Communicating the Role of Genetics in Management

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Abstract.—Three current issues serve as examples to convey the role of genetics in management. (1) Consequences of silvicultural systems on the genetic resource of tree species are limited to one generation of study and isozyme (qualitative) data. Results of simulated data for diameter (quantitative data) over several generations, illustrate the pitfalls of working towards balanced uneven-aged silvicultural systems in northern red oak, under natural regeneration constraints and existing management direction. (2) Comparisons of section boundaries within an ecological classification system and climatic zones (homoclines) as surrogates for managing genetic resources, are of limited utility in describing patterns of genetic variation for adaptive, growth, and disease resistance traits. (3) Reporting gains and seed yields from tree improvement programs in Forest Service decision documents is recommended as means of showing consequences of 'action vs. no action' for genetic resources, thereby placing genetics in a more active role in the Agency's next round of forest planning.

INTRODUCTION

An effective communication method for highlighting the role of genetics in ecosystem management is to relate genetic principles and tree improvement programs in the context of current events and issues driving land management practices. DeWald and Mahalovich (1997) and Mahalovich (1995) highlight the importance of improving forest health and conserving genetic diversity by the application of seed transfer guidelines and breeding for insect and disease resistance in tree improvement programs. This paper extends those considerations to (1) the consequences of managing species under natural regeneration constraints and uneven-aged silviculture, (2) the application of coarse-filters, e.g., ecological classification systems and homoclines in regulating seed movement and structuring tree improvement programs, and (3) infusing genetics in the Agency's next round of Forest Plan revisions.

Consequences of even- and uneven-aged silvicultural systems on genetic resources remains an open field of study. Research into the impacts of even-aged silvicultural systems has empirically shown little change in the genetic constitution of forest tree populations in one generation of shelterwood harvests in Douglas-fir (Neale 1985) or seed-tree harvests in Scots pine (Yazdani et al. 1985). The resiliency of the genetic structure has been presumed to be due to high within-stand and individual-tree heterozygosity (trees are relative new comers to domestication), maintenance of large effective population size after reduction in density of the parental population, and a high rate of outcrossing within shelterwoods (Neale 1985). These landmark studies however were based on isozyme data, which have shown no direct correlation among adaptive, growth, or insect and disease traits in forest tree populations (Mitton 1995, Savolainen and Kärkkäinen 1992).

CONSEQUENCES OF UNEVEN-AGED SILVICULTURE

Mahalovich (1993) designed a model (NATGEN) to overcome some of the limitations of previous even-aged studies in an attempt to address the longer term issues of uneven-aged silvicultural prescriptions, using a quantitatively inherited character. The first version of the northern red oak model allows the end user the opportunity to evaluate the consequences of various cutting levels on tree diameter for up to 10, 80-year rotations: (1) cutting from below, (2) cutting from above, and (3) a combination of cutting from above and below. Following harvest, the stand of 100 trees is naturally regenerated using the leave-trees as parents. The modeling scenario that focuses on diameter-limit cutting of trees 18 inches and above, results in the inability to achieve larger diameter trees after 5-7 rotations. Stated from a genetics perspective, once the heritability for diameter drops from 0.2 to below 0.1 and/or the desirable gene frequency drops from 0.5 to 0.01, the population of 100 trees is unable to recover without artificial regeneration, albeit genetically improved northern red oak.

The author was further challenged by Eastern Region silviculturists to evaluate mitigating factors, i.e., larger population size, variable cutting intervals, and advanced reproduction. For a population of 600 trees, cutting from above (18 inches or greater) results in fewer, larger diameter trees over time. This result is also mirrored by a decline in the genetic resource with the initial heritability for tree diameter falling below a value of 0.2 and desirable gene frequencies dropping below a value of 0.5. This model also shows that even if several 20-year cutting cycles are skipped, rotation ages are extended beyond 80 years, or advanced reproduction is chosen as the natural regeneration option, it is difficult to achieve 30-inch or greater, diameter trees in this population of 600 trees.

