To Breed or Not To Breed…That Is the Question for the Minnesota Red Pine Program

C. Pike and A. David
Department of Forest Resources, University of Minnesota

Abstract

Red pine is the most planted tree in Minnesota, but genetic gains are low due to limited genetic diversity within the species. Thus the ability for a tree improvement program to capture gains (estimated at 12 percent for tree volume) remains in question. Family ranks and heritabilities are compared between two fairly homogeneous and intensively managed seedling-seed orchards orchards, one located in northern Minnesota and the other in central Wisconsin. Analysis of variance reveals significant differences among families and reps but no significant family by site interaction. Tree ranks revealed eight families at each site that performed well and nine families that performed poorly at both sites. These results support the notion that select families in red pine outperform others on a range of sites, and gives further credence to a breeding program to capture and advance the genetic improvements in red pine.

Introduction

Genetic variation for most wind-pollinated conifers is relatively high, permitting moderate to high genetic gains in a tree improvement program. Red pine (*Pinus resinosa* Ait.), the official state tree of Minnesota, is the exception. Despite the lack of genetic variation, red pine was a logical candidate for a tree improvement program in Minnesota given the high degree of artificial regeneration that is practiced. Red pine stands are usually regenerated artificially, either as a single species or in combination with eastern white pine. The number of seedlings planted in Minnesota is difficult to calculate due to the diverse ownerships across the state, but are estimated at over one million red pine seedlings planted annually. Thus, in Minnesota alone, small increments of genetic gain can have a significant impact on productivity across the landscape.

The paucity of genetic variation in red pine has been confirmed from various field and laboratory trials. In spite of its homogeneity southerly sources were favored in provenance trials in all but the extreme northern sites planted (Wright et al. 1972). In addition, family differences have been observed (Guries and Ager 1980) but the species has not undergone extensive progeny testing. Genetic gains in red pine are estimated to be as high as 12 percent for volume (David et al. 2003), a figure that surpassed early expectations, but is in line with at least one other study (Guries and Ager 1980). Several studies recommend advanced generation breeding but offer no methodologies for capturing gain in a species where genetic gains can be elusive.

The objective of this study was to compare the performance of open-pollinated seedlings at three locations, calculate genetic gains, and to describe a program to produce advanced-generation orchards through tree breeding.

Methods

Two seedling-seed orchards are the focus of this investigation. One is located in central St Louis County (Minnesota) on land owned by the St Louis County land department, another in south central Wisconsin on land owned by Plum Creek Timber Company. The orchards were

established using open-pollinated seed collected from over 100 selected "mother" trees with 76 families common to both orchards. Both sites were planted with 24 randomized complete blocks of single-tree plots. Tree heights were measured with a Haglof® hypsometer to the nearest centimeter. Tree diameters were measured with a caliper to the nearest millimeter. At age 15, survival at the Minnesota site was 93 percent. The Wisconsin site was also measured at age 15 and posted 75 percent survival. Means for the orchards (all families) are shown in Table 1. Type III analysis of variance (Mixed models, SAS 2005) was used to compare significance at p<0.05 and for obtaining variance components on the 76 common families.

Results

Tree heights and diameters were generally larger in Minnesota than Wisconsin. The site in Minnesota was more homogenous than the site in Wisconsin (Table 1). ANOVA revealed highly significant differences (p<0.001) among families, sites, reps with no significant (p>0.05) family x site interaction (data not shown). The mean for the largest family at each site exceeded the site mean by 36 percent in Wisconsin and 10 percent in Minnesota (Table 2). Individual heritabilities (h^2i) were 0.195 and 0.338 in MN and Wisconsin respectively while family heritabilities (H^2f) were 0.552 and 0.689, respectively. Blocking and family variances each accounted for 5-13 percent of total variance. Genetic gains were estimated at approximately 12 percent (tree volume) at both sites in the rogued orchard, with 15 percent selection intensity (unpublished data).

Table 1. Means for tree height, diameter, volume and coefficient of variation at two seedling-seed orchards.

	Minnesota	**Wisconsin**
Height (m)	5.4	4.8
DBH (cm)	11.2	9.8
Volume (m^3)	0.03	0.02
Coeff. of Var.	26.3	46.4

A scatterplot of family ranks (Figure 1) revealed that family ranks were generally weakly correlated (r = 0.55) between sites. However, a group of well-correlated families representing the top 9 and lowest 8 families were clustered in each tail of the plot. The percent of site mean for tree height of each of these families is presented in Table 2.

