North Carolina State University Cooperative Tree Improvement Program

Annual Report

Department of Forestry & Environmental Resources College of Natural Resources - May 2008 **Inc STATE UNIVERSITY**

EXECUTIVE SUMMARY

A New Era for the NC State University Cooperative Tree Improvement Program

The Cooperative took the first steps in a major restructuring this past year. With the loss of breeding capacity by members and the recognition that breeding, testing, and selection can be done more efficiently at regional centers, the Breeding Center at the Georgia Forestry Commission's Arrowhead Seed Orchard was initiated. Funds from our new Contributing Members are the primary source for work that was started in 2008.

Note that the name of the program is now the North Carolina State University Cooperative Tree Improvement Program. This better reflects the diverse membership that is no longer predominantly the vertically integrated forest products companies.

SELECTION, BREEDING, AND TESTING

To increase the gain possible from the Atlantic Coastal Elite Population, clonal testing in progeny trials will be used. Seedlings from 76 crosses were screened at the US Forest Service Resistance Screening Center, and the surviving seedlings will be hedged to produce rooted cuttings for field trials.

Mainline breeding and testing continues to progress, with 57% of the total PMX breeding complete and over 60 PMX established in field trials.

With improvements in computer power and software such as the ASReml program, solving large mixed model equations for genetic analysis has become feasible. With the new BLUP protocol, the Coop will be analyzing progeny data on a continual basis for all our deployment regions.

SEED PRODUCTION

Almost 19 tons of loblolly pine seed were harvested by Cooperative members in 2007. Second-generation orchards contributed about 77% of total seed, and coastal orchards accounted for 76% of total seed production. Third-cycle orchards are starting to produce a significant amount of seed, currently 12% of the total.

RESEARCH

Substantial genetic variation among families in the Lower Gulf Elite Populations for the percentage of trees having sawtimber potential means that selecting parents with high volume and sawtimber-potential breeding values will be important not only for deployment decisions, but also for population management and the improvement of elite germplasm in the Cooperative.

BLUP analyses of forking in the subset of diallel tests with forking between 20% and 80% showed that substantial genetic variation exists for this serious defect. Across the 123 test series analyzed, the average half-sib family mean heritability was 0.76, and the average full-sib family mean heritability was 0.71, indicating that reasonably strong family differences for forking can be exploited in our breeding programs.

The Conifer Translational Genomics Network (CTGN) is a four-year, \$6 million effort funded by USDA and the US Forest Service, with the objective of moving marker assisted selection and breeding (MAS/MAB) toward application in tree breeding over the next few years. The CTGN project includes the four major university-based US tree breeding cooperatives at Oregon State, Texas A&M, University of Florida, and NC State and is headed by Dr. David Neale at UC Davis.

ASSOCIATED ACTIVITIES, GRADUATE STUDENTS, COOPERATIVE STAFF, MEMBERSHIP

2007-08 had to be a record year for Cooperative meetings. The highlight was the Crossnore Summit where strategic decisions about the program's future were made. Several workshops, the short course, and Contact Meeting kept everyone very busy.

The 6 graduate students funded by the Cooperative all made significant progress in their programs. Tyler Eckard completed his MS in 2007 and is the tree improvement forester for Smurfit-Stone Container Corp.

The staff remained relatively stable this year except for the addition of Josh Steiger as a research assistant with primary responsibilities towards the CTGN

The Cooperative benefitted from several facility changes and upgrade in the College of Natural Resources (CNR) and within the Department of Forestry and Environmental Resources.

Full membership is now at 12, the same number that started the Cooperative in 1956. There are 5 new Contributing Members with more likely to join in the coming months.

52nd ANNUAL REPORT North Carolina State University Cooperative Tree Improvement Program

TABLE OF CONTENTS

Pag	e
EXECUTIVE SUMMARY	i
TABLE OF CONTENTS i	ii
A New Era for the NC State University Cooperative Tree Improvement Program	1
SELECTION, BREEDING, AND TESTING	2
New Breeding Center at Georgia Forestry Commission's Arrowhead Seed Orchard Clonal Testing of Atlantic Coastal Elite (ACE) Population Third-Cycle Mainline Breeding Progress Third-Cycle Elite Breeding Third-Cycle Progeny Testing	2 2 3 4 5
"BIG BLUP" Analysis of Progeny Test Data	6
SEED AND CONE YIELDS	8
RESEARCH	9
Lower Gulf Elite Population Summary. Genetic Control of Forking: Analyses of the Cooperative's Diallel Tests of Loblolly Pine 1 Grants Received	9 2 3 4
ASSOCIATED ACTIVITIES	5
The Crossnore Summit1Meetings, Workshops, and Short Courses1Visiting Scientist.1Teaching1New Cooperative Website1Facilities Changes and Impacts to TIP.1	5 7 8 9 9
<u>GRADUATE STUDENTS</u>	1
<u>COOPERATIVE STAFF</u>	3
<u>MEMBERSHIP</u>	4
PUBLICATIONS OF SPECIAL INTEREST TO MEMBERS	5

A New Era for the NC State University Cooperative Tree Improvement Program

It is fair to say that the last year has been rather *significant* for the Cooperative Tree Improvement Program. Words such as "rebirth", "reinvention", "reinvigoration", "restructuring", and a "new era" are all legitimate descriptors of the changes that have occurred over the past 12 months. At last summer's strategic planning effort at the NC Forest Service Training Center in Crossnore, NC (*The Crossnore Summit* – see p. 15) cooperators and staff worked diligently to map out the Cooperative's future. Here are some of the highlights from the Summit and the past year:

- What's in a name? Note that "Industry" was dropped from the official name of the Cooperative. This is simply recognition that the traditional supporters of the program, the vertically integrated forest products companies no longer are our dominant supporters. Forest landowners, both big and small are our primary customers and beneficiaries of tree improvement.
- With the continued mergers and divestitures of forest land in the South, we are down to 12 full members of the Cooperative, the same number of members that started the program 52 years ago. With ArborGen's acquisition of the International Paper Company and MeadWestvaco breeding programs and nursery and orchard businesses, we went from 2 ½ members to 1 full member (ArborGen was a Research Associate Member).
- Tree improvement capacity by members of the Cooperative has dramatically declined in recent years. My best estimate is that cooperators have gone from having 33 tree breeders in the late 1990's to approximately 15 breeders in 2008. The consequences of these losses have had overwhelming impacts on the way we now do business in the program.
- Unlike only 10 years ago, members of the Cooperative own or manage less than half the acreage that is regenerated each year with loblolly pine that originates from our breeding program. Most users of genetically improved loblolly pine do not pay for the tree improvement to develop the genetic material.
- We have a new class of membership; there are now 5 Contributing Members that play a major role in the future of the program. We hope to add more Contributing Members in the coming months.
- Funds from Contributing Members are being used to support the operational breeding program.
 - Work at the new Breeding Center at the Georgia Forestry Commission's Arrowhead Seed Orchard (see cover) is possible because of these funds.
 - Topgrafting of the new Sawtimber Elite Population (SEPop) commenced at the Breeding Center.
 - The clonal testing regime for the Atlantic Coastal Elite (ACE) Population is underway (details page 2), and Contributing Member funds paid for the rust assessments at the Resistance Screening Center, supplies for establishing clonal hedges, and labor to get the job done.
- BIG BLUP has become a reality. We now have breeding values that are more reliable and valuable than ever for much of our deployment area. By year's end, all our data will be analyzed using ASREML for growth traits and all the binary traits.
- The Cooperative is part of a science team that received \$6 million from the USDA Coordinated Agricultural Project (CAP) entitled the Conifer Translational Genomics Network. This collaborative effort among scientists and tree improvement cooperatives at the University of Florida, Texas A&M, Oregon State, UC Davis, the USDA Forest Service Southern Institute of Forest Genetics, and NC State is focused on moving marker assisted selection and breeding (MAS/MAB) toward application in tree breeding over the next few years.
- With the use of Cooperative funds, significant contributions from the Department of Forestry and Environmental Resources and the College of Natural Resources at NC State, and a major donation of equipment from ArborGen, our new marker lab is up and running.
- To show off all this exciting news and information, take a look at our new and much improved web site <u>www.cnr.ncsu.edu/tip</u>.

