

North Carolina State University – Industry Cooperative Tree Improvement Program

49th Annual Report

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Front Cover

Despite the destruction from Hurricane Ivan in September, 2004, there were some bright spots. Sam Campbell is very proud of the 300 bushels of cones that were collected from Joshua's 3rd-cycle seed orchard at Wildfork in southern Alabama. Cone production is just getting started in this 7-year-old, 17-acre seed orchard and should increase dramatically in the coming years.

Fortunately, young orchards survived the wind damage from Ivan much better than the numerous older 2nd-generation and 1.5-generation seed orchards in the area. A summary of the impacts that Hurricane Ivan had on tree improvement activities in western Florida and southern Alabama is in this Annual Report.

EXECUTIVE SUMMARY

BREEDING, TESTING, AND SELECTION

For the third-cycle breeding, more than 17,000 bags with flowers have been pollinated, most of which were done in the last three years. Approximately 18.5% of the PMX breeding and 5.5% of the full-sib breeding is complete. The first pollen mix tests for the 3rd-cycle breeding program were established in 2005 in the Coastal Breeding Zone. A second series for the Coastal Zone and the first series for the Piedmont Zone will be established next year. Seeds have also been sown for the first of the checklot comparison trials. The impacts of the 2004 hurricane season were far reaching. Severe damage to breeding and testing programs in western Florida and southern Alabama resulted from Hurricane Ivan.

PROGRESS REPORTS FOR RESEARCH

Considerable genetic variation in wood density was found among elite parents in Coastal SC, GA, and AL (Regions 3, 4, & 5), Piedmont of GA (Region 7), but not for Upper Gulf (Region 6) (Table 3). Variation among parents in Region 1 (VA) was modest. Other wood properties (microfibril angle, cellulose and lignin content, and stuff) are being analyzed for this population of trees.

The effect of positive assortative mating combined with efficient redirection of resources to the best parents may have a tremendous positive impact on the outcome of forest tree breeding programs.

Genetic variation in stem taper and bark thickness was found in a 13-year-old genetics x silviculture trial in GA. Nonetheless, D²H measurements capture a great deal of the genetic variation in total inside-bark volume.

From detailed analyses of diallel tests of cad-n1 heterozygous parents, the increased wood density and growth associated with the cad-n1 allele were limited to specific crosses between heterozygous and wild type trees. There is also a trend of presenting pleiotropic growth and wood density which is apparently controlled by the cad-n1 gene interacting with other genes contributed from the second parents.

SEED PRODUCTION

The 2004 seed collection for the Cooperative was substantially lower than in previous years. The crop was not terribly big to begin with, and the damage from Hurricane Ivan, limited harvest from only selected parents, and low market demand for seedlings all contributed to the low yield. Yields per pound were not lower in 2004.

ASSOCIATED ACTIVITIES

Two graduate students completed their programs, and two new students began graduate studies. Nobel Prize Laureate, Dr. Norman Borlaug visited NC State in April 2005. He lectured to students and staff about the benefits of crop and tree breeding and their positive impacts on humankind. The Cooperative hosted the IUFRO Conference on Forest Genetics and Tree Breeding in the Age of Genomics in Charleston, SC. The focus of this year's contact meeting in Fernandina Beach, FL was on breeding and testing activities. Membership in the Coop stands at 16, with 5 state agencies and 11 private corporations. CellFor joined the Coop as a full member, and the SC Forestry Commission withdrew. A new Research Associated Membership category started with ArborGen as the first associate member. On a sad note, Dr. Dave Bramlett died in April 2005. Dave was a pioneer in tree improvement and reproductive biology and was a dear friend to all of us in the Cooperative.

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INTRODUCTION

2004 –2005 can best be described as a year of change and a year of big events. For Cooperative members and for the staff in Raleigh, the biggest change was Bailian Li and Steve McKeand taking over as Co-Directors of the program. Tim Mullin is leaving NC State in June 2005 after 5 years as Director of the Cooperative. We wish Tim the best.

As southern forestry and forest management continue to changes, our Coop membership reflects the unprecedented change in forest land ownership over the past 20 years. We currently have 16 members and one associate research member, including 5 integrated forest products companies, 5 state forestry agencies, 1 nursery company, 1 landowner, 2 REITs (Real Estate Investment Trust), 1 TIMO (Timber Investment Management Organization), and 2 Biotechnology Companies (1 as an associate member). In 1985 at the height of membership in the program, there were 29 members, with 24 integrated forest products companies, 4 state forestry agencies, and one nursery company. Who would have predicted 20 years ago that our two newest members, CellFor as a full member and ArborGen as an associate member, would be biotechnology companies? Back then, who knew what a TIMO or a REIT was? Our “traditional” players in tree improvement and forest management have changed and will likely change in ways few can predict. We welcome our newest members Cell For and ArborGen, and we will prepare our program to meet new challenges in the future.

The hurricane season of 2004 was the most devastating in recent memory. The state of Florida took the direct hit from 5 major storms. While the impacts were much less serious, North Carolina felt the direct effects or aftereffects of 7 different storms. There were few places in the Southeast not affected. Fortunately, relatively few tree improvement programs were seriously impacted, but don’t tell that to folks at International Paper Company in Jay, FL, Joshua Timberlands near Monroeville, AL, or Smurfit-Stone Container Corporation in Brewton, AL. These programs, especially the seed orchards and breeding programs were all set back dramatically (see story later).

The Cooperative hosted one and will host another prestigious conference this year. In November 2004, we hosted a joint conference of multiple working parties related to breeding and genetic resource management of IUFRO Division 2. Over 100 papers and posters were presented at this conference entitled "Forest Genetics and Tree Breeding in the Age of Genomics - Progress and Future" (details later). In June 2005, we will host the 28th Southern Forest Tree Improvement Conference in Raleigh.

At the University, the past 12 months have seen big changes for us in the Department of Forestry and Environmental Resources – starting with a new name that better reflects what we do. Barry Goldfarb took over as our new Department Head August 1, 2004. Barry is no stranger to our Cooperative and southern forestry. He has headed the Rooted Cutting Program since 1994 and is an old friend and colleague of the Coop. We look forward to working with Barry, and we welcome Fred Cubbage, former Department Head, back as a full-time faculty member in the Department.

We have a new Chancellor at NC State. Dr. Jim Oblinger, former Provost and prior to that, Dean of the College of Agriculture and Life Sciences, became the big boss January 1. Our Dean, Larry Nielsen is filling in as interim Provost, but Larry promises that he is returning to our College of Natural Resources the minute the new Provost starts. As a part of the chain reaction, who better than J.B. Jett to fill in as the interim Dean? J.B. spent 26 years with our Coop and has done a yeoman’s job the past several months as acting Dean of CNR. We know that he looks forward to returning to his “quiet life” as Associated Dean for Research when Larry gets back.

And finally, all of us are proud as the North Carolina State University – Industry Cooperative Tree Improvement Program starts its 50th year of operation come July 1, 2005. We have enjoyed 49 years of a very productive partnership with the forest products industry, forest landowners, state and federal agencies, and the citizens of the South. At this year's Advisory Meeting in conjunction with the 28th Southern Forest Tree Improvement Conference we will commence our golden anniversary year with a reception to honor our past and celebrate our future. Current and former company and state personnel, current and former staff members, friends and family all will come together to toast to our well-being.



Many 3rd-cycle orchards such as this one that supplies seeds for Hancock's reforestation programs in the Piedmont are just reaching the cone production stage.

SELECTION, BREEDING, AND TESTING

THIRD-CYCLE MAINLINE BREEDING PROGRESS

The total third-cycle breeding population for mainline has reached 925 in 2005. This is a census numbers representing all selections from three breeding zones within the Coop., which includes Coastal = 384, Piedmont = 364, and Northern = 177 (Table 1).

All selections have been assigned into sublines within each of three breeding zones. A total of 77 breeding sublines were formed for the three breeding zones, e.g., 32, 31 and 14 sublines for Coastal, Piedmont and Northern Zones, respectively (Table 1). All sublines are assigned to cooperators within each breeding zone, most with 8-15 selections, except one with 22 selections. Subline selections have been grafted into breeding orchards or top-grafted on to big trees for breeding by each of the cooperators.

The third-cycle breeding is progressing well with great progress by Cooperative members in 2005. A complementary design with polycross mating for among family selection and full-sib mating for within-family selection is being done. More than 17,000 bags with flowers have been pollinated, most of which were done in the last three years. The numbers of crosses that have been completed or are in progress are summarized in Table 1. Crossing was much more active in the Coastal Zone than Piedmont and Northern Zone.

Cooperative members within each breeding zone have grafted all parents selected for generating the pollen mix (PMX) for polycross mating. Three 3rd-cycle check seed lots are being created for each of the three regions by using the same 20-parent PMX applied onto 10 of the selections in the mix (Table 1). Checklot crossing progressed well last year in the Coastal and Piedmont regions (Table 1). Sufficient quantities of checklot seeds have been produced for all three regions (Coastal, Piedmont, and Northern) for establishing the PMX tests in 2005. More seeds will be needed to support more test series that will be established in the future.

In addition to the 3rd-cycle checklots, several well-characterized families (common family checks) from the first two cycles of breeding are being crossed with the pollen mix. These families will be included in all tests to contribute to estimates of variance components and provide better comparisons. Seeds from some common family checks have been collected for each zone (Table 1).

