

Early Assessment on Realized Genetic Gains from Second-Cycle Western Hemlock Tree Improvement

Terrance Z Ye¹, Keith JS Jayawickrama¹, and Eric C Turnblom²

¹ Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR, 97331, USA; ² School of Environmental and Forest Sciences, University of Washington, Seattle, WA 98195, USA

INTRODUCTION

Western hemlock (*Tsuga heterophylla* (Raf.) Sarg.) is an economically important tree species in the western North America. As an extremely competitive species on moist sites, it occupies large acreages of the coastal humid zone of Oregon (OR), Washington (WA), British Columbia (BC), and Alaska (3). First-cycle western hemlock tree improvement in the US Pacific Northwest has resulted in 2,283 selections of which 2,102 were tested using open-pollinated seed starting from 1975 (2). The best selections went into seed orchards and were also used as the parents in the second cycle breeding program in 1992. A total of 539 full-sib families were tested in OR and WA in this cycle. The third-cycle breeding was initiated in 2011 with its objectives to achieve higher genetic gains in growth, wood stiffness, adaptability, and tree health than the previous breeding cycles as well as to reduce stem defects.

While the second-cycle progeny tests have predicted large genetic gains over the unimproved stands, those sites were established as single-tree plots with a variety of genotypes under tight spacing and therefore unsuitable for long-term gain estimation (1, 5, 7). Thus, through the joint effort of the Stand Management Cooperative and the Northwest Tree Improvement Cooperative, long-term realized gain trials were established in OR and WA in large block-plots at operational spacing. The objective of this study is to verify early realized genetic gains in growth from those trials with the gains predicted from progeny tests.

MATERIAL AND METHODS

Two genetic entries were included in the tests:

- *Unimproved seed lot*: two separate woodsrun lots, one from WA and another from BC.
- *Improved seed lot*: a mix of nine top-performing second-cycle full-sib families.

The trials were established at four locations on a regular grid with 10' spacing in 2017 with a total of 18 unimproved and 18 improved plots. Each plot had 121 measure trees for a measurement plot of 0.28 acres. Three buffer rows were planted between plots. Total height (HT, cm), diameter at breast height (DBH, mm), and crown width (CW, cm) were measured for all trees in measurement plots after five growing seasons. Volume index (VOL) was calculated as $HT \times DBH \times DBH / 100,000$.

Data were analyzed using two linear models based on (1) plot means, and (2) individual tree measurements. Model 1 includes the following effects: population mean, site, seed lot, site by seed lot interaction, and residual. Model 2 includes all effects in model 1 plus family within seed lot as well as its interaction with site. All effects were considered as fixed effects except for residuals which were deemed as random. Hypothesis tests were conducted via Wald Test. Realized genetic gains were calculated as percentage increase of the improved materials over the unimproved using the estimated least-squares (LS) means.

RESULTS AND DISCUSSIONS

Significance tests

Significance tests were conducted by pooling all data across sites at both plot-mean level and individual-tree level. At plot-mean level (Table 1), there were significant differences in all traits among sites and between seed lots. The site x seed lot interaction effect was also significant for HT and VOL. While plot-mean based analysis usually required lots of replicates (e.g., 30 or more per treatment) and/or sites in order to detect statistical significances (4, 6), the differences between improved and unimproved seed lots in our data set appeared to be large enough to be detected statistically. Similarly, all effects including family and site x family interaction were significant for all traits in the individual-tree based analysis as well (results not shown).

Table 1. Significance tests based on plot means across all sites

Trait	Source	Degree of freedom		Wald statistics	P-value
		Numerator	Denominator		
HT	Site	3	14	119.72	<.001
	Seedlot	1	12	90.12	<.001
	Site x Seedlot	3	14	4.47	0.021
DBH	Site	3	13.1	44.75	<.001
	Seedlot	1	19	26.2	<.001
	Site x Seedlot	3	13.1	2.38	0.116
VOL	Site	3	11.8	61.85	<.001
	Seedlot	1	20.1	29.66	<.001
	Site x Seedlot	3	11.8	5.7	0.012
CW	Site	3	11.7	60.71	<.001
	Seedlot	1	22.2	4.52	0.045
	Site x Seedlot	3	11.7	2.35	0.125