Wow! What a year it's been!

Steve McKeand May 2008

SELECTION, BREEDING, AND TESTING

NEW BREEDING CENTER AT GEORGIA FORESTRY COMMISSION'S ARROWHEAD SEED ORCHARD

In 2007, the Cooperative made the decision to move towards developing Cooperative-managed Breeding Center(s), Testing Centers, and Archiving Centers. The idea is to consolidate efforts so that future breeding and testing will progress more efficiently and securely and so that breeding populations will be established in secure archives. The traditional model of individual cooperators doing all of the tree improvement efforts then pooling germplasm has served us well for years, but times have changed, and a new model is needed. For the 4th-cycle breeding program, the Cooperative will have a Breeding Center where most breeding will be conducted. Exactly how this will be managed has not been finalized, but the Cooperative staff will likely be the managers of the Center.

We made our first effort at this sort of organization in 2008 when we established the Breeding Center at the Georgia Forestry Commission's Arrowhead Seed Orchard near Cochran, GA. This February/March, we topgrafted the Sawtimber Elite Population (SEPop) selections and planted rootstock for 4thcycle topgrafting. The SEPop breeding will be done over the next 4-5 years, and rootstock will be managed so that topgrafting the 4th-cycle breeding populations will be possible in 5-10 years.

GFC has donated the orchard trees and land at least for the next 5-7 years for the Cooperative. It is quite likely that we will make a long-term commitment to the Arrowhead Breeding Center, but initially our arrangement is a "handshake". To protect the interests of all cooperators and GFC, more formal agreements will be necessary.

Our intention is that the BC will be funded and operated by the Cooperative, and that GFC will be a "good neighbor" but not bear the brunt of the costs. With existing funds and new funds from our Contributing Members, we will be able to operate the Arrowhead BC for the time being. We appreciate the efforts that Russ Pohl and others at GFC have put forth to date, and we look forward to working with them in the coming years.



Topgrafting (foreground) at the Arrowhead BC got started this spring as did rootstock establishment (background). We appreciate all the effort put forth by the Georgia Forestry Commission. (More pictures on front and back cover pages.)

CLONAL TESTING OF ATLANTIC COASTAL ELITE (ACE) POPULATION

Background: The elite breeding populations in the NC State Tree Improvement Program are intensively managed subsets of the mainline population selected for short-term genetic gain for each of the three geographic regions in the Cooperative. Elite populations are much smaller than the mainline so they can be bred and tested much faster than the mainline population. Elite populations in each region are being bred as a single breeding population to achieve maximum gain and will be managed mainly for short-term gain and to provide genetic material for full-sib deployment strategies and vegetative propagation for clonal forestry.

To increase the gain possible from the Coastal Elite Population, clonal testing of the progeny trials will be used to increase the within-family heritabilities and also allow for among family selections to be made. The increased within-family selection power gives higher likelihood that the forward selections themselves can be confidently grafted directly to production orchards.

With the Coastal Elite Series near completion (76 of 84 crosses completed with 400 seed), the decision was made in June 2007 to clonally multiply individual genotypes within each full-sib family using rooted cuttings. At the NC State Horticulture Field Laboratory (HFL), the Cooperative has the capacity to handle hedge management and cutting production at a reasonable cost.

Since fusiform rust resistance is such a critical trait for most of the Coastal Plain, all seedlings were screened at the USDA Forest Service Resistance Screening Center (RSC) in Asheville, NC. We used a high spore load (50,000 spores/ml) of a mix of broad-base field inocula that covered the entire range of deployment for these genotypes. The intention was to significantly challenge the seedlings with rust and cull the galled seedlings at 6-9 months. Our assumption is that a seedling with "no-gall" response at the RSC would be more likely to be resistant in the field than seedlings with galls. Through this culling, we eliminate genotypes that may be susceptible in the field to rust, and we are able to focus on selection for growth and quality traits in the remaining seedlings.

Status, May 2008: We just finished the 6-month assessment of rust infection at the RSC, and the results are very promising. Overall mean infection was 48%, ideal for assessing genetic differences. The genetic control for gall formation was very high with half-sib family mean heritability = 0.95, and full-sib family mean heritability = 0.93. These extremely high heritabilities with very low standard errors are a tribute to the outstanding job that is done by Josh Bronson and the crew at the Resistance Screening Center. We could not have had better results, and we appreciate their effort.

Along with high heritabilities, there was a wide range in breeding values for rust infection for the 24 parents. The average half-sib BV was 51% and ranged from 5% (best) to 81% (worst). Based on these rust data and the growth and form data from field trials, two of the parents will be dropped completely from the ACE population along with 5 to 7 other crosses.

Seedlings from the remaining 60+/- crosses plus some of the checklots are being transplanted into 3gallon pots at the HFL and will be managed as hedges to produce cuttings to be rooted in 2009. We intend to transplant 3300 seedlings with the intention to manage 2500 hedges. There is always some fall down when seedlings are hedged, and some latent rust galls are likely to appear. We anticipate that clonal field trials will be established in the fallwinter of 2009-2010.



Big projects require a team effort. Tag making for ACE was enjoyed by all... OK by most, OK by some. Well they enjoyed the pizza at the end.

THIRD-CYCLE MAINLINE BREEDING PROGRESS

Mainline breeding continues to progress, with 57% of the total PMX breeding complete. An additional 14% is in progress with some seed in hand. Following the reduction in population sizes as described in the Fall 2007 update of the Third Cycle Implementation Plan, the Cooperative is poised to rapidly complete PMX testing.

We are using a complementary design, with polycross mating for among family selection and full-sib mating for within-family selection. The coastal region has made the most progress with 70% of PMX breeding and 55% of Mainline Full-sib breeding complete (Table 1).

Cooperative members within each region have grafted all parents selected for generating the pollen mix (PMX) for polycross mating. Three third-cycle check seed lots are being created for each of the three regions by using the same 20-parent PMX applied to 10 of the selections as females. Checklot crossing has progressed well in the Coastal and Piedmont regions (Table 1). Thanks to breeding efforts in recent years, checklot seed for the Coastal and Piedmont regions is complete, while the Northern region is approximately 45% complete.

In addition to the third-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 family comparisons. Seeds from most of the common family checks have been collected for each breeding region (Table 1). Progress continues for full-sib controlled crossing made this year although changes in the Fall 2007 Third Cycle Implementation Plan have placed priority on completing PMX crosses (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.

