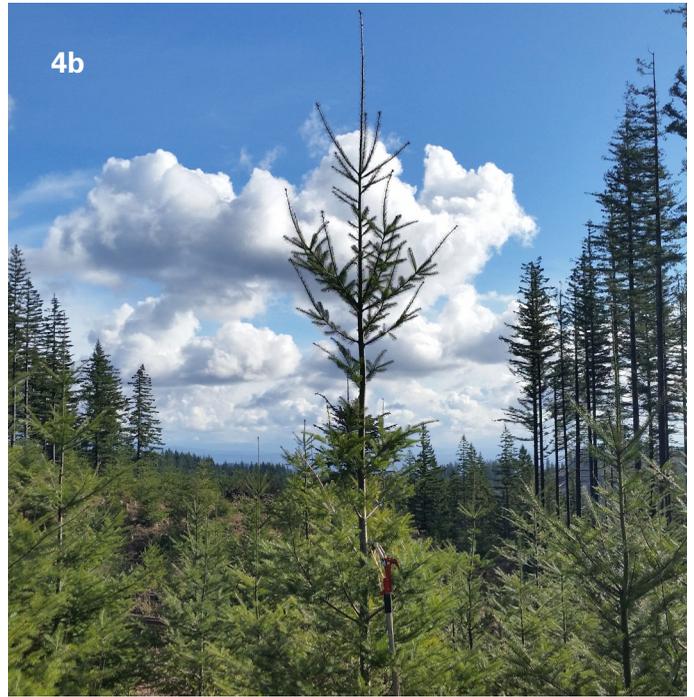




# NORTHWEST TREE IMPROVEMENT COOPERATIVE REPORT

*JANUARY 1, 2016 TO JUNE 30, 2017*





Measurement of Phase 2a of the WACTIC tests and subsequent analysis permitted selecting and grafting trees from Phase 2, the final series from 2nd cycle WA Douglas-fir tests.

4a, b and c. show promising forward selections.

4d. Grafting a WACTIC selection. (photo credits: Florian Deisenhofer and Dan Cress)




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Front Cover. Clockwise: Advancing one breeding cycle in 15 years. Sara Lipow and Keith Jayawickrama with the first seedling planted for 3rd cycle South Central Coast, March 2017; Al England with the first seedling planted for 2nd cycle South Central Coast, February 2002. 2nd-cycle western hemlock gain trial being planted on Hampton's "Rooster" site near Astoria.; 2nd-cycle Douglas fir realized genetic gain trial planted at BLM's Tyrrell seed orchard.

# NORTHWEST TREE IMPROVEMENT COOPERATIVE

*Report January 1, 2016 to June 30, 2017*

Text and photographs by Keith J.S. Jayawickrama, Terrance Ye and Hao Truong  
Layout and formatting by Sandie Arbogast

*June 2017*

## **FOR INFORMATION REGARDING NWTIC CONTACT:**

- Keith J.S. Jayawickrama, Director, NWTIC  
Department of Forest Ecosystems and Society  
College of Forestry, Oregon State University  
321 Richardson Hall  
Corvallis, OR 97331-5752  
Email: keith.jayawickrama@oregonstate.edu

## **MISSION OF 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



*Progeny test sites sometimes produce insights or information quite different from the original purpose. Photo 5a: This 40-year old Tillamook Western Hemlock trial near Neskowin on the Oregon Coast shows the contrast between the large, healthy hemlock trees and the Douglas-fir trees planted adjacent at the same time but severely affected by Swiss Needle Cast; Photo 5b: Jim Hargrove's Grays Harbor trial is an example of a mature, intensively managed western hemlock plantation from an era when planting of this species was uncommon; Photo 5c: Tim Truax at the Miller Flyway site (South Central Coast Phase I) 15 years after planting; Photo 5d: Florian Deisenhofer and Keith Jayawickrama at the Neskowin site (Trask Coast I) 13 years after planting. These photos demonstrates the potential of coastal sites to promote fast growth (but sometimes with poor stem form) in Douglas-fir.*

*Photos 6a, 6b: During the October 2016 annual meeting at the OSU NWREC campus in Aurora, we marked 30 years since NWTIC started operation and 50 years since the start of IFA-Progressive Tree Improvement System. Jim Hargrove and retirees Mike Bordelon, Nancy Mandel and Howard Dew shared some historic insights with the large group of current cooperators representatives present.*



*Photo 7: The Teeples test site from the Molalla cooperative, owned by Port Blakely Tree Farms, was sown in 1969 and is one of the oldest surviving first-generation test sites. It is conveniently located, within an hour from Portland, to demonstrate tree improvement to many visiting groups, such as this group organized by Clackamas County Extension and Clackamas County Small Woodland Owners Association.*



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## DIRECTOR'S FOREWORD

During the 18 months since the last report, NWTIC completed 30 years of continuous operation (with the first meeting being held in September 1986) and we also marked 50 years since the IFA-Progressive Tree Improvement program got underway in 1966. This long-standing investment in tree improvement is a tribute to the staying power and focus of the members: a few such as the Oregon Department of Forestry, Starker Forests and the Bureau of Land Management have stayed involved and active since the late 1960s, while others (such as Hampton, Quinault, Rayonier, Stimson) have stayed active for around 40 years. We marked the dual anniversary at the 2016 NWTIC annual meeting, which had several participants who had also been present at the first NWTIC meeting in 1986.

The various second-cycle- cooperatives have continued to measure test sites and make selections. Crossing for MEDTIC got off to a rapid start in 2016 and 2017. Third-cycle crossing has continued in South Central Coast, North Coast, CASTIC), HEMTIC and the emerging 3rd cycle Washington co-op. Six 3rd-cycle test sites were established by South Central Coast, almost exactly 15 years after their second-cycle tests were established.

Second-generation Douglas-fir and western hemlock realized gain trials were established on nine locations in March 2017. These are simpler trials than the previous Molalla and Grays Harbor trials, with two levels of genetic gain (elite and woodsrun) and one spacing (operational). We also expect the difference in gain between improved and woodsrun to be larger than in the earlier tests.

We are happy to report addition of several new members or additional divisions of existing members: Indian Hill, Perpetua Forests, Murphy Timber Investments, Josephine County, Hood River County Forestry, Fruit Growers Supply (California), Michigan-California Timber Company, and Green Diamond Resource Company (Oregon Operations) into NWTIC over these past 18 months. Weyerhaeuser Company purchased Plum Creek Timberlands, but remained involved in NWTIC as the largest cooperator in MEDTIC. With these additions, NWTIC is privileged to further members' tree improvement interests from Vancouver Island in British Columbia to the northern tip of California, and east to the Hood River area and to Klamath Falls.

Responding to cooperator interest, NWTIC gathered and synthesized information and helped with exploratory meetings on developing browse-non-preferred western red cedar for use by NWTIC members (Inset 1).

## INSET 1: ADVANCING THE GENETIC IMPROVEMENT OF WESTERN RED CEDAR IN OREGON AND WASHINGTON

### *Introduction*

Western red cedar is a native conifer which was originally widespread in western Oregon and Washington. While very much secondary to the dominant Douglas-fir species, several NWTIC cooperators remain interested in planting a small proportion of cedar. Reasons are:

1. Consistently high log prices as long as the wood is sound
2. Probably the most economically valuable reforestation option for areas affected by Laminated root rot (which precludes reforestation with Douglas-fir for up to 10% of the landbase in some areas).
3. Providing an additional reforestation option in areas with intensive Swiss Needle Cast pressure on Douglas-fir.
4. Providing another option to increase species diversity in the planting portfolio and the landscape.
5. Cultural importance to the native American tribes of the PNW.

Low-intensity tree improvement programs for cedar have been underway for decades in these two states. The Bureau of Land Management, Washington Department of Natural Resources, the Oregon Department of Forestry, the US Forest Service and Willamette Industries established seed orchards; the first three agencies continue to manage their orchards and obtain seed. A strong motivation for relying on orchard

seed has been evidence for a high selfing rate within woodsrun\wildstand seed (Lipow et al. 2002).

Many of these US PNW selections, plus other selections made by Dr. John Russell of the British Columbia Ministry of Forests, were infused into the BC red cedar breeding and testing program in the 1990s; nearly half of the ~1,200 first-generation trees tested in that program originated from the USA. The BC program made rapid strides from that time, with intensive testing for browse preference, growth rate, resistance to cedar leaf blight, and wood decay: a combination of clonal field tests, open-pollinated field tests, penned deer studies and laboratory assays (monoterpenes and tropolones) have been used. It has also become apparent that introducing some level of physiological maturity and toughness, by using cuttings from older donor plants or large seedlings, also generally reduces browse. Examples of the potential to reduce browse are shown in the contrast of photos 12a and 12b.

The largest deterrent to a higher proportion of red cedar in the US PNW planting mix has been the preferential browse (compared to Douglas-fir, western hemlock, Sitka spruce, Noble Fir etc.) by deer and elk and the increasing population of these ungulates. At its worst, repeated browse can lead to WRC never becoming free to grow and eventually being overtopped by other conifers. Vexar tubes are often installed at considerable cost, while careful site selection (colder north

facing slopes, riparian areas, accumulated logging slash, and areas with frequent human activity) provide some mitigation of browse damage. Red cedar has frequently been used to fill in areas affected by laminated root rot within fenced progeny test sites. If browse could be reduced to a manageable level, NWTIC members could be planting 2 to 2.3 million western red cedar seedlings\ cuttings per year, which would make it the third most important species for westside reforestation after Douglas-fir and western hemlock. As it is, 1.2-1.3 million WRC are being planted a year based on the survey conducted by NWTIC.

At the October 2016 NWTIC Annual Meeting, Florian Deisenhofer (Hancock Forest Management) opened a discussion on additional testing and development of the western red cedar resource. The idea of a low-cost program primarily focused on reducing browse was well received. Plans

have evolved over the last eight months, and would emphasize growing red cedar seedlings or rooted cuttings in a common environment (typically a greenhouse), collecting foliage in fall, and having the monoterpenes assayed allowing selection of a subset of high-monoterpene parents. Meanwhile, small “proof-of-concept” field trials are being installed to see if high-monoterpene, older and larger planting stock sufficiently deter browse to make reforestation cheaper and more viable. There is also the potential to make additional selections allowing for greater intensity of selection, and limited testing for growth rate. Cooperation with the BC western red cedar program to the extent possible would be highly desirable.

Lipow, S.R., St. Clair, JB and Johnson, GR. 2002. Ex Situ Gene Conservation for Conifers in the Pacific Northwest. USDA Forest Service Pacific Northwest Research Station, *General Technical Report PNW-GTR-528*.

## SECOND-CYCLE BREEDING AND TESTING

The main second-cycle activity (Table 1 and Table 2) has been measurement of growth and form traits (now including incidence of second flushing), date of budbreak, and acoustic velocity measured around age-12 using the TreeSonic tool (WACTIC Phase I and HEMTIC). Four NOCTIC tests have been thinned, removing alternate diagonals. A new 2nd cycle cooperative (MEDTIC) was formed, and got off to a flying start with 35 pollens collected in 2015, 74 crosses attempted and 186 pollen collections in 2016, and 45 crosses

attempted and 45 pollens collected in 2017. Unfortunately, a significant number of the 2017 crosses aborted due to frost or some unknown reason. More details of the MEDTIC cooperative are shown in Inset 2.

Acoustic velocity was also measured in some first-generation Douglas-fir programs in western Washington (Skagit, Snoqualmie, and Cowlitz). So far, acoustic velocity has been measured on 16,937 first-generation progeny and 17,231 2nd cycle progeny.

Table 1. Status of cooperative 2nd-cycle Douglas-fir and western hemlock breeding populations as of 2017.

Location	Status	Number of Crosses		Test Establishment		
		Planted	Local Crosses made (planned)	No. Es- tablished (planned)	Start planting in spring of	Complete planting in spring of
Washington Cascades	Test establishment completed	291	300	16	2006	2011
Puget Sound	Test establishment completed	292	90	10	2003	2009
Washington Coast	Test establishment completed	106	137	5	2008	2008
Vernonia/ Ryderwood	Test establishment completed	416	325	10	2001	2005
North Oregon Cascades	Test establishment completed	377	350	11	2001	2005
Trask (Coast + Inland)	Test establishment completed	500	427	21	2004	2007
South Central Coast	Test establishment completed	604	604	20	1983	2006
ROSETIC- Umpqua	Test establishment completed	178	250	10	2007	2010
ROSETIC- Roseburg Low	Test establishment completed	228	157	7	2012	2012
ROSETIC-Roseburg High	Test establishment completed	116	40	5	2012	2012
MEDTIC - Low	Crossing		12 (200)	(7)	(2024)	(2024)
MEDTIC - High	Crossing		47 (160)	(8)	(2022)	(2022)
TOTAL Douglas-fir		2,699	≈2,680	118		
HEMTIC	Test establishment completed	539		19	1997	2001

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

Table 2. Status of measurements and selections of second-cycle programs as of June 20175.

	Bud-burst	Fall Cold hardiness	First growth & Form	Needle Retention Score	No. of forward selections made	Second growth & 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			√		181		
WACTIC Phase IIb			√				
ROSETIC Umpqua II			√				
ROSETIC Roseburg Low	2016, 2017		2017				
ROSETIC Roseburg High	2016		2017				

## THIRD-CYCLE BREEDING AND TESTING

Third-cycle crossing has progressed rapidly in three Oregon programs (SCC, North Coast, CASTIC) and has begun for HEMTIC and 3rd cycle Washington (Table 3). Six 3rd-cycle test sites were established by South Central Coast; almost exactly 15 years after their second-cycle tests were established (Table 4). In 2017 the following crosses were attempted: CASTIC - 40, SSC – 40, North Coast – 97, HEMTIC – 38.

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 feet or so, smaller high-elevation and coastal testing programs, and three population tiers (growth and form elite, multi-trait

main population, and a high-wood-stiffness elite). Crossing will largely be within the breeding groups defined in the 2nd cycle (first-generation breeding programs) with about 20 selections per breeding group for most breeding groups.

Using resampling techniques and 2nd cycle data from Washington Douglas-fir programs, NWTIC is currently investigating the effect on precision and predicted gain of varying the number of sites, and individuals per cross per site, for the planned 3rd cycle Washington program. The goal of this study is to provide cooperators with information to make decisions regarding how large the tests need to be, since progeny testing in the PNW is very expensive.

Table 3. Status of cooperative 3<sup>rd</sup>-cycle Douglas-fir and western hemlock breeding populations, after harvesting crosses made in 2016.