Full-sib controlled crossing has also commenced in the last few years and full-sib seeds have been produced (Table 1). Seed production from full-sib cross mating is expected to rise in the coming years as the third-cycle selections produce more flowers. These full-sib crosses will generate seeds for within-family selection for the next breeding cycle.

Controlled pollination of loblolly female strobili.



Table 1. Summary of third-cycle breeding progress, as of winter 2004-05.

Type of crosses	Breeding Region	# Coop-erators	# Sublines	Total # Parents	#Crosses producing Seed	#Crosses of Sufficient Seed	% Done Crosses
Polycross	Coastal	10	32	384	170	113	29.4 %
	Piedmont	9	31	364	77	46	12.6 %
	Northern	6	14	177	34	13	7.3 %
	Total	16	77	925	281	172	18.5 %
PMX checks	Coastal	10	--	10	10	9	90 %
	Piedmont	9	--	10	10	8	80 %
	Northern	6	--	10	10	3	30 %
PMX CFs	Coastal	10	--	7	4	4	57 %
	Piedmont	9	--	7	2	2	28 %
	Northern	6	--	7	2	1	14 %
Full-Sib	Coastal	10	32	235	39	21	9.0 %
	Piedmont	9	31	186	11	7	3.8 %
	Northern	5	13	81	6	3	3.7 %
	Total	16	76	502	56	31	5.5 %

#Crosses of Sufficient Seed: A parental cross is counted here if the "total seed requirement" has been met for that cross; i.e. if enough seeds have been produced for that cross to establish a full test series.

PMX checks: Polycrossed checklot mixes

PMX CFs: Polycrossed Common Family checks

THIRD-CYCLE PROGENY TESTING

Polycross tests

The first series of 15 third-cycle polycross (PMX) tests was established for the Coastal region in 2004. Nine members of the Cooperative contributed to this ground-breaking effort. With the seeds harvested in the fall of 2004, we have now sufficient quantity of seeds to establish a set of PMX tests for the Piedmont region this year, as well as another set of Coastal PMX tests. Seeds have been distributed to members this spring for establishing 5 tests for both the Piedmont and Coastal PMX test series. For the Coastal test series, the tests will be distributed across the region from coastal North Carolina to southern Alabama. Five Cooperative members in each region will be responsible for establishing these five progeny tests in winter 2005-06.

As we continue to make progress for breeding programs in all three breeding regions (Table 1), it is expected that additional test series will be established in 2006 and beyond.

Checklot comparison tests

The purpose of the Checklot Comparison (CComp) tests is to link second-cycle checklots (CC) from eight test areas with the new third-cycle checklots from each zone for gain estimation. By fall 2004, sufficient quantity of checklot seeds had been harvested to establish a set of CComp tests. Seeds were distributed to members for establishing 5 tests next winter. The tests will represent the second-cycle test areas 3, 4, 5, 6, and 7. In each test, checklots will be planted in block plots, with 4 blocks per test. Five suitable CC's and the third-cycle checklots will be planted in each test.

Ivan the Terrible

On September 16, 2004, Hurricane Ivan struck the Gulf Coast of Alabama and Florida with incredible force (see pictures on back cover). The devastating impacts on forestry and tree improvement programs in western Florida and southern Alabama will be felt for many years. International Paper Company's seed orchard and breeding complex in Jay, FL, Smurfit-Stone Container Corporation's Escambia Seed Orchard in Brewton, AL, and the Joshua Timberlands Wildfork Seed Orchard all suffered significant damage. In addition, the Florida Division of Forestry's Munson Seed Orchard was damaged.

While many progeny tests in the region were destroyed or damaged, in many ways, the Cooperative was very fortunate with the timing of the storm. Had Ivan hit a few years earlier when cooperators were in the middle of measuring dozens of diallel tests, we would have had a real mess trying to collect data and salvage tests. Fortunately, relatively few tests were impacted. Tests older than 12-15 years were usually completely lost, but only one Early Diallel Measurement Series was destroyed. The younger tests such as those in the Lower Gulf Elite Population Program were damaged, but all can be salvaged.

Seed orchards on the other hand were substantially damaged, and many were destroyed. Cone production will be seriously impacted for 2 or 3 years, but most cooperators have substantial seed inventories and the shortage can be managed with minimal pain. An overriding impression after seeing the orchards in the region is that old is not always good (this is hard for us "middle-agers" to say). Without a doubt, the older the orchard, the worse the damage. First-gen and 1.5-gen loblolly orchards were hit badly but most were salvageable.

Amazingly some ramets were snapped like twigs, blown over, or had most of the crown taken out, and others looked as if they were hardly touched. Everything in a seed orchard is clonal, so why wouldn't hurricane resistance be?

Unfortunately, many of the old slash and longleaf orchards in the region were essentially 100% loss. Why these orchards took such hits, is not clear.

Second-generation loblolly orchards typically looked pretty awful, but they were not as bad as first-gen and 1.5-gen blocks. Ballpark estimates of 60-70% loss for 1.5-gen orchards and 40-50% loss in 2nd-gen orchards seem reasonable. Even with such damage, seed production should recover in 2-3 years.

The one 3rd-cycle loblolly orchard in the region looked fantastic given what it had been through. Sam Campbell with Joshua estimated the loss to be less than 5% in the 7-year-old blocks at Wildfork (see front cover). A few tops and branches were broken, but few ramets were destroyed. Some trees will struggle to recover, but overall the young ramets came through like champs.

Topgrafting for breeding suffered big losses in the region, but it was interesting that the grafts did not break at the graft union. The top of the tree or branches may have broken, but we didn't see any broken at the graft union. It's always surprising that for southern pines, orchard trees essentially never break at the graft union. This appears to be true for the topgrafts also.

It is amazing how little damage there was to seedling crops in the S-SCC and Joshua nurseries. Seedlings looked beautiful. Few if any entire beds were washed out; some seedlings were lost on the outside of some beds. The one bright side of Ivan was the lack of torrential rains for 2 or 3 days.

RESEARCH

Wood density variation among elite parents of the Cooperative's Coastal, Piedmont and Northern breeding populations of loblolly pine

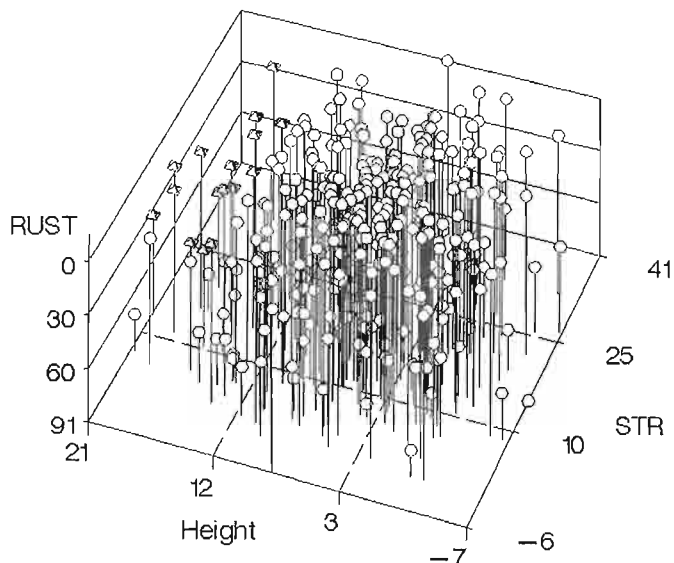
The Cooperative has achieved considerable improvement in growth, stem form, and fusiform rust resistance over the two cycles of selection and testing efforts in the last 49 years. Genetic improvement and intensive cultural treatment have improved productivity and reduced rotation ages, but wood quality traits have not been formally incorporated into the breeding program. As a part of strategy to improve juvenile wood properties in plantation loblolly pine, a research project has been carried out to characterize the genetic variation in wood quality within the elite breeding populations based on the 2nd-generation progeny tests. The purpose is to develop efficient breeding methods for genetic improvement of wood quality traits and for

operational deployment of these elite parents for desirable wood quality traits.

Materials

Based on the breeding values of 2nd-generation progeny tests, 179 elite parent trees with the highest breeding values for growth, stem straightness, and fusiform rust resistance were selected from the Coop database (Figure 1). For each elite parent, the best three full-sib families were selected. Wood samples (12 mm increment cores) from five progeny were sampled for each full-sib family. A common checklot was sampled from each test to be used to adjust the environmental effects.

Figure 1. Selection of elite parents (pyramids) in Region 6 of the Piedmont breeding population using truncation selection in the order of height, stem straightness, and fusiform rust breeding values.



A total 3273 samples were collected from 72 tests from three breeding zones, Coastal, Piedmont, and Northern, in the southern U.S. (Figure 2). Wood samples were processed to get a 2 mm thick wood strip. Wood strip of each core were scanned with an x-ray densitometry. Using the ring area as a weight factor, weighted core density values were estimated.

