

Flow cytometric assessment of microbial abundance in the near-field area of seawater reverse osmosis concentrate discharge



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HIGHLIGHTS

- Microbial abundance changed as a function of distance away from the discharge.
- Changes in relative abundance might be a result of normal dilution.
- Higher conductivity showed marginal variances, with cyanobacteria least affected.
- Differences in diversity could occur, which was not detected with the FCM analysis.

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ABSTRACT

The discharge of concentrate and other process waters from seawater reverse osmosis (SWRO) plant operations into the marine environment may adversely affect water quality in the near-field area surrounding the outfall. The main concerns are the increase in salt concentration in receiving waters, which results in a density increase and potential water stratification near the outfall, and possible increases in turbidity, e.g., due to the discharge of filter backwash waters. Changes in ambient water quality may affect microbial abundance in the area, for example by hindering the photosynthesis process or disrupting biogenesis. It is widely accepted that marine biodiversity is lower in more extreme conditions, such as high salinity environments. As aquatic microbial communities respond very rapidly to changes in their environment, they can be used as indicators for monitoring ambient water quality. The objective of this study was to assess possible changes in microbial abundance as a result of concentrate discharge into the near-field area (<25 m) surrounding the outfall of the King Abdullah University of Science and Technology (KAUST) SWRO plant. Flow cytometric (FCM) analysis was conducted in order to rapidly determine microbial abundance on a single-cell level in 107 samples, taken by diving, from the discharge area, the intake area and two control sites. FCM analysis combined the measurement of distinct scatter of cells and particles, autofluorescence of cyanobacteria and algae, and fluorescence after staining of nucleic acids with SYBR® Green for a total bacterial count. The results indicate that changes in microbial abundance in the near-field area of the KAUST SWRO outfall are minor and appear to be the result of a dilution effect rather than a direct impact of the concentrate discharge.

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1. Introduction

Seawater reverse osmosis (SWRO) desalination is expanding globally as a means to provide potable water [1]. While the societal benefits of desalination are well recognized, concerns are often raised over potential adverse environmental impacts of SWRO plants, especially with regard to the possible adverse effects of concentrate discharge (in this paper 'concentrate' refers to the brine of SWRO plants as waste stream and the process effluents discharged with it into a marine environment). It is widely suggested that the concentrate discharge may result in negative impacts on the marine environment, but what is stated

about the issue is in many cases not based on actual monitoring in the discharge sites of SWRO plants [2]. Most important in this respect are the possible changes in species composition, species diversity and population density with the most acute effects in the vicinity of the discharge outlet (near-field) [3]. Salinity is generally considered to be a dominant environmental factor regulating aquatic community structure, but it is not well understood whether this is primarily due to the direct physiological effect of salinity stress [4]. Existing literature has postulated that microbial research in saline environments could contribute to the study of the broad scale distribution of microbial communities and help to discern the potential factors underlying microbial diversity patterns in extreme environments [5]. Thus, it is expected that microbial studies along salinity gradients could shed additional light on this topic. The majority of current studies investigated the

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influence of salinity on the distribution of microbial diversity on temporally dynamic saline systems [6], whereas virtually nothing has been reported on microbial abundance in the near-field areas of hyper saline concentrate discharges from desalination.

The unicellular cyanobacteria (autofluorescent phytoplankton) of which *Prochlorococcus* sp. and *Synechococcus* sp. are the most abundant photosynthetic marine microorganisms are very important components of planktonic food webs. They play an imperative role in the ocean's carbon cycle and contribute significantly to marine primary production [7]. Microbial cell concentrations are typically about 10^5 cells/mL in the ocean surface layer (0–300 m) [8] and may respond very rapidly to changes in their environment [9]. Although there is a growing

understanding of the biogeochemical importance of microbial communities in most marine and coastal environments, the factors that shape their distribution are not properly understood. Nevertheless, in these environments, factors such as resource availability, salinity, temperature and light, latitude, depth, vertical mixing, bacterivory (grazing by protists that can influence bacterial community structure), and viral lysis are believed to be key ecological determinants that shape the biogeography of marine microorganisms [10]. Changes in microbial communities may reflect environmental changes within a few hours or over much longer periods and can be measured in response to the introduction of environmental pollutants, such as a sudden increase in salinity [11].

