Third-Cycle Breeding Strategy for Slash Pine by the Cooperative Forest Genetics Research Program

T. L. White, D. A. Huber and G. L. Powell [1]

Abstract: The Cooperative Forest Genetics Research Program (CFGRP) third-cycle slash pine tree improvement program will span 11 years (2003-2013), involving a breeding population of 360 third-cycle selections and 20 full-sib (FS) progeny tests with a total of 75,000 measurement trees. Of the 360 selections, two-thirds are forward selections (selections made in 1400 second-cycle full-sib selection plots) and one-third are backward selections (excellent first- and second-cycle selections brought forward into the third cycle). Selections will be top-grafted into sexually-mature, insect-protected, seed orchard trees where third-cycle breeding can begin as soon as one year after grafting. The main breeding population is divided into ten sublines with approximately 36 selections per subline. The top 6 selections from each of the 10 sublines comprise an elite population (6 per subline x 10 sublines = 60 elite selections). The ten sublines are divided into two superlines (the orange and blue superlines). Each superline has 5 sublines containing a total 180 selections of which 30 comprise the elite population for that superline.

The breeding for the main and elite populations is scheduled for three breeding seasons (2004-2006) and consists entirely of FS matings planted in replicated tests with single tree plots in incomplete block designs. For the elite population, a circular mating design will create 75 crosses in each of the 2 superlines (5 crosses for each of the 30 selections) for a total of 150 total elite FS families (75 crosses/superline x 2 superlines). Ten third-cycle elite FS progeny tests will be planted with each test having 3,000 measure trees (150 families/test x 20 blocks/test) for a total of 30,000 FS seedlings. For the main population, the circular mating design will attempt 72 crosses within each of the 10 sublines (averaging 4 crosses per selection) for a total of 720 main population crosses (72 crosses/subline x 10 sublines). Ten third-cycle main population FS progeny tests will be planted with each test containing FS progeny from half of the sublines (2 series with 5 tests for the orange subline and 5 for the blue). Assuming that only 600 of the 720 attempted FS families are successful, each test will contain 4,500 measure trees (300 families/test x 15 block/test of single tree plots) for a total of 45,000 FS progeny planted in main population tests (2 series * 5 tests/series * 4500 trees/test).

Keywords: Breeding strategies, *Pinus elliottii* var *elliottii,* third-cycle, selections, top grafting, breeding, progeny testing

INTRODUCTION

The Cooperative Forest Genetics Research Program (CFGRP), founded in November of 1953 (Perry and Wu, 1955), includes the University of Florida's School of Forest Resources and Conservation, forest industries and state agencies as cooperators.

T. L. White is Professor, D. A. Huber is Research Associate and G. L. Powell is Senior Biological Scientist with the School of Forest Resources and Conservation, University of Florida, Gainesville, Florida, 32611-0410

Our mission is to develop genetically-improved varieties of southern pines for reforestation of harvested timberlands in the lower coastal plain of the southeastern United States.

Throughout the 50 years of the CFGRP slash pine tree improvement program, several aspects have remained consistent: 1) Members of the CFGRP (industries and state forestry agencies from Florida and Georgia) conduct the selection, breeding and testing on their timberlands and provide policy and strategic direction; 2) CFGRP staff at the University of Florida provides strategic planning, technical support, supportive research, data management and analysis; 3) The program employs a single breeding unit aimed at creating broadly-adapted improved varieties for the entire slash pine native range in the lower coastal plain; and 4) The two most important traits are volume growth and fusiform rust resistance *(Cronartium fusiforme* sp. *fusiforme).*

Many other factors have changed over the 50 years of slash pine breeding: 1) The number of members and their names (only two of the original 10 members remain after 50 years, Rayonier Inc. and International Paper Company); 2) Breeding strategies; 3) Selection methods; 4) Genetic test designs; and 5) Data analysis methods. The purposes of this paper are to summarize the first 2 cycles of slash pine breeding by the CFGRP and detail the strategy for the third-cycle. We compare and contrast the breeding, selection and testing strategies and methods used in each of the three cycles.

