Tree Improvement in the 21st Century: Planning for the Future

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Andrew David

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Department of Forest Resources
College of Food, Agricultural and Natural Resource Sciences
University of Minnesota
St. Paul, Minnesota

For more information about the Department of Forest Resources and its teaching, research, and outreach programs, contact the department at:

Department of Forest Resources
University of Minnesota
115 Green Hall
1530 Cleveland Avenue North
St. Paul, MN 55108-6112
Ph: 612.624.3400
Fax: 612.625.5212
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POSTER ABSTRACTS

Tree Improvement in the 21st Century: Planning for the Future

September 6-8, 2006
Cloquet Forestry Center
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Abstract/Summary

The 3rd Northern Forest Genetics Association Meeting was held September 6-8, 2006, in conjunction with the Minnesota Tree Improvement Cooperative's 25th anniversary celebration. Approximately 40 people with a general interest in forest genetics from the United States and Canada gathered at the University of Minnesota's Cloquet Forestry Center in Cloquet, Minnesota, to present and discuss the status of their research and programs. The meeting opened with keynote presentations that reviewed the history of forest genetics research in the Lake States, the current successes and struggles at the North Carolina State University tree improvement program, and research on what changes future climate may bring for native plant populations. This meeting demonstrated activity in a wide variety of forest tree species with presentations falling into three broad categories: tree improvement of conifers and fine hardwoods, novel approaches to mitigate the impacts of diseases and pests, and potential impacts of climate change on populations and seed source recommendations. Participants also toured the Cloquet Forestry Center, including the white pine breeding arboretum, and various cooperator seed orchards in the Minnesota Tree Improvement Cooperative.

Mission Statement

Tree improvement in the northeastern United States has undergone tremendous re-alignment since the NFGA last met in 1993. Funds for tree improvement programs have dwindled due to a myriad of factors. A new global economy has emerged, resulting in companies outsourcing supplies and labor. Mills in Minnesota are increasingly dependent on imported wood while unproductive forests lay idle. Urbanization and fragmentation decrease parcel size, enhanced by company mergers and subsequent land sales. Land managers are pressured to reduce the size and scale of monocultures in exchange for mixed species and mixed-age plantings. In addition to anthropomorphic pressures, global climate change may affect species distribution and genetic by environment interactions. What is the future of applied forest genetics in the northeastern US? This conference aims to address these and other topics so we may better assess the needs for applied tree improvement and forest genetics research in the next century.

Rationale

Since the last meeting of the Northern Forest Genetics Association in 1993 tree improvement programs in the region have advanced their breeding programs and made great strides in the establishment and management of seed orchards. In addition, a new emphasis on hardwoods has emerged, reigniting interest in tree improvement efforts and vegetation management regimes for both fine hardwoods and short rotation woody crops.

Conversely, tree improvement has encountered a few obstacles as well. Mergers among forest industry companies have created unique opportunities and difficulties for tree improvement cooperatives. Land ownership is increasingly fragmented while the sale of industry-owned lands to TIMOs (timber investment management organization) and REITs (real estate investment trust) have resulted in profit models that differ from "traditional" forest industry. The advent of forest certification has increased pressure to favor mixed-species stands over single species plantations, and the specter of global climate change raises a myriad of questions regarding forest productivity and the ability of individual species to react and adapt to change.

What is the future of applied forest genetics in the 21st century? This conference aims to address these and other topics so we may better assess the needs for applied tree improvement and forest genetics research in the coming decades.

Acknowledgements

Special thanks to all who attended the 3rd meeting of the Northern Forest Genetics Association in Cloquet, Minnesota. Without your participation and interest none of this would have been possible. Recognition also goes to Ron Overton who organized the meeting of state tree improvement specialists at Kemp Biological Station in 2004, which resulted in the reformation of the Northern Forest Genetics Association. Regarding the Minnesota Tree Improvement Cooperative, a debt of gratitude goes out to Dr. Carl Mohn who first organized the MTIC with financial seed money from the Blandin Foundation and a cadre of forward thinking individuals who recognized early on the value that tree improvement could bring to modern forest management. Additionally, I would like to recognize Dr. Robert Stine, who acted as the Director of the MTIC for most of its early years and established the plantings and trials that the cooperative depends upon today. Finally, special recognition goes to Carrie Pike and James Warren for their efforts behind the scenes and in front of the participants to make this meeting run as smoothly as it did and for their steadfast devotion to the cooperative these past 10 years.

The Legacy

Don Riemenschneider
USDA Forest Service, Northern Research Station
Rhinelander, WI

The USDA Forest Service, Northern Research Station and one of its organizational predecessors, the Lake States Forest Experiment Station, has conducted a program of tree genetics research since the 1920s. In the Lake States (Minnesota, Wisconsin, Michigan) alone we have established dozens of field studies including experimental seed source and progeny tests on Agency lands and on the lands of collaborating institutions including the University of Minnesota. After 80 years of conducting this program of scientific research we have come to know much about the genetics of our major tree species. Unfortunately, while much of our knowledge has been published, more remains poorly published or unpublished. The reasons for this are many. Research projects are often closed and retirements occur with little warning leaving no time for a research team to capture what was left unwritten. Also, methods of analysis improve over time, especially those that require powerful computing ability. We find many instances where data analyses done between 1930 and even 1970 would be considered cursory and inadequate by today's standards. Further, research context and justification constantly change. Thus, the measurements we might have taken and the analyses we might have done in 1940 and 1950 to support *tree improvement* work might not be the same methods we would apply today as we attempt to understand the possible implications of global climate change. And people, even in the best of circumstances, rarely have the opportunity to publish personal expert opinion in the scientific literature. Each retiree who walks out the door for the last time carries invaluable yet undocumented knowledge that, absent extraordinary measures, is lost. My goal here is to capture that portion of our corporate knowledge related to forest genetics research conducted in Minnesota, Wisconsin, and Michigan.

One objective of the legacy project is to make existing data and metadata available to the public. The first objective, while necessary, does not take the project far enough because data are devoid of feeling. We should seek to know why the work was undertaken in the first place. What was the state of the landscape and our forestry institutions that justified the start and near 80-year continuance of forest genetics research? I am assembling our old records so that we might understand what people thought and why they did what they did. I have many old photographs that I use to convey a feeling for the condition of the landscape in those days. One of them is included in this paper. I seek to create a *community of interest*, an audience that having seen the images and read the stories will be motivated to take a closer look at the research and perhaps use our data and knowledge as an aid in the pursuit of their own interests. As an example, I present here a brief summary of one of the first forest genetics projects ever undertaken in the Lake States, a red pine seed source test.

Tree planting began in the Lake States much earlier than tree genetics research. From the beginning, red pine (a.k.a. Norway pine) became a preferred species for nursery growers and tree planters and it was assumed that the species would continue to play a large part in reforestation in the northeastern quarter of the US. The great wave of logging had passed through the Lake States, the Peshtigo and Hinkley fires had burned thousands of cutover acres and a strong feeling prevailed that intervention was needed to reforest the land. It was by then known that many, perhaps most, living species consisted of geographic races that differed in their adaptation to various environments. It was logical that Lake States trees would exhibit such racial variation and that it would be important to match the genetic characteristics of planted trees to the environment in which they were planted. Thus, tree genetics research was initiated at the Lake States Forest Experiment Station. I can only guess at the reasoning that led to the design of the first experiments, of which a red pine seed source test was the earliest. The oldest document I can find that describes the experiment is a *Working Plan for 1931* written by Carlos O. Bates, then Senior Silviculturist for the Lake States Forest Experiment Station. Mr. Bates described the beginnings of the work with some sense of frustration "Following the spring planting operations in the source-of-seed experiments, on the Chippewa and Superior National Forest, and the hasty and inadequate preparations which had to be made for those operations, with insufficient funds, the following plan is laid out for keeping up current observations during 1931, growing new planting stock, and preparing the sites for the next and final field plantings."

Too little time and too few resources plagued Bates and his colleagues then just as the same issues plague us now. Yet, seed was collected, seedlings were grown, field test sites were prepared and planted, and data were collected, analyzed and reported. Several field test sites were planned for the Superior, Chippewa and Huron National Forests. Of these plantings, all begun in 1931, only the planting on the Superior National Forest grew well enough to be tended over the long haul. The Huron National Forest planting succumbed to drought. The Chippewa National Forest planting succumbed to the misguided efforts of an *errant plowman*. A planting on the Chippewa National Forest was successfully established years later, in 1937, with a smaller set of seed sources than was used earlier. Work on this project began in 1927 with seed collections from individual trees, groups of trees, or stands throughout Minnesota, Wisconsin, and Michigan. Trees were climbed for cone collection or cones were taken from *squirrel caches*.

Figure 1. This photograph was taken during a seed collection expedition in 1930. The site is a roadside parking place in Itasca State Park in northern Minnesota.

Cones were shipped to a headquarters laboratory in St. Paul, MN, for germination and other testing. In total, more than 150 collections were made between 1927 and 1934. Collection records were detailed in those days and often included hand-sketched maps to individual trees and photographs of those trees.

What kind of thinking, what kind of commitment to the future led Bates and others to take the time, and it must have been a great amount of time, to document their work so thoroughly? Whatever their reason or motivation, the record provides opportunities for us today. Of the more than 150 collection locations, many with maps and photos, most can still be found. Thus, it is possible to revisit collection sites, resample populations, and test whether forest management practices have altered population characteristics. It is also possible to compare the landscape of 1928 with the landscape of today, more than 75 years later.

Preparation of a test site on the Superior National Forest began in May, 1931 according to Paul. O. Rudolf, a LSFES silviculturist. The plot corners were laid out by transit or compass with distances measured by chain or pacing. Once the plots were located, it was necessary to remove the stumps left over from logging. So, "the stumps were all blown by means of comparatively heavy center shots and, as a general rule, rather large holes were made." Once blown, "A Fordson tractor, borrowed from the Lake County road crew working on the Ely-Finland road, was used to complete the removal of the stumps." These means of preparation, having apparently been judged inefficient led to refinement. Thus, "It was attempted to blast the stumps with the smallest charge of dynamite which would loosen them up satisfactorily...Along this same line, instead of placing the entire charge below the center of the stump, two or three smaller charges were placed under the main roots...a 50-shot electric blasting machine, which had been borrowed from the Lake County road crew, was used part of the time."

The drastic means of site preparation is described here mostly because it is interesting to contemplate the time it would take today to prepare the requisite environmental analyses and then obtain the approval, safety training and certification prior to blowing the first stump. Things were different in the old days. At any rate, we know that the total cost for site preparation, including supervisory labor, was $1,087.34. Again, we see the attention to detailed record-keeping. Seed obtained from the collection expeditions was grown in the Cass Lake, MN, USDA Forest Service nursery. Collection numbers 10 to 88 were planted at the test site in 1931. Collection numbers up to 262 were planted in the nursery in 1931 and seedlings field planted in 1933. Many problems were encountered and overcome in the ensuing years. In a memo to then Station Director Raphael Zon from a Mr. Eyre on the National Forest we find "An error in the status records of the Superior National Forest which affect us has just come to light. The site upon which the Bates plantation was made this spring … proves to be private land." Bates writes some days later that "It is certainly a shock to me to learn that we have been playing around all of this time on private land at Camp 8…. tough luck!!" In due course, however, the land was acquired in return for *adjustment in taxes* which went before the County Commissioners in 1932. Weed control, mostly aspen sprouts, was a continual problem and a local forester "made arrangement with a Mr. Stickney, who lives by Chub Lake, to cut more aspen during January." A bill from Mr. Stickney in the amount of $1.50 for "cutting popel" was received and duly paid on January 20, 1933.

Many measurements of this experiment were made over the years including height and diameter of the trees, crown density, stem soundness, damage and its causes, and stem taper. It is tempting to notice the absence of what we might now consider *ecological attributes* of the experiment such as abundance of nontimber plant species, presence of migratory birds, nongame animal species, and infer thereby some error of omission. But, we were not yet attuned to the coming importance of such observations in those years; the work was still driven by the perceived need to reforest the landscape using the most expeditious means. In a memo to Bates, a field forester notes that "Pieces of apple, poisoned with strychnine, were distributed at the woodchuck holes. The woodchucks seem to be scarce and no new damage was noted." Case closed.

The last damage to the experiment occurred sometime around 1960 due to "a relocation plan for Highway 1 through the Stony River red pine plots." About 60 trees stood within the new right-of-way and were removed. The last measurement of the experiment was done in 1964 and the plantation has subsequently been managed as a normal part of the forest. Some trees still remain, but plot and seed source identities are lost. Little visual evidence remains to suggest to the casual or even professional visitor that those large, *old-growth* red pine represented the beginnings of forest genetics research in the Lake States

This may rank as one of the greatest ironies in the history of USDA Forest Service genetics research. The species we chose to study first ended up being the species that possessed the least amount of genetic variation in growth rate of any species studied subsequently. When growth data are analyzed it is rare, to this day, to find an experiment where more than about 5 percent of the variation in tree height or diameter is attributable to seed sources or families of trees. Yet, Carlos Bates found seed-source-related variation in cold hardiness. In an experiment conducted under artificial conditions in what later became the University of Minnesota Cold Hardiness Laboratory, Bates found that "northern sources of seedlings survived much better than those from the warmer portions of the range of Norway pine" (link to web document). Even then, it was recognized that seed sources did not always perform according to expectation as "Group 4 shows less hardiness than Group 5, the latter being composed almost entirely of samples taken very close to the southern limit of the Norway pine range in a diagonal line across Wisconsin and Minnesota." Very high hardiness was characteristic of seed source number 60. "The collection ... from Kilbourne, Wisconsin, which, except for sandstone outcrops occurring along the Wisconsin River, would apparently be outside the natural range of Norway pine." So, the racial patterns that did exist sometimes were consistent and sometimes were in conflict with expectation.

In 1956, Paul O. Rudolf used measurements of the Superior National Forest experiment to test much the same phenomenon using field data. The research lead to one of the first *seed zone* recommendations ever published for the Lake States. The work was reported as significant because "Most forest tree species probably have developed races that differ from one another physiologically rather than morphologically….For this reason it is important to establish homogeneous seed collection zones and to designate as to origin each lot of seed used in reforestation." What differences in seed source growth existed were related to climatic zones based on summer growing-degree-days and winter minimum temperature. Sufficient differences were found to justify certain boundary recommendations that are still in use (albeit modified) today. As best I can discern, data from the Chippewa National Forest planting was never used to corroborate any results based on data from the Superior National Forest field test.

Rudolf reported later in 1964 that "When it comes to picking out a pattern there is some difficulty. The best lots were from northeastern Minnesota, northwestern Minnesota, north-central Minnesota, northeastern Wisconsin, and adjacent southern Upper Michigan." Further, "This general pattern seemed to hold for the various characteristics measured or computed." Yet, Rudolf maintained support for his 1956 results stating that "Again we have the picture that there is better development of reasonably local sources in considering this one particular planting area..." But he hedges his rhetoric with "… sources from quite a distance away from the planting site still may perform quite well." At the same meeting where Rudolf presented his results, Hans Nienstaedt, in an analysis of only those collections that came from single trees (called an open-pollinated half-sib family), found that when those sources were grouped according to Rudolf's zones no differences among zones in tree height or diameter could be declared significant. In recommending a tree improvement protocol for red pine Nienstaedt held that "… measurements must be of sufficient accuracy to permit evaluation of small differences," a recognition that variance attributable to genetic causes might be small. Nienstaedt concluded in the end that "to write, on the basis of these results, that a red pine breeding program is feasible is perhaps unconvincing. What we need is an analysis of ...costs and...ultimate economic gains." Nienstaedt's reasoning was that a little bit of improvement spread over a large acreage of valuable timber might justify the research and development investment.

