Understanding Trends in Methane Production and Producers in Anaerobic Waste Water Treatment

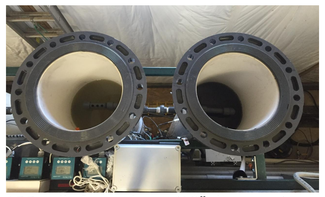
Jennifer Feigin[1], Andrew Pfluger[2], Lynne Albert[2], Mengyuan Yu[2], Gary Vanzin[2], Linda Figueroa[2], Junko Munakata Marr[2]

[1]Oberlin College, [2]Colorado School of Mines

BACKGROUND

Current large-scale aerobic waste water treatment methods often produce large amounts of activated sludge waste and have high operational costs due to pumping and aeration. Anaerobic treatment, by contrast, produces less sludge waste, requires less energy, and has the potential for biogas recovery in the form of methane. Treatment of waste water with anaerobic baffled reactors (ABRs) has been studied and shows promise for full-scale wastewater treatment. This study aims to assess methane production of microbial populations and quantify methanogenic DNA in ABRs. The impacts of system disturbances, Chemical Oxygen Demand (COD), and temperature were examined at different stages in the ABR treatment processes.

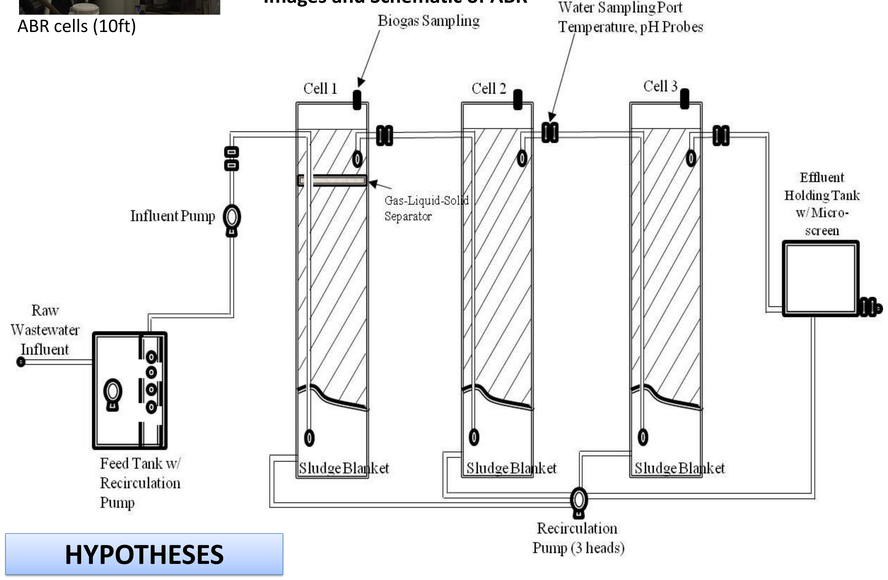
ABR cells (10ft)



ABR cells from above (12" diameter)

Floating Disturbance

Images and Schematic of ABR



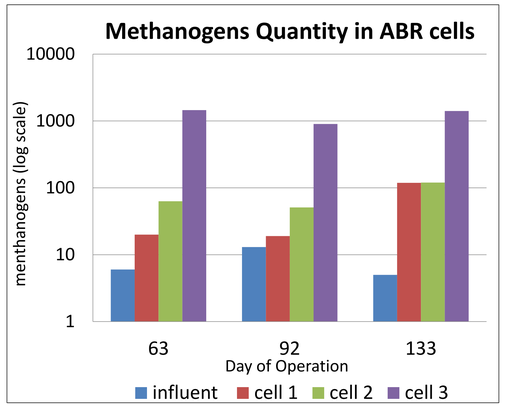
HYPOTHESES

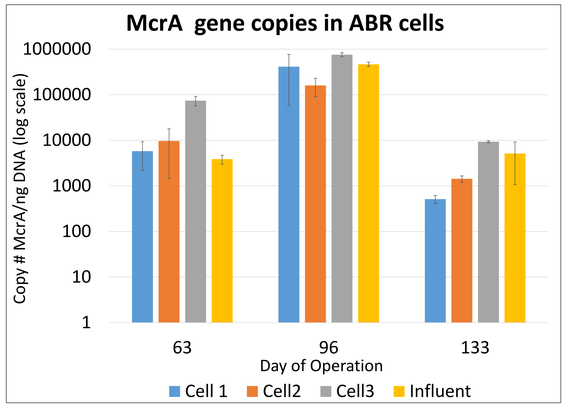
1. Methanogenic populations and methane production will increase throughout the reactor (from influent to cell 1 to cell 2 to cell 3.)
2. Rising temperatures will encourage methanogenic activity.
3. Disturbances in the ABR will impact the microbial and chemical functions of the system in the short-term, but will have a limited effect on long-term stability.
4. As time goes on, total COD removal will continue to approach EPA standards.

