

Abstract

We used eDNA techniques to analyze and compare differences in microbial diversity in Artist Lake, Upper Yaphank Lake, and Lake Panamoka. Our hypothesis was that the bacterial profile would be different in these three lakes, and that the difference might be correlated with the environments surrounding them. We collected water samples and extracted the DNA, then used a microbial primer to amplify the bacterial sequences. Our sequencing results yielded a total of almost one million species of bacteria, which were analyzed using the Purple Line of the DNA Subway program. The bacteria were compared between lake sources and estimated pollution levels (observed turbidity). Our results indicate that there are differences in microbial diversity between each lake, and that more turbid water shows lower relative frequency distributions. Our data indicate that eDNA shows promise in future monitoring efforts of natural bodies of water that are at risk for contamination by human activities.

Introduction

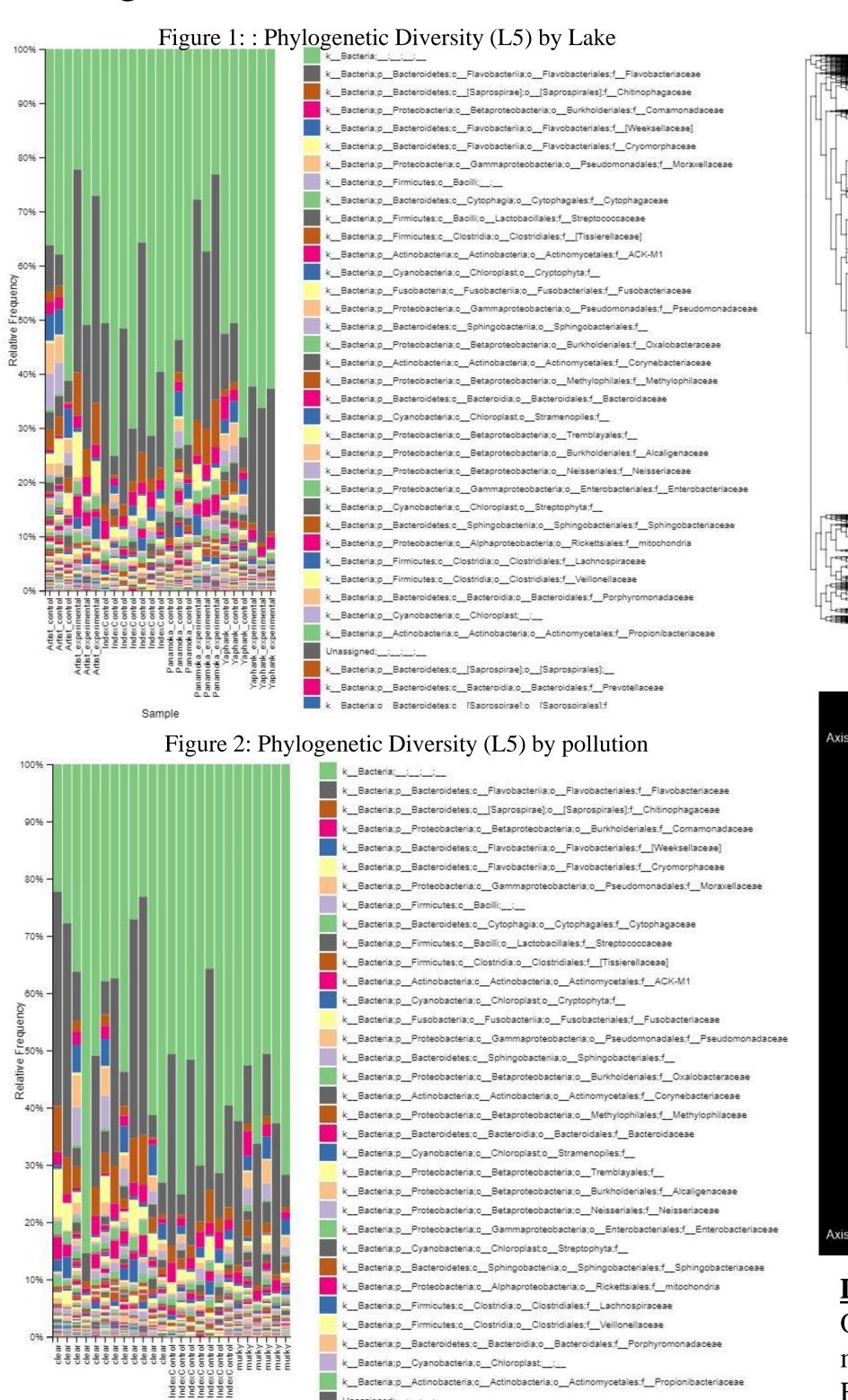
Artist Lake, Upper Yaphank Lake and Lake Panamoka have different environments. Upper Yaphank Lake, located beside Long Island Expressway, is used for recreational purposes which is leading to overfishing, duck waste exposure and introduction of invasive species. An aquatic invasive species known as fanwort was found in Upper Yaphank Lake, but the most recent 2016 DEC report states that there are generally only minor impacts to recreational use (1) Artist Lake is a glacial kettle hole lake located next to a large apartment/condominium complex in Middle Island. This lake naturally provides home to many sport fish which are regularly consumed(2). Lake Panamoka is surrounded by residential areas, recreational spots and roadways. Recent (June 2018) water quality testing of Lake Panamoka found no significant pollution and coliform levels were far below acceptable levels (3). The hypothesis that different level of pollutants can affect the microbiome can be addressed by using eDNA techniques to compare the microbiome profiles of lakes in different environments, and interpreting these results using the most recent water quality reports available for these lakes.