	Status	Number of Crosses with sufficient seed to sow	Target date to start planting tests	Entries Sown
South Central Coast	Crossing, planted phase I tests	224	2017	137
North Coast	Crossing	283	2019	N/A
CASTIC	Crossing	177	2019?	N/A
Washington Advanced Generation	Crossing	24	2021?	N/A
HEMTIC	Crossing	34	2022?	N/A
TOTAL				

Table 4. Summary of advanced - generation progeny trials established in 2017.

Type of trial	Planting Year	Number of		
		Entries	Locations	Test Trees
3 <sup>rd</sup> cycle South Central Coast	2017	137 families + 6 woodsrun controls	6	11,600

## INSET 2: THE MEDTIC 2ND CYCLE TREE IMPROVEMENT COOPERATIVE

The 2005-2006 NWTIC report outlined the genesis of the ROSETIC cooperative, and the story and nature of the MEDTIC cooperative (10 years later) has many parallels.

First-generation testing in the Medford District (Jackson and Josephine Counties) got underway slightly later than in the Oregon coast range, with the first sowing taking place in 1979 (Jacksonville – 1) and the last plantations installed in February 1991. Age-15 measurements were completed by 2005. The USDA Forest Service (78 test sites) and the USDI BLM (55) shouldered nearly 85% of the testing load of 157 plantations, and also took the lead in grafting the better parent trees in orchards (Provolt and Tyrrell by BLM; Zimmerman and Needle by USFS). The testing effort was challenging, and several of the sites failed from the difficult conditions of southern Oregon: high summer temperatures, prolonged summer drought, frosts and large diurnal variation of temperature, damaging weed species, gophers, and incomplete understanding of optimum stock types. Frosts and droughty soils were a problem even at the Provolt seed orchard and led to heroic efforts such as the use of smudge pots to protect flower crops. These tough environmental conditions were also important reasons for the cooperative Forestry Intensified Research (FIR) program (coordinated by Oregon State University) which ran from 1978-1991 to help forest owners and managers successfully reforest timberlands in this area.

A little further south Jay Kitzmiller outlined a forest tree improvement plan for the state of California in 1976 using a slightly different approach than the “Progressive” system implemented in Oregon and Washington, with fewer selections, fewer test sites, and a different experimental design. USFS Region 5 was the main player in this program. Over two hundred miles away to the north and east, straddling the Columbia river with comparable environmental conditions and in the Douglas-fir-Ponderosa pine transition zone, the Mid-Columbia cooperative tested 720 parents on 13 sites with a final measurement in 1995. Mid-Columbia orchards were established by the USFS, Champion International and later by SDS Lumber Company. All told, over 4,000 first-generation parents were tested in the three areas (Medford District, Mid-Columbia, and the northern part of California).

By the end of 2014, several changes had occurred from the start of these first-generation programs (1) the US Forest Service was almost entirely out of the tree improvement picture meaning that leadership would have to come from elsewhere (2) first-generation orchards had been established for the three areas mentioned and were mostly in full production, with the Provolt orchard largely growing above the height of damaging frosts (3) the entire Douglas-fir zone in western Oregon and western Washington, from Douglas County north had moved to 2nd or even 3rd cycle breeding and testing (4)

timber supply from federal land had greatly reduced, squeezing local sawmills and veneer mills and increasing the importance of timber from private land (5) advances in reforestation techniques (primarily in site preparation, weed control and seedling quality) meant that plantation failures were less frequent and plantation productivity higher. Despite the environmental challenges, the area did have some advantages for a Douglas-fir timber economy: absence of Swiss Needle Cast, lower incidence of stem defect, lower timberland costs, strong mill infrastructure and demand for wood, proximity to the California housing market or to eastbound rail routes, and lower population pressure and urbanization than parts of the I-5 corridor.

Based on the suggestion by Jim Smith (Plum Creek), NWTIC attempted to recruit timberland owners and managers in a second-cycle program. The response was surprisingly strong, and over the course of 2015 and 2016 the new cooperative ("MEDTIC") took shape with Jim as the first chair. By the end of 2016, fourteen members had joined declaring 655,000 Douglas-fir acres. Pollen was first collected

in 2015 (at Schroeder) and a substantial crossing effort took place in 2016 (along with a bumper Douglas-fir crop regionwide). Crossing is mostly taking place at Provolt seed orchard even as operational production in that orchard complex is gradually being replaced by production at other consolidated orchards (Horning and Tyrrell). Some pollen collection is taking place at the Chico facility near Redding, and Mid-Columbia crossing is planned in the SDS orchard. Two testing zones based on elevation are envisaged with the break around 3,000 feet: perhaps seven sites below (~200 crosses) and eight sites above (~160 crosses). Slight modifications may be necessary in the testing scheme: the use of smaller container stock mirroring stocktypes used in reforestation, freezing the stock for the high-elevation sites and planting them in spring, and a slightly older measurement age compensating for slower tree growth. Careful site selection and rigorous weed control will be crucial in seedling survival, with the margin for error being slim. Photographs on the final page present some aspects of forestry and tree improvement in the MEDTIC zone.

## DATA MANAGEMENT, ANALYSIS AND REPORTS

Key statistics about the database are summarized in Table 5. Hao Truong has recently began re-formatting the database. As the NWTIC database grew over the last 16 years, it had become complicated and not very efficient. The complexity came from the growing number of tables needed for different generations and the special measurements from different cooperatives. With regard to generations, there were different sets of tables for first generation programs vs. second generation programs with a third cycle getting started. The second generation tables were produced to accommodate the expanding amount of metadata that needed to be stored. The additional tables were for special measurements, such as acoustic velocity, budburst and cold hardiness: these were housed in their own separate tables because the current format was limited to a set amount of columns, and adding additional columns to the Generations table would increase the size of the database making it very inefficient. With regards to inefficiency, the effects were felt in both data retrieval and data management time. The additional tables were added because not every progenyID will have every measurement: for example there were about 3.3 million progenyIDs but only about 35,000 had acoustic velocity values. The additional table decreased the storage size of the database but increased the retrieving time of queries. The other problem with additional tables was the time spent to manage them, to keep track of different tables and especially to generate “views” to query and distributing subsets data.

The solution was to re-format the database. Regarding multiple generations, we are combining the generations to one table. With

regards to multiple tables, all cooperatives have a common set of columns (e.g. “progeny ID”, “owner”, “ht”, “dbh”, “damage”) but some also kept track of other columns like “living replanted”, “space” and “sequence number” in addition there are more columns for second measurements and potentially third measurements and so on. Currently the number of columns for just the progeny information and measurements is over 100.

We will employ a combination of a wide data format with a long data format. The wide format is what cooperators see in the Excel spreadsheets. The long data format uses the rows as both column names and column values. The wide format is for the columns that everyone program shares, while the long data format is for special columns and additional measurements (third, fourth and higher). This task has been challenging because of the scale, scope and unexpected issues that arise.

After the database has been completely reformatted, the data manager will no longer need to search the database for all relevant tables, or have to craft a specialized query that includes all the fixed, special and measurement columns. All progeny data can be viewed through a centralized program that pulls the relevant data in the database. The centralized program will also be incorporated into the new NWTIC website that is being developed. The time-consuming part of the old NWTIC website updating over 100 views that get the data that cooperators were used to seeing; every new view had to be manually added. The new website will create the same view automatically, but getting there has been time-consuming.

Table 5. Highlights of information in core NWTIC Database tables.

Table	December 15, 2015			June 15, 2017				
	Total # Records	# of 1st-generation records	# of 2nd-cycle records	Total records	Total # Unique Progeny Records	# of 1st-generation records	# of 2nd-cycle records	# of 3rd cycle records
Acoustic velocities (AV)	39,307	39,307		78,621	32,025	15,164	16,861	0
Address Phone	447			406				
Advanced Generation Seed Usage	1,607		1,607	1,607			1,607	
AV Wood Quality Measurements	11,266	11,266		11,266		11,266		
Budburst Measurements	101,819	45,407	56,412	116,851	78,285	18,848	59,437	0
Clone Bank Seed Orchard Inventories	66,928	66,388	540	66,928		66,388	540	
Clone Banks and Seed Orchards	171			171				
Contacts	3,003		3,308	3,003			3,308	
Co-ops	38			38				
Cross Tested Parents	1,895	31	7	1,895		31	7	
Crosses (includes fillers)	7,020	1,876	19	7,648	5,278	1,095	4,161	647
Fall Cold Hardiness	3,308		661	11,044	11,044		11,044	0
Gain Trial Measurements	41,716			41,716				
Gain Trial Sites	12			12				
Gen1/Gen2/Gen3 Progeny	3,352,305	3,352,305		4,053,358	4,053,358	3,385,040	667,143	1,175
Gen1/Gen2/Gen3 Progeny Measurements	3,352,248	3,352,248		9,510,261	3,798,666	3,268,175	530,491	0
Generational Gains	9,439	3,879	5,560	9,439		3,879	5,560	
Genetic Gains	2,620,607	2,579,730	40,877	2,620,607		2,579,730	40,877	
Later Genetic Gains	199,789	198,874	915	199,789		198,874	915	
Later Progeny Measurements	253,691	252,606	1,085	253,691		252,606	1,085	
Metadata Variables	2,225			2,225				
Owners	66			66				
Parent Tree Coordinates	31,718	31,627	81	32,602		32,242	360	
Polymixes	149	122	27	149		122	27	
Program Images	38		38	38			38	
Program Layouts	148	130	17	148		130	17	
Program Views	147	130	17	147		130	17	
Programs	154	135	19	165		141	23	
Seed	5,857	981	4,872	5,857		981	4,872	
Selected First Generation Parents	2,355	2,355		2,453		2,453		
Selected Progeny Individuals	2,735	2,735		4,490		2,701	1,804	0
Site Thinning Archiving	976	976		976		976		
Sites	1,152	1,013	133	1,187		1,034	152	1
Sowing Schedules	1,342	1,198	138	1,342		1,198	138	
Specific Gravity	14,509	13,829	680	14,509		13,829	680	
Swiss Needle Cast Monitoring	32,764	32,764		32,764		32,764		
Tree Identifiers	41,499			45,431				
View Metadata	62,265	52,604	8,837	64,061		52,604	8,837	
Z Scores	19,111	19,111		19,111		19,111		

Table 6. Summary of genetic gain predictions using BLUP, reports and other quantitative tasks, completed January 2016 through June 2017. Analyses are coastal Douglas-fir unless otherwise indicated.

First-Generation Analyses	Trait
Snoqualmie-1	Acoustic velocity
Snoqualmie-2	Acoustic velocity
Cowlitz-2	Acoustic velocity
Skagit	Acoustic velocity
Burnt Woods Phase II age-24 to age-31 data	Evaluate selection strategy in Needlecast zone, verify stability of ranks and gains over time, identify the most valuable selections.
Second-Generation Analyses	
Puget Sound Phase I acoustic velocity data	
Puget Sound Phase II fall cold hardiness data.	
WACTIC1 acoustic velocity data	
Acoustic velocity data collected by HEMTIC and by the PNWTIRC (western hemlock)	
WACTIC Phase 1+2 age-7 data (16 sites) including separate Low/Mid elevation and High elevation analyses	
ROSETIC Roseburg Low and High date of budbreak	
Other Quantitative Tasks	
NARA/SCC data: SNP information on 600 1st-gen and 2nd-gen trees + phenotypic information	
Simulation on sensitivity analysis to changes in number of sites and reps/site, in genetic parameters and predicted gain, for 3rd cycle WA Douglas-fir program	

NWTIC data analysis service is featured by pedigree- or marker-based genetic analyses for continuous, dichotomous, and polytomous traits in big data sets, in order to provide in-depth understanding of the main findings from the valuable genetics trials and draw guidelines for future selection and breeding. We applied spatial analysis to estimate and account for spatial environmental variation in the field, and estimate various genetic parameters, predict breeding values and genetic gains for multi-generation trials with mixed experimental and / or mating designs using univariate and / or multivariate mixed models. We also routinely conduct Monte Carlo simulation and resampling techniques to provide optimal breeding strategies for tree breeding programs.

In the past 18 months, we continued to improve the analytical strategy and

methodologies to meet members' needs better. Here are a few highlights.

1. Refined common analytical models to improve model fit for progeny test data.
2. Ran sophisticated multivariate models more effectively (e.g., using factor-analytical covariance structure, etc.) so that we are capable of analyzing G x E patterns for more than 100 test sites simultaneously.
3. Provided genetic parameter estimates using a number of model fitting methods.
4. Consolidated the predicted breeding values and gains into a single database for easy comparison and making selections.
5. Provided more maps and graphs for better visualization of the analytical results, e.g., density maps showing distribution and pattern of damage in the field, and graphs of family stability and G x E patterns, etc.

6. Implemented statistical methods for genomic selection (GS), including GS model training, cross-validation, and GEBV

prediction from various models using Bayesian and mixed model approaches.

Examples of output in NWTIC analyses are shown in Figures 1 - 4.

Figure 1. Example of plot of parental origins and test sites from NWTIC 2nd-cycle analysis.

