

NORTHWEST TREE IMPROVEMENT COOPERATIVE

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APRIL 1, 2004 TO MARCH 31, 2005

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NORTHWEST TREE IMPROVEMENT COOPERATIVE

A n n u a l R e p o r t

*Report April 1 2004 to
March 31 2005*

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Photo 1. Fast-growing conifers and superb scenery: two of the attributes of forest tree improvement in the PNW on view at Green Diamond's advanced-generation western hemlock test site near Rockaway. The age-5 measurement of the western hemlock test sites in Oregon and Washington took place this same fall. Photo courtesy of Steve McKeand.

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COOPERATIVE SECOND-GENERATION BREEDING AND TESTING OF COASTAL DOUGLAS-FIR

The overall progress and status of the various advanced-generation programs is summarized in Table 1.

Table 1. Summary of advanced-Generation Douglas-fir trials established in 2005

Program	Entries	Number of			Purpose
		Locations Trees	Test Fillers + Buffers	Test Trees +	
TRASK Inland Phase I	150 families + 2 woodsrun controls)	5	15,309	20,532	Rank families and parents Verify breed- ing zone(s)
NOCTIC Phase II	181 families + 3 woodsrun controls	5	18,366	23,567	Make forward selections

Puget Sound and Washington Coast

The Puget Sound metacooperative Phase I tests were visited regularly and maintained (abating browse damage including damage by grouse, brush and weed control) in 2004-5. Crossing continued for the Washington Coast program.

Washington Cascades (WACTIC)

Crossing continued for WACTIC, with notable success accessing and crossing in the USFS Planting Creek orchard. Relatively light snow in winter 2004-5 made it possible to access this high-elevation orchard in time for isolation and pollination.

WACTIC sowed the first four of eight Phase I sites at IFA Nisqually, as 515A container seedlings in early 2005. This crop included a total of 163 crosses: "local" crosses from the Cowlitz, Snoqualmie and Skagit cooperatives, DNR programs, and "non-local" crosses from WA Coast, Puget Sound, Vernonia/Ryderwood and NOCTIC. Crown Pacific ceased to exist in 2004, but the new landowner (Cascade Timberlands) continued membership in WACTIC. By March 2005, three test sites had been selected in the northern end of the testing zone (from 800 to 2,800 feet in elevation).

Vernonia/Ryderwood

The Vernonia / Ryderwood metacooperative Phase I and Phase II tests were visited and maintained in 2004-5. Replacement of mortality with western hemlock seedlings, and planting cedar in areas considered vulnerable to root rot, were only moderately successful; replanting with Douglas-fir plug seedlings was much more successful. All five Phase II sites had been tagged by spring 2005. Work continued on correcting errors in the Phase I plantation maps and database, in preparation for the first measurement expected in 2005 or 2006.

TRASK

Seedlings for TRASK Inland Phase I were grown at Sylvan Vale, and outplanted on five sites in February 2005. This planting included 150 crosses and

two woodsrn controls. Unusually dry weather in February and early March led to anxious discussion that many of the newly-planted trees might die. The dry spell was followed by heavy rain starting in late March, however, and when the tests were visited in late March it appeared that most of the seedlings would survive. A high-quality nursery tag printed with large font was adopted, and was universally well received by all concerned including the nursery and the planting and mapping contractor.

Trask Coast Phase I tests were visited in 2004 and early 2005. For the most part weed control and maintenance have been excellent. About 1,300 dead trees were replaced, with 1+1 western hemlock seedlings or surplus seedlings from Trask Inland Phase I. Three of the six test sites have been tagged; the remainder are to be tagged in summer 2005 along with the five Inland Phase I sites.

Four good sites had been located for the Inland Phase II tests, and three for Coast Phase II. Both these series of tests are to be established in winter 2006-7. Having test sites selected well in advance in this way is very helpful for good test establishment.

NOCTIC

Seedlings for NOCTIC Phase II were grown at Sylvan Vale, and outplanted on five sites in February 2005. They differed from Trask in being 615A cavities instead of 515A. This planting included 181 crosses and three woodsrn controls. As in the Trask Inland Phase I tests, unusually dry weather in February and early March led to concern about possible mortality in the newly planted tests; however the rains returned in late March. When the tests were visited in late March, it appeared that some mortality had taken place but that most of the seedlings would survive.

Several Phase I tests were visited in October 2003. After four growing seasons, some test trees exceeded ten feet in height. Work continued on correcting errors in the Phase I plantation maps and database, in preparation for the first measurement expected in 2006.

South Central Coast

For the most part, the South Central Coast (SCC) tests grew well during their third growing season. All the sites were visited in October 2004. On productive sites where weeds could be controlled with herbicides, some trees exceeded 12 feet in total height (see photo).

SCC revisited the decision to extend the testing zone, resulting in only a slight extension south and east. Gold Beach was not incorporated and South Coast Lumber therefore chose not to join the program. The final crossing season (winter 2003-4) proved to be successful, and a group of 73 highly-selected crosses (including elite crosses from Trask Coast) were sown in December. These were to be grown in 615A cavities similar to the Phase I seedlings, at Sylvan Vale nursery.

