

NORTHWEST TREE IMPROVEMENT COOPERATIVE REPORT

OCTOBER 1, 2012 TO DECEMBER 31, 2015



Front Cover:

Top left to right

Trees in some 2nd cycle South Central Coast test sites approach saw log size at 15 years from seed, 12" ruler for scale.

(Photo: Jim Carr)

First generation Cowlitz test site prepared for data collection.

(Photo: Lauren Magalska)

Lower

The Mollala Genetic Gain Verification trial has passed age-20. Mike Mosman and Mike Warjone at the Port Blakely site at Colton.

Inside Cover:

Top, right

NOCTIC Genetic Gain Demonstration planting showing row plantings of a good cross, a cross near the population mean, and woodsrun seedlings. Both height poles are set at the same height.

(Photo: Cascade Timber Consulting)

Lower, left to right

Paul Wagner highlights remarkable growth in a high elevation ROSETIC Roseburg High test site in the fourth year after planting.

Genomic selection study with 3rd cycle South Central Coast crosses outplanted in March 2015.



NORTHWEST TREE IMPROVEMENT COOPERATIVE

Report October 1, 2012 to December 31, 2015

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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



Jim Smith making 3rd cycle Douglas-fir crosses in the breeding orchard at Plum Creek Timber Company, Cottage Grove.



Oldrich Hak making 3rd cycle western hemlock crosses in the HEMTIC breeding orchard block at Green Diamond Resource Company's orchard near Shelton.



Stimulation of hemlock ramets for 3rd cycle breeding.



Western hemlock ramets in the HEMTIC breeding orchard block at Colton's BLM orchard. (Photo: Andrea Kelsey)



Seed were counted for the first sowing of a third cycle test series (South Central Coast) and the second-generation South Central Coast genetic gain trial. (Photo: Sara Lipow)

CONTENTS

Director’s Foreword	1
Second-Cycle breeding and testing.....	2
Inset 1: APHIS/Quinault Indian Nation / WA Coast Swiss Needle Cast Trial.....	7
Inset 2: The Effect of Fertilizer Application on Genetic Parameters in a 2nd-cycle Douglas-fir Progeny Test Series	8
Inset 3: Genetic Variation and Selection for Swiss Needle Cast Tolerance in the Washington Coast 2nd-cycle Douglas-Fir Breeding Populations, Based on Age-7 Assessments at Three Sites.....	10
3rd-cycle Breeding and Testing.....	11
Data Management, Analysis and Reports	12
Genetic Gain Verification Trials, and Gain Estimates from 2nd cycle tests.....	17
Inset 4: Age-9 Results from Grays Harbor Genetic Gain / Type IV Trials at Six Sites.....	27
Inset 5: Strategic Planning for Second-Generation Douglas-fir and Western Hemlock Realized Genetic Gain Trials	30
Training, Technical Updates, Research Projects	32
Associated Research Projects.....	34
Inset 6: Agenda for 2014 NWTIC Tree Improvement Short Course.....	35
Inset 7: Geographic Variation and Local Growth Superiority for Coastal Douglas-fir: Rotation-age Growth Performance in a Douglas-fir Provenance Test (Published in <i>Silvae Genetica</i>).....	36
Inset 8: Effects of Silviculture and Genetics on Branch/Knot Attributes of Coastal Pacific Northwest Douglas-fir and Implications for Wood Quality – a Synthesis(published in <i>Forests</i>).....	37
Inset 9: Proposal—An Examination of the Economics Related to Tree Improvement Pro- grams for Douglas-fir/Western Hemlock and the Economics of using Genetically Improved Stock by Family Forest Owners.....	38
Inset 10: A High-density Single Nucleotide Polymorphic Genotyping Array for Douglas-fir	41
Inset 11: Screening Elite Douglas-fir Families for Tolerance to Drought	47
The deployment of genetically improved forest tree seedlings.....	50
NWTIC Membership and Representatives	52

DIRECTOR'S FOREWORD



(Photo: Paul Wagner)

Slightly more than three years have gone by since the last report, and NWTIC and the various advanced-generation cooperatives have stayed very active. The major round of second-cycle test establishment tailed off in 2012, but it now appears that another series of sites will be established by a new Douglas-fir cooperative (MEDTIC, successor to the first-generation Medford cooperative) towards the end of the decade. The summer of 2015 was one of the driest in recent years, dry enough to kill or damage Douglas-fir in marginal Douglas-fir sites (e.g., adjacent to pastures in the Willamette Valley), but so far

very little drought-induced mortality has been reported within the progeny tests.

Third-cycle crossing has progressed rapidly in three Oregon programs (South Central Coast, North Coast, CASTIC) and has begun for HEMTIC and Puget Sound. Seeds were counted in November for SCC's first sowing. A strategy for 3rd-cycle crossing in western Washington is emerging, with a single low-elevation testing zone below 2,000 ft or so, a smaller high-elevation testing program, and possibly three population tiers (growth and form elite, multi-trait main population, and a high-wood-stiffness elite).

NWTIC delivered perhaps its most advanced and sophisticated data analysis yet, a four-zone multivariate analysis with 18 Douglas-fir test sites in Washington. Age 20/21 results of the Molalla Genetic Gain trial were studied intensively. While percent gains decreased from age-15, absolute gains had increased dramatically. A genetic gain \times spacing interaction still seemed evident. Interest and support for realized genetic gain trials are strong enough to motivate establishing second-generation trials in both Douglas-fir and western hemlock. A review of 2nd-cycle data analyses has provided estimates of the predicted gain of the 2nd-cycle populations compared to woodsrun controls in every testing program, with an average of 7.5% predicted gain in height and 22.8% $n \text{ ht}^2 \times \text{DBH}$ at age-7, and 6.1% and 16.5% predicted gain at age-10/12.

Operating in an area with great contrasts in climate, topography, and site conditions requires forest owners to deploy multiple species. NWTIC supported small ventures in two more conifer species: making selections for a 1.5-generation noble fir orchard for the Washington Cascades, and analyzing data for the Mid-Columbia Ponderosa Pine program.

SECOND-CYCLE BREEDING AND TESTING

No mainline 2nd-cycle tests were established in the 2013, 2014, or 2015 planting seasons. Given how dry the summer of 2015 turned out, it is fortunate that only a limited number of trials relevant to advanced-generation breeding and testing were established: namely the Quinault Indian Nation / WA

Coast Swiss Needle Cast trials (described in inset 1), the Bureau of Land Management (BLM) Douglas-fir Drought Hardiness study in southern Oregon (perhaps appropriately timed!) described in inset 2, and the Northwest Advanced Renewables Alliance (NARA) Genomic Selection Study.

Table 1. Summary of advanced - generation Douglas-fir trials established in 2013-15. The purpose of these trials was specifically to rank families in the presence of severe Swiss Needle Cast on the Washington coast.

Program	Planting Year	Number of		Test Trees
		Entries	Locations	
WA Coast Swiss Needle Cast sites	2014	50 families + 2 woodsrun controls + 1 western hemlock orchard control	3	4,050

It appeared that the 12 ROSETIC Roseburg Low and High tests established in early 2012 marked the end of the cooperative 2nd-cycle test-establishment phase; however, it now appears that sites will be established by a new cooperative (MEDTIC) in the southernmost part of Oregon towards the end of the decade. Similar to ROSETIC, MEDTIC plans a series of low-elevation sites as well as a series of high-elevation sites above 2,750 ft elevation or so; higher elevation forestland in Douglas, Josephine, and Jackson counties may actually provide better growing conditions due to greater availability of moisture.

The trees in the large network of 117 active Douglas-fir test sites are maturing and data are steadily being collected (Table 3); so far, only one site has been abandoned due to damage from drought, and one was dropped from the

across-site analysis for very poor survival and growth (cold, weed competition). As shown in Table 3, many of the older testing programs have received their second growth and form measurement at 10, 11, or 12 years from seed. As we expected, there were trees as tall as 53 ft at age-12 in the South Central Coast Phase I sites. Interestingly, one of the most productive sites was one selected as a Swiss needle cast test in 2002. The merger of Trask with Vernonia/Ryderwood, forming the combined 2nd and 3rd cycle North Coast cooperative, became effective in early 2015, as evaluation of the 2nd-cycle results indicated little marginal benefit of keeping the programs separate.

Acoustic velocity, a surrogate for wood stiffness, was measured in three 2nd-cycle test series (NOCTIC I and II, PSMC I) using the TreeSonic device and also in four first-generation Douglas-fir testing programs in

Table 2. Status of cooperative 2nd-cycle Douglas-fir and western hemlock breeding populations as of 2015.

Location	Status	Number of Crosses Planted	Test Establishment, Spring of		
			Number Established (planned)	Start planting	Complete planting
Washington Cascades	Test establishment completed	291	16	2006	2011
Puget Sound	Test establishment completed	292	10	2003	2009
Washington Coast	Test establishment completed	106	8	2008	2014
Vernonia/Ryderwood	Test establishment completed	416	10	2001	2005
North Oregon Cascades	Test establishment completed	377	11	2001	2005
Trask (Coast + Inland)	Test establishment completed	500	21	2004	2007
South Central Coast	Test establishment completed	604	20	1998 ³	2006
ROSETIC-Umpqua	Test establishment completed	178	10	2007	2010
ROSETIC-Roseburg Low	Test establishment completed	228	7	2012	2012
ROSETIC-Roseburg High	Test establishment completed	116	5	2012	2012
MEDTIC - Low	Crossing				
MEDTIC - High	Crossing				
TOTAL		2,640	118		
HEMTIC	Test establishment completed				

Figure 1. Distribution of cooperative 2nd-cycle Douglas-fir and western hemlock test sites in Oregon, Washington, and British Columbia.



Washington (DNR SW, Cowlitz1, Cowlitz 2, and Snoqualmie 1). This builds on the work done by the PNWTIRC in the Port Gamble, Trask and NOCTIC programs and the work on four first-generation North Oregon Cascade programs; a total of 23,000 trees have so far been assessed for stiffness in progeny tests considering all the different projects. We were pleased to find, instead of any loss of stiffness in the 2nd-cycle NOCTIC population compared to the wood-srun lots, a small gain; we speculate this arose from work by cooperators in the 1980s and 1990s to obtain wood-specific gravity

Table 3. Data collection and selection status of second-cycle programs as of December 2015.

Location	Bud-burst	Fall Cold hardiness	First growth and Form	Needle Retention Score	# of forward selections made	Second growth and Form	Acoustic Velocity
CL98			√		49	√	
NOCTIC I	√		√		48	√	√
Vernonia/Ryderwood I	√		√		89	√	
HEMTIC			√		125	√	
South Central Coast I	√		√	√	97	√	
Puget Sound I	√	√	√		155	√	√
Trask Coast I	√		√	√	84	√	
Vernonia/Ryderwood II	√	√	√		63	√	
Trask Inland I	√		√		75	√	
NOCTIC Phase II	√	√	√		55	√	√
WACTIC Phase Ia	√	√	√		173		
WACTIC Phase Ib			√				
Trask Coast II	√		√		45		
Trask Inland II	√		√		27		
South Central Coast II	√		√		27	√	
ROSETIC Umpqua I	√		√		58		
WA Coast	√	√	√	√	90		
Puget Sound II		√	√		120		√
WACTIC Phase IIa			√				
ROSETIC Umpqua II			√				
WACTIC Phase IIb			2016				
ROSETIC Roseburg Low	2016		2016				
ROSETIC Roseburg High	2016		2016				

data prior to making forward selections in the open-pollinated progeny tests.

No additional data were collected during this period in the 2nd cycle western hemlock test sites planted in 2001, but in October 2015 HEMTIC cooperators showed interest in collecting acoustic velocity data from these tests. In some recent instances, the value gap between Douglas-fir and western hemlock logs has nar-

rowed or even disappeared, and maintaining hemlock wood stiffness and evaluating the impact of tree improvement on stiffness were seen as relevant.

Two special studies are reported: work done in Phase II NOCTIC sites to investigate the impact of fertilizer on heritability (Inset 2, Table 4), and needle retention was assessed at three Washington Coast sites in June 2014 (see Inset 3).

Table 4. Differences between fertilized and non-fertilized blocks at two sites (i.e., 50th Avenue and Jack 32) using the 56 crosses present in both trials.

	No spatial												
	ht12		dbh12		vol12		fork12		rami12		sinu12		
	Reg	Fert	Reg	Fert	Reg	Fert	Reg	Fert	Reg	Fert	Reg	Fert	
# crosses	5656	56	56	56	56	56	56	56	56	56	56	56	
# tree	2,115	996	2,115	996	2,115	996	2,115	996	2,115	996	2,115	996	
Raw mean	951.7	966.5	111.4	116.9	125.3	139.6	0.13	0.17	0.43	0.39	1.18	1.22	
Variance components	Residual	9,052.7	8,009.0	280.0	273.1	1,836.7	2,148.2	0.0298	0.0359	0.0849	0.0721	0.3892	0.3677
	family	2,001.3	0.0	0.0	0.0	0.0	0.0	0.0000	0.0000	0.0000	0.0043	0.0000	0.0000
	female	0.0	1,927.9	14.7	0.0	132.9	150.9	0.0011	0.0008	0.0074	0.0003	0.0173	0.0394
	male	1,004.4	1,608.1	76.1	104.6	524.5	777.5	0.0000	0.0000	0.0000	0.0000	0.0366	0.0086
	Rep(site)	283.5	510.9	5.1	7.8	47.0	75.3	0.0001	0.0005	0.0004	0.0000	0.0000	0.0121
	site*family	0.0	43.0	5.4	0.0	48.4	0.0	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
	site*female	0.0	0.0	0.0	15.0	0.0	37.7	0.0000	0.0014	0.0000	0.0000	0.0000	0.0000
	site*male	207.5	0.0	1.7	0.0	12.8	38.4	0.0002	0.0000	0.0000	0.0000	0.0000	0.0076
	VA	2,009	7,072	182	209	1,315	1,857	0.0023	0.0017	0.0148	0.0007	0.1078	0.0959
VP	12,266	11,588	378	393	2,555	3,153	0.0312	0.0382	0.0923	0.0768	0.4431	0.4233	
Individual-tree heritability(h ²)	0.164	0.610	0.481	0.533	0.515	0.589	0.073	0.044	0.161	0.009	0.243	0.227	

INSET 1: APHIS/QUINAULT INDIAN NATION / WA COAST SWISS NEEDLE CAST TRIAL

Jim Hargrove

The Quinault Reservation is within 20 miles of the Washington Coast, an area where Swiss needle cast has the potential to heavily affect growth of the commercially most-valuable species, Douglas-fir, especially with predictions of growth impacts spreading and increasing due to climate change. As a result, the Quinault Indian Nation secured a grant from the USDA Animal and Plant Health Inspection Service (APHIS) to install three new test sites in areas of the reservation and the Olympic Peninsula heavily impacted by SNC, and then compare the results with WA Coast test sites established for evaluating growth outside the badly impacted zone (normal protocol in 2nd cycle testing), in order to calibrate the results from the WA Coast test sites. The grant also funded an intensive assessment of Swiss needle cast traits in the existing WA Coast test sites (details provided in this report).

The goals were to (1) show the correlation between ranks in the different test series and whether such auxiliary SNC test sites are needed, (2) help Douglas-fir timberland owners with standard progeny sites calibrate their screening information to use in seed deployment, and (3) identify seedlings with resistance deployed in reforestation programs that will make the forests more resilient to climate change in the coastal zone.

Seedlings from existing families (seed was already available and donated by WA Coast Tree Improvement Cooperative and other owners) were grown at a nursery and outplanted. Each site was placed in a somewhat sheltered area so that direct exposure to salt spray was minimized. The three sites were 2.7-3.2 acres in size. One site is on Rayonier ground near Hoquiam, another is on Hancock Forest Management ground near Nemah, and the last is on the Quinault Reservation (QIN) near the southern border. The QIN site received mechanical site preparation; the other sites were treated with an operational site-preparation spray. Each site was fenced with 8-ft fencing. The design is a single-tree replication design, with each of 50 separate crosses plus three control lots (53 entries) comprising one replication. The sources are as follows:

1. 32 high-gain and 5 low-gain crosses from the WA Coast 2nd cycle DF program (7 year data)
2. 3 top crosses based on results from the Grays Harbor Genetic Gain /Type 4 Trial
3. 5 top crosses from the Trask Coast 2nd cycle DF program
4. 2 top crosses from DNR South Sound, 2 from DNR NW, 1 from DNR Central

5. 1 North WA Coast woodsrain control, 1 South WA Coast woodsrain control
6. Double replication of 14% gain western hemlock from QIN seed orchard 1st generation program

Each site contains 25 such replications. The spacing is 9 × 9 ft on a hexagonal pattern. Trees were separately tagged at the nursery and mapped as they were planted. A follow-up tagging with aluminum tags of half of the test trees (every other row) was just completed. Locations too close to stumps or in wet depressions were planted with non-test filler trees. Two rows of filler trees surround the test replications' exterior boundary.

Sites will be measured and evaluated for SNC at ages 1,-3,-7 and 12 years. Information from existing test sites will be evaluated at ages 7 and -12 years. This will give us an evaluation of early examinations, as well as comparison to the current age 7-12 screening. Test efficacy results will be published and made available to other landowners in the region. Actual family information will be available to WA Coast cooperators, and other landowners will benefit if they obtain improved SNC-tolerant seed from seed orchards with these parents or selections from these crosses this material. Staff from the SNC cooperative and the NWTIC, both located at OSU, will provide test design, expertise, and analysis of data.

