Assessing Fern Biodiversity through DNA Barcoding and Measuring Abiotic Conditions

Makkena, Taneesh (School: Lake Highland Preparatory School)

Florida is the second largest state in the production of ferns. Ferns rely on high soil moisture levels to thrive. With the threat of drier soils from global warming, it is important to analyze the effects on fern populations. The purpose of this study to assess the fern biodiversity from DNA Barcoding and measure the abiotic conditions in the local area. After the plant samples and the data on abiotic conditions were collected, the DNA from the samples were extracted. Once the DNA extraction was complete, the samples underwent PCR amplification to augment the gene region that will be needed to sequence. To check the PCR results, the samples were observed through Gel Electrophoresis. The DNA samples were shipped to a sequencing center in order to produce the gene sequence data. When the sequence results were retrieved, the data was analyzed through an online bioinformatics tool to compare the sequences and identify the species. For the samples that were not fully sequenced, morphology identification helped classify the unknown species. With all the samples identified, the biodiversity of the fern community was calculated through the Simpson's Diversity Index. With a range from 0 to 1, the fern population’s Simpson’s Index of Diversity value was .65, revealing to be on the higher end of diversity. In the final analysis, DNA Barcoding proved to be an effective tool to help determine the biodiversity. The information from this experiment will serve as a baseline for future work to determine the changes to fern populations.

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