Umpqua-Roseburg

There were serious discussions on starting a second-generation program for the eastern part of the landbase served by the Umpqua cooperative, and the northern part of the land served by the Roseburg cooperative. Crossing work done by two BLM district geneticists (Al England and Rich Kelly) may make it possible to start test establishment as early as 2007; their foresight, interest and effort are much appreciated. Roseburg Resources, Seneca Jones and Lone Rock Timber are likely players in this program. Such a program would serve an important area of productive Douglas-fir timberland.

Table 2. Status of / plans for cooperative second-generation Douglas-fir breeding populations as of April 2005.

	Status	Number of Local & Semi-Elite Crosses		Test Establishment			
		Target	Sufficient Seed ¹ or Tested ²	Target no.	No. Established	Start planting in spring of	Complete planting in spring of
Washington Cascades	Seed sown for first sowing of Phase I (4 sites)	260	235 ¹	16	0	2006	≈2010
Puget Sound	Planted 5 sites in 2003 (Phase I, 143 crosses)	94	90 ¹	10	5	2003	≈2007
Washington Coast	Crossing	176	137 ¹	6	0	≈2008	≈2008
Vernonia/ Ryderwood	Test establishment completed	404	325 ²	10	10	2001	2004
North Oregon Cascades	Test establishment completed	414	350 ²	11	11	2001	2004
Trask (Coast + Inland)	Planted 6 sites (Coast Phase I, 215 crosses) in 2004 and 5 sites (Inland Phase I, 150 crosses) in 2005.	550	495 ^{1,2}	21	11	2004	2007
South Central Coast	Planted 6 sites in 2002 (283 Crosses) + 3 Swiss Needle Cast sites + 1 family block planting; 6 sites in 2006	7601	604 ^{2,3}	203	14	19983	2006
Umpqua	Likely to sow 6 sites in winter 2005-6	200	250	12	0	2007	2011
TOTAL		2,658	≈2,486	106	51		

³ Including Plum Creek's advanced-generation Coos Bay program which was amalgamated to South Central Coast in 2003

COOPERATIVE SECOND-GENERATION BREEDING AND TESTING OF WESTERN HEMLOCK

The local diallel and elite "diallel" sites planted in Washington and Oregon in 2001 were measured in fall-winter 2004-5. The data (from the Oregon and Washington sites only) were analyzed shortly thereafter, showing appreciable realized gain from the selection of 150 parents based

on first-generation testing, and substantial differences in gain between seed sources. A more complete analysis (multivariate BLUP including all test sites, possibly adjusting for spatial correlation and variation) is planned for later in the year.

GENETIC GAIN VERIFICATION / DEMONSTRATION TRIALS

The first three sites of the Grays Harbor Genetic Gain/ Stand Management Type IV trial were successfully established in March 2005. Sites were provided by Rayonier, Quinalt Nation and Weyerhaeuser. To work around some scheduling issues, the seedlings were lifted in January and kept in freezer storage to the begin-

ning of March (unlike the advanced-generation trial seedlings which have usually been stored in coolers). This proved very fortunate, because the trees were planted just in time to catch the return of rainy weather after the dry winter experienced in the region. Site layout, pinning and fencing were handled by the SMC, while NWTIC was

responsible for producing the seed, and growing, transporting and planting the seedlings. All possible care was taken in the aspects of growing, storing and planting the seedlings, mindful of the

failure of the Noti Genetic Gain trial planted four years previously.

The paper on age-5 results of the Molalla gain trial was published in summer 2005.

GENETIC GAIN DEMONSTRATION PLANTINGS

Three gain demonstrations were established using overrun from Trask Inland Phase I: two on Hampton land (see photo) and one on Stimson land. Two were planted using overrun from

NOCTIC phase II (CTC, ODF). This brought the total of NWTIC-led demonstration plantings to 11. Of these, the oldest (Boise's, established in 2001) was visited in February 2004.

DATA MANAGEMENT, ANALYSIS AND REPORTS

Work has continued on updating the database. Of the 32,567 parent-tree records expected, the database contained complete data for 30,783 records (94% of the total) by March 2004. There were also data on 1,453 cross-tested parents involving 84 programs; a minority of first-generation parents were tested in two (or perhaps three) programs; cross-testing was typically in adjacent breeding zones. NWTIC plans to analyze and interpret this information to further our knowledge of the effect of wider seed source movement for Douglas-fir.

As of March 31, 2004, data were complete for:

- 99 first-generation programs (of 127)
- 801 first-generation test sites (of 982)
- 886 first-generation sowing schedules (of 1156)

Starting in mid-2003, the main focus in data management was in loading progeny measurement files into SQL server and making them available through views that could be called up in Microsoft Access or on the web. By March 31, 2005 2,275,038 records had been loaded, and 775 views had been created.

Information on full-sib and polymix crosses were updated as information was received. These were mainly crosses made by the advanced-generation Douglas-fir and western hemlock metacooperatives, but also included crosses sown in the first generation tests. By March 31 the database contained records on over 3,900 full-sib and polymix crosses.

NWTIC maintained a strong emphasis on data analysis, completing genetic gain predictions and reports for 27 first-generation breeding units and 3 advanced-generation programs.

Table 3. Summary of genetic gain predictions using BLUP, and reports, completed April 2004 through March 2005.