INSET 2: THE EFFECT OF FERTILIZER APPLICATION ON GENETIC PARAMETERS IN A 2ND-CYCLE DOUGLAS-FIR PROGENY TEST SERIES

Terrance Ye

The NOCTIC 2nd-cycle Douglas-fir breeding program is located in the northern part of the Oregon Cascades. Three hundred seventy-eight full-sib crosses from 442 parents were tested over 11 sites, 6 sites in Phase I (2001) and 5 in Phase II (2005). Data from the most recent assessment were analyzed (height: *HT12*, diameter: *DBH12*, and volume: *VOL12*), stem forking: *FORK12*, and ramicorn branches: *RAMI12*), stem sinuosity: *SINU12*, and second flushing: *FLUSH12* at age 11 (phase 2) or 12 (phase 1). Data from one phase 1 site were dropped from the analysis due to its slow growth, high coefficients of variation, close-to-zero

heritability in growth traits, and very low Type-B genetic correlations with other sites. Overall survival at age-11/12 was 90% in phase 1 and 89% in phase 2 tests.

Small fertilized sections (56 crosses, 10 reps) were attached to Cascade Timber Consulting's two phase-2 sites (i.e., 50th Avenue and Jack 32) to examine whether fertilizing with a site-specific blend would increase within-site environmental homogeneity and thereby increase heritability estimates. Fertilizer was applied as per recommendations by Neal Kinsey, and was aimed to balance nutrients and micro-nutrients for long-term site productivity. Table 4 shows the effect of fertilizer by comparing the performance and variation of the fertilized and unfertilized sections at the two sites.

While trees in the fertilized portions were slightly larger prior to spatial detrending, the fertilizer effect may have been confounded with reps at each site, due to the experimental design. We understand there are other studies in the region (larger, better replicated) that would more reliably assess the effect of fertilizer on growth and yield of forest stands. More relevant to the tree improvement community, the estimates of heritability (h^2) in HT12 were noticeably higher with fertilizer (unfertilized $h^2 = 0.16$ vs. fertilized $h^2 = 0.61$). The estimates of h^2 increased only slightly for both diameter (from 0.48 to 0.53) and volume (from 0.52 to 0.59). By contrast, we saw that h^2 for forking, ramification, and sinuosity decreased slightly after fertilization.

While it has long been assumed that fertilizing would boost h^2 by homogenizing the micro-environment, results from this study did not provide unambiguous evidence to support this hypothesis. The variance components analysis indicated that the boost in height h^2 was mainly due to the increase of additive genetic (or GCA) effect and the reduction of non-additive (or SCA) effect. The estimates of residual variance fluctuated slightly without much impact of fertilizing for most traits.

Compared to the age-7 results, the age-11/12 difference in h^2 with and without fertilization faded greatly for both diameter and volume, but increased considerably for height. This may suggest a time lag for fertilizer to take effect.

Acknowledgements

This study took place due to the initiative of Howard Dew. Fertilizer application and site preparation was funded by Cascade Timber Consulting. NOCTIC cooperators paid for the establishment and data collection of the fertilized sections.

**INSET 3: GENETIC VARIATION AND SELECTION FOR SWISS NEEDLE CAST TOLERANCE
IN THE WASHINGTON COAST 2ND-CYCLE DOUGLAS-FIR BREEDING POPULATIONS,
BASED ON AGE-7 ASSESSMENTS AT THREE SITES**

Terrance Ye and Keith Jayawickrama

Many Douglas-fir stands in coastal areas of the Pacific Northwest suffer from Swiss needle cast (SNC) disease. A project, led by the Quinault Indian Nation and funded by the USDA Animal and Plant Health Inspection Service (APHIS), was initiated in 2013, with its goal to breed and deploy DNC-tolerant Douglas-fir germplasm to mitigate the effects of the disease. The Washington Coast Douglas-fir Cooperative (WACOAST) provided test sites for measurement, and the Swiss Needle Cast Cooperative (SNCC) gave input in designing this project. This report was based on the assessments of needle retention (BRET7) and pseudothecia count (BSPOR7) at three 2nd-cycle Douglas-fir progeny trials (5,600 trees from 106 full-sib crosses) on the western coast of the Olympic Peninsula.

Trees at two of the five WA Coast sites had too little needle loss or pseudothecia to justify assessment. While three sites displayed observable needle loss, Donkey Creek had about 30% more needles than the other two sites. The pseudothecia count was similar among the three sites. There was great variation among the 106 full-sib families for both BRET7 and BSPOR7. Family rankings on BRET7 were relatively consistent from site to site, with Type-B genetic correlation being 0.84 ~ 0.98.

The estimated across-site narrow-sense heritability of individual trees for BRET7 was 0.34 (family-mean heritability = 0.89), which was higher than that for the growth (0.16 ~ 0.19) and branch / stem traits (0.10 ~ 0.29) measured on the same trials, as well as the foliage traits (0.11 ~ 0.20) reported previously in an Oregon study. BSPOR7 was less strongly inherited, with individual-heritability estimate of 0.10; family-mean heritability was remarkably high at 0.69, given that it is based on only two needles per tree. Dominance effect was estimated at close to zero for both traits, suggesting that the breeding program for improving SNC tolerance should focus on using additive genetic variation.

Age-7 growth was not significantly correlated with either BRET7 ($r_g = 0.223 \pm 0.112$) or BSPOR7 ($r_g = 0.197 \pm 0.126$). There are a few possible reasons. First, needle loss at juvenile ages may be not severe enough to cause significant reduction in growth, and the impact of defoliation on growth may appear only after trees reach a certain size or age. Second, needle retention scored on individual

branches may not be fully representative of total crown biomass or foliage/ha. Thus, it is important to continue to examine the long-term impact of the disease, and assess how defoliation affects trees' future growth. In addition, adding stand-level measurements (e.g., foliage/ha, crown density, etc.) at later ages could be useful.

Age-4 spring budburst appeared to be moderately correlated with BRET7 ($r_g = -0.577 \pm 0.076$) and weakly correlated with BSPOR7 ($r_g = 0.252 \pm 0.115$), with early-bursting families suffering more needle loss and having slightly less SNC disease spores. BRET7 also correlated significantly with longitude, with parents originated from coastal areas tending to have less needle loss ($r = -0.41$, $P < 0.001$).

The average predicted gains of the best 15 parents were 11.5% for BRET7 and -8.2% for BSPOR7. For full-sib family selection, the average predicted gains of the best 15 crosses were 9.2% and -6.2% for BRET7 and BSPOR7, respectively. It is worth noting that if we select the top 10 full-sib families based on predicted gains on age-7 height growth or age-8 needle retention, half of the selections would be in common. The WA Coast South woodsrun control showed 8% more needle loss and 6% more SNC spores over the mean of the testing population, while the other control (WA Coast North) performed close to the population mean. These results suggest that there is good chance of improving both growth and needle retention through genetic improvement, and also that genetic selection had slightly improved tolerance to SNC in the overall WA Coast breeding population.

3RD-CYCLE BREEDING AND TESTING

Third-cycle crossing has progressed rapidly in three Oregon programs (SCC, North Coast, CASTIC) and has begun for HEMTIC and Puget Sound. Seed was being counted in November for SCC's first sowing (over 130 3rd-cycle crosses, 11 linkers from the 2nd cycle, five elite seed orchard controls, and a woodsrun control). A strategy for 3rd-cycle Douglas-fir breeding in western Washington is emerging, with the likely configuration being a single low-elevation testing zone below 2,000 ft or so, a smaller high-elevation testing program, and possibly three population tiers (growth and form elite, multi-trait main population, and a high-wood-stiffness elite).

Table 5. Status of cooperative 3rd-cycle Douglas-fir and western hemlock breeding populations as of 2015.

Location	Status	Number of Crosses >100 seed	Target date to start planting tests
South Central Coast	Crossing, sowing	186	2017
North Coast	Crossing	156	
CASTIC	Crossing	139	
Washington	Crossing	24	
HEMTIC	Crossing	8	
TOTAL		513	

DATA MANAGEMENT, ANALYSIS AND REPORTS

NWTIC maintained a strong emphasis on data analysis, completing genetic gain predictions and reports for 28 first-generation breeding units, 15 analyses involving advanced-generation programs, and 10 other quantitative analyses. (Table 6).

Key statistics about the database are summarized in Table 7. It now contains many more acoustic velocity observations, more crosses, and older genetic-gain trial measurements than the previous report. We also augmented test-site maps with driving directions to test sites. Hao Truong has recently begun to automate aspects of database management, he has written a custom executable program using Microsoft Studios as the integrated development environment and C sharp as the

programming language that allows data managers to process and load important data directly into the database. The process includes checks that will prevent any erroneous data from entering the database. For instance when processing progeny measurements the program takes three key columns to create a primary key, it then aligns the input data with the data in the database, and lastly the program outputs a file for the manager to spot check. This process can be completed in a day and loading the data is as simple as clicking a button.

We have also made changes to the database itself, adding new columns to tables not only for quicker access and understanding but also preventing duplication of data such as

different crosses or different parents being assigned the same GID. During the last year, Hao has successfully migrated NWTIC database from Microsoft SQL Server 2008 to 2012 versions, as the College of Forestry was moving away from SQL server 2008. This include recreating over 70 access databases to connect to the new 2012 server, and enabling the old website to the new connections.

In addition to maintaining the existing website, Hao has started in build a new NWTIC website. The website will have a newer fresher look, and functionality that is more useful such as integrated tables that are more specific to what the members want to see and user friendly such as a help menu and mouse of tool tips. The Microsoft Studios Web as the integrated development environment and C shape as the programming language. This will be all consistent with requirements of the College of Forestry. NWTIC members will provide input to what they want they see and how they access their data.

We have recognized a fundamental shift in priorities and needs in NWTIC information management. The "Data Management" phase, which started in year 2000, is clearly tailing down: the vast resource of first-generation parent and progeny data streams has almost dried up, first-generation parent GIDs and locations have been entered, almost all 2nd-cycle tests have been established, the

majority of 2nd-cycle data collected, and 3rd-cycle data will not be available for several years. On the other hand, we could say that "Result Management" needs are increasing: great numbers of predicted gains have been generated (multiple ages, traits, testing zones), and a parent or cross may have dozen of variables generated from a single analysis. With retirements and turnover of personnel, we find new co-op reps facing a large amount of catch-up in order to assemble all results relevant to the seed orchards they are involved in and the seed inventory. NWTIC has not focused recently on loading the predicted gains to the database; the predicted gains have instead been delivered to cooperators in Microsoft Excel and Microsoft Access tables distributed after each analysis.

At the October 2015 NWTIC meeting, members supported an initiative to shift our thinking from a "Database" or "Data Warehouse" approach to an "Information Delivery System." Starting in 2016, we plan to emphasize loading predicted gains to the database, following input from cooperators on what would be most useful to them. NWTIC has also been frequently approached about merging genetic gains into lists of seed orchard parents or into seed inventories; we will look toward building tools and routines to do such merging via the NWTIC "Information Delivery System."

Table 6. Summary of genetic gain predictions using BLUP, reports and other quantitative tasks, completed October 2012 through September 2015. Analyses are coastal Douglas-fir unless otherwise indicated with a 1.

First-Generation Analyses	
DNR Moose site	Acoustic Velocity
Mid-Columbia Ponderosa Pine1	HT
Mid-Columbia Ponderosa Pine1	HT, DBH, stem defect
Cowlitz-1	Acoustic Velocity
Simpson Puget Sound full-sib	HT, DBH
Mount Baker Snoqualmie Noble Fir1	HT, DBH
Second-Generation Analyses	
WACTIC Phase I (8 sites) + Puget Sound Phase I (5 sites) age-7 data (growth, form)	
Trask Coast and Inland, Phase I and II; VRTIC I and II; age-7 data (growth, form, budbreak)	
ROSETIC Umpqua Phase I age-7 data (growth, form, budbreak)	
SCC Phase I age-12 data	
WA Coast fall cold hardiness (full data set)	
Puget Sound, WACTIC and WA Coast fall cold hardiness data	
Second-Generation Analyses	
Higher-elevation Trask and VRTIC sites (Military, Sock, Stock Tank A, Stock Tank B, Cargo) age-7 data	
WA Coast (5 sites) age-7 data (growth, form)	
Draft on site grouping strategy across WA programs	
Vernonia/Ryderwood I and II Age-11/12 data	
Final version WA-wide 2nd-cycle analysis strategy	
Puget Sound Phase I Age12 data	
NOCTIC fall cold hardiness data	
Combined analysis of 2nd cycle tests in WA (18 sites, 3 meta coops)	
NOCTIC AV data	
Trask Coast Phase I, T96, VRTIC Phase I and II, Age11/12 data, Combined analysis	
Puget Sound Phase I + II Age7 data	
ROSETIC Umpua Phase I and II age-6/7 data (growth, form, budbreak)	
WA Coast SNC data (needle retention, spore frequency)	
OR statewide predicted gains, and patterns of growth and G x E interaction (in progress)	

Other Quantitative Tasks

Gold Beach BU-3: Compare gains from clonal vs. seedling orchard
Grays Harbor gain trial age-9 (3 sites)
Grays Harbor gain trial age-9 (6 sites)
Trask and VRTIC2 age-7 forking, ramcorns and sinuosity data. Investigate: Are rankings in Trask Coast, Trask Inland and V/R sufficiently different to justify 3 breeding zones, or do age-7 data indicate these could be combined to one or two zones?
Seed orchard designs
Grays Harbor gain trial age-9 (6 sites)
Molalla Gain trial age-20 data (4 sites)
Molalla Gain trial age-20/21 data (final analysis with all 5 sites)
1959 Provenance trial rotation-age growth data
Starker Forests genetics x nutrition study
Determine optimal experimental design strategy for future realized gain trials via stochastic resampling technique

Table 7. Highlights of information in core NWTIC Database tables

Table	Total No. of Records: December 2015	Total No. Records: September 2012
Acoustic_Velocities	51,528	39,307
Address_Phone	406	447
Advanced_Generation_Seed_Usage	1,607	1,607
AV_Wood_Quality_Measurements	11,266	11,266
Budburst_Measurements	120,805	101,819
Clone_Bank_Seed_Orchard_Inventories	66,928	66,928
Clone_Banks_and_Seed_Orchards	171	171
Cold_Hardiness	9,328	3,308
Contacts	2,583	3,003
Coops	38	38
Cross_Testing_Parents	2,049	1,895
Crosses	7,648	7,020
Gain_Trial_Measurements_Age_3	14,797	14,797
Gain_Trial_Measurements_Age_5	14,797	14,797
Gain_Trial_Measurements_Age_7	14,797	14,797
Gain_Trial_Measurements_Age_8	26,920	26,920

Gain_Trial_Measurements_Age_9	13,920	
Gain_Trial_Measurements_Age_13	8,784	8784
Gain_Trial_Measurements_Age_15	21,736	21,736
Gain_Trial_Measurements_Age_20	15,552	
Gain_Trial_Measurements_Age_21	10,369	
Gain_Trial_Progeny	41,718	41,716
Gain_Trial_Sites	12	12
Gen2_Progeny_Measurements	545,527	432,891
Gen2_Progeny_Trees	667,634	582,019
Gen2_Selected_Progeny_Individuals	1,626	818
Generational_Gains	9,439	9,439
Genetic_Gains	2,620,607	2,620,607
Later_Genetic_Gains	199,789	199,789
Later_Progeny_Measurements	254,640	253,691
Metadata_Variables	2,384	2,225
Owners	70	66
Parent_Tree_Coordinates	32,518	31,718
Polymixes	177	149
Progeny_Measurements	3,383,288	3,352,248
Progeny_Trees	3,383,345	3,352,305
Program_Images	38	38
Program_Layouts	148	148
Program_Views	147	147
Programs	162	154
Seed	5,857	5,857
Selected_FirstGen_Parents	2,453	2,355
Selected_Progeny_Individuals	2,741	2,735
Site_Thinning_Archiving	976	976
Sites	1,185	1,152
Sowing_Schedules	1,365	1,342
Specific_Gravity	14,509	14,509
Swiss_Needle_Cast_Monitoring	32,764	32,764
Tree_Identifiers	45,287	41,499
View_Metadata	62,265	62,265
Z_Scores	19,111	19,111

GENETIC GAIN VERIFICATION TRIALS, AND GAIN ESTIMATES FROM 2ND CYCLE TESTS

Age-20/21 data were obtained from the five Molalla Genetic Gain trial (MGT) sites, and age-9 data from all six Grays Harbor Genetic Gain / Type IV trials. Results are provided in this report in Figures 2-11 and Inset 4. The substantial realized gains (especially in volume per acre) from this study indicated that progress from genetic selection and breeding of Douglas-fir is demonstrable and real. Realized gains obtained in the MGT are by no means the upper limit that might have been obtained, even in the Molalla breeding zone, due to the way the original parents were selected (e.g., based on index rather than breeding value; full-sib families were not genetically tested) and certainly not for the first generation of testing. Top 2nd-cycle selections are expected to have much higher realized gains.