THIRD-CYCLE ELITE BREEDING

The expected gains from the Elite Breeding programs make it clear that getting this breeding underway is very important, and the cooperators have made great strides in accomplishing this task. A sufficient number of the Coastal region elite crosses were collected allowing the cooperative to move forward with clonally testing this population (details p. 2). Piedmont is now 23% complete with 45% assigned crosses made; and Northern is 7% complete with 23% assigned crosses made.

Table 1. Summary of third-cycle breeding progress, as of Fall 2007.

Type of crosses	Breeding Region	# Coop- erators	# Sublines	Original # Parents	Total Parents w/ Reduction	#Crosses producing Seed	#Crosses of Sufficient Seed	% Done Crosses with Reduction
Deberra	Occestel	7	20	204	200	070	000	700/
Polycross	Coastal	<u>/</u>	30	384	326	270	229	70%
	Piedmont	7	28	364	308	183	143	46%
	Northern	4	14	177	177	132	96	64%
Polycross	Total	12	72	925	826	585	468	57%
	Coastal	7		10		10	10	100%
PMX	Piedmont	7		10		10	10	100%
checks	Northern	4		11		11	5	45%
	Coastal	7		7		7	7	100%
PMX CFs	Piedmont	7		7		7	6	86%
	Northern	4		7		7	7	100%
Full-Sib	Coastal	7	30	321 ¹		*	178	55%
	Piedmont	7	28	220 ¹		*	69	31%
	Northern	4	13	127 ¹		*	28	22%
Full-Sib	Total	12	71	668		*	275	41%

#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

¹Number of parents does not reflect unassigned diallel mating schemes.

^{*}Insufficient Data

THIRD-CYCLE PROGENY TESTING

<u>Polycross tests</u>: In the fall/winter of 2007-2008, a total of twenty-one PMX tests were established within the cooperative (Table 1). Ten tests were established in the Coastal region from two tests series, seven tests were established in the Piedmont region from one test series and four tests were established from one test series in the Northern region. Since the number of tests per series was reduced for all regions, the PMX breeding and testing can move faster as we work together to complete the third cycle breeding and testing. Tests were established in AL, FL, GA, NC, SC, and VA.

In April 2008, seed was sent out to cooperators for the establishment of PMX tests in 2008-2009. A total of 5 tests were sent to Cooperative members. Thanks to all the Cooperative members for their efforts to get these tests in the ground!

<u>Full-Sib controlled cross tests</u>: A small number of Full-sib block plots are being installed and will continue to increase with the availability of full-sib seed. These plots will be a source for selections as the program moves forward. Each member is encouraged not to delay the installation of these tests. Once enough seed is collected from a few crosses, block plots can be installed

Region	Test Series	2004- 2005	2005- 2006	2006- 2007	2007- 2009	Total
Coastal	CPMX1	15				15
Coastal	CPMX2		5	5		10
Coastal	CPMX3			5	5	10
Coastal	CPMX4				8	8
Piedmont	PPMX1		3	5		8
Piedmont	PPMX2				8	8
Northern	NPMX1				4	4

Table 1. Third-cycle progeny tests to be established through 2009.



Good progeny tests start with good seedling care in the container nursery. Glenn Free and Tommy Conwell with Westervelt have produced excellent PMX seedlings and are showing them off to Tori Brooks.

"BIG BLUP" Analysis of Progeny Test Data

Since October 2007, the Cooperative staff has been working on the 'BIG BLUP' project. This is a new data analysis protocol for the Cooperative's progeny test data, statistically known as Best Linear Unbiased Prediction (BLUP). The first release of results is expected to be wrapped up this spring.

Why did we decide to make drastic changes in progeny test data analysis? In previous generations, the Cooperative had mostly distinct breeding and testing cycles. Data were based on well-designed experiments with relatively minor imbalance. Age differences between tests were not a concern because almost all the measurements were at age six or eight. There was not much relatedness among genotypes. Mating designs produced simple family structures, such as half-sibs and full-sibs. For selections, we focused on a few traits, namely growth, straightness, and rust resistance.

As the Cooperative program moves to more advanced generations, there will be a greater demand for more complex statistical and genetics models. Data will be more complex from various kinds of experiments. Increasing numbers of factors, such as different ages, sites, mating designs, multiple generations, pedigree relationships and even molecular genetic markers will contribute to this complexity. More traits will be measured compared to previous generations, such as sawtimber quality, wood characteristics, and bioenergy related traits. Data from cloned progeny tests or clonal selection tests are becoming available, which introduces another layer of complexity.

With improvements in computer power and software such as the ASReml program, solving large mixed model equations for genetic analysis has become feasible. With the new protocol, the Coop will be analyzing progeny data on a continual basis. As new data become available, breeding values can be recalculated and updated each year for selections.

Here are some of the advantages of the 'BIG BLUP' method:

- BLUP can integrate large sets of data from different sources, such as multiple mating designs (open-pollinated, polymix, control pollination), test series, and multiple test regions and generations.
- The information available from all relatives across test series or generations will be utilized in the BLUP analysis. For example, breeding values of 7-56 will be based on all the relatives of that parent tested in different test series and generations.
- Connection between genotypes across test series or generations will be enhanced using the pedigree relationships as well as checklots.
- Correlations among the parental GCA values across sites can be accounted for resulting in better predictions. Such an approach will take into account genotype by environment interactions in predictions.
- Variation in test quality (e.g. test precision) can be fully accounted for in the analyses. For example, each test site can have its error variance or additive genetic variance for predictions of breeding values.



Besides being an outstanding tree planter, Dr. Fikret Isik has taken the lead on 'BIG BLUP'. We're not sure which is his first love!

- The new BLUP method can better analyze categorical traits (e.g. tree form classes, forking, and fusiform rust infection) using generalized linear mixed models.
- Breeding values and gain estimates for generations, checklots, parents and progeny can be obtained simultaneously. Such breeding values and gain estimates would be comparable across generations, test regions, and test series.

These new breeding values and genetic gain estimates will allow us to better compare selections that have been made over the past decades. In addition, they will be very useful for our cooperators, landowners, and foresters as a tool for selecting the most valuable genotypes to deploy in their planting programs.

Ultimately, we will incorporate these new breeding values into the Loblolly Pine Performance Rating System (LP-PRS), which is proving to be a useful and practical tool for our cooperators and customers for genetically superior seedling marketing.



Establishment of pollen mix tests like this excellent CPMX3 test by Plum Creek in Ridgeville, SC continues to be a major activity of the Cooperative. Every effort is being made for these tests to be as uniform as possible. With fewer tests per series, each installation must be done with great care.

Kudos to Keith Palmer, Andy Volf, and the Plum Creek crew for a job well done.

SEED AND CONE YIELDS

Almost 19 tons of loblolly pine seed were harvested by Cooperative members in 2007, substantially lower than the 2006 harvest of 26 tons. In both the Coastal and Piedmont regions there was a decrease in the harvest of all generations of improved seed, while seed harvested in the northern region increased. The 2007 average seed yields per bushel were essentially the same as 2006 seed yields. Second-generation orchards contributed about 77% of total seed, and coastal orchards accounted for 76% of total seed production. Third-cycle orchards are starting to produce a significant amount of seed, currently 12% of the total. As yields from these young orchards continue to increase, substantial improvement in growth and quality will be realized in the coming years.