For the larger population size of 600, the concept of genetic diversity is evaluated by defining effective population size as the number of reproductively mature parents for both the seed tree and advanced reproduction, natural regeneration options. Effective population size described in this manner is over-simplified because it doesn't directly address the genetic constitution of parent trees, but is useful for end users with a limited background in genetics. When adequate numbers of parents are left for natural regeneration, further evaluation of their ability to meet the criteria for reproductive maturity (minimum of 10 inches in diameter and 80 years of age) can result in an effective population size of zero when diameter-limit cutting is practiced from above or when the target residual basal area drops below 80 square feet per acre.

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Table 1.—Hierarchical classification systems in ecosystem management: (a) ecologic and (b) genetic

(a) Ecological	Unit Size	(b) Genetic	Unit Size
Province	Multiple States	Genus	Varies by Species at All Levels
Section	1,000s of Square Miles	Species	
Subsection	10s to 100s of Square Miles	Race	
Landtype Association	100s to 1000s of Acres	Variety	
Ecological Land Type	10s to 100s of Acres	Provenance, Stand	
Ecological Land Type Phase	1s to 10s of Acres	Family	
Site	Up to about 1 Acre	Individual (Clone)	

Both versions of NATGEN begin to provide insights into the long-term consequences of practicing uneven-aged silviculture under natural regeneration constraints and pressures to meet high harvest levels. These preliminary results highlight the potential problems in managing the genetic resource of forest tree populations exposed to more than four generations of dysgenic selection practices. Modeling a population of northern red oak under these constraints limits the users ability to meet timber targets after six rotations and fails to meet desired future conditions for larger diameter trees, even for a species that readily lends itself to uneven-aged silvicultural prescriptions. Diameter-limit cutting and high-grading are expected to have negative consequences over the long-term for both pioneer and intermediate species managed under natural regeneration constraints.

LANDSCAPE ASSESSMENTS AND GENETIC RESOURCES

Land management practices have recently included stronger inter-agency collaboration and the development of landscape-level assessments for proposed, desired future conditions of federally-owned lands, e.g., the Interior Columbia Basin Ecosystem Management Project and the Southern Assessment. A primary planning and management product of these assessments is the development of ecological classification systems (ECS). Managing genetic resources using an ECS or other coarse filters for individual species, has a high potential for inappropriate management of genetic resources, if applied to seed transfer guidelines in reforestation programs or in the development of seed orchard and breeding populations. There are beneficial examples of using an ECS for managing threatened and endangered species when genetic data are lacking.

Ecological Classification System and Seed Transfer

An ecological classification system is hierarchical in nature as are patterns of genetic variation within individual species (Table 1). An ECS is based on soils, landform, climate, and potential natural vegetation. Only 10-20 percent of an ECS is based on biological factors. In contrast to these predominantly physical factors, forces that shape patterns of genetic variation over time are selection, drift, mutation, and migration. Very few species show patterns of genetic variation based on physical factors. Notable exceptions are patterns of variation based on soil type in Bishop pine (Millar 1989) and white spruce (Khalil 1985) and differences in wet and dry sites with Engelmann spruce (Mitton et al. 1989). Presently, there is no information supporting patterns of genetic variation based on habitat type in western Oregon (Campbell and Franklin 1981) nor in Inland Northwest conifers, as long as elevation is included in the models for adaptive characters (Rehfeldt 1974a, 1974b). This lack of a direct relationship between these two systems can be further illustrated in the following example from the Eastern Region, using an ECS as a substitute for established seed transfer guidelines.

Stand or provenance differences in conifer species are best described in magnitude by thousands of square miles. The scale that "best" fits that size of magnitude in an ECS is the section level. When seed zone boundaries (FSH 2409.26f) are superimposed over section boundaries in the Lake States, there are no meaningful linkages or similar geographic boundaries. As an example, there are parts of three sections (16, 22, and 13) encompassed by the most southern seed zone of breeding zone B in northern Wisconsin (Figure 1). There is no biological basis for further subdividing this seed zone into three additional sub-seed zones defined by section boundaries. The application of sections or smaller scales within an ECS artificially manages the patterns of genetic variation of tree species and unnecessarily limits the flexibility of available seed sources for reforestation. Ecologic and genetic classification systems are based on different factors and operate at different scales. An ECS regardless of scale, should not be used in guiding seed movement when genetic data are available.

