CHAPTER 12

Microbial Communities in the Process and Effluents of Seawater Desalination Plants

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12.1 INTRODUCTION

Scarcity of potable water due to the combined effects of climate change (driving changes in precipitation patterns and draughts) and population growth [1] has increased the global demand for desalination. At the end of 2015,[1] global desalination capacity was estimated at 86.6 $Mm^3\,day^{-1}$ with seawater (SW) desalination accounting for ca. 60% of the global desalination effort [2,3]. From 1997 to 2008, the compound annual growth rate of desalination was 17%, and increased exponentially at a rate of 14% $year^{-1}$ from 2007 to 2012. Although the yearly rate of increase then declined to 3% $year^{-1}$ from 2012 to 2015 [3,4], desalination and in particular construction of large-scale seawater desalination plants are expected to continue expanding worldwide. At present, two desalination technologies dominate the desalination industry: the thermal process Multistage Flash (MSF), and the membrane-based Reverse Osmosis (RO), the latter accounting for more than 60% of the market share [4].

Regardless of the technology used in seawater desalination, SW (feed water) is pumped into the desalination plant and brine is discharged back to sea—impacting the marine environment [5]. Intake of seawater entrains and impinges marine organisms [6,7]. Yet, its impacts on populations and communities are rarely characterized. Brine discharge effects are associated with increased salinity, accompanied by higher temperatures for thermal processes: brine from SWRO is discharged with about twice the seawater salinity, while brine from MSF has about 1.5 seawater salinity and a temperature higher by ca. 5°C. Environmental effects can be associated also with the

[1] http://www.iwa-network.org/desalination-past-present-future/

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chemicals used in the desalination process that are then discharged at sea. Those may include coagulants in the pretreatment stage (iron or aluminum salts, polymers—RO only); antifoaming agents (MSF only), corrosion inhibitors, biocides (such as chlorine), and neutralizers (sodium sulfite); antiscalants to prevent fouling of the membranes (such as polyphosphates, polyphosphonates, polyacrylic acid, polymaleic acid); cleaning solutions for RO membranes (acidic and alkaline solutions and detergents); pH and hardness adjustors for the product water (limestone). Thermal desalination plants are also subject to corrosion and subsequent discharge of metals (such as copper) with the brine [7].

In contrast to a continuously expanding number of papers published on desalination technologies, a relatively small number of studies have been published quantifying the environmental impacts of discharging brine in situ or in laboratory experiments [7a] (Fig. 12.1). Although the number of publications on environmental impacts is gaining in the last few years, there still exists a large gap between the two perspectives reflecting the high investment in technologies and the lag in funds and regulations for environmental research and impact studies.

The published studies are site specific, demonstrating variability that is also influenced by the desalination process, the size of the plant, the discharge composition, and the sensitivity of the receiving environment.

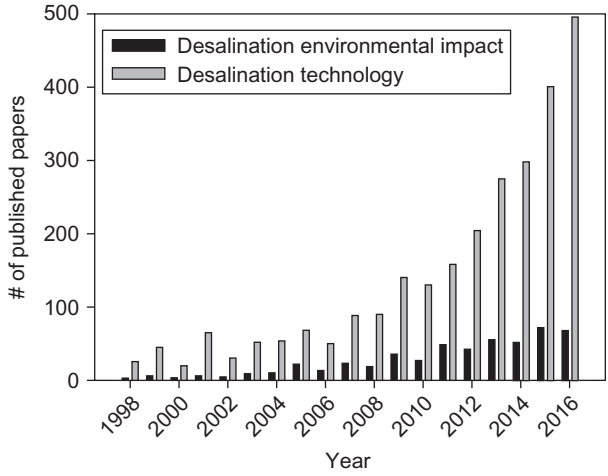

Fig. 12.1 The number of published peer-reviewed scientific papers from 1998 to 2016 on the subjects: Desalination technology; Desalination environmental impact. *Source: Web of Science, 3/5/2017.*