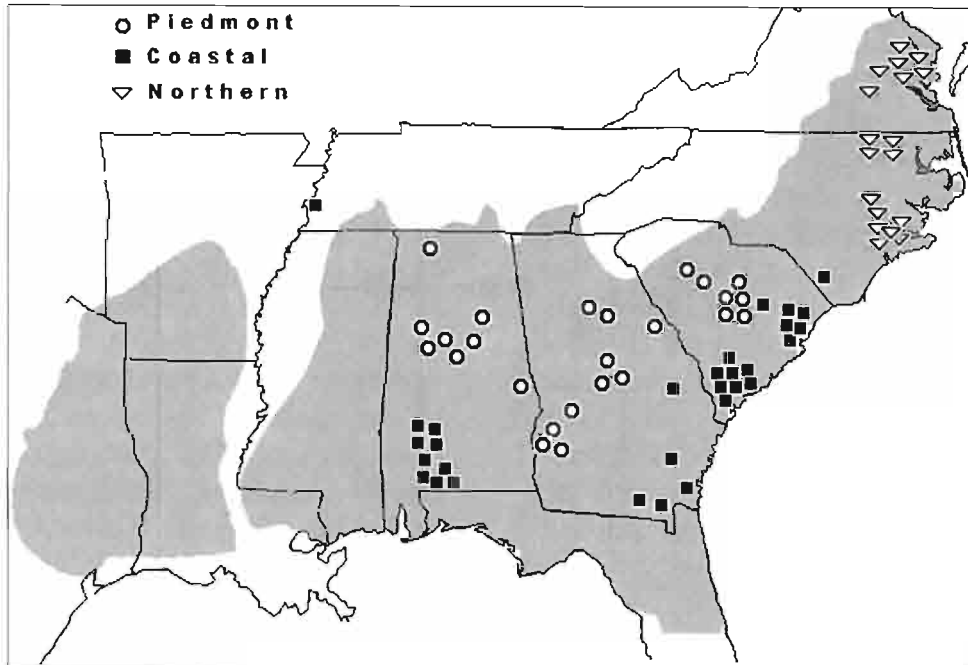


Figure 2. Location of test sites where the elite parents were sampled out for three breeding zones of loblolly pine. The shaded area depicts the natural distribution of the species.

Statistical analysis

Most elite parents were sampled from a different location. The only connection between locations was a checklot (seed orchard mix of a region). The checklot mean was used as a reference population to remove the confounded location and age effects in the data. First, individual tree wood density values were regressed on the checklot mean at each location using a linear fixed model ($y = \mu + X\beta + e_1$). Then, the residuals ($r = y - X\beta$) from the fixed model were used as data for random genetic model to estimate best linear unbiased predicted breeding values of parents. Most elite parents selected were used as female and male. An inverse relationship matrix was created using a pedigree file and was implemented by the ASReml software (Gilmour et al. 2001). Stability of checklot

means across sites was evaluated by the joint regression analysis concept (Finlay and Wilkinson 1963). Univariate and index selection methods were used to make selections among elite parents in each region. Smith-Hazel (SH) index values for each parent were developed using BLUP breeding values.

Results

As expected, the Coastal zone had greater (489 kg/m³) wood density than the Northern (444 kg/m²) and the Piedmont (431 kg/m³) breeding zones. Variation in wood density within each region was similar across all regions as shown by the coefficients of variation (Table 1).

Table 1. Descriptive statistics of unadjusted wood density for the geographic regions (2nd-generation regions) and the 3rd-cycle breeding zones of loblolly pine.

Region (Zone)	Mean (kg/m ³)	Std	CV(%)	Min	Max
Region 1 (North)	444	44.3	10.0	345	593
Region 3 (Coast)	485	46.4	9.6	373	607
Region 4 (Coast)	506	50.9	10.1	356	626
Region 5 (Coast)	479	42.4	8.9	396	619
Region 6 (Piedmont)	416	33.3	8.0	335	507
Region 7 (Piedmont)	435	41.4	9.5	333	580

The checklot was generally stable from one location to another and predictable. As the site density mean (average of parents) increased, the checklot density means also increased accordingly (R^2 ranged from 0.86 to 0.96). Using the checklot mean as a basis, all density values were normalized for the site effects, and age effects were also removed with a regression model. The BLUP (best linear unbiased prediction) was used to estimate the breeding value for wood density of parents and individual trees.

We detected considerable genetic variation in BLUP wood density breeding values among elite parents in Coastal SC, GA, and AL (Regions 3, 4, & 5), Piedmont of GA (Region 7), but not for Upper Gulf (Region 6) (Table 3). Variation among parents in Region 1 (VA) was modest. SC Coastal had greater variation among parents compared to all other regions. The difference between adjusted breeding values of parents ranged from 19 kg/m³ (in VA) to 90 kg/m³ (Lower Gulf). Parents in the Upper Gulf did not differ in density values due to a small sample size (n=10 parents).

Table 2. Descriptive statistics of adjusted BLUP breeding values of elite parents for wood density for the loblolly pine breeding populations.

Region	Mean (kg/m ³)	Std	CV(%)	Min	Max
Region 1 (VA)	396	6.4	1.6	381	418
Region 3 (Coastal SC)	403	35.0	8.7	326	461
Region 4 (Coastal GA)	505	20.0	3.9	479	561
Region 5 (Lower Gulf)	390	14.9	3.8	361	417
Region 6 (Upper Gulf)	423	-	-	-	-
Region 7 (Piedmont)	432	13.5	3.1	398	460

Other wood properties (microfibril angle, cellulose and lignin content, and stuff) are being analyzed for this population of trees. When complete, the Cooperative will have a genetic resource that will be extremely valuable for breeding and deployment of trees that are ideal for different end products. Such strong variations in these elite populations provide opportunities for

wood density improvement in the loblolly pine breeding program. Since these parents are highly desirable in growth, form, and rust resistance, the high-density families could be used for deployment for improved wood density. These parents could also be used in an elite breeding program for improvement of all traits simultaneously.

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- Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J., and Thomson, R. 2002. *ASREML User Guide*, Release 1.0. VSN International Ltd, Hemel Hempstead, HP1, IES, UK. 267 p.

Potential to enhance the efficiency of forest-tree breeding - a simulation study¹

Computer simulation is very useful to study complex systems and has become a standard tool in many research areas. As trees species have long life cycles, it is difficult to analyze and predict outcomes from an applied tree improvement program. A stochastic modeling approach, with a source of randomness in the model, was used in this study to investigate various aspects of a tree breeding program.

Recurrent selection was generally implemented for tree improvement as per Figure 1. Parents in the founder population were sampled from a population of unrelated and non-inbred individuals (natural stands). Founder trees were progeny tested and crossed. Progeny tests were established and results were evaluated. All progenies in the test were referred to as the “recruitment population”. Progenies in the test were candidates for selection of individuals used for the next generation of breeding, the “breeding population” (BP). Throughout all generations, the size of the BP was constant and generations were discrete (non-overlapping). In every breeding generation, top-ranking genotypes were selected out of the BP. These were symbolized as the “production population”, (PP) and used for the large-scale deployment of improved genetic material for reforestation.

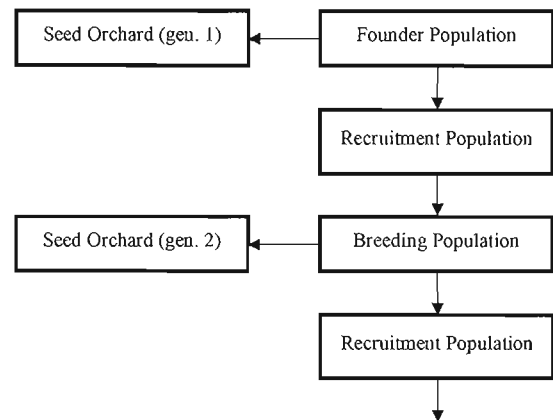


Figure 1. Schematic description of the conceptual breeding strategy implemented in the simulation.

Open-nucleus system and positive assortative mating

Nucleus breeding systems have been incorporated into various tree breeding programs. In such a system, top individuals in the BP are transferred into a nucleus (elite) population, while diversity is maintained in the mainline population (Cotterill et al 1989; Williams and Hamrick 1996). In an “open-nucleus” population, the highest-ranking trees are transferred from the main to the nucleus population and from the nucleus to the main population (two-way transfer of genetic material). The nucleus is thus enriched with both gain and diversity and becomes sustainable (James 1977, 1978).

The genetic advantage of an open-nucleus scheme is due to the assortment of mates into two hierarchical groups (subpopulations). The assortment leads to non-random parental associations,

¹ This is a summary of Milan Lstibůrek’s PhD dissertation. Milan completed his degree under the direction of Tim Mullin and Dag Lindgren in spring 2005.

reflected by positive correlation among values in observed characters of mated trees (positive assortative mating). This assortment into two hierarchical groups has its origin in animal breeding (Roden 1994), where animals tend to be managed in distinct groups (e.g., herds of sheep), thus breeding performed in open-nucleus schemes makes more practical sense. In tree-breeding programs, the breeder has the ability to perform controlled crosses without being much constrained by specific physical location or mating preferences of a tree. It is therefore possible to perform the assortment on an individual basis (rather than in a few distinct groups), resulting in larger similarities (correlation) among mates. Larger correlation contributes to higher genetic gains and variance in the BP due to non-random mating. Such enhancement leads consequently to higher genetic gains in the PP (seed orchards, family or clonal mixtures), thus more gain is available for forest plantations. The general advantage of positive assortative over random mating for forest tree breeding was demonstrated in a computer simulation study by Rosvall *et al.* (2003). The comparison between the assortment on an individual basis with that based on open-nucleus was performed by Lstibůrek *et al.* (2004a). The study revealed that individual parental assortment results in larger genetic gains in the PP (than achieved under open-nucleus) and that this conclusion holds at any target level of gene diversity carried in the improved regeneration material (e.g., seed orchard crop). This conclusion was verified over six breeding generations.

