Theme: Radiata Management

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Testing the Performance of the 300-Index Growth Model for Major Genotype Groupings Across New Zealand

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EXECUTIVE SUMMARY

Using a large national series of genetic gain trials, the 300 Index was estimated for each PSP plot and analysed. The averaged values of the 300 Index were not consistent, but generally increased with increasing GF rating, showing the gradual improvement in growth rate achieved by several decades of selection and tree breeding. These trends are generally apparent in all growth model regions with only a minor GxE interaction apparent in the analysis.

The summary of drift factors gives an indication of how well the 300 Index Growth Model performs for each GF rating. These show that the model is unbiased for GF14 and for most of the higher GF rated seedlots. This means that when predicting harvest volume for the GF14 seedlots from a mid-rotation inventory, the model will on average across these trial sites, have a bias in predicted harvest volume of less than 1%. Similar low levels of bias would be achieved using the model with higher GF rated seedlots.

These results imply that the 300 Index model can be used without adjustment for most seedlots rated GF14 and higher when projecting forward from plot measurements. In other words, the plot measurements themselves must adequately account for any level of genetic improvement, and there is no need to make any additional genetic gain adjustment to the growth model.

There may be some exceptions to this general result for some individual seedlots. It has been shown that the model under-predicts for a specific GF22 seedlot, especially on more fertile sites. These results suggest that adjustment to the model using drift factors may give improved results for a limited number of specific seedlots.

In general, the 300 Index Growth Model does not require adjustment when used with higher GF ratings.

INTRODUCTION

The radiata pine breeding programme has developed a wide range of improved breeds and clones. Growth and form (volume and crown) were selection criterion for earlier breeds; wood quality is a recognised selection criterion in the later breeds and clonal varieties. From an industry perspective, growth and wood quality models need to be sensitive to the effects of tree improvement, and applicable to a wide range of breeds and clonal varieties on a wide range of sites and applied silviculture regimes.

Previously, stand-level models accommodated the effects of tree improvement through the incorporation of genetic gain growth-rate multipliers in the basal area and height prediction equations (Carson S, *et al.* 1994). To-date, neither the 300 Index Growth Model (Kimberley *et al*, 2005), nor associated wood property algorithms, explicitly include the effects of tree improvement, nor is it clear if explicit inclusion is necessary.

Another consideration is the influence of site on genetic gains. It is well known that site factors (soil, climate, etc.) strongly influence growth rates and wood quality attributes. However, the existence or non-existence of interactions between genetics and site is the subject of debate. Although not the primary focus of this study, we also consider the question of whether genetic gains in growth operate independently across sites. If this is not true, models may potentially require regionalisation.

The objectives covered in this report are to:
- Tabulate the 300 Index in a 2-way table of genotype grouping by site type.
- Test the performance of the 300 Index Growth Model for major genotype groupings across a range of sites. If necessary, derive drift factors to allow the model to be run without bias.

METHODS

Meeting these objectives required extensive data from field trials testing genotype groupings across a wide range of sites. Ideally, these trials would be large-plot genetic gains trials, to avoid plot-edge effects which could potentially influence the growth rates. To meet these objectives, genetically improved radiata pine trials established by the Stand Growth Modelling Cooperative (SGMC) between 1978 and1994 throughout New Zealand were used. These trials consist of three series, namely the Genetic Gains, Silviculture Breed, and Special Purpose Breed series.

The growth data from these trials have been managed by the Permanent Sample Plot (PSP) team of Scion (Ellis *et al*, 1997). Hayes (2001) documented the workplans including the plot layout and genotype history. Each plot was classified into a genotype grouping on the basis of its assigned Growth and Form (GF) rating. The trials were classified into eight growth model (GM) regions, namely Canterbury (CY), Clays, Central North Island (CNI), East Coast (EC), Hawkes Bay (HB), Nelson/Marlborough (NN), Sands and Southland (SD). In total, growth data from 47 trials containing 1377 plots were analysed in this study.

