

MGM Research Note #2022-1

Modeling Genetic Gain in MGM

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Incorporating estimates of genetic gain into growth models is needed to enable evaluation of yield implications from deployment of seed produced by tree breeding programs. While TIPSy (Table Interpolation Program for Stand Yields) includes genetic worth in its yield calculations for B.C., there are currently no models available for Alberta which provide the ability to estimate yield implications arising from planting improved stock.

Flewelling (2008) recommends that using genetic worth values to develop modified top height-age curves, based on applying multipliers to natural stand top height-age curves could be fast and straightforward to implement. TIPSy uses the Lambeth equation (Lambeth 1980) for estimating change in top height as a function of selection age (age at which genetic worth is determined) and stand age. This approach effectively modifies the site index curve, but it results in a decrease in the magnitude of the height increase between selection age (where height would be increased by a percentage equal to genetic worth) and older ages.

Recently, Luo and Thomas (2021) analyzed data for white spruce and lodgepole pine provenances and found that an adjusted Lambeth equation was the most robust model for use in Alberta.

Their adjusted Lambeth equation has the form:

$$r_{t,T} = B_0 + B_1(LAR)$$

Where $LAR = \ln(t/T)$;

And, when $T > t$, T = age of interest and t = selection age;

With B_0 and B_1 varying by species.

Values for B_0 and B_1 for white spruce and lodgepole pine are summarized in Table 1.

Table 1. Parameter estimates, R^2 and residual degrees of freedom for the adjusted Lambeth equations for white spruce and lodgepole pine in Alberta (from Luo and Thomas 2021 Table 2).

Species	B_0	B_1	R^2	df
white spruce	0.993	0.255	0.761	65
lodgepole pine	1.017	0.445	0.723	22

The adjusted Lambeth equation can be used to calculate adjusted top height (H_{gw_i}) of improved material using the following equation:

$$H_{gw_i} = (((GW/100) * r_{t,T}) + 1) * H_{t0,i}$$

where:

H_{gw_i} is the calculated top height for the gw value at $T=i$

GW is genetic worth expressed as a %

$H_{t0,i}$ is top height for a stand with wild seed ($gw=0$)

Figure 1 illustrates the effects of GW on top height values for white spruce and lodgepole pine with a site index of 20 m at age 50. Table 2 illustrates the % increase in top height at age 50 associated with changes in genetic worth at age 15.

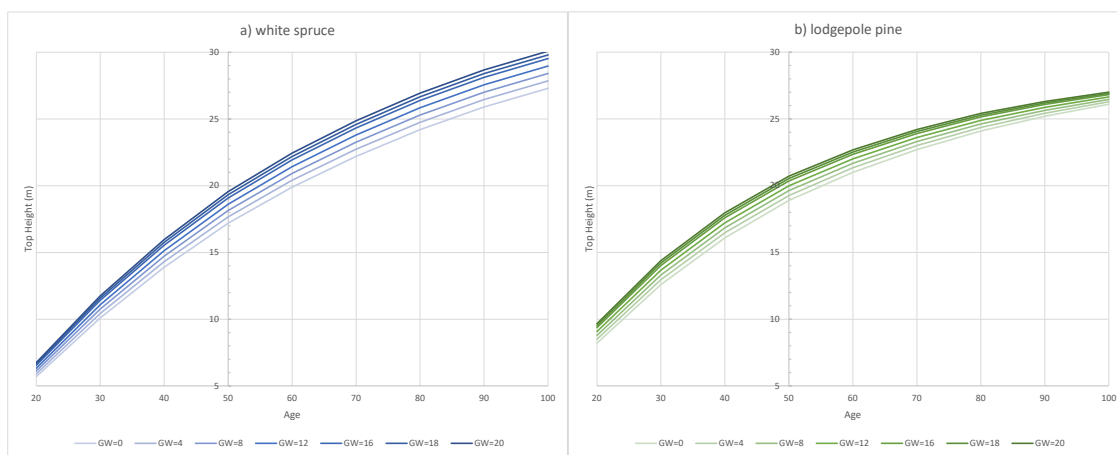


Figure 1. Estimated top height – age trends for a range of values of GW (assessed at age 15) for a) white spruce; and b) lodgepole pine with a site index of 20 m at 50 years. (Site index was calculated following Huang et al. 2009).

