GENETIC GAINS OF SECOND GENERATION SELECTIONS FROM THE NCSU-INDUSTRY COOPERATIVE TREE IMPROVEMENT PROGRAM

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Abstract: Data from 93 open-pollinated progeny tests of second-generation selections were analyzed to obtain genetic parameter estimates and breeding value predictions for height, volume and rust resistance. The 623 selections were grouped into four major geographic regions: 1) Virginia and northern North Carolina with 124 parents, 2) Atlantic Coastal Plains of North Carolina, South Carolina and Georgia with 131 parents, 3) Piedmont regions of North Carolina, South Carolina and Georgia with 285 parents, and 4) Lower Gulf region with 83 parents. The best linear unbiased prediction was used to estimate breeding values for 8-year height, volume and rust infection at a 50% infection level (R-50). The estimated gains for height from 2ndgeneration seed orchards in the four regions ranged from 13% to 21% over unimproved checklots. Roguing these seed orchards intensively to the best 10-15 parents could boost the gains to as much as 20-24% in height growth and an even greater improvement in volume production at harvest. A substantial number of 2nd-generation selections have not only demonstrated outstanding growth but also had less rust infection, R-50 values of 20% to 25% below the unimproved checklots. The best family from each population was generally 10-20% above the 1 st-generation seed orchard mix in height growth, indicating additional gain above the 1st generation selections. Although genetic gain for stem straightness is difficult to quantify, most of the 2nd-generation families had a higher percentage of trees with above average straightness than the checklots.

<u>Keywords:</u> breeding value, genetic gain, open-pollinated family, second-generation, seed orchard, rust infection.

INTRODUCTION

The N.C. State University-Industry Cooperative Tree Improvement Program has completed 41 years of loblolly pine genetic improvement. Members of the Cooperative, currently 16 industry members and five state agencies, annually plant 600 million trees on 900,000 acres accounting for 37% of the total annual tree planting in the U.S. The impact on forest productivity has been substantial through the two cycles of breeding, testing and selection by cooperative members. Trees grown from seeds of first-generation seed orchards have produced 8-12% more volume per acre at harvest than the trees grown from wild seed (Talbert et al. 1985). With additional improvement in value from quality traits (stem straightness, disease resistance, wood density),

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the estimated genetic gain in plantations from first-generation breeding is about 20% (Weir and Todd 1993). Second-generation seed orchards are now producing more than 50% of the total seed harvest in the region. Data from open-pollinated progeny tests of these 2nd-generation seed orchards are now available to provide genetic gain estimates.

MATERIALS AND METHODS

Second-generation selections were made from progenies of incomplete factorial matings of the 1st-generation parents where each of 20 to 30 females was mated to four to six males. These selections were grafted to establish 2nd-generation seed orchards by each cooperative member. Open-pollinated seeds from each seed orchard were collected, and 2nd-generation progeny tests were established by each member organization throughout the Southeast. The number of families in each test series ranged from 19 to 44 including several check seedlots. Families common to multiple seed orchards were included in several test series within each region. Each test series generally included 4 tests established over a two year period in two locations. The experimental design was a randomized complete block with six blocks and 6-tree row plots. All tests (93 in total) were measured for tree height and some were measured for DBH, stem straightness and rust infection. Since open-pollinated loblolly pine families generally show little genotype by environment interaction and high family stability in performance across a wide geographic area (Li and McKeand 1989, McKeand et al. 1990), the tests were grouped into four general geographic regions (Figure 1): 1) Virginia and northern North Carolina with 124 families in 5 test series, 2) Atlantic Coastal of North Carolina, South Carolina and Georgia with 131 families in 5 test series, 3) Piedmont regions of North Carolina, South Carolina and Georgia with 285 families in 12 test series, and 4) Lower Gulf region with 83 families in 3 test series.