This study utilised an Excel-based VBA application which can be used to estimate the 300 Index and Site Index for each PSP plot measurement. To obtain tables of mean 300 Index by GF and GM region, indices were firstly obtained for each PSP using the measurement closest to age 20 years. The following mixed model was then fitted using the SAS procedure PROC MIXED:

$$I300_{ijk} = a + t_i + g_j + e_{ijk}$$

where $I300_{ijk}$ is the 300 Index estimated for the kth plot in the jth genotype class in the ith trial, a is the overall mean, t_i is a random term representing the ith trial, g_j is a fixed effect representing the jth genotype class, and e_{ijk} is the residual error term. From this model, means for each genotype class adjusted to account for imbalance between genotype classes across the trials and trial series were obtained. The analysis was performed across all trials to obtain national 300 Index means for each genotype class, and separately for each GM region to obtain regional means.

The 300 Index was next calculated for each plot measurement and tests were performed for any systematic 'drift' in the index over time within each measurement plot. A systematic drift in the index is evidence of model bias. A negative drift in the index indicates that the model will over-predict yield, while a positive drift indicates that the model will under-predict. When a systematic drift in the index is absent, it can be concluded that the model is providing unbiased predictions of yield over time. This technique was used by Kimberley *et al.* (2006) and Kimberley (2007) in the validation of the growth model. The 300 Index Growth Model has a facility to cancel such bias using a linear drift factor. Potentially, different drift factors could be used to account for differences in growth trajectory between genotypes.

To test for differences in 300 Index drift between genotype groupings, the following random coefficient regression model fitted using PROC MIXED:

$$I300_{ijkl} = g_j + t_i + p_{k(i)} + gd_j \times Age + td_i \times Age + e_{ijkl}$$

where $I300_{ijkl}$ is the 300 Index estimated for the lth measurement in the kth plot in the jth genotype class in the ith trial, g_j is a fixed effect term for the jth genotype, t_i is a fixed effect for the ith trial, $p_{k(i)}$ is a fixed effect term for the kth plot in the ith trial, gd_i is a fixed effect drift slope term for the jth genotype class, td_i is a fixed drift slope term for the ith trial, Age is the age of the measurement, and e_{ijkl} is the residual error term.

RESULTS

Productivity Index Table

Mean 300 Indices are plotted in Figures 1-3 and tabulated in Table 1. Overall means of 300 Index for each GF class are shown in Figure 1. These indicate a general trend for the index to increase with GF rating. Compared with GF2, an unimproved seedlot, the mean 300 Index is 10% higher for GF14, 15% higher for GF22, and 17% higher for GF30. The average 300 Index for each GM region (Figure 2) indicates that the Sands and Canterbury regions had the lowest mean 300 Index while the Clays, East Coast and Hawkes Bay regions had the highest mean 300 Index.
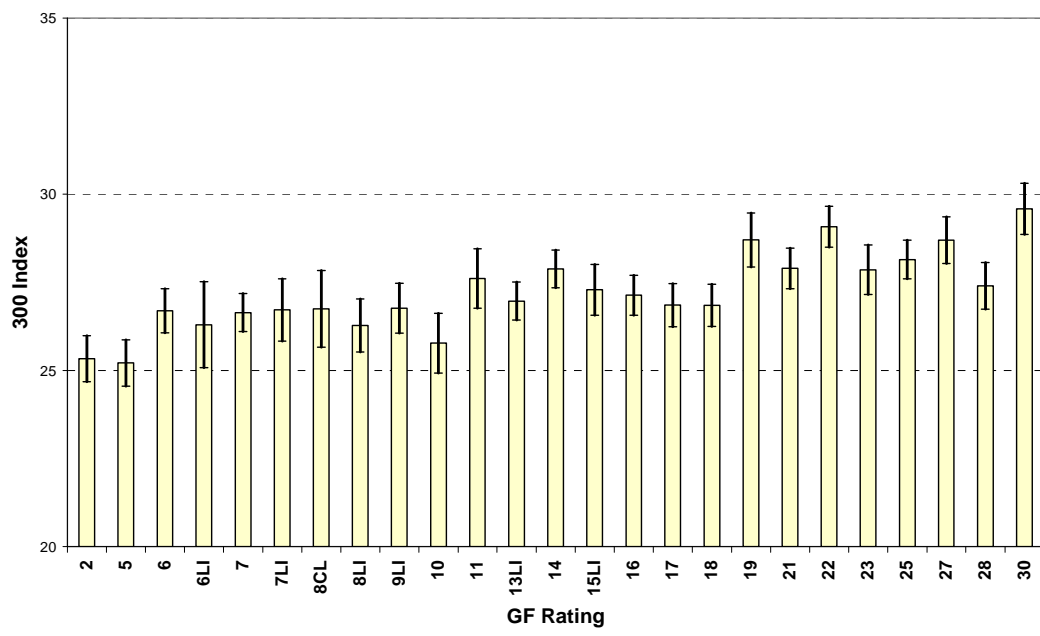

