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From Forest Nursery Notes, Winter 2008

© 73. **Limited reintroduction does not always lead to rapid loss of genetic diversity: an example from the American chestnut (*Castanea dentata*; Fagaceae).** Pierson, S. A. M., Keiffer, C. H., McCarthy, B. C., and Rogstad, S. H. *Restoration Ecology* 15(3):420-429. 2007.

Limited Reintroduction Does Not Always Lead to Rapid Loss of Genetic Diversity: An Example from the American Chestnut (*Castanea dentata*; Fagaceae)

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Abstract

In restoring species, reasons for introducing limited numbers of individuals at different locations include costs of introduction and maintenance, limited founder supply, and risk “bet hedging.” However, populations initiated from few founders may experience increased genetic drift, inbreeding, and diversity loss. We examined the genetic diversity of an isolated stand of more than 5,000 American chestnut trees relative to that of the 9 surviving stand founders (out of 10 total) planted in the 1880s. We used minisatellite DNA probes to reveal 84 genetic markers (circa 24 loci) among the nine founders, and their genetic diversity was compared with three separate plots of descendant trees, as well as with two natural stands. The descendants were circa 7.3% more heterozygous than the founders (mean estimated $H = 0.556$ vs. 0.518 , respectively; $p < 0.0001$). Genetic differentiation was not pronounced ($F_{ST} < 0.031$), and no markers, including those at

low frequency among the founders, were lost in the descendants. The founders and natural transects were not significantly different in H or similarity (mean proportion of bands shared). Special planting or mating protocols for establishment of a vigorous American chestnut population from a low number of founders may not be required to avoid strong effects of genetic drift and inbreeding. These results demonstrate that loss of genetic diversity following reintroduction of a limited number of founders is not always inevitable, such as this case where the species is highly outcrossing, expression of heterozygous advantage may occur, the original founders remain as gene contributors over generations, and the establishing population expands constantly and rapidly.

Key words: conservation genetics, endangered species, founder effects, population bottlenecks, population genetics, species restoration.

Introduction

Conservation of declining species often involves attempts to restore them back to habitats where they were formerly present. This is usually a costly and labor-intensive process. Generating or harvesting individuals to be reintroduced, specialized reintroduction protocols, maintenance and protection during establishment, and the need to reintroduce a species over a large range of habitats can all contribute to the costs required to protect a threatened species. Although normally it is advised to reintroduce large numbers of founders (e.g., Frankham et al. 2002), due to the above constraints this is not always possible, and frequently, only a very limited number of individuals are used in restoration projects.

Populations initiated from a low number of founders often have reduced genetic variation due to founder effects (Frankham et al. 2002). Post-founder reduction of

genetic diversity also often occurs due to the combined effects of random genetic drift and inbreeding, both of which intensify in populations that are, and remain, small in size (population bottleneck effects). Moreover, the frequency of homozygosity of rare, deleterious recessive alleles can increase by inbreeding in small populations, promoting inbreeding depression (reduced population fitness; e.g., Thornhill 1993). Loss of alleles and reduced heterozygosity may negatively affect the future evolutionary potential of bottlenecked populations (Burger & Lynch 1995; Robichaux et al. 1997). We investigated whether aspects of genetic diversity have changed in a stand of American chestnut (*Castanea dentata* [Marsh.] Borkh.; Fagaceae) since its establishment with a low number of founders.

The American chestnut was one of the most important, and often the local dominant, hardwood species in eastern forest ecosystems, ranging from Maine to western Tennessee and Mississippi (Gravatt 1949; Anagnostakis 1982). In the early 1890s, the Chestnut blight fungus (*Cryphonectria parasitica* (Murr.) Barr; formerly *Endothia parasitica* [Murr.] And. & And.) was introduced to North America from Japan, being first documented in New York (Merkel 1906). By 1910, the blight had invaded 10 states and later progressed rapidly throughout its range (McKay & Jaynes

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