Thus, while brine discharge typically increases salinity (and sometimes temperature) at discharge sites, the areas affected are highly variable. In SE Spain, high salinity (45, compared with the ambient 37–38) was observed up to 2 km from the SWRO outfall in winter, while in summer it was confined to the vicinity of the outfall [8]. In Israel, brine co-discharged with cooling waters of a power plant at the Mediterranean shoreline increased salinity (by up to 1.84) and temperature (up to 7.8°C) with spatial impacts reaching 2 km from the discharge point [9]. In contrast, brine discharged through a marine outfall at 10-m depth increased salinities (45, ambient average 39) of the bottom 1–2 m water layer with a spatial effect of up to1 km from the outfall [10]. In Western Australia, brine discharged through an outfall increased salinity by 1 in bottom layer waters, yet remained within the range of natural variability (ambient salinity of 33 to 37, [11]). More widespread increases in offshore salinity could also occur as reported from Kuwait [12]. The salinity at the discharge area increased from 36–41.5 to 41–43 from 1993 to 2002, while the natural seasonal variation decreased, with no concurrent change in temperature [12]. Following the expansion of the plant, dispersion of higher salinities increased to several kilometers from the outfall. Other chemical characteristics of water quality may be affected by the discharges, yet data are extremely limited. Whether this is valid for all other sites, and at different spatial and temporal scales is currently unknown.

Brine discharges also affect the coastal biota—both benthic and pelagic. Short-term (15 days) mesocosm experiments examining the impacts of salinity increase (by 1 above the natural range) on the seagrasss *Posidonia oceanica* resulted in significant reduction in leaf growth, increased necrosis, enhanced senescence, and an increase in mortality rates [13]. In an in situ salinity manipulation experiment, *P. oceanica* exposed to desalination brine with a salinity of 1 and 2.5 above ambient for a 3-month period showed a decrease in the number of leaves, the maximum leaf length, growth rates, biomass, and plant survival when compared with the control ambient populations [14]. A field survey of a shallow *P. oceanica* meadow exposed to RO brine discharge for more than 6 years revealed low shoot abundance, significant reduction in leaf size, and overload of epiphytes in the area nearest the outfall (salinity of 38.4–39.8) [15]. In contrast, three tropical seagrasses (*Thalassia testudinum*, *Halodule wrightii,* and *Ruppia maritima*) were highly tolerant of hypersaline conditions. The stress indicators (shoot decline, growth rates, and quantum yields of photosynthesis) demonstrated tolerance up to salinities of 55 to 65 [16]. Moreover, total shoot mortality was not affected for any of the three species across the range of salinities examined (35–70 salinity over 30-day

exposures) [16]. Discharges at a site on the southeastern Mediterranean coast of Spain increased coastal salinity and changed the benthic community from a mixed polychaeta, crustacea, and mollusca to one dominated by nematodes [17], while at the same site the amphipod populations decreased in abundance and diversity [18]. Discharges did not show any impacts on benthic communities from the northwest Mediterranean [19], examined for 12 months prior and 12 months following start of operations nor in Antigua [20], following 6 months of exposure to higher salinity and temperature or in Australia (Perth) after 15 months of operations. In the latter, however, benthic communities changed in the whole Cockburn Sound as a result of altered sediment composition, unrelated to the brine discharge [21]. These results emphasize the importance and lack of long-term quantitative studies as well as on the different trophic levels of the marine food web.

Currently, only a few studies investigating the impacts of desalination intakes and discharges on marine microorganisms (heterotrophic bacteria, cyanobacteria and unicellular eukaryotes) have been published [9,22–24]. Marine microorganisms dominate the abundance, diversity, and metabolic activity of the oceans, representing the "unseen majority" of the marine environment [25]. They sustain marine organic productivity (both autotrophic and heterotrophic), comprise a vast and dynamic reservoir of genetic variability, and are a fundamental link within the oceanic biogeochemical cycles of carbon and other nutrients [26,27]. Microbial communities, which are the basis of the marine food web (Fig. 12.2), constitute the primary and direct path of energy and biomass to the higher trophic levels in the ecosystem, and thus can influence the response and vulnerability of the whole ecosystem [28]. The interaction between primary (autotrophic) and heterotrophic