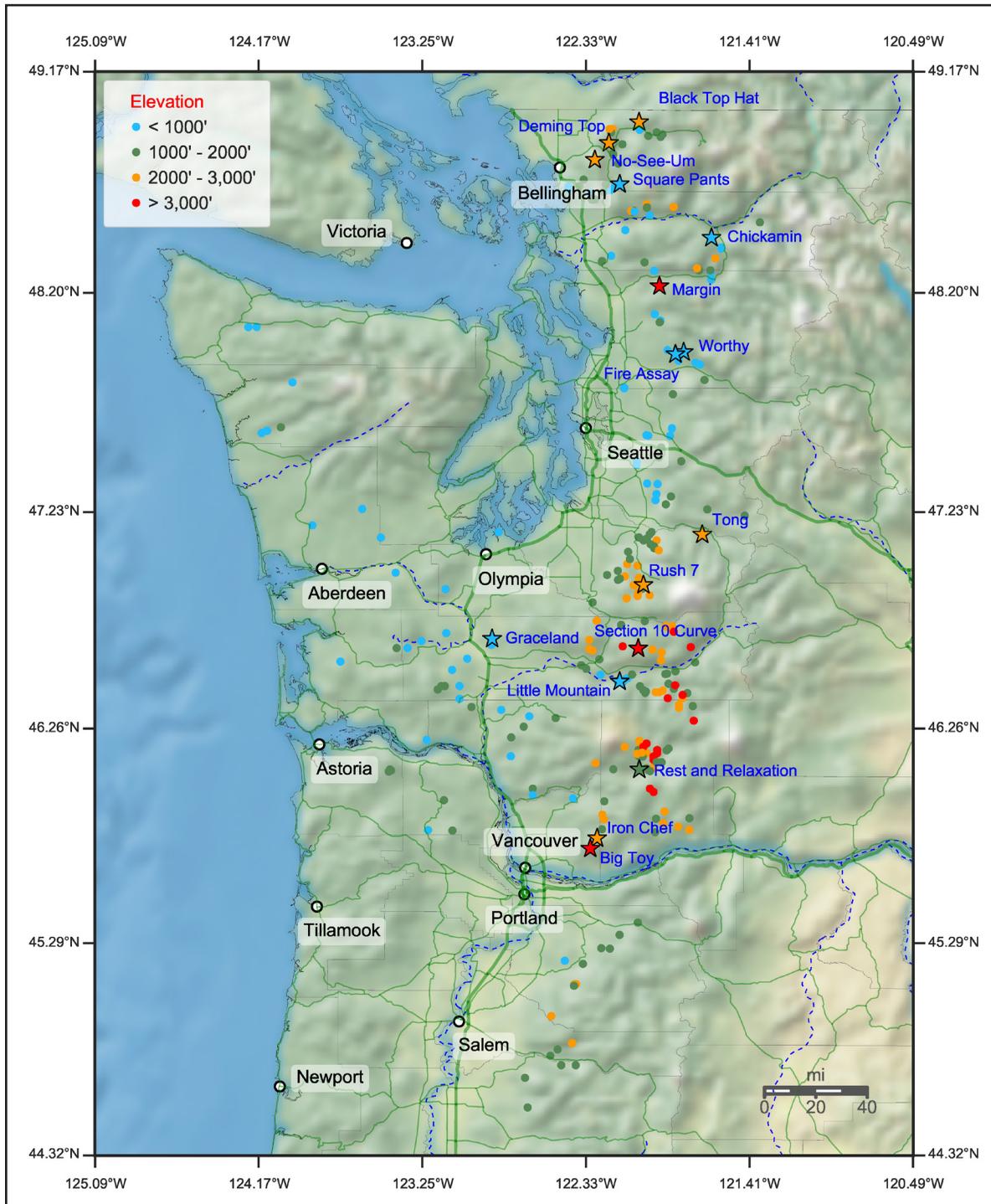


Figure 2. Example of site regression GGE biplot visualizing interactions of sites and genotypes.

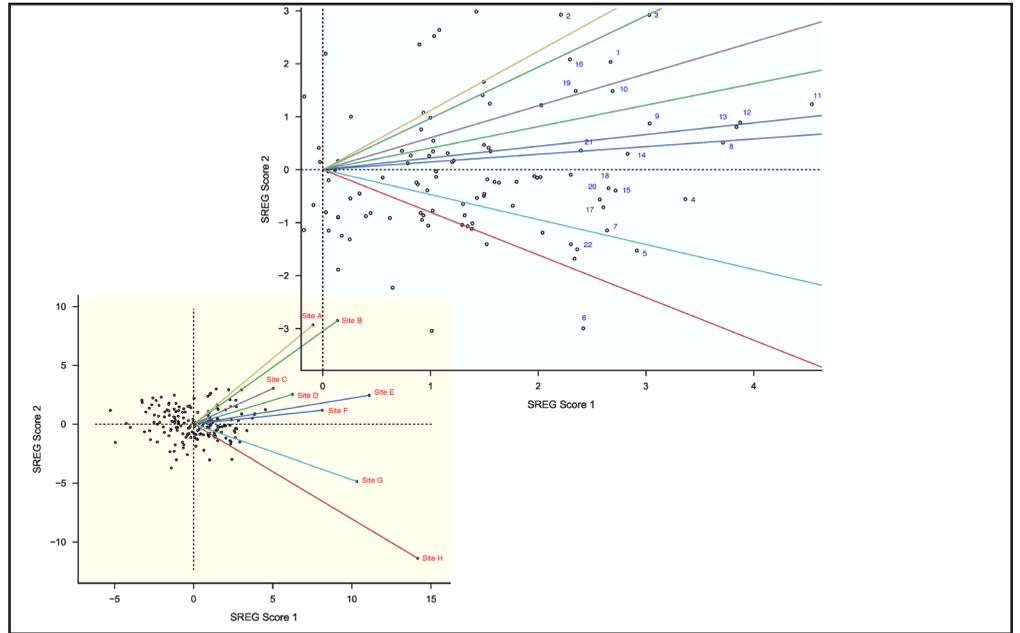


Figure 3. Visualization of parental GCA ranking change from site to site in a NWTIC 2nd-cycle analysis.

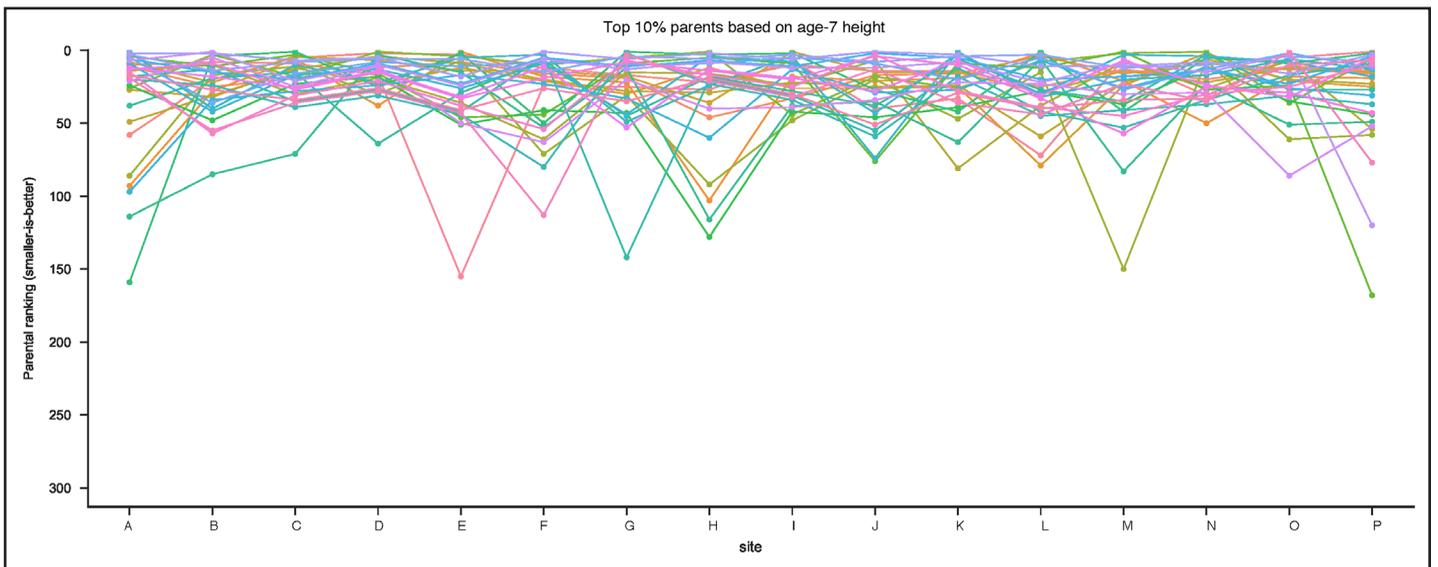
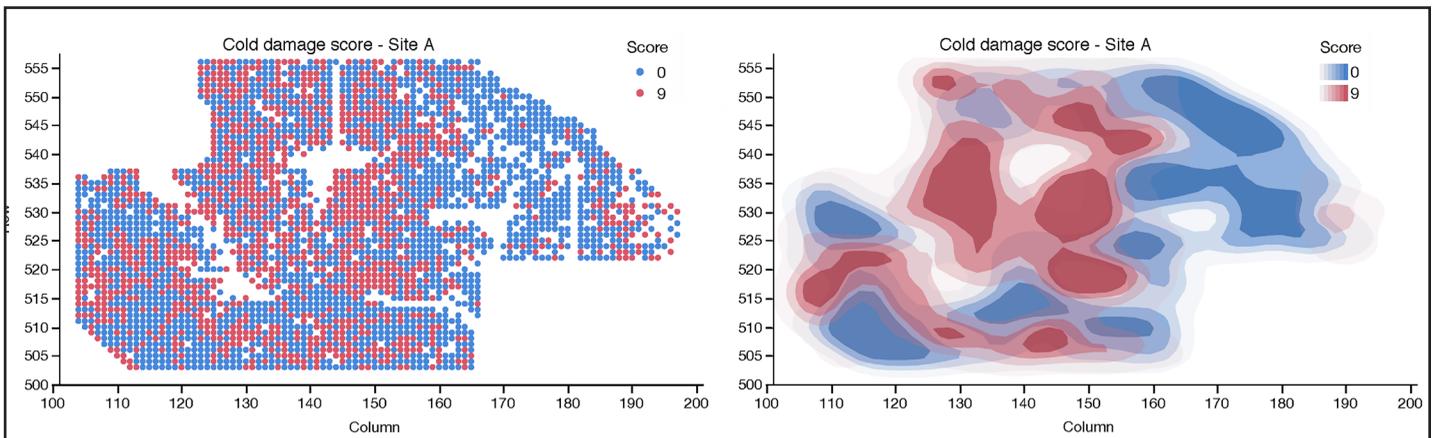


Figure 4. Visualization of spatial patterns of variation within a test site.



## GENETIC GAIN VERIFICATION TRIALS

Age-13 data were obtained from the 2005-planted cohort of the Grays Harbor Genetic Gain / Type IV trials during this period. Meanwhile Sukhyun Joo, working on his PhD in the College of Forestry with Doug Maguire as major professor, is focusing on the Molalla Gain Trial for his research.

Part of his work involves taking detailed measurements on branch characteristics, while the other part involves modeling tree growth from the obtained measurements to rotation. Progress on installing 2nd cycle genetic gain trials is described in the Inset 3 and Table 7.

Table 7. Summary of 2<sup>nd</sup> cycle realized genetic gain trials established in 2017.

Type of trial	Number of				Spac- ing	Size of measure- ment plot (acres)	Predicted % Gain <sup>1</sup> Based On 2 <sup>nd</sup> Cycle Data, Over Woodsrun						
	Entries	Loca- tions	Plots	Test Trees			HT	DBH	VOL	STEM- FORK	BASAL FORK	RAMI- CORNS	SINU- OSITY
South Central Coast Douglas- fir	8 elite crosses, 12 woodsrun lots, buffers	11' x 11'	37	6,316	11' x 11'	0.278	16.0	16.7	45.1	2.2	N/A	5.5	12.3
HEMTIC Western Hemlock	9 elite crosses, 2 woodsrun lots, buffers	10' x 10'	36	8,651	10' x 10'	0.278	11.1	12.3	34.3	0.8	-7.3	-1.9	N/A

<sup>1</sup>Age-10 or age-12 for South Central Coast depending on the cross, age-10 for HEMTIC

### INSET 3: INSTALLATION OF SECOND-GENERATION DOUGLAS-FIR AND WESTERN HEMLOCK REALIZED GENETIC GAIN TRIALS

Plans to establish these trials, and its objectives, were mentioned in the previous report (2012-15), and the various analyses to estimate the optimum number of sites and plots/site. We aimed to build simple trials focusing on some of the highest-gain and reliably performing genetic material available today. Based on these, we opted for the following broad strategy:

- Two genetic treatments: A. elite crosses that performed very well in 2nd cycle tests, compared with B. a broadly based and representative woodsrun (unimproved) seedlot.
- Single, operational spacing wide enough to run through rotation without thinning
- Unfenced
- 8 sites with 4 replicates per treatment per site (minimum of 32 plots per treatment)
- Measurement plots large enough to carry to rotation (over 0.25 acres)

#### *Douglas-fir*

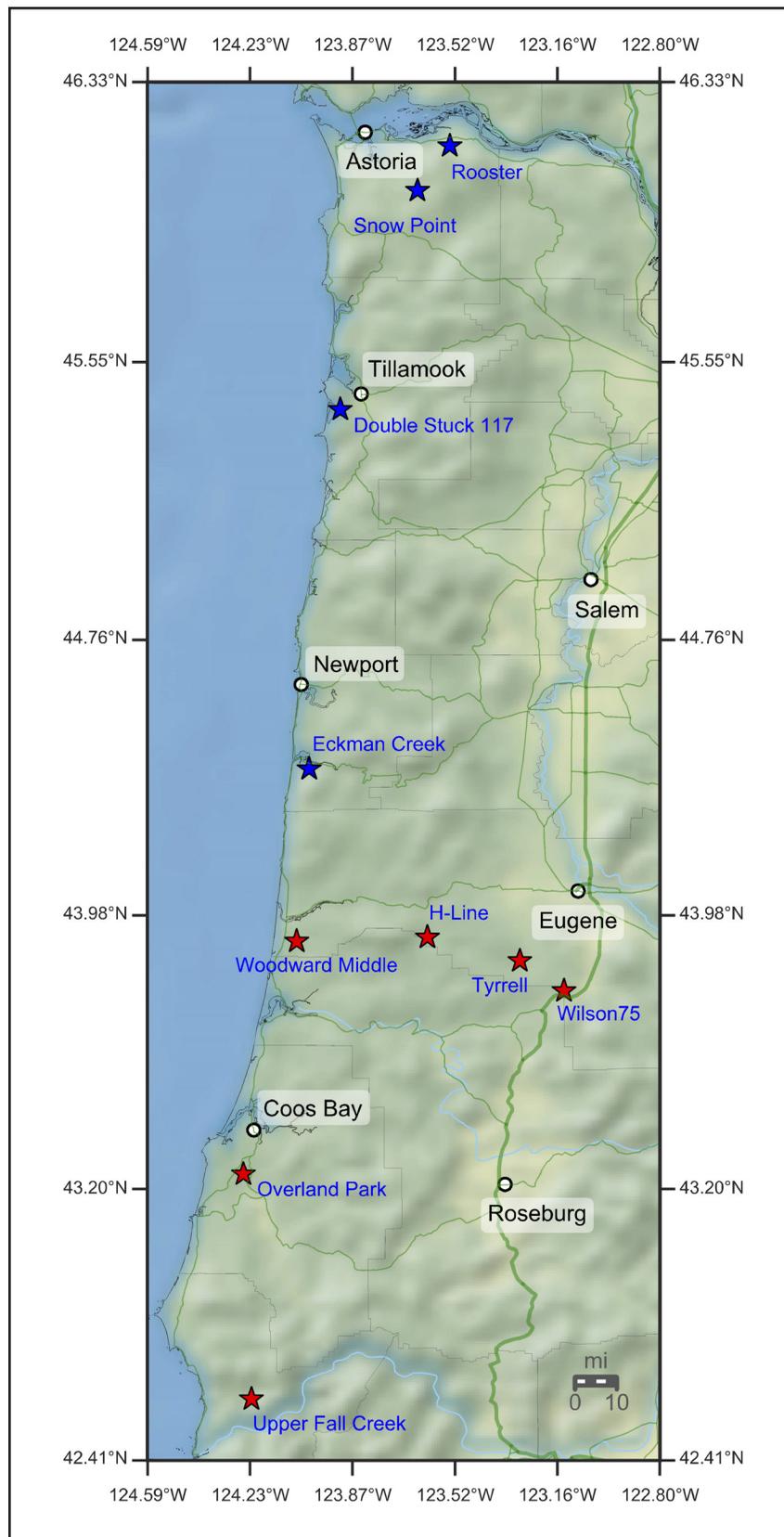
The Douglas-fir portion was based on the South Central Cooperative which is the process of installing 3rd cycle tests. There were economies of scale (seedling production, site preparation, planting, mapping, weed control, monitoring) available from being to co-locate five of the gain trial sites adjacent to 3rd cycle – Phase I test sites. Styro-20 seedlings were grown at Arbutus Grove Nursery on Vancouver Island, frozen in January and trucked down in mid-February. The plantations were established in March, on land owned/managed by Roseburg Forest Products, the Bureau of Land Management, Campbell Global, Lone Rock Timber, and

Rayonier. The planting was done by preferred operational planting contractors hired by the companies. Phase II of 3rd-cycle SCC test sites and the SCC gain trial are not due for several more years.