Brovonanco —	Bushels	of Cones	Pounds	of Seed	Pounds per Bushel		
FIOVENANCE	2007	2006	2007	2006	2007	2006	
Coastal 1.0	2915	4024	4027	5795	1.38	1.44	
Coastal 2.0	12839	21149	20291	34758	1.58	1.64	
Coastal 3.0	3715	4450	3996	5300	1.08	1.19	
Piedmont 1.0	21	129	40	190	1.90	1.47	
Piedmont 2.0	1510	3912	2106	5214	1.39	1.33	
Piedmont 3.0	391	670	522	693	1.33	1.03	
Northern 2.0	3463	183	6387	178	1.84	0.97	
Totals	24855	34516	37369	52127	1.50	1.51	

Table 1. Comparison of 2007 seed and cone yields with previous year.

Annual seed yields have varied over the years due to regeneration needs, changes in membership within the Cooperative, environmental factors, and growth and technology within the industry (Figure 1). For the last 7 or 8 years, cooperators have produced sufficient quantities of improved seed, and therefore have been making selective harvests of about 20 tons of seed per year.

From 1968 to 2007, over 2.2 million pounds of improved seed have been produced by Cooperative members. At 12,000 seedlings per pound, this is enough seed to grow over 26 billion improved seedlings. We look forward to greater production from advanced generation seed orchards in the near future!



Figure 1. Annual seed yields from 1968 to 2007.



Flowering in 2008 was heavy, even on young trees like this NC Forest Service ramet. The 2009 cone crop should be phenomenal throughout the region.

RESEARCH

Lower Gulf Elite Population Summary

Improving the value of our forests in the southeastern United States is becoming increasingly important to the stability and long-term productivity of Cooperative members as well as the industry as a Increasing the value and amount of whole. sawtimber from each acre of forest plantation is one opportunity for adding value to forest landowners in the South. With sawtimber prices 5 times greater than pulp prices, even small increases in the proportion of sawtimber can significantly increase the value of timber. While it has been widely observed that variation exists among families, it has not been characterized within the breeding populations of the Cooperative. Over the last year, the Cooperative has made efforts to assess the variation in traits thought to influence sawtimber quality.

The Lower Gulf Elite population was a joint effort between the NCSU-CTIP, WGFTIP, and CFGRP programs formed in the mid 1990's with elite material from the Atlantic Coastal Plain, Florida, and Livingston Parrish/East Texas provenances. At the time it was created, this was the most elite material from these provenances considered to be suitable for the development of a land race for the lower Gulf Coastal Plain. This combination of provenances provided an excellent population to quantify the variation in growth and sawtimber quality in loblolly pine. The objectives for this research effort were to 1) estimate genetic parameters for age 6 year growth and stem form and 2) determine potential gains in sawtimber quality by family selection.

The experimental design consisted of six 8-tree, disconnected diallels that resulted in approximately 128 crosses. Four tests in Alabama, Florida, and Georgia were measured; each test was a 20replication single-tree-plot design. Data were analyzed using a mixed model approach with ASReml. A total of nine traits were measured in the LGE diallel tests: Height, DBH, Volume, Rust, Forking, Sweep, Branch Angle, Branch Diameter, Branch Frequency, and Sawtimber Potential (on a 1-4 scale with 1=high sawtimber potential, 4=cull).

Individual-tree heritability estimates ranged from 0.08 for sawtimber potential up to 0.24 for tree height (Table 1). The half-sib family-mean heritability estimates ranged from a low of 0.71 in branch angle to a high of 0.97 for branch frequency. Full-sib family mean heritability estimates were lower than half-sib estimates ranging from 0.66 for branch angle to 0.91 for rust incidence. While some individual tree estimates seemed low (below 0.10), the half-sib family mean heritability estimates suggest there is genetic variation at the family level that could be utilized for population improvement. While branching characteristics were found to be heritable, it is perhaps most encouraging that the more subjective sawtimber potential score was heritable at the half-sib level with $h_{HS}^2=0.85$. The potential to grade a progeny test tree for multiple stem form characteristics with a single score could make sawtimber potential assessments rapid and cost-effective for tree improvement programs.

Table 1. Heritability estimates for traits measured in four Lower Gulf Elite tests.

Trait	h² _i	h ² _{HS}	H^2_{FS}
Height	0.24	0.95	0.89
DBH	0.12	0.87	0.77
Volume	0.15	0.87	0.78
Rust	0.22	0.96	0.91
Forking	0.15	0.91	0.82
Sweep	0.16	0.94	0.78
Branch Angle	0.16	0.71	0.66
Branch Diameter	0.09	0.91	0.69
Branch Frequency	0.13	0.97	0.71
Sawtimber Potential	0.08	0.85	0.70

Where:

 h_{i}^{2} = narrow-sense individual tree heritability,

 h^{2}_{HS} = narrow-sense half-sib family mean heritability,

 H^{2}_{FS} = broad-sense full-sib family mean heritability.

Based upon correlations among parental breeding values for growth and stem form traits (Table 2), there are no relationships that would prevent the improvement of stem form and growth in the Lower Gulf Elite population. Sawtimber potential was most highly correlated (between breeding values) volume and height (0.54 and 0.53, with respectively) but was not highly correlated with any branching traits (Table 2). A relationship between growth and sawtimber potential was expected since above-average growth was a criterion for sawtimber The modest correlations suggest that grading. volume was not unfairly weighted for sawtimber evaluation. In addition to growth traits, sawtimber potential was also negatively correlated (favorable) to sweep (-0.52) and rust infection (-0.38). Both of these relationships are favorable as lower sweep values indicate straighter trees and rust is scored as a binary variable (0 = no rust, 1 = rust). These traits are also factors in sawtimber potential scoring since stem rust disqualified a tree from being a potential sawtimber tree, and large sweep (>3") penalized a tree from being potential sawtimber. These relationships will be further explained through the development of a predictive model for estimating sawtimber potential from existing Cooperative breeding values.

In addition to the potential improvement of sawtimber quality in breeding populations, gains in sawtimber quality can also be captured through the deployment of select first- and second-generation parents. Figure 1 demonstrates the range in sawtimber and volume growth by full-sib family means. Since correlations were not high between growth and sawtimber potential, it is important to quantify both the growth and sawtimber quality of each family. Selecting only on volume for deployment will not always result in the families with higher proportions of potential sawtimber trees. This consideration is also seen in Figure 2 where the top fifteen parents for volume show a range in sawtimber potential from less than 40% to Selecting parents with high greater than 70%. volume and sawtimber potential breeding values will be important not only for deployment decisions, but also for decisions in population management and the improvement of elite germplasm in the Cooperative for future breeding efforts.

Table 2.	Parental Breeding	Value Correlations	(and p-value)	among selected	growth and	stem form	traits in
four Low	er Gulf Elite tests.						

	Height	Volume	Sweep	Branch	Branch	Branch	Rust	Sawtimber	Forking
				Angle	Diameter	Frequency		Potential	
Height		0.86	-0.06	-0.10	0.37	0.52	0.00	0.53	0.35
		<.0001	0.68	0.48	0.01	<.0001	0.99	<.0001	0.01
Volume			0.06	-0.28	0.53	0.32	0.00	0.54	0.28
			0.67	0.04	<.0001	0.02	0.99	<.0001	0.04
Sweep				-0.25	0.35	0.16	0.22	-0.52	0.10
				0.07	0.01	0.26	0.11	<.0001	0.48
Branch Angle					-0.40	0.03	0.11	-0.11	0.26
					0.00	0.85	0.44	0.41	0.06
Branch Diameter						0.36	0.39	-0.04	-0.05
						0.01	0.00	0.79	0.73
Branch Freq							0.11	-0.01	0.26
							0.43	0.95	0.06
Rust								-0.38	-0.01
								0.01	0.96
Sawtimber									-0.12
Potential									0.38

52nd ANNUAL REPORT North Carolina State University Cooperative Tree Improvement Program



Branch angle (steep-angle tree left, flat-angle tree right) was assessed on all trees in the LGEPop. While the genetic control was reasonably strong $(h^2_{HS}=0.71)$, the correlation with sawtimber potential was very low.