FIRST-CYCLE SLASH PINE BREEDING PROGRAM (1953-1986)

The first breeding cycle for slash pine spanned 34 years with the selection phase beginning in 1953 and terminating in 1986 with the first second-cycle selections. Selections were grafted into first-cycle seed orchards from 1955-1982. Breeding began in 1965 and was completed in 1985. Open-pollinated (OP) tests were established between 1959-1985 and full-sib (FS) tests were established between 1978-1986.

First-cycle Slash Pine Selected Population

The first-cycle selected population included 3969 selections made in natural stands throughout the native range of slash pine between 1953 and1980 (Table 1). Of these 3969 selections, 2516 were tested in progeny tests and/or subsequently used for breeding. Of the 2516, approximately 2000 first-cycle selections were high-intensity selections for growth and form using the comparison tree method in which candidate trees were graded against dominant neighbors for various form (straightness, branch diameter, branch angle, pruning, crown diameter etc.) and volume characteristics. Candidate trees were also free of disease; however, most stands were low in disease incidence, so selection intensities for rust and pitch canker resistance were very low.

During the 1960's and early 70's, it became apparent that fusiform rust resistance was a very important trait for our tree improvement program. So, beginning in 1972 a concentrated effort was made to introduce an acceptable level of rust resistance into the selected population. As a result, the other 500 first-cycle selections were dominant, rust-

free trees selected in high hazard, 10-year-old or older plantations in which at least 70% of the trees were infected with fusiform rust. This resulted in immediate gains for fusiform rust resistance (Goddard *et al.* 1975).

	Cycle 1	Cycle 2	Cycle 3
Cycle Duration			
Start (year)	1953	1987	2003
Finish (year)	1986	2002	2013
Years (#)	34	16	11
Size			
Selected Population *(#)*	3969	1051	500
Breeding Population (#)	2516	1017	360
Effective Number (Ne)	2516	665	NA
Types of Selections			
Backward (#)	2016	396	180
Forward (#)	0	330	320
Infusions (#)	500	291	0
Population Structure			
Elite Population?	No	Yes, 75 selns	Yes, 60 selns
Main Population:			
Sublines (#)	1	24	10
Selections/Subline (#)	2,516	42	50
Genetic Gain			
Volume (%)	9	15	23
Rust (R50)	45	39	31

Table 1: Selected and breeding populations for 3 cycles of slash pine tree improvement by the CFGRP. Selected populations include all selections made by the cooperative, while breeding populations include only those selections used in breeding and/or testing. Effective size of the breeding population was calculated from Falconer and Mackay (1996). Infusions are untested material added to the breeding population. Genetic gain is estimated as the mean BLP-predicted breeding value of all selections in the breeding population. Individual-tree volume gains are percentage (at 15 years) above unimproved slash pine. R50 values are rust incidence of improved material relative to an unimproved incidence of 50% of the trees infected. Figures for Cycle 3 were estimated in 2003 when approximately 3/4 of the selections had been made with 1/4 still to be made in 2004.

Genetic gains for the 2516 members of the first-cycle breeding population (9% for volume and an R50 of 45%) are a weighted average of the gains from the 2000 high-intensity selections for growth and form (10% for volume and little gain in rust resistance with R50=48%) and the 500 rust-free selections in high hazard stands (5% volume gain and R50=35%). The R50 value of 45% means that seedling offspring obtained from random matings among the 2516 first-cycle selections are expected to incur rust incidence of 45% when 50% of unimproved slash pine trees are infected with stem or branch galls.

First-cycle Slash Pine Breeding and Testing

In the first cycle of slash pine tree improvement, progeny testing and breeding were conducted in tandem. Progeny testing using orchard OP seed was done first to rank selections with OP field trials being planted mainly in the 1960s and 1970s as the first-cycle grafted orchards reached seed production. Then, in the 1970s and 1980s, the results of the OP trials were used to identify better parents (approximately 1000 of the first-cycle selections) to include in control-pollinated breeding to produce FS families for field trials in which second-cycle selections were made. The tandem approach, progeny testing followed by breeding, resulted in good genetic gain, but lengthened the first cycle to 34 years.