First Generation Analyses

Molalla
North Umpqua BU-3
Marial BU-2
North Umpqua BU-4
Riddle BU-1
BLM BU-32
Sunday Creek
BLM BU-11
BLM BU-31
Tye 2
Powers Low
Cave Junction BU 2
Dallas High
Nehalem
Grays Harbor
BLM McKenzie
Snoqualmie BU-1
Burnt Woods I
Burnt Woods II
Snoqualmie BU-2
Alsea Waldport Low Series 1
Alsea Waldport Low Series 2
Hebo Low 1
Hebo Low 2
Ryderwood
Snow Peak High
Snow Peak Low

Second Generation Analyses

Green Diamond Shelton
HEMTIC Age-5 (OR and WA sites)
Plum Creek Coos Bay (CL98)

GETTING GENETIC GAIN IN OPERATIONAL PLANTATIONS

Infusion of high-gain parents continued in several cooperative orchard blocks (Interim Burnt Woods, Interim Dallas, Nehalem) at the JE Schroeder complex. Based on a new BLUP analysis combining both Burnt Woods programs, cooperators chose to infuse several original first-generation parents and were successful in locating these parents and collecting scion from them.

This pilot Controlled Mass Pollination (CMP) project in the Interim Burnt Woods orchard proved very successful, producing 7.3 lbs (over 260,000 seed) derived from high-gain parents at a very reasonable cost. This was aided by having a very good seed year. Encouraged by the success of this project, there were sizable pollen collections over these 12 months in the Molalla orchard block and in the Breeding Unit 12, 13, 30 and 33 blocks at

BLM's Horning orchard, as well as an opportunistic CMP effort in the Vernonia orchard using leftover pollen from the Vernonia/Ryderwood program. The Interim Vernonia and Molalla orchard blocks were rogued. NWTIC analyses were used to rogue and stimulate other orchards as well.

Sara Lipow led an effort to establish high-gain cooperative orchard blocks for timberland west of Eugene and in the Roseburg vicinity. There is high demand for orchard seed in this area, both from industry and non-industrial timber owners. Rootstock were sown with the possibility of grafting getting underway in 2006.

There were also discussions on a cooperative orchard for the Washington Cascades area. Potential sites included two established orchard sites on Whidbey Island and one near Bellingham.

TRAINING

A workshop on cold-hardiness testing in advanced-generation cooperative genetic improvement programs was jointly organized by the NWTIC, the PNWTIRC and the PNW Research Station Genetics group. The meeting was attended by representatives of 11 NWTIC members. Presentations included an overview of cold-har-

diness in conifers, testing methods, the genetics of cold hardiness in conifers, and implementing cold hardiness testing in an applied program. It appeared likely that a simple assessment of cold-hardiness (spring budflush scored on one or two sites) would be implemented in a couple of the Douglas-fir metacooperatives.

OTHER PROJECTS

The high-elevation Oakridge site (USFS) of the 1959 Douglas-fir provenance trial was measured in early 2005. Added to the three sites measured recently in British Columbia, four of the original 17 sites have been measured at an age close to rotation (nearly 50 years from seed). NWTIC and BCMoF agreed to exchange their data to get a more complete picture of the effects of seed source movement.

Terrance Ye ran detailed simulations evaluating the benefits of using first-generation progeny data when analyzing second-generation tests. Results were presented at the IUFRO Conference

in Charleston in November 2004¹. When backward selection was used in the first-generation, including first-generation information helped increase both accuracy and precision of second-generation selection in all scenarios. However, the percent increase in effectiveness of selection was high when $h^2(1)$ is high and $h^2(2)$ is low, and

¹TZ Ye, KJS Jayawickrama, and GR Johnson. 2004. Efficiency of Using First-generation Information during Second-generation Selection: Results of Computer Simulation. In: Li, B and S McKeand eds. "Forest Genetics and Tree Breeding in the Age of Genomics: Progress and Future". IUFRO Joint Conference of Division 2. November 1-5, 2004, Charleston, South Carolina. http://www.ncsu.edu/feop/iufro_genetics2004/proceedings.pdf.

decreased as $h^2(1)$ decreased and $h^2(2)$ increased. This is expected since first-generation data contains more genetic information than random noise when $h^2(1)$ is high.

When forward selection was used in the first-generation, the first-generation information did little to increase the accuracy of ranking in the second-generation. The main reason was that selecting the best trees within families is relatively

imprecise and the rank correlation between true and estimated parental breeding values was quite low ($r = 0.2$ when $h^2(1) = h^2(2) = 0.25$ and $V_D = V_{GxE} = 0.5V_A$). When $h^2(1)$ was very low, the first-generation data simply added random noise for the second-generation selections. The precision of ranking would be increased up to 10~15% probably due to the increase the effective number of observations.

MEMBERSHIP CHANGES

BC Ministry of Forests withdrew from HEMTIC and NWTIC at the end of 2004. Oregon State University College Forests joined NWTIC and

Trask in 2005 with 12,000 acres. Recruiting new members remains a very high priority in 2005 and beyond.

COOPERATORS

Randall Greggs (Simpson Resource Co./Green Diamond Resource Co.) completed his tenure as NWTIC Chair at the 2004 annual meeting; his help during the transition of NWTIC from an independent entity to an OSU-based cooperative is appreciated. Jeff Madsen (Port Blakely) was elected NWTIC chair at that meeting.