Figure 1. Plot of Sawtimber full-sib breeding values vs. whole-tree 6-year volume full-sib breeding values (r = 0.53).



Figure 2. Half-sib breeding values for volume gain (%) and sawtimber potential (%) for the fifteen highest volume parents.

Genetic Control of Forking: Analyses of the Cooperative's Diallel Tests of Loblolly Pine¹

Forking defects are probably the most serious stem-quality problems in loblolly pine. Our assessment of forking included forked stems and major ramicorn or steep-angled branches that greatly reduce wood yield and wood quality. Assessing forking in elite pedigrees will enable us to more successfully breed and deploy non-forked phenotypes. The genetic control of forking and the correlation of forking to growth and stem straightness were investigated in 6-year-old diallel tests, located throughout the Southeast. There were 123 diallel series (12 parents, 30 crosses \times 36 trees per cross per site \times 4 sites) with sufficient forking between 20% and 80% for genetic analysis. As forking is a threshold or dichotomous trait with only two categories (Non-forked=0 or Forked=1), the generalized linear mixed model was fit to data to understand underlying additive and non-additive genetic effects controlling forking in loblolly pine.

Forking in this selected series of tests with high forking, varied across the different regions* (Figure 1). The genetic control for forking also varied (Figure 2). Region 3 (South Carolina Coastal Plain) had the highest fullsib family mean heritability of 0.78, and the greatest half-sib family mean heritability was in region 6 (Upper Gulf). Region 2 (North Carolina Coastal Plain) had the lowest full-sib family mean heritability as 0.60, and region 4 showed the lowest half-sib family mean heritability was 0.76, and the average full-sib family mean heritability was 0.71, indicating that reasonably strong family differences for forking can be exploited in our breeding programs. High heritability will result in high response of selection against forking.



Overall, the genetic correlation of forking and height is unfavorable with the average value of 0.28 (Table 1). While not a large unfavorable relationship (and the standard errors are large), selection for height will result in a slight increase in forking. The genetic correlation of forking and straightness is favorable with the value of 0.33. Straight trees have a tendency not to fork, but we suspect that measurement crews tended to call most forked trees as below average for straightness, which caused positive correlation between forking and straightness.

¹As part of her PhD research, Jin (Sherry) Xiong has analyzed the diallel test series that had sufficient forking to evaluate genetic variation. This is a brief summary of her findings.

For threshold traits (yes or no), an individual's phenotype is estimated very imprecisely; while the mean of the family is much more precisely known from the proportion of forking. So, selection at the family level against forking should be more effective in breeding programs. Based on the breeding value from the best linear unbiased prediction (BLUP) analysis, the gains from the selection of top 2 best parents in a test series were predicted. The highest predicted gain was 23.9, which means the forking proportion could be reduced 23.9% through half-sib family selection with the selection differential of 16.6% (2 out of 12). The lowest gain in a series would only result in 1.1% reduction of forking.

This analysis shows that forking is under reasonably strong genetic control, with moderately high heritability at the family mean level. The correlations between forking & height and forking & straightness are relatively low, but we do need to be aware of the possible negative consequences on stem form for selecting for growth. The best linear unbiased prediction showed that half-sib family selection against forking will provide lower-forking progeny, which would be significant in improving stem quality in the breeding program.

Table1. Genetic correlations between forking & height, and forking & straightness.

Region	<u>rg</u> fork-ht	Std error	<u>rg_fork-strt</u>	Std error
1	0.23	0.31	0.19	0.29
2	0.78	0.28	-0.41	0.41
3	0.19	0.28	0.43	0.25
4	0.16	0.29	0.41	0.27
5	0.00	0.31	0.51	0.23
6	0.20	0.31	0.49	0.24
7	0.18	0.30	0.45	0.25
<u>8</u>	<u>0.47</u>	0.26	<u>0.59</u>	0.23
Mean	0.28	0.29	0.33	0.27

Forking defects are probably the most serious stem-quality problems in loblolly pine. On some sites, forking and ramicorn branching are serious defects. Some families are less prone to forking than others, and Sherry Xiong's PhD research should help us understand the cultural and genetic control of forking.



Grants Received

Fikret Isik, Bailian Li, Bronson Bullock. USDA Forest Service Agenda 2020. \$169,125. Prediction of Whole-Stem Wood Quality of Superior Loblolly Pine Clones for Deployment. 05/05 - 05/07

Lauire Schimlek, Alex Clark III, Bailian Li, Fikret Isik. USDA Forest Service Agenda 2020. \$181,000. Rapid techniques for screening wood properties for genetic improvement of loblolly pine. 05/05- 05/07

Steve McKeand, Fikret Isik, Ross Whetten. Subcontract with the University of California – Davis, USDA Coordinated Agricultural Project (CAP). NCSU portion \$548,819. Conifer Translational Genomics Network. 9/07 to 9/11

The Conifer Translational Genomics Network - CTGN

A major new project for the Cooperative Tree Improvement Program is known as the Conifer Translational Genomics Network (CTGN). This four-year, \$6 million effort was funded by USDA and the US Forest Service starting in September 2007, with the objective of moving marker assisted selection and breeding (MAS/MAB) toward application in tree breeding over the next few years. The CTGN project includes the four major university-based US tree breeding cooperatives at Oregon State, Texas A&M, University of Florida, and NC State.

The amount and nature of genetic variation in pine populations (both natural and breeding populations) allow genetic variation within functional genes to be directly tested for association with phenotypes of commercial relevance. We will combine our 50+ years of tree breeding experience and population development with the experience of David Neale's group at UC Davis in the molecular dissection of complex traits, to further develop MAS/MAB tools that can accelerate the rate of tree breeding. Single nucleotide polymorphisms (SNPs) in functional genes previously shown to be associated with commercially-relevant traits in experimental populations will be tested for similar associations in operational breeding populations. New modules for handling conifer data will be added to software packages developed for use in marker-assisted breeding of crop plant species, and methods for implementing MAS/MAB in applied tree breeding programs will be defined and economically evaluated using assumptions derived from study results. Additional objectives for the project are to develop improved methods for detecting marker-trait associations and for finding complementary ways to combine phenotypic selection and MAS in conifers. Project outcomes will be delivered directly to breeders and documented in databases maintained on the web at the project website. More information about this project is available at http://www.pinegenome.org/ctgn/.



ASSOCIATED ACTIVITIES

The Crossnore Summit

In August 2007, Cooperative members and NCSU staff joined for a 2-day meeting at the NC Forest Service Mountain Training Facility in Crossnore, NC to discuss the future of the Tree Improvement Cooperative. The changing membership and the impact on members' ability to complete tree improvement activities (i.e. their inkind contributions) as well as their ability to fund the Raleigh staff have been well documented. The planning meeting was called to address some fundamental questions and issues:

- Does the Cooperative have a future?
- If so, what will it be?