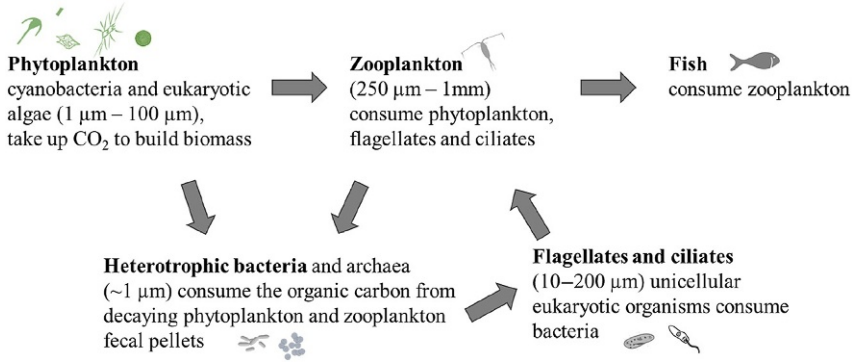

Fig. 12.2 Simplified marine food web and the basic components and functions of the microbial loop.

production within the microbial community is highly variable, and this variability impacts ecosystem function [29]. Moreover, a change in the physical and/or chemical environment due to the combined pressures of climate change and human impacts is often followed by a shift in structure and/or metabolic function change of the planktonic microbial community [30]. This may have potentially deleterious effects on biodiversity, abundance, productivity, and the ecological health of the marine ecosystem.

In this chapter, we will focus on the effects of desalination on the microbial community in seawater. This review complements and expands on Chapter 11. Section 12.2.1 discusses alterations to the microbial communities throughout the seawater desalination process from intake to discharge, while Section 12.2.2 assesses the effects of desalination discharges on coastal microbial communities using data from laboratory and in situ experiments. We conclude (Section 12.3) by addressing gaps in knowledge and with recommendations for plant operations that could mitigate the effects of desalination on the marine microbial community.

12.2 DESALINATION IMPACT ON MICROBIAL COMMUNITIES

Assessment of possible desalination impacts should begin with an environmental impact assessment (EIA) at the planning stages of a desalination plant and continue during construction. Although most of the impacts are assumed to be localized and cease after the construction phase, they could significantly affect populations during the process [7,31]. Seawater quality and microbial communities will most probably be affected by coastal construction that induces sediment resuspension, increases turbidity, and can release nutrients and pollutants to the water column. To the best of our knowledge, no data have been published comparing microbial community structure and function before, during, and postconstruction stages of large-scale desalination plants.

The assessment of possible impacts of desalination on the microbial community can be followed using the parameters and functions of the microbial community summarized in Table 12.1. During plant operations, the first stage affecting microbial populations is the intake of seawater (feed water), which entrains and transports the microbial biota with the flow of seawater into the desalination plant. We know of no published studies that have quantified the loss of entrained biota at either population or regional levels. The common assumption is that the organisms entering the

Table 12.1 Suggested parameters and required methodologies to assess microbial community structure and function

	Parameter/function	Indicator	Methodology	Reference
Autotrophs Phytoplankton	Biomass	Chlorophyll *a*	– Acetone extraction Fluorometric or spectrophotometric estimation – Chlorophyll *a* in situ fluorescence	[32], [33]
	Community composition	Microphytoplankton composition	– Microscopic determination of the microphytoplankton species – Taxonomic discrimination based on pigment combinations and ratios	[34]
		Picophytoplankton composition	Taxonomic discrimination based on the natural fluorescence of photosynthetic pigments, side-scatter and forward-scatter of the cells, enumerated by flow cytometry	[35]
		OTUs assignment	Molecular analysis—16S (cyanobacteria) and 18S (eukaryotic algae) rRNA gene extraction, sequencing, and Operational Taxonomic Units (OTU) assignment	[36]
	Diversity within community	Effective number of species	Calculated from the OTUs count	[37]
	Community composition shift	Diversity shared between communities	UNIFRAC metric for beta diversity measurements based on sequences from molecular analysis	[38]
	Productivity	Primary productivity	^{14}C or ^{13}C incorporation method	[39], [40]

Heterotrophs Bacteria	Biomass	Bacterial cell abundance	Nucleic acid staining, enumerated by flow cytometry	[35]
	Community composition	OTUs assignment	Molecular analysis—16S (cyanobacteria) rRNA gene extraction, sequencing, and Operational Taxonomic Units (OTU) assignment	[36]
	Diversity within community	Effective number of species	Calculated from the OTUs count	[37]
	Community composition shift	Diversity shared between communities	UNIFRAC metric for beta diversity measurements based on sequences from molecular analysis	[38]
	Productivity	Bacterial productivity	^{3}H leucine incorporation method	[41]

desalination plant will perish during the different stages of the desalination process, including when biocides are applied. However, this assumption is not always valid (see Section 12.2.1) and resistant microbial populations may remain in the water during the desalination process.