Table 2. Effects of Genetic Worth (GW) assessed at age 15 on estimated increases in top height at age 50 for white spruce and lodgepole pine with site index for wild stock of 20 m@age 50.

GW	% increase in top height at age 50	
	White spruce	Lodgepole pine
0		
4	2.7%	1.9%
8	5.5%	3.8%
12	8.2%	5.8%
16	11.0%	7.7%
20	13.7%	9.6%

This approach provides a method for calculating increases in top height and height growth associated with using improved seedlots. Since diameter growth is predicted as a function of height growth and competition in MGM, adjusting height growth provides a starting point for estimating potential yield gains associated with planting improved material.

Incorporation of genetic gain equations into MGM

These genetic gain equations and parameters for both white spruce and lodgepole pine were coded into MGM21. Several modifications in coding were necessary to support implementation of a stand level modelling approach in MGM which is an individual tree model.

In MGM, the top tree (largest DBH tree) grows on the site index curve while subordinate trees have reduced height due to competition. Maximum height increment for the top tree is the difference between site height at a given age and the site height at the age plus one year.

Maximum height increment for tree improvement is the difference between top height at a given age and the top height at the age plus one year for improved trees. For lodgepole pine, top heights at both ages are calculated directly using the top heights calculated as part of normal projection, adjusted upward using genetic gain equations and corresponding coefficients for selection age and genetic worth. Maximum height increment is applied to each tree as in a normal projection.

Maximum height increment for white spruce is complicated because MGM annually adjusts tree age to match the age required to reach a tree height on the site index curve (step 2 below). For lodgepole pine, this process is only done once at the beginning of the projection. For white spruce, the process for calculating maximum height increment is as follows:

- 1) The tree height provided in the tree list is tree-improved height (includes genetic gain). However, genetic gain is an adjustment on the top height of non-improved stock, therefore it was necessary to calculate the top height as if it were non-improved stock. This was done by subtracting the genetic gain adjustment from actual height using a re-arranged genetic gain equation and corresponding parameters for a given selection age and genetic worth. The result is site height at a given age.
- 2) For this new non-improved site height, the corresponding breast height age from the site index curve was determined.
- 3) The site height for breast height age plus one year is then calculated from the site curve.
- 4) The new tree improved top height is calculated based on site height at breast height age plus one year, using the genetic gain equations, and the corresponding selection age and genetic worth parameters.
- 5) Maximum height increment for improved trees is the difference between the tree improved top height at a given age and the tree improved top height at the age plus one year.

Additional constraining assumptions:

- Height increment for improved stock cannot be less than the height increment from the base site index curve.

The “Options” event and dialogue were updated in the MGM crop plan interface to toggle tree improvement and accept the user selectable tree improvement variables: species, selection age and genetic worth (Figure 2).