Results were also produced from the Pennsylvania experiment by A.F. Hough of the Northeastern Forest Experiment Station. Hough justified the work with some passion writing "In the Lake States, in New England, and in the Middle Atlantic States thousands of acres of abandoned farm land and land denuded by ax and fire have been planted with red pine" and "out conditions of planting sites far distant from its seed source?" Quite well apparently because Hough found "grouping of these 50 seed sources into nine geographic-climatic (Rudolf's zones) regions brings to light highly significant differences as measured by the value of F" and that "Seedlings of many of the Lake States seed sources outstripped those from the best Northeastern sources." He asked "why did the seed...70 airline miles from the Kane plantation, fail to produce the best height growth of all?" The question was asked and we still do not know the answer.

Overall, the story on red pine racial variation is anything but straightforward; local sources were often outpaced in growth by exotic sources. This is not altogether bad because the first seed sown in the new USDA Forest Service nursery in Rhinelander, Wisconsin, in 1932 was not local. More than 400 pounds of white pine and red pine seeds were sown to produce seedlings for planting in Wisconsin.

There are many more stories to write in addition to the red pine seed source test I have described. Similar research has been done with all our major conifer species and some hardwoods by the USDA Forest Service, the University of Minnesota, the University of Wisconsin, and Michigan State University. Yet, some wonder whether such work has a strong future. It is difficult to envision how *tree improvement* can remain a viable activity unless there is an increase in acres devoted to tree plantations. One logically asks whether there is any sense developing a *domesticated* tree crop if the means of deployment is lacking. Tree plantations will probably be needed, if not for the production of wood for the fiber-using market then for bioenergy feedstock. I agree that under a low-energy-price paradigm our forest inventory data make it difficult to justify plantation R&D in the short term. We do grow more wood than we consume. But, the North Central region will ultimately need to increase the wood supply for many reasons. Our energy demand dwarfs our current biomass production. As energy prices increase all kinds of biomass production systems will become economically viable and ecologically important as they act to shift demand away from the forest. Given such a future, the need to understand our past work and the opportunities it provides seems powerful.

How Do Today's Landowners Value Tree Improvement and Silvicultural Impacts on Forest Productivity in the Southern US?

S. E. McKeand, B. Li, R. C. Abt, and H. L. Allen
Department of Forestry and Environmental Resources, College of Natural Resources,
NC State University, Raleigh, NC

In the southern United States, tree improvement and silviculture are impacting today's loblolly pine plantations in unprecedented ways. When the best genetic material is planted and given the necessary resources to grow, mean annual increments of 10 tons a^{-1} yr^{-1} can be readily achieved on many sites. There are few other regions in the world where the use of integrated silvicultural systems and use of genetically improved planting stock is having as positive an impact on plantation productivity. Today's plantations are growing more than twice as fast as plantations of the previous rotation.

Forest managers have recognized that intensive plantation silviculture is like agronomy; both the plant and the soil need to be actively managed to optimize production. Genetic gains after two cycles of breeding can exceed 35 percent in volume production compared to unimproved loblolly pine. Based solely on growth gains, we have estimated that landowners can realize net present values of $50 to more than $300 per acre across a range of productivity and silvicultural management regimes simply by planting the best genotypes that are currently available from commercial and state forest nurseries. Landowners could pay more for the best genotypes, and the best seedlings would be well worth the additional costs.

The legacy of the large integrated forest products companies being the dominant players in southern forestry has changed dramatically over the past 5-10 years. Changes in forest ownership are impacting the way that landowner value silvicultural inputs and tree improvement. If landowners intend to establish, manage, and harvest plantations, then investment in tree improvement is a straightforward analysis. When land is *flipped* at shorter intervals, and given current appraisal methods for evaluating forest stands, the answer is much more *confused*. We will present results showing the benefits of tree improvement from various land ownership scenarios.

Adaptive Evolution in Response to Climate Change

Julie R. Etterson
Department of Biology, University of Minnesota-Duluth

Why is adaptive evolution important to this discussion?

Adaptive evolution is an almost universal response of the global biota to environmental change. Theoretical models suggest that adaptive evolution can enhance the persistence of populations in a changing environment even when migration is possible (Pease et al. 1989; Lynch et al. 1991; Lynch and Lande 1993; Bürger and Lynch 1995). As climate continues to change into the future, natural selection on wild populations will be altered (Etterson 2004a). The potential of species to respond to such changes in selection depends upon a number of genetic considerations that must be examined at the population level. Species are not uniform across their ranges but comprise a series of populations that have been molded by evolutionary forces such as founder events, genetic drift, gene flow, and selection. Each population differs in the extent to which it is adapted to local conditions and each has its own ecological amplitude and evolutionary potential. Thus, the ultimate fate of a species depends upon the evolutionary response of these genetically differentiated populations across the species range, not just at the margins of climate tolerance.

In general we think of three possible responses of populations to climate change: extinction, migration and adaptation. However, all of these processes are interrelated and adaptive evolution influences both of the former. The probability of extinction is influenced by population growth rate which is higher in populations that are well-adapted to their environment. The rate of migration may be increased by selection favoring greater dispersal ability. The migratory process itself, however, may reduce the potential for adaptive evolution by eroding genetic diversity during founder events and by genetic drift in small populations at the leading edge of the migration front (Cwynar and MacDonald 1987).

What are the critical factors that determine the potential for evolutionary response to selection?

The most fundamental requirement for adaptive evolution is that populations harbor genetic variation for relevant traits (Fisher 1930). The level of genetic diversity within populations is most often inferred from measures of molecular variation (Morgan et al. 2001 and citations therein). However, molecular variation will not necessarily correspond to genetic variation in complex phenotypic traits that will most likely be the direct targets of selection with climate change (Bonnin et al. 1996; Yang et al 1996; Lynch et al. 1999; Morgan et al 2001) such as timing of reproduction, dispersal ability, and drought tolerance.

An alternative indicator of genetic variation is the quantitative genetic parameter, heritability. Heritability (h^2) estimates the fraction of the total phenotypic variance (V_P) that is genetically based (V_A) and thus can be mobilized by selection for adaptation to changing environments (Falconer and MacKay 1996) and is described by the equation:

$$h^2 = V_A/V_P \qquad (1)$$

The heritability of traits is of great evolutionary significance because it reflects the degree to which progeny inherit their parents' phenotype. The speed of evolutionary response to selection (R) is a function of heritability and the strength of selection (S):

$$R = h^2S \qquad (2)$$

Populations are predicted to evolve rapidly if traits under selection are highly heritable and selection is strong. However, there is little information available about the spatial distribution of quantitative genetic variation across species' ranges for traits relevant to adaptation to climate change because of the laborious and protracted nature of the research required to obtain the estimates.

Predicting the evolutionary potential of populations: A case study

In an effort to examine the potential for adaptive evolution to future climates, I conducted a quantitative genetic experiment on the native prairie legume, *Chamaecrista fasciculata* in the Great Plains of the United States. To mimic predicted temporal change in climate, three natural populations of the annual legume, *Chamaecrista fasciculata*, were sampled from a climate gradient and progeny of formal crosses were reciprocally planted back into common gardens across this climate gradient (Minnesota, Kansas, Oklahoma from north to south). Traits that influence fitness were measured, including the rate of phenological development, leaf number, and leaf thickness. In each site, native populations produced significantly more seed than the other populations providing strong evidence of local adaptation (Etterson 2004a). Clines in selection corresponding to latitude were observed and are predicted to move northward in the future (Etterson 2004a). Populations had significant heritabilities for most traits under selection, although the size the estimates varied widely and were generally lower for the northern population at the periphery of the species range (Etterson 2004b). Despite appreciable selection and genetic variance, a multivariate analysis suggested that the rate of adaptive evolution would be slower than the anticipated rate of climate change. Slow rates of evolutionary response are attributed to genetic correlations among traits that are antagonistic to the direction selection under a changed climate (Etterson and Shaw 2001). For example, selection favored plants with many thick leaves in the southern environment but when northern plants were grown in this site, they produced either many thin leaves or few thick leaves indicating a fundamental genetic tradeoff (Figure 1b).

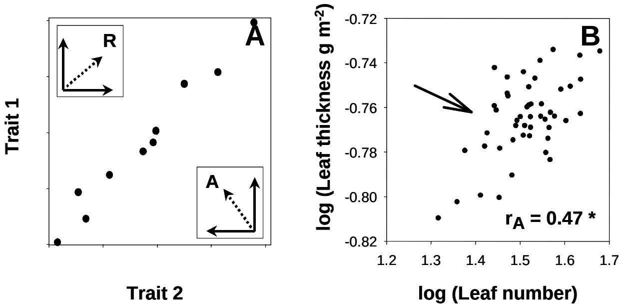

Figure 1. The influence of genetic correlations among traits on selection response. (A) Hypothetical positive genetic correlation (r_A) between two traits (each point representing a family). Two selection scenarios: "R", selection is in the same direction on traits; the depicted r_A is in accord with the direction of selection, enhancing evolutionary response; thus, the genetic correlation is "reinforcing". "A", selection is in the opposite direction for both traits; r_A is "antagonistic" to the direction of selection inhibiting evolutionary response. (B) Scatter plot of leaf thickness and leaf number of Minnesota families when grown in the southern environment in Oklahoma showing significant positive genetic correlation that is antagonstic to the negative vector of joint selection. (after Etterson and Shaw 2001)

Genetic correlations that are antagonistic to the direction of selection are due to either to pleiotropy, where an allele has positive fitness effects on one trait but negative effects on another, or linkage disequilibrium, where alleles at different loci are in close association. Antagonist genetic correlations may reduce the likelihood that the combination of traits that results in highest fitness will evolve. The lability of genetic correlations among traits and thus the severity of genetic constraint depends on the underlying cause of the correlation which is not readily determined.

In principle, populations could respond immediately to climate change, maintaining fitness by adaptive plastic responses (Bradshaw 1965; Schlichting 1986; Sultan 1987; van Tienderen 1991;

Schlichting and Pigliucci 1998; Donohue et al. 2001). For leaf number and thickness, the populations of this study exhibited substantial phenotypic plasticity that could be considered adaptive because it was in the direction of trait values favored by selection. However, even though plasticity was found to be in an adaptive direction, it did not maintain fitness across environments. Nevertheless, responses to selection on genetically based plasticity may help mitigate fitness losses as climate gradually changes.

Overall, this study suggests that if climate changes as predicted, northern populations of this species will face a severe evolutionary challenge in the future because of modest heritabilities, cross-environment genetic correlations antagonistic to selection, and demographic instability due to lower seed production in a hotter and drier climate.

Conclusions

It is uncertain whether the ongoing rate of evolution can keep pace with the rate of climate change. Rapid genetic adaptation to climate has been documented in studies of clinal variation of introduced species (Reinartz 1984; Lacey 1988; Weber and Schmid 1998; Huey et al. 2000) and a few studies have documented genetic changes in wild populations in recent decades (Bradshaw and Holzapfel 2001; Reale et al. 2003). Genetic detail is essential to furthering our understanding of the limits to adaptation. New insights into the risk of extinction may be found by coupling information on the current genetic architecture of populations, expected selection regimes in future environments, and other ecological parameters such as dispersal ability.

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Incorporating Wood Density in Black Spruce and Jack Pine Breeding Programs in Ontario for Maximum Fiber Yield Production

Paul Charrette
Superior-Woods Tree Improvement Association
Lakehead University, Thunder Bay, Ontario

Abstract

An operational-level evaluation of growth traits and wood density, including a new selection trait, dry fiber weight, was conducted in a black spruce and a jack pine tree improvement program in northwestern Ontario. Estimates of genetic variation, heritability and age-age correlation of wood density, growth traits (e.g., height, dbh, and volume) and dry fiber weight at different ages in black spruce and jack pine were completed. In addition, the impact of different selection scenarios on genetic gain was estimated. For black spruce a negative but weak genetic correlation between wood density and growth traits was found, resulting in no loss of genetic gain in dry fiber weight production due to selection based on growth traits, such as height and DBH. For jack pine, estimates of genetic correlation between wood density and growth traits were negative and moderately strong, especially between DBH and wood density, indicating that faster growing trees are genetically associated with lower wood density. If the primary objective of a jack pine tree improvement program is to increase wood production for solid wood products then, based on these results, it is recommended that wood density be considered.

Age 41 Results of a Half-Sib Red Pine Progeny Test on Three Michigan Sites

Paul Bloese
Department of Forestry, Michigan State University
East Lansing, MI

Abstract

Age 41 diameter and survival were measured in two Lower and one Upper Michigan plantings of a half-sib red pine progeny test (Figure 1). The majority of families in the test originated from Michigan's Upper and Lower Peninsulas, although families from New Brunswick, Maine, New York, Ontario, and Manitoba were also included. There were no significant differences ($Pr > \chi^2 = 0.05$) in survival among collection regions or among families. Collection region, collection region X site, family and family X site effects were all significant ($Pr > F = 0.02$) for diameter.