Resources allocation to better trees

In a study by Rosvall *et al.* (2003), it was further demonstrated that the use of positive assortative mating (within an ordinary BP and without any additional resources), combined with a slight imbalance in parental contributions (more from the best and fewer from the worst), either through mating

or selection, can further increase gain in the PP while conserving greater gene diversity per unit of gain achieved. In general, the imbalance is best achieved by a restricted increase in contributions per parent. The imbalance could also be imposed under open-nucleus scheme by allocating more resources into elite population, at the expense of the main population. In fact, this redirection of resources and focusing more on better trees in the elite group has been one of the key features, favouring such implementation in forest tree breeding (Cotterill *et al.* 1989). Nonetheless, imposing the imbalance under individual parental assortment was found superior to unbalanced open-nucleus schemes (Lstibůrek *et al.* (2004b), confirming the earlier conclusion under balanced parental contributions.

These concepts are schematically illustrated in Figure 2. PP (seed orchard) genetic gain is plotted as a function of the orchard's gene diversity. It is important to note that all such population management schemes in the figure consider constant total budget. Thus, one could interpret lines in the figure as describing the proficiency of a tree breeder to maximize genetic gain in the PP, while conserving genetic diversity in the BP (available for future improvement) under given resources. Each line is a continuum of situations, from one extreme to another that could be achieved under practical settings. At one extreme, where the diversity is minimum, all that is considered during selection is genetic gain. At the other extreme, the only source of gain is that generated by selecting top individuals within each family, preserving equal parental contributions, thus minimizing the loss of gene diversity. Any point in between these extremes then reflects a unique compromise between the genetic gain and the diversity.

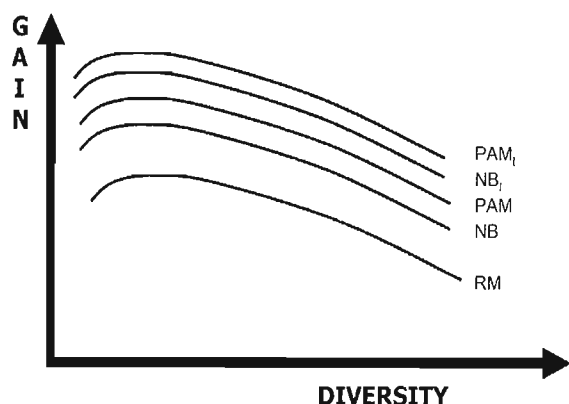


Figure 2. Genetic gain in the seed orchard as a function of gene diversity – schematic description. Different lines correspond to different management strategies discussed in the text: random mating (RM), open-nucleus (NB), positive assortative mating (PAM). NB and PAM strategies with imposed imbalance are designated as NB_I and PAM_I.

Utilizing all available information

Under real conditions, trees in the BP could be ranked by their value and such rank used as a quantitative indicator to assign the unbalance. Unfortunately, the unbalance would not in this way relate directly to the actual distribution of parental values, thus the potential (and costly) information would not be fully utilized. In a study that followed (Lstibůrek 2005a), the unbalance was imposed directly using a family size, which was derived for each family as a function of mid-parent breeding values. Wide range of

distributions of such family sizes was studied (Figure 3). In a breeding strategy, where balanced within-family selection is practiced, it is recommended to maximize the variation in family sizes, meaning that large effort should be redirected to higher-ranking families at the expense of lower-ranking families, but considering the actual distribution of parental breeding values. Such implementation may result in much larger genetic gains in the PP (additional 10 to 20% in the simulation, on top of additional gain generated by the effect of positive assortative over random mating), while having only a marginal impact on genetic diversity in the BP.

Practical implementation

This research suggests that spending equal amount of resources on every parental combination does not lead to the efficient use of available resources in tree improvement. It is proposed to assign the imbalance according to the actual predicted breeding values. The effect of positive assortative mating combined with such efficient redirection of resources may have a tremendous positive impact on the outcome of forest tree breeding programs and may provide a significant benefit to the forest industry.

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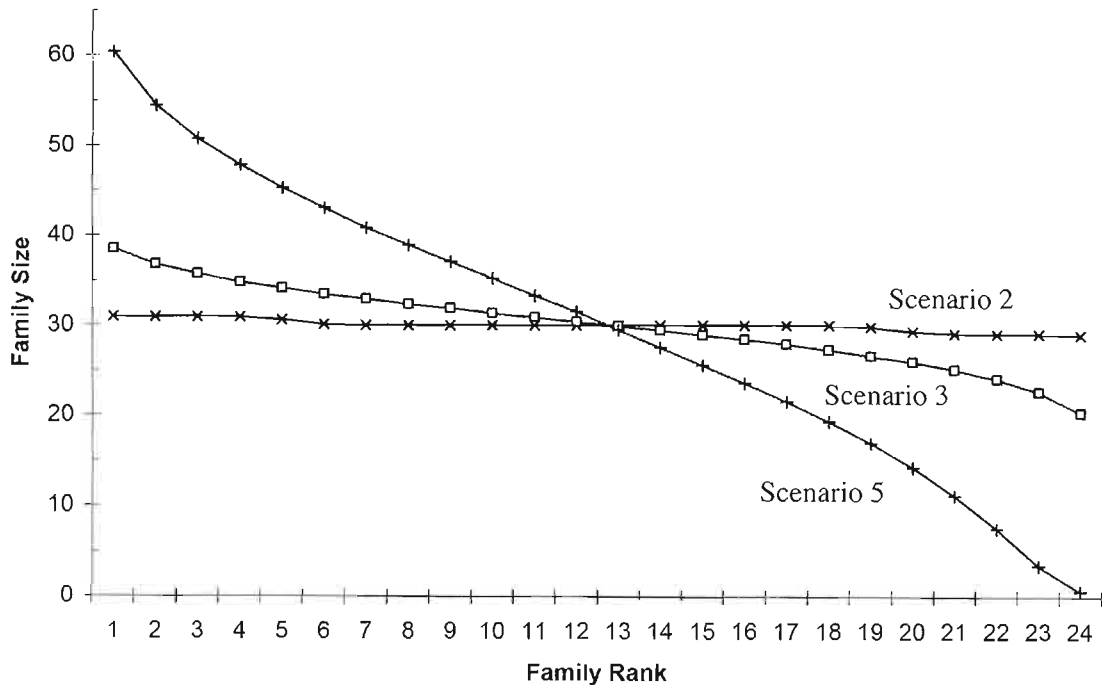


Figure 3. Examples of distributions of family sizes derived as a function of mid-parent breeding values. The family size is on the Y-axis, and the family rank is on the X-axis. Average values are shown in the figure; distributions in individual simulation iterations would vary, depending upon particular distribution of parental breeding values. For the three “balanced” scenarios shown, the variance in family size relative to the maximum possible variance in family size (V_f / V_{fmax}) was: Scenario 2 (2×10^{-5}), Scenario 3 (1×10^{-3}), Scenario 5 (1.25×10^{-2}).

Total Inside-Bark Volume Estimation for Loblolly Pine in Genetic Trials¹

Many tree breeding programs select genotypes based on volume more than any other trait. These programs commonly estimate volume using a combined-variable equation that uses diameter at breast height (D) squared multiplied by total tree height (H) as a regressor on inside-bark volume. The NC State Cooperative has a long history using the Warner and Goebel (1963) combined-variable equation (Warner-Goebel equation). The Warner-Goebel equation was derived from 74 loblolly pine trees from the upper South Carolina Piedmont using least-squares regression. Combined-variable equations have been effective in fitting prediction equations for total inside-bark volume. However, differences in taper and bark thickness among individuals or families are not accounted for with a combined-variable equation. One of the objectives of this study was to evaluate selection with the Warner-Goebel equation.

A genotype by cultural treatment study on lands of International Paper Company in Bainbridge, GA was measured in the 13th growing season. This study was a two by two factorial of weed control and fertilizer treatments in a split-plot design. For the main cultural treatment plots, the control had no herbicide applications until age five and no fertilizer

treatments. The herbicide treatment consisted of early woody and herbaceous competition control, and all treatments were aerially released at age five. The fertilization treatment was ground applied five times up until age 9.

There were 25 open-pollinated first- and second-generation families arranged as individual-tree subplots. Each complete block was replicated 5 times. Some known relationships existed among female parents and were acknowledged in the estimation of genetic parameters. Approximately 40 individuals from each of 25 families were sampled, 10 from each treatment. Two trees from each family were sampled in most replication/treatment plots for a total of 985 measurement trees.

