat to human and fish health. In this study *E. coli O157:H7* was isolated from four different ballast water samples (Altuğ et al.2013). This situation also showed that current international regulations (IMO, Regulation-D2) are insufficient to understand the possible bacteriological risk involved in the transportation of ballast waters in marine environments. For example B. melitensis is also an important bacterial pathogen that causes abortion in cattle and Malta fever in humans. In this study, *B. melitensis* was isolated from two different samples. Due to the fact that it is not known as a ubiquitous species of bacteria, the isolation of *B. melitensis* from ballast water was surprising. Likewise, after the isolation of *B. melitensis* from ballast water, it was also isolated from seawater samples taken from Caddebostan beach in Istanbul in July 2010 (Altuğ et al., 2010).

Many important pathogens belong to the Gamma Proteobacteria class. Gamma Proteobacteria was recorded to be the most common group in terms of species count. The members of the Bacilli class have high enzyme secretion capacity. Due to the fact that bacteria play an important role in organic matter turnover and carbon cycle, the metabolic characteristics of these bacteria arealso important for the marine ecosystem. In this Turkish Seas, the Bacilli class was recorded as the second most common group. In this

study a large number of pathogen bacteria in from various marine enviroments to the Turkish Seas were presented for the first time.

Bacterial contamination in coastal waters may change seasonally depending various environmental variables such as temperature, rainfall and other influences. The pathogenic bacterial inputs are undesirable situations with respect to public health, ecology and the environment.

Fig 6. Top map horizontal distribution of SST annual linear trends (°C/yr) over the period 1985 to 2008. Bottom – minimum values of the anomalies obtained from the composite forecast (out of the six scenario simulations) of sea surface temperature for the 2070 to 2099 period (vs. 1961 to 1990). Units are in °C (Top, adapted from Skliris et al., 2012; Bottom, adapted from Adloff et al., 2015).



Recent warming of the Mediterranean Sea (from the early 1990s) results from the combination of natural climate variability and climate change. (Figure 6a Skliris et al., 2012). The available

estimates of future surface warming in the Mediterranean range from +1.73 °C to +2.97 °C in 2070 to 2099 in respect to 1961 to 1990 (Figure 6b; Adloff et al., 2015) while surface salinity anomalies are forecast to increase from +0.48 to 0.89 over the same period. The frequency of heatwaves is expected to increase from about two days per year in the past century to about 6 to 24 days per year in 2021 to 2050 (Fischer and Schär, 2010). Over 2100, the Black Sea is also projected to warm, from a maximum of 2.81 °C per century in summer to a minimum of 0.51 °C per century in winter (Shaltout and Omsted, 2014), with little spatial variability in the annual trends (Cannaby et al., 2015). The sea surface salinity is estimated to have shown a gradual decrease (0.02/year) over the last 50 years (1960 to 2015; Miladinova et al., 2017) while future projections indicate a possible increase by the end of the century (Cannaby et al., 2015).

Rising temperatures may facilitate the occurrence and distribution of pathogens such as Vibrio bacteria (Lloret et al., 2016). An economically important disease of livestock, have already emerged in Turkey in response to climate change, and larger, more frequent outbreaks are predicted to occur in the future. For certain waterborne infections by pathogenic *Vibrio* spp., poleward spread correlates with increasing global temperature and lower salinity of marine environments in coastal regions (such as estuaries) caused by increased precipitation Baker-Austin et al., 2013). These changed conditions can promote the growth of *Vibrio* spp. in the environment Increasing sea surface temperatures also correlate with increases in *Vibrio cholerae* infections in Bangladesh (Pascual et al. 2010), infections with several human- pathogenic *Vibrio* spp. in the Baltic Sea region and the abundance of *Vibrio* spp. (including human pathogens) in the North Atlantic and North Sea (Vezzulli al., 2016).

Climate change affects the occurrence and spread of diseases in marine environments biota (Harrell et al. 2002) , depending on diverse socioeconomic, environmental and pathogen (Altizer et al. 2013). Understanding the spread of disease and designing effective control strategies requires knowledge of the ecology of pathogens, their vectors and their hosts, and the influence of dispersal and en-

vironmental factors (McDougald et al., 2006, Johnson et at. 2015).

The ubiquitous presence and further spread of pathogen bacteria indicate that these marine areas are able to easily adapt to changing environmental conditions including those caused by climate change. Several studies have previously examined their adaptation by analyzing phenotypical and gene expression changes taking place in pathogen species facing different stress conditions (Montánchez et al., 2019)

If global climate change continues in this direction in the coastal regions of the Mediterranean, the increased frequency and spread of some marine diseases may have potential consequences on human health. In the past, the ‘‘Vibrio cholerae paradigm’’ has represented the first important example of the cascade effects of climate change on human health. Vibrio cholera, indeed, lives attached to the exoskeleton of marine copepods, which depend on phytoplankton blooms for their nutrition. These in turn are influenced by climate change. We propose phenomena such as epidemics and mucilage as a potential new paradigm of ecosystem change caused by the synergistic effect of climate change and the misuse of naturel resources management.

4. **CONCLUSION**

Human activity that directly affects microorganisms, pollution, which positively feeds back on climate change, pollution, agricultural practice and the spread of disease. Human activity that alters the ratio of carbon uptake relative to release will drive positive feedbacks and accelerate

the rate of climate change. By contrast, microorganisms also offer important opportunities for remedying human- caused problems through improved agricultural outcomes, production of biofuels and remediation of pollution. The development of innovative microbial technologies to minimize and mitigate climate change impacts, reduce pollution and eliminate reliance on fossil fuels.

To understand how microbial diversity and activity that govern small- scale interactions translate to system fluxes, it will be important to scale findings from individuals to communities and to

whole ecosystems. Earth system modellers need to include microbial contributions that account for physiological and evolutionary responses to biotic and abiotic forcings.

We can recognize the effects of microorganisms on climate change and climate change on microorganisms. It is therefore not surprising that challenges exist for defining causes and effects of anthropogenic climate change on biological systems. As well as guiding future policy developments, together these indicate a considerable role for research in areas surrounding complex issues of climate change and public health.

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