

Omics Platform for in-operando Biological Characterization Systems Design

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Challenge

Biofouling is the uncontrolled growth of microorganisms (a biofilm) on membrane surfaces, and is a pervasive problem in desalination and other membrane-based water and wastewater treatment processes. Biofilms reduce the flux and increase the operating pressures, which significantly increases energy requirements and operational cost. Membrane elements can be cleaned (or replaced in severe instances), but must be taken offline to do so, limiting clean water production and increasing costs. Developing a fundamental understanding of how biofilms form could lead to the development of predictive tools that mitigate against biofouling, minimizing downtime and reducing costs.

Research Approach

This project will build a comprehensive “omics” platform to empower the research community to fundamentally understand biofilm formation and mitigate biofouling in water treatment and distribution systems. The term “omics” refers to the collection and analysis of DNA from the biofilm through the lenses of:

metagenomics (“who’s there?”)

meta-transcriptomics (what genes are active?)

metaproteomics (what proteins and enzymes are active?)

metabolomics (what is the biofilm metabolism doing, as a whole?)

Biofilms will be collected from real reverse osmosis (RO) elements in a large-scale desalination facility as well as from other RO elements in geographically diverse areas, and will be collected as single samples, or as time-series samples, to better understand how biofilms change from benign to harmful.

Impact

The resulting omics platform will provide an unprecedented opportunity to generate predictive understanding of biofilm formation and lead to more precise and efficient approaches to control membrane biofouling. The outcomes will inform

materials selection and operational parameters to reduce down time, decrease energy consumption and pretreatment requirements, extend RO module cleaning cycles, and enhance treatment system resiliency.

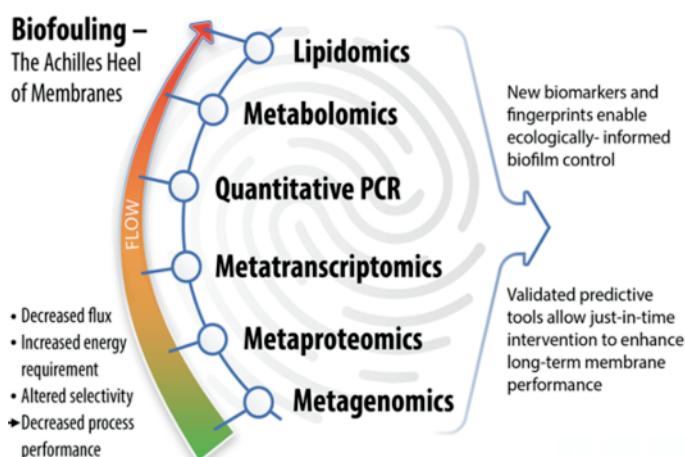


Figure 1. Proposed Omics Platform workflow to better understand the transition of biofilms from benign to destructive.

RESEARCH TEAM MEMBERS

Oak Ridge National Laboratory (ORNL): Dawn MarieKlingeman, Frank Löffler, Kellie Peyton, Mircea Podar, Randy Metheney; Rice University: Jacques Mathieu, Lauren Stadler, Pedro Alvarez; The University of Texas at Austin: Manish Kumar.

PUBLICATIONS AND REPORTS

Podar M., A. May, W. Bai, K. Peyton, D. Klingeman, C. Swif, D. Linson, J. Mathieu, D. Siljeström, I. Beneyto, L. Stadler, Y. Pinhas, F. Löffler, P.J.J. Alvarez, and M. Kumar (2021). Microbial diversity analysis of two full-scale seawater desalination treatment trains provides insights into detrimental biofilm formation. JMS Letters 1(1)100001.

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Accomplishments & Findings

Biofouling is a pervasive problem in desalination, wastewater reclamation, and other membrane-based water treatment processes, responsible for up to 25% of operating costs. Biofouling is currently treated as a “black box” in which bulk cleaning and disinfecting strategies are used without understanding the underlying microbial ecology. This Year 1 “Seedling” project set out to develop a methodology and sampling system to precisely measure the microbial communities that inhabit all water treatment systems, with the goal of enabling future biofilm management strategies based on biology and “precision treatment” rather than chemical treatments that drive up cost and can damage membranes and associated subsystems.

The project scored an early win by successfully installing a Membrane Fouling Simulator (MFS) system at Orange County Water District’s (OCWD) Groundwater Replenishment System and recovering samples for detailed ‘omics characterization from both the MFS and from cartridge filters ahead of the RO system at both OCWD and Tampa Bay, FL. The team developed robust standard operating procedures (SOPs) for sampling and handling of desalination plant biofilm material for downstream ‘omics analyses of nucleic acids (16S rRNA gene amplicon sequencing, shotgun metagenomics, metatranscriptomics), proteins (metaproteomics), and metabolites (metabolomics). This is the first time such detailed sampling has been carried out in an operating desalination environment.

The project confirmed that MFS systems are a practical method for enabling representative sampling of biofouled surfaces during plant operations and could be installed at any membrane-based water treatment plant. The study showed that feedwater and RO membrane biofilm communities are distinct. Microbial communities of the feedwater are very different from the communities associated with the prefilter cartridges and RO membranes. Cartridge filters do NOT prevent small bacteria (e.g. SAR11) from passing through and seeding the RO modules, potentially serving as food for other biofoulers. Better prefiltration could help reduce the presence of these

microorganisms. The team also discovered that predatory Bdellovibrionota were enriched on prefilter cartridges and likely impact microbial community composition and biofilm formation.

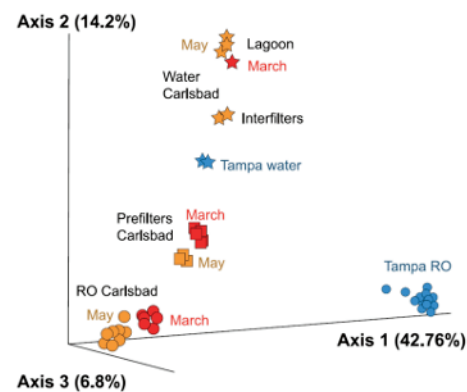


Figure caption: Beta diversity analysis of microbial communities across samples. See Podar et al., 2021.

Related Accomplishments

One related technical development that has greatly accelerated the efficiency and effectiveness of microbial ecology studies of this kind has been the use of AI in research. Noisy complex systems, as the microbial ecologies that affect biofilm formation in water systems, are much easier to study and decipher now.

Opportunities for Further Research

The team transitioned these insights to NAWI project 3.13 in which they evaluated more benign disinfectants such as peracetic acid, and novel approaches such as catalytic membranes, nutrient balancing, phages, and chlorine resistant RO membranes.

This project has shown that cartridge filters in common home water treatment systems preserve the community of microorganisms ambient in the water system. This suggests that cartridge filters can be sampled and monitored as “sentinels” for the detection of pathogenic microorganisms in water systems.