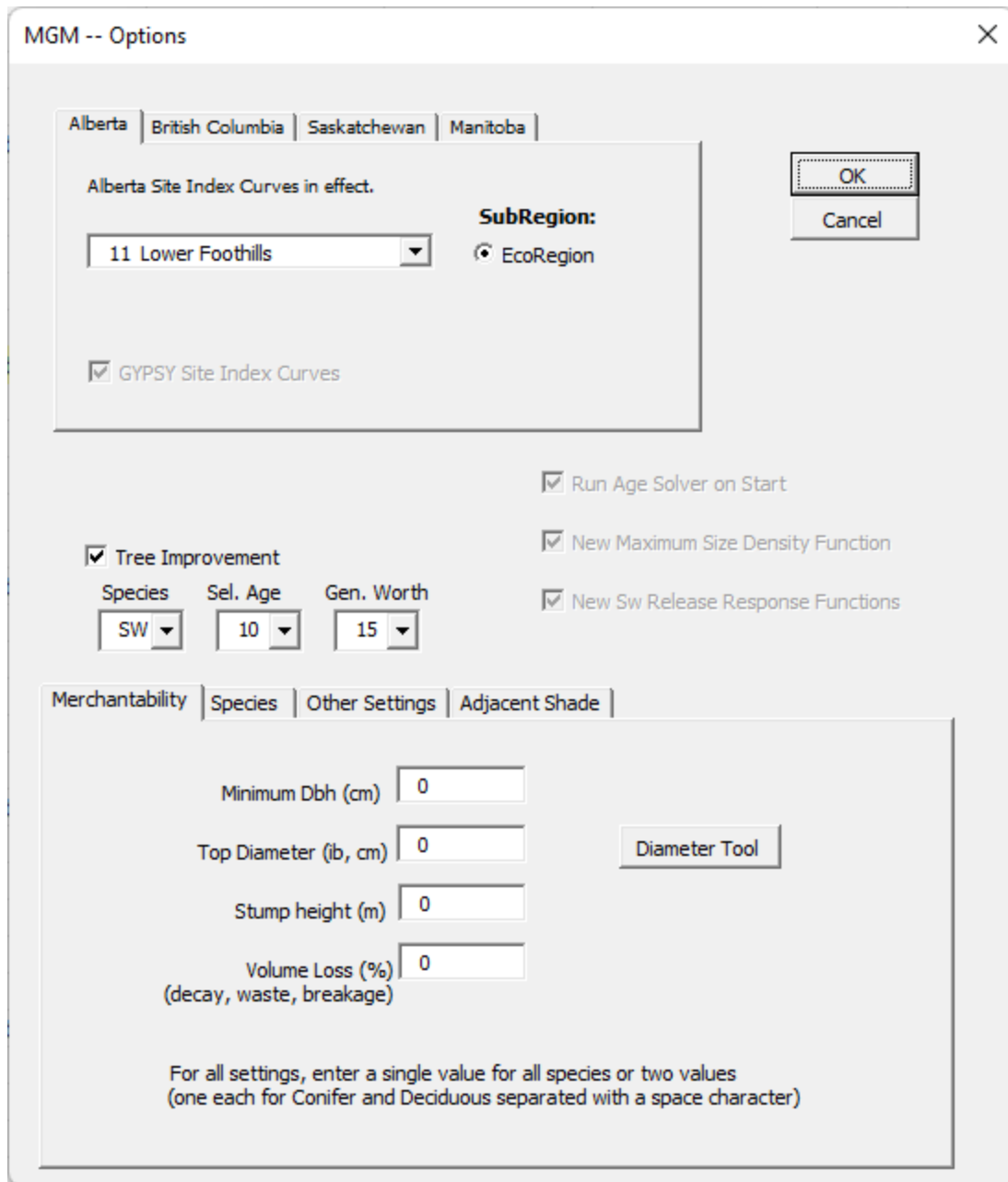


Figure 2. MGM options window with the new Tree Improvement option shown as selected.

Demonstration of Results

To demonstrate effects of genetic worth on volumes predicted by implementing the Luo and Thomas (2021) age-age correlation functions for white spruce and lodgepole the MGMs tree list generator was used to initialize the model for five scenarios ranging from planting stock derived from wild seed (0% genetic worth) to planting stock with 20% genetic worth. At initialization

(age 10) improved material was assumed to be larger by an amount equal to genetic worth (GW) for height, diameter and maximum height.

Table 3 summarizes tree sizes input into the MGM tree list generator to initialize simulations at age 10. Initial densities at age 10 were set to 1600 sph for white spruce and lodgepole pine. Additional MGM settings were: Lower Foothills Natural Subregion, GYPSY site index curves, site index = 22m, CMI = 10, maximum size density adjustment = on.

Table 3. Values used to initialize MGM for 5 levels of genetic worth assessed at age 10 using the MGM tree list generator. Standard deviation (shown in parentheses) of average height for GW =0 was based on values observed in spruce and pine performance surveys while for other values of GW SD was increased by the GW% value. Standard deviation for DBH was set to maximum values accepted by MGM.