Our hope was for a Rebirth of the NC State University – Industry Cooperative Tree Improvement Program. Specifically, we wanted to accomplish:

- What is our Mission/Vision? Strong consensus is critical
- Determine Cooperative objectives
- How to accomplish these objectives and the Cooperative structure



Below is a summary of the key decisions and recommendations approved by the Advisory Committee.

The "working version" of the Cooperative's Mission Statement is:

To Increase Value to Landowners and Citizens Through Continuous Genetic Improvement of Forest Trees

We wanted the statement to be concise yet broad enough to reflect the concept of value rather than only productivity as was stated in our previous mission statement. "Value" has implications beyond harvested timber to include carbon sequestration, bio-energy production, and other ecosystem services. "Continuous genetic improvement" reflects the comprehensive nature of our breeding program both for short-term financial gain and long-term management of genetic diversity.

The key objectives for the Cooperative are:

To conduct a comprehensive breeding program for loblolly pine and other species of regional importance that balances the need for short-term genetic gain for financial benefit and the need for long-term management of genetic diversity for the future.

To conduct research that will provide an improved knowledge and technology base for development and utilization of genetic resources in the future.

To enhance program progress, efficiency, and benefit through technology transfer activities.

Given the change in membership of the Cooperative and the need to have our name be more reflective of who we are, the Cooperative will now be known as the:

North Carolina State University Cooperative Tree Improvement Program

The concept and movement towards consolidating the breeding program at Breeding Centers and Testing Centers was unanimously and enthusiastically adopted (see page 2).

Discussion of a new membership category revolved around the reality that fewer landowners are involved in the development of our genetic material. The Cooperative's new Contributing Membership is designed for consulting firms, small to medium forest products companies, TIMOs, REITs, nurseries, and landowners who want to have the best knowledge possible about what loblolly pine genetics to plant. The fee that a Contributing Member pays is based upon the number of acres that are being established with genetic material from the NC State Tree Improvement Cooperative. Contributing Members have access to the Cooperative's performance data base (breeding values of all the families available from the Cooperative). With this knowledge, landowners are fully-informed customers and can be assured of obtaining the best genetic material possible for their land. For more information on Contributing Membership, go to:

http://cnr.ncsu.edu/tip/membership_class_descript/contributing_descript.htm

Our old friend, Dr. Lee Allen helped lead this strategic planning effort. Lee helped us all take a step back and obiectivelv look at the Tree Improvement Cooperative and see where we needed to be headed in the coming years and decades. Lee helps lead the Forest Nutrition Cooperative (www.forestnutrition.org/) and has faced many similar challenges over the years with changes in forest land ownership and membership in the program. We owe Dr. Allen a tremendous debt of gratitude, and we wish him the best as he starts his new career as a Professor Emeritus – ves, Lee retires this summer.

Southern Forest Tree Improvement Conference

Texas A&M and the Texas Forest Service hosted the 28th Southern Forest Tree Improvement Conference in Galveston, TX in June 2007. NC State students and faculty were well represented at the conference, giving four volunteer papers and one of the invited talks at the plenary session.

Tree Improvement Short Course

In September 2007, we had our Tree Improvement Short Course in Fernandina Beach, FL. Thanks to Rayonier for hosting the field trips and special thanks to Dr. J.B. Jett for his valuable contributions in teaching. Few others bring the experience and knowledge of tree improvement with more enthusiasm than J.B.

Genetics – Silviculture Workshop and 2007 Contact Meeting

In November 2007, the Cooperative held a Workshop for Foresters and Forest Landowners in conjunction with the Forest Nutrition Cooperative. Our theme was **Profiting from Planting and Managing Elite Loblolly Pine Genotypes**. Attendees from within the Cooperative as well as foresters and landowners from outside the program learned about opportunities to profit from appropriate management of elite genetics.

ArborGen's field trip to look at MCP and clonal forestry

research and operations helped to make the workshop and Contact Meeting a big success. We thank Phil Dougherty and the rest of the ArborGen folks for their efforts.

At the end of the week, our Contact Meeting and a special Advisory Committee Meeting was held.

Profiting from Intensive Plantation Silviculture

Over 40 foresters and landowners attended the April 2008 workshop at the NCSU Hofmann Forest in Onslow County, NC. Lee Allen and Steve McKeand hosted the workshop and field tour with one of the objectives to recruit members to the Tree Improvement and Forest Nutrition Cooperatives.

Collaboration with SLU Faculty of Forestry and SkogForsk in Sweden

For almost 20 years the Nicholson Fund has provided support to faculty in the Department of Forestry and Environmental Resources to facilitate interactions and collaborations with colleagues in Sweden. The Nicholson Fellowship has provided financing to Swedish students to study forest management and forest genetics at NC State. Daniel Gräns (see p. 19) is the current Nicholson Fellow.

In November 2007, forest genetics students and faculty from <u>SLU</u> and <u>SkogForsk</u> visited Raleigh and Summerville, SC to learn about forestry and tree improvement in the southern US. We appreciate the hospitality from ArborGen during the field tour.

Visiting Scientist

Dr. Bilgin Guller, Assistant Professor from Suleyman Demirel University, School of Forestry in Isparta, Turkey spent six months (October 2007 to March 2008) with the Cooperative Tree Improvement Program. During her stay Bilgin worked on a Turkish red pine (*Pinus brutia*) wood quality research project using the x-ray densitometry laboratory. She also gained some experience with new rapid wood quality screening tools & methods, such as the Resistograph method developed by the Cooperative and the TreeSonic. The Resistograph is used for rapid screening of genotypes for wood density whereas the TreeSonic is used to measure relative stiffness of live trees. Dr. Guller also followed some statistical data analysis classes and learned the SAS software for data analysis. We enjoyed having Bilgin with the Cooperative and wish her best for her career.

Teaching

FOR 411 (Forest Tree Genetics and Biology), our undergraduate tree improvement course was taught this spring along with FOR 725 (Forest Genetics – formerly FOR 611). Ross Whetten and Steve McKeand had a great group of students in class, and they enjoyed the tour of the NC Forest Service seed orchard and nursery at Goldsboro. From left \rightarrow right are Emily Grigsby, Michael Harris, George Khan, Steve McKeand, John Whitfield, Nick Williams, Chris Sharpton, Mike Adams, and Chris Letourneau (Maxie Maynor – photographer extraordinaire!).

New Cooperative Website (<u>www.cnr.ncsu.edu/tip</u>)

Our redesigned website was launched in August 2007. Those familiar with our old site will see many changes and improvements. There are new features such as the <u>News</u> tab, where one can find TIP news, seminars, and events of interest, and the updated <u>Publications</u> tab, where a list of current publications and all previous TIP annual reports can be found. <u>Research</u>, <u>Prospective Members</u>, and a <u>FAQ</u> sections are other new additions. The Mapper-Excel macro, courtesy of Richard Bryant (ArborGen) and the Seed Orchard Design Assistant (TIP-SODA), coded by our own Mike Jett, are examples of our intent to use the website more actively as a tool for our cooperators. We also intend for the website to be an approachable and easy-to-navigate site for those interested in learning more about the Cooperative.