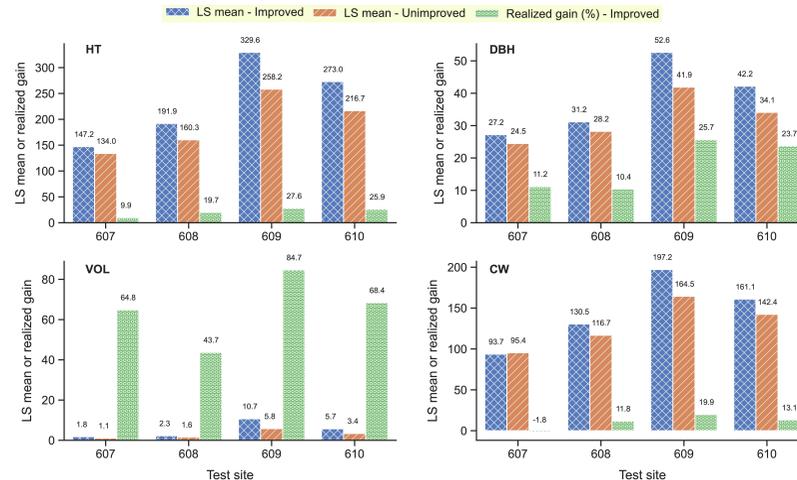


Figure 1. Least-squares means and realized gains at each site

Realized genetic gains

Realized genetic gain varied greatly among sites, from 9.9% to 27.6% for HT, 10.4% to 25.7% for DBH, and 43.7% to 84.7% for VOL (Figure 1). CW had positive realized gain on three out of the four sites. The improved seed lot performed consistently better than the unimproved seed lot at each site, suggesting that the significant site x seed lot interaction was non-crossover which resulted in no rank changes of seed lots.

When combining data from all four sites, the improved seed lot had realized gain of 22.4% for HT, and 19.1% for DBH, 72.8% for VOL, and 12.2% for CW (Figure 2). These values exceeded the expected genetic gains and were up to 200% higher than age-10 predicted genetic gains from progeny tests.

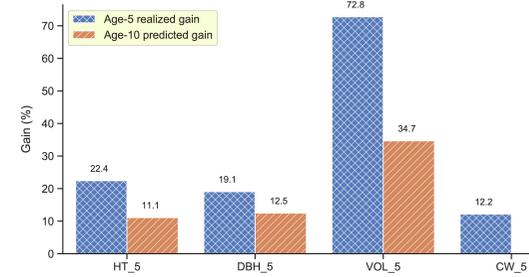


Figure 2. Realized gains at age 5 vs. predicted gains at age 10

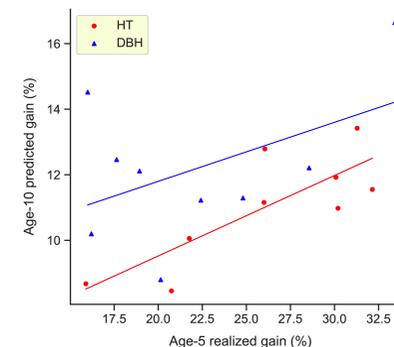


Figure 3. Age-5 realized gains vs. age-10 predicted gains for full-sib families

All full-sib families showed positive realized gains in growth (Figure 3). The large differences in realized gain between the highest- and lowest-gain tested families (i.e., 45% for HT, 44% for DBH, 130% for VOL, and 50% for CW), suggesting large possible gain in the next breeding cycle of western hemlock. The correlation coefficients between the age-5 realized gain obtained in this study and the age-10 predicted gain from progeny tests were 0.8 for HT, 0.5 for DBH, and 0.4 for VOL. Given the fact that these nine families were among the best selections for growth, these correlation estimates were likely underestimated due to sampling errors caused by the strong truncation selections.

CONCLUSIONS

Our study confirmed the hypothesis that there were significant differences in early growth between the elite full-sib families and the unimproved checklots. Even though these juvenile growth gains are likely to be higher than gains at rotation, the results demonstrated that tree improvement programs for western hemlock have been very effective in the US Pacific Northwest.

REFERENCES

- (1) Foster, G.S., 1989. Proc. 20th So. For. Tree Improv. Conf., pp. 21–35.
- (2) Jayawickrama, K.J.S., 2003. *Silvae Genet.* 52, 26–36.
- (3) Packee, E.C., 1990. *USDA Forest Service Agriculture Handbook* 654, pp. 613–621.
- (4) St Clair, J.B., et al., 2004. *West. J. Appl. For.* 19, 195–201.
- (5) Vergara, R., et al., 2004. *Can. J. For. Res.* 34, 2587–2600.
- (6) Weng, Y.H., 2011. *Silvae Genet.* 60, 178.
- (7) Ye, T.Z., et al., 2010. *Silvae Genet.* 59, 29–39.