The discussion thus far has focused on scale and geographic boundaries, i.e., two-dimensional concepts. Slightly different conditions exist in Inland West conifers. Patterns of genetic variation for adaptive traits are best described in three dimensions. These patterns of variability are summarized in seed transfer guidelines and breeding zones for tree improvement programs based on significant changes elevation, latitude, and longitude (Rehfeldt 1990). Attempting to apply a zonal, or two-dimensional approach to a three-dimensional system can be characterized as another example of artificially managing single species. Meaningful patterns of genetic variation are predominantly based on changes in elevation and to a lesser extent, geographic distance.

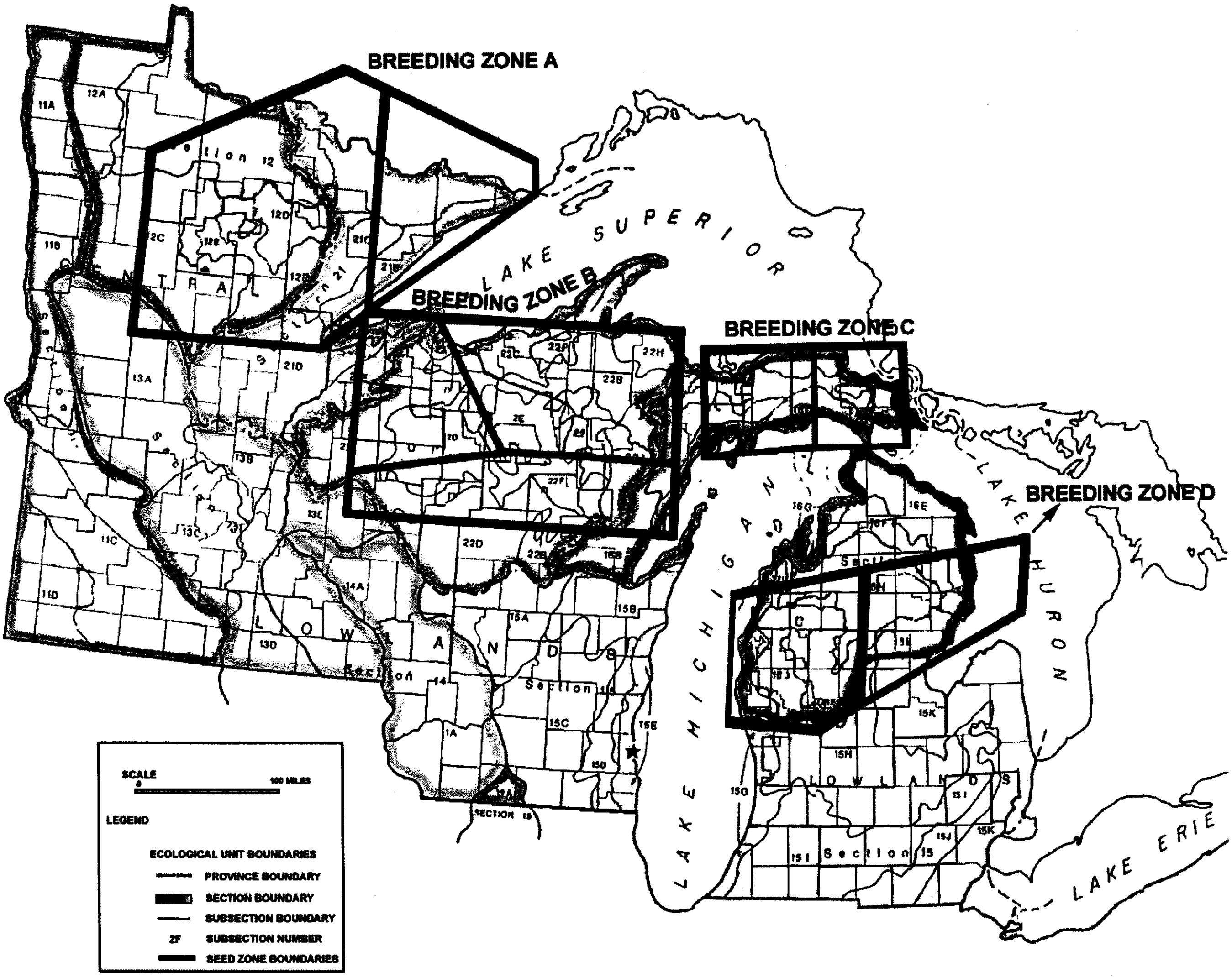

Figure 1.—Lake States breeding and seed zones superimposed on sections of the ecological classification system, USDA Forest Service Eastern Region.