Sectional data were collected along the stem every 1.2 m to a 7.6-cm top. Inside-bark diameters were used in Smalian's log volume equation to find the inside-bark volume of each stem section. In addition to diameters, total height was measured for volume estimation

Volumes estimated from the Warner-Goebel equation were compared to those determined by stem analysis of the felled trees. The Warner-Goebel equation was expressed as

$$\hat{V}_{ib} = 0.03371 + 0.0196128 \left(\frac{D^2 H}{10} \right)$$

where \hat{V}_{ib} is the estimated total inside-bark volume in cubic feet and $D^2 H$ is the combined variable in squared inches x feet.

The effectiveness of selecting trees based on the $D^2 H$ equation versus the more direct but time consuming estimate of volume using stem analysis was evaluated using the selection efficiency equation:

$$S = \frac{h_x h_y r_a}{h_y^2} \quad \text{where } h_x \text{ is } \sqrt{\text{heritability of trait } x}, h_y \text{ is } \sqrt{\text{heritability of trait } y}, r_a \text{ is the genetic correlation}$$

between traits x and y, and h_y^2 is the heritability of trait y.

The family-mean heritabilities of the measured volume from stem section data and the estimated volume using the Warner-Goebel equation were 0.69 and 0.72, respectively. The standard errors for these two values were

0.10 and 0.09, respectively. The genetic correlation between these two traits was high (0.99 with a standard error of 0.0056). Consequently, the selection efficiency for selection of estimated total inside-bark volume to make gains in measured inside-bark volume was 1.01. The Warner-Goebel equation generally over-estimated the total inside-bark volumes measured in the field (Figure 1). However, this did not affect selection.

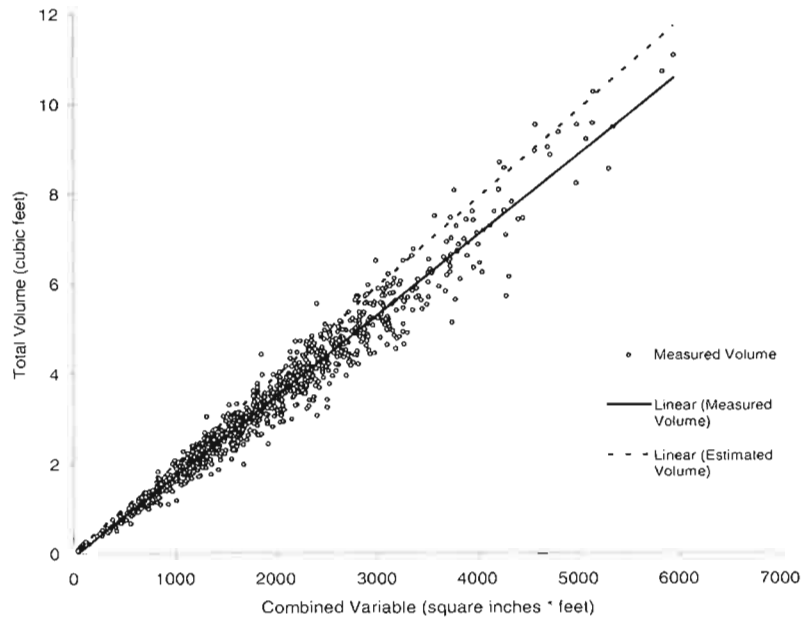


Figure 1. Comparison of prediction lines for estimated volume from the Warner-Goebel equation and measured inside-bark volume.

Combined-variable equations are commonly used to estimate volume in many research applications. For TIP trials, individual stems are generally compared using the Warner-Goebel total inside-bark volume prediction equation. Selection for true inside-bark volume by estimating volume with this equation has been an effective practice based on selection efficiency. In fact, family selection for volume estimated by prediction equations was slightly more favorable than by destructively sampling. This high selection efficiency may have resulted from less error variance being associated with estimated volume than with the detailed volume measurement.

The measured volume may have had more error variance due to variation in stem taper, bark thickness, environmental variation, and unknown factors. Nonetheless, D and H measurements capture a great deal of the genetic variation in total inside-bark volume. Differences in volume not accounted for by estimating volume with the combined-variable equation are probably small enough for indirect selection to be effective. It is recommended to continue using a combined-variable equation for selection of superior loblolly pine genotypes in the Southeastern US.

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¹ This is a summary of Josh Sherrill's M.S. thesis under the direction of Tim Mullin and Bronson Bullock (Assistant Professor and biometrician). The research was funded by the Cooperative with in-kind and field support from International Paper Co.

Association of the *cad-nl* allele with increased growth and wood density in full-sib families of loblolly pine

One of the fastest-growing loblolly pine selections made by the Cooperative, whose progeny are widely planted, 7-56 is also the only known natural carrier of a rare gene (*cad-nl*). This allele codes for deficiency in an enzyme, cinnamyl alcohol dehydrogenase (CAD), which catalyzes the last step in the biosynthesis of lignin precursors. The extent that the *cad-nl* mutation affects the breeding value of 7-56 has been an important question in our breeding program. Wu et al. (1999) reported that heterozygous *cad-nl* trees produced 14% more debarked wood volume at age 4 years, compared to wild-type trees. Previous studies of *cad-nl* heterozygotes yielded inconsistent results on pulping and bleaching. We recently examined the effects associated with this allele by comparing wood density and growth traits of *cad-nl* heterozygous trees with those of wild-type trees in a 10-year-old open-pollinated family trial growing under two levels of fertilization. Our results indicate that the substitution of *cad-nl* for a wild-type allele (*Cad*) was associated with a significant effect on wood density, but not for growth (Yu et al. 2005 in press).

Verification of the *cad-nl* effect is necessary to predict the magnitude of the *cad-nl* expression at a given age or in a particular environment and genetic background. In this summary we extend these findings to include three *cad-nl* heterozygous selections with four different genetic backgrounds in two test sites measured at two different ages.

Materials

Three *cad-nl* heterozygous descendants of 7-56 were studied. These parents produced 20 full-sib families from three disconnected half-diallel progeny test series of loblolly pine in South Carolina and Georgia. Full-sib progenies produced by *cad-nl* heterozygote selections crossed with 5 wild type parents were sampled and measured for growth and wood density traits. Genetic background is defined as a particular heterozygous selection in a particular series, so there are four genetic backgrounds in this study (Table 1). At age 15, total

height and diameter at breast height (DBH) were measured, and DNA samples were prepared and genotyped for *cad* as described in Yu et al. (2005). All tests in each test series had growth measurements at age 6. A 12-mm core was sampled from each tree at breast height for wood quality analyses using densitometry.

Results

On average, the four genetic backgrounds, height, diameter and volume at age 6 and age 15 were higher for *cad-nl* heterozygous than for wild type trees, and 2.7%, 2% and 6.6% greater at age 15, respectively. In separate analyses, volume of A-S1, C-S2 and A-S3 was 4.3%, 5.3% and 10.8% higher for *cad-nl* heterozygotes than wild type trees, respectively. However, S1-B was 4.5 % lower in volume at age 15. The effect of *cad* genotype was significant only for genetic background S3-A for height both at age 6 ($p=0.04$) and age 15 ($p=0.004$), and marginally significant for volume at age 6 ($p=0.096$) or at age 15 ($p=0.07$).

For most wood density traits, heterozygous and wild type trees were about the same averaged across the four genetic backgrounds. However, there are large differences between A-S3 and the other three genetic backgrounds in expression of *cad-nl* for wood density traits. In A-S3, weighted wood density and weighted latewood percentage were 2.6 % and 6.5% significantly higher for heterozygotes than wild type trees, respectively, whereas no significant differences for A-S1, B-S1 and C-S2 were found.

We did not find *cad* genotype x test interactions for growth traits both at age 6 and age 15, and wood density at age 15. There is also not a *cad* genotype x age interactions for growth traits. The differences for growth traits between the two genotypes are consistence at age 6 and age 15.

The difference between heterozygotes over wild type trees for volume and wood density on five full-sib families for selection A is presented in Figure 1. There are large *cad-nl* effects on volume and density among the five full-sib families (Figure

1). The two families A x A6 and A x A9 showed a significantly higher volume growth for heterozygous than wild type trees. Volume was not significantly lower for heterozygous than that for wild type trees in volume growth for all the 20 full-sib families.

Discussion

It appears that there are large effects on growth and wood density, associated with the *cad-n1* allele. When all three test series were considered in a combined analysis, *cad-n1* heterozygotes were found to have 5% ($p = 0.11$) greater volume than their wild-type full-sibs. Remington and O'Malley (2002) found apparent overdominance at the *Cad* locus on growth for both year 2 and year 3, although overdominance did not show statistically significant association with *cad-n1*. Yu et al. (2005) found that *cad-n1* heterozygous trees have greater wood density than wild type trees, but there was no association of *cad-n1* with growth. Wu et al. (1999) found that *cad-n1* heterozygous trees had faster growth than wild-type trees in the same half-sib family. Possible explanations for this discrepancy included different material used (open pollinated or diallel test), environmental differences between field trials, and statistical power to detect small effects.

There are large differences among genetic backgrounds in the expression of *cad-n1* mutant gene on growth and wood density, although these comparisons are confounded by the differences in the environments of the test sites. The significant

difference between the two genotypes on growth and wood density traits is strongly dependent on the particular selection in a particular genetic background growing in a particular environment. This may be due to either different genetic background between diallel series 1 or series 3, or different growing environments (Georgia and South Carolina). The effect of *cad-n1* allele may show up better at good site (series 3) than at poor sites (series 1).