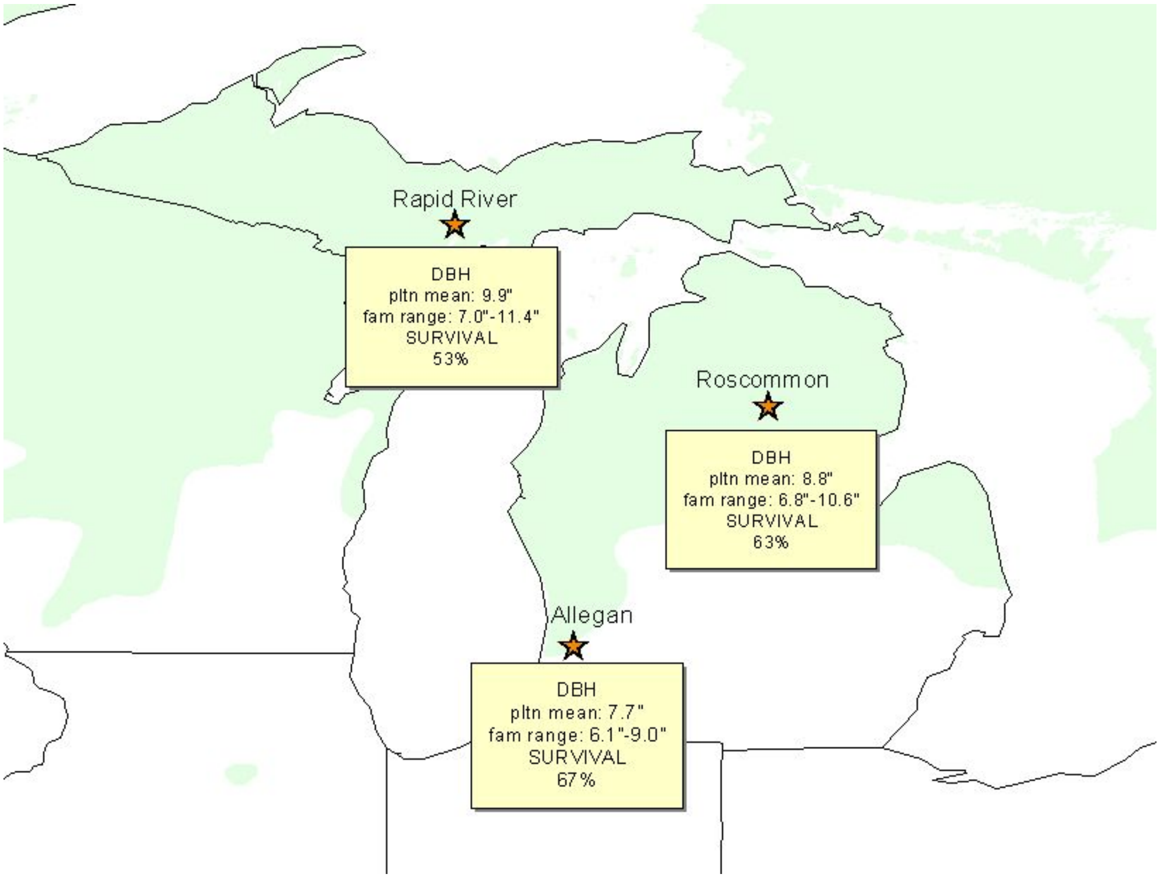

Figure 1. Mean survival and DBH at age 41 of half-sib red pine families planted on three Michigan sites. Shaded area denotes native range of red pine within mapped region.

Diameter of Michigan families was under relatively strong genetic control on an individual site basis (Table 1). However, single-tree and family heritability estimates for multiple-sites were substantially lower due to strong family X site effects (Table 2). The importance of family by site effects were also evident in low r_B estimates (paired-site r_B estimates: 0.16 – 0.45) and must be considered in the design of future genetic improvement programs. Broadly adapted families were identified and various strategies for using them to produce genetically improved red pine for Michigan discussed.

Table 1. Age 41 DBH single-site heritability estimates for 85 half-sib Michigan families planted at the Allegan, Roscommon, and Rapid River test sites. Standard errors of h^2_{tree} in parentheses.

Test Site	h^2_{tree}	h^2_{fam}
Allegan	0.41 (0.10)	0.69
Roscommon	0.30 (0.11)	0.49
Rapid River	0.18 (0.14)	0.37

Table 2. Age 41 DBH multiple-site heritability estimates for 85 half-sib Michigan families planted at the Allegan, Roscommon, and Rapid River test sites. Standard errors of h^2_{tree} in parentheses.

Test Sites	h^2_{tree}	h^2_{fam}
Allegan - Roscommon	0.19 (0.08)	0.44
Allegan – Rapid River	0.13 (0.09)	0.28
Roscommon – Rapid River	0.03 (0.08)	0.07
All 3 sites	0.13 (0.06)	0.36

Summary of Black Cherry Improvement at the Hardwood Tree Improvement and Regeneration Center (HTIRC)

Keith Woeste, Jim McKenna, and Paula Pijut
USDA Forest Service Hardwood Tree Improvement and Regeneration Center,
Department of Forestry and Natural Resources, Purdue University

Background

Black cherry (*Prunus serotina*) is found in southeastern Canada and throughout the eastern US. It is the only native species of the genus *Prunus* that is of high commercial value for timber and sawlog production. Black cherry wood is one of the most valued woods in North America for cabinets, furniture, fine veneer, and architectural woodwork. Hardwood lumber mills are constantly seeking high-quality sources of this species, because stands of large, straight-stemmed, black cherry trees are becoming increasingly difficult to find. Attack by several species of insects causes gum defects in black cherry, resulting in reduced timber quality, especially for veneer (Rexrode and Baumgras 1984). Gum spots (gummosis) in the wood are often associated with the feeding and activity of the lesser peachtree borer (*Synanthedon pictipes* Grote and Robinson) [Lepidoptera]. Damage to the parenchyma cells causes a discoloration and production of lysigenous gum canals or gum spots. Gum spot defects drastically reduce the yield of marketable lumber and veneer from otherwise excellent logs. Logs rejected for veneer stock because of gum spots may be reduced in value by as much as 60 to 70 percent.

In 1966, the USDA Forest Service began a tree improvement program based on plus-tree selection of black cherry primarily from the Allegheny National Forest (ANF), the most important timber production area for the species. Mature plus-trees in even aged stands were selected in areas where black cherry was dominant. The goal of the program was to provide local, genetically improved planting stock for reforestation on the National Forest. For each plus-tree, three comparison trees of similar age were evaluated. Traits selected for were: merchantable volume, apical dominance, absence of black knot (caused by the fungus *Apiosporina morbosa*), gummosis, ice damage, and quality timber form. Detailed records for each select tree have been maintained by the ANF and the USDA-FS Region 9 Geneticist, providing the opportunity to re-evaluate and collect these trees. The breeding value of these selections remains to be fully investigated.

In March, 2005, HTIRC staff re-visited 36 of these trees to evaluate them and collect scion wood for our breeding research at the HTIRC. At the time of collection we re-measured DBH, recorded incidence of black knot and gummosis, and noted the general health of each tree. The trees were 64 years-old, on average, when they were selected in the 1960s, with an annual average DBH growth rate of 0.31 in/yr. Today they average 102 years-old, with an annual DBH growth rate of 0.20 in/yr. Eighty-six percent (31/36 trees) remained black knot free in the 38 years since selection (Table 1).

Table 1. Summary of growth and quality of select black cherry from the Allegheny and Monongahela National Forests.

			Orig. select traits[A]			**Ann. DBH growth (in/yr)**[B]		**Black knot**		**Gummosis**	
Tree	**Age**	**DBH (in)**	**Ap. dom.**	**Ht.**	**Vol.**	**Initial**	**last 40 yrs**	**Initial**	**last 40 yrs**	**Initial**	**last 40 yrs**
B-7	137	24.7	5%	11%	9%	0.19	0.15	0	0	0	0
B-10	96	26.9	31%	7%	100%	0.31	0.24	0	0	0	0
B-13	174	36.3	6%	5%	26%	0.21	0.21	0	0	0	0
B-16	77	23.0	9%	4%	27%	0.36	0.23	0	0	0	+
B-19	92	22.3	27%	8%	40%	0.26	0.21	0	+	0	+
B-24	104	33.4	115%	0%	32%	0.32	0.33	0	0	0	0
B-30	101	21.3	35%	11%	23%	0.23	0.17	0	+	0	0
B-31	104	30.7	22%	1%	22%	0.27	0.33	0	0	0	0
M-1	110	23.7	41%	-2%	17%	0.24	0.17	0	0	0	0
M-2	88	28.9	38%	1%	85%	0.45	0.18	0	+	0	0
M-7	111	36.4	-27%	18%	112%	0.33	0.33	0	0	0	0
M-9	91	26.2	82%	6%	140%	0.39	0.15	0	+	0	0
M-13	98	33.6	16%	29%	187%	0.45	0.17	-	-	-	-
M-16	125	25.3	-3%	16%	35%	0.24	0.11	0	0	0	0
M-17	93	25.2	81%	-2%	21%	0.34	0.18	0	0	0	0
M-20	85	27.5	36%	11%	93%	0.44	0.18	0	0	0	0
M-23	87	27.7	69%	8%	26%	0.31	0.33	0	0	0	0
NE-8	105	23.8	38%	8%	7%	0.28	0.14	0	0	0	0
R-12	137	30.7	37%	6%	32%	0.24	0.18	0	0	0	0
R-21	102	22.3	127%	13%	45%	0.24	0.17	0	0	0	0
R-23	97	30.1	15%	9%	42%	0.34	0.27	0	0	0	0
R-24	78	18.6	13%	9%	60%	0.31	0.15	0	0	0	0
R-27	83	18.3	42%	0%	0%	0.27	0.15	0	0	0	0
R-36	104	21.3	42%	13%	96%	0.26	0.09	0	0	0	0
S-5	85	19.6	62%	9%	0%	0.27	0.18	0	0	0	0
S-7	88	23.6	48%	9%	40%	0.33	0.19	0	+	0	0
S-11	90	25.8	41%	6%	20%	0.35	0.19	0	0	0	0
S-12	87	31.0	53%	4%	31%	0.42	0.28	0	0	0	0
S-17	94	22.5	36%	2%	12%	0.27	0.20	0	0	0	0
S-18	115	22.7	37%	9%	23%	0.23	0.13	0	0	0	0
TV-1	139	35.8	23%	15%	43%	0.26	0.25	0	0	0	0
TV-2	113	25.8	-4%	6%	34%	0.30	0.10	0	0	0	+
TV-3	102	23.4	90%	0%	-7%	0.25	0.19	0	0	0	0
AVG	**102**	**26.37**	**40%**	**7%**	**46%**	**0.31**	**0.20**	**0**	**0.16**	**0**	**0.10**
SD	20	5.08	33%	6%	43%	0.07	0.07	0	0.37	0	0.30

[A] Improvement of each select tree in comparison to the average of 3 companion trees for: apical dominance (Ap. dom.), total height (Ht.), and merchantable volume (vol.).

[B] Average annual diameter growth calculated by dividing DBH by age at the time of selection (initial) and from that time to the present (*c.a.*last 40 yrs).

The 1982 Klondike #685 Evaluation Planting

In the fall of 2005, we measured a 23-year-old planting (essentially a progeny test) containing open-pollinated seedlings from ramets of some of the ANF selections and seedlings from local, non-select parents planted as controls. The three-acre planting site, Klondike #685, was a clear-cut in the ANF (McKean Co., PA) that had failed to naturally regenerate.

Select and control seedlings were planted in full alternating rows at ~3m × 3m. Adjacent select and control rows were paired and analyzed as blocks (10 rows = 5 blocks) by ANOVA. Initially, the site was intensively maintained. At present, the site is fully stocked with the surviving planted black cherry and naturally regenerated pin cherry, red maple, and yellow birch. Because of the competition, the silvicultural class of each tree was determined, and only dominant and codominant trees were analyzed. Volume was calculated by Doyle's log rule with log lengths to the first fork. We rated the trees for apical dominance, straightness, self-pruning, and clarity of the bole. The seedlings from selected parents were significantly larger than the comparison seedlings in height, diameter, and volume. The incidence of black knot was not significantly different between sources.

The ANF Superior Trees and the HTIRC Breeding Program

Black cherry improvement began at the HTIRC in 2001, when 100 seedlings derived from a grafted seed orchard of selected PA black cherry (Penn Nursery c/o Mr. Alex Day) were obtained and planted at Martell. These trees exhibit a wide range of phenotypes and began setting seed in 2006, their fifth full growing season. These parents will be evaluated as clonal selections and in progeny tests.

In 2004, seed was collected for a limited range provenance test to examine the phenotypic diversity, quality, and adaptability of black cherry from five sources: IDNR commercial stock (seed sources from northern and southern Indiana), run-of-the-mill fence row trees at Purdue (north central Indiana); plus trees in a natural forest in southern Indiana (Harrison Crawford State Forest); plus trees selected at the Vallonia Nursery growing in an improved seed orchard; and seed collected from the ANF, primarily the Kane Experiment Station, Kane, PA. The seed was sown at the Vallonia nursery, and 1-0 trees planted in 2006 at 3 sites. A minimum of 100 seedlings per provenance were planted in a RCBD at each site. The plantings will be used to evaluate the adaptedness of the ANF sources, to determine how widely adapted southern and northern Indiana sources are, to evaluate phenotypic range of black cherry growing in Indiana in terms of growth and form, and to provide material for selection in the future.

In 2005, scions from the ANF superior trees were collected and grafted onto seedling rootstocks at Purdue. Grafted trees were planted in: (1) a clone bank with other first generation selections; (2) a seed orchard comprised of only PA selections; and (3) mixed seed orchards comprised of PA, IN, and selections from other states.

As of July 2006 there were 101 black cherry (*Prunus serotina*) accessions in the HTIRC black cherry improvement germplasm, not including the trees from the Penn Nursery. Nearly all the accessions are grafted ramets of select trees from the following areas:

60% (n=60) from the Allegheny Plateau in Pennsylvania
24% (n=24) from Indiana
13% (n =13) from Michigan
2% from West Virginia and Vermont (n=2 for each state).

Each clonal accession was grafted onto a seedling rootstock, and three ramets were randomly placed into a clone bank. Evaluation of the trees in the clone banks will provide initial data regarding their growth rate, timber qualities, and phenology. The clone bank also serves as a repository, a source of propagation material to establish breeding/seed orchards, and a source of scion wood or cuttings for further clonal testing. As the clone banks produce seed, they will be progeny tested. Controlled pollinations among clones will be performed to investigate their specific combining ability.

HTIRC has propagated four black cherry seed orchards. The Edinburgh, IN orchard, in cooperation with Danzer Forestland, is comprised of grafted selections from PA; the orchards at Martell contain either grafted selections from PA (orchard 2) or IN (orchard 3). The fourth orchard, located just west of the Purdue campus at the FNR farm, contains grafted accessions from Indiana and Michigan. All will be evaluated for straightness, growth rate and freedom from disease, used as sources of scion wood, seed for progeny testing, and as locations for controlled crosses.

Clonal production of black cherry

Clonal reproduction of commercially important hardwood tree species is necessary, in a tree improvement program, in order to provide improved planting stock for use in progeny testing and for production forestry. In vitro and vegetative propagation methods will be required to produce clones of elite black cherry genotypes or genetically improved genotypes. Genetic modification of hardwood tree species to produce trees with herbicide tolerance, disease and pest resistance, improved wood quality, and reproductive manipulations for commercial plantations is also a major aspect of a tree improvement program. Development of an effective gene transfer and efficient in vitro regeneration system for black cherry, that can be easily adapted for many genotypes, will be required to produce genetically improved black cherry trees.

Rooted cutting results from 9-year-old black cherry trees appear promising (Pijut and Espinosa, 2005). Forty-two percent rooting was achieved overall for softwood cuttings collected mid-June and treated with K-IBA or IBA. The greatest rooting success (54 percent) was with 12 mM K-IBA. Fifty percent rooting was achieved with 15 or 74 mM IBA. The number of roots per cutting increased with increasing concentration of K-IBA. Rooted cuttings survived (80 to 100%) overwintering in a controlled cold-storage environment. This protocol is being utilized to establish rooted cuttings from elite selections of mature black cherry trees. Establishment of in vitro shoot cultures for three genotypes of black cherry, and regeneration of adventitious shoots with rooting from in vitro leaf explants, has been successful (Espinosa et al. 2006). The maximum mean number of shoots regenerated per explant (5.05 ± 1.14) was obtained with 2.27 µM TDZ plus 0.54 µM NAA. The highest percent shoot regeneration (38.3) and mean number of shoots (4.13 ± 0.97) was obtained with 6.81 µM TDZ plus 1.07 µM NAA. The highest rooting (27%) of adventitious shoots and number of roots per shoot (2.3 ± 0.2) was obtained with 2.5 µM IBA when shoots were maintained for 7 days in the dark on rooting medium before transfer to a 16-hour photoperiod. The highest rooting (70%) of nodal explant-derived stock cultures and number of roots per shoot (2.7 ± 0.9) was also obtained with 2.5 µM IBA, but when shoots were maintained for 4 days in the dark before transfer to a 16- hour photoperiod. In total, 86% of the plantlets survived acclimatization to the greenhouse and 100 percent survival after overwintering in cold-storage. In vitro shoot cultures from elite, mature black cherry selections have been established and will be used to further optimize this regeneration system for genetic modification and rooting studies. The development of transgenic elite black cherry trees with resistance to pests or engineered for reproductive sterility will potentially have great economic benefits to landowners, lumber mills, and the forest products industry. Genetic gain in black cherry genotypes through this research will complement traditional tree improvement efforts.

