ESTABLISHING RESTORATION SEED RESERVES IN NATIONAL FOREST SYSTEM SEED ORCHARDS

Craig S. Echt,[1] Barbara S. Crane, and C. Dana Nelson

[1]Southern Institute of Forest Genetics, Southern Research Station, USDA Forest
Service, Saucier, MS

The role of the nine National Forest System seed orchards in the Southern Region is to support reforestation and restoration programs on the region's national forests. Traditionally, the emphasis of the seed orchards has been with commercially important tree species. Recently, emphasis is shifting to gene conservation aspects of restoration of ecologically important imperilled tree species. The main threats facing these species are shrinking ranges and declining populations that result, in part, from global climate change. Many factors influence the ability of forest species to adapt to changing conditions, but our focus is on the genetic factors affecting adaptive traits. The challenge is to ensure that imperilled species in national forests are managed to maximize their genetic adaptability to changing environments. So how can National Forest System seed orchards best support the response to this challenge?

Our basic concept is to establish seedling seed orchards that can produce seed with sufficient genetic diversity to impart to restored populations an ability to adapt to rapidly changing environments. When properly designed, the seed product from these "restoration seed reserves" (RSRs) should improve the resiliency of restored populations enough to avert extinction or extirpation of priority species in southern national forests. This model does not involve traditional genetic improvement, but rather involves enhancing adaptive potential of deployed germplasm. Although traditional tree improvement has long sought to maintain genetic diversity while improving marketable traits for a few commercial species, we are advising something different by developing a program for the genetic management of broader range species that have ecological value. Therefore, RSRs should rely not on artificial selection for specific traits or genotypes, but on managing gene flow among populations to increase their adaptive genetic diversity (Kramer and Havens 2009). A guiding principle in restoration plans that use seed from these RSRs will be to let natural selection do the heavy lifting and produce well-adapted tree populations. The supporting mission of RSRs, therefore, will be to supply "restoration ready", high quality, and genetically diverse seed for imperilled species management.

Twelve priority tree species and groups have been identified for RSR establishment: Atlantic white cedar, red spruce, Table Mountain pine, American chestnut, Carolina and Eastern hemlocks, seven threatened and endangered oaks, several ashes, butternut, longleaf pine, pitch pine, Fraser fir, September elm, yellow buckeye, and Ozark chinquapin (Crane 2011). These species were selected from a ranking of 140 southern species evaluated by the ForGRAS model for various risk factors associated with changing environments in the Southern Appalachian Mountains (Potter and Crane 2010).

We recommend harvesting at least 200 seed from each of 200 trees, *i.e.*, half-sib families, distributed across 20 to 40 separate populations. Mother trees should be spaced at least 100 m apart, as the collection area permits. The target of 200 trees is maintained regardless of the number of populations sampled. Therefore, collect seed from 10 to 5 mother trees from 20 to 40 populations, respectively. As reproductive isolation increases among populations, then sample more populations, with fewer trees each. Collections from immediately imperilled or rare species could be extended to as many as 50 populations. However, that many distinct populations may not be available for a species in decline. In such cases, we recommend collecting from all available populations. This sampling design will capture virtually all alleles across the extent of the sampled range (Lawrence et al. 1995; Gapare et al. 2008). While a more comprehensive collection target might include 250 to 300 mother trees, our prescribed number of 200 will suffice when resources are limited.

A general RSR design for a species is as follows: germinate enough seed to establish twelve seedlings for each family, plant the seedlings in 4 x 3-tree family block plots, then at maturity evaluate trees for seed production and rogue each plot to one tree. This plan requires no progeny testing or family selection. Individual tree selection criteria are limited to flowering synchrony and fecundity. Selection for disease and pest resistance should be incorporated into a traditional tree improvement program, if warranted for a species. The result is 200 seed production trees in an RSR. Allocation of family plots in the orchard is not randomized, but rather is optimized to manage gene flow (cross-pollination) among families and groups. One type of optimized RSR design could maximize genetic diversity in the seed product by maximizing pollen exchange among populations. An alternate design could preserve ecotype traits by promoting pollination among populations whose families are planted in proximity. Orchard design optimization software is available that can weight or penalize family allocation by factors such as seed zone, ecotype, population, or kinship. (Fernández and González-Martinez 2010). We recommend establishing a species' RSR under the same or similar climatic and soil conditions found at the intended restoration sites or at least within the same seed zone, if known. To ensure a continuous supply of seed, successional RSRs should be established from new seed collections in anticipation of an eventual decline of RSR productivity or imbalance of family representation.