The effect of *cad-n1* allele on growth and wood density was consistent at age 6 and age 15 in the four genetic backgrounds. There is no *cad-n1* genotype x age interactions on growth and wood density. The *cad-n1* effects on growth and wood density that are detectable over multiple growing seasons may be mostly valuable in a wide range of breeding programs. For full-sib A x A6, we found that the *cad-n1* allele is associated with a significant increase in wood density at 15 years (Figure 1). This increase can be attributed to higher earlywood density, latewood density, and a greater proportion of latewood in *cad-n1* heterozygotes. These results are similar to the previous study of Yu et al. (2005) in *cad-n1* half-sib family.

In conclusion, the increasing wood density and growth associated with the *cad-n1* allele were limited to specific crosses between heterozygous and wild type trees. There is also a trend of presenting pleiotropic growth and wood density which is apparently controlled by the *cad-n1* gene interacting with other genes contributed from the second parents.

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Table 1. Sample collections from three series of diallel tests.

Series	Heterozygous parents (descendants of 7-56)	Genetic background	Mate (second parents)				
			A1	A2	A3	A4	A5
S1	A	A-S1	A1	A2	A3	A4	A5
S1	B	B-S1	B1	B2	B3	B4	B5
S2	C	C-S2	C1	C2	C3	C4	C5
S3	A	A-S3	A6	A7	A8	A9	A10

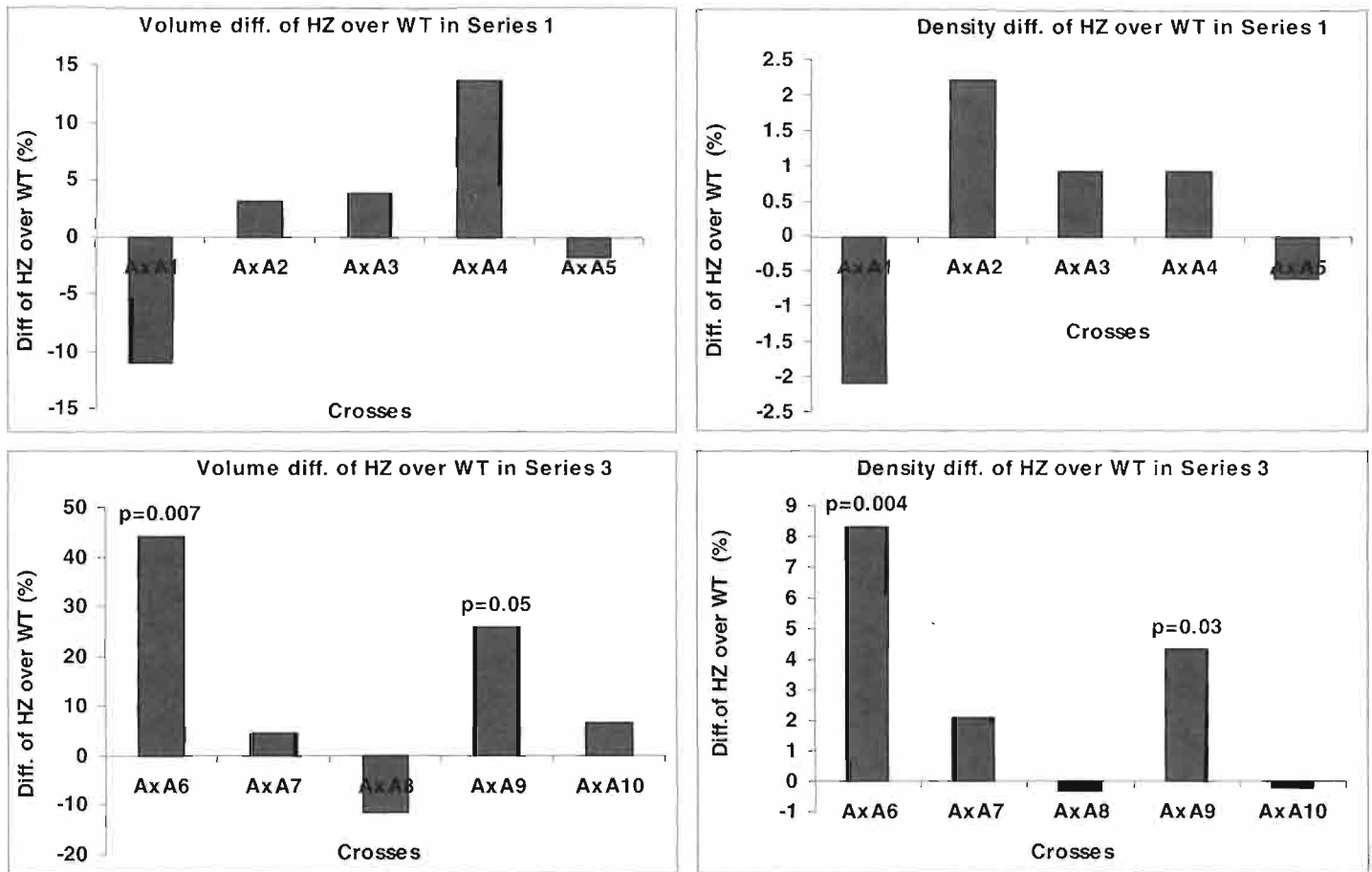


Figure 1. The difference (Diff.) of heterozygotes (HZ) over wild-type (WT) trees for volume and wood density in five full-sib families in heterozygous parental selection A at age 15.

EXTERNALLY FUNDED RESEARCH GRANTS 2004-2005

Chang, H.-M., J. Kadla, R. Sederoff, B. Li and B. Goldfarb. USDA-IFAFS: \$3,000,000. Wood and fiber quality of juvenile pine: characterization and utilization. 08/16/01-08/15/05.

Chang, H.-M., J. Kadla, D. O'Malley and B. Li. DOE Agenda 2020: \$585,000. Exploiting genetic variation of fiber components and morphology in juvenile loblolly pine. 07/01/01-02/15/05.

T.J. Mullin, Bailian Li, John F. Kadla, and Hasan Jameel. DOE Agenda 2020. \$1,125,410. Performance and Value of CAD-Deficient Pine. 05/03-05/06.

Robison, D., L.J. Frampton, R. Bardon, B. Goldfarb, G. Hodge, B. Li, J. Kadla, Steve McKeand and S. Moore. USDA: \$266,005. Integrated Biotechnological and Genetic Systems for Enhanced Forest Productivity and Health. 06/01/03-05/30/05.

Amerson, H., S. McKeand, T. Mullin and B. Li. USDA-IPM. \$100,000. Development of Stable and Predictable Deployment Populations of Loblolly Pine to Minimize Fusiform Rust Impacts in Southern Pine Plantations.

SEED AND CONE YIELDS

Year 2004 appears to have been a below-average year for seed collection in the Tree Improvement Coop. Pounds of seed collected came in at about half the previous year's, at approximately 13 tons. Several factors appear to have contributed to the lower yield, including Hurricane Ivan, general cone crop quality, and market demand for seed. Fortunately, the third cycle seed collection continues to make good progress, increasing from 262 to 377 pounds between 2003 and 2004.

Average seed yields in pounds per bushel were almost identical to those of 2003. About 80% of the total seed came from second generation orchards and about 86% of the collection was from the Coastal source (Table 1). Seed yield rankings between orchards changed little from 2003 to 2004, with the exception of those cooperators unfortunate enough to be in Hurricane Ivan's path.

Table 1. Comparison of 2004 seed and cone yields with previous year.

Provenance	Bushels of Cones		Pounds of Seed		Pounds per Bushel	
	2004	2003	2004	2003	2004	2003
Coastal 1.0	3,414	9,200	5,098	13,931	1.49	1.51
Coastal 2.0	12,336	17,807	17,941	24,532	1.45	1.38
Coastal 3.0	382	295	377	262	0.99	0.89
Piedmont 1.0	19	415	33	452	1.74	1.09
Piedmont 2.0	3,060	15,336	3,772	19,924	1.23	1.30
Totals	19,211	43,053	27,221	59,101	1.38	1.37

ASSOCIATED ACTIVITIES

Visit from Dr. Norman Borlaug



The College of Natural Resources had the honor of hosting Dr. Norman Borlaug (center) for a visit in April 2005. Dr. Borlaug, who is best known as the “father of the green revolution”, has had an incredible impact on agricultural productivity and feeding a hungry world. Through his breeding programs with cereal grains in the tropics, he revolutionized agriculture and provided farmers in developing countries the means to feed their peoples. His many recognitions include the Medal of Freedom, over 35 honorary Doctorate Degrees, and the 1970 Nobel Peace Prize for his contributions to humanity.

In Steve McKeand’s FOR 725 (Forest Genetics) class, Dr. Bruce Zobel (left) joined Dr. Borlaug in giving a campus-wide address to students on factors that have shaped their careers. Dr. Borlaug emphasized that his training and education as a forester was instrumental in shaping his career. The broad training in forestry at the University of Minnesota gave him many of the tools that he used in his distinguished career as a crop breeder. Dr. Zobel emphasized the need for tree breeders to demonstrate their results as early as possible. Long rotation ages and the lack of certainty remain problems today, but 50 years ago, skepticism about tree improvement was pervasive. Both spoke of the need to “carry the message” of the benefits of crop improvement and intensive cultural systems to provide the food and fiber for mankind. They also emphasized the need to remember common sense when it comes to science, agriculture, and forestry. As Dr. Borlaug said, some interest groups seem to have lost the “common sense” gene when they criticize the positive impacts that increases in agricultural and forest productivity have had on mankind.