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Butternut Canker and the USDA Forest Service Response

Paul Berrang, Milwaukee, WI
Mike Ostry, St. Paul, MN
Keith Woeste, West Lafayette, IN
Manfred Mielke, St. Paul, MN

Butternut canker is caused by the fungus *Sirococcus clavigignenti-juglandacearum* and is killing butternut (*Juglans cinerea*) throughout the range of the species. Surveys from about five years ago indicated that about 80 percent of the trees in parts of the northern range were infected. The situation has probably gotten worse since then. The USDA Forest Service is composed of separate parts that have different legally defined functions. Three parts of the agency play a role in helping to preserve butternut.

Forest Service Research (FSR) supports both basic and applied research on butternut canker. Mike Ostry and his coworkers in St. Paul, Minnesota, have shown the pathogen has very limited genetic diversity, suggesting that it is of exotic origin. They have refined techniques for inoculating butternut with the pathogen. These techniques have already been used to define the host range of the pathogen. These techniques could be used in the future to screen butternut for resistance to butternut canker. Ostry and his coworkers have shown that some trees remain disease free for up to ten years even when surrounded by severely infected trees. This indicates that some trees may be resistant to the disease. They have refined techniques for clonally propagating butternut. These techniques can be used to establish clone banks and breeding orchards. Keith Woeste and his coworkers at West Lafayette, Indiana, have shown that hybrids between Japanese walnut and butternut are not unusual, particularly near towns and farms. He has found that some of the most vigorous butternut are actually hybrids or species intermediates and that some nursery stock sold as butternut is actually a mix of butternut, hybrids and intermediates. He is developing a DNA test that could be used to distinguish between pure butternut and intermediates. Jim McKenna, who also works at West Lafayette, has searched for disease-free butternut over a multi-state area and propagated them into clone banks where they can be evaluated and re-propagated.

State and Private Forestry (S&PF) is involved with a variety of technology transfer, technology development and pest surveys that relate to butternut. S&PF was the first part of the USDA Forest Service to work on butternut canker. Bob Anderson and Leon Lamadeleine published the results of a survey for butternut canker in 1978, one year before the fungus that causes butternut canker was first described. Since then S&PF has issued a number of pest bulletins on butternut canker. Cindy Ash is cohosting a workshop on butternut canker in Niagra Falls, Ontario, in October 2006. More recently S&PF has funded a number of environmental monitoring and technology development projects that relate to butternut canker with university researchers. These projects have supported surveys for butternut canker in a number of states. One of these projects at the University of Tennessee has shown that there are differences in resistance to butternut canker among open-pollinated families. This shows that resistance to butternut canker is genetically determined and suggests that it would be possible to breed for resistance to this disease. Manfred Mielke of S&PF has cooperated with Mike Ostry of FSR to publish management guidelines for butternut.

The National Forest System is the land management branch of the USDA Forest Service. Its activities are focused on managing butternut on the National Forests. Butternut has been identified as a sensitive species on all of the Forests where it occurs. This means the species is given special consideration during land management activities and records are maintained of where butternut are found. Jan Schultz, formerly of the Hiawatha National Forest, worked with researchers and contractors to prepare a Conservation Assessment for butternut. This document summarized what was known about butternut, butternut canker and their management. Employees of the Chequamegon-Nicolet National Forest have cooperated with Mike Ostry of FSR to evaluate the effects of various silvicultural practices on butternut and butternut regeneration.

A number of National Forests have planted butternut in restoration projects. One problem with restoration projects is getting genetically diverse seed that is known to be pure butternut. Recently the Genetics Program within the National Forest System has started a program that will help preserve a portion of the butternut genome and make genetically appropriate seed available for restoration projects. This work applies techniques developed by researchers in an operational setting. It includes searching for relatively healthy butternut, collecting scion, grafting it onto walnut rootstock, and testing it to determine whether it is pure butternut. Material was collected from the Chequamegon-Nicolet National Forest in Wisconsin last winter and grafted this spring. We expect to plant it in a clone bank next spring. When this material starts to bear seed it will provide a seed source for restoration projects on the Forest. We expect to search for and collect additional material from nearby parts of Wisconsin this winter. We expect to expand this work to other National Forests in the Northeast in the future.

Advances in Breeding American Beech for Resistance to Beech Bark Disease

Jennifer L. Koch, Mary E. Mason and David W. Carey
USDA Forest Service, Northern Research Station

Introduction

Beech bark disease (BBD) is a complex disease that is initiated by the feeding activities of the beech scale insect (*Cryptococcus fagisuga*). As the insects feed, groups of parenchyma cells collapse and die resulting in the development of small fissures in the bark (Ehrlich 1934). These provide entryway for fungal inoculation with either the native pathogen *Neonectria galligena*, or *Neonectria coccinea* var. *faginata*, a pathogen believed to have been introduced from Europe. As the fungal mycelia grow, large areas of tissue become weakened and die. Eventually complete girdling of the tree may occur. Often, cankers form resulting in wood defects. Large numbers of severely deformed American beech trees persist in forests long-affected by BBD, complicating stand management practices due to prolific formation of root suckers by these diseased trees. This can result in the formation of dense “thickets” of small diameter susceptible beech. Such thickets are of little value and may actually interfere with the regeneration of desired species (Houston & O’Brien 1983).

The spatial and temporal spread of BBD has been classified into three distinct stages (Houston & O’Brien 1983). The advancing front is the first stage of the disease and refers areas recently invaded by the beech scale insect. Large diameter, mature beech trees are normally the first to be infested. The second stage is termed the killing front and refers to the situation where extremely high levels of beech scale infestation are coupled with severe *Neonectria* attacks, resulting in heavy mortality. The last phase of the disease is termed the aftermath forest. This is an endemic stage persisting in regions where heavy mortality has occurred in the past and the remaining beech trees are mostly small, highly deformed and defective, and often of root-sprout origin. These younger trees provide a continual source of inoculum of both the scale insect and the *Neonectria* fungi.

Fortunately, even in aftermath forests long-affected by BBD, there are American beech trees that remain disease-free. Insect challenge trials have demonstrated that such trees are resistant to the scale insect and extensive *Neonectria* infections are typically not observed without prior scale infestation (Houston 1982). Resistant trees are commonly found clustered in close proximity to one another. This indicates they are likely related, originating either as clones of nondiseased individuals established through root- and stump-sprouting or as full- or half-sib seedlings clustered due to a limited radius of seed dispersal (Tubbs & Houston 1990). Currently, suggested management strategies for stands infested by or about to become infested by BBD include reducing the proportion of susceptible beech and retaining the resistant trees so that they may reproduce increasing the frequency of resistant individuals (Leak 2006). However, retaining only the estimated 2-5 percent of beech trees that are resistant may result in a significant loss of genetic variability due to the high degree of relatedness among resistant trees in a stand. The number of resistant genotypes in a stand could be far less than the number of actual resistant stems. In fact, studies using both isozymes (Houston & Houston 1994; Houston & Houston 2001) and RAPD markers (Carey et al. 2001) have confirmed the close relationships between resistant trees clustered in close proximity.

Therefore, conservation of genetically diverse resistant trees will be critical to the long-term survival of healthy, productive American beech. In addition to conserving the genetic mechanisms involved in resistance, it is of equal importance to maintain diversity related to adaptation to local environments. Development of a beech breeding program is an integral part of achieving these goals. Our early research has focused on developing tools required for investigating and eventually understanding the genetics behind the scale-resistance phenotype and to establish methods for preserving and propagating a genetically diverse array of resistant selections.

Controlled Cross-Pollinations in American Beech

The first step in developing a breeding program is to identify the desired traits and determine the underlying genetics responsible for the heredity of those traits. Due to the fact that *Neonectria* infections are not a significant problem in beech in the absence of the scale insect, our research has focused on the scale-resistant phenotype.

The parent trees used in our cross-pollination experiments were located in Ludington State Park, Ludginton, MI. This region is considered a *killing front* having an abundant scale population and the presence of *Neonectria coccinea* var. *faginata*. Although the disease at this location was first reported in 2001 (O'Brien et al. 2001), anecdotal evidence suggests the scale has been present for ten years or more. All parent trees have had their phenotype confirmed by using the artificial infestation technique (Houston 1982) that involves placing insect eggs directly on the bark of the tree. Productive controlled cross-pollinations were achieved between two resistant parents (R x R), and between a resistant and susceptible parent (S x R) (Koch & Carey 2004). Half-sib families were derived from seed collected from two of the parent trees as well as an additional susceptible tree. Also obtained was a half-sib family from a tree (ME) located in a stand in Maine that had been managed for BBD by removal of all susceptible beech stems (Farrar & Ostrofsky 2006). Because the specific trees that provided pollen were not identified nor was their resistance level confirmed, this cross is considered a R x pseudo R cross. A summary of the full- and half-sib families that were obtained is listed in Table 1.

Table 1. Summary of full- and half-sib families.

Female parent	Male parent or open-pollinated	Number of seedlings
1505 (R)	1504 (R)	47
1506 (S)	1504 (R)	50
1504 (R)	OP	33
1506 (S)	OP	89
1510 (S)	OP	22
ME (R)	OP (pseudo R)	71

R=resistant; S=susceptible; OP=open-pollinated

To determine the proportion of the scale-resistant phenotype among individuals in each of these families, the artificial infestation technique was carried out on one-year old seedlings in 2004 and the data have been reported (Koch & Carey 2005). Insect challenges were performed again in 2005 and 2006. The data from 2004 were collected during a different phase of the insect life cycle than those collected in 2005 and 2006. Despite this, the data from all three years did identify the same trends (Koch et al. in prep.). Data from the current year, 2006, are summarized in Figure 1. The largest proportion of resistant progeny is observed in both the R x R controlled-cross and the ME open-pollinated (R x pseudo R) population. Where there is only one resistant parent (S x R) the proportion of resistant offspring is smaller than that seen when both parents are resistant, but greater than what is observed in progeny from open-pollinated susceptible parents. Open-pollinated seed from a resistant parent (1504) yields a proportion of resistant to susceptible individuals much like the S x R cross. This is presumably because the majority of available pollen donors are susceptible, unlike the situation in Maine. The proportions of resistant individuals in the half-sib families from susceptible parents appear to be related to distance between the maternal tree and a potentially resistant pollen donor. For example, 1506 is located within 20 feet of a resistant tree while 1510 is at least 600 feet from the closest resistant tree. The effect of genotype or family on the number of scale insects populating an individual tree was determined to be significant (p < .001) based on an analysis of variance (Koch et al. in prep.). A separate breeding effort headed by Dr. Judy Loo of the Canadian Forest Service has produced seedlings that have been challenged and in the summer of 2007 will yield data available for comparison with the studies reported here.

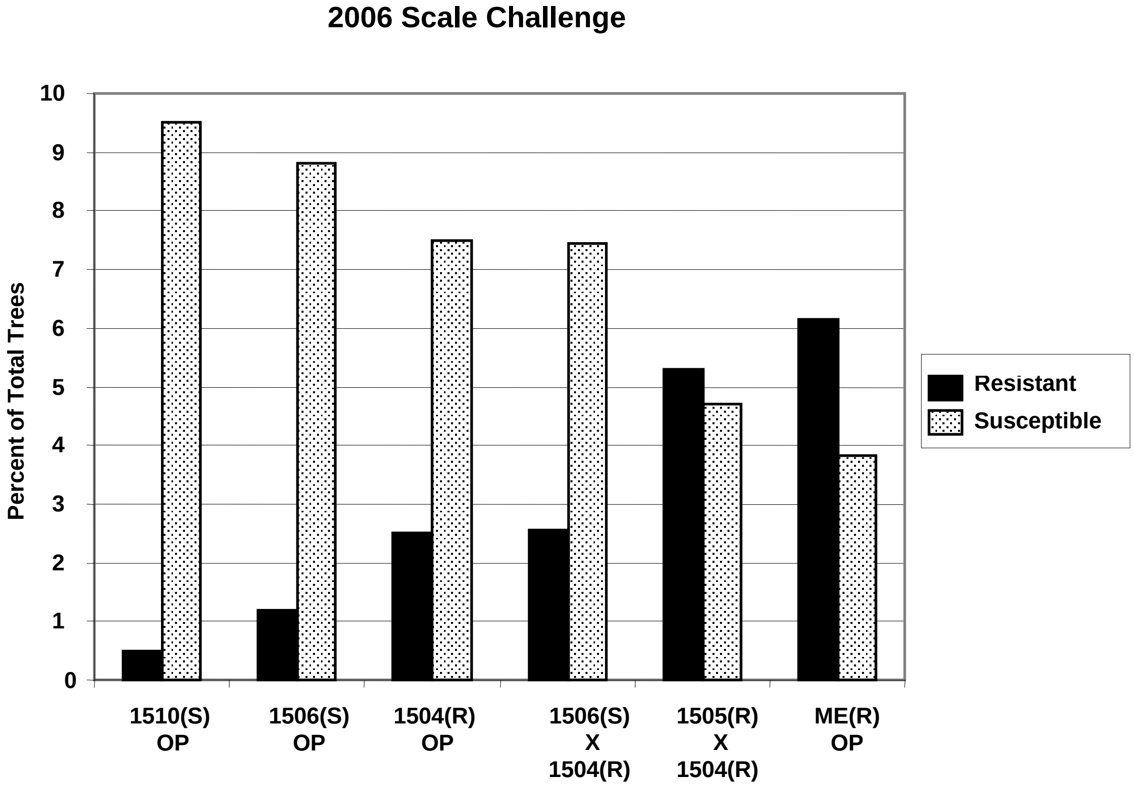

Figure 1. Results of 2006 scale challenge experiment of full- and half-sib families.

Containerized Greenhouse Seed Orchards

The scale-challenge data on the full- and half-sib families demonstrate that scale-resistance is a highly heritable trait with potential for considerable genetic gain in resistance. However, the establishment of seed orchards is a daunting task for several reasons. American beech does not reach sexual maturity until roughly 40 years of age at which point it can be upwards of 70-120 ft.

tall. Flowers are produced at sporadic intervals and good seed crops occur only once every 2 to 8 years (Tubbs & Houston 1990). To facilitate breeding efforts in American beech, effective methods for inducing flowering at younger ages, increasing successful reproduction and facilitating seed collection are needed. Furthermore, effective means to propagate selected parent trees are not available for this intractable species. Micropropagation techniques have been attempted and have proven to be inefficient (Barker et al. 1997; Loo et al. 2005). Traditional grafting methods have proven to be more successful, with a reported average success rate of 33 percent (Loo et al. 2005).