Table 2. Percent of site mean (tree heights and volumes) for top 8 and lowest 9 ranked families.

| | | % of Site Mean | | | |
| | | Tree height | | Tree volume | |
	Family	WI site	MN site	WI site	MN site
Best	518	11.3	3.9	36.6	10.6
Families	106	3.7	-1.8	28.1	11.1
|	101	3.6	1.8	28.8	16.0
|	271	8.3	3.7	31.8	7.5
|	207	4.3	0.6	27.3	6.1
|	448	2.1	1.2	24.5	11.6
|	452	5.3	2.2	24.0	9.9
V	471	5.4	2.2	22.6	6.6
Worst	496	-2.6	-2.9	-18.9	-11.2
Families	242	-5.6	-2.4	-20.8	-10.7
|	277	-6.6	-1.8	-26.1	-14.4
|	285	-13.0	-8.7	-30.0	-24.3
|	280	-3.9	-2.2	-17.7	-10.5
|	231	-14.1	-1.8	-28.9	-14.2
|	498	-7.7	-2.7	-37.6	-5.0
|	504	-8.1	-1.8	-37.7	-11.1
V	287	-10.4	-1.4	-42.0	-12.6
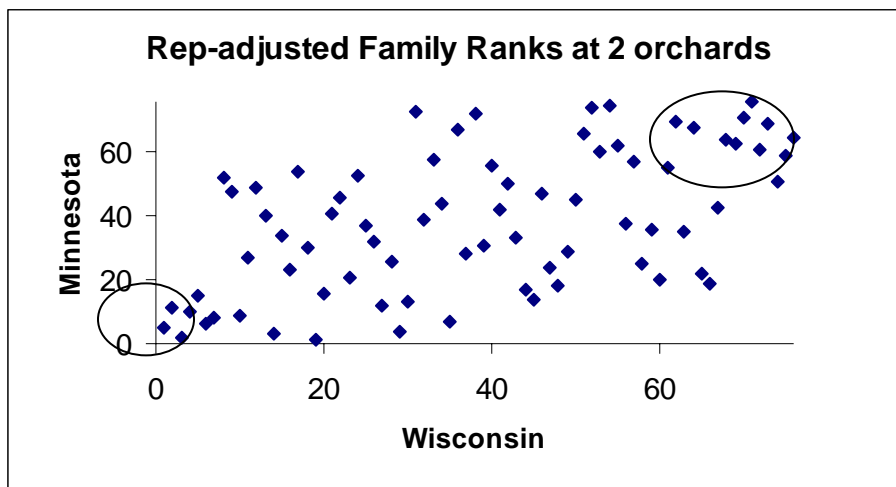
Figure 1. Family ranks (obtained from rep-adjusted least squared means for tree volume) for 76 common families for Wisconsin and Minnesota seedling-seed orchards. Circled trees in lower left of graph are the top-performing families at both sites, and those in the top right are the lowest-performing families.

Discussion

Predicted genetic gains, at 12 percent for tree volume, are not as high as other wind-pollinated conifers but are valuable given the number of seedlings planted in this region. Family-by-site interactions were not significant, but merit additional assessment to ascertain the weak correlation of family performance between sites. Eight families were top-performers at both sites, while the poorest performing nine families ranked lowest at both sites. The sites represent

two vastly different ecotypes; one being located in north central Minnesota and the other in south central Wisconsin. The fact that several families ranked well and poorly at these different sites bolsters the possibility that genetics of red pine are important and significant contributors to tree growth.

Cost for tree breeding are high, but an advanced-generation breeding scheme could produce a second-generation population in as few as 45 crosses. Cotterill (1985) details a variety of low-cost strategies which all feature the use of sublines to structure the breeding program. The advantage of a subline scheme is that crosses within sublines can take place for several generations without inbreeding, after which crosses among sublines could be used to reinvigorate the breeding population. One subline would contain the top-performing individuals of six unrelated families. Breeding within a subline would be accomplished with assortative single-pair mating to further maximize the number of unrelated offspring. We are proposing that 15 sublines, each containing six families, be produced. Sublines would be determined based on tree rank, so top performing trees would be crossed with other top performers. Each six-tree subline would result in three unrelated full-sib families for a total second-generation population of 45 unrelated families. In practice, poor families would not be utilized for future orchards but would serve as a negative control. Full-sib seed would be outplanted together to create the next generation parents, and in concert with a control, would verify the additive gains associated with breeding best with best parents. In addition, an open-pollinated woods run control would be included in a field trial to quantify growth of breeding vs. nonbred material.

The orchards will be maintained as sites for conducting controlled breeding work and will continue to be used for seed collection. Both orchards were rogued using combined index selection which simultaneously retains the best individual performers within best families while maximizing diversity (David et al. 2003). Roguing is taking place over a number of years, and will eventually be thinned to the top 15 percent of trees.

References
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