12.2.1 Entrainment of Microbial Communities and Their Fate Along the Desalination Process

In the desalination literature, microbial populations are mostly addressed in the context of membrane biofouling [42–51]. Several other investigations examined group-specific contributions such as harmful algae blooms (HABs) and their effects from the perspectives of plant operations and product water [52–54]. However, the main impact of entrainment on the marine environment, the quantification of the biomass lost during the desalination process, is usually mentioned only qualitatively. To the best of our knowledge, there are no publications of quantitative data excluding several studies on power plants, mainly concerning fish larvae [55]. Yet, the membrane biofouling literature provides the basis for future research on entrainment effects on the microbial community: loss during the desalination process and the communities, if any, returned to the sea with the brine.

The studies on membrane biofouling usually address the diverse bacterial communities in various compartments of the desalination process: feed and product water (free-living) and biofilm-forming communities in pretreatment filters and compartments and in membranes (usually RO). Following are some results taken from studies performed at operational RO desalination plants. *Alphaproteobacteria* and *Planctomycetaeota* dominated the longest operated SWRO membrane (330 days), while in the less used membrane (10 days) *Betaproteobacteria* predominated [49], hint of succession and temporal changes of the biofilm community. In parallel, the microbial composition of the RO membranes in Southern California was mainly *Alphaproteobacteria* (60%) followed by *Gammaproteobacteria* [50]. Similarly, in Israel, the bacterial community on the RO membrane was dominated by *Alphaproteobacteria* in spring and winter and *Gammaproteobacteria* in the summer, reflecting the feed water free-living communities that included mainly *Alphaproteobacteria* followed by *Gammaproteobacteria* [47]. All studies emphasized the dynamic interaction between the feed water planktonic communities and the biofouling on the membranes. These groups of planktonic heterotrophic bacteria, prevalent in the surface seawater, change their relative abundance seasonally according to the environmental conditions such as temperature, salinity, carbon source, and nutrients levels.

The biofouling on the membranes and the possible effects on the environment are probably also process dependent, in addition to being site and season specific as demonstrated in a bench scale (4-day) laboratory study [51]. The prevalent class in the feed water was the *Alphaproteobacteria*, which was superseded by *Betaproteobacteria* (*Burkholderiales*) in the membrane distillation (MD) filter and *Alphaproteobacteria* in the RO filters. The altered microbial populations for the two different membranes were attributed to the different processes: the community under RO is exposed to high pressure at low (room) temperatures while under MD the temperatures are high (50–80°C) with no hydraulic pressure [51].

Currently, we know of a sole study that addressed the communities discharged with the brine [47]. The general findings demonstrated that free-living communities at the feed waters did not highly differ from other free-living communities along the desalination process. The biofilm-forming communities did differ however and were related to the original seawater communities and therefore were site specific and characteristically seasonally dependent. Importantly, no significant differences were found between bacterial communities from the feed water to those discharged in the brine, showing that SWRO did not promote or stimulate proliferation of nonambient or exotic populations [47].

Free-living bacteria and eukaryotes were quantified in the water along the desalination process in Saudi Arabia, but not in the brine [43,44]. The resulting product water was not sterile and contained both bacteria (i.e., Firmicutes) and eukaryotes (i.e., Fungi). The source of these organisms in the product water was suggested to be bacteria (or only DNA) transferred at the time of installation, or/and intrusion through the membrane during normal plant operation.

12.2.2 Impact of Seawater Desalination Discharges on the Coastal Microbial Communities: Results from Laboratory, Mesocosm, and In Situ Studies

12.2.2.1 Salinity Effects: Mesocosm Study

In addition to impacts from brine discharges and the increasing salinities, the receiving environments of thermal desalination plants are often exposed to higher temperatures that may also affect the microbial populations. Halophilic and thermophilic species may thrive while other species, less tolerant, may dwindle and disappear. The relative contribution of the different species to the microbial communities is expected to change, and in turn, influence the higher trophic levels.