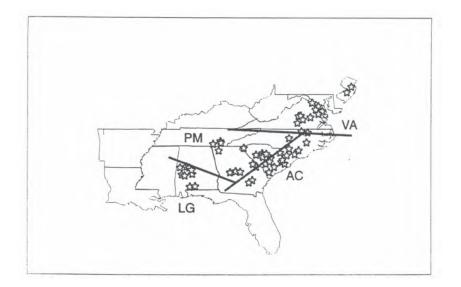


Figure 1. Distribution of 2nd-generation open-pollinated tests in four geographical regions. Note: VA=Virginia and northern NC, AC=Atlantic Coastal, LG=Lower Gulf, PM=Piedmont. All data were adjusted for age and scale effects before estimating the genetic parameters and breeding values in each region. The best linear unbiased predictions (BLUP) was used to estimate parental breeding values because the data are unbalanced with different parents, ages and test qualities (Huber 1993). The BLUP for parental general combining abilities (GCA) were estimated and then breeding values were estimated using the GCA estimates. Breeding value estimates were based on 8-year height and volume measurements. For ranking parents within a given geographic region, percent genetic gain over local checklots was calculated from the predicted breeding values for height. Breeding values for rust infection at a 50% infection level (R-50) were also calculated for ranking parents for rust resistance.

RESULTS AND DISCUSSION

Family-mean heritabilities for individual test series ranged from 0.51 to 0.87 for height and from 0.43 to 0.87 for stem volume. The family-mean heritabilities for rust infection varied with the test infection levels and ranged from 0.01 to 0.86. Breeding value estimates are summarized by regions for percent gain over local checklots for height (Figure 2). Only height gain is presented here because not all tests had DBH and rust measurements.

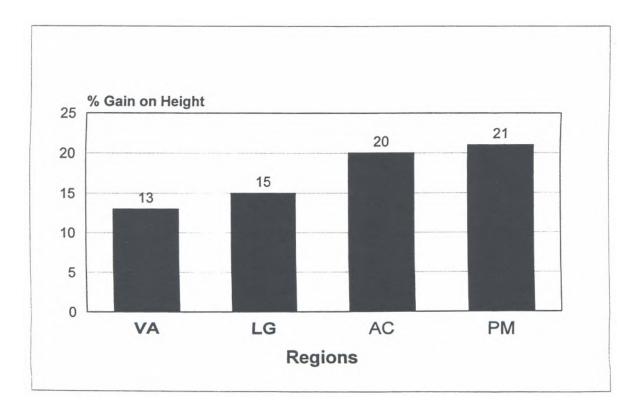


Figure 2. Genetic gain estimates (%) for 8-yr height over local unimproved checklots for the four geographical regions, VA⁼Virginia and northern NC, AC⁼Atlantic Coastal, LG=Lower Gulf, PM=Piedmont.

It is evident from these estimates that 2nd-generation selections have produced substantial gains over unimproved checklots. The genetic gain for 8-yr height from the top 30% of families was 13% above the local checklots for Virginia/NC, 15% for the Lower Gulf, 20% for the Atlantic Coastal Plain, and 21% for the Piedmont region. The gain for the Piedmont families ranged from 11.6% over the NC Piedmont checklots to 20.9% over the Piedmont checklots of SC. Volume gains over unimproved checklots should be greater than those based on height (Talbert et al. 1985). These estimates indicated that, in general, second generation breeding and selection has been effective for improving loblolly pine growth even with the limited selection intensity due to the tester mating design used in the 1st-generation breeding program.

Rust infection (R-50) was generally lower for 2nd-generation families than for the checklots. For example, in the Atlantic Coastal population, about 80% of the families had lower R-50 breeding values than all three checklots. The top ranked 30% of families for rust in the Atlantic Coastal population had an R-50 of 29.6%, significantly lower than the three checklots (above 63%). Similar differences in R-50 were observed for the Piedmont population which averaged 28% for the best 30% families and 56% for checklots. No strong correlations were found between height growth and R-50 breeding values except in the Lower Gulf population. While rust infection was generally high for tests in the Lower Gulf, the R-50 was moderately correlated (r=-0.48) with height growth. Because of this favorable correlation, it is possible to select fast growing families with relatively low R-50 values.

Much greater genetic gains can be expected from utilizing the best families since large differences were observed among 2nd-generation families. The best Atlantic Coastal family had 31.6% gain over the unimproved checklots of NC and 17.1 over the checklots of SC, while the best Piedmont family had 29.3% gain over the unimproved checklots of SC. The best family from each population was generally 10-20% above the checklot of lst-generation seed orchard mix, indicating additional gains above 1st generation selections. These gain estimates were based on open-pollinated progeny. Additional genetic gains could be achieved by selecting a few outstanding parents and making controlled mass pollination, assuming that specific combining ability is negligible for a full-sib cross. Although genetic gain for stem straightness is difficult to quantify because of different ages and scoring systems in different tests, it is evident that most of the 2nd-generation families had a higher percentage of trees with above average straightness than the checklots.

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