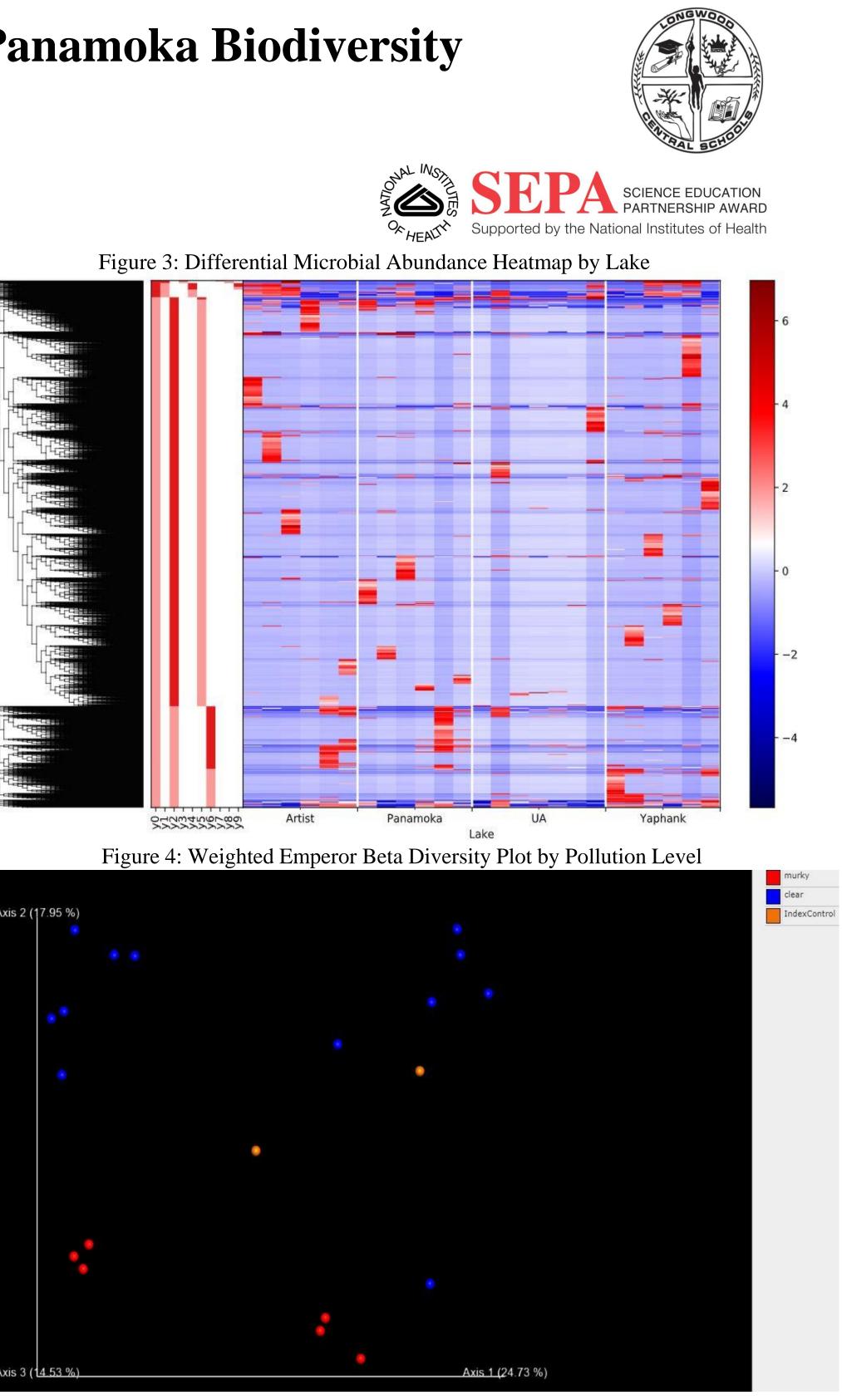
Materials & Methods

In early March 2019, we collected water samples in triplicate from each lake, recording the GPS data. Water samples were filtered and distiled water was used as controls. DNA was extracted from the filters using the PowerSoil Protocol.. A bacterial 16S primer amplified the bacterial regions, and gel electrophoresis was used to determine which PCR products could be sent out for next-generation Illumina sequencing. After uploading the sequencing data, identification of species as well as analysis and comparison of the microbiome profiles were carried out using the taxonomic diversity, alpha- and beta-diversity routines of the Purple Line in DNA Subway.

Results Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae Our results indicate that eDNA techniques can be used successfully to k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae Analysis revealed a total of almost one million bacterial species represented. A Level 5 k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae clear monitor microbial biodiversity in different bodies of water. As seen in k__Bacteria;p__Cyanobacteria;c__Chloroplast;__ phylogenetic comparison of species in water samples from Artist Lake, Lake Panamoka, and Index Index Index Index k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Propionibacteriaceae Figures 3 and 4, there are differences in both overall frequency of abundance Unassigned: Upper Yaphank Lake reveals differences in microbiome profiles (Fig. 1). When samples were of species in each lake, as well as differences related to observed water **References** compared using a visual measure of water quality (clear vs. murky), we also saw differences in quality. A detailed analysis of the