Examining the Impact of Antibiotic Loading on Bacterial Communities in AnMBRs

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Introduction

Antibiotic resistance is a growing threat to public health and environment. Wastewater treatment plants, which act as gateways to the environment, are believed to be hotbeds for antibiotic resistance proliferation.

The nutrients, bacteria, and antibiotics in wastewater influent could allow for propagation of antibiotic resistance.

Fig. 1 - Global Antibiotic Consumption[1]

Little is known about the resulting bacterial Communities in emerging biotechnologies such as anaerobic membrane bioreactor or AnMBR. Therefore, our research project delves into the effects of antibiotic loading on bacterial communities within AnMBRs.
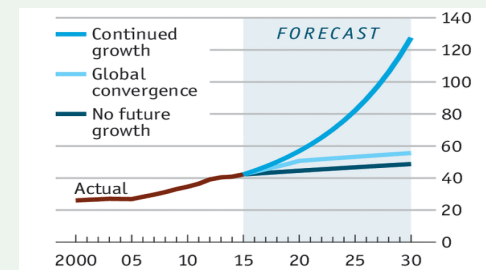
Motivation and Objectives

Elucidating the effects of antibiotic loading in bacterial community structure will inform on the resilience and susceptibility of certain bacterial taxonomies to antibiotics. This in turn enables the creation of a better-represented database, which could be referenced by other environmental samples subjected to antibiotic loading.

Fig. 2 – Relative Abundance Graph By Phyla[2]

Even so, future work that correlates antibiotic resistant genes with resilient bacterial communities can inform the likelihood of certain bacterial hosts to the antibiotic resistant genes.

Skills Learned

Research
• Techniques of many lab equipment and tools, such as the Illumina MiSeq Sequencer and the mothur bioinformatics tool
• Proper lab etiquette and procedures despite the obstacle of virtual learning and research

Fig. 3 - mothur

Academic
• Explored the intersectionality between technology and sustainability, an area that I'm now even more passionate and excited about
• Better understood the role and place of environmental engineers in today's world, a career path I've always been interested about pursuing

Fig. 4 – Illumina MiSeq Sequencer[3]

Results and Discussion

The rarefaction curve (Fig. 5) revealed that the effluent samples were better represented than the biosolid samples. In addition, the biosolid samples had more OTUs than the effluent samples, implying greater richness.
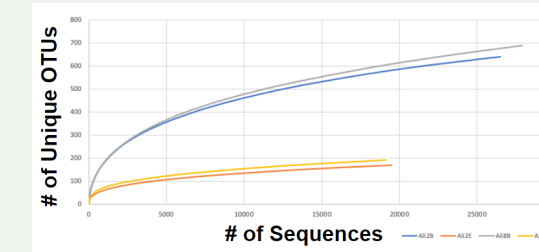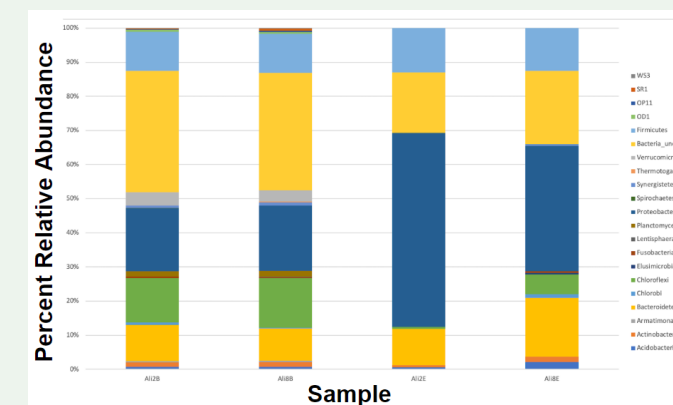

Fig. 5 - Rarefaction Curve

Fig. 6 – Relative Abundance Graph By Phyla

The relative abundance graph by phyla (Fig. 6) revealed that the effluent samples had higher relative abundance of Proteobacteria and lower relative abundance of unclassified bacteria compared to the biosolid samples.

In addition, the effluent samples had fewer less abundant phyla. Upon antibiotic loading, the effluent sample experienced a notable decrease in the relative abundance of Proteobacteria, paired with an increase in relative abundance of unclassified bacteria, less abundant phyla, and OP11 bacteria.

