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Marine Biology
Investigation into the presence of Cyanobacteria in the Quinnipiac River
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The area surrounding Quinnipiac River is known to have an assortment of point and nonpoint pollution sources which have led to elevated levels of nutrients and bacterial pollution (QRWA 2013, Todd Trench 2000). Increased nutrients can result in an excess growth of algae, known as an algal bloom. It has been shown that urban development can cause a rise in nutrients, and therefore impact the frequency and extent of these blooms (Huisman et al. 2018). Algal blooms can cause particularly serious health complications in aquatic and land organisms, including humans, when they result from cyanobacteria species that produce toxins (Codd et al. 1999). Toxic cyanobacteria have been identified throughout the state of Connecticut (CT DEEP 2011); however, little research has been done on the Quinnipiac River to determine the presence of potentially toxic cyanobacteria. The intention of this study is to identify the presence of cyanobacteria in the Quinnipiac River, as well as nutrients and water qualities that may aid in its development. We aim to identify cyanobacterial communities and their potential for toxicity within the river through collection and isolation of individual cyanobacterial species.

Samples for species isolation were collected from both the surface water, as well benthic scraping at four collection sites along the Quinnipiac River. Additionally, nutrient levels and water quality readings were measured at each collection site with the use of the eXact Echo-Check kit and YSI water quality meters respectfully. Samples were processed by plating on agar discs and incubated at 23°C until they reached maturity. Individual species were then identified using microscopy and isolated on new agar plates or suspended in liquid media. DNA was then extracted from the species isolates using the Qiagen DNeasy plant mini kit, PCR was performed using the Universal Plastid Amplicon (Sherwood and Presting 2007), and PCR products were sent to Yale for sequencing. Sequences were then analyzed using Geneious software (<https://www.geneious.com>) and by using the Basic Local Alignment Search Tool (BLAST) to find reference sequences in order to identify individual species.

Sequence analysis has identified a variety of microalgae species present in the Quinnipiac River, but cyanobacterial species have not been isolated to date. This could be due to the latency of development that cyanobacteria has demonstrated, requiring additional time to accommodate culturing and collect complete data from cultures. Alternatively, the absence of identifiable cyanobacteria may be due to significantly low levels present in the river. Confirmation of cyanobacteria in similar waterways throughout the state of Connecticut (CT DEEP 2011) indicates that further research, with an emphasis on identifying toxin producing cyanobacteria, is necessary to confirm findings.

Continued investigation of all samples collected during the May-August collection period will be performed as cultures mature to identify all species, including cyanobacteria, present. In addition, water quality and nutrient patterns will be compared to fluctuations in the type and amount of species present to determine any correlations. Examination of current and future species isolates will provide a through community assessment, as well as provide a broad range of reference sequences to support an overarching study of environmental sequences of the Quinnipiac River.

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