Single-Factor Coarse Filters and Seed Transfer

Another proposed seed transfer method for individual species involves a coarse-filter approach using similar climatic zones, referred to as homoclines (Rauscher 1983). In this example, breeding and seed zones are again superimposed over homoclines in the Lake States (Figure 2). The use of climatic zones is too liberal of an approach to guide seed movement. For example, seed from homocline #14 in Michigan can be transferred to homocline #14 in Wisconsin.

An historic example of this type of liberal seed transfer involves jack pine seed putatively from Michigan, planted during the 1930s on the Chequamegon National Forest in Wisconsin. It was during this time that seed was in short supply and the development of seed transfer guidelines was still in its infancy. Beginning in the late 1980s, silviculturists began to note that jack pine around the Sunken Camp area began to prematurely exhibit signs of decline and over-maturation. Subsequent analysis of these populations relative to local seed sources pointed towards a problem of an off-site seed source[2]. It is likely that this problem could have been avoided by using locally adapted seed. Using climatic zones or homoclines as a surrogate for seed transfer is also, not recommended when genetic data are available.

Native Plants and Species Recovery Programs

Broad-scale assessments and coarse filters become more useful in genetic resource programs for species lacking genetic information for adaptive characters. These assessments and coarse filters have the potential to provide a first-cut at seed transfer guidelines in native plant programs. The goal however, should be to continue to work towards defining seed transfer guidelines based on genetic data for adaptive characters (Rehfeldt 1990).

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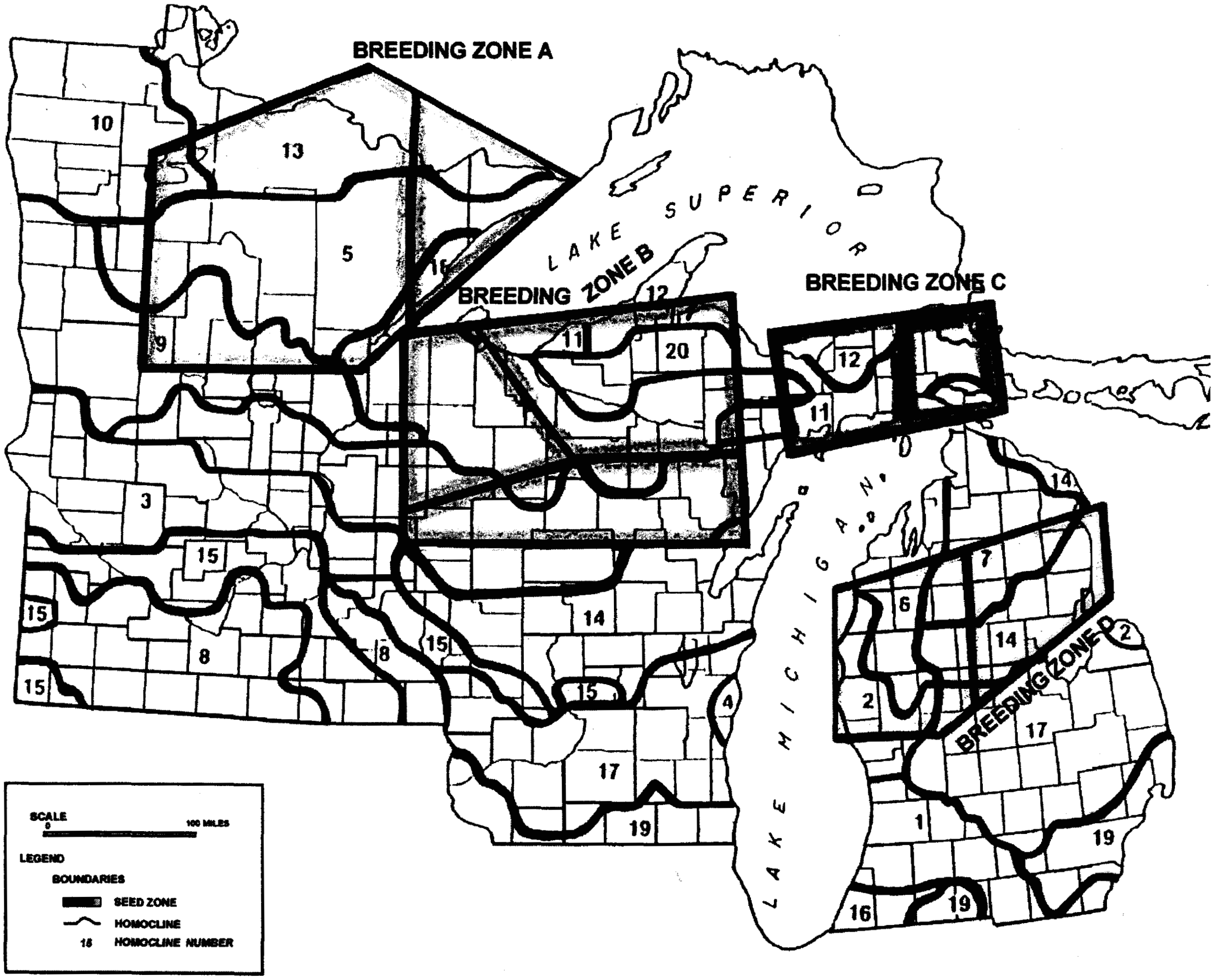