Similar to age-15 results, significant genetic level \times spacing still existed at age-20. This may have implications for our current testing approach. With constant h^2 , higher age-age correlation led to higher genetic gain. Due to the existence of a significant genetic level \times spacing interaction, realized gain may be impaired by using narrow-spacing settings in our progeny trials. If significant genetic level \times spacing interaction exists widely in other

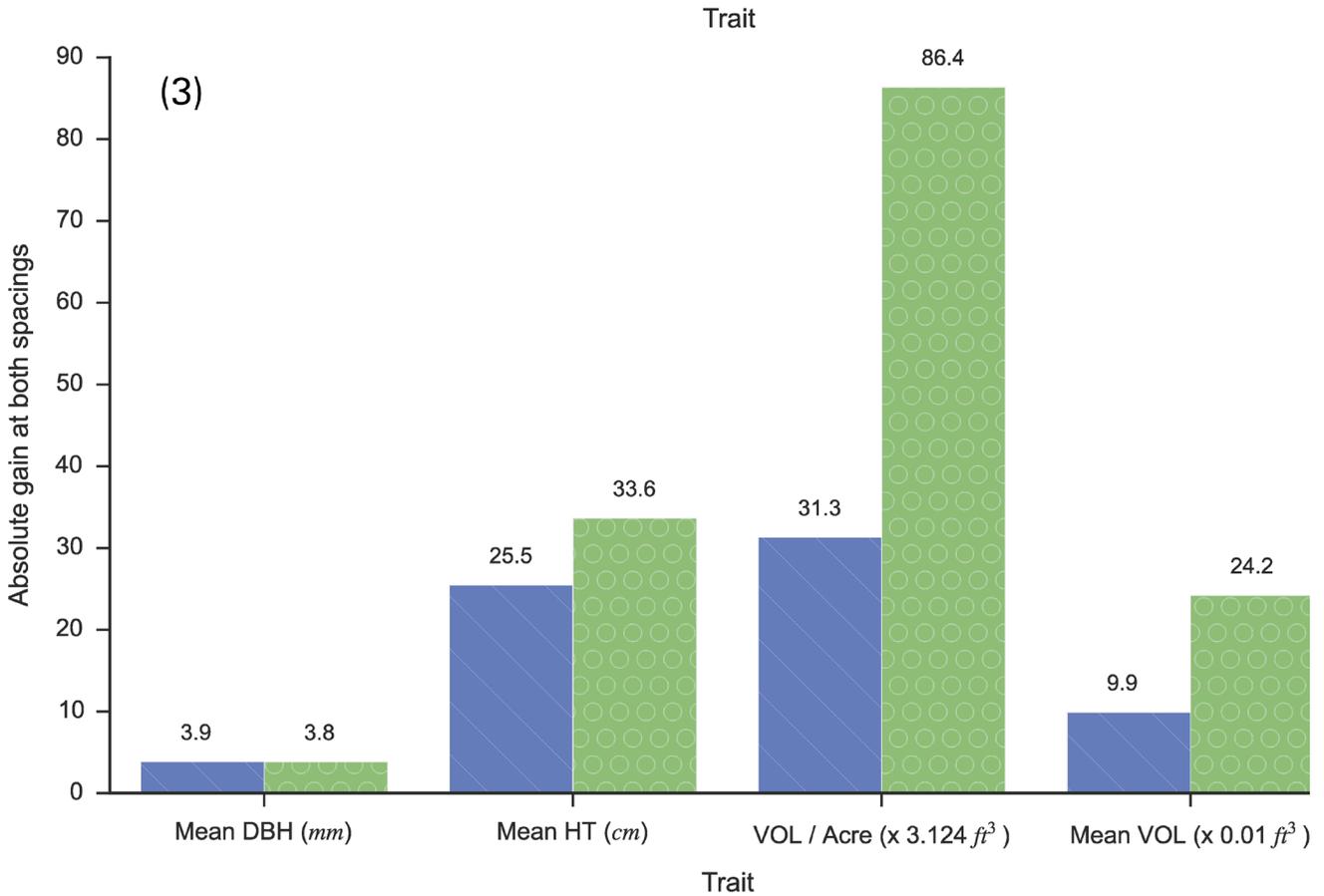
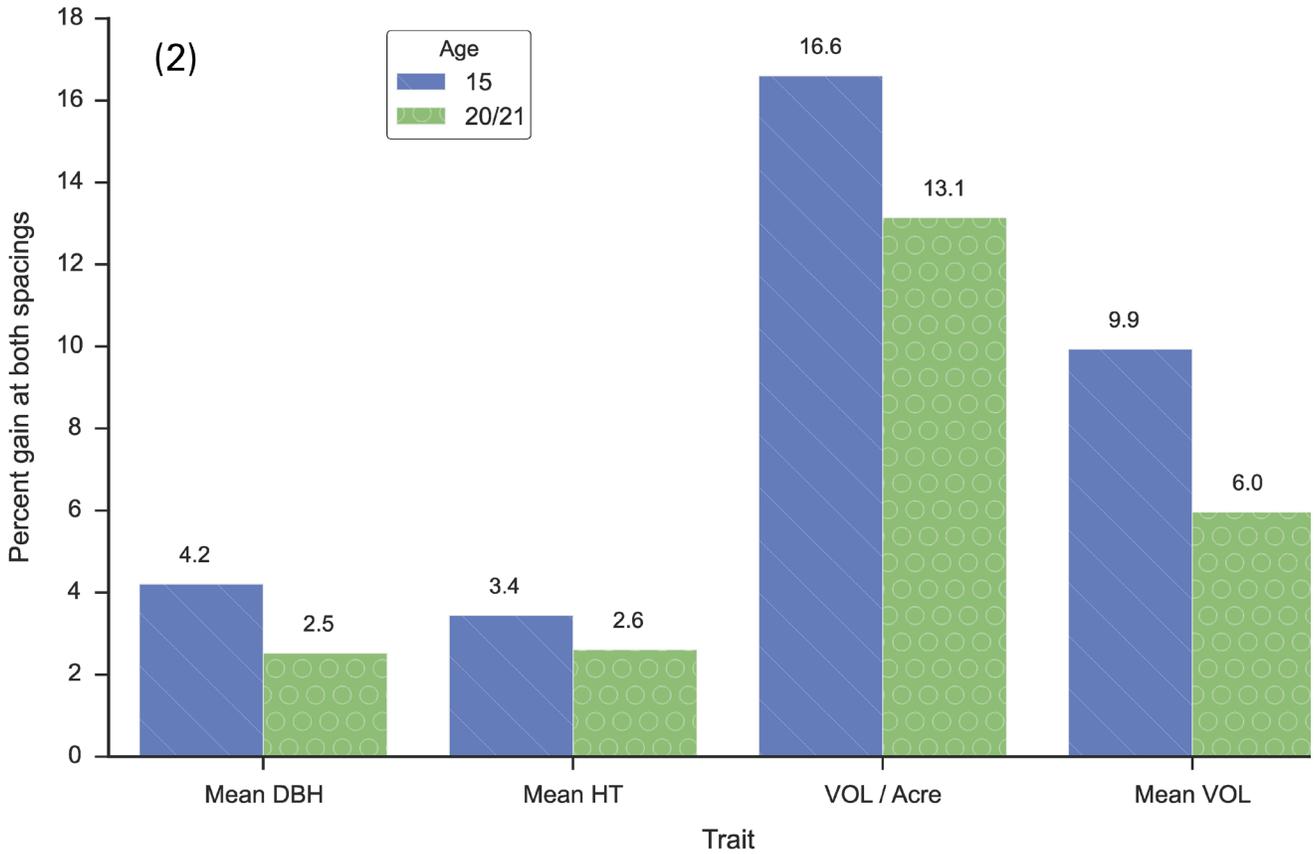
NWTIC breeding zones, spacing closer to operational planting may be advisable for future progeny trials.

Interest and support for realized genetic gain trials are strong enough to motivate establishing second-generation trials in both Douglas-fir and western hemlock.

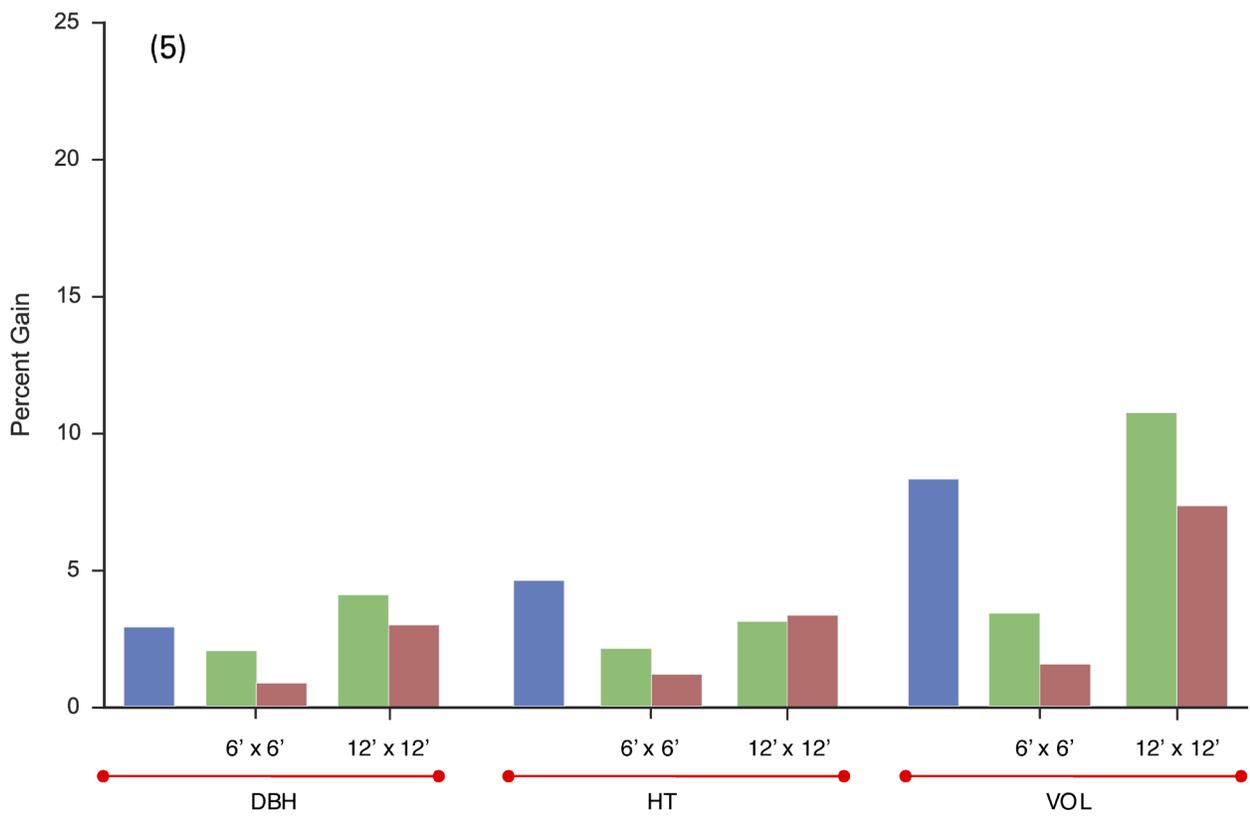
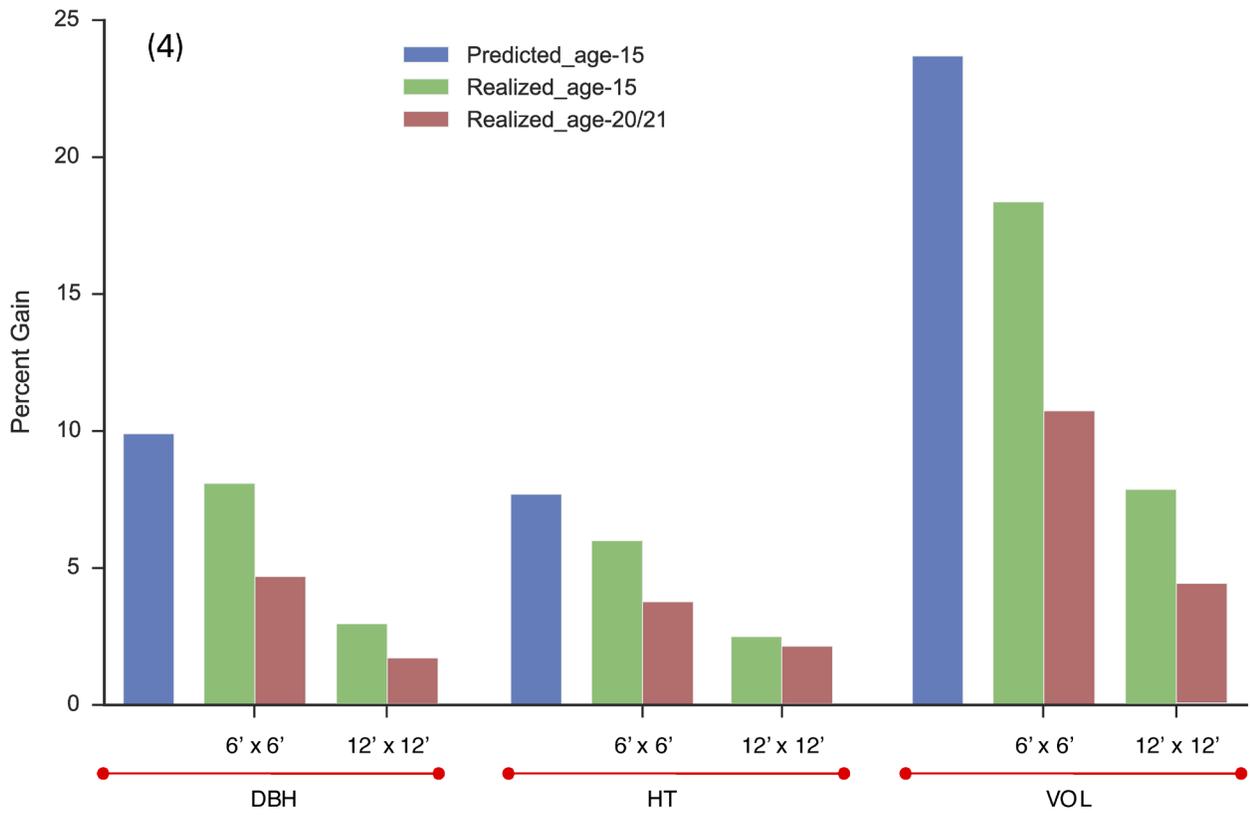
The objectives of these new trials are as follows:

1. Compare realized and predicted genetic gains for seed lots similar to those that are being produced or will be produced from second-generation tree improvement and seed orchards.
2. Produce data sets that represent tree growth using current best silvicultural management coupled with top genetic improvement (i.e., the upper limit of coastal Douglas-fir and western hemlock tree growth currently achievable).
3. Visually demonstrate the impact of Douglas-fir and western hemlock breeding programs and of using high-gain reforestation stock.

Some strategic planning studies and results for those studies are shown in Figures 12-16 and Inset 5.



Figures 2 & 3: Realized genetic gains at age 20/21 in the Molalla Genetic Gain Verification trial expressed as (2) percent gain and (3) absolute gains over woodsrun/unimproved population.



Figures 4 & 5: Realized genetic gain of (4) Elite and (5) Intermediate Seedlots over woodsrun/unimproved population at age 20/21 in the Molalla Genetic Gain Verification trial, compared to predicted gains.

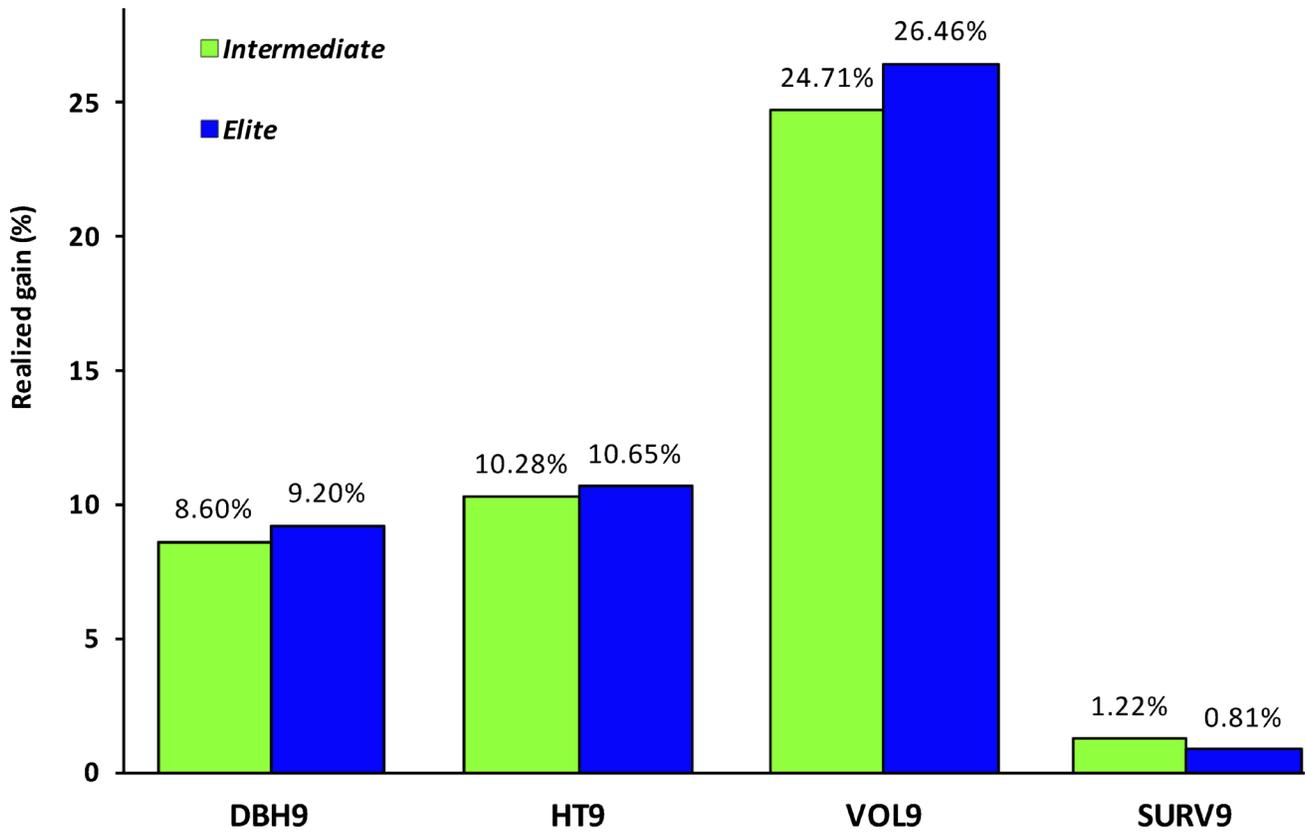


Figure 6: Realized genetic gains over woodsrun/unimproved population at age 9 in the Grays Harbor Genetic Gain / Type IV trial.