The main impact driver of the desalination effluent is the elevated salinity of the brine. Hypersalinity effects on the structure and function of natural assemblages of planktonic microbial populations were studied in large-volume (1 m^3) mesocosm experiments in the Eastern Mediterranean Sea (EMS) [56]. Excess salinities of 5% and 15% above ambient, simulating the natural salinity increases near desalination plant outfalls were examined. Rapid (within 2 h upon treatment application) community physiological responses were detected at the 15% salinity treatment: primary productivity decreased (by 25%–60%) while heterotrophic bacterial productivity increased (by 36%–180%; Table 12.2) [56]. Similar physiological responses may occur in situ when the residence time of plankton at the discharge site is relatively short. Longer-scale responses (11–12 days) occurred mostly in the composition and structure of bacterial and eukaryotic communities accompanied by functional changes of enhanced primary and heterotrophic bacterial productivity (by 100%–150% and by 0%–200%, respectively; Table 12.3). The response was seasonally dependent, with a more distinct difference in the summer communities. The relative abundance of large cyanobacteria (*Oscillatoriophycideae*) and the heterotrophic *Alphaproteobacteria* (*Rhodobacterales*) increased. Concurrently, decrease was measured in the relative abundances of the small cyanobacteria (*Prochlorococcus*), heterotrophic *Alphaproteobacteria* (*Pelagibacteraceae*), and *Gammaproteobacteria* (*Altermondales*). The experiment simulated the in situ continuous brine discharge to the coastal areas with low turbulence that may retain the phytoplankton and bacterial communities under salinity stress. This may in turn lead to altered community composition caused by selection for salinity-tolerant microorganisms that may then reduce subsequent community diversity.

12.2.2.2 Chemical Discharges Along With Salinity Effects: Mesocosm Study

Microbial communities may be affected also by the chemicals discharged with the brine. These chemicals could have both negative (toxic or inhibiting) and positive (increasing bioavailability) impacts on the microbial populations. Coagulants and antiscalants are typically added during the desalination process to aid in the precipitation of large particles to facilitate their removal by prefiltration (coagulants) and to prevent membrane blockage by inorganic scaling (antiscalants). Iron hydroxides serve as common coagulants while antiscalants are characteristically comprised from different compounds including phosphonates. As in other topics covered in this review, only limited published data exist examining the effects of chemical additions to desalination discharges on the microbial populations.

Table 12.2 Immediate (within 2 h) biomass, productivity, and diversity changes (in percent from control treatments) in microbial communities during mesocosm experiments (compiled from Refs. [24,56])

		Treatment			
			Fe	Phosphonate (Pn)	
Parameter		Salinity (Sal)	[% changes from control treatment]		Fe + Pn + Sal
Phytoplankton	Biomass	30 ↓	40–70 ↑	10–40 ↑	20–30 ↑
	Primary productivity (per chl *a*)	25–60 ↓	30–45 ↓	10–25 ↓	80–125 ↑
Heterotrophic bacteria	Cell abundance	No change	45–50 ↓	0–25 ↓	35–45 ↓
	Bacterial productivity (per cell)	40–180 ↑	125–185 ↑	0–25 ↑	30–85 ↑
Bacteria (autotrophs and heterotrophs)	Diversity	No change	45 ↓	No change	50 ↓
Eukaryotic algae	Diversity	No change	80 ↓	No change	60 ↓

Table 12.3 Biomass, productivity and diversity changes (calculated as a percent from the control values) after 10 days of incubation of microbial communities during mesocosm experiments (compiled from Refs. [24, 56])

		Treatment			
			Fe	Phosphonate (Pn)	
Parameter		Salinity (Sal)	[% changes from control treatment]		Fe + Pn + Sal
Phytoplankton	Biomass	100–400 ↑	0–50 ↓	No change	No change
	Primary productivity (per chl *a*)	100–150 ↑	30–50 ↓	No change	No change
Heterotrophic bacteria	Cell abundance	No change	No change	0–25 ↓	No change
	Bacterial productivity (per cell)	0–200 ↑	0–100 ↑	0–300 ↑	50–200 ↑
Bacteria (autotrophs and heterotrophs)	Diversity	85 ↓	20 ↑	75 ↓	40 ↑
Eukaryotic algae	Diversity	70 ↓	70 ↓	250 ↑	75 ↑

Simulation of such discharges was performed by examining the impacts of iron hydroxide and polyphosphonate additions on coastal microbial populations of the EMS under ambient and elevated salinities [24]. Immediately upon addition, the coagulant (iron hydroxide) changed the composition of the bacterial communities, increased the heterotrophic productivity (by 150%), and reduced primary productivity (by 40%) (Table 12.2). At the same timescale, adding only the antiscalant relieved the phosphorus stress of the community, while the combination of coagulant with antiscalant and elevated salinity (15% above ambient) resulted in synergistic effects reflected by the increased productivity of both primary and bacterial producers (by 100% and 50%, respectively) [24]. These effects may be found in situ during high turbulence and short residence time of the microbial communities within the discharge-affected areas.

