## Who's on First: Temporal Analysis of PDMS Biofouling in a Marine Environment

Keyana Roohani<sup>1</sup>, Kayla Kurtz<sup>2</sup>, Vinka Craver<sup>2</sup> & Christopher W. Reid<sup>1</sup>

<sup>1</sup>Science & Technology, Bryant University, Smithfield, RI <sup>2</sup>Civil & Environmental Engineering, University of Rhode Island, Kingston, RI

Biofouling on instrumentation deployed in the marine environment is one of the biggest challenges of long-term monitoring activities. As part of the RI C-AIM sensor development effort, microfluidics- based devices are currently in development. Understanding the dynamics of biofilm formation is essential to design antibiofuling strategies.

To investigate the biofouling of microfluidic devices, we have developed an *in vitro* biofouling assay and metagenomics pipeline to assess colonization and development of biofilm in polymers commonly used for microfluidics manufacturing. Initial experiments have employed a 1 cm<sup>2</sup> PDMS polymer incubated in Narragansett Bay seawater over a three-week time course. Total genomic DNA was extracted from incubated PDMS chips and 16srDNA amplified by PCR, library preparation, and sequencing performed on an Oxford Nanopore MinION. The initial pioneers (first 48 hours) of the PDMS polymer were predominantly alkane-degrading bacteria from the genus *Alcanivorax* and *Marinobacter* in addition to *Pseudomonas* and *Acrobacter*. Temporal changes in the microbial community were observed in the biofilm. While the pioneer species was a constant presence in the community after three days, increased microbial diversity was observed with colonization by *Aerobactium* and *Spongiibacter*. By the end of the three weeks, the biofilm presented a high diversity of gamma- and alpha- proteobacteria with a high abundance of chemoorganotrophic and photoheterotrophic Rhodobacteriaceae.