In an attempt to improve the efficiency of vegetative propagation of American beech, we adapted a hot-callus grafting system (Strametz 1984) for use with *Fagus grandifolia* (Carey & Koch in prep). Using this technique in the first year of grafting, 2005, successful graft rates were between 50-60 percent for both scion sources: seedlings (cross-progeny) and mature scion. In one case, several mature scions taken from the resistant tree 1505, produced flowers post-grafting. These flowers were successfully pollinated and went on to produce viable seed (Table 2.) In 2006 the seedling take rate was increased to 71 percent with the overall mature scion take rate of 60 percent. Graft success rates varied depending on the genotype and on the time of year the grafting was performed. Grafts from some genotypes are routinely 90-100 percent successful. In 2006, scions from 19 different mature resistant genotypes gave an overall grafting success rate of 85 percent. Of these 19 genotypes, 16 went on to flower post-grafting. All of the grafts that produced viable flowers were pollinated in the greenhouse and kept there until seed could be harvested. To date, a portion of this seed has begun to germinate and Table 2 demonstrates the significant increase in germination rates in containerized greenhouse pollinations compared to field pollinations. In 2004, resistant tree 1505 was pollinated in the field at Ludington State Park, MI, with pollen collected from Sebois County, Maine. The same pollen, Sebois 23, was also used in 2005 to pollinate containerized grafts of 1505 in the greenhouse. Only 14 percent germination was achieved in the seeds collected from the field pollinations, but 92 percent of the seed collected from the greenhouse pollinations germinated. In all cases, dramatic increases were observed when comparing germination rates of field-pollinated seed to greenhouse-pollinated seed. The highest germination rates obtained in the field were 30-32 percent, and the lowest germination rates reported to date for the greenhouse pollinations are 58-62 percent, representing a minimum twofold increase over the field pollinations.

Discussion

The developmental fate of the flower-producing buds was predetermined at the time the scion was harvested. At this time, it is unknown whether or not these grafts will continue to flower in future years or if grafting will have a rejuvenation effect delaying any subsequent formation of reproductive structures. If this is the case, future research will focus on developing methods to promote flowering. Regardless of the developmental fate of these mature scions once they are grafted, containerized greenhouse seed orchards will greatly expedite the American beech breeding program in a cost-effective manner. Travel costs and other expenses such as repeated bucket truck rental are reduced by greenhouse pollinations, and seedling yield is increased dramatically. This increase in high quality seed production can most likely be attributed to the controlled greenhouse environment where seed-producing grafts receive an adequate supply of water and nutrition which promote vigorous growth and prevent drought and nutrient stresses. Flowers are protected from damaging frosts and developing fruits from herbivore damage. The seedlings obtained from these greenhouse pollinations will be tested for scale-resistance. If they exhibit the same high proportion of resistant offspring as was that observed for field pollinations between two resistant parents, the greenhouse approach may be used in the future to supply landowners with a source of resistant seed or planting material. Resistant seedlings could be planted ahead of the killing front as a way to minimize the impact of beech bark disease and in aftermath forests for restoration purposes.

Table 2. Summary of results of field pollinations and greenhouse pollinations.

Female parent	Male parent	Year/field or greenhouse	# of grafts or branches	Total # of flowers	Total # of seed	# of seed germinated	Percent germination
1506 (S)	1504 (R)	2002/F	4	98	241	77	32
1504 (R)	1506 (S)	2002/F	6	249	675	11	2
1504 (R)	1501 (I)	2002/F	2	69	133	13	10
1505 (R)	1504 (R)	2002/F	2	115	231	51	22
1505 (R)	1503 (R)	2004/F	2	80	33	10	30
1505 (R)	Sebois 85 (R)	2004/F	5	260	206	23	11
1505 (R)	Sebois 52 (R)	2004/F	2	52	21	5	24
1505 (R)	Sebois 23 (R)	2004/F	4	228	109	18	14
1505 (R)	Sebois 23 (R)	2005/GH	14	NA	48	44	92
1201 (R)	1208 (R)	2006/GH	17	71	134	87*	65*
1209 (R)	1219 (R)	2006/GH	16	39	128	80*	63*
1211(R)	1228 (R)	2006/GH	20	38	55	54*	98*
1228 (R)	1211 (R)	2006/GH	16	56	112	71*	64*

*Seed are currently germinating, this number represents only those that have germinated to date. It is expected that this number will increase.

NA=data not available; S=susceptible; R=resistant; I=intermediate; F=field; GH=greenhouse

Previous work has shown that American beech does not self-fertilize readily and there are indications that closely related trees do not efficiently produce beechnuts (Nielson & De Muckadelli 1954; Koch & Carey 2004). The mature resistant trees that remain in aftermath forests are frequently found in clusters and have been shown to be closely related (Houston & Houston 1994, 2001; Carey et al. 2001). Presumably, these closely related clusters will not effectively interbreed. By planting resistant trees with a high level of genetic variation cross-breeding may be facilitated to promote natural regeneration. Further research is needed to determine the parameters that influence the ease with which resistant beech may be restored to aftermath forests.

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The Minnesota Tree Improvement Cooperative: 25 years of meeting tree improvement objectives for the forest products industry in Minnesota and Wisconsin

Carrie Pike, Jim Warren, Andy David
Department of Forest Resources, University of Minnesota

Abstract

The Minnesota Tree Improvement Cooperative (MTIC) was established in 1981 in response to a surge in demand for seed for reforestation efforts. In its 25 years, membership has waxed and waned with the health of the forest products industry in the upper Midwest. The MTIC exists primarily from membership dues of which the majority is paid by public agencies. Orchard-produced seed is used exclusively in planting programs for several tree species, primarily jack pine and white spruce where demonstrable gains and abundant seed production in orchards has driven demand for improved seed. Advanced-generation orchards have been established for jack pine and white spruce, and are planned for red pine and white pine.

The Cooperative Model in Minnesota

Worldwide, tree improvement programs are often executed in a cooperative model to facilitate resource-sharing toward a common goal. In Minnesota, this model is especially applicable because of the high degree of public land ownership. In the state, 54 perent of forest land is managed by public agencies, including federal (14 percent), state (27 percent) and county-level (13 percent) ownership. Public agencies can cooperate openly due to a lack of proprietary issues concerning forest management. In addition, competition between private industries is minimal due to the diversity of products that are produced, i.e., no two mills are competing in the same market. The longevity of the tree improvement program has been achieved largely to the high degree of cooperation among its members.

The primary mission of the MTIC, as stated in its 1981 charter, is to “apply genetic principles through breeding and management to increase the quantity and quality of timber yields in Minnesota and Wisconsin.” Two levels of membership are offered within the MTIC. Full members generally manage at least one orchard, attend meetings, and have voting privileges. Supporting members are invited to attend meetings and workshops but are not entitled to a vote. An advisory committee, consisting of one representative per member agency, provides general direction for projects and budgets for the MTIC. Within the MTIC, decision-making power is not proportional to dues, and all full-members are entitled to one vote per agency. Voting is utilized to legitimize dues increases, and to assure cooperative support for projects. No bylaws are maintained; all decisions are made by consensus of the committee.

The MTIC is based at the University of Minnesota’s Cloquet Forestry Center, which is operated by the College of Food, Agricultural, and Natural Resource Sciences. The MTIC is staffed by one full-time Research Fellow who coordinates day-to-day activities, and one part-time Research Fellow who provides field and technical assistance. The University of Minnesota’s Department of Forest Resources assists with salaries, fringe, and funds the Forest Geneticist who serves as director. The director assists in setting long-range objectives and breeding designs. Two business meetings are held annually, and one workshop is sponsored annually to promote education related to tree improvement or silviculture.

MTIC staff is responsible for assisting members with orchard design and management, along with conducting all tree breeding. Data and pedigree information of all orchard trees are maintained centrally in a database. MTIC staff also coordinates the planting of genetics tests, and is responsible for data collection, analysis, interpretation and distribution of findings. The staff maintains regular communication with cooperative members, distributes monthly and annual reports, and manages the budget. Finally, the MTIC serves to link members with resources at the University of Minnesota in St Paul.

Financial History

Membership in the MTIC has grown from three members in 1981 (Minnesota DNR, Potlatch Corp, Blandin Paper Company) to 20 in 2006. Twelve additional agencies initiated and later rescinded membership over the course of the MTIC's 25 years. In the early years, member dues were supplemented by seed money from the Blandin Foundation. By 1987, seed money expired and membership dues, with support from the University of Minnesota's Department of Forest Resources, became the sole source of funding. In 1998, the Minnesota legislature approved money for white pine blister rust research which continues to cover a portion of salaries and fringe for MTIC staff. In 2006, state agencies paid the highest share of MTIC dues (38 percent), followed by county land departments (33 percent), industry (25 percent), and tribal forest units (4 percent). A biennial contract with the DNR Division of Forestry accounts for the majority of state agency dues. Throughout the MTIC's history, additional dollars have been obtained for specific projects that helped leverage MTIC membership dues. Some of these funding sources included the Wilderness Research Foundation, Iron Range Resources, Blandin Paper Company and the Minnesota DNR Division of Forestry.

Genetic Gains: the value of a tree improvement program

Tree improvement programs are inherently expensive. In addition to dues, each member is required to fund costs associated with orchard establishment and maintenance. All costs related to tree improvement are theoretically offset by the added gains achieved from planting orchard seed. This added gain, or genetic gain, is calculated as the percent of additional wood that can be expected in a forest planting when orchard seed is utilized over woods run material. In general, tree improvement is usually justifiable in economic terms, although most tree improvement research takes place in warmer, subtropical climates. In Minnesota, the economic benefits of a tree improvement program are more difficult to justify due to the long rotation ages. Despite the extended growth required, genetic gains of up to 30 percent in volume have been demonstrated in white spruce which is economically justifiable in northern Minnesota. Additional benefits are possible in terms of improved tree form (straighter trees), survival (improved resistance to disease or superior adaptability), and increased wood density for papermaking. Again, these *gains* are difficult to quantify but can add significant value to a stand.

Seed orchards provide several advantages over woods-run collections. The amount of seed that is produced, the genetic diversity of seed and genetic gains can all be controlled through orchard design. The genetic makeup of the orchard can be changed by removing poor-performing sources while maintaining and propagating productive parent trees. Orchards also provide safe, accessible places for seed collection where cone production can be monitored and manipulated through fertilization and irrigation. In addition, grafted orchards also serve to conserve genotypes that are either remote (i.e., superior white spruce genotypes from southeastern Ontario) or at risk from timber harvests, fire, and windstorms. Thus, the value of orchards from a seed production and gene conservation standpoint cannot be ignored.

Progress to Date

In its 25-year history, the MTIC has advanced programs for five tree species: black spruce, white spruce, jack pine, red pine and white pine. Projects with Norway spruce, Scotch pine, tamarack, and black walnut were initiated but not continued due to poor survival or waning interest. Early work with native tamarack was abandoned, but recent efforts to build a new seed orchard through the MN DNR began with seed collections made in fall 2006.

Black spruce - *Picea mariana.* Black spruce is commonly found in lowland areas across northern Minnesota. Its range extends into the far northern reaches of the east and west coasts of Canada. Black spruce is a relatively slow-growing species, compared with its upland cousin white spruce. Known for its broad genetic diversity and dense wood, black spruce is highly prized in some markets for its pulpwood.

The majority of artificial regeneration in Minnesota is accomplished through aerial seeding, using woods run seed exclusively. Because tree planting represents a small percent of black spruce regeneration, the MTIC has not advanced the black spruce program in recent years. Several orchards have been established and provide seed when it is needed. Four open-pollinated progeny tests, converted to seedling-seed orchards through roguing, have become the primary source of improved seed. In addition, seed is occasionally collected from four grafted orchards. Genetic gains in black spruce are approximately 9 percent for tree heights.

White spruce - *Picea glauca.* White spruce was the first species developed for tree improvement in Minnesota, thus great strides have been made. Plus-tree selections from wild trees in Minnesota, Wisconsin, and Michigan supplement selections from southeastern Ontario, a provenance that is notorious for producing the fastest growing genotypes. The MTIC program continues to measure and manage an open-pollinated progeny test planted in 1986, which features offspring of 292 genotypes. Orchards have been rogued based on early results and three new grafted orchards have been established with the top-ranking families. A second-generation population was created through controlled pollinations using an assortative, single-pair mating scheme. The resulting seedlings were out-planted in 2003 and 2005 at five different locations.

The first white spruce seed orchard was planted on land owned by Blandin Paper Company in 1976. Formerly known as the *Audette farm* and later the *Zigmund* orchard, the now *Latimer* seedling-seed orchard contains open-pollinated offspring from 239 seedlots selected from Minnesota. Originally planted as a progeny test, this site was later converted to a highly successful and productive seedling-seed orchard that is still in use today. Several selections from Latimer were included in the MTIC progeny test, and four trees tested within the top 10 percent of all progeny. Expected gains from newly established grafted orchards are approximately 12 percent for tree heights.

Several seed-source trials have been established to observe measured differences in tree volume between orchard and woods run material. Using ten-year data, tree volumes of improved seed exceeded a woods run source by approximately 30 percent. Gains are expected to be higher with subsequent roguings that took place since seed was collected for this trial. In 2003 a similar trial was planted in order to compare seed from several orchards, including top-ranking trees, along with seed from a woods run source. Genetic gains are expected to meet or exceed those found in the previous trial.

Jack pine - *Pinus banksiana.* Jack pine tree improvement efforts were launched in 1974 with the first seedling-seed orchard *Kallstrom* on Potlatch land. Since then, 15 seedling-seed orchards have been established, and currently nine are actively maintained for seed production. Each orchard contains a set of unique families selected from nearby forests in addition to sources that are replicated at other orchards.

A vast breeding program was undertaken in 1993 and was completed in 1996. A total of 286 crosses were made from the top-performing trees unique to each of eight orchards using assortative single-pair mating. No genotype was used more than once within or across any orchard. In 1999, 143 unrelated full-sib families were out-planted at four sites. By 2000, only two sites remained due to biotic and abiotic calamaties. One of the two remaining sites is located on land owned by Crow Wing County in partnership with the Minnesota DNR. The other site is located at the St Louis County orchard complex in partnership with Iron Range Resources. Both sites are in excellent condition with good survival. Eventually the second-generation populations will be thinned and function as seedling-seed orchards. Controlled pollinations will be performed to advance program further. In 2003, grafting of selected parents from first-generation orchards was begun, to build orchards that will provide a reliable seed source until the second-generation populations can be used for seed collections.

Red pine - *Pinus resinosa.* Three red pine orchards were planted in 1981 by Minnesota DNR (Cotton and Eaglehead) and Potlatch (Gillogly Rd). Additional orchards were later planted by St. Louis County, Cass County in partnership with Beltrami and Hubbard counties, and Wausau-Mosinee. Two orchards were established on land owned by Plum Creek Timber Company, one in northern Wisconsin (Bayfield) and the other in central Wisconsin near Wisconsin Rapids (Petenwell).

