

Genetic Variation of *Spartina alterniflora* Loisel. in the New York Metropolitan Area and Its Relevance for Marsh Restoration

Ari Novy^{1,2}, Peter E. Smouse³, Jean Marie Hartman², Lena Struwe^{1,3}, Josh Honig¹, Chris Miller⁴, Melissa Alvarez⁵ and Stacy Bonos¹

¹Department of Plant Biology and Pathology, ²Department of Landscape Architecture, ³Department of Ecology, Evolution & Natural Resources

Rutgers University, New Brunswick, New Jersey
⁴USDA-NRCS Plant Materials Center, Cape May, New Jersey
⁵U.S. Army Corps of Engineers, New York District, New York City
 *arinovy@rci.rutgers.edu



ABSTRACT

We determined the genetic population structure of *Spartina alterniflora* in Jamaica Bay, Queens, NY and the surrounding area by microsatellite genotyping in order to assist the ongoing restoration of Jamaica Bay by the U.S. Army Corps of Engineers. AMOVA analysis indicated that population differences accounted for only 15% of molecular variance ($\Phi_{PT} = 0.15$, $p = 0.001$). Observed heterozygosity (H_o) ranged from 0.62 to 0.73 from locus to locus. A Mantel test indicated a weak and non-significant correlation between Nei genetic distance and geographic distance matrices ($r = 0.34$, $p = 0.12$). A PCA revealed no obvious grouping pattern for the sampled populations. Based on these data, we determined that the studied populations contained similar genetic variability to other populations in the New York vicinity and to those of the entire region. It seems likely that collection of germplasm from within the general region will provide sufficient variation to maintain overall genetic variation in restoration plantings. Given the small amount of genetic structure among populations within Jamaica Bay, however, it would be prudent to collect widely within the target marsh. We also recommend the practice of propagating plugs of *S. alterniflora* from wild seed, as opposed to vegetative propagation, when creating planting stock, in order to maximize genetic diversity in restored marshes.

MATERIALS AND METHODS

We obtained vegetative samples from marshes in NY, NJ, CT and RI (Figure 1), encompassing the range of *S. alterniflora* that is expected to provide propagules for restoration in the NY City area. This includes four of the marsh islands within Jamaica Bay itself. Samples were collected from marshes in Narragansett, RI ($N = 6$), Barn Island, Stonington, CT ($N = 6$), Joco Island, Jamaica Bay, NY ($N = 10$), Big Egg Island, Jamaica Bay, NY ($N = 9$), Elders Point, Jamaica Bay, NY ($N = 9$), Floyd Bennett Field, Jamaica Bay, NY ($N = 5$), Cheesequake Sate Park, Mattawan, NJ ($N = 9$), and Cattus Island Park, Toms River, NJ ($N = 6$). We collected samples a minimum of 5 meters apart and across the longest transect of each marsh whenever possible. We transported all samples to Rutgers University (New Brunswick, NJ) for DNA extraction from fresh leaf tissue.

We scored microsatellite loci for 56 sampled individuals from the 8 populations. We then analyzed the resulting allelic data in Genalex ver. 6 to generate measures of heterozygosity. We also conducted an Analysis of Molecular Variance (AMOVA) to quantify population structure (Φ_{PT}), where Φ_{PT} is a measure of population differentiation. We generated a geographic distance matrix for the sampled populations and then compared it with the pairwise Φ_{PT} matrix using a Mantel Test. Significant similarity between a pairwise Φ_{PT} matrix and geographic distance matrix is seen as evidence of isolation by distance, or limitation of gene flow by geographic separation. Finally, we conducted a Principal Coordinates Analysis (PCA) in SAS version 9.1 to determine whether observed patterns in the molecular data support the partitioning of the samples into specific groupings.

RESULTS

Location	N	H_o	H_e	n_e^*
Narragansett	5	0.61	0.53	3.03
Barn Island	6	0.73	0.65	5.01
Joco Island†	10	0.67	0.70	6.63
Elders Point†	9	0.72	0.75	6.21
Big Egg†	9	0.67	0.62	3.47
Floyd Bennett Field†	5	0.64	0.75	6.78
Cheesequake	8	0.67	0.68	4.71
Cattus Island	3	0.62	0.46	2.06

Table 1: Genetic diversity measures for *Spartina alterniflora*; N - sample size; H_o - observed heterozygosity; H_e - expected heterozygosity; n_e^* - bias corrected effective number of alleles; † indicates populations from Jamaica Bay, Queens, NY

RESULTS

The 11 microsatellite primer pairs yielded a total of 139 alleles and amplified between 7 and 27 alleles per locus, with an average of 12.6 alleles per locus. Observed heterozygosity (H_o) ranged from 0.62 to 0.73, expected heterozygosity (H_e) from 0.46 to 0.75, and the effective number of alleles (n_e^*) ranged from 2.06 to 6.63 (Table 1). The AMOVA indicated that the majority (85%) of molecular variance was found within populations. We also performed a hierarchical AMOVA, in which we defined three regions: populations north of, within and south of Jamaica Bay. We found no inter-regional variance, indicating that the molecular variance characterizes population differences, but shows no regional grouping within our study area. The Mantel test indicated no credible correlation between the Φ_{PT} matrix and geographic distance matrix ($r = 0.34$, $p = 0.12$), again suggesting that populations showed no compelling geographic structure that might be compatible with isolation by distance. Spatial separation of *S. alterniflora* populations along a coastal continuum does not appear to be the dominating factor in determining microsatellite genetic structure over the limited latitudinal range of this study. The PCA (Figure 2) also revealed no obvious grouping pattern for the sampled populations.