In total, 363 first-cycle OP progeny tests were planted by CFGRP cooperators in Florida, Georgia, Alabama and Mississippi to rank 2516 parents for volume growth and rust resistance (Table 2). Each test contained 10 to 150 OP families (typically 20 to 40 families), and the field design was randomized complete block (RCB) with 6 to 10 blocks established with row plots containing 6 to 10 trees per plot. In total, the 363 OP tests contained approximately 580,000 total measure trees.

All first-cycle breeding was conducted in a breeding population that was unstructured in any way (no sublines, no elite population and no multiple populations). The most common mating design utilized was 6-parent disconnected diallels, but some were disconnected factorials in which pollen from 4 rust-free selections was used as males with 6 original selections used as females. As a result of control-pollinated breeding, 277 first-cycle genetic tests containing over 2700 FS families were planted by CFGRP cooperators in Florida, Georgia, Alabama and Mississippi (Table 2). The purposes of these tests were to rank the parents and make second-cycle forward selections. The field design of these tests was RCB with row plots. A typical test has 20-30 FS families, 6-10 blocks and 6-10 trees per plot for an average of 1600 measure trees per test. In total, more than 440,000 test trees were planted as a result of the first-cycle FS breeding efforts.

Site preparation and test maintenance (weed control, fertilization, mowing) were minimal in first-cycle tests resulting in relatively low h^2 for volume (0.09) and rust (0.21), while G x E interaction was relatively high with type B genetic correlations of 0.6 for volume and 0.7 for rust (Table 2).

First-Cycle Propagation Population and Deployment

In 1955, CFGRP members began establishing first-cycle, grafted seed orchards. Each member's seed orchard contained that company's 40 to 200 selections (i.e., selections were not interchanged among members). Approximately 50 orchards were established by members in this manner. For many years (1960s and 1970s) the main deployment method was to use bulk seed collections obtained from these OP first-cycle, slash pine seed orchards. Expected genetic gains in harvest yields at 20 years from the operational plantations established with bulk collections from unrogued, first-cycle seed orchards

averaged 7.6% and 12.9% on low hazard and high hazard fusiform rust sites, respectively (Figure 2). The actual gains varied among the 50 orchards.

	Cycle 1	Cycle 2	Cycle 3
OP and PM Tests			
Test Sites (#)	363	16	0
Purpose	Rank parents	Rank parents	NA
Mating Design	OP from orchards	PM in clone bank	NA
Field Design	RCB, row plots	RCB+IBD, STP	NA
Families (#)	2,500	315	NA
Trees (#)	580,000	54,400	NA
Full-sib Tests			
Test Sites (#)	277	10	20
Purposes	Rank parents and Make selections	Make selections	Rank parents and Make selections
Mating Design	Disconnected diallels and factorials	Stratified in sublines	Circular diallels in sublines
Field Design	RCB, row plots	Unreplicated blocks	IBD, STP
Families (#)	2700	1407	750
Trees (#)	440,000	105,000	75,000
Heritability (h2)			
Volume	0.09	0.31	NA
Rust	0.16	0.26	NA
GxE(r			
Volume	0.6	0.8	NA
Rust	0.7	0.8	NA

Table 2. Characteristics of breeding and genetic testing for 3 cycles of slash pine tree improvement by the CFGRP. Abbreviations are: G x E= genotype x environment interaction; h^2=individual, pooled-site heritability; IBD=incomplete block design; OP=open-pollinated; PM=pollen-mix pollinated; RCB=randomized complete block; STP=single tree plots; and rb=type B genetic correlation of family performance for the same trait across sites.

As OP progeny test data became available, seed orchard clones were ranked and poor performing clones were removed (rogued) from the orchards. Average estimated gains from members' rogued seed orchards rose to 12.8% and 17.9% in 20-year harvest yield on low and high hazard sites, respectively (Figure 1). This is a gain of slightly more than 5% from roguing seed orchards based on OP progeny test information and varied among orchards depending on the quality and quantity of progeny test data available to rank the clones in each orchard. This seed was the main source of operational seed from 1980 to 1995 (White and Duryea 1997).

