

Ecological Genetics at the USGS National Wetlands Research Center

The Ecological Genetics Program at the USGS National Wetlands Research Center (NWRC) employs state-of-the-art DNA fingerprinting technologies in characterizing critical management aspects of the population biology of species of concern (fig. 1). The overarching themes of this program have been (1) the critical role that genetic diversity plays in maintaining population viability and (2) how management strategies might incorporate genetic information in preventing the decline of desirable species or in controlling the spread of invasive species.

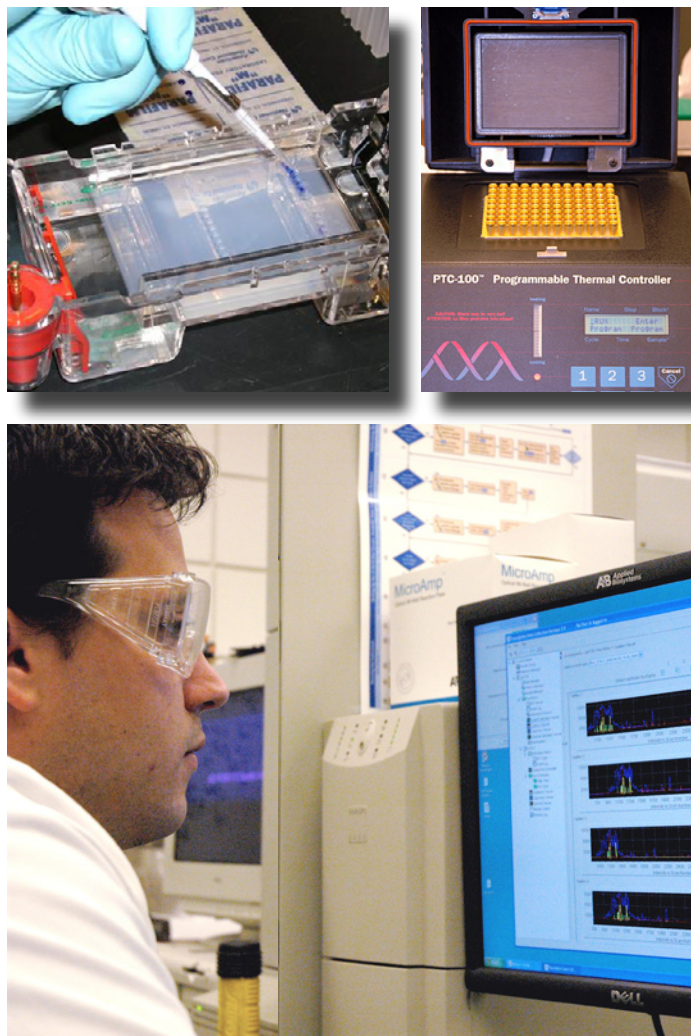


Fig. 1. Clockwise from top left: DNA quantification using Agarose gel electrophoresis; programmable thermal controllers for amplifying DNA via the polymerase chain reaction; researcher analyzing microsatellite data on an automated DNA sequencer.

Supporting Recovery of Threatened and Endangered Species

The importance of properly delineating population units for species conservation is now universally recognized; therefore, much of the genetics research at NWRC focuses on assessments of genetic population structure. For example, NWRC scientists have taken a leading role in investigating two endangered plants that are threatened by habitat fragmentation in the Lower Rio Grande Valley of Texas, star cactus (*Astrophytum asterias*) and Zapata bladderpod (*Lesquerella thamnophila*). The goals in this study are to augment U.S. Fish and Wildlife Service recovery plans through an understanding of current levels of gene flow and to determine how gene flow will affect the success of transplantation and/or controlled breeding efforts.

Work in Arizona has highlighted key differences in hybridization histories among four extant populations of the endangered Arizona cliffrose (*Purshia subintegra*) (fig. 2). Whereas two of these populations were shown to represent the species as it was originally described, a third population was identified as a genetically distinct species, and a fourth population was shown to exhibit evidence of recent hybridization with a common congener. Previously, the genetic status of these populations could only be guessed through traditional morphological measurements, but this new and more accurate information is now available to resource managers for the development of more appropriate management strategies.



Fig. 2. Left: Wild growing Arizona cliffrose (*Purshia subintegra*). Right: An experiment to determine the reliability of morphology as an indicator of hybrid status, conducted at The Arboretum at Flagstaff in Arizona (photographs by Joyce Maschinski).

Plant Restoration Genetics

NWRC scientists have also been applying the principles of conservation biology to wetland restoration projects throughout the northern Gulf of Mexico. Here, the focus is on plant species that form the dominant, or keystone, component of their respective communities.

Smooth cordgrass (*Spartina alterniflora*), for example, is used extensively in the restoration of low-elevation salt marshes throughout southern Louisiana. Studies have highlighted the comparative advantages of allowing passive colonization versus pursuing an active planting program at restoration sites created from dredged sediments. Because smooth cordgrass is capable of rapid clonal spread via underground rhizomes (fig. 3), research has shown that a critical aspect of any restoration strategy is the degree to which it promotes clonal diversity. Low clonal diversity not only reduces the ability of restored populations to respond adaptively to environmental disturbances, but it also reduces their capacity to replace themselves through sexual reproduction (fig. 4), thereby compromising their long-term viability.