The PCoA plot (Fig. 7) showcased that the biosolid community structure was clearly distinct from the effluent community structure. Though the biosolid communities before and after antibiotic loading were similar, the effluent communities before and after antibiotic loading were comparatively different.
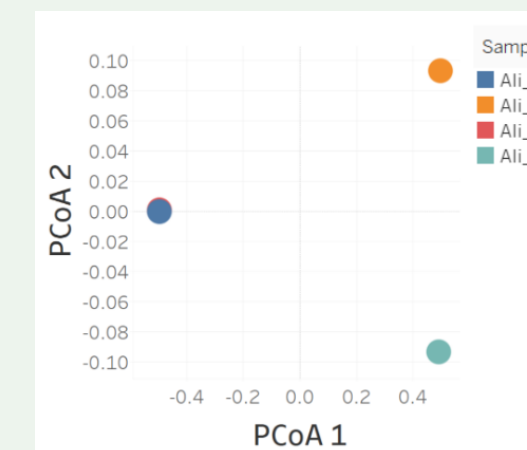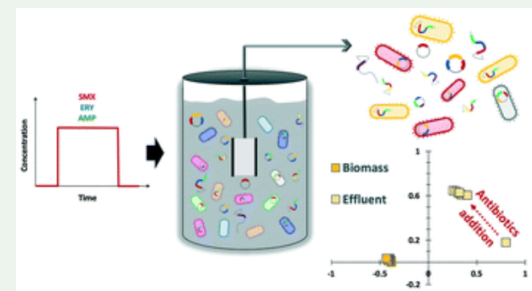

Fig. 7 - Principle Coordinate Axis Plot

From our results, we were able to qualitatively determine which phylum was more resistant to antibiotic stress. We also showcased that AnMBRs are capable of retaining high levels of bacteria in the reactor, inferring their capacity to decrease antibiotic resistance loading into the environment compared to conventional treatment systems.

Citations

1) Klein, E. Y., Van Boeckel, T. P., Martinez, E. M., Pant, S., Gandra, S., Levin, S. A., Goossens, H., & Laxminarayan, R. (2018). Global increase and geographic convergence in antibiotic consumption between 2000 and 2015. Proceedings of the National Academy of Sciences, 115(15), E3463–E3470. https://doi.org/10.1073/pnas.1717295115

3) Kozich JJ, Westcott SL, Baxter NT, Highlander SK, Schloss PD. (2013): Development of a dual-index sequtencing strategy and curation pipeline for analyzing amplicon sequence data on the MiSeq Illumina sequencing platform. Applied and Environmental Microbiology. 79(17):5112-20.

2) Zarei-Baygi, A., Harb, M., Wang, P., Stadler, L. B., & Smith, A. L. (2020). Microbial community and antibiotic resistance profiles of biomass and effluent are distinctly affected by antibiotic addition to an anaerobic membrane bioreactor. Environmental Science: Water Research & Technology, 6(3), 724-736.

Zarei-Baygi, A., Harb, M., Wang, P., Stadler, L., Smith, A. (2019). Evaluating Antibiotic Resistance Gene Correlations with Antibiotic Exposure Conditions in Anaerobic Membrane Bioreactors. ACS Publications. https://pubs.acs.org/doi/10.1021/acs.est.9b00798

How This Relates to Your STEM Coursework

Through this research project, my knowledge and understanding of the environmental issues that pervades our society and environment have grown significantly.

Through my Physical Computing and Machine Learning courses this coming school year, I'm excited to build environmental impact-driven technologies addressing these new issues and utilize everything I've learned, as well as make room for further education.

In addition, I'll also be taking Genetics I and Marine Biology where I'm confident the skills and experience, especially in nucleic acid sequencing and analysis, that I've picked up through SHINE will come in handy.

Next Steps and Advice for Future SHINE Students

Next Steps for Me
I'll be flying back to Exeter and continue spearheading sustainability initiatives on-campus such as fossil fuel divestment and campus terracycling.

Advice for Future SHINE Students
This experience is such a wonderful time to explore your interests in STEM. Dr. Mills, your professor, your mentors, and your colleagues are all amazing and interesting people; Take the time to get to know them. Simply put, have fun, learn from your mistakes, and ask questions.

Acknowledgements