Species	GW (%)	Average height (m)	Average DBH (cm)	Maximum height (m)
white spruce	0	1.80 (0.90)	1.60 (0.48)	2.5
	5	1.89 (0.95)	1.68 (0.50)	2.63
	10	1.98 (0.99)	1.76 (0.53)	2.75
	15	2.07 (1.04)	1.84 (0.55)	2.88
	20	2.16 (1.08)	1.92 (0.57)	3
lodgepole pine	0	2.20 (0.80)	2.40 (0.72)	3
	5	2.31 (0.84)	2.52 (0.76)	3.15
	10	2.42 (0.88)	2.64 (0.79)	3.3
	15	2.53 (0.92)	2.76 (0.83)	3.45
	20	2.64 (0.96)	2.88 (0.86)	3.6
trembling aspen	0	3.2 (1.0)	2.3 (0.69)	4.5

Results illustrate predicted effects of genetic worth on gross total stand volumes and top height, (Figures 3 and 4) for spruce and aspen stands with base SI=22m. The results for projections of gross total stand volume to age 100 for white spruce and lodgepole pine provided in Figures 3 and 4 indicate that there is a consistent trend of increasing conifer volume with increasing genetic worth.

Yields estimated at age 100 for white spruce and 75 for lodgepole pine are shown in table 4. These ages were selected for this presentation because they correspond to commonly used rotation ages for these species. For white spruce, volume at age 100 increases from 462.1 m³/ha for stands regenerated using wild seed with site index of 22m to 546.4 m³/ha for a stand with a

genetic worth of 20. This translates into a gain of 84.3 m³/ha or 18.2% for material with GW 20 over the wild origin material. For lodgepole pine, volume at age 75 increases from 402.1 m³/ha for wild seed to 438.6 m³/ha for a stand with a genetic worth of 20, representing a 36.5 m³/ha (9.1%) gain at age 75.

Figures 5 and 6 illustrate interactions between aspen density and GW for spruce and pine, and suggest that gains are still realized in the presence of aspen while the magnitude of gains are reduced by increasing aspen densities. It is interesting to note that increases in genetic gain for either spruce or pine led to reductions in aspen volumes due to accelerated growth and increased competitiveness of the conifers.