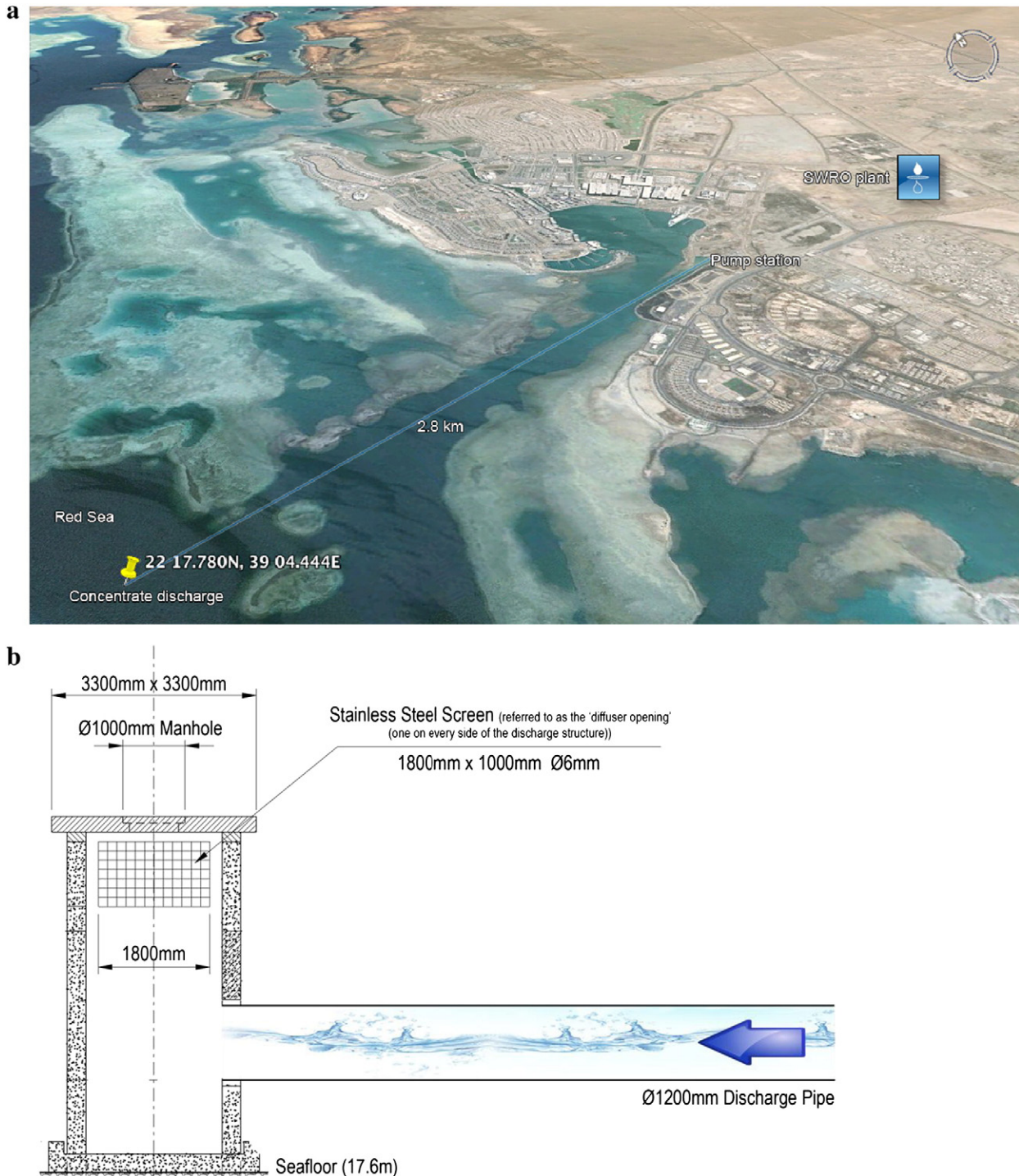


Fig. 1. a: KAUST SWRO offshore discharge locality (source: Google Earth). b: Schematic of the discharge structure.

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