Identification of Bacteria in Otsego Lake Using DNA sequencing Technology
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Abstract
Water samples were collected from various locations in Otsego Lake, NY. Using standard recombinant DNA techniques, such as Polymerase Chain Reaction (PCR) and DNA cloning, bacterial DNA was isolated and extracted from the samples. The DNA will then be sequenced. This type of sequencing is known as environmental sequencing, which is the retrieval of genetic information from environmental samples. Prior to this type of sequencing, the bacteria from the sample would have to be grown under extreme conditions. This is an obstacle because the laboratory conditions can be very hard to satisfy and the bacteria would have to be identified based on their growth, rather than directly determining them based on their genetic material. Studies show that over 99% of bacteria cannot be grown in a lab setting (1). This is part of a larger field known as Metagenomics, which has become increasingly more popular within the last decade due to the large variety of research applications. Such applications include the human gastrointestinal tract and pathogen function.

Metagenomics has also been used to analyze the various types of bacteria in different parts of a hospital. The same techniques were utilized on water-associated samples, such as sink drains, ice machines, and other surfaces. The research was found to be effective in identifying bacteria that would have not been identified had the samples been grown in a laboratory setting (2). This type of sequencing also has many other applications that apply to fields such as biofuels and agriculture.

Methods and Results
Water samples (2 sets consisting of 4 samples each) were collected from Otsego Lake. The location and depth of each set was different. The samples were purified and the DNA was extracted using standard DNA isolation protocol. A highly conserved genetic sequence, which is the 16s rRNA gene, was targeted for amplification by PCR. PCR allows for a high volume of copies within a short time, and with little preparation.
The fragments of DNA were cloned into a DNA vector (bacterial plasmid). The recombinant DNA molecule was then inserted into a common nonpathogenic strain of E. coli (host cell). The bacteria synthesized large amounts of DNA, which will then be sequenced. Once sequenced, Bioinformatics databases that contain DNA sequence maps of various genomes will be used to help identify the specific species of bacteria present.
The DNA that was amplified by the PCR reaction was run on an agarose gel, as shown in figure 2. The bands circled are the PCR products that were obtained.

Future Work
Further analysis will be done to determine the protein coding regions of these sequences as well as other information including the determination of relationships between these bacteria, and how the roles of these bacteria effect their ecosystem.

References