#### *Western hemlock*

Similar to the Grays Harbor Genetic Gain \ Type IV trial, this is being established as a collaborative effort between the Northwest Tree Improvement Cooperative and the Stand Management Cooperative (SMC) based at the University of Washington. 3rd cycle HEMTIC trials being still some years out, we decided to move forward with a first group of four sites established on the Oregon coast in 2017, and a second group of sites established in Washington in 2018. Seedlings for the first group were grown at Sylvan Vale Nursery on Vancouver Island, and the same nursery is growing the second cohort of seedlings. Cooperators cleaned the sites to a higher standard than operational sites, to facilitate laying out the sites on regular, even-spaced grids and decades of future work (especially measurement on a 2-year then 4-year schedule). The SMC field crew and a contractor took care of surveying the plots and installing the pin flags. The seedlings were transported from Vancouver Island along with the South Central Coast seedlings and planted in March. Liz Cole (OSU College of Forestry) and Keith Jayawickrama provided supervision of planting with the help of representatives of the four cooperators (Hampton, Greenwood Resources, Stimson and Starker) and the mapping. The planting was done by preferred operational planting contractors hired by the companies.

Map1. Geographic locations of 2nd-cycle genetic gain trials. Douglas-fir trials shown by red stars, western hemlock trials by blue stars.



## TRAINING, TECHNICAL UPDATES AND RESEARCH PROJECTS

NWTIC has scheduled a second two-day tree improvement short course in September 2017 at the BLM's Horning Seed Orchard.

College of Forestry Forest economist Tammi Cushing's NPV calculator on tree improvement costs is available now, and examples of its output for coastal Douglas-fir and western hemlock are shown in Table 8. In this example of site index 120 ground, the NPV gain from tree improvement for both species at age-45 was almost the same for both species. A higher wood value for Douglas-fir (\$596\MBF vs. \$463\MBF) was compensated by more seedlings\lb. of seed for western hemlock (125,000 vs. 20,000) and greater harvest volume per acre. If we were to adjust for increased productivity from genetics, keeping the harvest volume the same and reducing the rotation age (3 years for DF, 2.25 years for WH), we could increase the NPV by a further \$38\acre for Douglas-fir and \$8\acre for western hemlock.

The Northwest Advanced Renewables Alliance (NARA) project was completed. Results from a preliminary genomic selection study are shown in Inset 4.

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

Joo, S., Maguire, D. and Jayawickrama, K. 2017. Simulation of Douglas-fir realized gain trials with ORGANON using genetic gain multipliers. Pp. 32-38 in D. Maguire and D. Mainwaring (eds). *CIPS 2016 Annual Report*. Center for Intensive Planted-forest Silviculture, College of Forestry, Oregon State University, Corvallis, OR, USA.

Joo, S., Maguire, D. and Jayawickrama, K. 2017. Variation in crown attributes among families in the COLton Douglas-fir realized gain trials. P0pp 39-45 in D. Maguire and D. Mainwaring (eds). *CIPS 2016 Annual Report*. Center for Intensive Planted-forest Silviculture, College of Forestry, Oregon State University, Corvallis, OR, USA.

Kolpak, S.E., Jayawickrama, K., Kling, J., Trappe, M., Hipkins, V., Ye, T., Guida, S., Cronn, R., Cushman, S.A., McEvoy, S. and Howe, G. T. 2017. *Development of a high-density Affymetrix Axiom genotyping array for genomic selection in Douglas-fir*. Poster presented at Forest Genetics 2017: Health and Productivity under Changing Environments. A Joint Meeting of WFGA and CFGA, University of Alberta, Edmonton, AB, Canada June 26-29, 2017

Table 8. Example of outcomes from an economic analysis of tree improvement for coastal Douglas-fir and western hemlock.

	Volume in board feet		Per Acre NPV	
	Douglas-fir	western hemlock	Douglas-fir	western hemlock
Wild seed	28,194	40,120	\$ 510	\$ 427
Genetically improved, same rotation (15% genetic gain)	32,423	46,138	\$ 626	\$ 539
Genetically improved, reduced rotation (15% genetic gain)	28,284	40,129	\$ 664	\$ 547
Gain from genetics - same rotation, increased volume	4,229	6,018	\$ 116	\$ 113
Gain from genetics - same volume, shorter rotation	N/A	N/A	\$ 154	\$ 121

## **INSET 4: MAKE SELECTIONS FOR INCREASED BIOFUEL PRODUCTION USING A COMBINATION OF PHENOTYPIC AND SNP GENETIC MARKER DATA**

*Terrance Ye, Glenn Howe, Scott Kolpak, Jennifer Kling and Keith Jayawickrama,  
College of Forestry, Oregon State University*

### ***Introduction***

In this study, we applied Genomic Selection (GS) to coastal Douglas-fir to investigate the accuracy and selection efficiency for the phenotypes of growth rate, biofuel product, wood chemistry properties, and branching characterless, by using SNP markers.

### ***Methodology***

This study was carried out using two series of coastal Douglas-fir full-sib progeny trials (previously described i.e. SCC and CL98) as training / validation populations. The overall objective was to explore the potential of accelerating breeding cycles of Douglas-fir through genomic selection (GS). In this process, 640 trees were genotyped using an Axiom 55K SNP array with Call Rate (CR)  $\geq$  80%. All monomorphic SNP markers were excluded, but SNPs with rare alleles were retained. As a result, a total of 22,126 polymorphic SNPs were used.

The marker effects and, therefore, genomic estimated breeding values (GEBVs) were estimated using best linear unbiased prediction model (GBLUP). Our preliminary study indicated that the differences in PA between GBLUP and various Bayesian models (e.g., BL, BRR, BayesA, BayesB, and BayesC) were small for all the traits studied.

To assess prediction accuracy (PA) of GS, we used 10 replications of 10-fold cross-validation where 90% of the total population was used as a training population

and 10% as the validation population. The PA was calculated as the mean Pearson correlation between the estimated breeding values (EBVs) from pedigree-based models and the GEBVs from the GS models. The relative efficiency (RE) of GS to traditional selection (TS) was estimated by comparing PAs from both schemes, assuming that the length of breeding cycle in GS is half of that in TS as a result of early selection.

For each of the 19 traits studied, we trained univariate genomic selection (UVGS) models with EBVs and validated GEBVs using the same (direct UVGS) or different (indirect UVGS) traits. In addition, we examined the consequences of including dominance variation in the UVGS models.

Since tree breeding programs normally deal with multiple trait selection, and some traits are difficult to evaluate, expensive, or they need a large sample size, we also evaluated and compared the accuracy of genomic predictions using multivariate genomic selection (MVGS) models. The following four scenarios were analyzed using MVGS models: (1) Training on total biofuel (TB), recalcitrance factor (RF), specific gravity (SG), or age12 volume (VOL12); validated on TB, (2) Training on TB, RF, pretreatment yield (PY), or holocellulose yield (HY); validated on TB, (3) Training on HT12, HT7, DBH7, or VOL; validated on HT12, and (4) Training on HT12, HT7, DBH7, or VOL; validated on VOL12.

## **Results**

The predictive accuracies from direct UVGS were relatively high for all the traits studied, ranging from 0.57 to 0.79 (Table 9). For example, the predictive accuracy was 0.65 for age-12 height (HT12) and 0.64 for total biofuel product (Figure 5). The corresponding REs of genomic selection to TS, assuming a conservative reduction of 50% in the length of the breeding cycle, were 1.79 and 1.92 respectively (Table 10 and Figure 6), highlighting the increase in efficiency per unit time.

The indirect UVGS revealed interesting patterns. For height and volume growth at age 12, the models developed at age 7 and age 12 performed equally well in predicting the growth at age 12 (Figure 7). For example, the predictive accuracy was 0.6 for the model trained on HT7 and validated on HT12. This number was almost the same as the predictive accuracy (=0.61) from the direct genomic selection on HT12. For wood chemistry and biofuel traits, however, predictive accuracies from indirect genomic selection were generally much lower than that from the direct genomic selection (Figure 8).

Results indicated that the additive model (A) and the combined additive and dominance model (AD) produced similar predictive abilities for all traits (Figure 9), despite the fact that dominance variation did contribute some genetic variance in some traits. This suggests that there is little merit of including genomic dominance effects in the GBLUP prediction models.

Multivariate genomic selection provided higher predictive accuracy and RE in each scenario; all were higher than their respective cross-validated univariate genomic selection results. It appears that multivariate genomic selection exploits even weak trait correlations,

and provided improved accuracy in a time and cost manner thus increasing genetic gain from selection among untested genotypes.

## **Conclusions/Discussion**

In conclusion, this study showed encouraging results of applying genomic selection in coastal Douglas-fir cooperative breeding programs. High predictive accuracies were found for all traits studied: around 0.60 for growth and biofuel product, and 0.75 for branching / stem straightness in univariate models. They are comparable to the accuracies estimated in the pedigree-based TS. For example 0.710 for HT12 (compared to 0.710 by pedigree-based selection), and .62 vs. .69 for VOL12.

For growth traits, accuracies remained high when using models generated at age 7 to predict phenotypes at age 12. For age-12 growth and branching traits, genomic selection models trained at age-7 had similar predictive abilities as models trained at age-12. Prediction using multivariate models were generally more accurate than using univariate models, but the increase of accuracy depends on the relationship among traits.

Assuming that the length of breeding cycle in genomic selection is half of that in field-based selection, the relative efficiency of genomic selection to field-based  $\approx 200\%$ . Prediction accuracies from some other studies in forestry species were as follows: Loblolly pine (Resende Jr et al. 2012a): 0.63 – 0.74 for HT6, 0.65 – 0.75 for DBH6; Eucalyptus (Resende 2011): 0.73 – 0.79 for HT3, 0.65 – 0.78 for SG4; Maritime pine (Isik et al. 2015): 0.47 for HT12, 0.43 for DBH12; Loblolly pine (Resende Jr et al. 2012b): 0.39 for HT, 0.46 for DBH; Interior spruce (Ratcliffe et al. 2015): 0.37 – 0.47 for HT (ages 3 - 40).

Figure 5. Direct genomic selection using single-trait additive model: mean prediction accuracy.

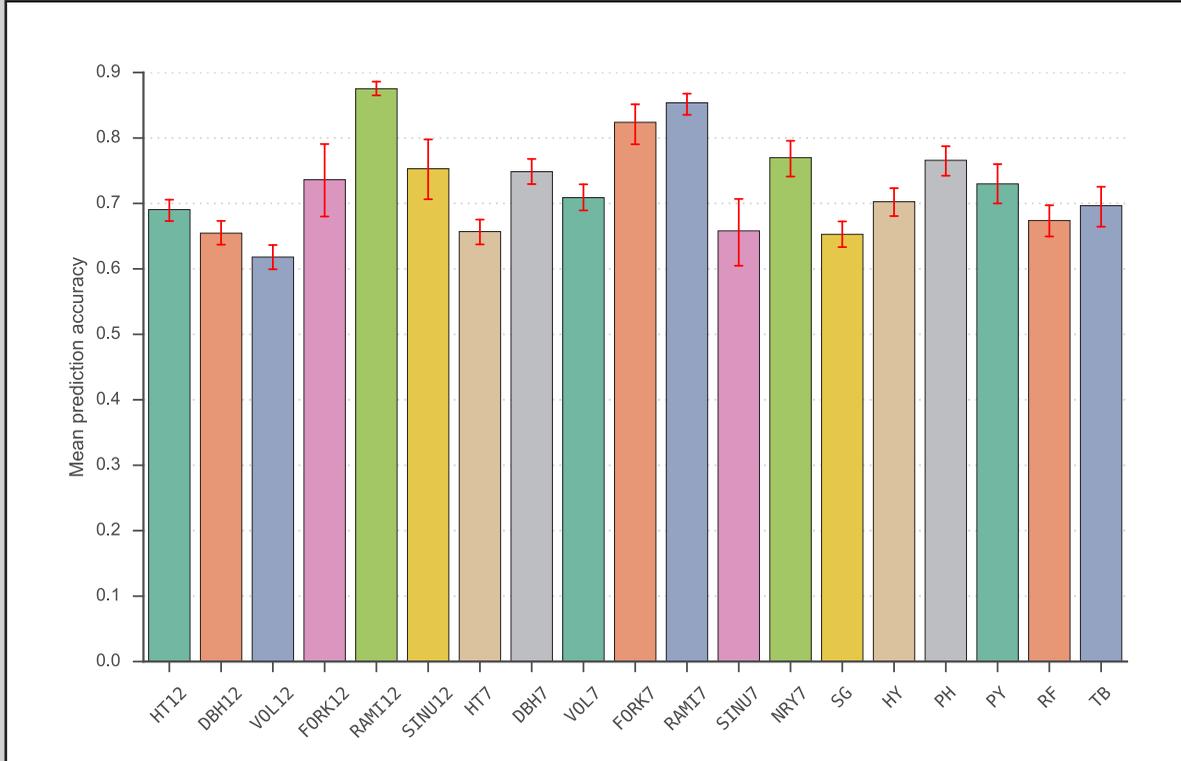


Figure 6. Direct genomic selection using single-trait additive models: mean relative efficiency of genomic selection.