Figure 2.—Lake States breeding and seed zones superimposed on Lake States homoclines (Rauscher 1983), USDA Forest Service Eastern Region.

Characterization of habitat types for Kirkland's warbler in Michigan and Karner Blue butterfly in Minnesota has made the Lake States' ECS particularly useful in identifying unknown populations for census surveys of rare species. Perpetuation of rare species however, is determined as much by the system of genetic variability as it is by habitat availability (Rehfeldt 1990). Geographic distributions and population demographics are not adequate predictors of genetic structure; designed genetic experiments remain the most reliable means of understanding patterns of genetic variation (Rehfeldt 1997). Recovery programs are just beginning to go beyond a demographic approach (census number, breeding pairs, and life histories) to a population viability analysis (Murphy et al. 1990), incorporating patterns of genetic variation that infer an adaptive advantage with threatened, endangered and sensitive species.

Conservation of genetic diversity, restoration of target species, and improving forest health require land managers and geneticists to focus on important biological levels within the genetic hierarchical system, which infer insect and disease resistance and adaptation. Broad-scale assessments and coarse filters are not recommended for managing the genetic resource of individual species, except as a temporary measure until genetic data become available. The last topic of this paper presents a means of capturing these concepts in land management decisions as it relates to genetic resources.

FOREST PLAN REVISIONS

An appropriate landscape-level unit is necessary for guiding Forest Plan revisions. Recent discussions within the Forest Service have focused on a planning unit roughly the size of hundreds to thousands of acres. This scale corresponds to the landtype association level with an ecological classification system. From a perspective of managing genetic resources, there are concerns of applying this small

Table 2.—Role of genetic resources within a proposed Record of Decision

VI. THE DECISION

Some major aspects of the Decision are:
Timber Supply, Forest Health, Restoration...

Consequences of using improved vs. unimproved seedlings:

Western White Pine	
Woodsrun	Little or no blister rust resistance; unknown achievement in conservation goals; unreliable seed source.
Phase I	65 percent blister rust resistant; does not meet conservation goals due to limited genetic base; medium to high risk of losing single-gene resistance; reliable seed source.
Phase II	100 percent blister rust resistant; exceeds conservation goals; medium to low risk of losing resistance; reliable seed source.
Western Larch	
Woodsrun	No improvement in cold hardiness, *Meria* needle cast resistance or height-growth; unknown achievement in conservation goals; highly *unreliable* seed source.
Phase I and II	Gains of 15-20 percent increase in cold hardiness, 5-15 percent increase in *Meria* needle cast resistance, and 20-30 percent improvement in early height-growth; exceeds conservation goals; reliable seed source.