NWTIC representatives for 2004 were:

- Jerry Anderson (Boise Cascade Corp)
- Charlie Cartwright (BC Ministry of Forests, Research Branch)
- Liang Hsin (Bureau of Land Management)
- Howard Dew (Cascade Timber Consulting)
- Jim Unsell (Crown Pacific-Hamilton Division)
- John Goodrum (Crown Pacific-Olympic Division)
- Beth Fitch (Hampton Tree Farms)
- Dean Stuck (Hancock Forest Management)
- Bryan Nelson (Lone Rock Timber)
- Erik Lease & Chris Lipton (Longview Fibre Co.)

- Jim Carr (Menasha Corp.)
- Joe Steere (Miami Corp.)
- Sara Lipow (Oregon Department of Forestry)
- Jim Smith (Plum Creek Timberlands.)
- Dan Cress (Pope Resources)
- Tim Truax & Jeff Madsen (Port Blakely Tree Farms)
- Jessica Josephs (Rayonier Timberlands)
- Dave Walters (Roseburg Resources)
- Randall Greggs (Simpson Resource Co. / Green Diamond Resource Co. – WA and OR operations.)
- Mark Diegan (Simpson Resource Co. / Green Diamond Resource Co.– CA Operations)
- Marc Halley (South Coast Lumber)
- Dick Powell (Starker Forests)
- Margaret Banks (Stimson Lumber Co.)
- Jim Hargrove (Quinault Indian Nation)
- Dave Rumker (The Campbell Group)
- Tim Crowder (Timber West Forest)
- Greg Johnson & Christine Dean (Weyerhaeuser Co.).

STAFF

There were no staff changes in 2004. NWTIC personnel were as follows:

- | | |
|------------------------------------|--------------------|
| Director: | Keith Jayawickrama |
| Quantitative Geneticist: | Terrance Ye |
| Information Management Specialist: | Denise Steigerwald |
| Test Coordinator: | Ron Rhatigan |



Puget Sound Phase I – Green Diamond Site near Matlock



Vernonia/Ryderwood Phase I – Weyerhaeuser's Mosquito Creek site



Puget Sound Phase I – Port Blakely site near Winlock



Vernonia/Ryderwood Phase II – perfect weed control on Stimson's Sock site



NOCTIC Phase I - Weyerhaeuser's Williams Lake 63 site



NOCTIC Phase I – Weyerhaeuser's Roaring River site



NOCTIC Phase II seedlings – full-sib cross vs. woodsrun control



TRASK Coast Phase I – Green Diamond's Neskowin site



TRASK Coast Phase I – Starker's Branch Flats site

TRASK Inland Phase I – Boise/Forest Capital's Fir Grove Orchard site



TRASK Inland Phase I seedlings at Burton Creek



Genetic gain demonstration established by Hampton Tree Farms

12 feet tall in three years – at South Central Coast's Lyon Ridge site (Menasha)



Plum Creek's Coos Bay second generation test at McMullen

VALIDATING PREDICTED GENETIC GAIN IN COOPERATIVE FIRST-GENERATION TESTING PROGRAMS

Keith Jayawickrama and Terrance Ye

Method Comparison

The NWTIC genetic gain prediction protocol, using BLUP, has been implemented and refined since September 2003. When a new protocol such as this (especially a complex one) is implemented, it is interesting and necessary to compare it with other measures of genetic worth. There is also a lot of interest by cooperators in whether the high predicted gains seen in some programs are realistic.

One way to validate the procedure is to divide the data into subsets, predict gains in one subset and validate in another subset. We therefore did the following:

1. Selected two Douglas-fir programs with strong heritabilities and high gains. Since the data are proprietary to the respective cooperatives, they are referred to as Program A (which had nine sites) and Program B (which had 10 sites). The absolute gains are not provided, but “realized” gains are provided compared to predicted gains.
2. Predicted parental (backward) gains using data from a random group of sites (four in the case of Program A, five in the case of Program B) using the normal BLUP procedure. Gain1 was predicted for all parents, for height, dbh and volume (dbh² x height).
3. Chose the top 5% of parents for Ht Gain1, and averaged their predicted gains.
4. Calculated the following (“Realized” gain) for those parent using data from the remaining sites:
$$2 \times 100 \times \frac{(\text{Mean of select families}) - \text{Overall mean of all the families}}{\text{Overall mean}}$$
5. Chose the top 10% parents for Ht Gain1.
6. Repeated step 3 and 4.
7. Chose the top 25% parents for Ht Gain1.
8. Repeated step 3 and 4.
9. Repeated steps 2 to 8 for dbh and volume.
10. Repeat steps 2 to 9 above, except use a second group of sites (five in the case of Program A, six in the case of Program B) to predict gains, and cross-validate on sites not used in the prediction.
11. Repeat steps 2 to 9 above, except use a third group of sites (six in the case of Program A, seven in the case of Program B) to predict gains, and cross-validate on sites not used in the prediction.
12. Get an average for the predicted and “realized” gains from the three separate estimates for each.
13. Calculate (realized/predicted) for Gain1 for all three estimates.