Figure 1. Mean 300 Index for each GF rating across NZ. The error bars show the standard errors of the means. LI = Long Internode and CL = Climbing select.
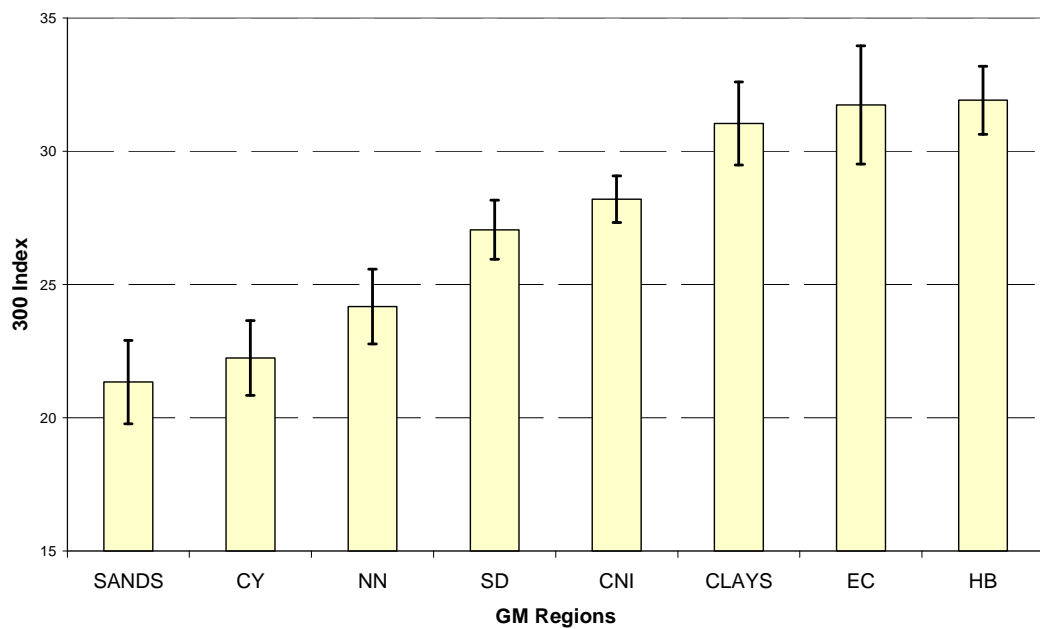

Figure 2. Mean 300 Index for the eight Growth Model regions. The error bars show the standard errors of the means.

