

## Microbial community dynamics of a membrane bioreactor treating hydraulic fracturing wastewater

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Wastewater generated during production of oil and gas, commonly termed produced water (PW), is challenging to treat due to the presence of a wide variety of characterized and uncharacterized contaminants such as hydrocarbons, heavy metals, and minerals, at high concentrations. Despite the complexity, some bioreactor studies have shown that PW is amenable to biological treatment. These bioreactors were inoculated with sludge from municipal wastewater treatment plants and incrementally acclimated to high salinity of PW. However, very little is known about the microbial communities within well-performing bioreactor or their dynamics during the acclimation phase.

To address this knowledge gap, we operated and monitored an aerated, 130 L PW-fed membrane bioreactor (MBR) seeded with municipal wastewater sludge. During acclimation phase, the MBR was fed with a gradually varying mixture of dechlorinated tap water and PW in order to increase the salinity until the MBR was fed by only PW (Salinity- 29 g/L); at which point salt was added gradually to 100 g/L to see how the community and bioreactor would perform at these salinity levels. Microbial communities were profiled via cultivation-dependent as well as by 16S rRNA amplicon sequencing techniques. In parallel, physicochemical analyses like dissolved organic carbon, ion chromatography and excitation-emission-matrices of both the feed and membrane permeate were performed to correlate microbial communities to carbon.

During acclimation, microbial community diversity decreased drastically with increasing salinity. However, there was little change in reactor performance as measured in terms of dissolved organic carbon removal. Towards the end of the acclimation phase, 4 major Amplicon Sequence Variants (ASVs) belonging to the genera *Iodidimonas*, *Roseovarius*, *Arcobacter*, and *Rehaibacterium* constituted close to 80% of the sequence tags. Of these major ASVs, we were successful in obtaining isolates of *Iodidimonas* and *Roseovarius*. We are further characterizing these isolates through whole genomic sequencing and biochemical tests to shed better light on their role in treating PW.

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