The RSR concept is similar to the tree breeding strategy of multiple origin polycrossing proposed by Ledig and Kitzmiller (1992) as a means to increase population heterozygosity in gene conservation programs. Broadhurst et al. (2008) proposed a related concept for seed transfer, "composite provenancing", to enhance genetic diversity in restoration populations. While rare, such forms of genetic blending can result in outbreeding depression or loss of local adaptation for some species, however, southern trees typically are generalists and not highly locally adapted (Schmitdling 2001). We maintain that the conservation paradigm of local-seed-is-best is a precautionary approach appropriate only when there is an abundant seed supply for direct seed transfer and when local populations are genetically diverse enough to endure throughout current and predicted ranges. However, if local seed is available from only small, isolated, inbred populations, then there may not be sufficient genetic diversity available to sustain local populations or maintain the species in the face of climate change. In such cases, augmenting the species' genotypic diversity with a variety of alleles and crosses from different populations could provide the necessary adaptive potential for forest restoration and sustainability.

Various options can mitigate potential risk in RSRs and species restoration plans. The most obvious is to establish duplicate RSRs for each species to minimize the chance of catastrophic loss from fire, severe weather, or even land development. For some species, this may require establishing additional seed orchards or seed production areas on national forest ranger districts. A second RSR or seed production area could be established in a different climatic zone or different seed zone; although there is no clear evidence this would improve restoration success over the expected life of the RSR. Another option, if a precautionary approach is desired for some species, is to establish supplemental seed production plot(s) dedicated to “local seed” production. Using different seed production plots with different rates of gene flow among sampled populations is an adaptable strategy because seed from different production plots could be mixed in desired ratios for deployment. Spare seed collected from mother trees could be archived in cold storage, though seeds of some species quickly lose viability in storage.

In summary, RSRs allow managed gene flow among sampled populations that is tailored to the restoration needs of the target species. The key features are that RSRs: 1) avoid inbreeding by having no clones or siblings, 2) limit selection to essential seed production traits, 3) manage gene flow with an optimized planting design, and 4) can increase adaptive diversity of restoration populations beyond what is currently available from native seed supplies.

References Cited

Broadhurst LM, Lowe A, Coates DJ, Cunningham SA, Mcdonald M, Vesk PA, Yates C. 2008. Seed supply for broadscale restoration: maximizing evolutionary potential. Evolutionary Applications 1:587-597

Crane BS. 2011. “CC projects summary R8 Southern Region Genetic Resource Management Program” .docx file. ftp://ftp2.fs.fed.us/incoming/r6/ro/genetics/cc_wksp/R8/

Fernández J, González-Martinez SC. 2010. SOFSOG: a suite of programs to avoid inbreeding in plantation designs. Molecular Ecology Resources 10:393-396.

Gapare WJ, Yanchuk AD, Aitken SN. 2008. Optimal sampling strategies for capture of genetic diversity differ between core and peripheral populations of *Picea sitchensis*. Conservation Genetics 9:411-418.

Kramer AT, Havens K. 2009. Plant conservation genetics in a changing world. Trends in Plant Science 14: 599-607.

Lawrence MJ, Marshall DF, Davies P. 1995. Genetics of genetic conservation. I. Sample size when collecting germplasm. Euphytica 84: 89-99.

Ledig FT, Kitzmiller JH. 1992. Genetic strategies for reforestation in the face of global climate change. Forest Ecology and Management. 50: 153-169.

Potter K, Crane BS. 2010. Forest Tree Genetic Risk Assessment System: A tool for Conservation Decision-Making in Changing Times. http://www.forestthreats.org/current-projects/project-summaries/genetic-risk-assessment-system-description-120610.pdf

Schmidtling RC. 2001. Southern Pine Seed Sources. Gen. Tech. Rep. SRS-44. Asheville, NC: U.S. Department of Agriculture, Forest Service, Southern Research Station . 25 p.