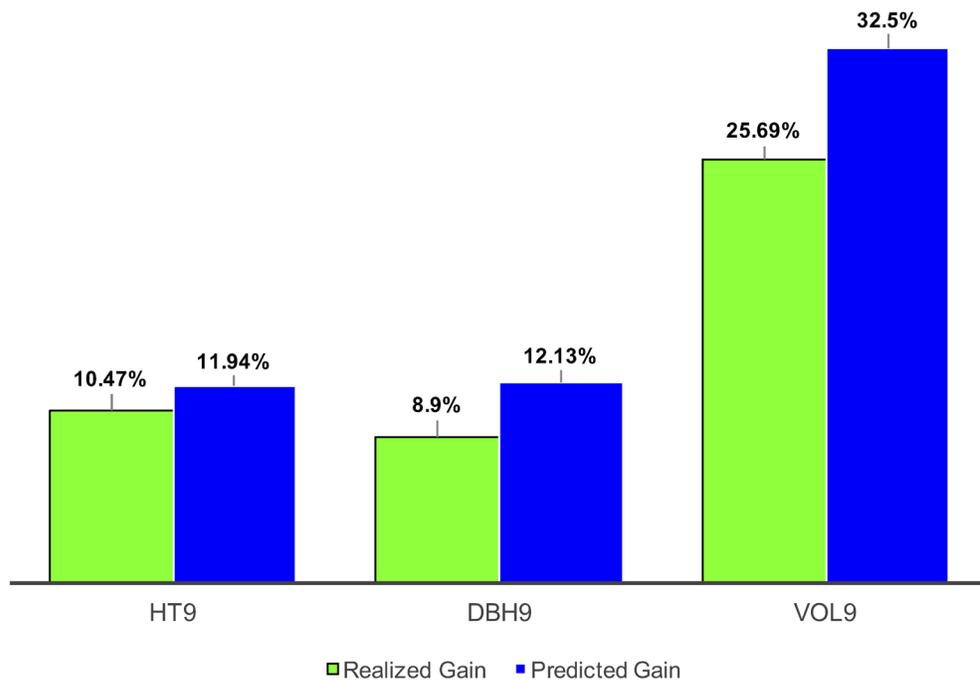


Figure 7: Realized genetic gains at age-9 over woodsrun/unimproved population in the Grays Harbor Genetic Gain / Type IV trial, compared to gains predicted at age-10.

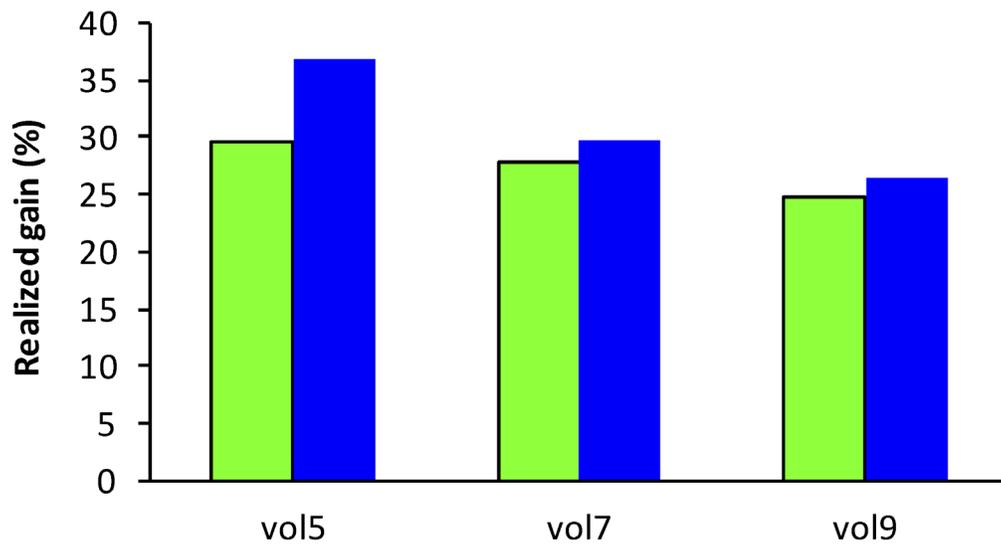
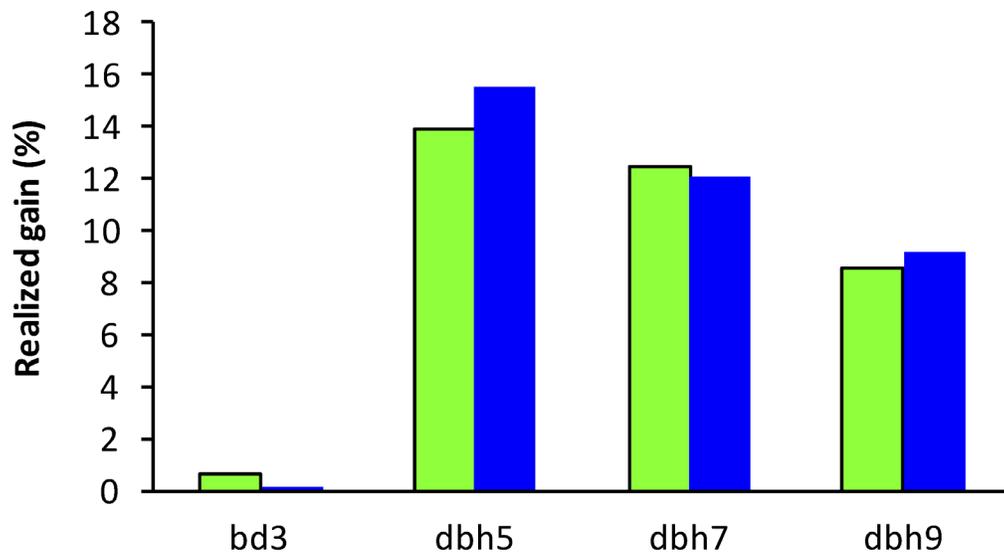
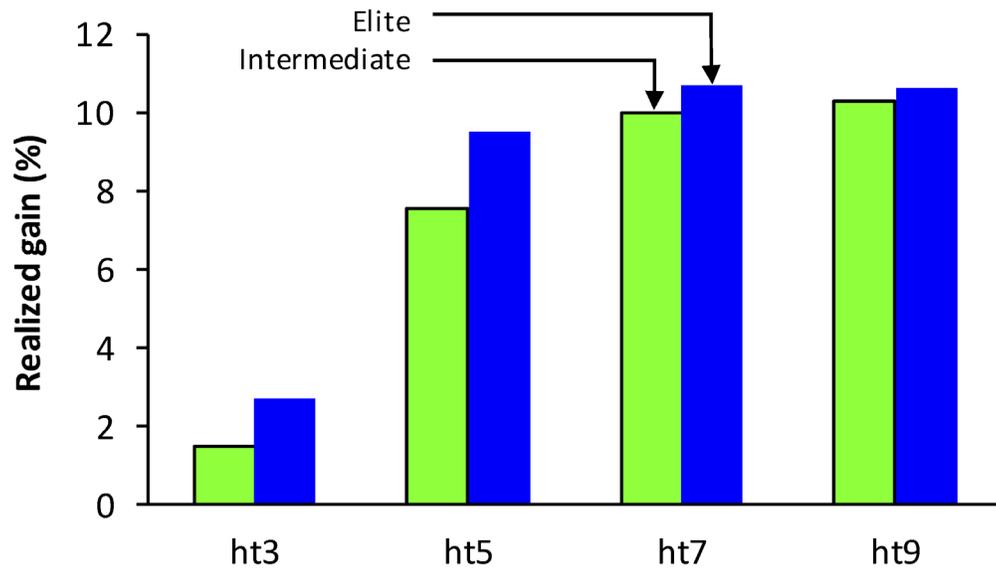


Figure 8: Changes in percent realized genetic gains with age over woodsrun/unimproved population in the Grays Harbor Genetic Gain / Type IV trial.

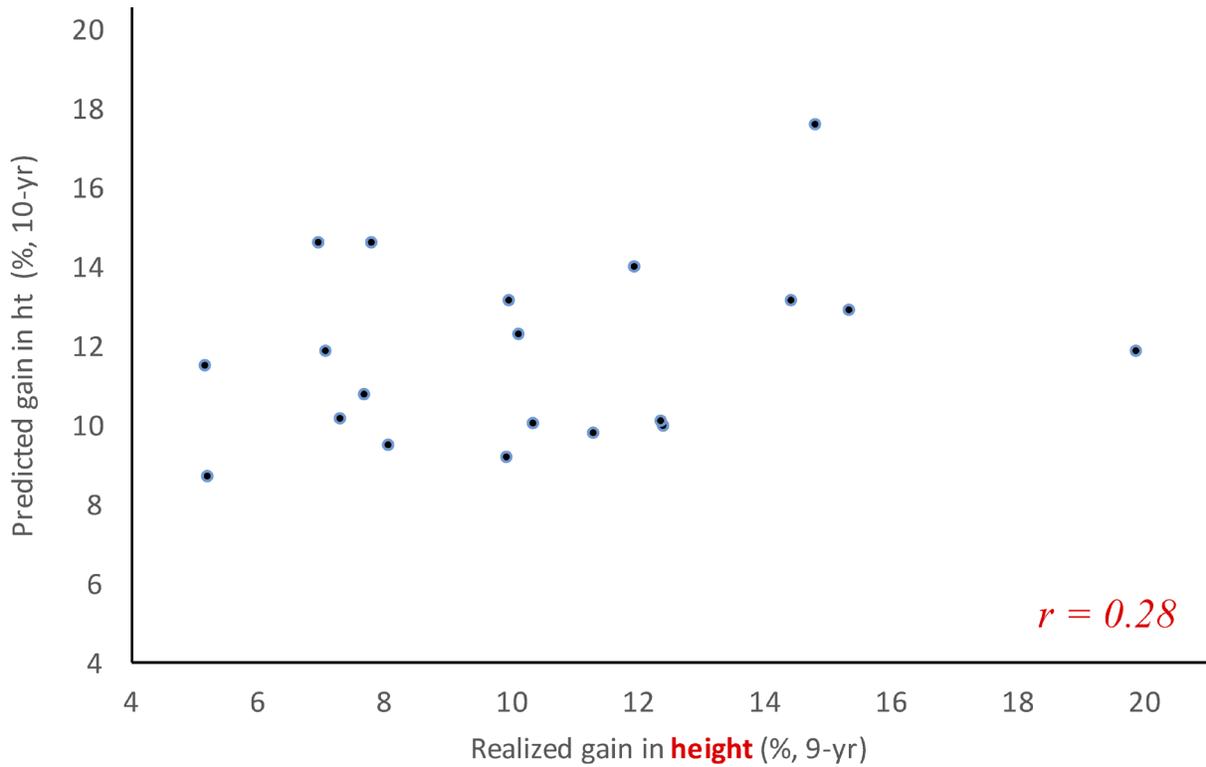


Figure 9: Regression of predicted and realized gains for HT in the Grays Harbor Genetic Gain / Type IV trial ($r = 0.28$).

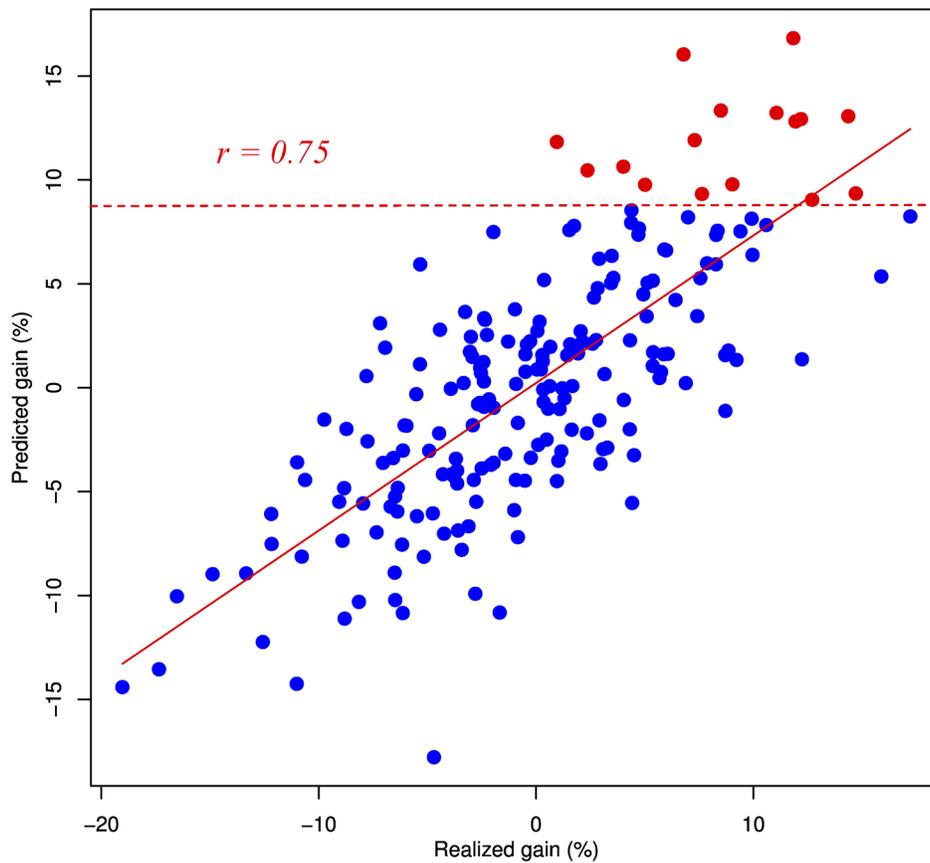


Figure 10: Simulation showing strong regression of predicted vs. realized gains in the presence of a wide spread of predicted gains ($r = 0.75$).

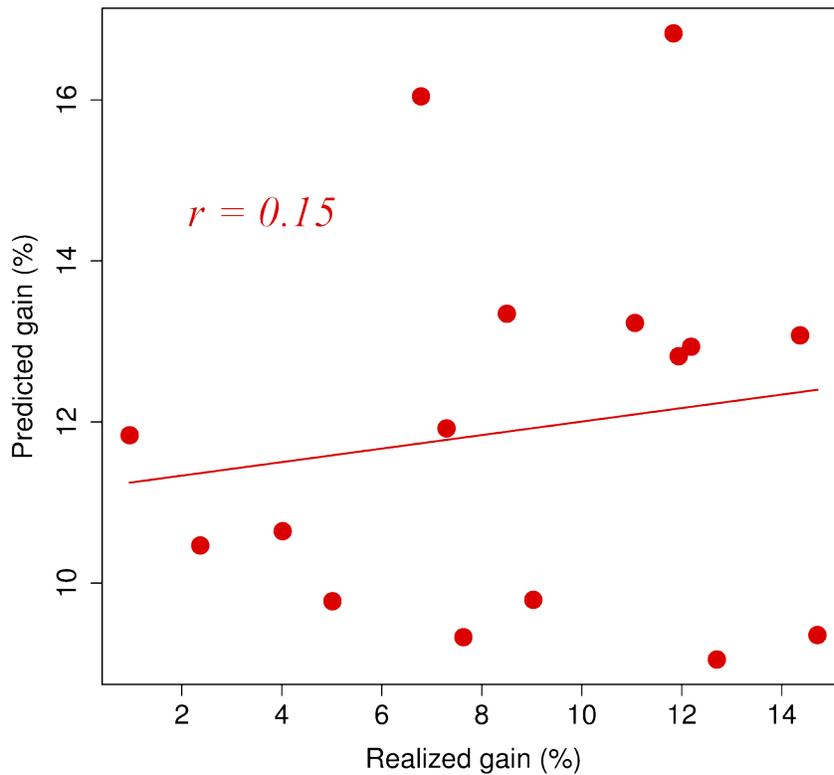


Figure 11: Simulation showing weak regression of predicted vs. realized gains in the presence of a truncated spread of predicted gains, if only considering the predicted gains in red from Figure 10 ($r = 0.15$).

