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Microbial community in seawater reverse osmosis and rapid diagnosis of membrane biofouling

Jinwook Lee, In S. Kim *

Center for Seawater Desalination Plant, Gwangju Institute of Science and Technology (GIST), 261 Cheomdan-gwagiro, Buk-gu, Gwangju 500-712, Republic of Korea

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ABSTRACT

Due to the acceleration of global warming and the stress that population growth has placed on the global water supply, seawater reverse osmosis (SWRO) desalination is arising as a promising technology to overcome the stress placed on current water resources. However, the biofouling of RO membranes is a common problem, as it causes flux decline, demands frequent cleanings, and consumes high energy, resulting in a shortened lifespan of the system. In an attempt to address these issues, detailed knowledge of the microbial bacteria present, which have a strong correlation between biofilm community structure and operational problems, is ultimately expected to lead to greater control of biofouling. Furthermore, a more rapid diagnosis of biofilm bacteria in SWRO processes is required for faster process feedback. In this study, previous approaches that have been proposed for understanding, diagnosing, and predicting biofouling are reviewed. Finally, the future outlook towards controlling biofouling in SWRO is discussed.

1. Introduction

As the acceleration of global warming induces climate changes, desertification, and drought, both current and future water shortages are recognized as being a significant problem throughout the world. Excaberating this problem is increasing populations and unbalanced distribution of water resources [1]. Thus, as concerns over water availability and demand increase, seawater desalination is garnering more attention as a solution for resolving projected water shortages.

Desalination is rapidly emerging as a promising technology for efficienlty producing freshwater from seawater (high salinity) or brakish water (moderate salinity). Desalination markets have become increasingly popular and reverse osmosis makes up about 72% of total desalination capacity in Europe [2]. Recently, seawater reverse osmosis (SWRO) processes are evloving since they have the potential to enable the economically feasible operation. To this end, a number of unit systems comprise the system used in SWRO plants, including intake, pretreatment, reverse osmosis (RO), and post-treatment systems. Large-scale, low-energy requirements, and low fouling are the major technical themes that should be achieved in SWRO implementations [3].

Among various fouling types, biofouling of the membrane system via biofilm formation from bacteria can cause flux decline, increase the frequency of membrane cleaning, incur a high-energy demand, and reduce the membrane lifetime [4].

For these reasons, estimation of the degree of biofouling is an important task in RO plant operation and management. Diverse bacterial communities and marine environments, which include viable, biofilm-forming cells, and nutrients for growth and proliferation, can severely affect both the pretreatment step in the RO membrane process for desalination as well as biofilm formation on the RO membrane. In addition, there is a high demand to more fully understand the microbial community comprising the biofilm on RO membranes in order to obtain information to prevent biofouling.

Generally it is accepted that biofouling problems from bacteria originate from seawater intake, so a detailed knowledge of the microbial community, which has a strong correlation between the community structure and operational problems, is necessary. The accurate control of biofouling in RO membranes can significantly reduce the overall costs incurred during plant operation. Therefore, understanding of bacterial community structure and changes in bacterial composition during SWRO are required for biofouling diagnoses and control.

2. Membrane biofouling

In RO membrane processes, feed water diffuses under the high pressure applied across a semipermeable membrane that preferentially rejects salts, as well as other organic and biological matter such as bacteria, viruses, and similar microorganisms. In spite of the pretreatment of feed seawater and crossflow in RO systems, however, feed substances still enter the RO module. These substances are then transported to and accumulate on the membrane surface, causing fouling. Fouling can be classified into particulate (scaling), chemical, and organic fouling, and biofouling, depending on their component

* Corresponding author. Tel.: +82 62 715 3382; fax: +82 62 715 2584.
E-mail address: iskim@gist.ac.kr (I.S. Kim).

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characteristics. Specifically, biofouling occurs due to the delivery of live biofilm-forming bacteria and organics, nutrients for bacterial growth and proliferation, to the membrane. Once the bacteria are attached, they grow, multiply, and contribute to biofilm formation on the RO membrane surface. As a result, severe biofilm formation decreases membrane performance, which is referred to as membrane biofouling.

Biofouling, as determined by established parameters and operational problems of RO membrane installations, has correlations with biomass accumulation. From autopsies of 45 RO membranes from 16 (pilot) plants, which were varied based on type of source water, pretreatment, temperature, and dosage of chemicals, biomass concentrations were previously investigated [5]. The autopsy results varied from 20 to 45,000 pg ATP/cm^2, from 1×10^7 to 1×109 cells/cm^2, from 1 to 250 mg/m^2 of iron, and from 0.001 to 4 mg/m^2 of manganese [5].

In the above case, the biomass was distributed unevenly over the individual membrane layers of all membranes. Most of the biomass measured (ATP, TDC, and HPC) was found on the feed side of the membrane and the feed spacer; the least was observed in the product spacer [6]. And severe biofouling was observed in cases where the feed water had BFR-values exceeding 120 pg/cm^2 day and/or the AOC value exceeded 80 μg Ac-C/L [5].

3. Microbial community structure in seawater intake

A number of previous studies have reported that the biological matter and environmental factors of seawater such as temperature, total dissolved solids, and biological quality have affected the pretreatment regimes of numerous desalination plants [7,8]. As examples, viable, biofilm-forming bacteria or dominant groups or specific bacteria, which increase the concentration of high molecular-weight organics or microbial extracellular polymeric substances, can negatively affect the pretreatment of desalination processes [9,10]. Therefore, a more comprehensive understanding of the microbial community structure in seawater intake sources is necessary.