Fig. 3. Smooth cordgrass (*Spartina alterniflora*) clones growing on a created site in the Sabine National Wildlife Refuge, La.

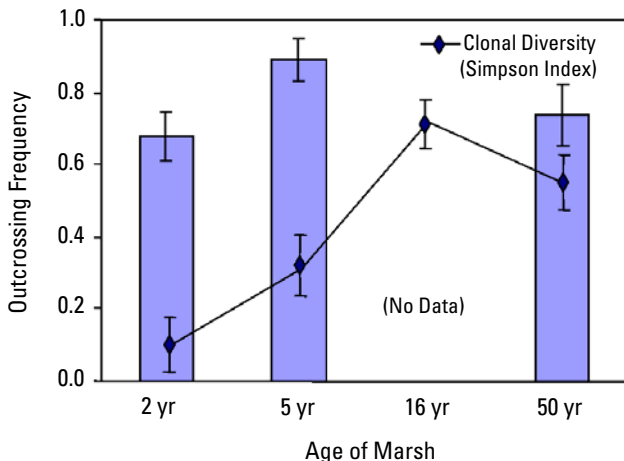


Fig. 4. Outcrossing, or the sexual reproduction of one clone with another, directly tracks clonal diversity as restored smooth cordgrass populations age.

Along the coast of Texas, NWRC researchers have been contributing to shoalgrass (*Halodule wrightii*) restoration efforts by helping evaluate the effectiveness of restoring populations from the combined donor materials of several spatially separated seagrass meadows. These studies have shown that both genetic diversity and recruitment potential are enhanced by such a strategy. In fact, a large population of spontaneous “volunteers” was genetically traced to a restored population growing less than a kilometer away, just 2 years after the restored population was established.

The red mangrove (*Rhizophora mangle*) is a dominant intertidal species found throughout the estuaries of southern Florida, which provide critical ecosystem services to the growing human population of the region. NWRC scientists have been studying the direct genetic impacts of environmental contaminants on red mangrove populations by assessing genetic mutation rates (fig. 5). The impacts of these mutations on population viability are the subject of extensive experiments being conducted in Tampa Bay, where seedlings from populations with highly variable pollution histories have been planted in a “common garden” to assess differences in their rates of growth and survival over time.

Understanding the Causes of Invasiveness

The importance of properly delineating population structure also extends to the control of invasive species, where an improved understanding of the genetic mechanisms behind invasiveness may be the key to devising adequate control measures. The use of genetics tools may also aid in the identification of exotic genotypes of a species into native populations of the same species.

NWRC scientists are working in cooperation with National Park Service personnel in the Western Great Lakes Region to document the incidence of cattail (*Typha* spp.) hybridization, which may have played a key role in the emergence of cattail as an invasive species over the past 20 years (fig. 6). Hybridization between native broad-leaved cattail (*T. latifolia*) and a European cattail species (*T. angustifolia*) introduced to North America nearly two centuries ago is thought to be contributing to invasiveness through the broadening of ecological niches and hybrid vigor. The hybrid status of individual cattails is being correlated, through multivariate analyses, with suites of morphological characters that will provide resource managers with a tool for identifying hybrids in the field and undertaking their removal where appropriate.

Purple loosestrife (*Lythrum salicaria*) is an invasive exotic introduced throughout the United States by the horticultural trade. The native range of this species extends from Scandinavia to the Middle East, and NWRC scientists are exploring the possibility that multiple introductions have contributed to invasiveness in much the same way as interspecific hybridization has resulted in invasiveness in cattails, that is, through a form of hybrid vigor. The inadvertent cross-breeding of plants from widely separated



Fig. 5 Top: Red mangroves (*Rhizophora mangle*) in Key West National Wildlife Refuge, Fla.; Bottom: A chlorophyll-deficient mutant (yellow) seedling and a normal (green) mangrove seedling.

Old World populations would clearly result in the mixing of gene pools adapted to very different suites of environmental conditions, potentially leading to the same sort of niche expansion as seen in cattails.

Finally, NWRC geneticists have been working to determine the incidence of a morphologically cryptic European genotype of the common reed, *Phragmites australis*, recently introduced to the Atlantic and Gulf of Mexico Coasts of North America where it has begun to behave as an invasive. This work has experimentally documented the competitive superiority of European *Phragmites* relative to native *Phragmites* of the gulf coast region and suggests that naturally low levels of clonal diversity may make gulf coast populations particularly vulnerable to invasion.

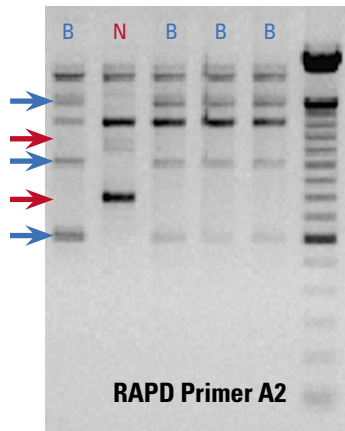


Fig. 6 Top: Flowering morphology of hybrid cattails (*Typha* spp.)
Left: DNA fingerprints, constructed from randomly amplified DNA polymorphisms (RAPDs), differentiating broad-leaved cattails (B) from narrow-leaved cattails (N).

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