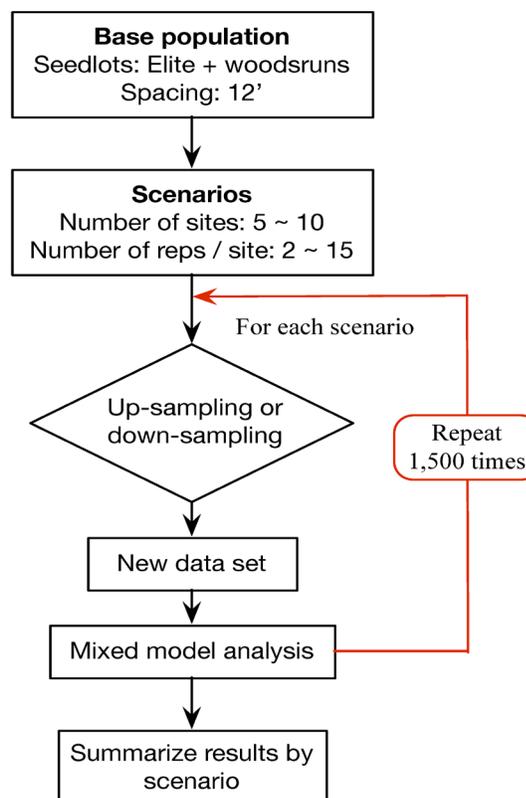


Figure 12: Procedure for investigating the number of sites and replications required for second-generation realized genetic gain trials

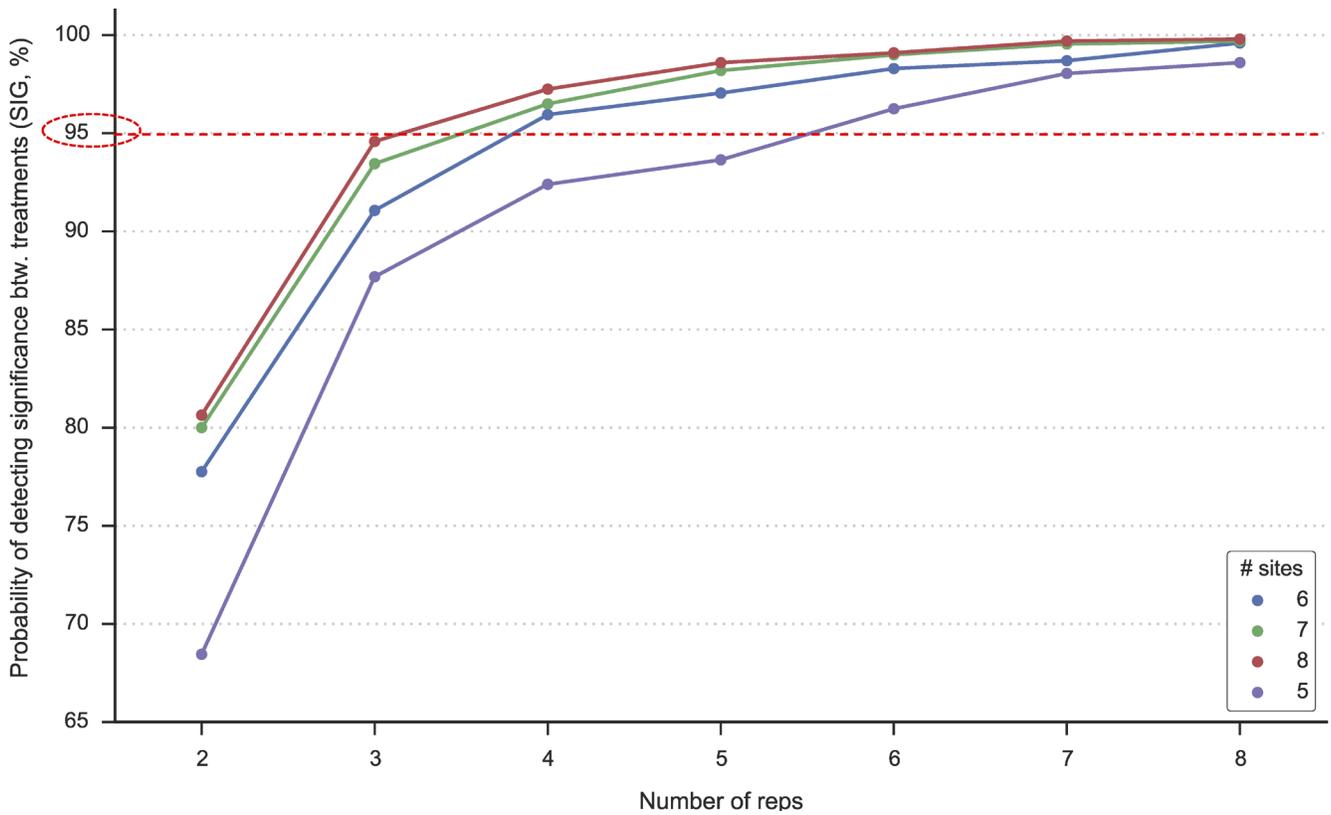


Figure 13: The effect of varying the number of sites and replications in a second-generation realized genetic gain trial on the probability of detecting significance between treatments.

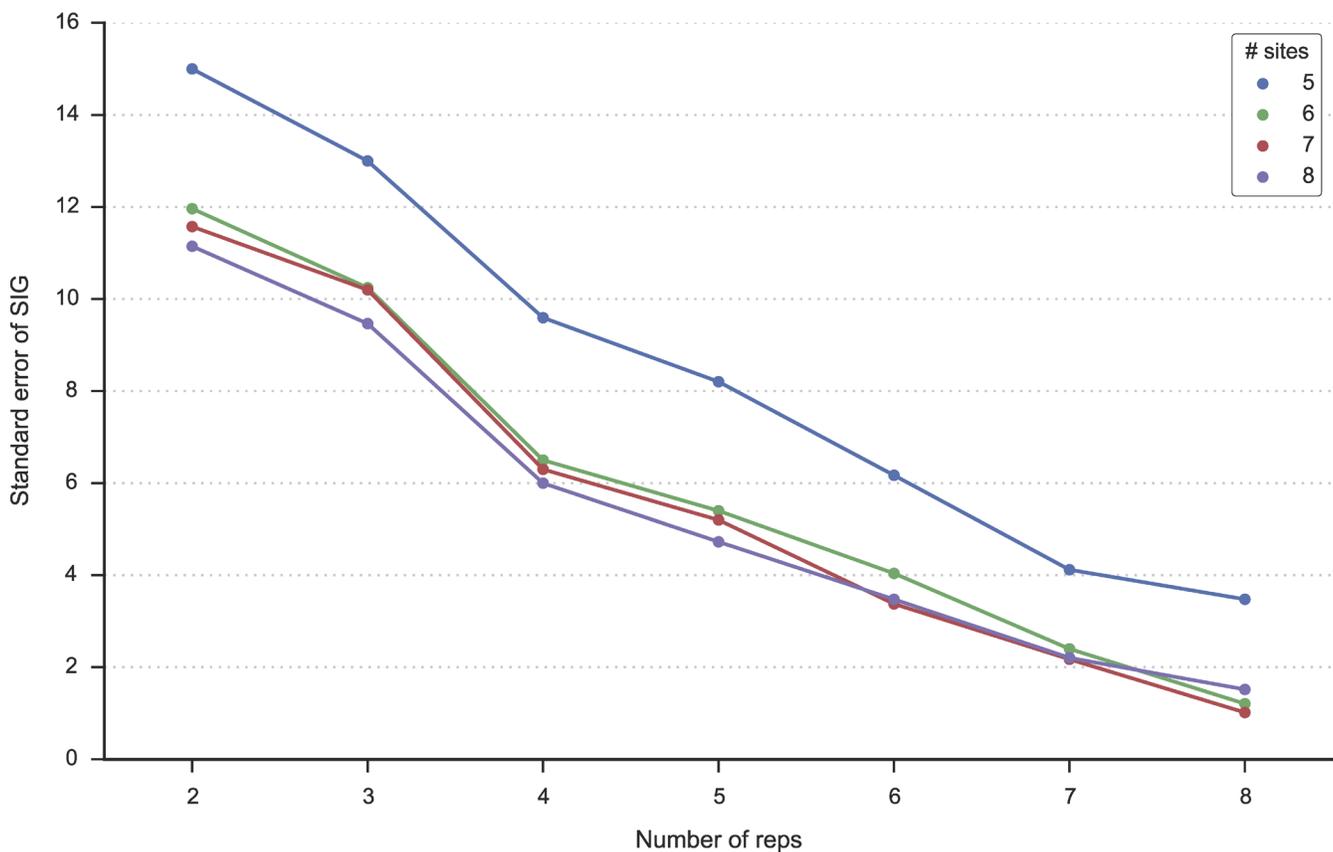


Figure 14: The effect of varying number of sites and replications in a second-generation realized genetic gain trial on standard error of SIG.

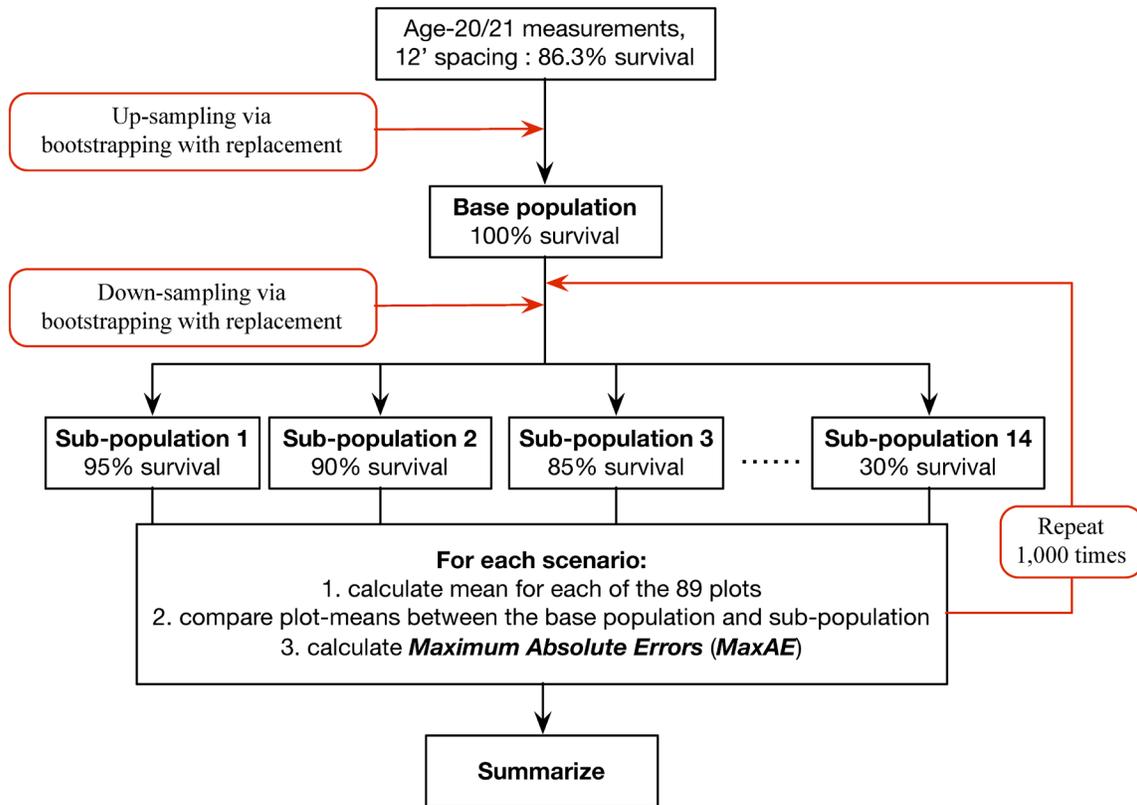


Figure 15: Procedure for investigating the effect of mortality within a second-generation realized genetic gain trial on the accuracy of the results.

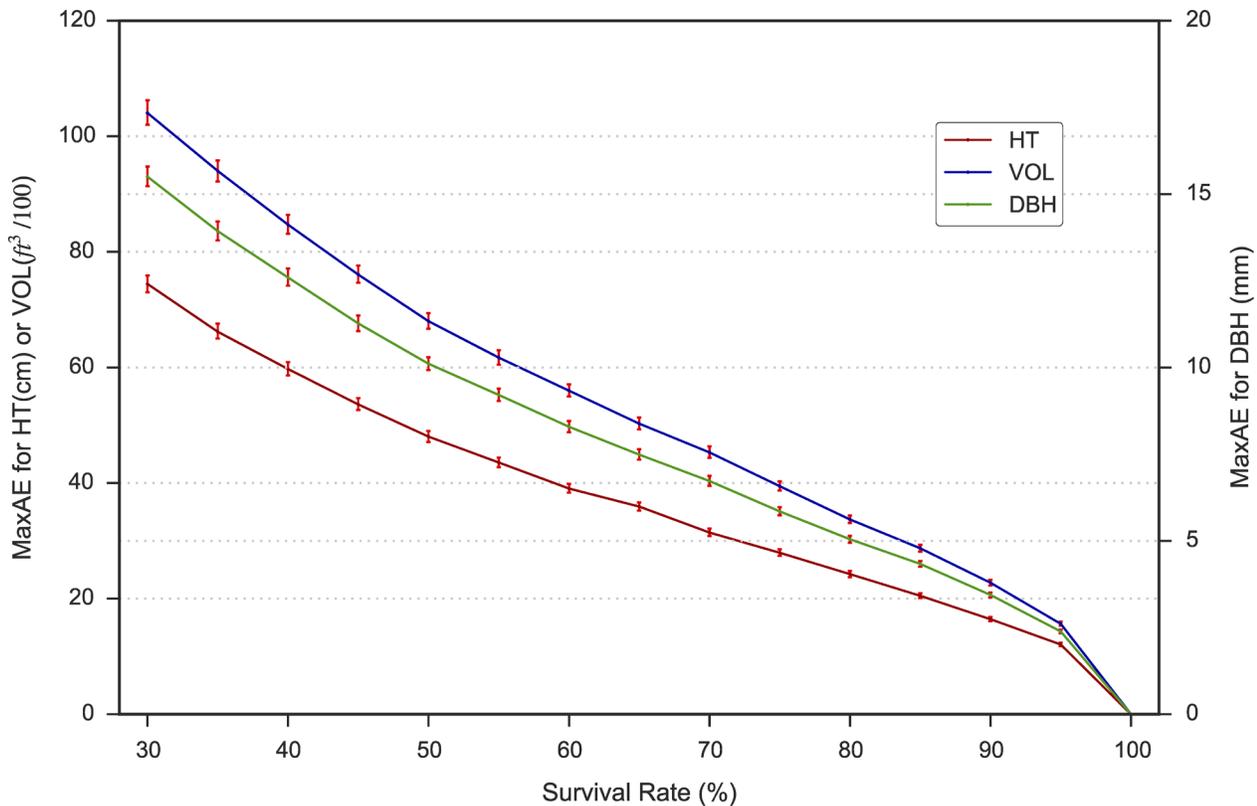


Figure 16: Stimulation results on the relationship between survival rate and Maximum Absolute Error for HT, DBH, or VOL in second-generation realized genetic gain trials.

All 2nd-cycle Douglas-fir programs established after 2001 included one or more woodsrun (unimproved) controls. The BLUP analyses have provided estimates of the gain superiority of the 2nd-cycle populations compared to these controls, with an average of 7.5% superiority in height and 22.8% superiority in $ht^2 \times DBH$ at age-7, and to 6.1% and 16.5% at age-10/12.

Table 8: Predicted genetic gain superiority of full-sib test populations compared to unimproved controls in cooperative 2nd-cycle Douglas-fir programs.

2nd-Cycle Program	Age from seed	Height	DBH	HT* DBH ²
A	7	11.2	16.6	35.4
B	7	8.9	12.0	27.5
C	7	10.0	10.5	26.5
D	7	5.6	9.8	25.2
E	7	6.6	9.7	22.9
F	7	8.0	8.2	21.5
G	7	6.5	7.0	18.2
H	7	6.1	6.8	16.7
I	7	4.9	5.0	14.3
J	7	7.0	7.6	19.5
		7.5	9.3	22.8
K	12	8.8	9.1	24.0
L	12	6.4	8.7	20.8
M	12	5.5	5.7	14.3
N	12	3.0	2.5	8.0
O	12	6.7	4.9	15.6
P	10/12	6.2	7.0	16.5
		6.1	6.3	16.5

INSET 4: AGE-9 RESULTS FROM GRAYS HARBOR GENETIC GAIN / TYPE IV TRIALS AT SIX SITES

Terrance Ye and Keith Jayawickrama (NWTIC); Eric Turnblom (SMC); Brad St Clair (USFS-PNW)

Introduction

Background on the objectives, experimental design, and linear model for data analyses of this trial were presented in the 2007-9 NWTIC report. Very briefly, the trial had the following notable features:

Treatments:

- Three levels of genetic gain: Unimproved, Intermediate Gain, and Elite
- Three density treatments: Low density (15 × 15 ft), Intermediate density (10 × 10 ft), High density (7 × 7 ft)
- Two vegetation control levels: Standard, Complete

Test design:

- Six sites
- 22 plots per site
- 64, 100, and 250 measurement trees / plot for den = 1, 2, and 3, respectively,
- Considered as a completely random design

Results and Discussion:

At the time of the age-9 measurement, there were 12,235 surviving trees. Survival (surv9) varied from 72 to 90% across sites. The following traits were measured: diameter at breast height (dbh9, inches), average crown width (acw9, ft), crown base height (cbh9, ft), basal diameter (above the collar) of the largest branch in the first whorl above breast height (bdb9, inches), number of living branches of at least 1/2 of the largest diameter in the whorl (nbw9), and number of living branches in the internode above the first whorl above breast height that are at least 1/2 of the diameter of the largest branch (nbi9). Total height (ht9, ft) was measured on about 50% of living trees (i.e., 68%, 47%, 45%, 39% and 52% at sites 601 – 606, respectively) to reduce the measurement cost. Thus, MARTIN and FLEWELLING's (1998) model (2) was fitted for each plot at each site, and then used to predict ht9 for the unmeasured trees.

Analyzed across all three sites, the genetically improved seedlots (both the elite and the intermediate) grew significantly faster than the unimproved seedlot ($P < 0.001$), with larger average crown width ($P < 0.001$) and more big living branches

($P \leq 0.003$) as well. Realized genetic gains were slightly higher for ht9 (10.3% for the intermediate, 10.7% for the elite) than for dbh9 (8.6% for the intermediate, 9.2% for the elite). For vol9, realized gains were 24.7% for the intermediate and 26.5% for the elite.