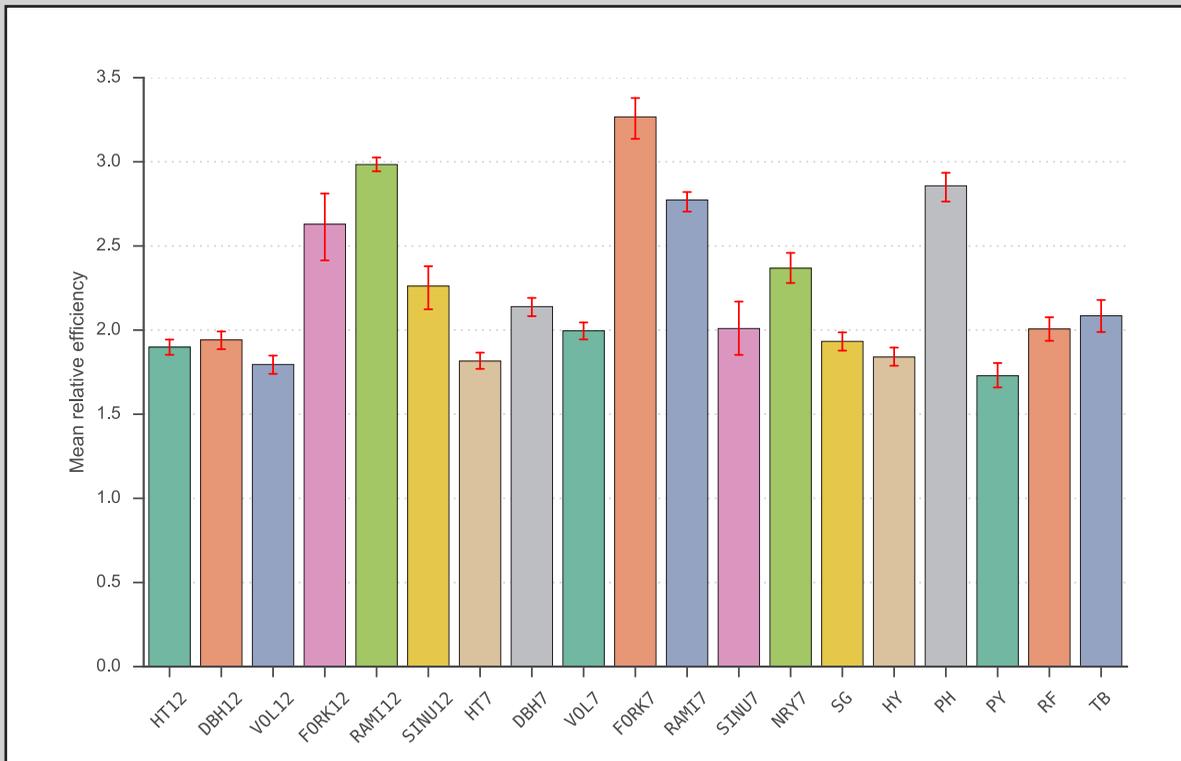


Figure 7. Mean prediction accuracy (PA) for all traits when training on age-7 height (HT7), age-12 height (HT12), and age-12 stem volume (VOL12).

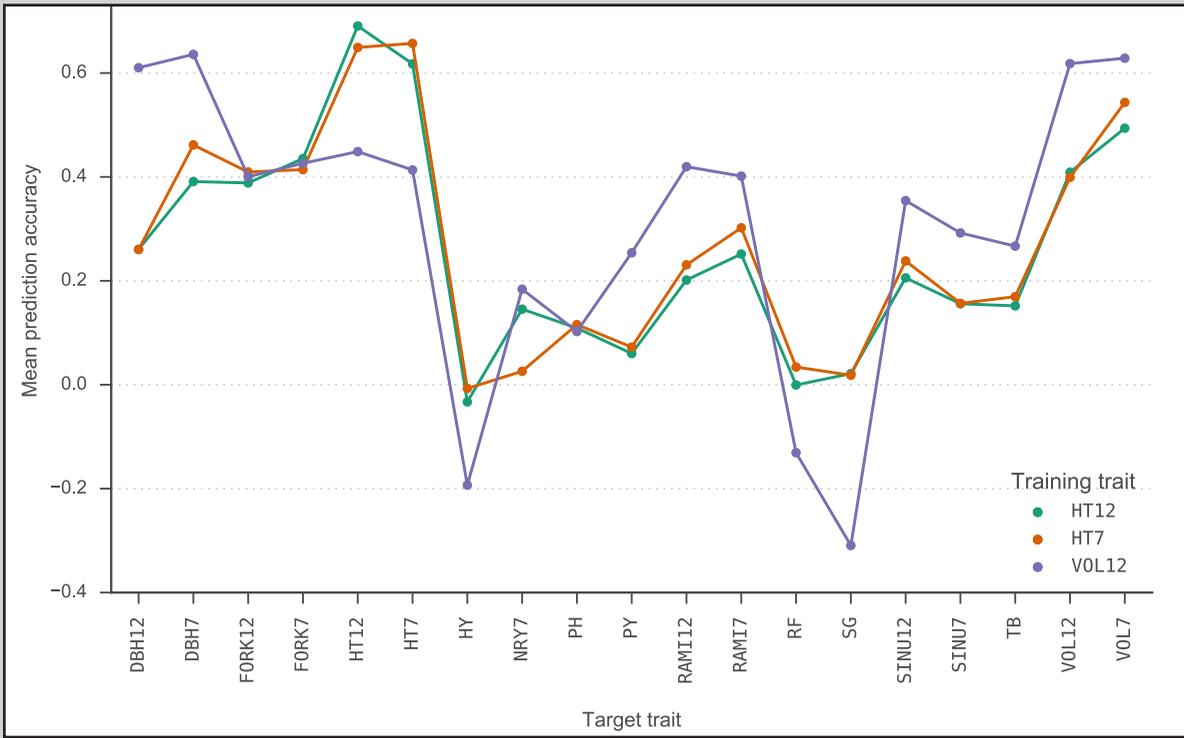


Figure 8. Mean prediction accuracy for indirect genomic selection using single-trait additive models: age-12 height (HT12) and total biofuel product (TB).

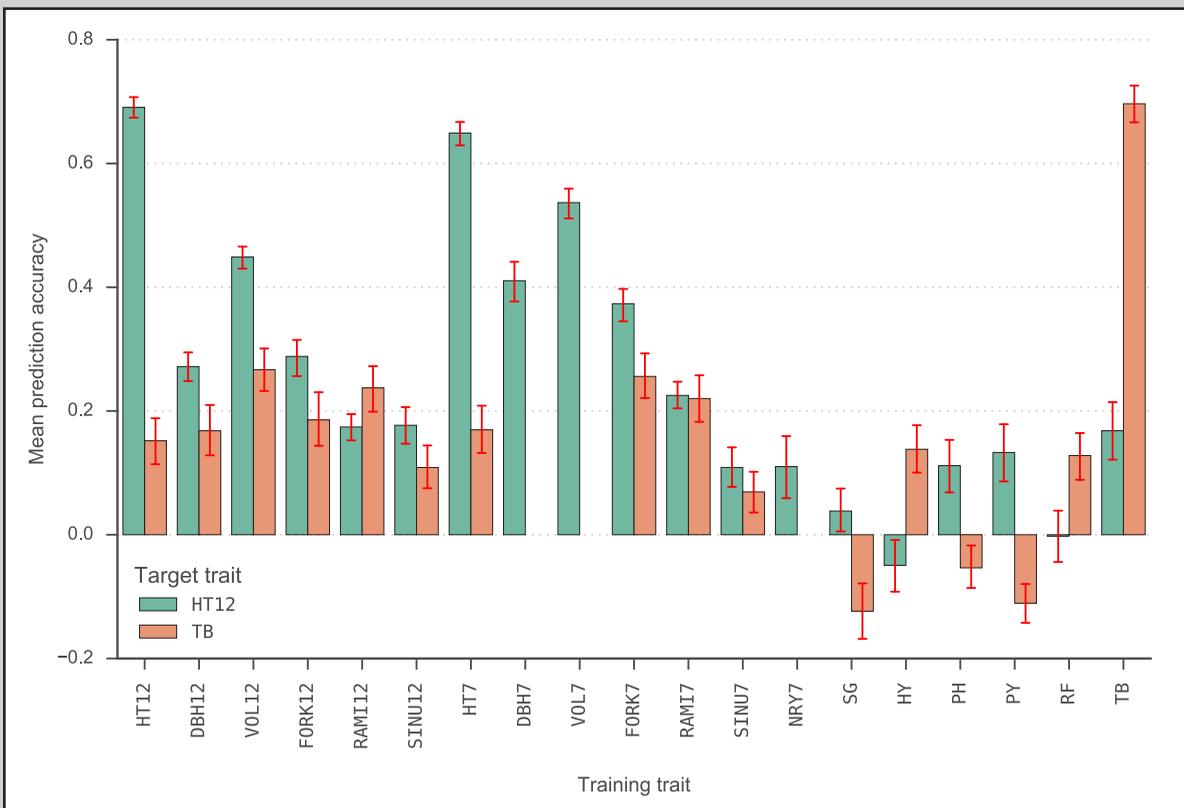


Figure 9. Mean prediction accuracy in direct genomic selection: additive model (A) vs. additive + dominance model (AD.)

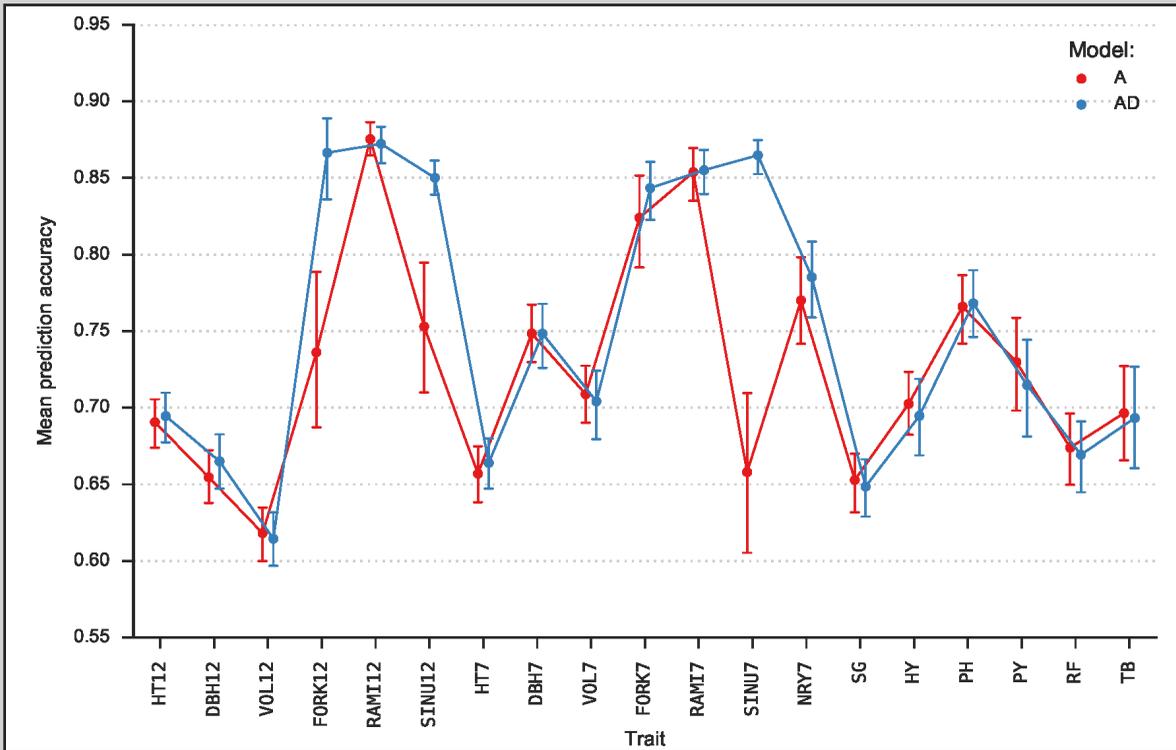


Figure 10. GEBVs vs. EBVs from a 10-fold cross-validation in direct genomic selection.

