Desalination 286 (2012) 120–130

Contents lists available at SciVerse ScienceDirect

Desalination

journal homepage: www.elsevier.com/locate/desal

Rapid sand filtration pretreatment for SWRO: Microbial maturation dynamics and filtration efficiency of organic matter

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ARTICLE INFO

Article history:
Received 4 July 2011
Received in revised form 3 November 2011
Accepted 4 November 2011
Available online 7 December 2011

Keywords:
Rapid sand filtration
SWRO pretreatment
Biofilm
Biodegradation
Maturation period
Filtration efficiency

ABSTRACT

Rapid sand filtration (RSF) is used today as an effective pretreatment procedure to enhance water quality prior to reverse osmosis (RO) membranes in desalination plants. RSF in newly operated desalination facilities requires a maturation period of about three months before the feedwater may be filtered efficiently. To date the desalination industry RSF has regarded RSF mainly as a physical barrier effectively retaining particles larger than 0.35 mm.

In this study we assessed the potential of the RSF as a biological filter by following the dynamics of bacterial colonization and metabolic activity within the filter bed and determining filtration efficiency in respect to particulate and dissolved organic carbon, chlorophyll *a* and transparent exopolymeric particles (TEP). Bacterial abundance and diversity were shown by DGGE and SEM analysis to increase gradually over a three month sampling period. Bacterial metabolic activity within the filter bed interstitial water increased erratically with time. With the outgrowth of a microbial population and biofilm development on the filter bed medium, significant removal of organic carbon from the source water was always observed. Our results indicate that current RSFs function as biofilters with moderate efficiency. Innovative design is needed to maximize the biofiltration potential of these filters.

1. Introduction

Limitations of global freshwater supplies have stimulated the application of desalination technology with desalinized water coming online worldwide at a rate of 40 to 50 million $m^3\ d^{-1}$ [1]. Currently, about 50% of global desalination is based on filtration through reverse osmosis (RO) membranes requiring effective pretreatment procedures upstream to reduce fouling, maintain performance and extend membrane lifetime and to ensure the manufacturers requirements for membrane recovery yield [1,2].

Due to its relative simplicity, low energy consumption, and relatively low operational costs, rapid sand filtration (RSF), based on granular gravity filtration, is the most common pretreatment presently used in large-scale SWRO facilities. RSF with flow rates ranging between 5 and 30 $m^3\ h^{-1}$ is a robust technology to physically remove suspended solids larger than 0.35 mm from water by size exclusion and adsorption. Flocculation and adsorption prior to the RSF are generally used to enhance the removal of particulate aggregates formed by coagulation procedures, while backwashing is the common procedure to clean and reset the RSF performance.

Slow sand filtration (SSF), with flow rates ranging between 0.1 and 0.2 $m^3\ h^{-1}$, has been a standard biofiltration treatment for decades in the wastewater industry. In these systems, biofiltration is accomplished by a diverse microbial community that colonizes and forms biofilm on the particle surfaces within the filter bed medium and acts to decompose various types of organic material [3–5]. The initial degradation steps are accomplished by extracellular enzymatic hydrolysis of macromolecules to smaller substrates, which can then be transported into the biofilm [6]. Further degradation takes place by a wide range of specific enzymes proliferated by a diverse microbial biofilm community and is completed by oxidation of organic carbon to CO_2 with the concurrent utilization of electron acceptors such as oxygen or sulfate [7].

Presently, little is known about the biological functioning of RSF systems. Due to the rapid flow of water through these filters (up to ~300 fold in comparison with SSF) it has been tacitly assumed that the biological impacts on water passing through RSF are minimal. The water quality at various pretreatment stages is usually followed by measuring parameters such as silt density index (SDI), available organic carbon (AOC), biodegradable dissolved organic carbon (BDOC) and turbidity. However, recent work [8,9] has pointed out the need for monitoring other water quality characteristics such as Chlorophyll *a* (Chl *a*), transparent exopolymer particles (TEP), particulate and dissolved organic carbon (POC and DOC respectively)

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0011-9164/$ – see front matter
doi:10.1016/j.desal.2011.11.010

that can affect the RO biofouling [10,11]. Chlorophyll *a* is a standard method to evaluate algal concentrations while TEP are microscopic (0.4–300 μm), organic gelatinous particles consisting mainly of acid polysaccharides, detected by staining with Alcian Blue [12], and are important components of the natural organic matter (NOM) pool. Current findings within the water treatment and desalination industries indicate a significant role for TEP in fouling RO membranes [9–11,13].

In this study we evaluated the potential of a RSF as a biofilter at the newly operational Hadera SWRO facility, Israel. We followed the spatial and temporal dynamics of bacterial colonization using DGGE and SEM visualization and heterotrophic bacterial activity within the filter bed media during the first three months of operation to assess the development of the microbial community during maturation of the RSF. The filtration efficiency of the RSF with respect to Chl *a*, TEP and dissolved and particulate organic carbon (DOC and POC, respectively) was measured at several times during the maturation period to determine the extent to which the RSF was functioning as a biofilter.

