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Capturing Genetic Variation during Ecological Restorations: An Example from Kankakee Sands in Indiana

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Abstract

Genetic variation in populations, both natural and restored, is usually considered crucial for response to short-term environmental stresses and for long-term evolutionary change. To have the best chance of successful long-term survival, restored populations should reflect the extant variation found in remnants, but restored sites may suffer from genetic bottlenecks as a result of founder effects. Kankakee Sands is a large-scale restoration being conducted by The Nature Conservancy (TNC) in northwestern Indiana. Our goal was to test for loss of genetic variation in restored plant populations by comparing them with TNC's seed source nursery and with local remnant populations that were the source of nursery seed and of the first few restored sites. Allozyme analysis of *Baptisia leucantha*, *Asclepias incarnata*, *Coreopsis tripteris*, and *Zizia aurea* showed low levels of allozyme diversity within

all species and reductions in polymorphism, alleles per locus, and expected heterozygosity between remnants and restorations for all species except *A. incarnata*. Almost all lost alleles were rare; restored populations contained almost 90% of alleles at polymorphic loci that occurred in remnants at frequencies greater than 1%. Allele frequencies for most loci did not differ between remnants and restored sites. Most species showed significant allele frequency differentiation among remnant populations and among restored sites. Our results indicate that seed collection techniques used at Kankakee Sands captured the great majority of allozyme variation present in seed source remnant populations.

Key words: allozyme, ecological restoration, genetic variation, prairie.

Introduction

The goal of ecological restoration is to reestablish historical ecosystem function in degraded or disturbed sites (Society for Ecological Restoration International Science & Policy Working Group 2004). Fundamental to this effort is the recreation of plant communities with the attributes of historical vegetation comprised of resilient, self-sustaining populations. Care is usually taken to include only species known to have been present prior to disturbance (Millar & Libby 1989) and to reestablish historical patterns of hydrology and other ecosystem processes (Society for Ecological Restoration International Science & Policy Working Group 2004). Less attention has been paid to genetics of plant populations in restorations, beyond the now widely appreciated notion that locally collected seed stock may contain locally adapted genotypes (variously referred to as ecotype collection, ecosourcing, or provenance-based sourcing) (Millar & Libby 1989; Handel et al. 1994; Montalvo et al. 1997;

Hufford & Mazer 2003; Gustafson et al. 2004b). Not much is known about how well patterns of genetic variation in restorations reflect patterns in natural seed source populations (Montalvo et al. 1997; Gustafson et al. 2004a). Genetic variation is hypothesized to be needed for long-term evolutionary change and short-term environmental adaptation (Ellstrand & Elam 1993; Guerrant & Pavlik 1997; McKay et al. 2005) and, thus, has the potential to influence restoration success (Huenneke 1991; Fenster & Dudash 1994; Knapp & Dyer 1998). Plant genetic diversity can also further the goals of ecological restoration by enhancing arthropod diversity and increasing annual net primary productivity (Crutsinger et al. 2006).

The Nature Conservancy (TNC) is undertaking a large-scale ecological restoration in northwestern Indiana (Fig. 1). Populations of prairie plants are the foundation of this restoration. Due to habitat conversion, prairie vegetation in the state is estimated to have been reduced from more than 2 million acres in pre-settlement times to fewer than 1,000 acres at present (Bacone 1997). The remaining habitat patches are small, fragmented, and isolated. The Efrogmson Restoration at Kankakee Sands is a 20,000-acre project to return marginal farmland to a historical matrix of wetlands, sand prairie, and *Quercus velutina* (Black oak) savannah, also linking several high-quality remnant natural areas. The goal, largely focused on wildlife

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