By this writing, all but two red pine orchards have been measured and rogued. Petenwell (owned by Plum Creek Timber Company) will be marked in summer 2006 for roguing in fall. Genetic gains are expected to be as high as 12 percent for volume. The remaining orchard, a partnership among Cass, Beltrami, and Hubbard counties, is slated for measurement in 2006 for roguing in 2007. In addition, a comparison trial is slated for planting in 2007 which will test seed from several MTIC orchards alongside a woods run source. Future breeding efforts are being considered and additional grafted orchards are planned.

White pine - *Pinus strobus.* White pine is a relatively new species of interest to the MTIC with the first seed orchards being established in 1985. Due to the close ties that white pine has to Minnesota's history, the state legislature created the white pine initiative in 1996. Designed to reduce the impact of white pine blister rust in Minnesota this funding not only helped jump start the MTIC's breeding and screening programs but also provided funding to state and county agencies for white pine planting and bud capping programs. Currently the MTIC has four grafted seed orchards, one breeding arboretum, and utilizes six progeny test/disease gardens established by the Wilderness Research Foundation.

Because of the introduced disease white pine blister rust, which is often fatal to younger seedlings and saplings, breeding work in this species is focused primarily on increasing disease resistance while growth and form improvements are secondary considerations. The breeding program has benefited from research by earlier researchers such as Cliff Ahlgren, Wilderness Research Foundation; Drs. A. J. Riker and R. Patton, University of Wisconsin; Drs. Scott Pauley and Carl Mohn, University of Minnesota; and Richard Meier and Bill Sery, USDA Forest Service. Their research sought out putative rust resistant individuals and used them to establish disease gardens, seed orchards, and the forerunners of our seedling screening programs. Because the true breeding value of these selected individuals remains unknown our white pine breeding program stresses controlled crosses and screening of progeny through exposure to white pine blister rust to determine which parents can produce seedlings with higher levels of resistance to the disease.

The Road Ahead

Anecdotal reports have indicated that improved seedlings generally perform well in forest tree plantings. In fact, foresters rely solely on improved seed, when available, for the vast majority of white spruce and jack pine tree plantings. In red pine, seed production in orchards is increasing, but demand cannot yet keep up with supply. Future orchards in red pine are being designed to maximize seed procurement efficiency. Ongoing research to improve the resistance of white pine to white pine blister rust has revealed some promising results. Orchards have been established, and are being expanded to incorporate the research results. A plan to incorporate improved black spruce seed into the aerial seeding program is being devised to help ensure that future seed supplies are adequate for future regeneration efforts.

The wood products industry has seen tremendous change in the last few years. Significant land sales and acquisitions have occurred. Several mills have closed, while others ponder expansion. Stumpage prices remain high, especially for *low-value* hardwoods. With all the shifts in the forest products industry that have occurred, conifers remain an important staple of the forest-products industry. Management of that resource is challenged with continued parcelization and fragmentation of existing forest lands. Increasing forest productivity will become essential to maintaining a healthy wood supply on a dwindling land base. The tree improvement program plays a critical role in meeting those increased productivity requirements. Additional progeny tests, seed source trials, and breeding are necessary to advance current tree improvement programs to adapt to future demand. Continued support for the MTIC is necessary for these projects to continue into the future.

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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

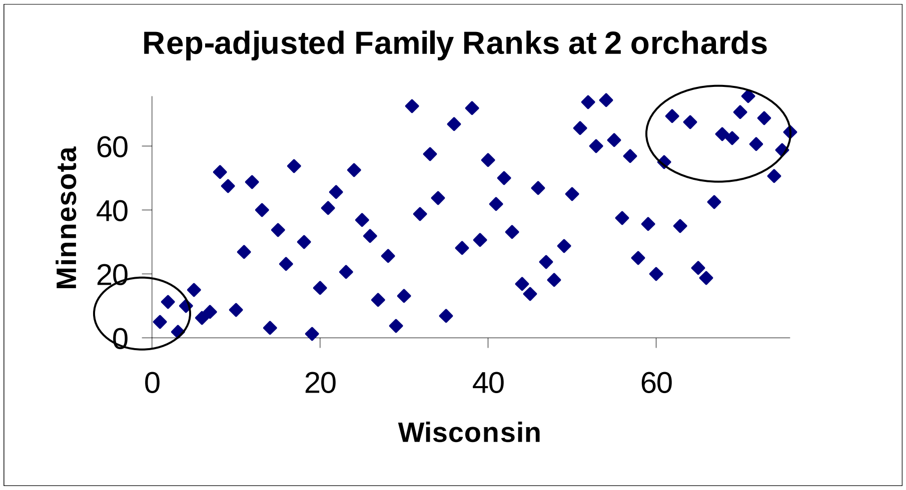

Figure 1. Family ranks (obtained from rep-adjusted least squared means for tree volume) for 76 common families for Wisconsin and Minnesota seedling-seed orchards. Circled trees in lower left of graph are the top-performing families at both sites, and those in the top right are the lowest-performing families.

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.

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Advances in Understanding the Host-Pathogen Interaction in Fusiform Rust Disease of Loblolly Pine

C. D. Nelson, T. L. Kubisiak, Southern Institute of Forest Genetics,
USDA Forest Service, Southern Research Station
H. V. Amerson, Department of Forestry and Environmental Resources,
North Carolina State University

Abstract

Fusiform rust disease continues to be the most destructive disease in southern US pine plantations. Our cooperative research program is designed to identify, map, and clone the interacting genes in both the host and pathogen. Eight resistance genes (*Fr1 - Fr8*) have been genetically mapped in loblolly pine (*Pinus taeda*) (Wilcox et al. 1996; H. V. Amerson unpub.). In addition, DNA marker analysis has proven extremely useful for understanding and manipulating the pathogen, *Cronartium quercuum* fsp. *fusiforme* (Cqf). Recently, we showed that mixtures of spores avirulent and virulent towards *Fr1* are capable of causing multiple infections on seedlings artificially inoculated under standard conditions (Kubisiak et al. 2005). However, only virulent spores are capable of causing disease on seedlings with the *Fr1*allele, while both types of spores cause disease on seedlings without *Fr1* (i.e., *fr1/fr1)*. These results encouraged us to hypothesize the presence of an avirulence gene (*Avr1*) corresponding to *Fr1* and suggested a means for proving its existence. In an ongoing study we inoculated a family segregating for *Fr1 (Fr1/fr1)* with an isolate segregating for avirulence and virulence to *Fr1*. Bulk segregant analysis (Michelmore et al. 1991) was performed on pycniospore drops collected from galls on trees with and without the *Fr1* allele within a single full-sib family. In total, 1,200 RAPD primers were screened against the bulk samples. Preliminary analyses suggests that four RAPD markers are significantly linked to *Avr1*, with one marker showing two recombinant progeny out of 96 and the other three markers showing eight recombinants. In addition, the eight recombinant progeny observed for the three cosegregating markers differ from the two observed for the most closely linked marker, indicating that *Avr1* is most likely within the genomic region flanked by these markers. We plan to use this information along with a recently developed fosmid (40 kb average insert size) library for Cqf to identify, clone and sequence the *Avr1* gene. Once achieved, *Avr1* allele-specific markers will be developed for use in assessing the occurrence and frequency of *Avr1* alleles across the pathogen population. Such information, for all known Avr genes, should provide a reliable means by which informed management decisions can be made regarding the deployment of host resistance genes.

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Resistance Mechanisms in *Pinus strobus* to *Cronartium ribicola*, Causal Agent of Blister Rust

Jason A. Smith, Robert A. Blanchette, Todd A. Burnes, James J. Jacobs,
Department of Pathology, University of Minnesota
LeeAnn Higgins, Bruce A. Witthuhn, Department of Biochemistry,
Molecular Biology/Biophysics, University of Minnesota
Andrew J. David, Department of Forest Resources, University of Minnesota
and Jeffrey H. Gillman, Department of Horticultural Science, University of Minnesota

Successful development and deployment of blister-rust resistant eastern white pine (*Pinus strobus*) depends on an understanding of the underlying mechanisms of resistance. In this study, mechanisms of resistance were explored utilizing germplasm selected by previously by the late Dr. Robert Patton of the University of Wisconsin. Epicuticular wax on needles was evaluated for its influence on *Cronartium ribicola* infection of resistant and susceptible selections of *Pinus strobus*. Environmental scanning electron microscopy comparisons revealed that needles from a resistant selection of eastern white pine, P327, had a significantly higher percentage of stomata that were occluded with wax, fewer basidiospores germinating at 48 h after inoculation, and fewer germ tubes penetrating stomata than needles from a susceptible selection H111. In addition, needles from seedlings that failed to develop symptoms 6 weeks after inoculation, from a cross between P327 and susceptible parent H109, had a significantly higher percentage of stomata occluded with wax compared with needles from seedlings that developed symptoms. In experiments where epicuticular waxes were removed from needles before seedlings were infected, resistant seedlings without wax developed approximately the same number of infection spots (as measured by spot index) as susceptible seedlings with wax intact. Gas chromatography/mass spectrometry comparisons of extracted epicuticular waxes revealed several peaks that were specific to P327 and not found in susceptible H111 suggesting biochemical differences in wax composition. These results implicate the role of epicuticular waxes as a resistance mechanism in *P. strobus* selection P327 and suggest a role for waxes in reducing spore germination and subsequent infection through stomatal openings. Although infection incidence of resistant selection P327 is low, successful infections are often arrested due to a hypersensitive-like reaction. In order to characterize this reaction, a proteomic comparison of needles from resistant and susceptible seedlings was undertaken using two-dimensional gel electrophoresis (2-DE). The results revealed 19 polypeptides specific to resistant seedlings and seven of these specific to infected resistant seedlings. There were 13 polypeptides up-regulated (≥3-fold increase) in resistant family P327 in comparison to needle tissue from susceptible and mock-inoculated seedlings. Electrospray ionization liquid chromatography and tandem mass spectrometry was used to sequence 11 proteins from the 2-DE gels. Sequences obtained from electrospray ionization liquid chromatography and tandem mass spectrometry were used for MSBLAST and Pro-ID database searches allowing identification with a 95 to 99 percent confidence level. Six proteins were determined to be homologs of proteins with known roles in disease resistance, five were determined to be homologs of members of the leucine-rich repeat (LRR) superfamily, and one was a homolog of heat shock protein 90, a protein that serves as a cofactor for certain LRR proteins. This is the first report of members of the LRR family with functional homologs in *Pinus strobus* and of a molecular basis for white pine blister rust resistance in *Pinus strobus*.

Strategies for Improving Forest Productivity in Minnesota

Alan Ek, Professor & Head
Department of Forest Resources, University of Minnesota

Preface

These strategies and suggested gains in forest and related productivity have been compiled by the author from a combination of first principles and experience gleaned from researchers, consultants, and professionals in the Great Lakes Region and beyond. They are intended as a guide to the possibilities in forest management.

Areas with potential for significant gains and estimated range of potential gains (in percent in brackets[ ])

Utilization

1. Smaller top diameters (say down to 2 inch) [1-3%]
2. Variable stick/log length harvesting and transport (including tree length) [2-7%]
3. Utilization of trees < 5" Dbh [1-3%]
4. Utilization of tree tops (branches) [5-20%]
5. Substitution of species currently in less demand for desired species, etc.
6. Biomass harvesting—logging residues, right of ways, WMAs, etc.
7. Mill improvements [mill improvements in utilization rates have shown increases of 2-3% per decade nationwide for more than 30 years]

Harvest Scheduling

1. Shorter rotation ages to reduce mortality, decay, and succession losses [5-20%].
2. Use of forest wide harvest scheduling models [such applications can avoid much of the allowable cut reductions with group grope (GG) approaches; e.g., GG may lead to a reduction of say 35 percent or lead to infeasible solutions. [Model applications hold such reductions to 15% or less and bring rigor to the process].

Stand Treatment

1. Improved guidance for species–site matching, e.g., in considering what to plant or encourage on wet, dry, light, heavy or other soil types, and in considering aspect, and other plant competition or animal damage [choices may simply avoid mortality and/or provide substantial gains in yields].
2. Genetically improved plant materials through conventional breeding [12-22% volume increase per generation of breeding]. Greatest gains are in combination with treatments described below. Hybrids [5-50%]. GMOs may have higher gains. However, hybrids and GMO gains are typically not without very intensive culture. Thus the gains are best compared with usual plant materials that also grown under very intensive culture.
3. Site preparation and early competition control including release [this is a major source of gains in survival and early growth; early height growth may increase 50-100%].
4. Thinning to salvage mortality before it occurs and to improve residual tree growth [5-15%].
5. Thinning early (in rotation), light, and often can salvage mortality, improve residual tree growth, extend tree life and rotation ages and allow for large tree sizes and dramatically increase stand yields [15-100+%]. Very early thinning may be noncommercial but still very

important in increasing yields over an entire rotation. Also, thinning can effectively reduce stress and promote tree health and vigor, e.g., by allowing for more photosynthetic area per tree. Of interest is optimal timing and extent of thinnings over a rotation. Note most thinning is in this region is late, heavy and seldom, i.e., not very productive. In practice, if the crown ratio has fallen much below 40-50 percent, you have waited too long to achieve a strong response.

6. Fertilization and nutrition (including micronutrients) are related. If there is poor nutrition, growth potential and health will decline. Such treatments have become important in other regions, but they have been studied little here. Responses are likely species, age and site specific and there is often a strong interaction with soil moisture. Possible gains [5-20% in growth, some gains in survival as well].
7. Pruning to increase value growth and yield. Typically up to 17ft. [5-20% in value over 15-20 years, i.e., over the period in which first log grades may be improved].
8. Combinations of the above, especially 1, 2, 3, plus 4 or 5 can double usual yields over a rotation.
9. Retention of herbicide options in silvicultural toolbox. Note increasing pressure from forest land certification agencies to eliminate use of herbicides, including Velpar and Accord.

Communications

1. Professionals, loggers and increasingly landowners will need to become familiar with the options. Classic research documents are essential but insufficient. Need electronic availability of information…see for example the beginnings of the regional web-based forest management guidelines at: http://ncrs.fs.fed.us/fmg/nfmg/species/index.html
2. An organized and focused system of demonstration sites is also needed…for each region, covertype and stand age grouping, preferably with treatments side by side. Such sites need not be larger than an acre for most purposes, but they need informative signage.

Major research steps to accomplish the above information needs

1. Synthesis of information on utilization options.
2. Synthesis of information on stand treatments discussed here, notably considering FIA data, and existing and new research plot data to shed light on the following points.
   a. Response to thinning early light and often for major cover types.
   b. Response to combinations of treatments for major cover types.
3. Synthesis of information on models/applications for harvest scheduling, including development of growth and yield models for managed stands (i.e., stands developed from using some of the most instructive stand treatment possibilities noted above).
   a. Assessment of stand treatment compatibility with wildlife habitat measures on a stand and forest basis, including development of comprehensive (many species or guild based) wildlife management guidelines for forest managers.
   b. Analysis of the micro (stand) and macro (forest and regional) economics of these treatments alone and in combinations for meeting various ownership objectives.
4. Rapid and widespread documentation and reporting of results, including continued development, refinement and expansion of web-based syntheses of forest management guidelines, especially management options and examples that foster productivity.
5. Continued monitoring / tracking of study and demonstration plots.