Note: The mean described in step 4 is a simple mean of all the trees for the families of the appropriate group of parents. The overall mean is the simple mean for all trees on those sites. The data are not adjusted in any way, and are purely the measured heights, dbhs and dbh²xheights.

Results

The results are shown in Tables 4 and 5.

Program A

“Realized” gains on the five comparison sites were considerably less than the predicted gain if only four sites were used in the prediction. When five sites were used in the prediction, “realized”

Table 4. Validation of predicted genetic gains, Douglas-fir program A.

Trait	Proportion of parents selected	Prediction based on:			Average Proportion (Realized/ Predicted)
		4 sites	5 sites	6 sites	
		Validation based on:			
	5 sites	4 sites	3 sites		
["Realized" Gain/ Predicted Gain] for Gain					
HEIGHT	Top 5%	0.67	0.89	1.15	0.90
	Top 10%	0.63	0.91	1.01	0.85
	Top 25%	0.68	0.99	1.09	0.92
DBH	Top 5%	0.91	0.70	1.17	0.93
	Top 10%	0.51	0.96	0.96	0.81
	Top 25%	0.68	0.80	1.02	0.83
VOLUME	Top 5%	0.42	0.80	1.27	0.83
	Top 10%	0.43	0.88	1.01	0.77
	Top 25%	0.40	0.85	0.99	0.75
Average Proportion (Realized/ Predicted)		0.57	0.85	1.11	

gains approached the predicted gains; when six sites were used, "realized" gains on the remaining three sites were, on average, as high as the predicted gains.

Program B

"Realized" gains on the comparison sites very closely matched the predicted gains for height and for dbh. The match was weaker for volume, especially for the top 5% of parents; in this case the predicted gains appeared to be too high.

Discussion

For the most part, gains predicted based on 2/3 of the total number of sites matched "realized" gains on the remaining 1/3 (independent) sites very well. This is very encouraging since they

Table 5. Validation of predicted genetic gains, Douglas-fir program B.

Trait	Proportion of parents selected	Prediction based on:			Average Proportion (Realized/ Predicted)
		4 sites	5 sites	6 sites	
		Validation based on:			
	5 sites	4 sites	3 sites		
["Realized" Gain/ Predicted Gain] for Gain					
HEIGHT	Top 5%	1.02	0.96	1.02	1.00
	Top 10%	0.96	0.91	0.97	0.95
	Top 25%	0.94	0.99	0.95	0.96
DBH	Top 5%	1.02	0.93	0.92	0.96
	Top 10%	1.01	0.93	0.97	0.97
	Top 25%	1.14	1.06	1.10	1.10
VOLUME	Top 5%	0.87	0.79	0.81	0.83
	Top 10%	1.00	0.85	0.94	0.93
	Top 25%	1.05	1.06	1.04	1.05
Average Proportion (Realized/ Predicted)		1.00	0.94	0.97	

are different trees on different sites, calculated using a very simple method involving few assumptions. Also note that since only 60-72 trees maximum were available for a family on 2/3 of the sites, the prediction of a family's gain is weaker than the prediction from the complete dataset (96-100 trees maximum per family). First-generation Douglas-fir programs typically had 100 or more trees planted per family.

Please note that these comparison gains are not true realized gains – though the sites were different, the seedlings were all grown together in the same nursery the same year, and outplanted in the same year. True validation requires independent nursery crops planted in different years on sites different from those used in the prediction, and in which trees compete with other trees of similar gain levels.

GENETIC GAIN PREDICTIONS FOR COASTAL DOUGLAS-FIR IN THE US PACIFIC NORTHWEST AND THEIR RELATIONSHIPS WITH PARENT TREE LOCATION

K.J.S. Jayawickrama and T.Z. Ye

Introduction

The IFA-PNW “Progressive Tree Improvement System” emphasized forming local cooperatives to share costs, and on progeny testing lots of trees using wind-pollinated seed in small testing zones. This phase ran from 1967 till 1993, during which over 26,000 first-generation Douglas-fir parents were tested in 109 breeding units, with over 3 million progeny test trees planted. A typical breeding unit was designed for 100,000 acres of commercial timberland, extended 70km north-south and 50km east-west, but due to the varied topography in the Pacific Northwest could contain parent trees spanning as much as 600m (2,000 feet) in elevation. In some cases families originating from outside the breeding zone were included in the tests.

Since late 2003, the NWTIC began to predict genetic gains for first-generation breeding programs using Best Linear Unbiased Prediction. These first-generation programs are the basis for seed production in most orchards and for advanced-generation breeding, and estimates of gain are useful for many purposes (roguing and establishing orchards, collecting and deploying seed, valuing the contribution of tree improvement to boosting productivity of plantations and selecting parents for advanced-generation breeding). Few estimates of genetic gain have been published for coastal Douglas-fir in Oregon and Washington.

Elevation, latitude and departure information are available for most first-generation parent trees. With a dominant species covering such a wide geographic range with possibilities of pollen flow and migration, continuous genetic variation seems likely. An early analysis of two of these programs suggested that growth rate increased

with decreasing elevation, and shifts to the east or north (Silen and Mandel 1983). While the first-generation programs are individually inadequate to give an adequate estimate of clinal variation, they provide many independent estimates of variation over a small north-south and east-west range, and represent the largest sample of wild Douglas-fir parent trees that will ever be tested in the Pacific Northwest.