2004 Contact Meeting

Smurfit-Stone Container Corporation with the assistance of Rayonier, Inc. hosted the annual Contact Meeting, December 1-3, 2004 in Fernandina Beach, FL. The usual array of topics were discussed, but the focus was on breeding and testing plans for the 3rd-cycle program. As the Cooperative enters the next big phase of testing, the need to have high-quality tests with good measurements was emphasized.



Topics for discussion at the Contact Meeting emphasized test establishment – from growing good quality seedlings (left) to establishing trials on the most uniform sites possible (right).



The lunch at Rayonier's Crandall picnic area along the Saint Mary River was a particularly lovely setting in December.



Participants in the 2004 Contact Meeting



Hofmann Forest Genetics Demonstration and Research Study

This past spring, we installed a rather large trial on the Hofmann Forest in Onslow County, NC. The 79,000-acre Hofmann Forest, near Jacksonville, NC is managed by the NC State University Forestry Foundation. Proceeds from the forest are dedicated to support of the College of Natural Resources and the Department of Forestry and Environmental Resources, including our Cooperative.

The objective of the trial is to demonstrate to students, visitors, and foresters the genetic gains obtained from two generations of tree improvement with loblolly pine. Fast-growing, high quality 2nd-cycle loblolly pine families were planted and will be compared to: 1st- and 2nd-generation seed orchard mixes; unimproved loblolly pine; and fast-growing, poor-form loblolly pine. In addition, several very fast-growing clones from the Rooted Cutting Program's Clonal Selection Study were also established. In the main part of the trial, 100-tree block plots were established for each seedlot for future assessments of stand-level growth and yield parameters. Along the edge of the study, 10-tree row plots were planted to demonstrate to visitors the dramatic differences that we see in improved loblolly pine compared to unimproved loblolly. In total, over 8 acres of seedlings were planted.

The Hofmann Forest is a very valuable resource for the Department and the Cooperative. Not only do we benefit financially from the revenue from timber harvests, we plan to continue using the Forest for research and demonstration of the benefits of tree improvement and intensive plantation management.



Outstanding open-pollinated families from the Cooperative's breeding program were planted on the double-bedded site near the Deppe Headquarters of the Hofmann Forest. Students, staff, and faculty all joined in for the festivities. Milan Lstibůrek (above) and Tori Batista (right) both appear to be enjoying themselves way too much while playing in the dirt.



IUFRO Conference on Forest Genetics and Tree Breeding in the Age of Genomics

Hosted by NC State University and the Tree Improvement Cooperative



In November 2004, North Carolina State University and several members of the Tree Improvement Cooperative organized a joint conference of multiple working parties related to breeding and genetic resource management of IUFRO Division 2. Bailian Li and Steve McKeand chaired the scientific program of the conference, while MeadWestvaco and ArborGen hosted the field tour for operational tree improvement operation and biotechnology. Over 120 papers and posters were presented at this conference entitled "Forest Genetics and Tree Breeding in the Age of Genomics - Progress and Future". This international conference brought together geneticists, breeders, applied and basic scientists, managers and professional foresters to exchange the latest information on forest genetics and tree breeding, with special focus on potential application of biotechnology and genomics in the future. Given that the topics were important, timely, and pertinent to scientists worldwide, a total of 231 people from 22 countries participated in this conference. The conference included invited, contributed presentations, and poster presentations. The main topics of the conference included:

- progress of major breeding and tree improvement programs,
- advances and challenges of clonal forestry,
- advances in forest biotechnology,
- advances in genomics and applications for tree breeding,
- genetic diversity and gene conservation,
- breeding strategies, progeny testing and selection strategies,
- advances in somatic embryogenesis technology and clonal forestry,
- social aspects of clonal forestry,
- genetic data analysis and modeling,
- advances in reproductive biology and seed orchard management,
- breeding for disease resistance,
- genetic gain modeling and prediction, and
- genetic improvement of wood quality

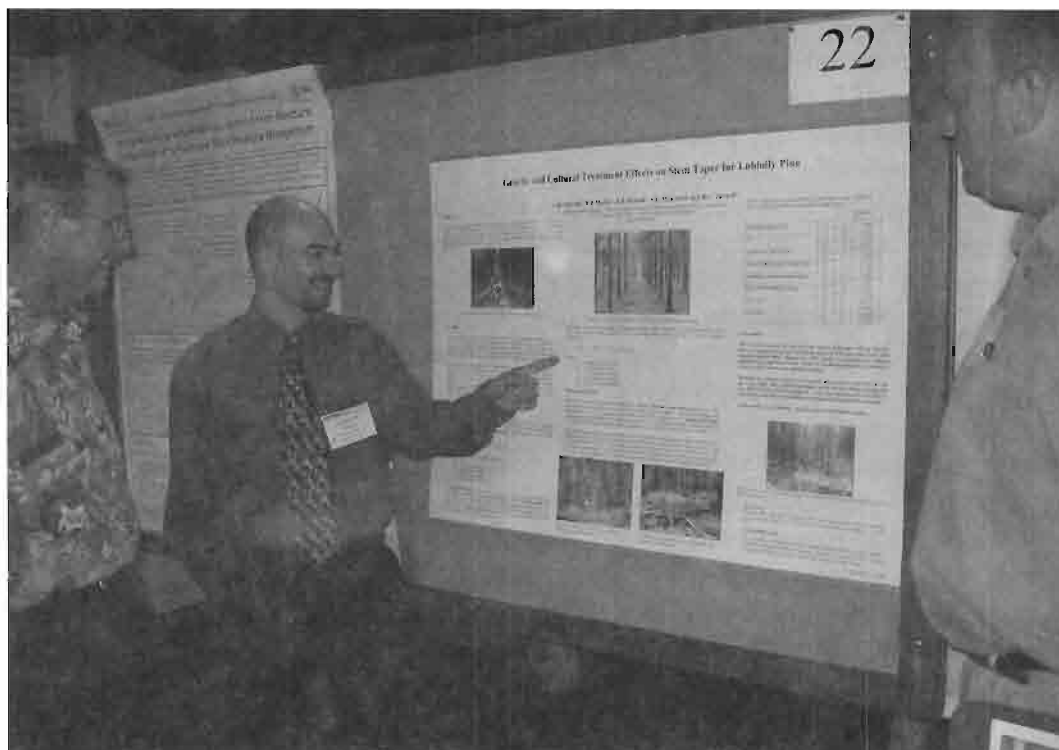


Partial attendees

North Carolina State University Alumni, Students, Faculty, and friends at the conference

Poster session

Graduate student Josh Sherrill presenting results to Early McCall and Ray Moody.



As a part of the conference, a field trip was organized to visit MeadWestvaco Corporation and ArborGen. At MeadWestvaco, participants saw all aspects of breeding and tree improvement with loblolly pine, including breeding facilities, progeny and clone testing, vegetative propagation, greenhouse, seed orchards, nursery, and improved pine plantations. At ArborGen, forest biotechnology and genomics research was displayed, including genetic transformation, somatic embryogenesis, and gene discovery.

Advances in Tree Breeding Programs: Tree breeders provided overviews of the major tree breeding programs in the world and updates on the breeding strategies of advanced generations, clonal testing and selection strategies, top-grafting for accelerated breeding and genetic gain predictions. Significant progress has been made in forest genetics research and tree breeding in the last three decades. Many breeding programs in the world have progressed rapidly from provenance testing to advanced-generation breeding. Substantial genetic gains have been achieved for most tree species in adaptation, productivity, pest resistance and wood quality. Genetically improved plantations from breeding programs have had and continue to make significant impacts on forest productivity, wood supplies, and sustainability of forest resources. Deployment of genetically improved genotypes, whether they originated from open-pollinated seed orchards or mass control-pollinated full-sib families, has been a standard practice for some species in many parts of the world. Recent progress in vegetative propagation in rooted cuttings and somatic embryogenesis has made possible the operational deployment of forest clones in plantations. New breeding strategies, selection and testing methods are being developed to improve breeding efficiency to capture much greater genetic gains in tree breeding programs. However, the traditional breeding programs are being challenged by the overwhelming level of new information in biotechnology and genomics. It is critical to explore opportunities on how to incorporate these tools into forest genetics research and tree breeding programs.

Advances in Biotechnology/Genomics and Integration with Breeding: New advances in somatic embryogenesis (SE) technology have had a great impact in recent years on the deployment of genetic materials for several major breeding programs. SE has also offered great opportunities for genetic transformation and production of clonal forestry with improved productivity, reduced disease, and enhanced wood quality in plantations. Major breakthroughs in genomics research have been in genome sequencing, genotyping with markers (including SNPs, SSRs etc.), transcript profiling (DNA microarrays and RT-PCR), and metabolite profiling. Based on the up-to-date information, conference participants explored opportunities for integration of new genomics and biotechnology into major areas of breeding and genetic resource management. Key biotechnology challenges are successful transformation systems for major species, gene expression, risk analysis and public acceptance. Although great progress has been made in quantitative trait locus (QTL) mapping for trees, limitations in markers and trait variation and low-resolution mapping have restricted the application to breeding. Association mapping, with gene space scan, abundant marker and trait variation, and high resolution mapping of QTL, may be more promising for integration with breeding. For successful implementation of marker assisted breeding, we need to improve high throughput genotyping, high resolution framework mapping, and reliable experimental approaches for tree phenotyping. Genetic diversity and gene conservation were discussed for implications on breeding, biotechnology, deployment and forest resources management.