For ease in remembering, the website's URL has been shortened to <u>www.cnr.ncsu.edu/tip</u>. Organization and information flow were the key principles that directed the overhaul, and we think you will appreciate the updated feel to the website. It was coded and designed by Colleen Liley, a recent graduate from the NCSU School of Design, and our thanks go to her for a high-quality, professional product.

Facilities Changes and Impacts to TIP

There have been quite a few facility changes in the College of Natural Resources (CNR) and within the Department of Forestry and Environmental Resources (FER) in the past year. The largest comes with the opening of the new addition of Jordan Hall (locally dubbed Jordan II) that provided 5 new floors of teaching, office, and lab space for the college.

While completion of the addition was welcome, there arose a challenge in that the college had grown beyond expectations in the years since the original plans were drafted. Within FER, department head Dr. Barry Goldfarb assembled a committee of faculty and staff, chaired by Dr. Ross Whetten, to explore options and implement consolidation efforts of all departmental labs into function-driven labs rather than program-driven spaces. The end results should prove to strengthen the abilities and research capacities of all of the programs in FER.

$52^{nd} \ ANNUAL \ Report$ North Carolina State University Cooperative Tree Improvement Program

<u>The Pollen and Seed Lab</u> has been relocated to the new wing of Jordan Hall. It has a new walk-in cooler and all the necessary tools for seed and pollen processing and storing. Mr. Michael Tighe, with CAMCORE, manages the facility. While the majority of activities on a departmental level will occur in these labs, the issue of storage space, both with respect to tools and refrigeration/freezer considerations, still needed to be addressed as all primary users of this space have different space requirements. As a result, TIP has retained a small space in Biltmore Hall, providing easy access to our materials in cold storage to conduct the day-to-day pollen and seed activities.

The Molecular Marker Lab resides in what many have historically known as the Tree Improvement Labs in Biltmore Hall. Renovations began as soon as the Jordan II move took place. At the time of writing, many months after the start of the project, the lab space is expected to be operational by early summer 2008. This lab has a pre- and post- amplification space, a dedicated purified water system, increased workspace capacity, and upgraded electrical capacities. The lab is managed by our own Saul Garcia. *We would like to give a note of special thanks and acknowledgement to ArborGen, who donated a tremendous amount of lab equipment and supplies that will be a large jump-start to research efforts in this lab.*

<u>The X-ray Densitometer Service Center</u> is a new service center within CNR that will provide a means to assist in covering the expense in operating the x-ray densitometer. The fee is a per scan charge on all cores passing through the densitometer. This service can be available to cooperators who want densitometry assessments on their own samples. Dr. Fikret Isik heads the center and makes sure that everything is in order, from servicing to general maintenance.

<u>The Horticulture Field Lab (HFL)</u> is the shared field space between the College of Agriculture and Life Sciences and CNR. This is where our rooted cutting clonal study materials are being produced and managed. CTIP has taken over the majority of the responsibilities of the CNR space, managed by Patrick Cumbie, since we will be the major users in the very near future. We already have a 300+ hedge project (FrCAD) producing cuttings, and with the addition of the Atlantic Coastal Elite (ACE) population with an estimated 2500+ hedges, the HFL will be a large and important resource in the Cooperative's future.

As a final note, CTIP now has access to secure, dedicated server space within the university infrastructure. While not physically a facilities change, the impact is very important for us. The largest implication is that this space allows us to backup our data to a system that is "disaster-recovery" secure, meaning that in the event that a massive catastrophe locally, everything we place in this space can be recovered. We see this as an important system to use given the decades of irreplaceable information we have amassed.

GRADUATE STUDENTS

The Cooperative continues to be dedicated to graduate education. Graduate students bring fresh ideas and facilitate collaboration with other faculty at NC State and in other institutions. Through the Tree Improvement Program, students are educated and trained to be the tree improvement leaders of tomorrow. Tyler Eckard is one of our recent success stories. Tyler completed his MS in fall 2007. He worked with Fikret Isik and Bronson Bullock looking at development of prediction models for whole-stem wood quality of superior loblolly pine clones for deployment. Tyler is now one of our cooperators working as Technical Forester – Geneticist with Smurfit-Stone Container Corporation in Fernandina Beach, FL.

We are fortunate to have 4 new graduate students joining us in August 2008. We'll let you know about them next year.

Mike Aspinwall completed his masters degree last summer. His project dealt with wood properties and the inherent variation present up the boles of different genotypes. Mike is now working on his PhD on a physiology / genetics project focusing on the Hofmann Forest Growth-Genetics-Spacing (GST) Study with John King and Steve McKeand.

Jesus Espinoza is working on a project jointly funded by the Forest Nutrition and the Tree Improvement Cooperatives. Jesus received his MS with CAMCORE in 2003 then worked with Carton de Venezuela before returning for his PhD. Jesus has made good progress on his project looking at genetics and cultural effects on stem quality with emphasis on stem sinuosity in loblolly pine.

Daniel Gräns's PhD research is looking at solid wood properties in loblolly pine and Norway spruce. Daniel's Nicholson Fellowship is supporting his work both in Sweden and with the Cooperative. His loblolly pine trial is a Genetics x Culture trial established by International Paper Company in Bainbridge, GA. Daniel hopes to finish his research and complete his dissertation this summer.

52nd ANNUAL REPORT North Carolina State University Cooperative Tree Improvement Program

George Khan began his masters degree in tree improvement / biotechnology last August working with Ross Whetten. George is developing speciesspecific SNP markers that can be used to distinguish different populations and species of pines.

Ben Smith is a PhD student on a Hofmann Forest Graduate Fellowship. His project is focusing on incorporating realized gain from genetic improvement into loblolly pine growth and yield models using trials established by MeadWestvaco in Walterboro, SC. Ben plans to complete his degree by 2009.

Sherry Xiong is working on her PhD in tree improvement / biotechnology with Ross Whetten and Steve McKeand looking at the genetic factors of forking in loblolly pine. She is using data from clonal trials of loblolly pine established by MeadWestvaco and now managed by ArborGen.

Student, Degree, Research Project

Mike Aspinwall, MS (completed 2007), PhD, Genetics / physiology in loblolly pine
Patrick Cumbie, PhD (part time), Association genetics in loblolly pine
Tyler Eckard, MS (completed 2007), Prediction of whole-stem wood quality of loblolly pine clones
George Khan, PhD, Develop species-specific SNP markers
Jesus Espinoza, PhD, Genetics and silvicultural effects on stem quality in loblolly pine.
Daniel Gräns, PhD, Variation in solid wood properties in Norway spruce and loblolly pine.
Ben Smith, PhD, Incorporating realized gain from genetic improvement in loblolly pine growth & yield models
Sherry Xiong, PhD, Genetic factors in forking of loblolly pine

COOPERATIVE STAFF

Fortunately the Cooperative team has remained fairly stable since last year. Josh Steiger joined us last fall as a research assistant with primary responsibilities towards the USDA-CAP grant entitled the Conifer Translational Genomics Network. Josh worked for the Cooperative as an undergraduate student and made himself indispensible. When the position with the CAP grant came around, Josh was an easy choice to make.

You've heard me say this many times; you will not find a more dedicated, hard-working, and collegial group of individuals to lead the Cooperative through this exciting time

Tree Improvement Staff: $L \rightarrow R$: Fikret Isik, Saul Garcia, Josh Steiger, Patrick Cumbie, Tori Batista-Brooks,
Jim Grissom, Steve McKeand, and Ross Whetten. And yes, some foresters still live in
Biltmore Hall.