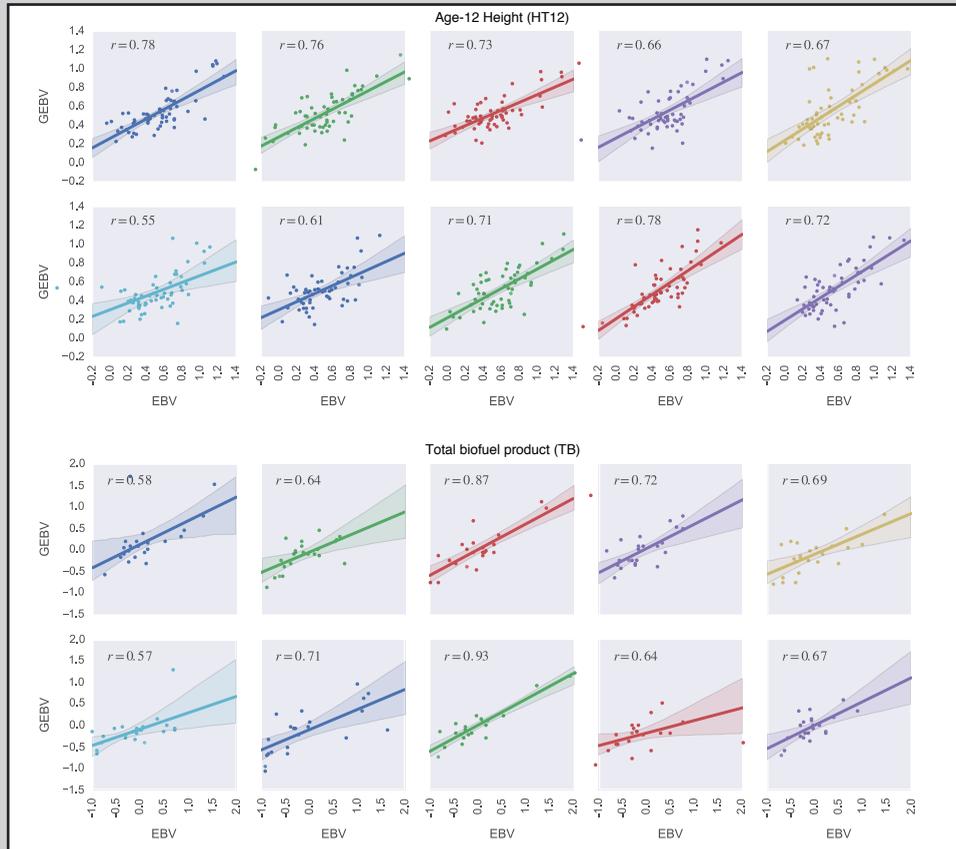
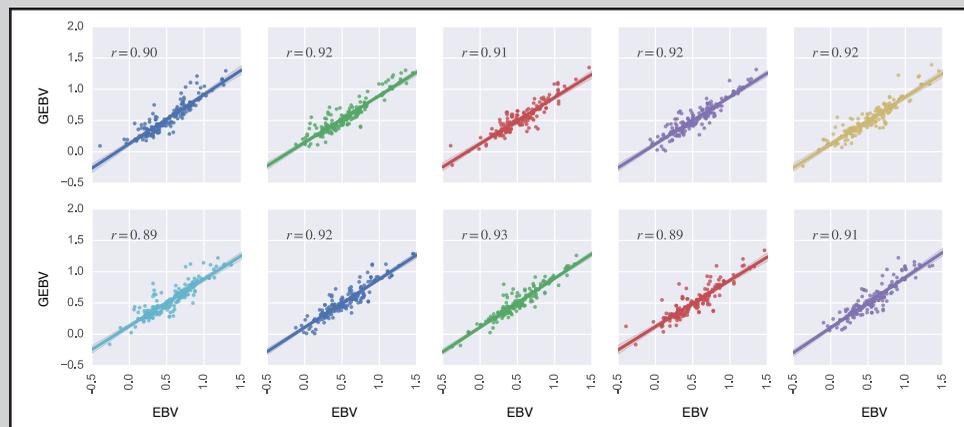


Figure 11. Genomic estimated breeding value vs. expected breeding value in a 10-fold cross-validation for HT12: multiple-trait model (HT7, DBH7, VOL7, HT12).



We have tried to optimize prediction procedures in genomic selection in the following ways:

*Compare different statistical approaches:* GBLUP vs. Bayesian methods: GBLUP method performed equally well as Bayesian methods in general. (Figure 12)

*Add non-additive component to the additive genomic selection model:* Including non-additive component in the genomic selection model did not improve prediction accuracy for most traits. For FORK12, SINU12 and SINU7, Adding dominance effect into the genomic selection model boosted prediction accuracy by 13 – 31%.

*Use multiple-trait models to make use of among-trait correlations:* Multiple-trait models are better than single-trait models even when the among-trait correlations were weak. However, multiple-trait models show no benefit for predicting new individuals without any phenotypic information.

*Use a subset of SNP markers to reduce genotyping cost:* It appears that similar predictive ability can be reached by using only a subset of SNP markers (~3K).

There are several outstanding issues for genomic selection in Douglas-fir:

- What is the optimal size / age / type of reference population? The efficiency of genomic selection largely depends on the design of the reference population.
- Can different breeding zones or regions share the same genomic selection model? Our data are only relevant to a single breeding zone. A study in loblolly pine also showed that prediction accuracy remained high across sites as long as they were used within the same breeding zones.
- How many generations does a genomic selection model need to be re-trained? Results from dairy cattle breeding suggested that prediction accuracy eroded quickly with generations.
- What is the cost-benefit analysis (genomic selection vs. TS)? The genotyping cost was \$75 / tree, the DNA extraction probably added \$5-10 more per tree. In contrast, growing, planting, measuring a Douglas-fir progeny tree is about \$10-20 / tree. However, relative benefits of genomic selection for Douglas-fir may be higher than other important conifer species (e.g., radiata pine, southern pines, and eucalypts). The testing cycle is longer for Douglas-fir,

Table 9

Table 9. Accuracy of genomic additive (A) and additive + dominance (AD) models for direct (i.e., same trait in training and validation) and indirect (i.e., different traits in training and validation) genomic predictions. HT, DBH, VOL, FORK, RAMI, SINU, and NRY are total height, diameter at breast height, volume index, number of incidents of forks, number of incidents of ramiforms, stem sinuosity score, and estimated years of needle retention, respectively. The trailing numbers refer to measurement ages. Age-17 wood chemistry traits include HY (hydrolysis yield), PH (pretreated holocellulose fraction), PY (pretreated holocellulose fraction), RF (recalcitrance factor), and SG (specific gravity). TB is an index of total biofuel product calculated as  $VOL_{12} \times SG \times RF$ .

Model	Training trait	Validation trait																		
		DBH12	DBH7	FORK12	FORK7	HT12	HT7	HY	NRY7	PH	PY	RAMI12	RAMI7	RF	SG	SINU12	SINU7	TB	VOL12	VOL7
A	DBH12	0.586	0.588	0.285	0.333	0.256	0.229	-0.198	0.177	0.024	0.244	0.427	0.383	-0.147	-0.339	0.284	0.244	0.188	0.534	0.529
	DBH7	0.551	0.674	0.445	0.583	0.396	0.420	0.037	0.037	0.132	0.153	0.528	0.497	-0.067	0.089	0.225	0.074	0.252	0.545	0.625
	FORK12	0.220	0.384	0.766	0.611	0.327	0.321	-0.079	0.132	0.161	-0.091	0.500	0.456	-0.041	0.093	0.217	0.139	0.283	0.297	0.405
	FORK7	0.264	0.492	0.615	0.765	0.363	0.323	-0.035	0.268	0.161	-0.091	0.529	0.499	-0.041	0.093	0.217	0.139	0.283	0.297	0.405
	HT12	0.225	0.363	0.367	0.409	0.650	0.567	-0.079	0.107	0.041	0.124	0.191	0.236	-0.053	0.019	0.199	0.151	0.194	0.371	0.463
	HT7	0.214	0.412	0.389	0.385	0.604	0.611	-0.035	0.006	0.039	0.102	0.201	0.271	0.001	0.014	0.199	0.131	0.222	0.355	0.499
	HY	-0.185	0.069	-0.128	-0.050	-0.087	-0.085	0.599	0.006	-0.205	-0.446	0.121	0.154	0.557	-0.066	-0.113	-0.113	0.125	-0.187	0.073
	NRY7	0.212	0.069	0.181	0.376	0.114	0.012	0.790	0.006	-0.205	-0.446	0.069	0.156	0.557	-0.066	-0.113	-0.113	0.125	-0.187	0.073
	PH	0.019	0.069	0.141	0.170	0.086	0.104	-0.199	0.790	0.006	-0.205	0.069	0.156	0.557	-0.066	-0.113	-0.113	0.125	-0.187	0.073
	PY	0.263	0.069	0.011	-0.090	0.150	0.144	-0.423	0.019	0.689	0.024	0.060	0.079	-0.119	0.188	-0.021	-0.021	-0.062	0.073	0.073
	RAMI12	0.336	0.438	0.489	0.515	0.169	0.171	0.080	0.058	0.060	-0.230	0.784	0.707	0.332	-0.079	0.213	0.118	0.106	0.253	0.390
	RAMI7	0.309	0.428	0.461	0.503	0.215	0.232	0.124	0.128	0.080	-0.226	0.733	0.738	0.090	-0.096	0.223	0.130	0.253	0.315	0.403
	RF	-0.115	0.069	-0.110	-0.041	-0.029	-0.023	0.567	0.128	-0.114	-0.348	0.090	0.128	0.570	-0.067	-0.144	-0.142	0.120	-0.111	0.403
	SG	-0.345	0.069	0.102	0.121	0.086	0.064	-0.065	0.201	-0.114	-0.348	-0.130	-0.146	-0.065	0.582	-0.126	-0.133	-0.141	-0.256	0.251
	SINU12	0.246	0.259	0.273	0.229	0.187	0.186	-0.071	0.096	-0.008	-0.051	0.238	0.239	-0.095	-0.082	0.727	0.669	0.143	0.269	0.251
	SINU7	0.206	0.117	0.116	0.148	0.141	0.123	-0.085	0.016	-0.010	-0.049	0.132	0.136	-0.112	-0.103	0.648	0.750	0.131	0.212	0.102
	TB	0.219	0.580	0.250	0.298	0.176	0.175	0.103	0.172	-0.068	-0.106	0.318	0.295	0.097	-0.134	0.102	0.119	0.642	0.282	0.581
VOL12	0.545	0.580	0.393	0.420	0.425	0.378	-0.188	0.172	0.055	0.220	0.420	0.394	-0.139	-0.294	0.319	0.262	0.273	0.569	0.581	
VOL7	0.518	0.639	0.488	0.588	0.523	0.521	-0.188	0.057	0.055	0.220	0.477	0.476	-0.139	-0.294	0.319	0.262	0.273	0.569	0.581	
AD	DBH12	0.586	0.581	0.290	0.335	0.250	0.222	-0.188	0.202	0.025	0.230	0.431	0.388	-0.141	-0.343	0.290	0.250	0.183	0.533	0.524
	DBH7	0.533	0.656	0.431	0.567	0.393	0.407	0.049	0.049	0.146	-0.014	0.517	0.486	-0.083	0.068	0.218	0.073	0.263	0.531	0.606
	FORK12	0.228	0.383	0.785	0.621	0.324	0.315	-0.094	0.138	0.146	-0.014	0.516	0.477	-0.083	0.068	0.278	0.131	0.263	0.302	0.403
	FORK7	0.267	0.493	0.621	0.769	0.366	0.322	-0.043	0.256	0.158	-0.075	0.529	0.499	-0.045	0.081	0.216	0.140	0.275	0.333	0.489
	HT12	0.229	0.358	0.372	0.409	0.650	0.568	-0.072	0.084	0.037	0.110	0.194	0.237	-0.045	0.013	0.195	0.149	0.198	0.376	0.460
	HT7	0.211	0.400	0.388	0.379	0.599	0.603	-0.060	0.008	0.037	0.106	0.200	0.271	-0.024	-0.008	0.204	0.138	0.213	0.350	0.482
	HY	-0.179	0.057	-0.137	-0.056	-0.085	-0.083	0.606	0.008	-0.212	-0.453	0.134	0.167	0.563	-0.074	-0.115	-0.116	0.108	-0.187	0.060
	NRY7	0.209	0.057	0.196	0.393	0.108	-0.012	0.606	0.783	-0.212	-0.453	0.103	0.185	0.563	-0.074	-0.115	-0.116	0.108	-0.187	0.060
	PH	0.013	0.057	0.126	0.160	0.088	0.110	-0.193	0.783	0.685	0.017	0.103	0.185	0.563	-0.074	-0.115	-0.116	0.108	-0.187	0.060
	PY	0.261	0.057	0.012	-0.093	0.140	0.136	-0.426	0.049	0.019	0.636	0.062	0.081	-0.111	0.189	-0.026	-0.026	-0.065	0.071	0.060
	RAMI12	0.339	0.435	0.501	0.523	0.169	0.165	0.088	0.041	0.078	-0.236	0.796	0.722	-0.319	-0.019	-0.034	-0.030	-0.096	0.246	0.380
	RAMI7	0.319	0.416	0.481	0.514	0.217	0.233	0.140	0.132	0.075	-0.247	0.753	0.759	0.044	-0.095	0.229	0.132	0.263	0.324	0.390
	RF	-0.123	0.057	-0.105	-0.034	-0.032	-0.024	0.580	0.008	-0.125	-0.344	0.074	0.116	0.585	-0.069	-0.161	-0.159	0.113	-0.119	0.390
	SG	-0.355	0.057	0.092	0.117	0.063	0.036	-0.053	0.783	0.205	-0.020	-0.124	-0.139	-0.053	0.590	-0.126	-0.132	-0.143	-0.275	0.255
	SINU12	0.248	0.265	0.294	0.243	0.181	0.183	-0.082	0.083	0.009	-0.049	0.254	0.259	-0.107	-0.111	0.742	0.672	0.130	0.266	0.255
	SINU7	0.206	0.103	0.126	0.153	0.128	0.113	-0.092	-0.005	0.007	-0.026	0.142	0.150	-0.117	-0.100	0.658	0.759	0.130	0.208	0.087
	TB	0.228	0.580	0.250	0.296	0.178	0.177	0.100	0.157	-0.077	-0.102	0.312	0.289	0.093	-0.150	0.100	0.117	0.639	0.289	0.087
VOL12	0.543	0.580	0.392	0.423	0.423	0.377	-0.177	0.157	0.045	0.208	0.423	0.400	-0.132	-0.299	0.318	0.260	0.264	0.567	0.583	
VOL7	0.506	0.628	0.481	0.584	0.508	0.511	-0.177	0.060	0.045	0.208	0.476	0.477	-0.132	-0.299	0.318	0.260	0.264	0.567	0.583	

Table 10

Table 10. Relative efficiency of genomic selection (GS) to traditional selection (TS) based on genomic additive (A) and additive + dominance (AD) models for direct (i.e., same trait in training and validation) and indirect (i.e., different traits in training and validation) genomic predictions, assuming that the length of breeding cycle in GS is half of that in TS. HT, DBH, VOL, FORK, RAMI, SINU, and NRY are total height, diameter at breast height, volume index, number of incidents of forks, number of incidents of ramiforms, stem sinuosity score, and estimated years of needle retention, respectively. The trailing numbers refer to measurement ages. Age-17 wood chemistry traits include HY (hydrolysis yield), PH (pretreated holocellulose fraction), PY (pretreatment yield), RF (recalcitrance factor), and SG (specific gravity). TB is an index of total biofuel product calculated as VOL12 x SG x RF.