Citations can continue with other species, e.g, ponderosa pine, Douglas-fir, lodgepole pine, based on regional tree improvement program emphasis.

of a scale relative to the larger scales that best describe meaningful patterns of genetic variation for individual species. Land managers need to make an extra effort to consider the implications of scale and place this in the context of managing and conserving the genetic structure of forest tree populations.

For planning purposes, a possible solution to bridge the gap between large-scale assessments or vegetation task groups that design protocols for ecological pattern and process, is to develop GIS layers based on genetic data for priority species. These genetic layers can be used to identify coincident polygons to link to a TSMRS database or to the Satellite Imagery Landcover Classification system. For the Northern Region, this approach would require 32 layers to reflect the three-dimensional patterns of genetic variation for western white pine, western larch, ponderosa pine, Douglas-fir, and lodgepole pine. Such an approach would help to standardize protocols among a broader sample of program areas, without having to rely on genetics terminology.

Another issue in Forest Plan revisions is a long-term commitment to tree improvement programs to help meet objectives of sustainable ecosystems, improved forest health, and conservation of biodiversity. Genetic programs are becoming increasingly vulnerable to reduced budgets and pressures to meet reforestation and timber stand improvement targets. Additional pressures on genetic resource programs can also occur when silvicultural projects are considered for non-commercial tree species or for lands classified as unsuitable. These pressures diminish the capacity of genetic resource programs to play a vital role in ecosystem management.

Tree improvement also has the potential to play a more visible role in the forest planning process. Several sections in Environmental Impact Statements, Record of Decisions and Forest Plans can emphasize the consequences of proposed actions on genetic resources: 'Introduction and Goals', 'Vision for the Future', 'The Decision,' and 'Alternatives Considered' (USDA Forest Service, Clearwater National Forest Record of Decision and Forest Plan 1987). Possible examples for the Northern Region are summarized in a hypothetical Record of Decision in Table 2. This information can be further expanded upon in the text of individual Forest Plans.

The basic premise is to document the consequences of 'Action vs. No Action' in identifying gains in production seed orchards based on insect and disease resistance and cold hardiness, to meet forest health and conservation of genetic diversity objectives. Seed orchards provide a more reliable seed source of higher seed yields and seed quality over woodsrun collections. Seed orchards serve a primary role in restoring lands decimated by fire, insects and diseases, particularly when natural regeneration is insufficient or inappropriate. Internal and external customers need to be made aware that without the genetic material in progeny tests or seed orchards, federal lands become vulnerable when entire collection areas of locally adapted seed sources are lost to due insects, diseases, or catastrophic fire.

Gains from improved seed also increase productivity in commercial tree species. Harvest levels among the alternatives considered in land management planning can be further characterized by projected increases in productivity per acre from using genetically improved planting stock (Howe and Raettig 1985).

Important linkages between genetic resource programs and other program areas also need to be emphasized in the forest planning process. An example is the linkage among tree improvement, reforestation, integrated disease management, and timber stand improvement programs to work together to place rust resistant white pine back in Inland Northwest forests. It is implied that where there is a commitment to tree improvement, there is a commitment to reforestation programs among regions. These are simple measures to portray a more complete picture of how federally owned lands are managed in the context of ecosystem management, while employing cost-effective measures to prevent further erosion of genetic resources.

CONCLUSIONS

Benefits of tree improvement programs in managing ecosystems and improving forest health are sometimes lost in changing management paradigms and in the development of new technologies. Potential consequences of uneven-aged silvicultural prescriptions and the replacement of broad-scale assessments and single-factor filters in lieu of genetic data have serious consequences on managing the genetic resource of tree species. Tree improvement programs have an active role in developing and maintaining appropriate seed transfer guidelines, seed production areas and seed orchards (designed for improved forest health, cold hardiness, and productivity), as well as gene banks. A means of documenting these benefits internally and externally in the Agency's decision documents will more formally address the benefits derived from tree improvement programs.

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