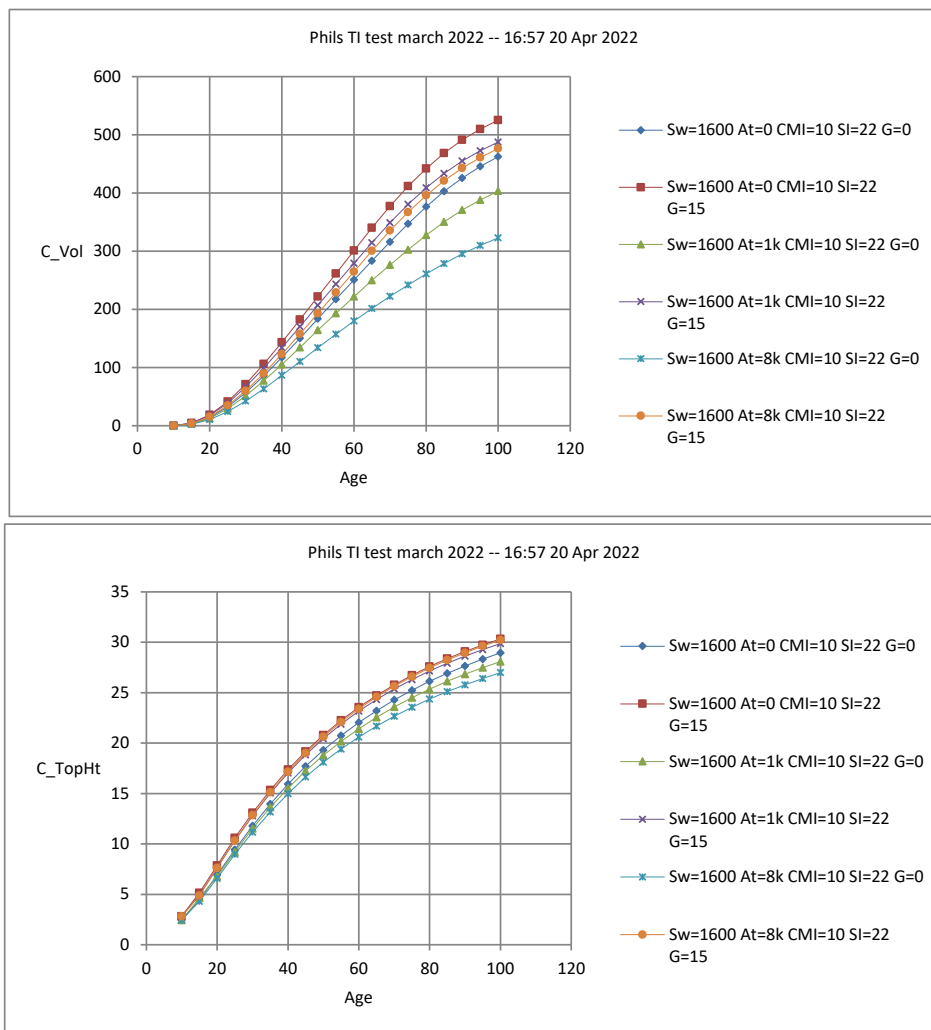


Figure 3. MGM projections of gross total white spruce volume (C_Vol, m³/ha) and top height (C_TopHt, m) to age 100 based on five values of genetic worth (0, 5, 10, 15 and 20) at a selection age of 10 years for a site index of 22m and CMI=10 in the Lower Foothills.