Some members also chose to graft new seed orchards containing only the highest ranking first-cycle parents based on the OP progeny test data. These 1.5 generation orchards required large-scale exchange of scion material among members, because most members had originally selected only a few of the high ranking parents. Average estimated gains in harvest yield from members' 1.5 generation seed orchards were 17.1% and 22.5% in low and high rust hazard areas (Figure 1). These seed orchards have been a main source of operational seed between 1985 and the present time. It is now common for members to collect seed by clone and deploy OP families operationally (McKeand *et al.* 2003).

SECOND-CYCLE SLASH PINE BREEDING PROGRAM (1987-2002)

The second-cycle slash pine selection, breeding and test establishment spanned 16 years (1987-2002). The selection phase began in 1987 and was completed in 1990. Selections were grafted into clone banks for breeding between 1988 and 1990. Breeding began in 1993 and was completed in 2001. Two series of polymix (PM) tests were established to rank many, but not all, of the parents in the selected population: Series I in 1998 and Series II in 2001. As part of the complementary mating design, FS breeding was conducted simultaneously with the PM breeding and 10 sites (1 per member) were established with unreplicated block plots of FS families for making third-cycle forward selections. A total of 1407 FS families were planted in unreplicated plots between 1995 and 1999 with third-cycle selections beginning in 2003. The second-cycle tree improvement program for slash pine is outlined below and detailed in White *et al.* (1993).

Second-Cycle Slash Pine Selected Population

The second-cycle slash pine total population size was 1051; however, thirty-four selections are for research purposes only and are in a non-breeding or testing subline (subline Q). Therefore the second-cycle breeding and testing population size was 1017 with an effective population size of 665 (Table 1). Our objectives for the selected population were to maximize genetic gain, while maintaining a broad genetic base. Potential candidates available for inclusion in the selected population were: 1) 2500 original first-generation selections (backward selections); 2) 440,000 trees from 2700 different FS families generated from crosses among first-cycle selections (forward selections); and 3) A number of promising, but generally untested, materials from a range of sources (infusions).

All forward and backward candidates were ranked according to their predicted genetic worth for volume and R50 using best linear prediction (Hodge et. al. 1989). Then, 3 selection indexes were developed: 1) Growth and rust combined; 2) Most weight on volume; and 3) Most weight on rust resistance. The best candidates identified by these three indices were selected with a maximum 7 relatives permitted for top ranking selections (to maximize gain) and fewer relatives for less-superior selections (to maintain genetic diversity). For each forward selection, a computer generated selection form was printed and CFGRP members visited the full-sib tests to make forward selections. This selection process was completed in 1990.
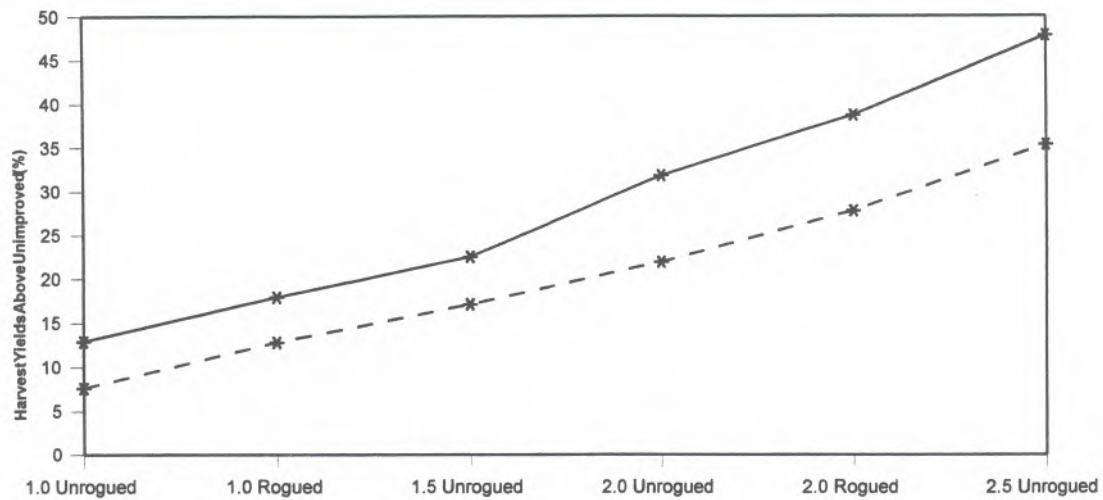
Figure 1. Estimated genetic gains in harvest yield from slash pine seed orchards when material is planted in low (lower dashed line) and high (upper solid line) rust hazard areas. First and second cycle gains are estimated from actual orchard compositions of members' orchards, while 2.5 orchard gains are mean breeding values of the top 20 available selections. These gains in harvest yield combine the effects of volume growth and rust resistance and are projected to a 20-year pulpwood rotation.