This paper therefore summarizes results to date in predicted gains and relationships between predicted gains and latitude, departure and elevation.

Methods and Materials

A typical first-generation program tested 200-300 wind-pollinated families (seed collected from parent trees in the wild) on eight to 10 sites, with 12 to 16 trees per family per site. To keep replicates small, families were usually grouped into sets of 25-30 families and tested using the “Reps-In-Sets” design. In this design, each set was essentially an independent experiment, with three to five replicates grouped together. Three to four trees were typically planted per family in non-contiguous plots. Sets were generally all represented on common sites. Some tests were established using the “Sets-In-Reps” design, with sets randomized in replicates; this design is better suited to compare families across sets than the “Reps-In-Sets” design. In some cases trees originating from different parts of the breeding unit were randomly allocated to sets, in others trees from different parts of the breeding unit were consciously grouped into different sets (“geographic sets”).

Gains are predicted for age-10 and age-15 height, age-15 dbh and age-15 volume (as dbh² x height). Gain1, Gain2, and Gain3 are predicted using three linear models respectively: model1 considers set to be a fixed effect, model2 considers set to be a random effect, and model3 drops set from the model. Model1 and model2 assume that all differences between sets are due to environmental variation within test sites, while model3 does not. Since unimproved controls were generally absent, the population mean is assumed to equal zero gain. This assumption should be reasonably valid, since the Progressive Tree Improvement system stressed collecting seed from well-separated parent trees during good seed years, rather than intensive plus-tree selection.

Genotype x environment interaction is investigated using a test of crossover interaction. Tests are conducted for each pair of families evaluated across each pair of sites based on least-squares means and standard errors derived from ANOVA for each set at each site. Finally, family stability is expressed as the significant *COI* as a percentage of the total number of interactions for each family.

For programs analyzed to date and for which both height and volume gains could be predicted (38 programs testing 10,346 parents, about 40% of the total number of Douglas-fir parents), average gains for the top 1% and top 5% of parents were calculated. These proportions are relevant since 1.5-generation orchards are being established combining approximately the best 2-5% of parents from several adjacent programs. Volume Gain1 and Gain3 were regressed on latitude, departure and elevation. The average regression coefficients and correlations were calculated.

Results and Discussion

Age-15 volume gain predictions for the top 1% of first-generation parents in a program typically exceeded 50%, and were typically three times as large as the age-15 height gain predictions.

Table 6. Predicted age-15 volume gains for top parents in first-generation cooperative Douglas-fir tests

Selection Intensity	Volume Gain1 %	Volume Gain3 %	Height % Gain1	Height % Gain3
Top 1% of parents	53.7	57.1	16.5	17.6
Top 5% of parents	40.4	42.5	12.9	13.7

If top parents with the highest predicted gains in several adjacent programs are all available, it seems feasible to build a 1.5-generation orchard with 40% predicted age-15 volume gain.

On average, parents tested in a program originated over 51.3 miles (82 km) north to south, 30 miles (48 km) east to west, and had an elevation range of 1,946 feet (590 meters). Within testing zones, predicted gains tended to decrease with increasing elevation (22 of 28 regression estimates with Volume Gain1, and 25 out of 29 regression estimates with Volume Gain3 were negative), but the correlation between predicted volume gain and elevation was weak (-0.08 and -0.10 respectively). Correlations between predicted volume gain and latitude, and predicted volume gain and departure, were essentially zero. In some cases Gain3 was more strongly related to parent tree location than Gain1, which might be explained by the fact that with "geographic" sets, adjusting out set effects partially removes geographic trends. The strength of the relationships with geographic variables varied from program to program.

Results obtained so far (from about 40% of the parents) provided little evidence to reconsider the amalgamation of first-generation zones in the second-generation testing program, at least for growth rate. Typically less than 10% of the crossover interactions in a family are significant. Any small incremental gain from progressing breeding in multiple smaller zones instead of the second-generation zones would be more than offset by increased cost. For example, we can consider the largest second-generation zone, which is 340km (210 miles) north to south and has a 600m

Table 7. Relationships with predicted age-15 volume gains in first-generation cooperative Douglas-fir tests.

Variable	Average Correlation Coefficient		Average Regression Coefficient	
	Volume Gain1 %	Volume Gain3 %	Volume Gain1 %	Volume Gain3 %
Latitude (km)	-0.02	-0.01	-0.0479 (1% reduction per 13.0 miles northward)	-0.0423 (1% reduction per 14.8 miles northward)
Departure (km)	-0.03	-0.03	-0.0006 (1% reduction per 1042 miles eastward)	-0.0114 (1% reduction per 55 miles eastward)
Elevation (m)	-0.08	-0.10	-0.0142 (1% reduction every 234 feet increase)	-0.0171 (1% reduction every 195 feet increase)

(2,000 ft) elevation range. Based on the overall trend, the difference in predicted volume gain north to south (for parents within the first-generation zones contributing to that zone) would be around 16%, and across the elevation range around 9%. The weak correlations between predicted gain and parent tree location also suggest it is possible to find high-gain parents throughout most first-generation breeding zones.