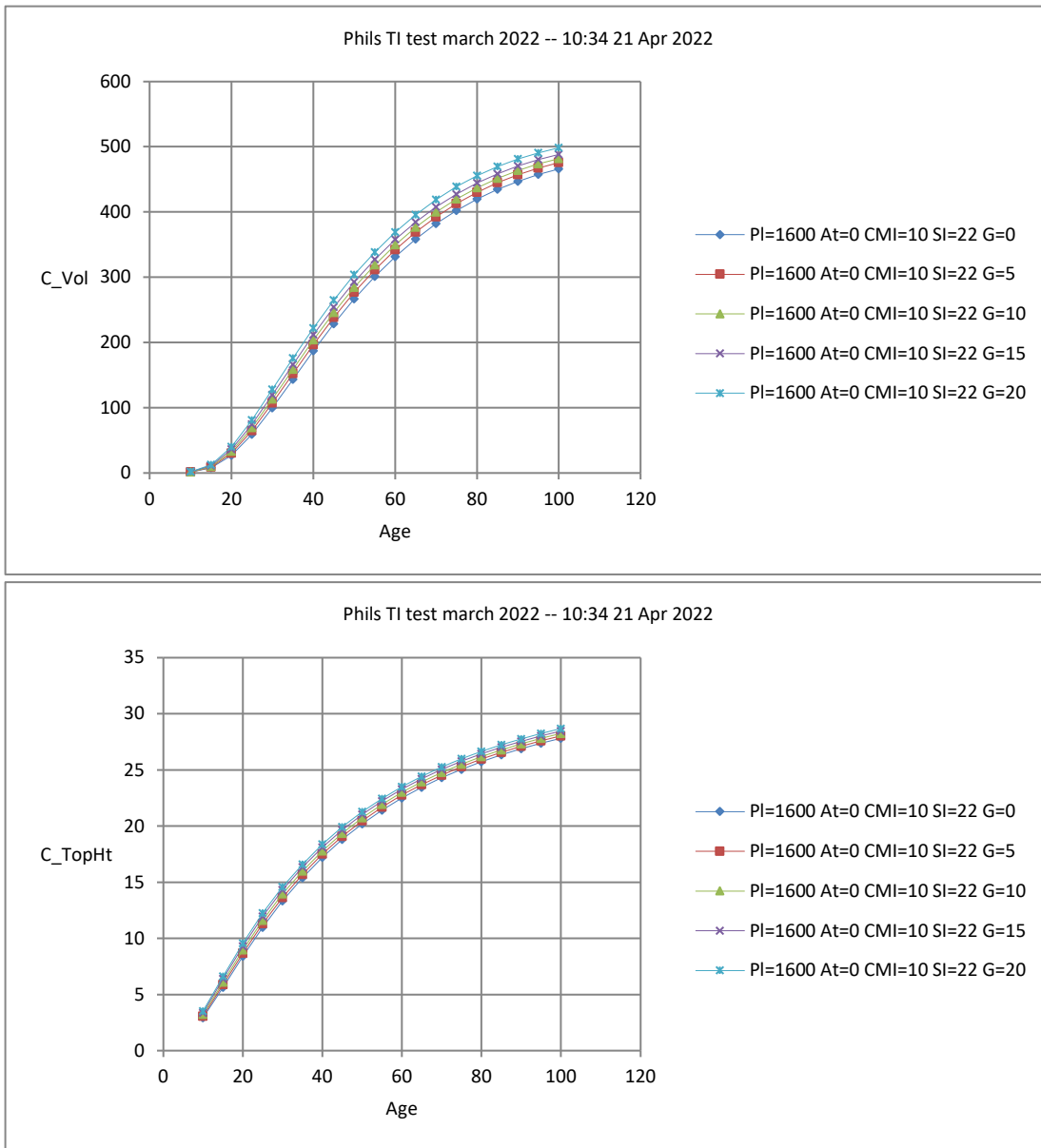


Figure 4. MGM projections of total lodgepole pine volume (C_Vol , m^3/ha), and top height (C_TopHt ,m) to age 100 based for five values of genetic worth (0, 5, 10, 15 and 20) at a selection age of 10 years for a site index of 22m and CMI=10 in the Lower Foothills.

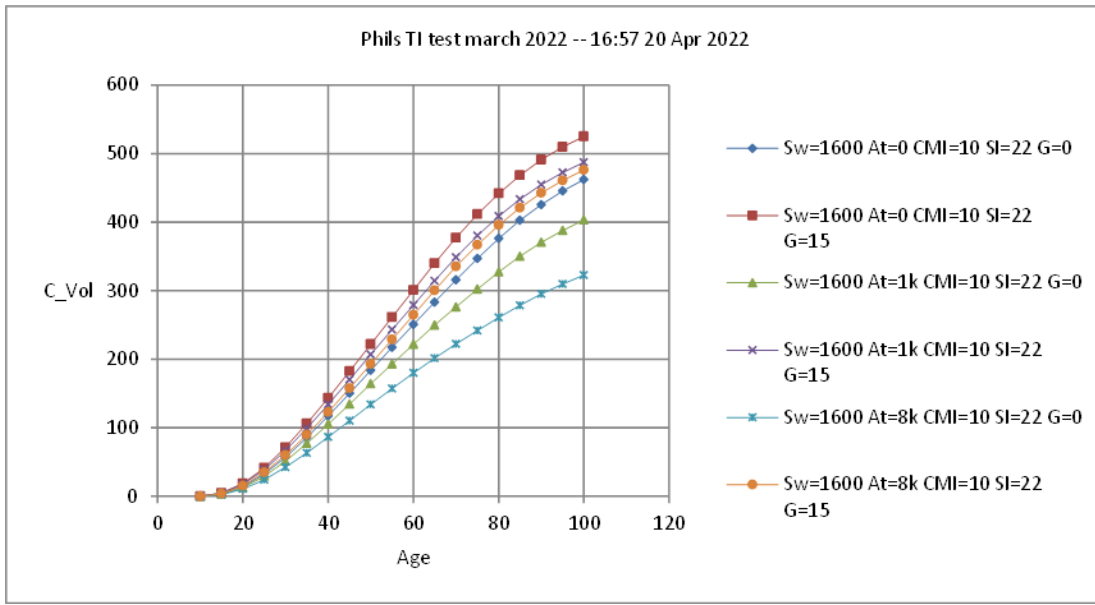


Figure 5. Effects of aspen density (0=0 sph, 1k=1000 sph, 8k=8000 sph) and genetic worth (G=0 and G=15) on predicted gross stand volumes (C_Vol , m³/ha), for white spruce with baseline site index of 22m and CMI=10.

