ISOLATION, GENOMIC IDENTIFICATION, AND CHARACTERIZATION OF CYANOBACTERIA SPECIES IN LAKE OKEECHOBEE, FLORIDA, USA

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Cyanobacteria are a diverse and widespread group of microorganisms. An overgrowth of these organisms limits recreational use of water resources and negatively impacts aquatic ecosystems. Moreover, some cyanobacteria can produce toxins, causing additional problems for human and animal health. Lake Okeechobee, the second largest freshwater lake within the contiguous United States, experienced extensive cyanobacterial blooms in 2016 and 2018. Although field studies have been conducted to examine phytoplankton communities in this lake, cultivation efforts are quite limited. This has diminished further laboratory research, which is valuable to study the ecophysiology of these algal species to understand their nutrient preference and the capability of toxin production. The objective of this research is to isolate some representative cyanobacterial species from Lake Okeechobee samples and to examine their genomic and ecological features. Water samples from multiple sites around Lake Okeechobee were cultured in the lab to isolate some species of cyanobacteria. A new batch of samples was cultured each month from April-September 2019 to see if different species show up at different times in the summer. Samples were also cultured from the Caloosahatchee River, a waterway of Lake Okeechobee. Strategies used to create unialgal cultures include serial dilutions, antibiotics, hydrogen peroxide treatments, and physical separation. Once a cyanobacteria species was isolated, a DNA sample was also prepared to determine its genome sequence. At least 60 strains of algae have been isolated and genomic DNA samples were prepared, and the DNA sequencing of 23S rRNA gene was determined over 15 strains. The determined DNA sequences were compared with other DNA sequences available in the GenBank. Our isolates included species of Synechococcus, Microcystis, Limnothrix, Planktothrix, Merismopedia, and some other eukaryotic algae. These cyanobacteria will be used in a whole-genome sequencing to determine their capability to produce toxins and fix dinitrogen.