We plan to revisit these summaries when the remaining analyses are completed. The predicted gains are to be calibrated by estimates of realized gain from realized gain trials: NWTIC established one such trial in 1997 (St Clair et al. 2004) and

a second one is to be planted in 2005 and 2006. NWTIC also plans to use the vast pool of progeny data for validation of gain predictions.

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EFFICIENCY OF SPATIAL ANALYSIS OF FIRST-GENERATION COASTAL DOUGLAS-FIR PROGENY TRIALS IN THE US PACIFIC NORTHWEST

Terrance Ye and Keith Jayawickrama

Nearly 1,000 first-generation progeny trials were established in the Pacific Northwest between 1967 and 1993, programs now associated with the NWTIC. These trials typically had 200-300 parents tested as open-pollinated families collected from the parent tree growing in the wild, and planted on 6-12 locations. Most trials were in “Reps-In-Sets” designs where all replicates of a single set of families planted together; with the rest established as “Sets-In-Reps” where each replicate included all the sets of families. Although efforts were taken to minimize micro-environmental variation, spatial homogeneity seldom occurs within replicates in forestry experiments. With increasing computational power and new spatial analysis techniques available, it may be possible to get greater efficiency and genetic gain in forest tree improvement programs at minimal added cost.

This paper reports an evaluation of efficiency of spatial analysis using autoregressive models relative to our current “Reps-In-Sets” or “Sets-In-Reps” analyses (base models), for 139 first-generation coastal Douglas-fir progeny trials from 18 different breeding zones in western Oregon and western Washington. Measurements of tree height (*HT*) were made at ages 5, 10, and 15 years from seed for most of the trials. Breast-height diameter (*DBH*) at ages of 10, 15, and 20 years were available for 15~82 sites, and stem volume (*VOL*) was calculated approximately as $HT \times DBH^2$ when both *HT* and *DBH* were available.

We found that 500 out of 506 trial \times trait combinations had significant spatial variation based on likelihood ratio test. Positive spatial

correlations among neighbors were found in all cases ($\bar{\rho} \approx 0.8$). Spatial analyses using AR1 \times AR1 models on average reduced the residual variance by 13~23% for *DBH* and 27~33% for *HT*. The resulting change in heritability after fitting spatial models varied among sites and traits with average increases from 0.20 to 0.24 for *DBH*, from 0.22 to 0.30 for *HT*, and from 0.32 to 0.37 for *VOL*. Spatial analysis also increased the accuracy of breeding value estimation (i.e. correlation between true and predicted genetic values) by 9~11% in most cases. Increases in relative genetic gain of changing from base models to spatial models were mostly less than 3% for backward selection (selecting the top 20% parents) and less than 5% for forward selection (selecting the best offspring from each of the 20% families). Sites with “Sets-In-Reps” design showed relatively higher spatial autocorrelation than sites with “Reps-In-Sets” design (0.88 vs. 0.79). Spatial autocorrelation was slightly higher in *DBH* (0.88) than in *HT* (0.80), and higher at age-10 than at age-5 or age-15. The pattern was rather random and patchy geographically and did not show significant longitudinal, latitudinal, or altitudinal trends (i.e. between breeding zones within the region).

Results indicated that adjustment for micro-environmental heterogeneity in progeny tests in the Pacific Northwest is desirable to improve estimates of genetic parameters and to maximize genetic gains from selection. It is therefore likely that spatial adjustment will be used in analyzing the second-generation data which is already coming available.

RELATIONSHIPS BETWEEN HEIGHT, DIAMETER AND VOLUME AT THE FAMILY LEVEL

Keith Jayawickrama

Introduction

Many selection decisions (for orchard establishment, second-generation breeding) in the Progressive/NWTIC program have been on age-10 or age-15 height. Recent analyses have shown rank changes, some dramatic, when using $dbh^2 \times$ height instead of height as a selection trait in Douglas-fir programs. This brief review looks at some unpublished NWTIC data and publications relevant to this topic.

Data Sources

A. For programs analyzed to date and for which both height and volume gains could be predicted (38 programs testing 10,346 parents, about 40% of the total number of Douglas-fir parents), linear family-mean correlations between raw family means and between Gain1 values were summarized.

Discussion and Conclusions

There is good evidence that while diameter and height are strongly related at the family level, the correlation is not perfect. The NWTIC data indicate the correlation is around 0.8; the ht: dbh correlation estimates do vary from program to program. Published height: dbh genetic correlation estimates (some based on much smaller numbers of parents and test sites) for several major conifers varied from 0.49 to 0.90. Thus recent NWTIC ht: dbh and ht: volume correlation estimates are no weaker than published estimates.

The correlation between dbh and volume is stronger than the correlation between height and volume in every one of the publications listed above, and in the results of the NWTIC analyses. This is true in the NWTIC data both for the raw family means, and the BLUP gain predictions. Obviously this is due to the fact that dbh is squared

Table 8. Summary of linear family-mean correlations from NWTIC BLUP analysis of first-generation Douglas-fir programs.

Number of programs	Number of parents tested	Between raw family means			Between predicted gains		
		Ht: dbh	dbh : vol	ht: Vol	Ht Gain1: DBH Gain 1	DBH Gain 1: Vol Gain 1	Ht Gain1: Vol Gain 1
32	8,918	0.84	0.96	0.88	0.79	0.95	0.86

B. Intertrait correlations (genetic or family-mean) were obtained from 15 publications describing genetic parameters of forest tree species.