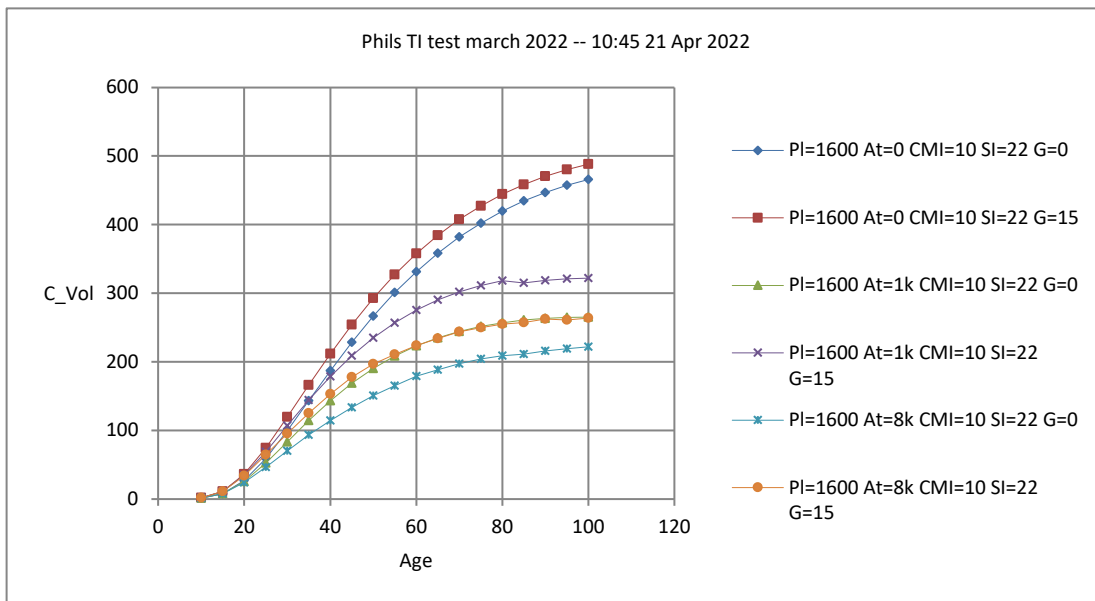


Figure 6. Effects of aspen density (0=0 sph, 1k=1000 sph, 8k=8000 sph) and genetic worth (G=0 and G=15) on predicted gross stand volumes for lodgepole pine with baseline site index of 22m and CMI=10.

Table 4. Effects of genetic worth (assessed at age 10) on gross total stand volume at age 100 for white spruce and at age 75 for lodgepole pine predicted by these MGM simulations (SI=22m). Relative gain % indicates % of volume provided by wild origin seed with genetic worth=0%.

Genetic Worth (%)	white spruce		lodgepole pine	
	Conifer Volume (m³/ha)	Relative Gain %	Conifer Volume (m³/ha)	Relative Gain %
0	462.1		402.1	
5	482.0	104.3%	412.6	102.6%
10	502.9	108.8%	419.7	104.4%
15	525.1	113.6%	427.3	106.3%
20	546.4	118.2%	438.6	109.1%

The lower gains shown for lodgepole pine than for spruce are somewhat surprising. Luo and Thomas (2021) confirm that age-age correlations for lodgepole pine are lower than for white spruce in Alberta, resulting in smaller yield gains.

In this implementation of genetic worth in MGM we assume that increases in diameter increment of both improved and wild material are effectively predicted as a function of increases in height increment and tree size. Further research is required to determine whether this assumption is correct, or if new compatible diameter increment models, which include height increment in the prediction of diameter increment, are required for improved seedlots.

Validation of MGM behavior against actual data was not possible at present as there are currently no realized gain trials old enough to permit this. Testing using data from plantations established using improved material, notably from realized gain trials which are 10 to 14 years old, should be undertaken when such data are available.

In addition to the acquisition of realized gains and other data to evaluate MGM, ongoing work is needed to determine if tree taper and diameter growth functions require modification to better model improved material. Evaluation of the effects of breeding on survival probability, maximum stand densities (stocking limits) and sensitivity to climate effects may also be required.

References

- Flewelling, J.W. 2008. Proposal for genetic gain estimation for three Alberta tree improvement programs. Report prepared for Alberta Sustainable Resource Development, Forest Management Branch.
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