Of the 1017 selections, 396 were backward selections, 330 were forward selections and 291 were infusions (Table 1). The selected population was structured in several ways to both control relatedness (within sublines and superlines) and to focus increased effort on more superior selections in the elite population and upper stratum of the main population. First, the selected population was divided into 2 superlines, orange and blue, each one consisting of an elite population and a main population of 12 sublines (Figure 2). Each subline contained approximately 42 selections which were divided into three stratum based on genetic worth (I, II, III, with selections of the highest quality in stratum I). All related selections were assigned to the same subline and each CFGRP member was given one or two sublines to breed. All forward selections, infusions and some backward selections were grafted into breeding clone banks (1988 to 90). All forward selections were established in at least two members' clone banks.

Compared to unimproved slash pine, the mean genetic gain (predicted as an average of the BLP-breeding values) for this population of 1017 selections was 15% for 15-year individual-tree volume and R50=39%. These second-cycle gains indicate a 6% increase in volume breeding value and a 6% reduction in R50 compared to the entire first-cycle population (Table 1). However, the second-cycle gains are decreased by inclusion of 291 untested infusions, most of which were assumed to have volume gains of 10% or lower and R50=40 or higher.
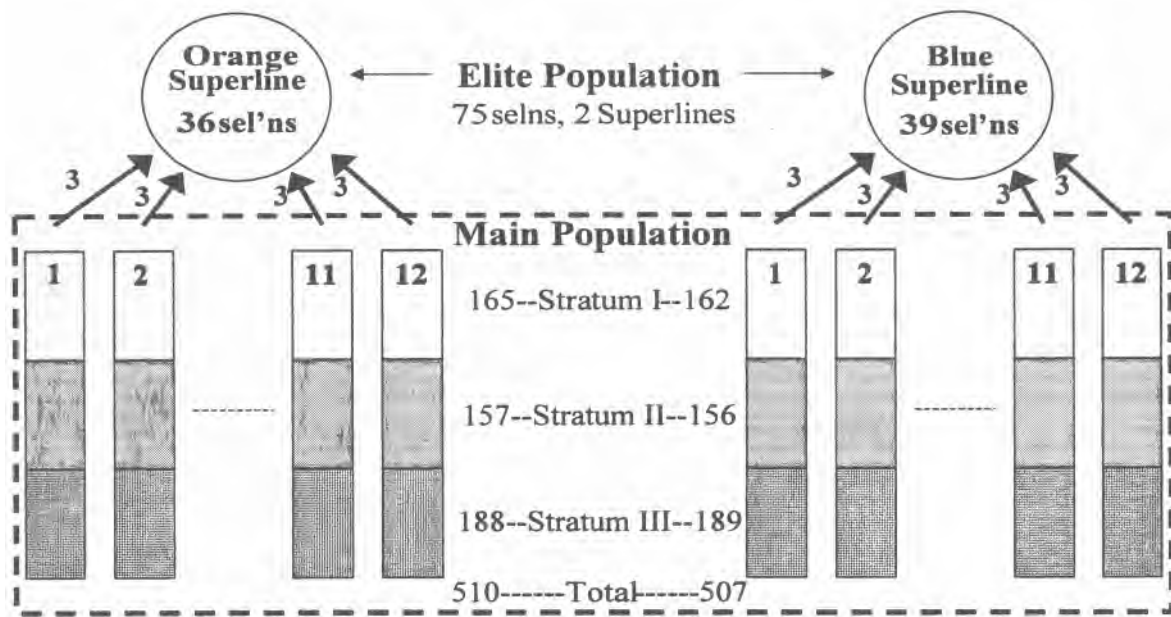
Figure 2. Breeding population for second-cycle slash pine. Selections were divided into 2 superlines, orange and blue, each one consisting of an elite population and a main population of 12 sublines. All relatedness was confined with sublines and superlines. Each subline was divided into three strata based on genetic quality (I, II, and III with selections of the highest quality in I).