The Eurasian Larch Project

Andrew David
Department of Forest Resources, University of Minnesota

Abstract

From 1996 to 2001 a team of forest geneticists, headed by Dr. Owe Martinsson of Mid-Sweden University, traversed the Russian Federation and collected seed and wood quality data from 1,005 individual larch trees representing four different larch species (*Larix cajanderi, Larix gmelinii, Larix sibirica* and *Larix sukaczewii*) in 49 stands from 17 regions. Ranging from 49º 08' to 66° 51' north latitude and 38º 15' to 152º 30' east longitude this is the largest organized collection of Eurasian larch seed ever and represents an unprecedented opportunity to assess the growth potential of these species around the world and northern Minnesota in particular. To date trials have been established in Alaska, Canada (Saskatchewan) Finland, Iceland, Norway, Russia, and Sweden. Additional trials will be established shortly in Japan, northern Minnesota, and Quebec, Canada. Analyses will be preformed by site as well as across sites to determine superior regions, stands, and families as well as growth patterns associated with latitude, longitude and elevation. As a cooperative effort access to growth data from other trials is assured and this presentation represents a summary of data presented at the recently convened Eurasian larch conference in Arvidsjaur, Sweden (www.siblarch.net).

International Eurasian Larch Project

The International Eurasian Larch Project grew out of conversations that commenced at the 1992 International Larix Symposium in Whitefish, Montana, USA. From 1996 to 2001 at least two different collection forays into Eurasia were made to collect open pollinated seed, wood cores and site characteristics for four different larch speices and their hybrids. By 2002 the first seed was being disseminated to cooperators and participants around the world after having been tested for germination and catalogued. In 2003 the first genetic trials were established and August 2006 the first international Eurasian larch meeting was convened in Arvidsjaur, Sweden.

The International Eurasian Larch Project has three main goals or foci. First, is to investigate the timber properties of Eurasian larch, especially as it relates to the modulus of rupture and the modulus of elasticity. Second, is to discern the genetic variability and adaptive potential of the four larch species. Third is to foster the establishment of native larch stands in Eurasia through active management that mimics natural processes.

Seed and wood cores were collected from more than 1,000 trees in 16 collection areas or regions with three to five stands in each region (Figure 1.) The four larch species that were sampled include *L. sukaczwii*, *L. sibirica*, *L. cajanderii,* and *L. gmelinii.*

As of late summer 2006 a total of 13 different genetic trials had been planted, three in Russia, three in Sweden, two in Finland, two in the US (Alaska), and one each in Norway, Iceland, and Saskatchewan, Canada. Four additional plantings are planned for the near future in Japan; the US (Minnesota); Quebec, Canada; and northeast China. Due to the limited availability of seed and the latitude of each site not all sites received all seedlots.

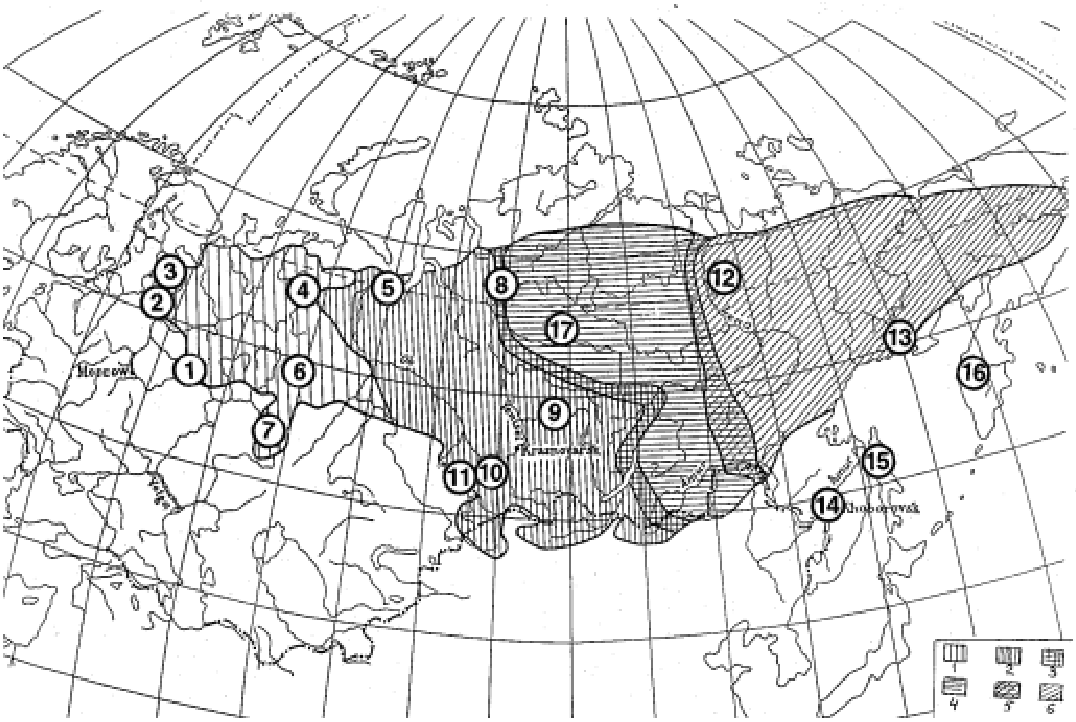

Figure 1. Sixteen collection regions of the International Eurasian Larch Project. Shaded areas represent the range distribution of the four native *Larix* species and their hybrids. From west to east they are *L. sukaczwii*, *L. sibirica*, *L. cajanderii,* and *L. gmelinii*.

The history of the Minnesota planting dates back to 1996 when Gary Wyckoff, the Director of the Aspen/Larch Genetics Cooperative, convinced the cooperators to contribute $10,000 USD to the Eurasian larch collection effort. In March 2003 the ALGC received a sample of seed and by August 2004 the first greenhouse measurements were made. Originally intended for use by cooperators in western Alberta and northern Minnesota the Minnesota planting was dealt a blow when the western Alberta cooperators withdrew from the Cooperative and another in June 2005 when Boise Cascade LLC lands in Minnesota were sold to Forest Capital Partners, Inc. (FCP). As FCP did not have an interest in the productive potential of Eurasian larch the original planting site was lost, an alternative site needed to be found and the 1-0 container seedlings were planted into the nursery. Seedling measurements were taken in September 2005 after two years of growth, one in the greenhouse and one in the nursery.

A search for a second site was conducted through the winter of 2005-2006. Ideally, it would be in northern Minnesota to take advantage of the higher latitude the colder winters and the moister summers that the area affords. By spring 2006 the search had focused on four sites in northern St. Louis County that were all operational forestry sites. In the final analysis none of these sites were acceptable, each for a different reason, and the seedlings were again put into the nursery for a third year of growth, with survival, growth and bud break measurements taken in August 2006. In the meantime site preparation for the genetics trial began on a parcel of land recently acquired by the University of Minnesota in southeastern Koochiching County for a scheduled spring 2007 planting of the 1-2 seedlings.

The interest in Eurasian larch springs primarily from the successes that the ALGC has seen with European larch. European larch is the fastest growing conifer in terms of kg dry weight/ha/year in the upper Great Lakes region and has obvious applications in biomass and biofuels as a feedstock and for enhancing the carbon sequestering capabilities of our northern forests. In the Nordic countries of Sweden, Norway and Finland the Eurasian larch are being considered as a natural substitute for treated Scots pine in an effort to decrease overall chemical usage in construction but also in recreational furniture and children's play equipment. In addition to being used for feedstock in biomass and biofuel situations larch are being used as a substitute for conifers in pulping studies where it pulps similarly to jack pine. It also is being used as a fiber for OSB which is one of the most common construction panels in the industry. From established ALGC trial at Haskell Lake in Itasca County we know that European larch outcompetes red pine in growth when planted on a former red pine cabin log site. Similar results were found in an ALGC trial on a former northern hardwood site with a high water table near Brookston, Minnesota, where European larch was superior in both height and diameter growth to white spruce.

On both of these sites browsing was very common either by deer (Haskell Lake) or by a combination of deer and moose (Brookston). On the Haskell Lake site deer browse was so sever that many of the red pine controls were killed. At Brookston some of the white spruce seedlings were browsed which indicates a high level of ungulate pressure. Larch is relatively tolerant of browse because it has a different architecture from most conifers. As opposed to most conifers where the branches are attached at whorls or nodes along the main stem larch is subopposite which means that the branches do not originate from opposing positions along the stem. Because browsing removes the leader in larch the next highest branch becomes the terminal leader and upward growth can begin immediately.

In other conifers the whorled branch arrangement means that each branch in the whorl directly below the browse line has an equal chance at becoming the next leader. This sorting out process delays upward growth and keeps the seedling short and branch tips within reach of ungulates. The browse tolerance exhibited by larch species exacerbates their growth potential when compared to the native conifers.

The objectives of the Minnesota trial are to compare growth and survival of different seedlots to red pine, determine the seed collection regions adapted to the local climate, identify individuals that would be suitable for use in a seed orchard and share information regarding patterns of growth and adaptability with other researchers participating in the international study.

The site that was chosen for the genetic trial is a former hay field with a high clay content located in southeastern Koochiching County. At latitude 47'57" and longitude 93'05" it is approximately 35 km west of Gheen, Minnesota, located in USDA plant hardiness zone 2.

The Minnesota site that will be planted in spring 2007 will be one of the most southern trials at just under 48' latitude. Many of the most northern collections will not be well adapted to the photoperiod and climate at this location. As a result only 10 collection regions will be planted. The experimental design for the Minnesota planting is shown in Figure 2. There are three replications, collection regions are represented in blocks to make the visual assessment of adaptation ability more obvious. Not all stands within regions and families within stands were available due to limitations in the numbers of seed. Larger numbers of families and stands will be planted from regions that are most likely to have a photoperiod and climate similar to northern Minnesota. Red pine will be planted as a control species.

Table 1. Experimental design for the Minnesota planting of the International Eurasian Larch Project. Numbers refer to collection regions (see Figure 1), red pine is a local control. Large plots (7, 11, 14, 15 and red pine) represent 100 seedlings, plots numbered 1 and 9 represent approximately 66 seedlings, while plots 2, 4, 5, 6, 12, and 13 represent approximately 33 seedlings.

Rep 1	7	2	14	15	1	11	12 13	9	red pine
		4							
		5			6		10 16	6	
Rep 2	1	14	2	11	red pine	15	9	7	12 13
			4						
	6		5				6		10 16
Rep 3	12 13	2	14	7	9	red pine	15	11	1
		4							
	10 16	5			6				6

First year height measurements of the Minnesota seedlings from the greenhouse and a subsequent two years of nursery measurements (2004-2006) indicate that seedlings from three collection regions have maintained their overall height ranks. Seedlings from Chabarovsk, Novgorod and Sachalin were ranked first, second, and third in height in each of the three years of measurements (Table 2).

In the summer of 2006 bud set was measured in the nursery (Table 3). Bud set for a region was defined as a minimum of 90 percent of the seedlings having formed a terminal bud on the leader. Results indicated that the regions that expressed the greatest height growth also tended to be regions with the latest bud set dates. This is not surprising, European larch has a similar growth rhythm which allows it to grow into August when the native conifers have ceased height growth by mid-July. Although this exposes these seedlings to early fall frost events if a terminal bud is formed early September there is usually sufficient time to initiate the cold hardiness process before an extremely hard frost.

Because bud set is typically correlated with photoperiod one would expect northern collection regions to set a terminal bud first and the most southern regions last. However, bud set date did not appear to correlate well with latitude across collection regions. In fact, if there was any trend at all it was for the interior regions, i.e.: 4, 6, 9 11, and 13, to set bud first by 18 July, then the easternmost regions, 1,2 and 7 to set bud by 26 July and finally regions 14 and 15, the westernmost regions to set bud last. This trend toward a regional pattern instead of a latitudinal pattern may indicate the influence of climatic forces such as aridity, or proximity to large water bodies that override the traditional latitudinal control on bud set.

Table 2. Mean height in centimeters for Eurasian larch seedlings from different collection regions, in Grand Rapids, Minnesota after one year in the greenhouse (2004), an additional year in the nursery (2005) and two additional years in the nursery (2006).

Region	Region Name	2004 height (cm)	n	2005 height (cm)	n	2006 height (cm)	n
1	Novgorod	27.7	264	33.2	264	45.0	195
2	Plezetsk	22.4	137	27.0	137	34.2	98
4	Petchora	13.2	124	14.6	124	20.3	95
5	Salechard	17.3	7	20.6	7		
6	Perm	25.0	282	30.1	282	40.4	197
7	Ufa	24.3	428	28.4	428	38.0	299
9	Boguchany	25.6	311	29.6	311	36.2	198
10	Novokutznetsk	26.5	15	31.6	15		
11	Altai	23.2	389	27.7	389	34.5	295
13	Magadan	23.2	119	26.7	119	31.8	51
14	Chabarovsk	30.5	399	37.4	399	54.4	273
15	Sachalin	26.6	439	32.2	439	44.2	298
16	Kamchatka	21.7	30	25.5	30		
		25.2	2944	30.0	2944	40.2	1999

Table 3. Effect of bud set on total height (cm) for three-year-old Eurasian larch seedlings grown at Grand Rapids, Minnesota.

Region	Region Name	Date Bud Set	2006 Height	Rank 2006 Height Growth
4	Petchora	18 July	20.3	10
6	Perm	18 July	40.4	4
9	Boguchany	18 July	36.2	6
11	Altai	18 July	34.5	7
13	Magadan	18 July	31.8	9
1	Novgorod	26 July	45.0	2
2	Plezetsk	26 July	34.2	8
7	Ufa	26 July	38.0	5
15	Sachalin	10 August	44.2	3
14	Chabarovsk	not set	54.4	1

Early International Results

The early international results presented here were compiled from presentations made at the SibLarch Conference in Arvidsjaur, Sweden, in August 2006 (Table 4). Although the collection regions are similar the stands and/or families may differ as these are reported as regional means without additional information. No attempt was made to estimate standard errors, perform a means comparison test or a combined site analysis. Moreover, the results reported here vary in the age of the seedlings and the way in which they were grown. Regardless, these reports provide the first evidence of how larch seedlings from the different collection regions are growing at different geographical sites.

Seedlings were four-years old at both the Canadian and the two Swedish sites, having been grown in the greenhouse first followed by three years of field growth. As mentioned earlier the Minnesota seedlings were three years old, one year in the greenhouse and two years in the nursery. Despite the differences in seedling age and geographic location there are similarities in height rankings. Regions 1, 14 and 15, (Novgorod, Chabarovsk, and Sachalin) were in the top three regions for total seedling height at three of the four sites. The results in Minnesota were similar to results reported in Saskatchewan, Canada, and two sites in Sweden.

Table 4. Total height for Eurasian larch seedlings from 18 different collection regions grown at four different locations. The three tallest performing regions at each site are highlighted for comparison.