Additional Information: The full conference proceedings can be accessed online at http://www.ncsu.edu/feop/iufro_genetics2004/proceedings.pdf.

Li, Bailian and Steven McKeand, eds. Forest Genetics and Tree Breeding in the Age of Genomics: Progress and Future, Proceedings of IUFRO Joint Conference of Division 2, November 1-5, 2004, DoubleTree Guest Suites, Charleston, South Carolina, USA

Field tour to progeny test, nursery, and seed orchard at MeadWestvaco.



VISITING SCIENTISTS

Dr. Sofia Valenzuela, a professor in the Faculty of Forestry Sciences at Universidad de Concepción, Chile, spent 3 months in Raleigh for a visiting research program with the Tree Improvement Program. She was supported by the University Concepción for doing research on marker assisted breeding work here and worked closely with us on a loblolly pine project with molecular markers. As a well-trained molecular geneticist, Sofia contributed a lot to our research program during her stay here. Her research used AFLP markers for detecting genetic variation within a population of related trees, and then relating molecular genotypes to breeding values of parents and progenies for selection. Her interactions with faculty, post-doc and graduate students have been beneficial to our research program. This collaborative research project will continued by a graduate student.



Dr. Sofia Valenzuela (left) working in the lab with graduate student Tracy Yu

GRADUATE STUDENTS

Graduate education continues to be a focus in the Cooperative. Graduate students bring fresh ideas and facilitate collaboration with other faculty at NC State and in other institutions. We also help to educate and train the tree improvement leaders of tomorrow. Two excellent examples of our success in graduate education are Milan Lstibůrek (picture p. 21) and Josh Sherrill (picture p. 23). Milan completed his PhD with Tim Mullin and Dag Lindgren and has returned to the Czech Republic where he has started his new career at the university in Prague. Josh Sherrill completed his master's degree with Tim and Bronson Bullock (biometrician / mensurationist) and just started as a tree improvement forester with Rayonier in Yulee, FL. We wish Milan and Josh the best.



Mike Aspinwall joined us in January 2005 as a masters student. His project will deal with wood properties and the inherent variation present up the boles of different genotypes. Mike is pictured above, looking a bit shell-shocked with some of his preliminary samples.

Tracy Yu (picture p. 26) joined us in August 2004 as a PhD student with a departmental assistantship. She is working with Bailian Li and Ross Whetten on a marker-assisted breeding project in loblolly pine.

Daniel Gräns returned to Raleigh in June 2004 from his leave of absence in Sweden to continue his PhD. Daniel's first weeks back in the South was a real shock to his system. He moved from *northern* Sweden (pictured below with his gar fish in the Baltic Sea) and immediately traveled to Bainbridge, GA to help Josh Sherrill for 3+ weeks of grueling field work. Daniel started having second thoughts about the wisdom of his move once the thermometer reached 100°F. Daniel's PhD research is looking at solid wood properties in loblolly pine and Norway spruce.



Student, Degree, Research Project

Mike Aspinwall, MS, Whole stem wood properties in loblolly pine

Daniel Gräns, PhD, Variation in whole-tree wood properties in loblolly pine.

Milan Lstibůrek, PhD, Population Response to Positive Assortative Mating in Forest Tree Breeding - *complete*

Josh Sherrill, MS, Genetic and Cultural Effects on Stem Taper and Bark Thickness for Loblolly Pine - *complete*

Tracy Yu, Ph.D., Marker-assisted selection with AFLP markers in loblolly pine with three-generation pedigrees.

COOPERATIVE STAFF

Bailian Li and Steve McKeand took over as co-directors of the Cooperative in the spring of 2005. Tim Mullin is leaving NC State June 30. Jim Grissom continues as Tree Improvement Analyst with primary duties of managing the Cooperative's database and making sense out of the mountains of numbers that are generated each year. Mike Jett is the Field and Laboratory Manager and spends most of his time fixing problems generated by the rest of us in Raleigh and many of the Cooperators. Kathie Zink has been on board for about one year as Administrative Secretary. That's been just about long enough to figure out where most of the skeletons are hidden, so we try to stay on Kathie's good side.

We are fortunate to have Drs. Fikret Isik and Qibin Yu as well as Tori Batista on board with funds from various research projects. Fikret has had primary responsibility for the IFAFS wood sampling project (see write up on previous pages), and Qibin and Tori have been working on the CAD project for almost a year. Their contributions to our program go way beyond these fairly narrow research projects, and we really appreciate their input.

Membership of the NCSU-Industry Cooperative Tree Improvement Program

The current membership of the Coop stood at 17, 16 full members and 1 associate research member, with 5 state agencies, 12 private corporations.

Alabama Forestry Commission
CellFor
Georgia Forestry Commission
Gulf States Paper Corporation
Hancock Timber Resources Group
International Paper Company
Joshua Land Management, L.L.C.
Mead Westvaco Corporation
North Carolina Division of Forest Resources
Plum Creek Timber Company
Rayonier, Incorporated
Smurfit - Stone Container Corporation
Temple-Inland Inc.
Tennessee Department of Agriculture
Virginia Department of Forestry
Weyerhaeuser Company

Research Associate Member
ArborGen

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David L. Bramlett, 1938-2005

In April 2005, the tree improvement and forestry communities in the South lost a dear friend and long-time professional colleague. Dr. David L. Bramlett died April 21 after a long illness. Dave's distinguished career with the USDA Forest Service lasted 35 years until his retirement in 1997. Dave's pioneering work in reproductive biology and tree physiology, pollination techniques, mass control pollination, and the genetic basis for cone and seed abortion helped shape not only our Cooperative's breeding program, but breeding and seed orchard programs around the world.

Dave was truly a gentleman and a scholar and a remarkable human being that I am proud to have known as a mentor, scholar, and buddy. As I came up through the forestry and tree improvement ranks as a "green as grass" scientist with the Tree Improvement Cooperative, Dave was always willing to advise and offer counsel in a way that was easy to take. Dave was such a well-known and internationally recognized scientist that we youngsters could have been easily intimidated. That simply was not Dave. From my first interactions with him, it was clear that his only motive was to be as helpful as he could possibly be. No doubt that I learned as much tree improvement and seed orchard management from Dave as from almost anyone else.

The indelible image I have of Dave is him up in the top of a loblolly pine graft in a seed orchard during the pollination season. The impact Dave has had on the productivity and sustainability of our southern forests will be felt for generations to come.

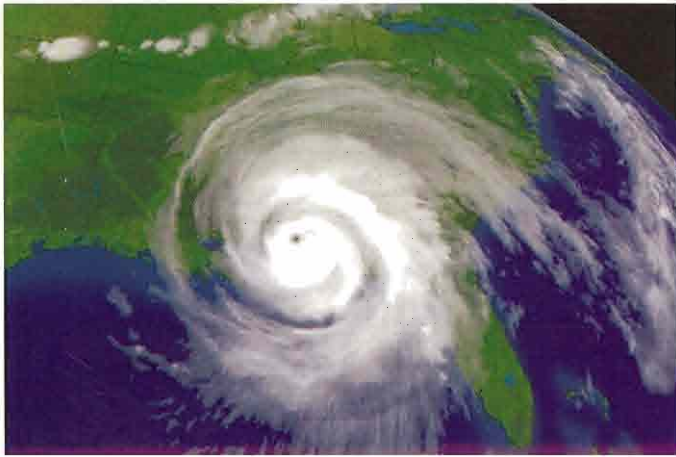


I've never known anyone who truly enjoyed his work more than Dave. He always seemed so happy when he was in the trenches or up a tree solving problems. I will always remember his pleasant smile, his ability to laugh and joke at himself and others, and his willingness to teach and share his wisdom with folks like me. The forestry and tree improvement communities will miss his intellect, wonderful sense of humor, warm personality, and friendship. We wish the best to Dave's wife Anne and the rest of his family.

Steve

Back Cover

The effects of Hurricane Ivan



Hurricane Ivan, September 16, 2004 3:45 am
Satellite imagery from the National Hurricane Center (<http://www.nhc.noaa.gov/>).



The devastation caused by Ivan in IPCo's clone bank in Jay, FL is a good reminder of the importance of having selections grafted in multiple locations. To our knowledge, no selections were lost from the Cooperative's breeding programs.



Older seed orchards such as the 1.5-generation loblolly (S-SCC, left) and first-generation longleaf (Joshua, right) were particularly hard hit by Ivan. Both slash pine and longleaf pine appeared to suffer more damage than loblolly pine in older (>20 years) seed orchards.



Older tests like this 1989 OP loblolly trial (left) in Brewton, AL were hit very badly by Ivan, but younger trials like the 1998 Lower Gulf Elite Population PMX test in Jay, FL were only moderately damaged.