Second-Cycle Slash Pine Breeding and Testing

The breeding and testing strategy for the second cycle employed complementary mating designs (van Buijtenen 1976, van Buijtenen and Lowe 1979): 1) Polymix (PM) crosses planted in randomized and replicated progeny tests to rank parents; and 2) Full-sib (FS) crosses planted in unreplicated block plots of 50 to 100 trees per family from which to make third-cycle forward selections.

Of the 1017 selections, 315 poorly-tested forward and backward selections were crossed with a single pollen mix and planted in PM tests. Infusions and selections that were well tested in the first cycle were not included in the PM testing, but rather used only in the FS breeding. The test design was an RCB with 20 blocks and single tree plots (STPs). A total of sixteen tests were established in two series of 8 tests. Series I was planted in 1998 and the 5 year measurements were taken in 2002. Series II was planted in 2002 and the first year measurements were taken in 2003. The total number of measure trees in these 16 tests are 54,400 (Table 2). Narrow sense heritability from these trials for volume at age 5 years is triple the heritability for the same trait from the first-cycle OP trials (Table 2) and we attribute this both to smaller size of replication with STPs and better site preparation, weed control and fertilization of the second-cycle trials.

The FS breeding phase began in 1993 simultaneously with the PM breeding. In total, 1407 families were created as part of the breeding in the main and elite populations. No specific mating design was followed; rather, more crosses were made with better selections contained in the elite and top stratum of the main breeding population (Lindgren 1986, Lindgren and Matheson 1986). In the main breeding population (Figure 2), all FS breeding was done within each of the 24 sublines, crossing selections together according to their strata: I X I, I X II, I X III, II X II (there are no crosses among strata II x III or III x III).

The 1407 FS families were established by CFGRP members in unreplicated block plots, with a total of 105,000 measure trees across the 10 sites (1 site per member with their FS block plots). These are the selection plots in which the third-cycle, forward selections are being made in 2003 and 2004.

<u>Second-Cycle Propagation Population and Deployment</u>

From 1988 to 1998, CFGRP members established 15 second-cycle, grafted seed orchards using a mixture of tested, first-cycle selections (backwards) and newly-selected second-cycle selections (forwards). The most common field design employed a systematic, repeating design that maximized distance between related clones (Hodge and White 1993). Clones selected for each seed orchard depended on the weight that each member put on volume growth and rust resistance. In total 194 (out of 1017) selections were grafted into one or more orchards, but the number utilized in several orchards is closer to 60. A typical second-cycle CFGRP seed orchard ranges from 5 to 50 acres (mean= 23) and started with 22-93 clones (mean=39). Many of these orchards are now in full seed production and are providing substantial quantities of operational slash pine seed. Most members collect seed by clone and operationally deploy OP families (McKeand *et al.* 2003).

Average genetic gains in plantations established from the 15 unrogued second-cycle seed orchards (based on bulk collection and no pollen contamination) are 22% and 32% for total harvest yield at age 20 on low and high hazard rust sites, respectively (Figure 1). Many members are currently roguing their second-cycle seed orchards, and while actual results from the roguing are not yet available, a simulated roguing leaving the best 20 clones in each of the second-cycle orchards increases expected gain in harvest yield approximately 6% above the unrogued orchards (Figure 1). Furthermore, a simulated 2.5 cycle orchard including only the best 20 selections, now that PM tests have provided rankings, would produce expected gains still higher (35% and 48%) gains in harvest yield in low and high hazard rust sites, respectively.

THIRD-CYCLE SLASH PINE BREEDING PROGRAM (2003-2013)

The CFGRP third-cycle slash pine selection, breeding and testing will span (2003-2013) beginning with the third-cycle selection phase in the winters of 2003 and 2004. Selections will be top grafted into seed orchards in the winters of 2003 to 2005. Breeding is planned from 2004 to 2006. No OP or PM tests are planned in the third-

cycle. Rather, FS families from breeding the 360 selections in the breeding population will be planted in 20 total field tests in 2008 with fourth-cycle forward selections from these tests planned in 2014.