Longer-term effect (10 days) revealed significant compositional shift only in the treatments in which coagulants, antiscalants, and high salinity were combined. This treatment reduced both function (photosynthetic rates) and biomass of primary producers by 50%, while the heterotroph bacterial activity and communities increased by 50% (Table 12.3) [24]. These effects may be found in situ during low turbulence and long residence times of the microbial communities within the discharge-affected areas.

12.2.2.3 In Situ Studies

While simulated experiments can isolate the specific factors impacting the microbial populations, in situ studies are necessary to assess the response of communities to the combined effects of these parameters in the natural setting. Changes in microbial communities were investigated from two different brine-discharge sites along the EMS coastline: (1) a submerged marine outfall equipped with diffusers, installed capacity of 90 $Mm^3\,year^{-1}$ and (2) open outfall at the shoreline that was mixed with power plant cooling waters and well amelioration brine [24] with an installed capacity of 127 $Mm^3\,year^{-1}$. Polyphosphonate-based coagulants were discharged by both plants, while iron-hydroxide coagulants were discharged at the open-discharge plant [57,58].

Seasonality governed the bacterial communities' structure at the nonaffected, ambient salinity stations [24]. Overall, the community shifts were weaker at the submerged outfall compared to an open outfall site, and occurred for the prokaryotic microorganisms (autotrophic and heterotrophic bacteria) at both sites, parallel to diversity changes (Table 12.4). The highest contribution to the shifts in community composition was attributed mostly to the interplay in the

Table 12.4 Biomass, productivity, and diversity changes (calculated as percent changes from the ambient station values) in microbial communities at the submerged outfall and open outfall sites of SWRO desalination brine discharges (compiled from Ref. [24, 56])

		Submerged outfall	Open outfall
		[% changes from control stations]	
Salinity elevation above ambient		10–38	4–5
Phytoplankton	Biomass	30–40 ↑ Summer 20–30 ↓ Winter	50–70 ↓
	Primary productivity (per chl *a*)	30 ↓ Summer	50 ↑ Summer 30 ↓ Winter
Heterotrophic bacteria	Cell abundance	No change	30 ↓ Winter
	Bacterial productivity (per cell)	No change	200 ↑ Summer 30 ↓ Winter
Bacteria (autotrophs and heterotrophs)	Diversity	50 ↓ Summer 27 ↓ Spring 21 ↓ Fall 60 ↑ Winter	5–40 ↓
Eukaryotic algae	Diversity	70 ↑ Summer	70 ↓ Summer 70 ↑ Winter

relative abundance of proteobacteria, cyanobacteria, and diatoms. Physiological changes accompanied the compositional ones. The community physiological responses to elevated salinity (and codischarged chemicals) was seasonal and site dependent (Table 12.4). At the submerged outfall site, only autotrophs were affected, mostly in summer, when reduced productivity (by 30%) was measured. At the open outfall site, the physiological changes were more prominent and included both phytoplankton and heterotrophic bacteria. The biomass was reduced, while productivities fluctuated between seasons. Although at the open outfall site the salinity elevation reached only 5% above the ambient, SWRO discharge included iron hydroxides (not present at the submerged outfall). Thus, the responses of the microbial community were similar to the iron-hydroxide treatment in the mesocosm approach [24].

An earlier preliminary study at the open outfall site was performed when backwash from the sand filters containing iron hydroxide was discharged in pulses with the continuous brine discharge at the shoreline [9]. This pulsed discharge increased turbidity, caused water discoloration, enhanced the concentrations of suspended particulate matter near the discharge point, and reduced phytoplankton densities and their productivity per chlorophyll *a* [9].