Significant differences were found between the elite and the intermediate seedlots for dbh9 and vol9 ($P < 0.05$), but not for ht9 ($P = 0.32$). The reason for the elite seedlot not outperforming the intermediate seedlot in height growth is not straightforward. However, competition effect and its interaction with seedlots might have played a role. The elite and intermediate were selected and classified based on their performance in the Grays Harbor first-generation progeny test. Due to the tight spacing (6×6 ft) used in the progeny test, we would expect crown closure and strong inter-tree competition at the time of final measurement (age-10). Hence, the elite seedlot may be a collection of families characterized with high competition ability, with highest gains at narrow spacing. Its superiority over the intermediate seedlot might not be evident prior to onset of strong inter-tree competition such as the current growth and spacing settings (10×10 ft) in the GGTIV.

Planting spacing had significant or marginally significant effects on all traits except for nbi9. The trees planted at the wide spacings (15×15 ft and 10×10 feet) were on average 8% fatter than those from the plots of narrow spacing (7×7 ft), while the trees planted at the narrow spacings (7×7 ft and 10×10 ft) were on average 5% taller than those from the plots of wide spacing (15×15 ft). Spacing did not exhibit a significant impact on tree survival ($P = 0.20$), indicating that tree survival was unlikely related to the among-tree competition at this age. In fact, survival rate at 7×7 ft spacing (86%) was higher than at 10×10 ft (81%) and 15×15 ft (80%) spacings. Low stand density might have created harsher environmental conditions (especially weed competition) before crown closure.

Differences between the two levels of vegetation control were insignificant for all growth traits but significant for acw9 ($P = 0.08$), cbh9 ($P = 0.003$), bdb9 ($P = 0.02$), and surv9 ($P = 0.03$), with the complete control having larger crown width, lower crown base height, larger living branches, and higher survival rate. The Grays Harbor area receives rainfall through most of the year, so periods of summer drought are shorter than in some parts of the Douglas-fir region. We would expect larger gains from complete weed control in areas subject to more severe summer droughts.

Realized gains varied greatly among full-sib families within each improved seedlot for all the traits studied. It is also obvious that within-seedlot variation was much larger than among-seedlot variation. The highest realized gains for ht9, dbh9, and vol9 for a full-sib cross were 19.9%, 20.3%, and 62.3%, respectively.

The overall predicted gains were quite comparable to (e.g., height) or a bit higher than (e.g., diameter and volume) the realized gains. The average realized gains (elite + intermediate) were 10.5% for ht9, 8.9% for dbh9, and 25.7% for vol9. The corresponding average predicted gains from the progeny trials were 11.9% for ht10, 12.1% for dbh10, and 32.5% for vol10 (Figure 8). However, it is evident that the degrees of closeness of the linear relationship between the two types of gains at the family level were relatively low ($r = 0.09\sim 0.28$). This is different from the three previous publications on Douglas-fir genetic gain trials. Many factors may have contributed to this, such as the small number of tested families (a truncated population), strong site \times family interaction, different measurement ages, and existence of seedlot \times silvicultural treatment.

Acknowledgments

Rayonier Forest Resources (RFR) and Quinalt Indian Nation (QIN) developed the Grays Harbor breeding population on which this trial was based. Mike Bordelon and Jess Daniels were early supporters of establishing realized gain trials in the PNW. The full-sib crosses were made by RFR (coordinated by Jessica Josephs), while the QIN (coordinated by Jim Hargrove) helped collect the unimproved seed. These trials were established through the collaboration of the SMC, NWTIC, and the USDA Forest Service PNW Research Station. Green Diamond Resource Company, Port Blakely Tree Farms, QIN, RFR, Washington Department of Natural Resources, and Weyerhaeuser Company provided the test sites. Ron Rhatigan and his field crew (OSU) measured three sites, while Williams Forestry measured the remaining three at age-7. Bob Gonyea and Bert Hesselberg (SMC) helped audit measurements on three sites, monitored the sites from the time of establishment, and provided maintenance as needed. Age-9 data were collected by the SMC field crew. Data management was done by Randy Collier (SMC) and Denise Cooper and Lauren Magalska (NWTIC).

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INSET 5: STRATEGIC PLANNING FOR SECOND-GENERATION DOUGLAS-FIR AND WESTERN HEMLOCK REALIZED GENETIC GAIN TRIALS

Terrance Ye and Keith Jayawickrama

Realized gain trials are among the more expensive tree improvement trials because of (1) plots large enough to measure through rotation and (2) the long duration of the trial. NWTIC cooperators have been supportive of such trials since 1992 and are interested investing in new trials for Douglas-fir and for western hemlock as well. One cost-saving measure would be to limit our goal to validate realized gains for the best selections. For this purpose, establishing elite selections at a single operational spacing would be adequate, with the caveat that we would not be able to get further information on the genetic level \times spacing interaction observed in the Molalla Gain trial.

It is also very important to design these trials with the right statistical power so that we have confidence in being able to answer the questions we ask. For example, what are the optimal number of sites and replicates within sites? They have been addressed a couple of times in the literature. Using the age-8 Douglas-fir in the Molalla Realized Genetic gain trials, St. Clair et al. (2004) concluded that to detect significant differences between the elite and woodsrun lots, 20 to 40 reps would be needed for HT, and 30 to 50 reps for DBH. Using age-5 data from black spruce realized gain trials, Weng (2011) concluded that to detect 5% to 10% gains at a significance level of 0.05 with a predetermined power of 0.80, four sites with five to ten blocks per site, or four to six sites with six blocks per site would be needed.

Potential limitations of these conclusions are that (1) both studies were based on early height or DBH growth (age-8 and age-5); and (2) the deterministic method used may be oversimplified, since the data from thousands of trees (16,000 in the MGT) and many plots go through an ANOVA step and a major information bottleneck to just four to six variance components. Then it is assumed that variance components are the same, regardless of changes in sites and reps (which is rarely true), and that various combinations of numbers of sites and reps are tested.

We therefore used a new, computer-intensive, stochastic approach, *bootstrap-ping stratified sampling with replacement*, based on age-20 VOL/acre (as well as plot-mean growth). This approach has very little information bottleneck. We then examined the probability of detecting significant differences between the top five crosses in the elite and woodsrun through 1,500 repeated runs (see Figures 12-14), assuming that the relative performance of the elite crosses vs. unimproved populations in the future 2nd-cycle gain trials is similar to that found in age-20 MGT. The effect of increasing mortality within the plots was also modeled, using the methodology shown in Figure 15.

How many sites and reps within sites are needed?

For per-acre volume or plot-mean height, six sites with four reps / site are required to detect statistically significant differences between the improved and the unimproved populations at 95% confidence level. Figures 13 and 14 for plot-mean volume, eight sites with five reps / site or seven sites with seven reps / site are required for the same. Fewer sites or reps are required if higher realized gains are to be achieved in the future gain trials.

How does within-plot survival rate affect the accuracy of plot-mean estimation?

We noted that the survival rate in the trial dropped with the increase of age, from: **91%** at age-8 → **88%** at age-15 → **85%** at age-20/21. Using the Maximum Absolute Error (*MaxAE*) of the gain estimate as a criterion, we found that mean *MaxAE* increased gradually with the decrease of survival rate, with no obvious cut points for determining optimal survival rate within plot (Figure 16). One way to set up the cut points is to ensure that mean *MaxAE* is smaller than the absolute gain of the improved populations (i.e., 33.6 for HT, 3.8 for DBH, and 24.2 for VOL). This is to make sure that the differences in plot means caused by mortality will not change the order of the improved vs. the unimproved treatments. With this criterion, the minimum survival rate can be determined as **68%** for **HT**, and **84%** for **DBH** and **VOL**. Note that the use of *MaxAE* here is very conservative. It tracks the most extreme plot, whose mean deviates the most from the true value. Thus, we propose it more reasonable to take an extra 10% to 20% deduction from the above percentages, giving tolerance limits of **54% to 61%** for **HT**, and **67% to 76%** for **DBH** and **VOL**.

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TRAINING, TECHNICAL UPDATES, RESEARCH PROJECTS

Mindful of the need to prepare for retirements and promotions of current representatives to the NWTIC, and the lack of forest tree improvement training provided to undergraduates from West Coast forestry programs, NWTIC organized a two-day tree improvement short course in May 2014 at the BLM's Horning Seed Orchard (Inset 6). This was well attended by co-operator representatives. Our thanks to the

presenters who shared their expertise, to the BLM (George McFadden, Jeannette Griese, Mike Crawford) for providing excellent facilities and support, and to Port Blakely Tree Farms for providing several tour stops. We had excellent weather on both days, and the unique opportunity of seeing many aspects of PNW tree improvement (orchards for multiple conifer species, greenhouses, progeny tests

of different ages, and a realized genetic gain trial) within a few miles of each other—plus a view of an 11,200-ft mountain (Mount Hood) as a backdrop!

In August 2015, we were happy to host the contact meeting of the NCSU Tree Improvement Program, including the co-op director and Keith's mentor Steve McKeand. We more or less repeated the May 2014 tour of sites at BLM Horning plus Port Blakely, followed by a trip west to the Greenwood Resources (GWR) poplar breeding station in Westport and to Hampton Tree Farms for a look at Pacific Coast forestry. The third day was spent on a visit to Mount St. Helens learning about forest recovery and replanting after the 1980. The visit culminated with a visit to Wind River Experimental Forest, where Brad St. Clair led discussion on the oldest forest genetics trial on the West Coast, and Jeff DeBell walked us through the Wind River Arboretum, where so many introduced species failed: both these plantings had profound impacts on forest geneticists and foresters.

References

NWTIC staff were involved in the following peer-reviewed publications, which appeared during this period:

Lowell, E.C., Maguire, D.A. Briggs, D.G., Turnblom, E.C., Jayawickrama, K.J.S. and Bryce, J. 2014. Effects of Silviculture and Genetics on Branch/Knot Attributes of Coastal Pacific Northwest Douglas-Fir and Implications for Wood Quality—A Synthesis. *Forests* 2014, 5, 1717-1736; doi: 10.3390/f5071717.

Ye, T.Z. and Jayawickrama, K.J.S. 2014. Geographic variation and local growth superiority for coastal Douglas-fir – rotation-age growth performance in a Douglas-fir provenance test. *Silvae Genetica* 59(1): 29-39.

Geleynse, S., Alvarez-Vasco, C., Garcia, K., Jayawickrama, K., Trappe, M. and Zhang, X. 2014. A Multi-Level Analysis Approach to Measuring Variations in Biomass Recalcitrance of Douglas fir Tree Samples. *BioEnergy Research* DOI:10.1007/s12155-014-9483-z.

Urhan, O., Kolpak, S.E., Jayawickrama, K.J.S., Howe, G.T. 2014. Early genetic selection for wood stiffness in juvenile Douglas-fir and western hemlock *Forest Ecology and Management* 320: 104-117.

Jayawickrama K.J.S., L.K. Miller and D.W. Cress 2013. Coastal Douglas-Fir Controlled Crossing Guidelines. *Tree Planters Notes* 56(1): 60-73.

Ye, T.Z. and Jayawickrama, K.J.S. 2012. Early Selection for Improving Volume Growth in Coastal Douglas-fir Breeding Programs. *Silvae Genetica* 61(4-5), 186-198. Abstracts of that work are shown in Insets 7-8.

Over the last couple of years, NWTIC has explored making use of an Oregon-wide combined analysis to investigate Genotype × Environment interaction and refine breeding zones. The full dataset available has age-7 data from 71 sites and eight 2nd-cycle programs totaling 217,351 trees; age-10/12 data are available from most of those trees as well. The strength of the dataset is its size and extent; its weakness is that connectivity is only partial. This work is ongoing.

Keith is working with one of the College of Forestry's more recent faculty, forest economist Tammi Cushing, to investigate the eco-

nomics of forest tree improvement for coastal Douglas-fir and western hemlock. Tammi's proposal is detailed in Inset 9.

ASSOCIATED RESEARCH PROJECTS

The Northwest Advanced Renewables Alliance (NARA) project on renewable production of aviation fuel from wood in PNW states, is nearing its end. Through this project a genomic-selection pilot study with 26 third-cycle crosses was planted near Elkton, Oregon; seedlings were grown by Plum Creek and the site provided by Roseburg Forest Products.

An even larger accomplishment was, in collaboration with Glenn Howe, having a Douglas-fir genotyping array with 55,000 Single Nucleotide Polymorphisms built and getting 1,920 samples collected and genotyped. Preliminary results of this study are shown in Inset 10. The BLM Douglas-fir Drought Hardiness Study mentioned earlier is described in Inset 11.

INSET 6: AGENDA FOR 2014 NWTIC TREE IMPROVEMENT SHORT COURSE

Date: May 12-13, 2014 Time: 9:00 AM

Location: BLM Horning Seed Orchard, 27004 Sheckley Road, Colton, OR 97017

<i>Item</i>	<i>Moderated / Presented by</i>
May 12 Classroom Topics	
Coffee	
Call to order, welcome	Margaret Banks (NWTIC Chair)
Basic overview of forest genetics and tree breeding	Terrance Ye (NWTIC)
Overview of 60 years of PNW Tree Improvement	Keith Jayawickrama
Short break	
Controlled crossing of Douglas-fir	Sara Lipow (Roseburg Resources)
Progeny testing and data collection	Jim Smith (Plum Creek)
NWTIC data management, information resources available to NWTIC members	Lauren Magalska (NWTIC)
Lunch	
Understanding and making use of genetic parameters	T. Ye
Seed orchards of major PNW conifer species	Larry Miller (OD F)
Realized genetic gain estimates	K. Jayawickrama
Short break	
Cost: benefit analysis of tree improvement	Mike Warjone (Port Blakely)
Effective participation in tree improvement cooperatives	M. Banks
Question: Answer session	M. Banks
Adjourn	
May 13 Field Visits	
50 years of operation for Horning seed orchard (lecture room)	Mike Crawford / Jim Fischer (BLM)
Overview of grafting and demonstration of pot grafting, greenhouse	L. Miller
Douglas-fir seed orchard blocks of various ages; Noble fir, western hemlock, western red cedar, sugar pine orchard blocks	M. Crawford / J. Fischer
Lunch at Horning Seed Orchard	
Load up vehicles and drive to Molalla progeny test site	
First-gen Molalla progeny test site (Port Blakely)	M. Warjone / K. Jayawickrama
Molalla Genetic Gain trial test site (Port Blakely)	M. Warjone / K. Jayawickrama
Second-cycle NOCTIC Phase II test site (Port Blakely)	M. Warjone / K. Jayawickrama / Bill Marshall (Cascade Timber)
Adjourn	

**INSET 7: GEOGRAPHIC VARIATION AND LOCAL GROWTH SUPERIORITY
FOR COASTAL DOUGLAS-FIR: ROTATION-AGE GROWTH PERFORMANCE IN A
DOUGLAS-FIR PROVENANCE TEST (PUBLISHED IN *SILVAE GENETICA*)**

Terrance Z. Ye and Keith J. S. Jayawickrama

Abstract

Rotation-age growth performance of 16 provenances and local growth superiority were assessed from a rotation-age reciprocal coastal Douglas-fir [*Pseudotsuga menziesii* var. *menziesii* (Mirb.) Franco] provenance test established in the Pacific Northwest of America. Provenance differences for total volume per plot were highly significant. Due to the significant provenance \times site interaction effect, the best provenances varied across planting sites in terms of rotation-age volume growth. Local provenance trees exhibited superior volume growth at two of the six planting sites. At the remaining four sites, local provenances performed equally well as average non-local provenances. At the three low-elevation (< 1500 ft) sites, low-elevation provenances performed significantly better than high-elevation provenances. By contrast, high- and low-elevation provenances had similar growth at the two high-elevation (> 2640 ft) sites. Southern provenances generally grew faster than northern provenances at the Oregon sites, while northern provenances performed better than southern provenances at the sites in British Columbia.

Regression analyses showed that although local growth superiority increased with the geographic distance between provenance's origin and the test site in general ($r = 0.47$, $P < 0.001$), it only became obvious when the geographic distance was larger than 270 miles 435 km in latitude or 1200 ft 370 m in elevation. Significant spatial autocorrelation was found via Mantel test, and geographically or climatically closely located provenances tended to have similar rotation-age volume growth.

The results suggested that breeding zones larger than the current second-cycle zones would lead to little loss of rotation-age total volume for coastal Douglas-fir in this region.

INSET 8: EFFECTS OF SILVICULTURE AND GENETICS ON BRANCH/KNOT ATTRIBUTES OF COASTAL PACIFIC NORTHWEST DOUGLAS-FIR AND IMPLICATIONS FOR WOOD QUALITY – A SYNTHESIS (PUBLISHED IN FORESTS)

*Eini C. Lowell, Douglas A. Maguire, David G. Briggs, Eric C. Turnblom,
Keith J. S. Jayawickrama, Jed Bryce*

Abstract:

Douglas-fir is the most commercially important timber species in the U.S. Pacific Northwest due to its ecological prevalence and its superior wood attributes, especially strength and stiffness properties that make it highly prized for structural applications. Its economic significance has led to extensive establishment and management of plantations over the last few decades. Cultural treatments and genetic improvement designed to increase production of utilizable wood volume also impact tree morphology and wood properties. Many of these impacts are mediated by crown development, particularly the amount and distribution of foliage and size and geometry of branches. Natural selection for branch architecture that optimizes reproductive fitness may not necessarily be optimal for stem volume growth rate or for wood properties controlling the quality of manufactured solid wood products. Furthermore, Douglas-fir does not self-prune within the rotation lengths currently practiced. This paper synthesizes extensive Douglas-fir research in the Pacific Northwest addressing (1) the effects of silviculture and genetics on branch structure and associated consequences for wood quality and the product value chain and (2) methods to measure, monitor, modify, and model branch attributes to assist managers in selecting appropriate silvicultural techniques to achieve wood quality objectives and improve the value of their Douglas-fir resource.