Third-Cycle Slash Pine Selected Population

Approximately 500 third-cycle selections will be made during the winters of 2003 and 2004 with two-thirds being forward selections (selections made in the 1400 second-cycle, unreplicated FS selection plots) and one-third being backward selections (excellent first- and second-cycle selections brought forward into the third cycle). All forward selections and some backward selections will be top-grafted into sexually-mature, insect-protected, seed orchard trees where third-cycle breeding can begin as soon as one year after grafting. The third-cycle main population is divided into ten sublines with approximately 50 selections per subline (Figure 3). The 24 second-cycle sublines (Figure 2) were condensed to 10 for the third cycle and all related selections are assigned to the same subline. The top 6 selections from each of the 10 sublines make up an elite population (6 per subline x 10 sublines = 60 elite selections). The ten sublines are divided into two superlines (the orange and blue superlines). Each superline has 5 sublines containing a total 250 selections (50 selection/subline x 5 sublines = 250 selections, of which 30 comprise the elite population for that superline).

The PM Series II trials from the second-cycle program along with FS unreplicated selection plots younger than 5 years in 2004 were not considered available for the third-cycle program. Rather, we decided to move ahead rapidly with the third-cycle selection phase in 2003-2004. Then, any excellent backward selections identified by the second-cycle PM tests and any excellent forward selections from the younger FS selection plots will be included in the fourth-cycle selected population (i.e., these will skip a cycle).

Genetic gains for the third-cycle selected population of 500 selections are anticipated to be 23% for individual tree volume with R50=31% (Table 2). These are the mean values of the 419 selections made in 2003 with still another 81 left for making in 2004. These gains are considerably higher than the mean for the second-cycle breeding population due to: 1) Few untested infusions being included; 2) Heritabilities from the PM trials are high, so excellent FS families were identified in which to make third-cycle selections; and 3) Unreplicated FS family selection plots were generally well maintained with 50 to 100 trees of the same family (meaning that within-family resulted in appreciable gain).

Third-Cycle Slash Pine Breeding and Testing

Starting with 500 third-cycle selections, we anticipate that only 360 will comprise the breeding population due to losses during grafting, flowering and breeding (Table 2). Crossing for the main and elite populations is scheduled for three breeding seasons (2004-2006) and consists entirely of full-sib (FS) matings planted in replicated tests with single tree plots in incomplete block designs (IBD). We have opted for this strategy instead of complementary mating designs, because all trees planted are used for both ranking parents and making forward selections (as opposed to CMD in which the PM

tests provide only information, not selections). A further advantage is that rankings will be available for a large number of well-tested FS families which benefits those CFGRP members deploying FS families operationally (such as through control mass pollination).
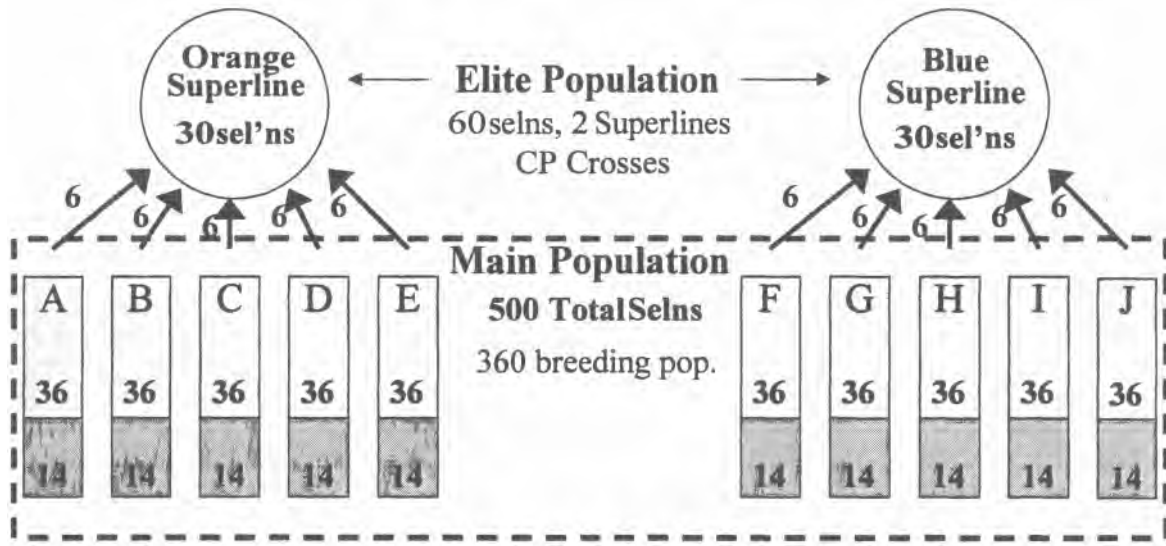