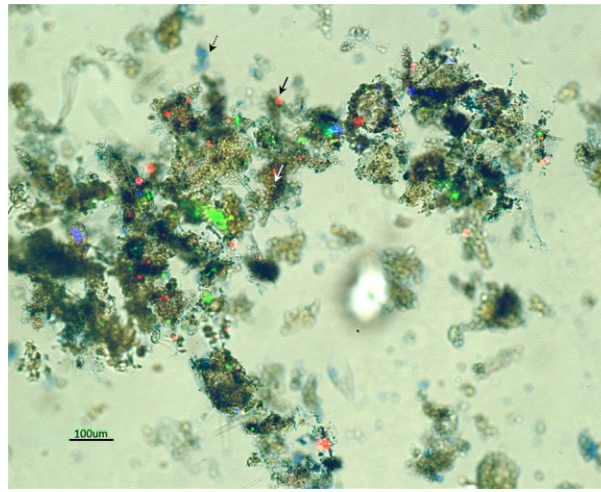

Fig. 12.3 Microscopic image of aggregates collected at the open outfall site on August 2012. Black arrow: phytoplankton, white arrow: bacteria, dashed black arrow: transparent exopolymer particles (TEP).

Mitigation measures stopped the pulsed discharge of the backwash by mixing it with the brine prior to its continuous discharge. This was expected to minimize the impact. Still, changes in community composition and function were detected in the vicinity of the discharge location [24], while aggregates (from the backwash discharge) containing bacteria and algae were present in the surface water (Fig. 12.3).

At other geographical sites, only minor changes were observed in the abundance of in situ microbial populations sampled at different distances from the submerged outfall site. Small variations in species abundance were attributed to a dilution effect, rather than a direct impact of the brine discharged, at the marine outfall of the King Abdullah University of Science and Technology (KAUST) SWRO Plant (Saudi Arabia, Red Sea) [23]. However, the plant is small (installed capacity of 15 $Mm^3 year^{-1}$) compared to the large capacity of the plants along the Mediterranean coastline discussed earlier. An early study from the coastal waters near Al-Jubail desalination plant (Saudi Arabia, Gulf) [22] also examined the plankton community. Higher primary production was evaluated in the coastal area that receives the water from the outfall bay, while the phytoplankton species composition did not change significantly. Concurrently, decreased abundances of diatoms, dinoflagellates, and cyanobacteria were measured at the outfall bay in comparison to those quantified from the open sea and the intake stations.

A summary of the measured effects of desalination discharges on microbial communities is compiled in Table 12.5. The composition of aquatic

Table 12.5 Summary of the effects of desalination brine and codischarged chemicals on the microbial communities based on in situ studies and on mesocosm and laboratory experiments

In situ studies

Area	Desalination technology	Stressor	Parameters	Observed effect (and stressor, when attributed)	Reference
Arabian Gulf	MSF	Salinity (S), Temperature (T)	Chl *a*, phytoplankton, zooplankton	*Increase:* PP *No change*: phytoplankton species composition *Decrease*: abundance of diatoms, dinoflagellates and cyanobacteria	[22]
Eastern Mediterranean Sea	RO with power plant cooling waters	Salinity (S), Temperature (T), Fe coagulant	Chl *a*, picoplankton number, PP, BP	*Inconclusive changes:* PP and BP *Decrease*: chl *a* and cell numbers (T and S) and phytoplankton growth efficiency (Fe)	[9]
Red Sea	RO	Salinity (S),	picoplankton number	*Reduced numbers* (Dilution of effluent)	[23]
Eastern Mediterranean Sea	RO with power plant cooling waters	Salinity (S), Temperature (T), Fe coagulant, Phosphonate (P) antiscalant	Chl *a*, picoplankton and bacteria numbers, PP, BP, 16S and 18S rDNA gene sequencing	*Increase*: *Gammaproteobacteria*, BP (Fe+P) and cell specific BP (Fe+P) *Decrease*: *Alphaproteobacteria* and cyanobacteria, chl *a* (Fe) and PP, diversity of bacteria and eukaryotes	[24]

Mesocosm experiments

Area	Experiment time	Stressor	Parameters	Observed effect (and stressor, when attributed)	Reference
Eastern Mediterranean Sea	Mesocosm, 10 d	Salinity (S)	Chl *a*, picoplankton and bacteria numbers, PP, BP, 16S and 18S rDNA gene sequencing	*Increase*: chl *a* (S), PP (S) *Inconclusive changes*: BP *Decrease*: biodiversity (S, seasonal dependent)	[56]
Eastern Mediterranean Sea	Mesocosm, 10 d	Salinity (S), Fe coagulant, Phosphonate (P) antiscalant	Chl *a*, picoplankton and bacteria numbers, PP, BP, 16S and 18S rDNA gene sequencing	*Increase*: PP (combined S, Fe, P), BP (combined S, Fe, P), eukaryotic diversity (P, combined S, Fe, P) and bacterial diversity (combined S, Fe, P) *Decrease*: Chl *a* (Fe), PP (Fe), eukaryotic diversity (Fe) and bacterial diversity (P)	[24]