Keywords: Douglas-fir; wood quality; silviculture; branch; genetics

INSET 9: PROPOSAL—AN EXAMINATION OF THE ECONOMICS RELATED TO TREE IMPROVEMENT PROGRAMS FOR DOUGLAS-FIR/WESTERN HEMLOCK AND THE ECONOMICS OF USING GENETICALLY IMPROVED STOCK BY FAMILY FOREST OWNERS.

Tamara L. Cushing, Starker Chair of Private and Family Forestry

I propose a two-pronged approach. The first approach would be to revisit the 1981 Forest Service publication, PSW-156, *West Coast Tree Improvement Programs: A Break-even, Cost-benefit Analysis*, by Ledig and Porterfield. The second would be to examine the economics of a family forest owner using genetically improved planting stock.

Part 1:

This part would focus on an update of Ledig and Porterfield (1981)). The original publication examined breeding programs for ponderosa pine and Douglas-fir. The analysis was based on a set rotation (expected rotations in the late 70s and early 80s, as well as pricing structures common at that time). Since its publication, there have been numerous analyses of the value of genetic improvements in the southern United States (typically focused on loblolly pine). Cabbage et al. (2000) evaluated the economics of fusiform rust protection research, which included genetic selection for fusiform rust resistance. Using a benefit-cost ratio, Cabbage et al. (2000) demonstrate whether fusiform rust programs were beneficial, using both fixed-rotation ages and solving for the optimal financial rotation age.

In the southeastern United States, gains from genetic improvement come from more than one direction. Gains may be from improved seedling survival, resulting in reduction in planting density (and thus reduced upfront costs per seedling), improvement in quality of stems (higher percentage of sawtimber grade products at harvests), reduction in susceptibility to pathogens, reduction in defects (less forking), increase in total volume, and a reduction in age of first commercial thinning and final harvest. Cumbie et al. (2012) examined the improvement in sawtimber potential due to genetic improvements. This study found an increase in the potential amount of sawtimber when measured at an early age for the traits that are desirable for sawtimber.

Most of the work in the South has looked at the genetic gains from improvement, with little examination of the economics. Even less attention has been paid to the impact on landowners of genetically improved material. McKeand et al. (2006) calculated the economics of forest landowners planting improved stock. This study used a range of improvement and site productivity levels and calculated the increase

in land expectation value (LEV). The resulting calculation illustrated the maximum increase in cost a landowner should be willing to pay for an improved seedling and still improve the net present value of the stand.

Revisiting the Ledig and Porterfield (1981) analysis should include the following changes and updates:

1. Replace ponderosa pine with western hemlock
2. Allow the rotation age to vary (this will allow users to see the impact of a change in rotation age on the economics)
3. Explore limiting the thinnings to what would reasonably be expected in a rotation: no thinnings if rotation is below a certain age, or show what happens when a thinning occurs below age 40 with certain economic conditions, and even pushing the age of a commercial thinning as low as realistically possible. Current practice for many landowners seems to be to plant many seedlings, thin pre-commercially (costing money and reducing the return), then do a commercial thin later. It would be good to look at the economics of planting fewer seedlings (assuming they have better survival than non-improved stock), reducing the need for the precommercial thin (which will improve the return), and commercially thinning earlier (since the volume gain should allow for that).
4. Vary log prices depending on whether logs are obtained from a thinning or final harvest. This will mainly be due to differences in logging and hauling costs. After the first thin, there is a reduction in harvesting costs that needs to be recognized. This will be put in with some default values and allow the user to alter as needed.
5. Use multiple site indices with volumes varying by site, which would also affect log prices through different log grades. The interactive spreadsheet will allow users to input site index (within reason, since volumes for those will have to be embedded in a table).
6. Allow genetic gains to vary, e.g., from 5% to 30% volume gain at rotation. Gains at commercial thinning age are believed to be higher, so we could use a range of 10% to 40% gain.
7. Perhaps allow input of modest improvements in survival. For example, if wood-srun has 80% survival, improved might have 85% or 90% survival. Thus, fewer trees could be planted.
8. Allow breeding and testing costs expressed as \$ per acre to vary (e.g., from \$0.5 to \$3/acre).
9. Allow seed production costs expressed as \$ per pound to vary (e.g., from \$250

to \$1000 for Douglas-fir, \$500 to \$2000 for western hemlock). Note that the number of seedlings / lb. will be a lot higher for western hemlock.

10. The analysis would then be available online for cooperators, behind a login. There would be flexibility to the inputs, but using a set methods of analysis. This is to protect the integrity of the analysis and avoid input of unreasonable values or modification of the methodology.
11. Use a benefit-cost ratio as well as a break-even analysis, as did Ledig and Porterfield (1981). The break-even analysis will allow us to specify what minimum price or volume would be needed.
12. Conduct a sensitivity analysis on inputs such as discount rate (online would allow the user to input a discount rate).

Published sources or contacts would be used for log prices, reforestation costs, and logging and transportation costs. I would need information related to any seed production costs (basically, any cost prior to actually growing the tree) and on expected volume gain from tree improvement practitioners.

Part 2:

This would analyze the benefits of using genetically improved planting stock for private landowners. Here I propose to use the information on volume gains and log improvement in a cash flow for private landowners. I would like to show changes to management (fewer trees planted per acre or earlier commercial harvests), plus any gain at final harvest from planting improved seedlings. I would not need any additional information for this other than the cost of seedlings to a private landowner (by private, I mean family owner). My intention here is to illustrate when a landowner should invest the extra money in genetically improved stock.

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INSET 10: A HIGH-DENSITY SINGLE NUCLEOTIDE POLYMORPHIC GENOTYPING ARRAY FOR DOUGLAS-FIR

Glenn Howe and Keith Jayawickrama, College of Forestry, Oregon State University

Abstract

We used the Affymetrix Axiom genotyping array to test 55,776 potential single nucleotide polymorphic (SNP) markers in Douglas-fir. Because the SNPs were derived from transcriptome sequence, the array targets SNPs in the expressed genes in the Douglas-fir genome. We tested the array on 1,420 Douglas-fir trees, and found that ~20K SNPs could be reliably genotyped. For 19,822 SNPs that had a call frequency greater than 85%, the median call rate was 99.3%, and the median minor allele frequency was 0.215. This array will serve as an excellent foundation for testing genomic selection in Douglas-fir breeding programs.

Introduction

Genomic selection may help tree breeding by allowing breeders to shorten the breeding cycle, reduce the costs of progeny testing, increase heritabilities, and select for mature traits such as wood properties at the seedling stage. The main goal of this project was to develop a large number of single nucleotide polymorphic (SNP) markers for Douglas-fir. Later, these markers will be used to test genomic selection in advanced generation breeding programs of Douglas-fir.

Having enough markers is critical to the success of genomic selection. The number of markers needed for genomic selection varies based on the biology of the species, including the genome length (cM), number of QTL controlling the trait, and trait heritability. It also depends on the effective size of the breeding population (N_e), which is about equal to the number of parents used in the breeding cycle. In Douglas-fir, 2,000 to 40,000 SNPs may be needed for effective population sizes of 25 to 100 ([Grattapaglia and Resende 2011](#); [Iwata et al. 2011](#); [Resende et al. 2012a](#); [Resende et al. 2012b](#)). Because typical advanced generation breeding programs of Douglas have effective population sizes closer to 30, the number of SNPs needed is expected to be about 5,000 to 20,000, depending on the factors described above and the distribution of the markers in the genome ([reviewed in Howe et al. 2013](#)).

We previously used transcriptome sequencing to identify 278,979 potential SNPs in ~20,000 Douglas-fir genes ([Howe et al. 2013](#)). We then tested a subset of these SNPs ($n=8067$) using an Illumina Infinium genotyping array, resulting in 5847 successful SNPs (i.e., polymorphic SNPs that can be reliably measured).

Although the Infinium array is highly robust, it is also expensive. Although costs have been decreasing, the cost at the time of purchase was \$122 per tree. Other, less-expensive genotyping arrays have become available more recently, most notably, the Axiom array manufactured by Affymetrix. Although the costs of this array varies widely based on the number of SNPs assayed and the number of trees genotyped, the entry point was about \$75 when we began this this project. The objectives of this work were to (1) increase the number of SNPs that can be assayed and (2) test the Affymetrix Axiom array, a lower-cost genotyping platform.

Methods

SNP resources

The potential SNPs chosen for the Axiom array were derived from transcriptome sequencing projects described by [Muller et al. \(2012\)](#) and [Howe et al. \(2013\)](#). We added the Muller SNPs to increase the number of genes that could be assayed, thereby increasing genome coverage for genomic selection. The Douglas-fir transcriptome (454 sequence data) and SNPs identified by [Muller et al. \(2012\)](#) were downloaded by Stephanie Guida (National Center for Genome Resources). These data contain ~170,000 putative transcripts and ~188,000 SNPs. We used this information to identify “new genes”—that is, genes that were absent from our transcriptome assembly—and then added the corresponding SNPs to our SNP database. To identify these new genes, NCGR compared the Muller transcripts to the Howe transcriptome assembly using BLAST and an e-value cutoff of 1e-10. Excluding singletons, 63,286 transcripts had no BLAST hits, and were classified as new genes. [Muller et al. \(2012\)](#) used three SNP detection programs (GSMapper, ssahaSNP, and bwa SAMtools) to identify 40,206 biallelic SNPs in the 63,286 unique transcripts described above. Of these 40,206 SNPs, 16,859 were detected by two or three SNP detection programs, and were the SNPs considered for inclusion on the genotyping array. These were added to our existing SNP database of 278,979 SNPs [Howe et al. \(2013\)](#).

Axiom array design

Two steps were used to filter the combined SNP database described above. First, we removed SNPs that were highly repeated in the Douglas-fir genome. This was done by comparing the SNP sequences to a draft of the Douglas-fir genome (v0.5) provided by Jill Wegrzyn (University of Connecticut). Second, we removed SNPs that had flanking sequences that did not meet minimum Affymetrix criteria for inclusion on the array. After filtering, we submitted 111,648 SNPs in 21,659 genes to Affymetrix for the final array design: 108,299 SNPs in 19,336 genes

came from the Howe SNP database, whereas 3,349 SNPs in 2,323 genes came from the Muller SNP database.

Because 111,648 SNPs exceeds the capacity of a 50K SNP array, we prioritized these SNPs for the final design phase. We ranked the SNPs sent to Affymetrix using various measures of SNP quality, giving high ranks to target SNPs that were successfully genotyped using the Infinium array, most likely to be true SNPs, and least likely to have other SNPs in their flanking sequences [Howe et al. \(2013\)](#). Affymetrix used our rankings and their proprietary “p-convert” values to choose the final set of 55,766 SNPs representing 21,639 genes that were included on the array. The p-convert value reflects the probability that a SNP will be assayed reliably using the Axiom array system. The array also included a set of non-polymorphic “control” probes that were used to judge array performance. Rich Cronn and Sanjuro Jogdeo developed these polymorphic sequences by identifying sequences that were identical between our Douglas-fir transcriptome and the loblolly pine genome. During processing, the control probes were used to calculate a quality control metric (DQC) that was used to identify and remove poor quality samples.

Results

We measured 55,766 potential SNPs on 1,536 trees using the Axiom array. Of the 1,536 DNA samples submitted to GeneSeek, 116 failed to meet Affymetrix quality control specifications, resulting in 1,420 trees for which we obtained SNP genotypes. Table 1 shows the number of SNPs falling into six SNP quality categories: PolyHighResolution, NoMinorHom, OTV, MonoHighRes, and CallRateBelowThreshold. The call rate (CR) is an important measure of SNP quality. CR is the proportion of trees that can be assigned a reliable genotype (called) relative to the total number of trees genotyped ($n = 1420$). The Affymetrix default threshold for call rate (CR) is 97%. That is, to be classified in the PolyHighResolution group, a SNP must have been successfully genotyped in 97% of the trees tested. In Table 1, we also provide results for SNPs that meet a CR threshold of 85%.

Discussion

SNPs classified as polymorphic and high-resolution (PolyHighResolution) are the ones that should work best for genomic selection. Using the default Affymetrix CR of 97%, 14,959 SNPs fell into this category (Table 1). However, for genomic selection, a CR of 85% is probably more than sufficient ([Rutkoski et al. 2013](#)). Therefore, we also calculated statistics using this lower CR threshold. In this case,

19,822 SNPS were classified as PolyHighResolution. For the SNPs that had a call frequency greater than 85%, the median call rate was 99.3% and the median minor allele frequency was 0.215, which is very encouraging for using these SNPs in genomic selection.

Two other categories of SNPs (NoMinorHom and MonoHighResolution) probably contain many true SNPs that can be measured reliably. However, their minor alleles may be too low in frequency to make them particularly valuable for genomic selection, at least in the populations we tested. Nonetheless, if we count all three categories of “converted” SNPs (PolyHighResolution, NoMinorHom, and MonoHighResolution), we have nearly 39,000 SNPs that could contribute to the success of genomic selection. On the other hand, many of these may not be of sufficient quality, and we may need to exclude other SNPs in the PolyHighResolution category because of other issues, such as deviations from Hardy-Weinberg equilibrium. Balancing these considerations, we conclude that we have between 20,000 and 30,000 SNPs that will allow us to practice genomic selection in Douglas-fir. This is probably more SNPs than are needed to practice effective genomic selection in NWTIC-type breeding programs.

Remaining Work

A further batch of 384 trees remain to be genotyped. Following that, the work of matching genotypic data with existing phenotypic data and testing the concept of genomic selection in Douglas-fir can begin.

Acknowledgements

We thank Stephanie Guida and Callum Bell for helping with the analyses of the SNPs described by [Muller et al. \(2012\)](#); Rich Cronn and Sanjuro Jogdeo for providing the non-polymorphic sequences used as control probes; Jill Wegrzyn for providing a draft sequence of the Douglas-fir genome; Scott Kolpak for general analytical help; Matt Trappe, Jim Smith, Bill Marshall and Sara Lipow for sample collection; Matt Trappe and Valerie Hipkins for the DNA isolations; and GeneSeek and Affymetrix for building the genotyping array and genotyping the samples. Funding was provided by the Northwest Advanced Renewables Alliance, members of the PNWTIRC, and the National Science Foundation Center for Advanced Forestry Systems.

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Table 9. We have about 20K SNPs available to practice genomic selection in Douglas-fir. This table shows the number of SNPs that were classified into six SNP quality groups (PolyHighResolution, NoMinorHom, OTV, MonoHighRes, and CallRateBelowThreshold) using an Affymetrix Axiom genotyping array. For each SNP, the call rate (CR) is the proportion of trees that were assigned a genotype (called) relative to the total number of trees tested (n = 1420).

Classification	No. of SNPs with call rate (CR) of:		Affymetrix abbreviation: description
	97%	85%	
Polymorphic high resolution	14959	19822	PolyHighResolution: These are the very best SNPs because they vary among trees (are polymorphic) and can be measured very accurately (are high-resolution). These SNPs pass all thresholds (CR.cut \geq 97; FLD.cut \geq 3.6; HetSO.cut \geq -0.1; HomRO2.cut \geq 0.3; HomRO3.cut \geq 0.9; nMinorAllele.cut \geq 2).
No minor homozygote	6140	6140	NoMinorHom: Minor alleles were found, but no minor homozygotes. Many of these are probably true SNPs, but the MAF may be too low to be valuable for genomic selection.
Monomorphic high resolution	12807	12814	MonoHighResolution: These SNPs are high-resolution, but they did not vary among trees (not polymorphic). They may not be true SNPs or the minor allele frequency may be very low, and not valuable for genomic selection.
Converted	33906	38776	This number (PolyHighResolution + NoMinorHom + MonoHighResolution) is a good indication of the success of the SNP genotyping platform itself.
Off-target variant	423	423	OTV: OTVs usually indicate that the DNA hybridized poorly to the genotyping array, perhaps because of other unknown SNPs near the target SNP. It may be possible to measure these SNPs after using the OTV_Caller program to re-call the genotypes.
Other	16493	16493	Other: These SNPs did not pass various quality thresholds for various reasons.
Call rate below threshold	4944	74	CallRateBelowThreshold: The SNP was below the 97% or 80% CR threshold, but the SNP passed all other thresholds except that the number of minor alleles was ignored. For genomic selection, a CR of 85% is probably more than sufficient (Rutkoski et al. 2013).
Not converted	21860	16990	OTV + Other + CallRateBelowThreshold
Total	55766	55776	Total number of SNPs attempted on the "50K" genotyping array.

INSET 11: SCREENING ELITE DOUGLAS-FIR FAMILIES FOR TOLERANCE TO DROUGHT

Keith J. S. Jayawickrama and Mike Crawford

Justification

Several members of the scientific forestry community propose that climates will change sufficiently in the 21st century to cause a mismatch of environmental conditions at planting sites in western Oregon with the seed sources developed for those sites. One change proposed is that the climate will become hotter and drier, or summer droughts will grow longer, compared to the baseline (from 1960-1990). The Bureau of Land Management (BLM) made an enormous investment in testing thousands of Douglas-fir (DF) families in western Oregon, establishing hundreds of test sites. The bureau also established three first-generation DF seed orchards between the 1960s and mid-1990s, and more recently developed smaller blocks of consolidated, higher-gain 1.5-generation and 2nd-cycle orchards at two of those sites. These consolidated orchards will soon form the reforestation basis for the BLM in western Oregon. There is interest within the BLM to supplement existing data for the elite families from first-generation and 2nd-cycle field tests (growth, stem form, and survival to age-12 or age-15) with specific information on ability to grow in hot, droughty conditions.