Model	Training trait	Validation trait																		
		DBH12	DBH7	FORK12	FORK7	HT12	HT7	HY	NRY7	PH	PY	RAMI12	RAMI7	RF	SG	SINU12	SINU7	TB	VOL12	VOL7
A	DBH12	1.738	1.681	1.017	1.322	0.705	0.632	-0.519	0.544	0.088	0.577	1.456	1.242	-0.438	-1.004	0.855	0.746	0.563	1.550	1.490
	DBH7	1.611	1.927	1.564	2.279	1.082	1.148	0.114	0.114	0.569	-0.015	1.762	1.581	0.264	0.665	0.665	0.222	0.756	1.565	1.761
	FORK12	0.653	1.098	2.735	2.424	0.899	0.886	-0.209	0.403	0.602	-0.215	1.705	1.480	-0.201	0.277	0.773	0.321	0.756	0.863	1.140
	FORK7	0.782	1.406	2.196	3.033	0.999	0.891	-0.093	0.821	0.602	-0.215	1.804	1.621	-0.123	0.277	0.653	0.424	0.848	0.955	1.367
	HT12	0.667	1.036	1.312	1.623	1.788	1.568	-0.208	0.326	0.154	0.294	0.651	0.767	-0.159	0.056	0.598	0.461	0.581	1.078	1.303
	HT7	0.634	1.177	1.387	1.527	1.662	1.688	-0.092	0.018	0.146	0.242	0.683	0.879	0.002	0.042	0.597	0.399	0.664	1.031	1.403
	HY	-0.551	0.609	0.606	1.396	0.307	0.034	1.568	2.429	-0.768	-1.057	0.416	0.506	1.660	-0.195	-0.339	-0.346	0.375	-0.545	0.207
	NRY7	0.056	0.056	0.507	0.681	0.234	0.286	-0.522	0.286	2.569	0.057	0.210	0.261	-0.355	0.555	0.158	0.043	-0.186	0.502	0.207
	PH	0.785	0.997	1.251	1.745	2.043	0.413	-1.109	0.071	0.071	1.498	-0.903	-0.905	-0.945	-0.068	-0.156	-0.145	-0.317	0.738	0.738
	RAMI12	0.917	1.223	1.647	1.995	0.590	0.642	0.324	0.180	0.222	-0.543	2.671	2.294	0.096	-0.233	0.640	0.359	0.792	0.947	1.097
	RAMI7	-0.342	-1.028	0.367	0.485	0.236	0.178	-0.172	0.392	0.298	-0.537	2.498	2.396	0.269	-0.284	0.672	0.397	0.758	0.915	1.136
	RF	0.612	0.729	0.977	0.910	0.514	0.514	-0.187	0.296	-0.028	-0.114	0.450	0.443	-0.333	-0.304	1.948	2.292	0.392	0.617	0.289
	SG	0.655	0.612	0.415	0.588	0.388	0.341	-0.224	0.048	-0.037	-0.114	0.450	0.443	-0.333	-0.304	1.948	2.292	0.392	0.617	0.289
	SINU12	1.616	1.657	1.405	1.669	1.168	1.046	-0.493	0.531	-0.254	-0.251	1.096	0.967	0.288	-0.397	0.308	0.367	1.922	0.823	1.638
	SINU7	1.515	1.827	1.713	2.302	1.426	1.427	-0.493	0.176	0.204	0.522	1.430	1.279	-0.415	-0.872	0.957	0.799	0.818	1.652	1.638
	TB	1.738	1.659	1.036	1.330	0.688	0.615	-0.493	0.622	0.094	0.545	1.470	1.260	-0.419	-1.017	0.872	0.765	0.547	1.549	1.473
	VOL12	1.559	1.877	1.515	2.217	1.074	1.114	-0.493	0.150	0.544	-0.033	1.724	1.543	-0.249	0.202	0.642	0.216	0.547	1.525	1.707
	VOL7	0.675	1.097	2.804	2.464	0.891	0.872	-0.245	0.424	0.544	-0.033	1.758	1.548	-0.249	0.202	0.836	0.403	0.787	0.877	1.135
	AD	FORK12	0.793	1.410	2.219	3.051	1.006	0.889	-0.114	0.788	0.590	-0.178	1.802	1.620	-0.136	0.241	0.650	0.427	0.822	0.967
FORK7		0.678	1.024	1.328	1.619	1.789	1.570	-0.189	0.255	0.137	0.260	0.660	0.769	-0.133	0.039	0.584	0.454	0.593	1.091	1.295
HT12		0.624	1.142	1.384	1.504	1.648	1.666	-0.158	0.022	0.136	0.251	0.680	0.879	-0.071	-0.024	0.612	0.419	0.638	1.016	1.357
HT7		-0.532	-0.492	-0.222	-0.222	-0.231	-0.229	1.587	0.022	-0.793	-1.074	0.460	0.547	1.675	-0.221	-0.348	-0.357	0.321	-0.542	1.357
HY		0.603	0.163	0.660	1.459	0.288	-0.032	2.407	0.022	-0.793	-1.074	0.460	0.547	1.675	-0.221	-0.348	-0.357	0.321	-0.542	1.357
NRY7		0.039	0.039	0.453	0.638	0.241	0.303	-0.506	2.407	2.557	0.042	0.336	0.572	-0.332	0.560	0.166	0.031	-0.194	0.498	0.170
PH		0.778	1.005	1.244	1.789	2.076	0.456	-1.116	0.069	0.069	1.506	-0.941	-0.935	-0.949	-0.056	-0.077	-0.078	-0.194	0.206	0.206
PY		0.947	1.189	1.718	2.040	0.596	0.644	0.368	0.406	0.288	-0.558	2.714	2.344	0.132	-0.281	0.689	0.402	-0.094	-0.288	0.717
RAMI12		-0.365	-1.059	-0.378	-0.135	-0.086	-0.065	1.519	0.130	0.288	-0.558	2.565	2.466	0.302	-0.327	0.729	0.448	0.815	0.930	1.098
RAMI7		0.327	0.327	0.464	0.464	0.169	0.096	-0.139	0.406	0.281	-0.585	2.565	2.466	0.302	-0.327	0.729	0.448	0.815	0.930	1.098
RF		0.736	0.736	1.051	0.963	0.498	0.505	-0.214	0.253	0.035	-0.116	0.866	0.841	-0.319	1.748	-0.383	-0.409	-0.427	-0.803	0.717
SG		0.612	0.295	0.448	0.605	0.351	0.313	-0.240	-0.018	0.027	-0.062	0.482	0.485	-0.350	-0.297	1.978	2.321	0.387	0.602	0.245
SINU12		0.681	1.611	1.398	1.676	1.164	1.043	-0.464	0.485	-0.288	-0.241	1.076	0.949	0.276	-0.444	0.303	0.360	1.912	0.843	1.642
SINU7		1.481	1.796	1.691	2.284	1.387	1.397	-0.464	0.181	0.170	0.493	1.442	1.298	-0.393	-0.885	0.956	0.793	0.789	1.646	1.795
TB		1.481	1.796	1.691	2.284	1.387	1.397	-0.464	0.181	0.170	0.493	1.442	1.298	-0.393	-0.885	0.956	0.793	0.789	1.646	1.795
VOL12		1.481	1.796	1.691	2.284	1.387	1.397	-0.464	0.181	0.170	0.493	1.442	1.298	-0.393	-0.885	0.956	0.793	0.789	1.646	1.795
VOL7		1.481	1.796	1.691	2.284	1.387	1.397	-0.464	0.181	0.170	0.493	1.442	1.298	-0.393	-0.885	0.956	0.793	0.789	1.646	1.795



Figure 13. Genomic selection using multiple-trait additive models. Mean prediction accuracy: single-trait vs. multiple-trait models.

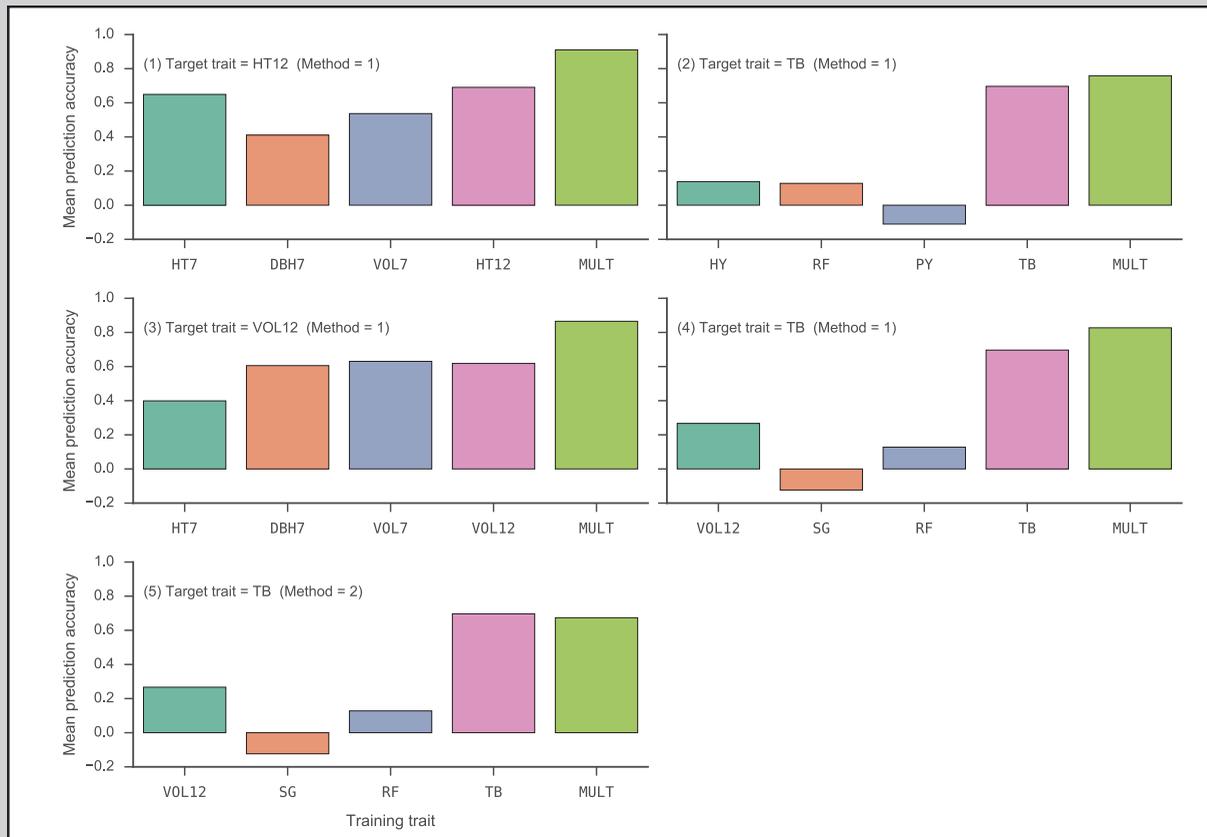
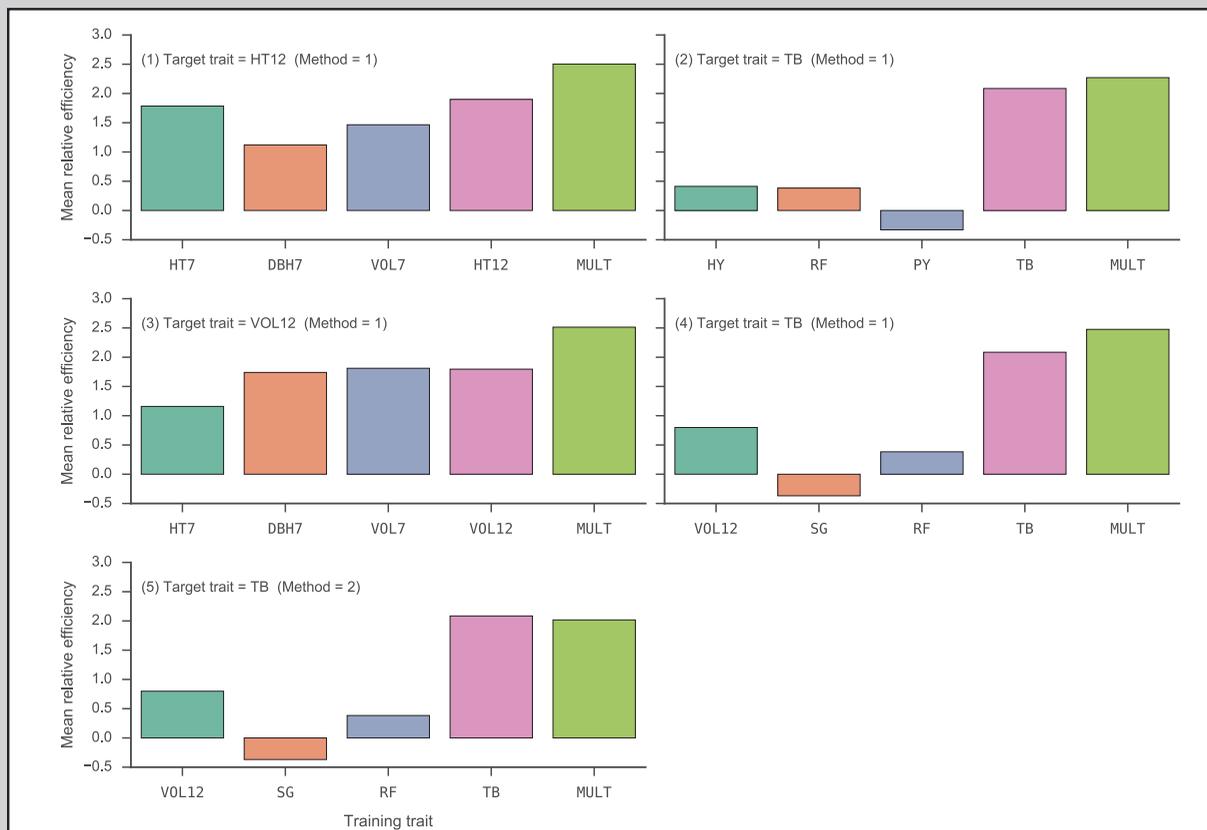


Figure 14. Mean relative efficiency of genomic selection: single-trait vs. multiple-trait models



