

DNA Extraction of *Halophila stipulacea* Plants for Genetic Variability around the Virgin Islands

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Invasive species, such as the seagrass *Halophila stipulacea*, pose a threat to the ecosystems that they invade by outcompeting native species for resources. The goal of this project is to determine the genetic variability of *H. stipulacea* and to use that information to help create an invasion history model. In order to achieve this goal, we used the 2bRAD method to identify single nucleotide polymorphisms (SNPs), and analyzed genetic structure and clonal diversity.

Approximately 8 samples were analyzed from Magen's, John Brewers, and Lindbergh bay on St. Thomas. From this, we noted 3 different genotypes. Samples collected from John Brewers and a Magen's Bay sample were clones, while the Lindbergh and 2nd Magen's Bay samples differed from all other samples. We found the richness of diversity (R) to be 0.28571 over 4 loci. Since this species is known to reproduce clonally outside of its native habitat, this implies that multiple invasions have occurred throughout the Virgin Islands. Currently, we are assessing genetic diversity of 56 additional samples from different bays around St. Thomas, Water Island and St. John, and in the future, we will determine whether environmental factors such as depth are associated with particular clones in Brewers Bay.

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