C. Across-site family-mean heritabilities were calculated for height, dbh, volume ($dbh^2 \times$ height) and taper (ht/dbh) for five first-generation Douglas-fir programs, and expressed as a percentage of heritability for height.

in the volume equation, but that in turn is the inevitable result of geometry.

Based on five independent programs, the family mean heritability estimate for taper was about 59% to 94% as strong as the family mean heritability estimate for ht15. There is therefore evidence for heritable differences between families for taper.

Table 9. Examples of intertrait correlations published for forest tree species.

Species	Height: Dbh	Height: Volume	Dbh: Volume	Type of correlation	Age	Reference
Douglas-fir	-	0.854	0.992	Genetic	20	Johnson et al. 1997
Douglas-fir	0.79	0.80	1.0	Genetic	7	Woods et al. 1995
Loblolly pine	-	0.76	0.95	Family Mean	16:20	Li et al. 1996
Loblolly pine	-	0.7-0.8	0.97	Genetic	8	Xiang et al. 2003
Loblolly pine	-	0.74	0.98	Genetic	25	Gwaze and Bridgwater 2002
Loblolly pine	-	0.57	0.70	Family-mean	10:15	Raley et al. 2003
Slash pine	0.533	0.826	0.983	Genetic	10	Hodge and White 1992
Radiata pine	0.69	-	-	Genetic	8	Jayawickrama 2000
Lodgepole pine	0.65	0.83	0.95	Genetic	15	Xie and Ying 1996
Scots pine	0.77	-	-	Genetic	11-24	Haapanen et al. 1997
<i>Pinus caribaea</i> x <i>P. tecunumanii</i>	0.49- 0.71	-	-	Genetic	age 5	Dungey et al. 2000a, 2000b
<i>Pinus caribaea</i> x <i>P. oocarpa</i>	0.69- 0.81	-	-	Genetic	age 5	Dungey et al. 2000a, 2000b
<i>Pinus tecunumanii</i>	0.80	0.91	0.96	Family-mean	12	Moura and Dvorak 1998
Sitka spruce	0.90	-	-	Genetic	10	Lee et al. 2002
<i>Eucalyptus globulus</i>	-	0.90	-	Genetic	5	Sanhueza et al. 2002

Table 10. Examples of relative family-mean heritabilities for height, dbh, volume (dbh²xheight) and taper (ht15/dbh15) for first-generation Douglas-fir programs.

Program	Across-site family-mean heritabilities (% of ht15 family-mean heritability)			
	ht15	dbh15	volume15	taper15
BLM12	100.0	88.5	82.1	94.9
BLM13	100.0	100.0	92.8	84.3
Ryderwood	100.0	89.7	93.1	74.1
Burnt Woods1& 2	100.0	92.8	97.6	59.0
Gold Beach1	100.0	85.5	89.2	74.7

Given that rank correlations are generally even weaker than Pearson family-mean correlations, and given the differences in taper, families could well have dramatically different ranks for height, dbh and volume. If the objective is genetic gain in volume in plantations, selecting on height only is likely to give less gain than selecting on volume. Some authors go so far as to state that selecting on DBH alone will give more gain than selecting on height alone (e.g. King et al. 1988, Li et al. 1996). Another study in Douglas-fir indicated that selecting for height and dbh were both equally effective in improving volume, but neither was as effective as selecting on volume (Adams and Joyce 1990).

Clearly the answer will depend largely on factors such as heritability and coefficient of variation. The phenotypic variation in volume is usually larger than height and/or dbh. Since volume has similar h^2 as dbh and height, direct selection on volume is expected to be better than indirect selections even the genetic correlations (dbh:vol or ht:vol) are high.

In a recent analysis, the BLUP gain prediction for DBH² x height was shown to have a estimated correlation of 0.999 with the BLUP gain prediction based on Bruce and DeMars volume equation for small Douglas-fir trees. In a study on loblolly pine, the estimated genetic correlation between total inside-bark volume (measured by cutting down trees and taking sections) and DBH² x height was 0.99 (Sherrill et al. 2004). DBH² x height is not the same as measured volume, but it should provide very good rankings of stem volume at a fraction of the cost of actually measuring the volume of every tree.

Measuring height can be imprecise when trees are tall, and, therefore, selection based on height would be more subject to measuring errors. However, dbh is more sensitive to stand density than height. Thus, some breeders tend to give an equal weight to both dbh and height during selection.

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Mission of the Northwest Tree Improvement Cooperative

- Oversee cooperative breeding of Douglas-fir, western hemlock and other species of the coastal forests of the Pacific Northwest
- Guide technical aspects of implementing these tree improvement programs
- Analyze and interpret genetic test data
- Store test data and breeding records
- Provide expertise and training in tree breeding



Grays Harbor Genetic Gain / Type IV site: Donaldson Creek (Weyerhaeuser)



Grays Harbor Genetic Gain / Type IV site: Donkey Creek (Rayonier)



1959 Provenance trial at Oakridge High – this site was measured in 2004-5



Some cooperatives have been very successful locating elite parent trees for grafting in 1.5 generation orchards