2. Materials and methods

2.1. Sampling strategies

Water and filter bed media samples were collected from a newly constructed, dual media RSF during the first three months of operation (11 sampling dates) from October 2009 to January 2010 comprising the "maturation period", at the Hadera SWRO desalination facility (Israel). The sampling was divided into two stages, 1) the first 4 weeks (0 to 27 days) when a single, 100 cm deep, fine layer of filter bed medium (grain size 0.5–1 mm ø) was in place, and 2) from 42 to 85 days, when two substrate layers were present; a crude substrate (grain size 1–3 mm ø) 100 cm thick overlying a fine layer, (100 cm). (*Note: this two stage process is a standard industry procedure*). Throughout the entire maturation period the RSF was subjected to frequent backwashing; for consistency, sampling was always performed ~15 h after backwashing.

The sampling locations were: 1. Plant intake (feedwater reference), 2. Pre-RSF. Water after treatment with coagulant and immediately overlying the RSF, 3–6. Four depths within the single-medium fine substrate filter bed (A, B, C, D) during the first stage, and four depths within the dual media filter bed (A*,B*,C*–D*) during the second stage, 7. RSF-effluent (filtrate). Sampling dates and locations are given in Table 1 and Fig. 1.

2.2. Water and particulate sampling within the filter bed

We used a specially constructed sampler/corer [14] to obtain samples of interstitial water and particulate media at different depths within the filter bed Particulate samples were stored in 15 ml polycarbonate tubes (Falcon) at 4 °C for denaturing gradient gel electrophoresis (DGGE) and scanning electron microscopy (SEM) analyses. Interstitial water (3 L) was pumped directly from each sampling depth into clean flasks and analyzed within several hours at the laboratory.

2.3. Dissolved Oxygen (DO) measurements within the filter bed

To measure dissolved oxygen (DO) concentrations at various depths in the filter media, we used a custom designed corer that contained a pre-calibrated combined DO optode and temperature sensor connected to a Microx TX3 oxygen meter (*PreSense Inc. OXY1*) and portable PC [14].

Table 1
Detailed description of the sampling depths within the RSF during the two operational stages, 1. single (fine grained) medium layer, and 2. two layer of media composite (crude and fine-grained).

Stage	Media depth (cm)	Media type	Key	Description
First (single-medium)	~100	Fine grains	A	Media near-surface
			B	Upper-mid filter bed
			C	Lower-mid filter bed
			D	Bottom of the filter bed
Second (dual media)	~200	Crude grains	A*	Upper media near-surface
			B*	Bottom of upper-media layer
		Fine grains	C*	Lower media near-surface
			D*	Bottom of the filter bed

2.4. Nucleic-acid extraction and PCR amplification

Filter bed media grain samples were rinsed with sterile sea water (10 ml) to remove planktonic bacteria. The grains were re-suspended with 1 ml lysis buffer (40 mM EDTA, 50 mM Tris pH = 8.3 and 0.75 M Sucrose) in 2 ml cryotubes and stored at −80 °C until extraction. Nucleic acids were extracted from the media using a phenol–chloroform extraction method modified according to Massana et al. [15] and Brinkof et al. [16]. The extracted DNA was amplified by polymerase chain reaction (PCR) using *GM5F-GC-Clamp* and *907R* [17]. Amplification conditions for the PCR included an initial denaturation step of 95 °C for 4 min, followed by 34 cycles of 94 °C for 30 s, 60 °C for 30 s, 72 °C for 30 s and a final extension step of 72 °C for 10 min.

2.5. Denaturing gradient gel electrophoresis (DGGE) and analysis

DGGE was performed with a 20 slot Hoefer TM SE 600 Standard dual cooled gel electrophoresis unit (Hoefer Scientific Instruments, San Francisco, CA, USA) and gel gradient (5 ml min^{-1}) using a peristaltic pump (Cole-Parmer Instrument Co.). Gels (18 × 16 cm), containing 6% (w/v) polyacrylamide (37.5:1 acrylamide/bis-acrylamide) and 50X TAE buffer (Tris/acetic acid/EDTA, pH 8.0), were 0.75 mm thick. A linear gradient from 20% to 60% denaturant was used for all analyses [18]. (100% denaturant contained 7 M urea and 40% formamide). Forty microliters of PCR product was loaded into the gel which was run at 65 °C at 100 V for 16 h. After electrophoresis the gels were stained for 50 min with a mix of 1× TAE buffer and Gel Star (Invitrogen Carlsbad, USA) and photographed using a Kodak KDS digital camera (Kodak Co., New Haven, CT, USA).

2.6. Scanning electron microscopy (SEM) and image processing

Filter-bed media samples (~0.5 ml of grains in an Eppendorf tube) were immediately fixed using 0.7 ml of Karnovsky solution and kept at 4 °C until SEM preparation. Samples were prepared for SEM imaging according to Gamliel [23]. When dry, samples were carbon coated for 60 s using a Denton Desk Vacuum IV, (LLC Inc.). From each sample, 3 to 5 grains were examined with a JEOL 840 scanning electron microscope at 4000× magnification. Counts of bacterial colonies were made at 5 random sites on single grains and averaged for 1 mm^2 of grain surface. When the abundance of colonies became too dense to enable discrete counting, the surface area (mm^2) covered by random colonies was evaluated by measuring the diameter (μm) of each colony.

2.7. Bacterial production (BP) as bacterial activity (BA)

BP was determined from water samples using the ^{3}H-leucine incorporation method [19,20] as modified by Smith and Azam [21]. All samples were run in triplicate with zero time controls. Leucine