In our previous study, more than 25 different strains of bacteria were isolated from seawater intake of SWRO process (Table 1) [11]. Note that traditional techniques for identifying bacteria based on phenotypic characteristics are not generally as accurate as identification based on genotypic methods; thus, a comparison of the bacterial 16S rRNA gene sequence has emerged as the preferred genetic technique to identify bacteria. From the results of the 16S rRNA gene sequencing of each colony, strains closest to *Pseudoalteromonas* sp. and *Bacillus* sp. were predominantly observed. Table 2 shows the phylogenetic diversity in the seawater sample, as a total of 93 partial 16S rRNA gene sequences were identified during a comparison to a GeneBank database using a BLAST search. The BLAST analysis of the sequences indicated that the screened clones were highly similar (mean = 96%) to the target clones [11]. The most abundant sequences in the seawater clone libraries were α-proteobacteria (53%) and a large fraction of the α-proteobacteria was uncultured *Rhodobacteraceae* bacterium. The next most abundant clones were Bacteroidetes (29%), with a significant fraction of the Bacteroidetes also being composed of uncultured Bacteroidetes bacterium; uncultured clones comprised 48.4% of the total clones. The fraction of γ-proteobacteria was relatively small, comprising approximately 5% of the community, and an unknown bacteria of unclear taxonomical identity accounted for 14%.

Interestingly, even clones related to pathogens such as *Rickettsiales* and *Roseobacter* sp. (oyster pathogens) appeared and bacteria that removed hazardous or non-degradable substances were also observed. For example, *Erythrobacter*, observed in both bacteria isolation and DNA-based 16S rRNA gene cloning, is known to be a critical component in the cycling of both organic and inorganic carbon in the ocean. Other clones, such as uncultured *Chromatiales* bacterium, a purple sulfur bacteria specializing in sulfite oxidation, and uncultured *Pseudomonas* sp., a biofilm-forming bacteria, were also found.

It is noted that the predominant populations or presence of specific strains in the intake sample were not sufficient to reflect either the entire microbial diversity or complexes present in the seawater since only a small fraction (<10%) of the total extracted DNA from 100 mL of

Table 1
Bacteria isolation from seawater and 16S rRNA gene sequencing. [11].

Best-matched organism	No. of isolates	Similarity (%)[a]
Firmicutes		
Bacillus cereus strain CTSP45	2	99–100
Bacillus pumilus strain duxiaoyabaoganjun	2	99
Bacillus subtilis isolate W51	2	100
Bacillus aquimaris strain SC0	1	100
Bacillus megaterium limp 4-1	1	99
Bacillus flexus strain TS10	1	00
Bacillus drentensis strain WN575	1	100
Bacillus sp.	3	99
Planococcus citreus strain TF-16	1	100
γ-Proteobacteria		
Pseudoalteromonas elyakovii	1	100
Pseudoalteromonas haloplanktis strain	1	100
BSi20582		
Pseudoalteromonas sp.	3	94–99
Altermonas sp.	2	94–99
ß-Proteobacteria		
Leptothrix sp. S1.1	1	97
α-Proteobacteria		
Erythrobacter sp.	1	99
Actinobacteria		
Micrococcus sp.	1	98

[a] Similarity is the percent of identity to previously identified sequences based on the best-matched bacteria in GeneBank.

Table 2
16S rRNA gene cloning of seawater sample and sequencing results identified by BLAST. [11].

Best-matched organism	No. of clones	Similarity[a] (%)
α-Proteobacteria		
Uncultured *Rhodobacteraceae* bacterium	11	96–99
Roseobacter sp.	7	96–99
Sulfitobacter sp.	5	95–98
Uncultured *Rickettsiales* bacterium	4	92–98
Ruegeria sp. MB2	4	96–98
CVSP bacterium CV1010-362	4	97–99
Uncultured alpha proteobacterium	3	95–99
Staleya japonica IGL5	2	98
Roseovarius crassostreae CV919-312	2	99
Uncultured *Rhizobiales* bacterium	1	98
Thalassobius mediterraneus CECT 5383^T	1	97
Kordiimonas gwangyangensis GW14-5	1	90
Erythrobacter sp. DG1288	1	99
Chelatobacter sp. Pht-3B	1	93
Caulobacter sp. MCS6	1	90
Alpha proteobacterium GMDsbM1	1	99
Bacteroidetes		
Uncultured Bacteroidetes bacterium	16	98–99
Formosa sp. 5IX/A01/134	6	95–99
Aureimarina marisflavi IMCC3054	2	97
Microscilla aggregans catalatica	2	92
Uncultured *Flavobacteria* bacterium	1	99
γ-Proteobacteria		
Marinobacterium sp. J5	1	97
Uncultured *Chromatiales* bacterium clone SIMO-1354	1	96
Uncultured *Oceanospirillales* bacterium clone SIMO-2851	1	97
Uncultured *Pseudomonas* sp. clone: BJS81-001	1	96
Unknown		
Uncultured marine bacterium	4	90–100
Uncultured bacterium	2	94–99
Marine bacterium ATAM173a_17	7	95–99

[a] Similarity is the percent of identity to previously identified sequences based on the best-matched bacteria in GeneBank.