

## Genetic Diversity of *Scaevola* Populations on Culebra, Puerto Rico

*Scaevola* is a coastal shrub that grows in many tropical islands in both the Pacific and Atlantic Oceans including the islands of Puerto Rico. On the island of Culebra, Puerto Rico the native species of *Scaevola*, *S. plumieri*, is co-occurring with an invasive species, *S. taccada*, introduced from the indo-pacific islands. The introduction of this non-native invader is hypothesized to have been facilitated by its use as decoration for commercial business such as hotels on the island as well as being dispersed from commercial businesses on the Virgin Islands. In other studies focusing on the relationship between *S. taccada* and *S. plumieri*, the invasive *S. taccada* has shown to flourish do to many physiological advantages for dispersal and disrupt the natural growth of *S. plumieri* when both species are co-occurring (Finkle and Elliott 2011).

The objective of this project begins with trying to understand the genetic differences between *S. plumieri* and *S. taccada*, exploring why *S. taccada* is observed to be so much more successful on Culebra when co-occurring with *S. plumieri*. We are interested in looking at populations within the same species to understand if there are populations with unique genotypes as well as looking at both *S. plumieri* and *S. taccada* to compare their genetic diversities. We have developed several genetic based questions about each of the species including wanting to assess whether the populations are in Hardy-Weinberg Equilibrium based on comparing the observed heterozygosity to the evaluated vales for expected heterozygosity. We study these experimental questions with populations of *Scaevola* on several different Culebra beaches looking at some locations where only one species is growing and other locations where the two species are co-occurring. The native species, *S. plumieri* would be expected to have a greater amount of genetic diversity than the invading species based on the fact that *S. taccada* has gone through a population bottleneck. Specifically, *S. taccada* has founded new populations on

Culebra rather than being already well established on the island like *S. plumieri*. Based on personal observation, *S. taccada* seems to be more successful and in most cases, is overtaking the native *Scaevola* species on Culebra. From these unexpected observations, we developed a hypothesis questioning if the *S. taccada* has a greater genetic diversity due to the populations originating from several individuals coming from different locations and introducing many different genotypes into the separate populations founded on Culebra.

The comparisons of genetic diversity among plant populations were constructed using data from microsatellite markers, short tandem repeats of DNA sequence that vary in length among individuals. Samples from both *S. plumieri* and *S. taccada* populations were collected from the island of Culebra during January of 2015 and March of 2017. The genomic DNA from each individual was extracted upon return to the lab. Using fluorescently labeled primers, microsatellite markers in the genome were amplified and analyzed using DNA fragment analysis. The data from the amplified fragments was analyzed using a program called Geneious (“Geneious 9” <http://www.geneious.com>, Kearse et al., 2012). Peaks representing the fragment size of each microsatellite allele were identified and recorded for each individual. This data was then evaluated using AMOVA through the program Arlequin which implements a series of tests to determine heterozygosity and grouped the population by haplotype to compare variability between plant populations (“Arlequin 3.5” Excoffier and Lischer, 2010). Based on preliminary data from populations on Culebra, P.R., the invasive *S. taccada* populations seems to have higher genetic diversity, meaning they have more unique genotypes present, than when compared to the *S. plumieri*. The data also currently shows that heterozygotes are only present in the *S. taccada* populations. These findings relate to our hypothesis showing that *S. taccada* seems to have a more advantageous genetic diversity which may play a large role in its ability to overtake *S. plumieri*.

populations. We plan to further analyze the *Scaevola* populations by including more populations from Culebra, P.R. in following studies to create a more complete analysis of the genetic diversity of the different species.

## Works Cited

Excoffier, L. and H.E. L. Lischer (2010). Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources*. 10: 564-567.

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