Figure 3. Third-cycle selected and breeding populations of slash pine. The 500 selections are divided into 10 sublines of 50 selections each. The top 6 selections in each subline are also in the elite population of 60 selections which is divided into 2 superlines, orange and blue. Assuming that 14 selections in each subline do not survive top grafting or do not flower, then the breeding population will consist of 360 selections (36 in each of 10 sublines).

For the elite population (Figure 3), a circular mating design will create 75 crosses in each of the 2 superlines (5 crosses for each of the 30 selections) for a total of 150 total elite FS families. Ten third-cycle elite FS progeny tests will be planted with each test having 3,000 measure trees (150 families/test x 20 replications/test) for a total of 30,000 FS seedlings in third-cycle elite tests.

For the main population, the circular mating design will attempt 72 crosses in each of the 10 sublines (averaging 4 crosses for each of the 36 selections) for a total of 720 main population FS families (72 crosses/subline x 10 sublines). All crosses in the main population will be made within a subline. Ten third-cycle main population FS progeny tests will be planted, with each test containing FS progeny from half of the sublines (5 tests containing FS families from the orange sublines and 5 tests for the blue sublines). Assuming that only 600 of the 720 attempted FS families are successful, each test will contain 4,500 measure trees (300 families/test x 15 blocks/test of single tree plots in an IDB) for a total of 45,000 FS progeny planted in main population tests (2 series x 5 tests/series x 4500 trees/test).

Tests of elite and main population FS families are scheduled for planting in 2008 with 6-year measurements in 2013 and fourth-cycle selections beginning in 2014. Counting the tests for both the main and elite populations, there are a total of 20 tests containing 750 FS families with 75,000 measure trees planned for the third cycle. This compares favorably with nearly 160,000 measure trees in second-cycle tests (summing PM and FS tests from Table 2) and over a million measure trees in genetic tests of the first cycle.

Third-Cycle Propagation Population and Deployment

Once all third-cycle selections are made (2004), third-cycle seed orchards will be developed using the very best of these selections. Clones selected for each seed orchard will again depend on the weights that each member wants to assign to volume growth and rust resistance. These would be orchards containing both untested, forward selections and some tested backward selections also.

CONCLUSIONS

It is valuable to reflect on breeding, testing and analytical strategies and how these have changed over the 50 years and 3 cycles of slash pine tree improvement. New developments by many people have resulted in changes in breeding strategies and methods including: 1) Structuring of the breeding population into sublines and superlines; 2) Increasing focus on elite material; 3) Use of overlapping generations (e.g., forward and backward selections); 4) Evolution of mating designs away from disconnected and complementary mating designs to interconnected full-sib designs; and 5) Top-grafting to obviate clone banks and reduce the duration of a breeding cycle by several years.

In genetic testing, recognition of the importance of single tree plots and incomplete block designs coupled with quality installation, maintenance and measurement have all contributed to increased precision of the trials (higher heritabilities and larger gains from selection). These developments allow substantial reduction in the number of test sites and measure trees in genetic tests, because each site is providing more information. In the CFGRP slash pine program, the number of trees in genetic tests has decreased steadily with no anticipated loss in genetic gain per cycle (Table 2).

It is only through the sustained efforts of the people involved and members of the CFGRP that this cooperative has maintained its long term tree improvement program for slash pine. Their commitment to this program for half a century (1953-2003) has produced ever-increasing genetic gains from slash pine seed orchards (Figure 1), an achievement that all members can be proud of!

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