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Genetic Structure of Threatened Native Populations and Propagules Used for Restoration in a Clonal Species, American Beachgrass (*Ammophila breviligulata* Fern.)

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Abstract

An important goal of native plant restorations was to reconstitute populations that are genetically similar to native ones, thereby increasing the probably of successful establishment and persistence. We examined the extent to which this goal has been accomplished in Great Lakes restorations of *Ammophila breviligulata* Fern., a beachgrass species that is widely used for habitat restoration and is considered threatened in the study areas. In parallel studies on Lake Michigan and Lake Superior, we used polymorphic Intersimple Sequence Repeat markers to assess genetic similarity between well-established and new native populations, restored populations, and restoration propagules obtained from two commercial suppliers. Native populations were generally more diverse than expected for a clonal species, whereas the commercially cultivated releases were monotypic. One of the commercial releases used in Minnesota was exclusively found in restored populations and did not occur in any other native population at this site. The propagules used in the newly planted restoration in Illinois were derived from a release that commercial suppliers maintain was derived from a native Michigan population, as opposed to a selected release. Diversity in this restoration was equivalent to that native Illinois' populations; however, many of the genotypes were not of local origin. Overall, study underscores the importance of obtaining baseline genetic surveys of remnant native populations and restoration propagules before restoration efforts are initiated, especially when the populations are threatened or endangered.

Key words: American beachgrass (*Ammophila breviligulata* Fern.), clonal plants, ISSR, molecular diversity, population genetic structure, restoration genetics.

Introduction

Native plant restorations have become an essential component of conservation biology as we strive to reconstruct habitats that have been degraded by human activity (Dobson et al. 1997). An important aim of any restoration was to create a sustainable population. The probability of success may increase if restored populations harbor fitness enhancing variability (Menges 1990; Gemmill et al. 1998; Batista et al. 2001). A paradox of restoration genetics is that although too little genetic variation may result in inbreeding depression (Barrett & Kohn 1991), interbreeding of genetically diverged populations can lead to outbreeding depression (Lynch 1991; Waser & Price 1994; Fenster & Galloway 2000; Luijten et al. 2002). Both scenarios can lead to a reduction in plant vigor and survivorship and may threaten the long-term population sustainability (Barrett & Kohn 1991; Fenster & Dudash 1994). An understanding of the genetic structure of natural populations and restoration propagules is important if we intend to recreate viable populations through our restoration efforts (Fenster & Dudash 1994; Montalvo et al. 1997; Batista et al. 2001).

For these reasons, there is mounting concern over the source of restoration plantings both in terms of genetic diversity and the extent of genetically divergence from local populations (Hufford & Mazer 2003). Restoration propagules may lack genetic diversity because of limited sampling of the original source population or because propagation techniques result in a disproportionate representation of a few genotypes (Robichaux et al. 1997; Williams 2001). Several studies have shown that restored populations harbor less genetic variation than natural populations (Williams & Davis 1996; Helenurm & Parsons 1997; Williams & Orth 1998; Williams 2001) and this can negatively impact population growth (Williams 2001). Introduction of restoration materials that are genetically distinct from native populations may also be problematic, as plants may fail to establish if they are maladapted to

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