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

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. 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.

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