		$47^{0}22'$	$52^{0}56'$	$57^{0}47'$	$65^{0}11'$
Region #	Region Name	United States	Canada	Sweden	Sweden
		Grand Rapids, MN	Birch Hills, SK	Österbymo	Järvträsk
1	Novgorod	45	100	119	46
2	Plezetsk	34	63	80	51
3	Onega			66	53
4	Petchora	20	20	31	42
5	Salechard		32	36	41
6	Perm	40	79	96	44
7	Ufa	38	95	117	46
9	Boguchany	36	75	78	50
10	Novokutznetsk		90	81	53
11	Altai	35	61	47	36
12	Yakutiya		30	0	40
13	Magadan	32	41	90	58
14	Chabarovsk	54	72	147	66
15	Sachalin	44	61	141	61
16	Kamchatka		42	76	44
18	Lassnmaa (so)			75	54

Summary

Cooperators in the International Eurasian larch project, which has its roots in the 1992 International Larix Symposium, will plant their final sites in the spring of 2007. These plantings will bring the total number of sites to 17 on three continents. Height data collected over several years on nursery grown seedlings in Grand Rapids, Minnesota shows consistent performance among provenances, with the Chabarovsk, Novgorod, and Sachalin regions the tallest. These regions are also among the latest to set bud in the Grand Rapids nursery which is likely contributing to their increased height growth. The seedling height data was fairly well correlated with height data from other plantings of the same provenances around the world; especially for sites planted at latitudes lower than 58º. This is not surprising if the provenances are genetically distinct and the species possess a broad level of adaptability. However, despite the correlations among provenances in different years at the same site or among provenances at different sites it is still too early to make recommendations about the suitability of these provenances for deployment in northern Minnesota. Thus these results can only be considered preliminary because the extremes in weather and not the means will dictate the level of adaptation to local climate.

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POSTER ABSTRACT

Seed Source Selections Under Climate Uncertainty

William H. Parker and Kevin A. Crowe
Faculty of Forestry and the Forest Environment, Lakehead University

There is broad consensus among meteorologists that the earth's climate is changing and will continue to change, although there is deep uncertainty over the rate and magnitude of future change. Planned adaptation to climate change is therefore a necessity of growing importance. To date, there exists no method or decision support model to determine the most suitable seed source to use in artificial regeneration of a given site under the conditions of a changing climate. The goal of this study was to develop and implement a decision support model to select a mixture of seed sources that minimizes risk of maladaptation at a given site under a number of equally probable climate change scenarios as indicated by several global circulation models. Elements of modern portfolio theory were combined with a species range impact model (SRIM) based on genecological data from a series of jack pine provenance trials to construct the decision support model. The SRIM was used to provide estimates of how well adapted a given seed source would be to a predicted climatic condition at a given site for each climate change scenario. The first field application of the model is a south to north implementation of the seed source portfolio selections for jack pine in north western Ontario. Completely randomized block trials of selected and local sources are being established as demonstration plots near Fort Frances, Dryden and Red Lake.

Crowe, K., and W.H. Parker. 2007. Using portfolio theory to guide reforestation and restoration under climate change scenarios. Climate Change (in review).

Jack Pine and White Pine: Wisconsin's Tree Improvement Approach

Ray Guries, University of Wisconsin-Madison
Gregory Edge, Wisconsin DNR
David Stevens, University of Wisconsin-Madison

Selection and breeding continued in four second generation populations of jack pine growing at the Ten Mile Creek Seed Orchard (Wood Co.). Height measurements in conjunction with scores for incidence of pine-oak gall rust (*Cronartium quercuum*) were used to select superior trees for breeding using a polycross mating scheme to produce progeny for third generation populations. Controlled pollinations were completed in the spring of 2005, producing 352 cones from which 4,997 seeds were extracted this past fall. The Ten Mile Creek populations were thinned in 2006 following completion of breeding. Fifty percent (1,700 trees) of the planting was removed to provide more space for crown expansion and facilitate development of a production seed orchard. Further thinning and pollarding of trees to control height growth will take place during the winter of 2007 and 2008.

Two eastern white pine family tests established in Wisconsin provide data on early survival and third-year height, and we can already observe patterns of variation related to provenance and planting location. For example, seed collected from populations in eastern Upper Peninsula Michigan (EUP) performed very poorly in north-central WI as did several provenances from Minnesota. In general, the best performing families came from Wisconsin counties south and west of the planting site in Oneida County. At the Black River Falls site, UP seed sources also fared poorly, as did some from Iron, Vilas, and other northern Wisconsin counties. In general, the best performers at Black River Falls were those sources originating in Jackson, Monroe, Sauk, and Burnett counties. Results after three years are inadequate for predicting long-term success, but these patterns are clearly different for north vs. central Wisconsin, suggesting that some care should be taken with the choice of eastern white pine seed source for reforestation even within Wisconsin.

Development of Novel Ash Species Hybrids to Introgress Resistance to Emerald Ash Borer from Asian to North American Ash Species

Mary E. Mason, David Carey, Richard Larson, Jennifer Koch
USDA Forest Service, Northern Research Station

Agrilus planipennis, a beetle native to Asia and called Emerald Ash Borer (EAB), has been introduced into the Great Lakes region and is rapidly spreading. No resistance has been identified in native North American ash species, so the entire ash resource of the eastern U.S. and Canada is at risk of loss due to EAB. In contrast, outbreaks of EAB in Asia appear to be isolated responses to stress and do not devastate the ash population. It is likely that heritable genetic resistance to EAB is part of the reason EAB damage is less severe in Asia.

Our current work is focused on utilizing heritable resistance to EAB to produce EAB resistant hybrids between North American ash species and Asian ash species. Two years of breeding efforts have produced very few putative interspecific hybrids. Current goals of the breeding program are (1) to identify successful species combinations for hybridization, (2) to identify barriers to interspecific hybridizations, and (3) develop techniques to circumvent hybridization barriers. Additional work is focused on developing markers to confirm hybrid parentage, and for later incorporation into marker-assisted breeding strategies. Seventeen microsatellite marker loci previously published for *Fraxinus excelsior* have been screened against a small sample size panel of the species of primary interest to the breeding program. In addition, ash seed germination studies are ongoing to develop reliable protocols for germinating seeds from difficult to germinate species, and to produce seedlings of Asian species for screening for resistance to EAB in North America.

Introduction to the History, Use, and Facilities of the Cloquet Forestry Center

James Warren
Department of Forest Resources, University of Minnesota

The University of Minnesota's Cloquet Forestry Center is the University's primary research and education forest and has been pursuing its mission "To conduct applied education, research and outreach related to northern forests" since 1909. The Center has more than 3,400 acres of contiguous, actively managed forest on the southern edge of the boreal forest. Facilities include more than 10,000 ft^2 of indoor learning space for up to 140 people, with lodging available for 72 people. In 2005, the Center hosted more than 10,000 user days in approximately 200 meetings and classes.

Attendee List for Northern Forest Genetics Association Conference

September 06, 2006 Cloquet, Minnesota
Participants: 39

Dr. Paul Berrang
Regional Geneticsist
USDA Forest Service
626 East Wisconsin Ave
Milwaukee, WI 53202
Phone: 414-297-3569
pberrang@fs.fed.us

Mr. Paul Bloese
Tree Improvement Supervisor
Michigan State University
Dept. of Forestry
126 Natural Resources Bldg
East Lansing, MI 48824
Phone: 517-355-5183
bloese@msu.edu

Mr. Lew Castle
Resource Supervisor
Potlatch
P.O. Box 504
Cloquet, MN 55720
Phone: 218-879-0430
Fax: 879-0452
lew.castle@ptlatchcorp.com

Mr. Paul Charrette
Tree Improvement Specialist
Superior-Woods Tree Improvement Association
Lakehead University
955 Oliver Road
Thunder Bay, ON P7B 5E1
Phone: 807-343-8502
Fax: 807-343-8116
pcharret@lakeheadu.ca

Dr. Andrew David
University of Minnesota
UMN / NCROC
1861 Hwy. 169 East
Grand Rapids, MN 55744
Phone: 218.327.4521
adavid@umn.edu

Mr. Gregory Edge
Forest Geneticist
Wisconsin DNR
3550 Mormon Coulee Road
La Crosse, WI 56401
Phone: 608-785-9011
gregory.edge@dnr.state.wi.us

Dr. Alan Ek
Professor and Head
University of Minnesota
Dept of Forest Resources
1530 Cleveland Avenue N
St. Paul, MN 55108
Phone: 612-624-3098
aek@umn.edu

Dr. Julie Etterson
Assistant Professor
University of Minnesota Duluth
Dept of Biology
153A Swenson Science Building
Duluth, MN 55812
Phone: 218-726-8110
jetterso@d.umn.edu

Mr. Mike Fasteland
Potlatch
P.O. Box 504
Cloquet, MN 55720
Phone: 218-879-0429
Fax: 218-879-0452
mike.fasteland@potlatchcorp.com

Mr. Adam Fink
Forester
Grand Portage NRM - Forestry
PO Box 428
Grand Portage, MN 55605
Phone: 218-475-2415 x-64
Fax: 218-275-2615
adamf@grandportage.com

Mr. Gene Grell
Forester
UPM Blandin Paper
115 SW 1st ST
Grand Rapids, MN 55744
Phone: 218-327-6606
Fax: 218-327-6898
gene.grell@upm-kymmene.com

Dr. Ray Guries
UW-Madison
1101 Union Rd
Oregon, WI 53575
Phone: 608-262-0449
Fax: 608-262-9922
rpguries@wisc.edu

Ms. Kathy Haiby
University of Minnesota
1861 Hwy 169 East
Grand Rapids, MN 55744
Phone: 218.327.4300
haiby001@umn.edu

Mr. Egon Humenberger
U of M - NCROC
1861 E. Highway 169
Grand Rapids, MN 55744
Phone: 218- 327-4523
Fax: 218- 327-4126
humen002@umn.edu

Mr. Rick Klevorn
MNDNR
500 Lafayette Rd
St Paul, MN 55155
Phone: 651-259-5274
rick.klevorn@dnr.state.mn.us

Dr. Jennifer Koch
Research Biologist
USDA Forest Service
359 Main Road
Delaware, OH 43015
Phone: 740-368-0188
Fax: 740-369-2601
jkoch@fs.fed.us

Mr. Quintin Legler
PFM Forester
UPM - Blandin
115 SW 1st Street
Grand Rapids, MN 55721
Phone: 218/327-6304
Fax: 218/327-6387
quintin.legler@upm-kymmene.com

Ms. Mary Mason
Research Associate
US Forest Service
Forestry Sciences Laboratory
359 Main Rd
Delaware, OH 43015
Phone: 740-368-0189
mmason@fs.fed.us

Dr. Steve McKeand
North Carolina State University
Department of Forestry
Raleigh, NC 27695
Phone: 919-515-6073
steve_mckeand@ncsu.edu

Richard Mergener
Mr. Tree Improvement Supervisor
Michigan DNR
23033 Maple Drive
McMillan, MI 49853
Phone: 906-341-2518
mergener@michigan.gov

Ms. Deb Moritz
Assistant Nursery Supervisor
MN DNR
PO Box 95
Willow River, MN 55795
Phone: 218-372-3182
Fax: 218-372-3091
deb.moritz@dnr.state.mn.us

Mr. William Murphy
General Manager
Forest Renewal Co-op Inc.
955 Oliver Road
Lakehead University
Thunder Bay, ON P7B 5E1
Phone: 807.343.8313
Fax: 807.343.8669
frcoop@lakeheadu.ca

Mr. Jake Mutchler
Forester
Itasca Forestry
PO Box 273
Cohasset, MN 55721
Phone: 218 328-6261
info@itascagreenhouse.com

Dr. Dana Nelson
Project Leader
USDA Forest Service
Southern Institute of Forest Genetics
23332 Hwy 67
Saucier, MS 39574
Phone: 228-832-2747 x 201
Fax: 228-832-0130
dananelson@fs.fed.us

Mr. Philip O'Connor
Tree Improvement Specialist
Indiana DNR
PO Box 218
Vallonia, IN 47281
Phone: 812-358-3621
Fax: 812-358-9033
poconnor@dnr.in.gov

Dr. Ronald Overton
Area Regeneration Specialist
USDA Forest Service
Purdue University
715 West State Streed
West Lafayette, IN 47907
Phone: 765.496.6417
Fax: 765.494.9461
roverton@fs.fed.us

Mr. Mark Pannkuk
Forester III
St. Louis County Land Department
5713 Old Miller Trunk Highway
Duluth, MN 55811
Phone: 218-625-3700
Fax: 218-625-3733
pannkukm@co.st-louis.mn.us

WDr. illiam Parker
Professor
Lakehead University
955 Oliver Road
Faculty of Forestry
Thunder Bay, ON P7B 5K9
Phone: 807 343 8484
Fax: 807 343 8116
bill.parker@lakeheadu.ca

Ms. Kristin Peterson
Tree Improvement Forester
Wisconsin Dept. of Natural Resources
Forestry Division - FR/4
101 South Webster Street
Madison, WI 53707
Phone: 608-264-6044
Fax: 608-266-8576
kristin.peterson@wisconsin.gov

Mrs. Carrie Pike
University of Minnesota
175 University Rd.
Cloquet, MN 55720
Phone: 2187266406
cpike@umn.edu

Dr. Don Riemenschneider
Research Geneticist
USDA Forest Service Forestry Siences Lab
5985 County Road K
Rhinelander, WI 54501
Phone: 715-362-1115
Fax: 715-362-1166
driemenschneider@fs.fed.us

Dr. Peter Schaefer
South Dakota State University
Horticulture, Forestry, Landscape & Parks Dept.
Box 2140A
Brookings, SD 57007
Phone: 605-688-4732
Fax: 605-688-4713
peter.schaefer@sdstate.edu

Dr. Jason Smith
University of Minnesota
495 Borlaug Hall
1991 Upper Buford Circle
St Paul, MN 55108
Phone: 612-625-6231
smit1278@umn.edu

Mr. David Stevens
Wisconsin State Forest Tree Improvement
Research Specialist
U.W.-Madison Forest Ecology & Management
1630 Linden Dr.
Madison, WI 53706
Phone: 608-263-6977
dstevens@wisc.edu

Mrs. Carrie Sweeney
Orchard Manager
USDA Forest Service
18100 Saul Spring Road
White Lake, WI 54491
Phone: 715-276-7400
csweeney@fs.fed.us

Mr. Thomas Toratti
Forester
Koochiching Lands & Forestry
P.O. Box 211
309 Front Street
Littlefork, MN 56653
Phone: 218 278 6643
Fax: 218 278 6249
ttoratti.koochlaf@frontiernet.net

Mr. Jim Warren
Research Fellow
University of Minnesota
175 University Rd.
Cloquet, MN 55720
Phone: 2187266405
Fax: 2188790855
warre036@umn.edu

Dr. Keith Woeste
Molecular Geneticist
USDA Forest Service
715 West State Street
Pfendler Hall 226A
West Lafayette, IN 47907-2061
Phone: 765-496-6808
Fax: 765-494-9461
woeste@purdue.edu

Dr. Ron Zalesny
Research Geneticist
USDA Forest Service Forestry Siences Lab
5985 County Road K
Rhinelander, WI 54501
Phone: 715-362-1132
Fax: 715-362-1166
rzalesny@fs.fed.us