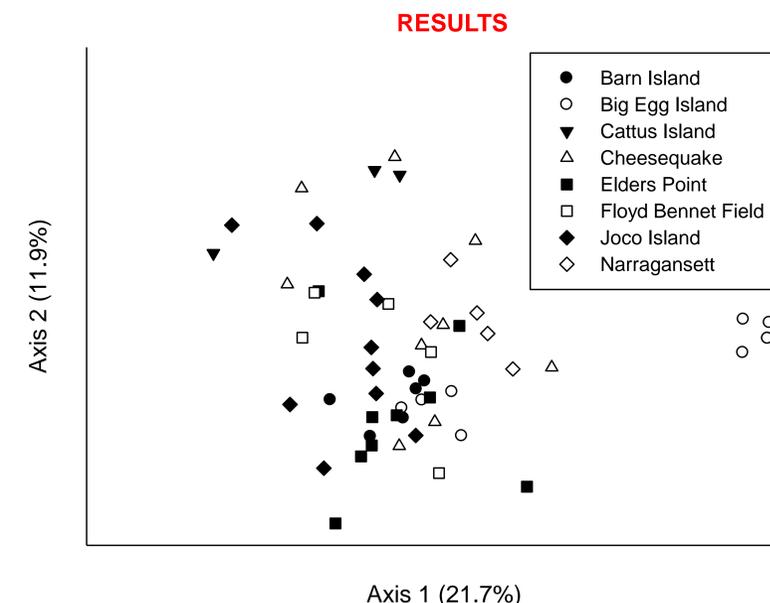


Fig. 2 Principal Coordinate Analysis (PCA) results of molecular data set utilizing 11 microsatellite loci. Values in parentheses on axis labels indicate the percentage of the total variance

DISCUSSION

This study was conducted to answer the question: How should one define 'local' propagules in marsh restoration efforts? If the goal of marsh restoration includes maintenance of the genetic structure of the pre-existing landscape, it is preferable to obtain genetically diverse propagules locally. The decision to maintain genetic structure is generally motivated by a concern for local adaptation, balanced by the need to allow for normal levels of gene flow, while avoiding maladapted genotypes. The term 'local' only makes sense in relationship to some larger spatial delineation. The most comprehensive delineation of *S. alterniflora* molecular genetic structure to date utilized Bayesian and AMOVA analysis of microsatellite variation and chloroplast haplotyping to subdivide the species into several broad regions: New England, North Mid-Atlantic, South Mid-Atlantic, South Atlantic and Gulf Coast, though precise boundaries between regions were not explicitly defined. The North Mid-Atlantic region includes Jamaica Bay, Queens, NY. While the significant Φ_{PT} value of 0.15 indicates some level of divergence among marshes, the Mantel and PCA analyses showed that there was no clear pattern to that divergence that would suggest any specific boundaries between marsh populations. Because Jamaica Bay marshes contain comparable genetic diversity, because Φ_{PT} is significant, and because wild collection of *S. alterniflora* has been mandated for the Jamaica Bay restoration, it would be prudent to sample widely from within Jamaica Bay to obtain propagules for the restoration.

CONCLUSIONS

Propagules of *S. alterniflora* can be defined as 'local', and should preserve the genetic integrity of the pre-existing landscape, as long as they originate from within the same region as the target marsh, but are no further than 300 Km from the target marsh (Travis in press), and contain ample genetic diversity. In the absence of a direct assessment of local adaptation for each restoration site and source, this strategy will maximize the chance that a restored marsh will play its intended ecological role.

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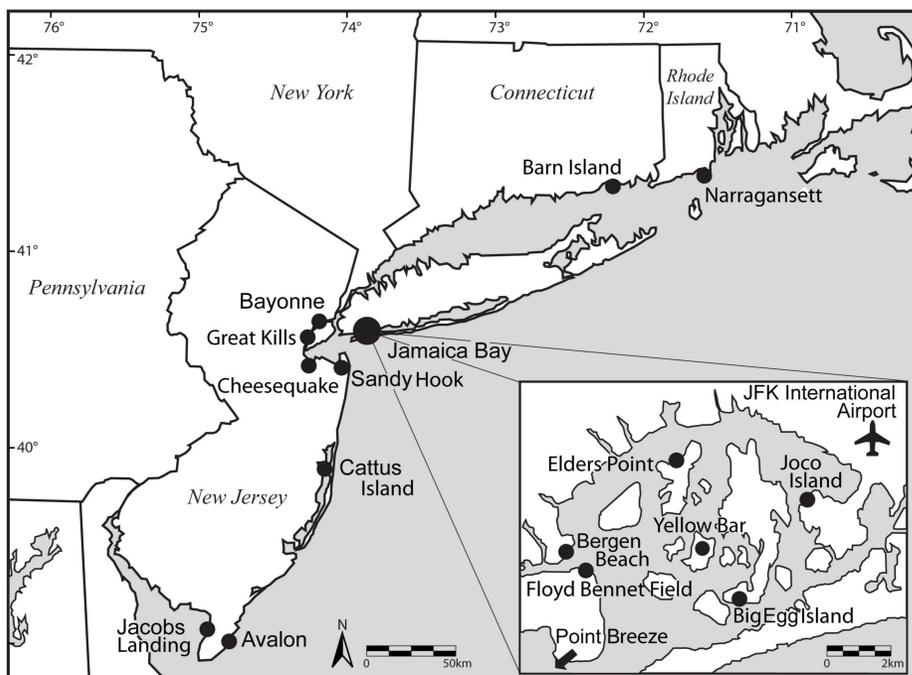


Figure 1: Sampling range and locations of *S. alterniflora* populations