Laboratory experiments

Area	Experiment type and time	Stressor	Parameters	Observed effect (and stressor, when attributed)	Reference
Pacific Ocean	Laboratory bioassay, 72 h	Salinity	EC_{50} of phytoplankton growth inhibition	Salinity range of 42–62 ppt	[64a]
Pacific Ocean (Australia)	Laboratory diatoms cultures, 14 d+14 d	Salinity	^{29}Si CP-MAS NMR	Changes in silica structure in one species (S)	[59]
Pacific Ocean (Australia)	Laboratory bioassay, 72 h	Brine (S and P)	NOEC of phytoplankton growth inhibition	At 11% brine in seawater (S and P)	[64b]

EC_{50}—Concentrations that caused an effect on 50% of the population, NOEC—No observed effect concentrations.

bacterial communities varies as a result of both natural (site specific and seasonal) variability and due to desalination impact. Compositional shifts in microbial community can reflect the chronic impacts of the outfall site. Such shifts may compensate for the metabolic stress encountered by some species at the site due to the salinity elevation or change in chemical composition of the local coastal water [60]. Yet, the altered microbial communities may also reduce the ecosystem's resilience to additional stressors such as climate change [61–64].

12.3 GAPS IN KNOWLEDGE AND OUTLOOK

Here we reviewed the potential impacts of seawater desalination on the marine planktonic microbial communities and described the scarce quantitative data available on the different components of the community's composition and functions. Accordingly, we believe the following gaps in knowledge should be addressed in future studies:

- Lack of baseline information on the ambient microbial communities (composition, abundance, metabolic, and growth rates) and their functions within the food web.
- No quantification of losses due to entrainment (including zooplankton, not addressed here).
- Lack of baseline information on the microbial communities discharged back to the coastal environment with the brine.
- Lack of short- and long-term in situ data at outfall areas.
- Lack of laboratory and mesocosm studies at relevant temporal scales.

These gaps may be filled by

- Incorporating the study of microbial communities to environmental impacts studies prior to plant construction and during long-term monitoring studies.
- Performing dedicated laboratory and mesocosm studies to assign a cause-response relationship among the different desalination stressors and their combined effects.
- Employing interdisciplinary in situ surveys and installing in situ automatic measuring devices to monitor changes in environmental parameters along the brine plumes (e.g., conductivity, temperature, density profilers (CTDs)).
    - Deploying new in situ instruments for continuous monitoring of biological parameters such as flow cytometry buoys and other imaging equipment for microbial and zooplankton populations.

- Utilizing newly available techniques such as hydrodynamic (e.g., Ref. [65]) and ecological (e.g., Ref. [66]) modeling.
- Determining eco-region specific ecological indicators, to be continuously monitored [67], including several indices for microbial species and communities.

In the meantime, based on the available knowledge and technology and on precautionary principles, several mitigation measures may be applied to reduce the possible effects of desalination on the marine microbial communities. Impacts can be reduced during the construction of the plants by more environmental sustainable construction measures. For example, pipeline installation by pipe jacking as far as possible from shore with controlled dredging beyond. Entrainment can be reduced by locating the intakes away from biologically productive areas, such as in deeper waters farther offshore, or by using underground beach wells, although the latter may be difficult to implement for large-scale desalination plants [6,68,69]. Brine management should strive to reduce brine discharge, improve its quality [70,71], and optimize its dilution. For direct discharge, the marine outfall should be equipped with a diffuser system, away from the shore so that exposure of the microbial populations to concentrated discharges is reduced. For open-channel discharges at the shoreline, dilution can be achieved by co-disposal, for example, with cooling waters from power plants. Alternative pretreatments for the desalination feed water, such as biofiltration and bioflocculation can be utilized instead of chemicals such iron hydroxide coagulants [72]. Other more environmentally friendly chemicals could replace more traditional antiscalants and coagulants. Alternatively, instead of discharging directly to the sea, the brine may be reused or a zero-liquid discharge policy promoted [31,73].

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