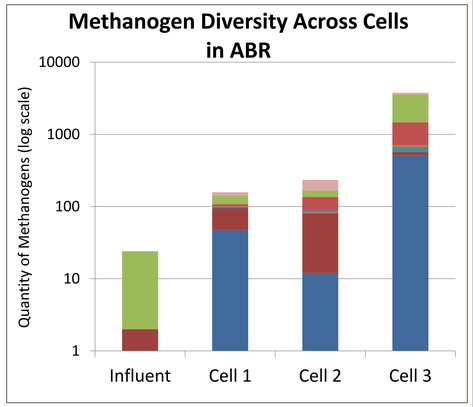
METHODS

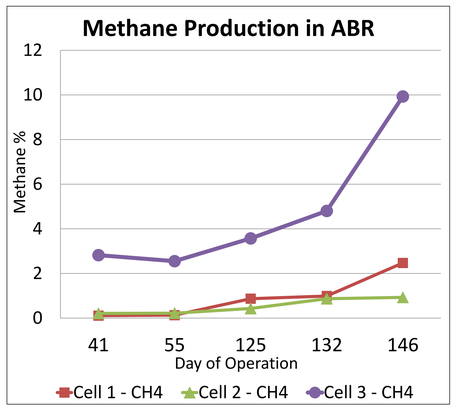
DNA extraction & purification of samples → Create primers & standard curve for PCR & qPCR →  qPCR & PCR of DNA with mcrA primers → Analysis of qPCR & preliminary sequencing data → Monitor & measure COD and temperature in all cells → Collect biogas grab-samples from ABR cells →  measure % CH_4 in cells using gas chromatography

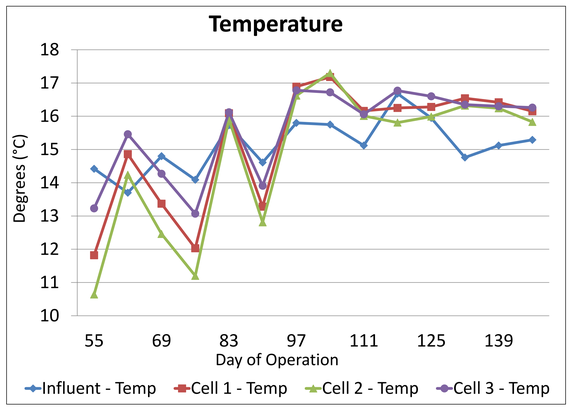
RESULTS

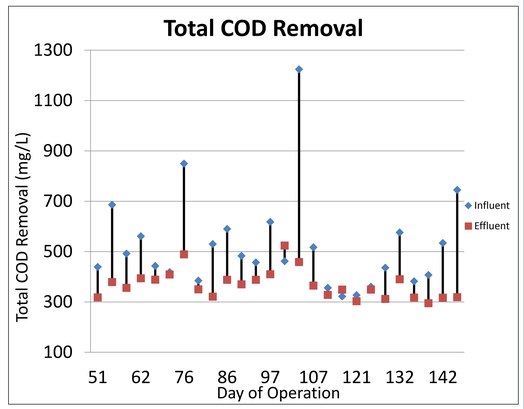












The microbial analyses of the mcrA gene and the sequencing data show that the quantity of methanogens detected increase from the influent to cell 3. The sequencing taxonomic results showed that all archaeal species detected in sequencing were methanogens. Overall microbial DNA, methane levels, and COD removal from influent cell 1 to cell 2 to cell 3 increased.

ANALYSIS & FUTURE DIRECTIONS

Methanogenic populations in each of cells in the ABR differ. While the microbial communities seem to be impacted by disturbances, indicated by decreased COD removal and changes in methanogen DNA quantities, they seem to resume normal function shortly afterwards. Floating events are largely thought to be due to biogas accumulation in reactors. The overall upward trend of both methanogen communities and methane production across the cells and over time indicate the potential for future biogas recovery and reuse applications, but further study is required to determine long term changes and patterns of stability in these populations and their methane production levels.

Acknowledgements:

This research was made possible thanks to the generous contribution of many experts who have dedicated themselves to raising the level of human and environmental standards of living by studying anaerobic waste water treatment. In this regard, I would like to thank Major Andy Pfluger and Dr. Lynne Albert for all that they taught me and whose care, commitment, guidance, and endless knowledgeable inputs made this project come alive. Thank you to Dr. Junko Munakata Marr and Dr. Linda Figueroa for all their contributions of time, suggestions, and knowledge in addition to their lab space and materials. Thank you to Mengyuan Yu for her contributions to data collection and chemical testing at Mines Park; thank you to Dr. Gary Vanzin for generously setting aside time to reorganize and patiently teach me about the sequencing data analysis; thank you to the ReNUWIt program coordinator Dr. Pamela McLeod for all she does to make this REU a truly wonderful experience. I am also thankful to The National Science Foundation for funding this REU.