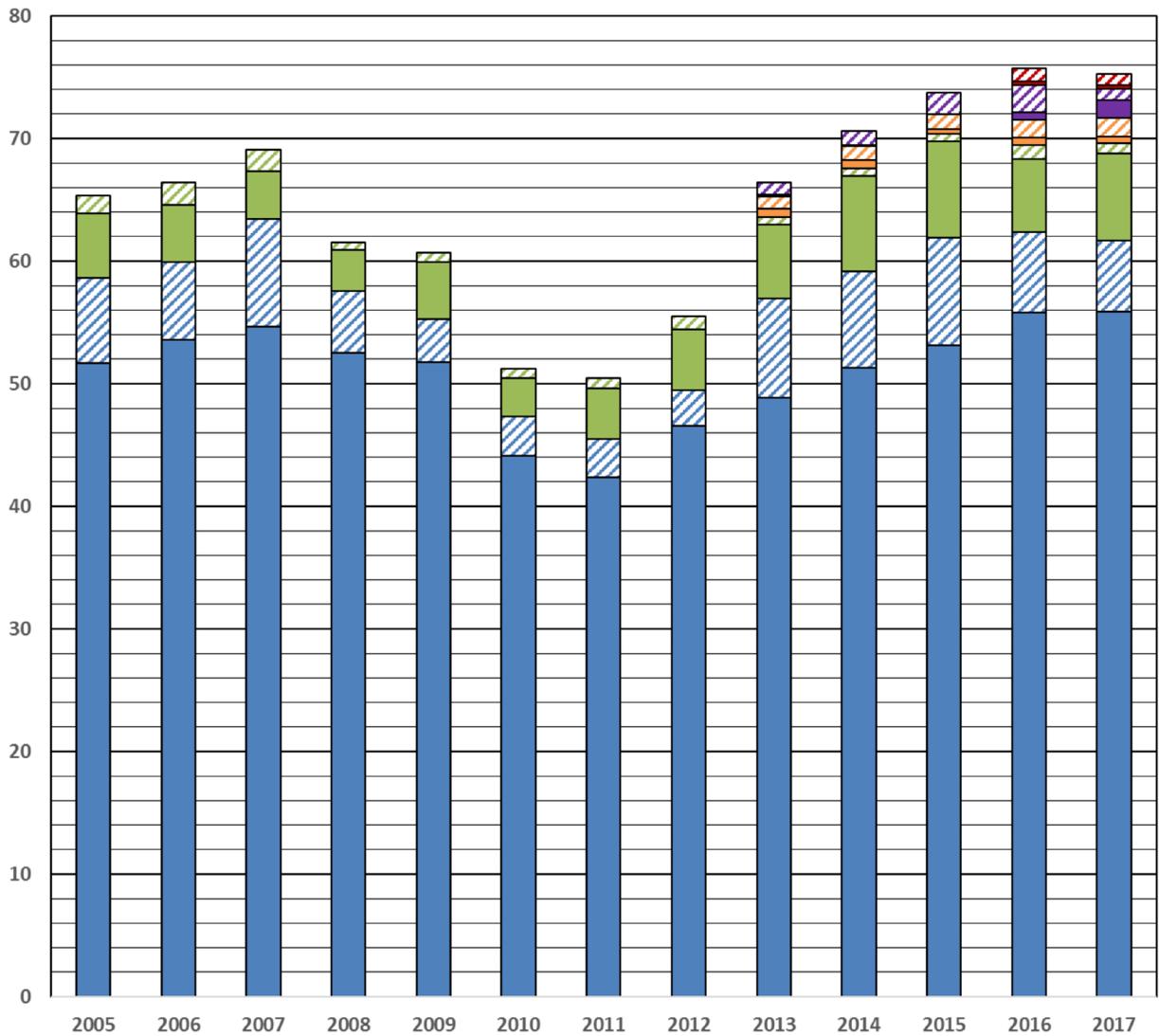
## THE DEPLOYMENT OF GENETICALLY IMPROVED FOREST TREE SEEDLINGS

NWTIC surveyed the number of coastal Douglas-fir, western hemlock, noble fir and ponderosa pine seedlings planted both by members and non-members, and added western red cedar as well. While these should be considered only approximate numbers (some assumptions and interpolations were unavoidable), they 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 the number of trees originating from tree improvement programs in 2017 (coastal DF, hemlock, ponderosa pine, and noble fir, and western red cedar), had increased slightly to about 65.2 million (compared to about 61.4 million trees in 2015). The number of woodsrun trees planted in 2017 (10.0 million) was lower than the corresponding figure for 2015 (12.3 million). It is also heartening to see planting

rise to about 75.2 million trees in 2015, from a low of just over 50 million in 2011, (however at that time NWTIC did not query planting of Noble Fir, Ponderosa Pine or western red cedar). The 2017 species summary was 61.7 million Douglas-fir, 7.9 million western hemlock, 2.1 million Noble Fir and 2.4 million Ponderosa Pine; supporting the idea of more emphasis on the improvement of western red cedar was the planting of 1.38 million seedlings in 2016 and 1.20 million in 2017.

With regards to seed production, 2016 was a good seed year in western Oregon and Washington, but this does not appear true for 2017 with conelet abortion observed by May despite the lack of particularly low temperatures. One concern has been the loss or scaling down of seed processing facilities in the PNW over the last few years, similar to the limited options for grafting contractors.

Figure 15: Numbers of trees planted originating from tree improvement programs vs. unimproved trees, by species, in Oregon and Washington west of the Cascades.



- Coastal Douglas-fir improved
- Western Hemlock woodsrun
- Ponderosa pine woodsrun
- Western Hemlock improved
- Noble fir woodsrun
- Noble fir improved
- Ponderosa pine improved
- Western Red Cedar woodsrun
- Western Red Cedar improved
- Coastal Douglas-fir woodsrun

## NWTIC MEMBERSHIP AND REPRESENTATIVES

Due to the establishment of MEDTIC we were happy to welcome eight new members: Indian Hill, Perpetua Forests, Murphy Timber, Josephine County, Hood River County Forestry, Fruit Growers Supply (California), Michigan-California Timber Company, and Green Diamond Resource Company (Oregon Operations) into NWTIC over these past 18 months. Weyerhaeuser Company purchased Plum Creek Timberlands but remained involved in NWTIC as the largest cooperator in MEDTIC. Keith also met with American Forest Management, Confederated Tribes of Grand Ronde, Cow Creek Forestry, Forest Investment Associates, Mason Bruce & Girard, Merrill and Ring, and Sierra-Pacific Industries (California) encouraging their participation. Growing the cooperator base is seen as vital to keeping PNW cooperative tree improvement vibrant into its sixth decade.

After the purchase of Plum Creek Timberlands and the sale of the Mosby Creek nursery and orchard complex to PRT Nurseries, Jim Smith ended his 39.5 year career at that location with Georgia-Pacific\The Timber Company\Plum Creek\Weyerhaeuser. During that time Jim effected the Toledo and Coos Bay first-generation programs, and the Toledo, CL98 and Coos Bay High 2nd cycle in-house programs, in addition to participating in and chairing the Trask and North Coast programs, being the first Chair of 2nd-cycle MEDTIC, and bringing Plum Creek into South Central Coast. In addition, he established numerous orchard blocks at Mosby Creek and even collected seed from some remote clone banks. All with his unique wry sense of humor and pleasant demeanor. Few people left such a

large tree improvement footprint and legacy in the region and so many well-wishers.

Other retirees through the end of June 2017 included Harry Bell (who led the Rayonier tree improvement program soon after its inception and brought Green Crow into NWTIC and 2nd cycle co-ops), Candace Cahill (starting with Rayonier in 1975), and Mike Albrecht (40 years with Weyerhaeuser\International Paper\Roseburg, almost entirely at the facility in Lebanon) and Rod Burns (Fruit Growers Supply).

This will be the last NWTIC report formatted by Sandie Arbogast, who has done the graphic work since the 2006-7 NWTIC report. Sandie retires from Oregon State University on June 30. Thank you for the help, Sandie!

NWTIC representatives as of June 2017, and the members they represented, were as follows:

### *Membership and Representatives*

- **Bloedel Timberlands:** Roy Bever
- **Bureau of Land Management:**  
Jeannette Griese and Michael Crawford
- **Campbell Global:** Dave Lortz and  
Dave Hamlin
- **Cascade Timber Consulting:** Bill Marshall
- **Fruit Growers Supply (Oregon):**  
Tom Shorey
- **Fruit Growers Supply (California):**  
Tom Young
- **Giustina Land and Timber:** Eric Kranzush
- **Giustina Resources:** Paul Wagner

- **Green Crow Management Services:**  
Jenny Knoth
- **Green Diamond Resource Co.:**  
Eric Schallon
- **Green Diamond Resource Co. (Oregon Operations):** Mike Williams
- **Hampton Tree Farms:** Beth Fitch
- **Hancock Forest Management:**  
Florian Deisenhofer
- **Hood River County:** Doug Thiesies
- **Josephine County:** Rick Kern
- **Lone Rock Timber:** Bryan Nelson
- **Miami Corp:** Joe Steere and  
Luke Bergey
- **Michigan-California Timber Company:**  
Bob Amesbury
- **Oregon Department of Forestry:**  
Don Kaczmarek
- **OSU College Forests:** Brent Klumph
- **Perpetua Forests:** Brian Sutch
- **Pope Resources:** Andrew Wodnik
- **Port Blakely Tree Farms:** Mike Warjone
- **Quinault Indian Nation:** Jim Hargrove
- **Rayonier Timberlands:** Josh Sherrill
- **Rocking C Ranch:** Paul Zolezzi
- **Roseburg Resources:** Sara Lipow
- **SDS Lumber:** Aric Lemmon
- **Sierra Pacific Industries:** Doug Sand and  
Josh Misenar
- **Silver Butte Timber Co.:** Darin McMichael
- **South Coast Lumber:** Marc Halley
- **Starker Forests:** Fred Pfund
- **Stimson Lumber Co.:** Margaret Banks
- **Timber West Forest:** Bevin Wigmore
- **Washington Department of Natural Resources:** Jeff DeBell
- **Weyerhaeuser Company:** Brian Baltunis

### ***Liaison Members***

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

### ***NWTIC personnel***

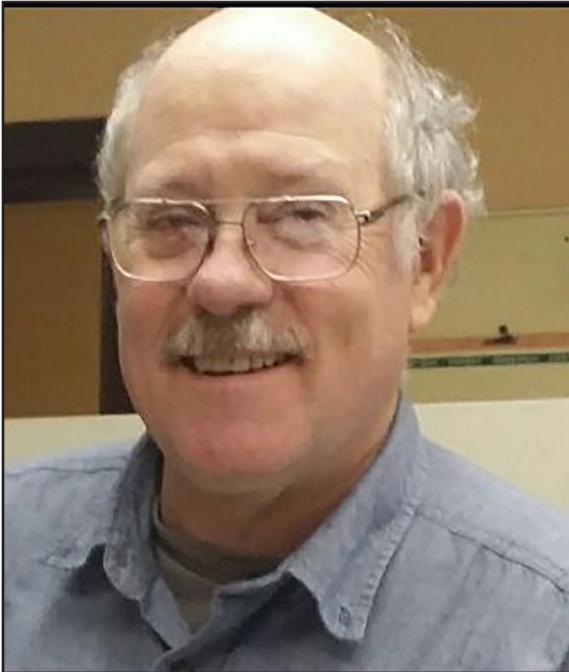
- **Director:** Keith Jayawickrama
- **Quantitative Geneticist:** Terrance Ye
- **Information Management Specialist:**  
Hao Truong



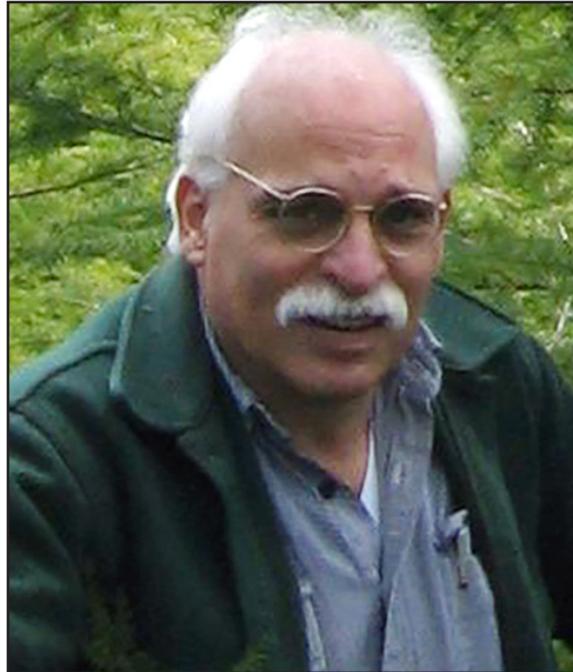
*Jim Smith*



*Candace Cahill*



*Mike Albrecht*



*Harry Bell*

*Long standing NWTIC representatives and tree improvement personnel continue to retire in numbers. Top Clockwise: Jim Smith, Georgia-Pacific\The Timber Company\Plum Creek\Weyerhaeuser; Candace Cahill Rayonier. (photo credit Josh Sherrill); Harry Bell, Rayonier\Green Crow; Mike Albrecht, International Paper\Roseburg. (photo credit Sara Lipow)*



9. Thinning 2nd-cycle NOCTIC test site. (photo credit John Jayne)

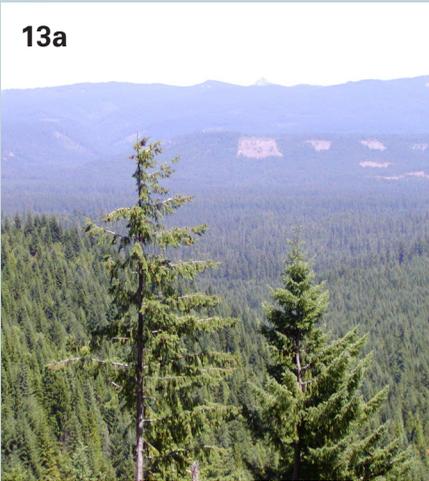
10. Collecting pollen at Green Diamond Resource Company orchard for HEMTIC crossing. (photo credit Dan Cress)

11. It is encouraging to be shown productive operational plantations: Jake Thiemens demonstrates impressive leader growth in a Hancock plantation near Neskowin.

12. NWTIC cooperators are exploring developing sources of western red cedar less susceptible to browse. Their motivation includes evidence from British Columbia where 12a. heavily browsed plots can be contrasted with 12b. adjacent free-to-grow cedar with high terpenes, and established at the same time using large stock. 12c. The Washington Department of Natural Resources is working on operational rooted cutting production at their Webster Nursery.

## THE MEDTIC 2ND-CYCLE COOPERATIVE

13a



13b



13c



13d



13e



13f



13g



13h



13i



The MEDTIC 2nd-cycle cooperative serves an area which though hot and dry in summer, is an important timber growing and manufacturing region. 13a. Medford timber stands; 13b. 5 year old plantation in Butte Falls (photo credit Eric Hippler); 13c., 13d. and 13e. Douglas-fir in Mid-Columbia.(photo credit Keith Jayawickrama and Doug Thiesies); 13f. A log pile near Glendale; 13g. Plywood manufacture at Bingen; 13h. Mike Crawford making crosses in the BLM's Provolt orchard; 13i. Crossing in Plum Creek's Butte Falls block.