Objectives

Screen 363 first-generation selections from the consolidated orchards, supplemented by 20 families provided by the Washington DNR, for survival and growth in hot, droughty conditions. These selections were made based on performance in both first-generation tests and, where available, 2nd-cycle tests. Emphasis will be on low- and medium-elevation orchards (up to 2,000 or 3,000 ft, depending on the zone) serving the Medford, Roseburg, Eugene and Salem Districts. It is assumed that (1) drought tolerance will be less critical for orchards serving the Oregon coast or high elevations, and (2) testing will be less critical in the pine species used by the BLM, given their greater tolerance of drought.

Methods

- Separate plantings were established in March 2015 on three locations, planting a total of up to 60 seedlings per family, plus 120 seedlings of the woods-run controls. We used single-tree plots in a randomized, replicated design for a total of 18,693 progeny and control trees planted on a 8 × 8 ft spacing. In

addition to a planting at BLM's Sprague seed orchard near Merlin, a large site was planted near Glendale on Silver Butte Timber Co., and a smaller site near Shady Cove on Plum Creek.

- To the extent possible, sites were prepared to reduce variation (subsoiling or disking) and allow for good root development. The Plum Creek site had a lot of subsurface rock limiting subsoiling.
- 60 cubic inch container stock, grown at the BLM's greenhouse at Sprague over two growing seasons, were used.
- All three sites have fences to exclude deer and elk, and have weather stations.
- Competition from brush and herbaceous vegetation will be controlled with means available: by herbicides on the two cooperator sites, and by weedmats and mowing at Sprague.
- 2015 was a challenging year for reforestation through much of western Oregon, due to prolonged drought and high temperatures. Conditions were especially harsh at the Sprague site, with many days exceeding 100° F. The seedlings at Sprague were irrigated once to help them survive their first year. Survival was close to 90% at the other two sites, and no irrigation was applied.

Significance of study

As seen in Figure 17, the study contains a unique set of high-gain tested Douglas-fir families from throughout western Oregon and a sample from western Washington. No such trial has been established in the cooperative domain in the 60 years since tree improvement was started in the PNW. We anticipate that the trial will yield many valuable conclusions over the years, both for the BLM and other members of NWTIC. With the 8-ft spacing used and the slower growth in these southern Oregon test sites, we anticipate that serious inter-tree competition will not begin until at least 10 years after planting. The study has already attracted a PNWTIRC graduate student (Erda Celer), who has begun her master's thesis research using these sites. We give special credit to Jeannette Griese and George McFadden for their vision and for obtaining the resources for this study.

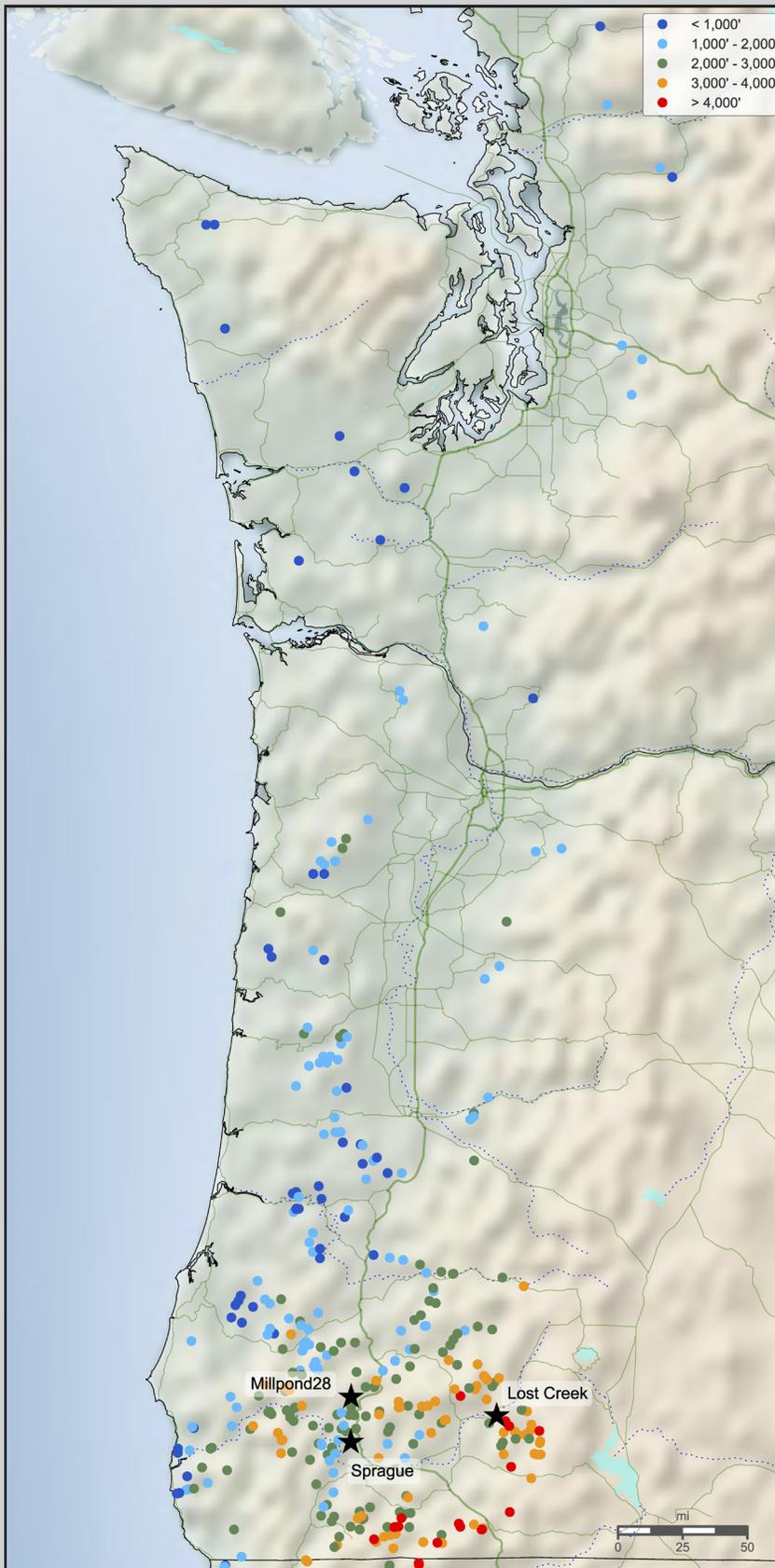


Figure 17: Location of test sites and origin of parents used in the Bureau of Land Management's Douglas-fir Drought Hardiness Study planted in 2015.

THE DEPLOYMENT OF GENETICALLY IMPROVED FOREST TREE SEEDLINGS

NWTIC again attempted to collate the number of coastal Douglas-fir and western hemlock seedlings planted both by members and non-members, and added noble fir and ponderosa pine as well. While some approximations were involved, these numbers are relevant, since there are no other published reports on the number of forest tree seedlings derived from orchard seed planted in in western Oregon and Washington. It appears that about 60.4 million trees originating from tree improvement programs were planted in 2014-15 (coastal DF, hemlock, ponderosa pine, and noble fir), and two NWTIC cooperators are producing enough seed from 2nd cycle orchards to meet their planting needs in their main deployment zones. Many others can meet their planting needs from 1.5-generation grafted orchards. It is also heartening to see planting rise to about 73 million trees in 2015, from a low of just over 50 million in 2011.

The survey indicated that annual planting of hemlock (WA and OR) had increased from 4 million in 2010 to 8.5 million in 2015; 78% of the hemlock planted in 2005 was improved while 93% was improved in 2015. The main driver of this is Swiss needle cast: the SNC cooperative/Oregon Department of Forestry aerial survey estimated 589,000 acres affected in 2015 (the largest figure reported in over 20 years of monitoring), and the USDA Forest

Service / Washington DNR aerial survey indicated 349,704 acres with either moderate or severe SNC symptoms in spring of 2015.

However, it also appears that 12.4 million woodsrun trees were still planted in 2014-15 (same four species), after 35–60 years of work and investment in breeding, testing, and seed orchard development. The year 2014 provided an exceptional cone crop from Douglas-fir seed orchards, 7,000 pounds from orchards in Oregon belonging to six NWTIC members. At 20,000 seedlings per pound, this would be sufficient for 140 million seedlings, perhaps three or four years of reforestation in western Oregon. Crops such as this give hope that the proportion of planting with woodsrun seed will continue to decrease, although, unfortunately, it was followed by a very poor seed year in 2015 (frost in some locations and heavy attack by cone and seed eating insects).

Numbers we can use to compare are the ~25 million coastal Douglas-fir, western hemlock, red cedar and Sitka spruce sown for British Columbia planting programs in 2014 (Forest Genetic Council of British Columbia Annual Report 2013/14) and an estimated average of 843 million tree seedlings planted per year by 31 cooperators in the southeastern United States in the 2011, 2012, and 2013 planting seasons (NCSU Tree Improvement Program Annual Report 2015).

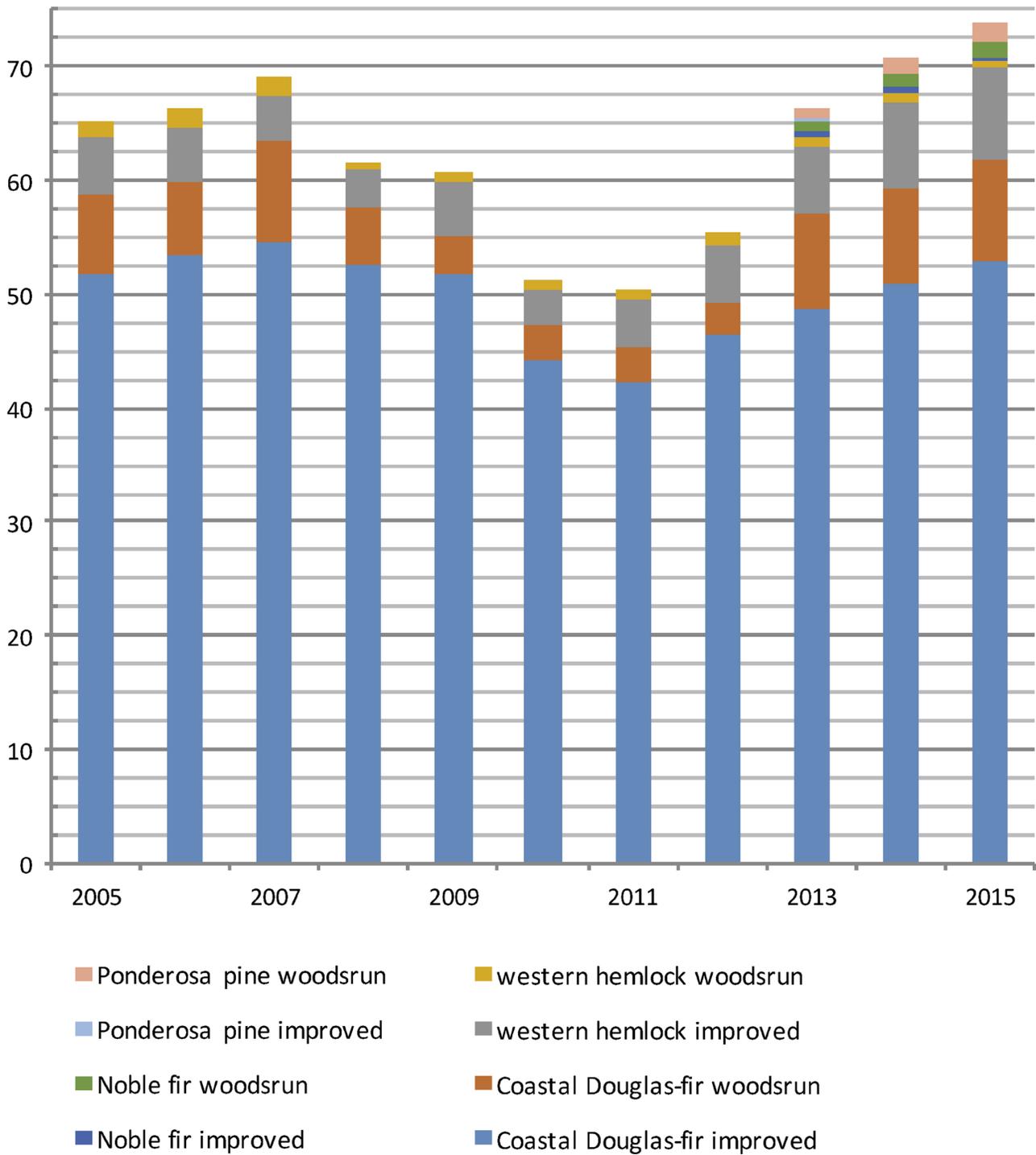


Figure 18: Numbers of trees planted originating from tree improvement programs vs. unimproved trees, by species, in Oregon and Washington west of the Cascades.

NWTIC MEMBERSHIP AND REPRESENTATIVES

The purchase of Longview Timberlands removed one more of the founders of cooperative tree improvement in the region (Longview Fibre was one of four members of the original Vernonia cooperative in 1967, along with Crown Zellerbach and International Paper), leaving just the Oregon Department of Forestry still active in the cooperative. West Fork Timber was purchased by Sierra Pacific Industries in 2015, so the acreage remained within NWTIC. The Lewis and Clark Tree Farm came under the management of GreenWood Resources (GWR) during 2015, with GWR continuing membership in North Coast, HEMTIC, and NWTIC. We also expect to welcome three new members: Indian Hill, Perpetua Forests, and Murphy Timber into NWTIC in 2016, with their participation in MEDTIC.

Retirements during this period included Larry Miller (Oregon Department of Forestry), Lew Howe (Silver Butte), Dave Russell (Roseburg Forest Products), Al Heimgartner and Steve Mitsuyasu (Hancock), and Tim Crowder (TimberWest). Larry Miller played a key role in getting 3rd-cycle tree improvement underway within the NWTIC, including many days collecting and processing pollen and making crosses.

Sadly, Randall Greggs (Green Diamond) passed away on May 11, 2015 after more than a year's battle with cancer. Randall was instrumental in getting the Puget Sound 2nd-cycle Douglas-fir cooperative (the first in Washington) established, and was a strong supporter of NWTIC, including being the first Chair of the Operations Committee after it was relocated to Oregon State University in 2000.

Mike Warjone was NWTIC chair for 2012-13, followed by Margaret Banks for 2013-14, and Bryan Nelson for 2014-15. NWTIC representatives for 2012-15, and the members they represented, are:

Bloedel Timberlands: Roy Bever

Bureau of Land Management: Jeannette Griese / Michael Crawford

Campbell Global: Dave Rumker / Dave Lortz / Dave Hamlin

Cascade Timber Consulting: Bill Marshall

Fruit Growers Supply: Rod Burns

Giustina Land and Timber: Mike Tucker / Cary Hart

Giustina Resources: Paul Wagner

Green Crow Management Services: Harry Bell / Jenny Knoth

Green Diamond Resource Company: Randall Greggs / Eric Schallon / Dan Cress

Hampton Tree Farms: Beth Fitch

Hancock Forest Management: Dean Stuck / Florian Deisenhofer

Lone Rock Timber: Bryan Nelson

Longview Timberlands: Rick Brooker / Dan Cress

Menasha Corporation / Campbell Global: Jim Carr
Miami Corporation: Joe Steere / Luke Bergey
Oregon Department of Forestry: Larry Miller / Don Kaczmarek
Oregon State University College Forests: David Lysne / Brent Klumph
Plum Creek Timberlands: Jim Smith
Pope Resources: Dan Cress / Andrew Wodnik
Port Blakely Tree Farms: Mike Warjone
Quinault Indian Nation: Jim Hargrove
Rayonier Timberlands: Candace Cahill / Josh Sherrill
Rocking C Ranch: Paul Zolezzi
Roseburg Resources: Sara Lipow
SDS Lumber: Aric Lemmon
Sierra Pacific Industries: Keith Greenwood
Silver Butte Timber Company: Lew Howe / Darin McMichael
South Coast Lumber: Marc Halley
Starker Forests: Fred Pfund
Stimson Lumber Company: Margaret Banks
Timber West Forest: Tim Crowder / Bevin Wigmore
Washington Department of Natural Resources: Jeff DeBell
West Fork Timber: Gene McCaul

Liaison Members

Pacific Northwest Tree Improvement Cooperative: Glenn Howe
USFS-PNW Research Station Genetics team: Brad St Clair

Staff

Director: Keith Jayawickrama
Quantitative Geneticist: Terrance Ye
Information Management Specialist: Lauren Magalska¹/ Hao Truong

¹Lauren Magalska left NWTIC in May 2014 to work for DNR, and was replaced as Data Manager in January 2015 by Hao Truong.

NWTIC bid farewell to many representatives during this period, notably:



Larry Miller, Oregon Department of Forestry.



Lew Howe, Silver Butte Timber Company.



Tim Crowder, Timber West.



Randall Greggs, Green Diamond Resource Company.



Second-cycle orchards are now coming online with significant amounts of seed produced. (photo: Sara Lipow)

2014 was a very good year for seed production from Douglas-fir seed orchards. (photos: Mike Crawford)



Establishing a 1.5-generation Noble Fir orchard, (A) Scion collection in Podunk orchard near Estacada. (B) French Butte orchard on Gifford Pinchot National Forest.



The 2014 NWTIC Tree Improvement short course: (A) Classroom session; (B) Grafting demonstration; (C) A large group in a great setting with Mount Hood in background.



NCSU Tree Improvement Program visitors at Wind River Experimental Forest. (A) in Douglas-fir Heredity Study, 100 years after the study was established in 1915; (B) In front of old-growth Douglas-fir tree. (Photo: Steve McKeand)