Membership of the NCSU Cooperative Tree Improvement Program

Cooperative Membership is very different today than it was only a few years or even months ago. In the past year, ArborGen took over the tree improvement programs of International Paper Company and MeadWestvaco, resulting in a loss of 2 full members and a change for ArborGen from being a Research Associate member to being a full member. Joshua Land Management dropped as a full member, but Molpus (land managers for Joshua) began as a Contributing Member in January 2008. The full members of the program provide the inkind support to make tree improvement happen in the field. Their financial contributions to NC State University support the operations, research, teaching, and outreach components of the program. Support from the Contributing Members is used primarily for the on-the-ground breeding, testing, selection, and archiving efforts by the full members and the Cooperative staff. We could not ask for a more dedicated and supportive group of cooperators.

> *Full Members* ArborGen CellFor, Inc. Georgia Forestry Commission Hancock Timber Resources Group North Carolina Division of Forest Resources Plum Creek Timber Company Rayonier, Incorporated Smurfit - Stone Container Corporation Tennessee Department of Agriculture Virginia Department of Forestry Westervelt Company Weyerhaeuser Company

Contributing Members Dougherty & Dougherty Forestry Services, Inc. Jordan Lumber & Supply Company Molpus Timberlands Management, LLC Resource Management Service, LLC South Carolina Forestry Commission

When Steve tried to convince Dave Gerwig to select this superior tree, Dave figured it was time to give up on tree improvement. While Dave is no longer directly involved in breeding at ArborGen, we stay in touch. We wish him the best with his new responsibilities.

PUBLICATIONS OF SPECIAL INTEREST TO MEMBERS (2005-2008)

From our inception in 1956, there have been over 800 publications written by Cooperative Scientists, Students, and Associates. Below is a list of publications from the last 3 years. The entire list is available at our web site: http://cnr.ncsu.edu/tip/publications_citations.html

2008

- Emerson, J.L., L.J. Frampton and S.E. McKeand. 2008. Genetic variation in early growth and bud production among natural populations of Fraser fir. HortScience (in press).
- Isik, F., M. Gumpertz, B. Li, B. Goldfarb, X. Sun. 2008. Analysis of cellulose microfibril angle (MFA) using a linear mixed model in *Pinus taeda* clones. Can. J For. Research 38: (in press).
- Isik, F, B. Li, B. Goldfarb, and S. McKeand. 2008. Prediction of wood density breeding values of *Pinus taeda* elite parents from unbalanced data: a method for adjustment of site and age effects using common checklots. Ann. For. Sci. 65: (in press)
- McKeand, S.E., B. Li, J.E. Grissom, F. Isik, and K.J.S. Jayawickrama. 2007. Genetic parameter estimates for growth traits from diallel tests of loblolly pine throughout the southeastern United States. Silvae Genetica (in press).
- McKeand, S.E., D.M. Gerwig, W. P. Cumbie, and J.B. Jett. 2008. Seed orchard management strategies for deployment of intensively selected loblolly pine families in the southern US. P. 177- 182, In: Lindgren, D. (ed.). Seed orchards, Proceedings from a conference at Umeå, Sweden, September 26-28, 2007 (ISBN: 978-91-85911-28-8)
- McKeand, S.E., B. Li, J.E. Grissom, F. Isik, and K.J.S. Jayawickrama. 2008. Genetic parameter estimates for growth traits from diallel tests of loblolly pine throughout the southeastern United States. Silvae Genetica (in press).
- Sherrill, J.R., T.J. Mullin, B.P. Bullock, S.E. McKeand, R.C. Purnell, M.L. Gumpertz, and F. Isik. 2008. An evaluation of selection for volume growth in loblolly pine. Silvae Genetica 57(1):22-28.

2007

- Espinoza, J., S. McKeand, L. Allen, J. Grissom, T. Brooks, and B. Smith. 2007. Response of several genotypes of loblolly pine to environmental stress for stem form traits at age 12. In: Proc. 28th South. For. Tree Impr. Conf., Galveston, TX. (in press).
- McKeand, S.E., B.J. Zobel, T.D. Byram, and D.A. Huber. 2007. Southern pine tree improvement a living success story. In: Proc. 28th South. For. Tree Impr. Conf., Galveston, TX. (in press).

2006

- Alizoti, P., B. Li, and S.E. McKeand. 2006. Early evaluation of intra- and inter-provenance hybrids of loblolly pine for planting in Piedmont regions of the southern US. For. Sci. 52:557-567.
- Emerson, J.L., L.J. Frampton, and S.E. McKeand. 2006. Genetic variation of spring frost damage in three-year-old Fraser fir Christmas tree plantations. HortScience 41:1531-1536.
- Hu, X. S., B. Li. 2006. Additive genetic variation and the distribution of QTN effects among sites. Journal of Theoretical Biology 243:76-85.
- Li, Hua, H. Amerson, Bailian Li. 2006. Genetic models of host-pathogen gene interaction based on inoculation of loblolly pine seedlings with the fusiform rust fungus. New Forests 31: 245-252.

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- Lstiburek, M., Mullin, T.J., and El-Kassaby, Y.A. 2006. The impact of differential success of somatic embryogenesis on the outcome of clonal forestry programs. I. Initial comparison under multi-trait selection. Can. J. For. Res. 36: 1376-1384.
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- McKeand, S.E., E.J. Jokela, D.A. Huber, T.D. Byram, H. Lee Allen, B. Li, T.J. Mullin. 2006. Performance of improved genotypes of loblolly pine across different soils, climates, and silvicultural inputs. For. Ecol. and Manag. 227:178-184.
- Myburg, H., A.M. Morse, H.V. Amerson, T.L. Kubisiak, D. Huber, J.A. Osborne, S.A. Garcia, C.D. Nelson, J.M. Davis, S.F. Covert, and L.M. van Zyl. 2006. Differential gene expression in loblolly pine (*Pinus taeda* L.) challenged with the fusiform rust fungus, *Cronartium quercuum* f. sp. *fusiforme*. Physiological & Molecular Plant Pathology 68:79-91.
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- Sykes, R., B. Li, F. Isik, J. Kadla, H.M. Chang. 2006. Genetic variation and genotype by environment interactions of juvenile wood chemical properties in *Pinus taeda* L. Annals of Forest Science 63 (8): 897-904.
- Yu, Q., B. Li, C.D. Nelson, S.E. McKeand, V.B. Batista, and T.J. Mullin. 2006. Association of the *cad-n1* allele with increased stem growth and wood density in full-sib families of loblolly pine. Tree Genetics & Genomes 2:98-108.

2005

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On a sad note, on May 12, 2008, the Cooperative lost a true friend and strong supporter. Dr. Dave Canavera lost his battle with cancer. We worked closely with Dave during his career with Westvaco and MeadWestvaco until his retirement last fall. All of us benefitted from Dave's sage advice and counsel over the years and most recently at the Crossnore Summit last August (see group photo p.15). Our sympathies go to the Canavera family.

A new era of Cooperative breeding began this year with the Breeding Center at the Georgia Forestry Commission's Arrowhead Seed Orchard near Cochran, GA. We are indebted to Russ Pohl and the GFC for their willingness to get this new venture started. We are fortunate to have hired John Hendrickson to get our Sawtimber Elite Population topgrafting off to a great start. Chuck Little and Patrick Cumbie were there to make sure John and Russ did things right.