species present and absent in each lake 1. WI/PWL Fact Sheets - Carmans River/Great South Bay Watershed (0203020203). (2016). profiles (Fig. 2). Murky water samples exhibit lower overall frequency as well as specific Retrieved November 13, 2018, from https://www.dec.ny.gov/docs/water_pdf/wiatlliscrgsb.pdf could provide clues regarding the current cumulative effect of pollution. 2. DEC.NY.GOV Factsheet on Artist Lake, from https://www.dec.ny.gov/outdoor/24149.htm differences in abundance of certain families of bacteria (Fig. 2). Differential abundance heatmaps Human pathogens may be more abundant in some lakes, which would be 3. Lake Panamoka Civic Association water quality site, also reveal different microbial profiles when comparing samples from the different lakes (Fig. 3). important information for the public. In summary, our results suggest that https://lakepanamoka.net/communitycenter/water-testing Beta diversity Emperor plots are more difficult to interpret, but when sorted by pollution level, Acknowledgements eDNA monitoring of microbial diversity in bodies of water used for the weighted Emperor plot of species from the three lakes appears to show smaller differences We wish to acknowledge the assistance of Dr.Aleida Perez at the BNL recreation by the public may become an additional valuable tool for between the profiles of each lake (Fig. 4). Open Lab, as well as the advice of Dr. Bruce Nash and Dr. Sharon monitoring possible human health risks in conjunction with regular water Pepenella for data analysis. quality testing

Effect of Human Population on Spring Lake, Yaphank Lake, and Lake Panamoka Biodiversity Amber Leon¹, Maha Mahmood¹, and Annisha Wazed¹ Mentor: Dr. Lucinda Hemmick¹ ¹Longwood High School, Middle Island, NY





Discussion