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In Figure 3, the mean 300 Index is shown for each genotype within each region. GF22 performed particularly well in Hawkes Bay, Nelson and Southland. In these regions, GF22 consists of seedlot '850-55x850-96', which is highly rated for growth but has a lower rating for straightness and branching when compared with most other high GF seedlots (Hayes *et al*, 1998).
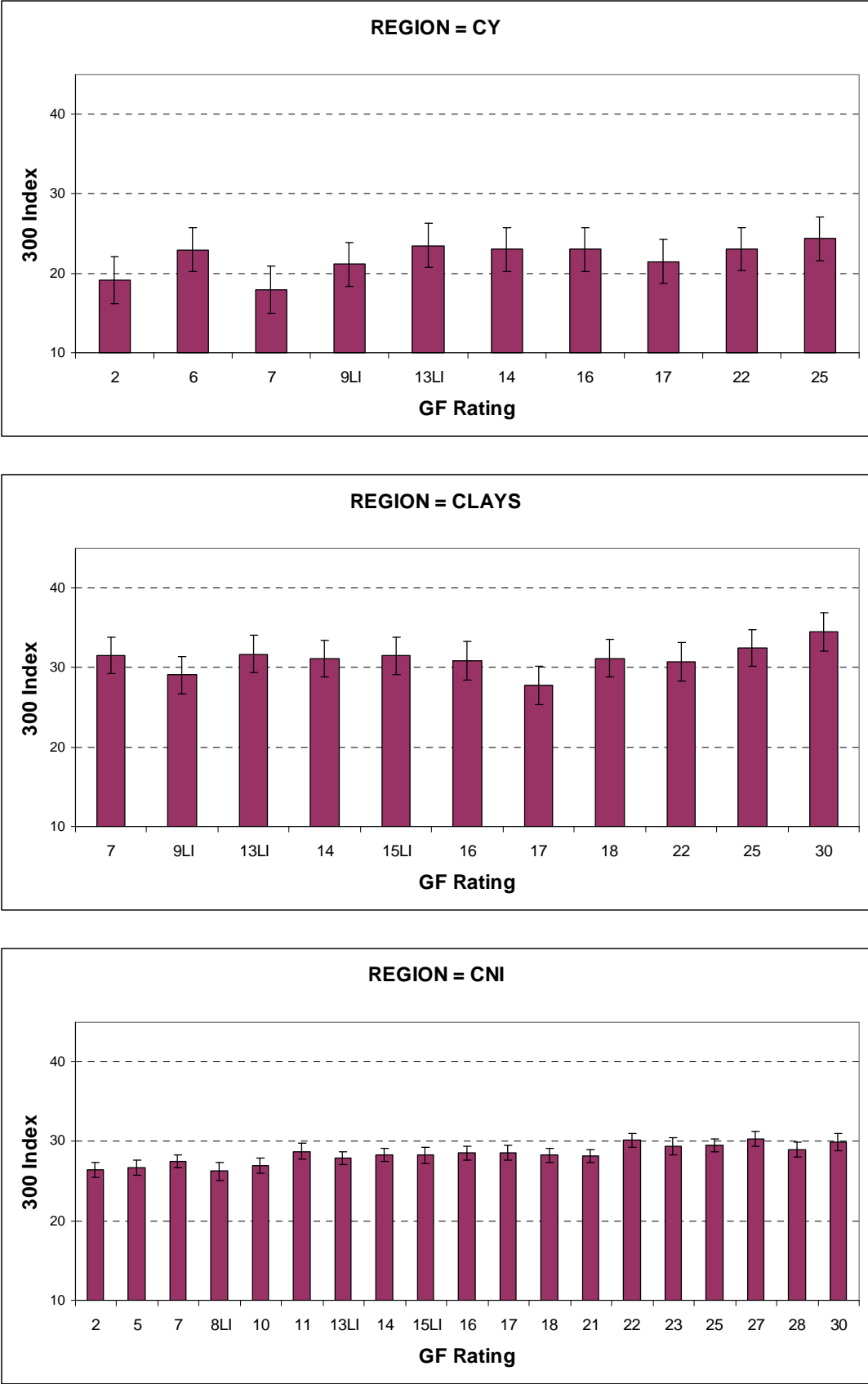

Figure 3. Mean 300 Index for each GM region by GF rating. The error bars show the standard errors of the means.
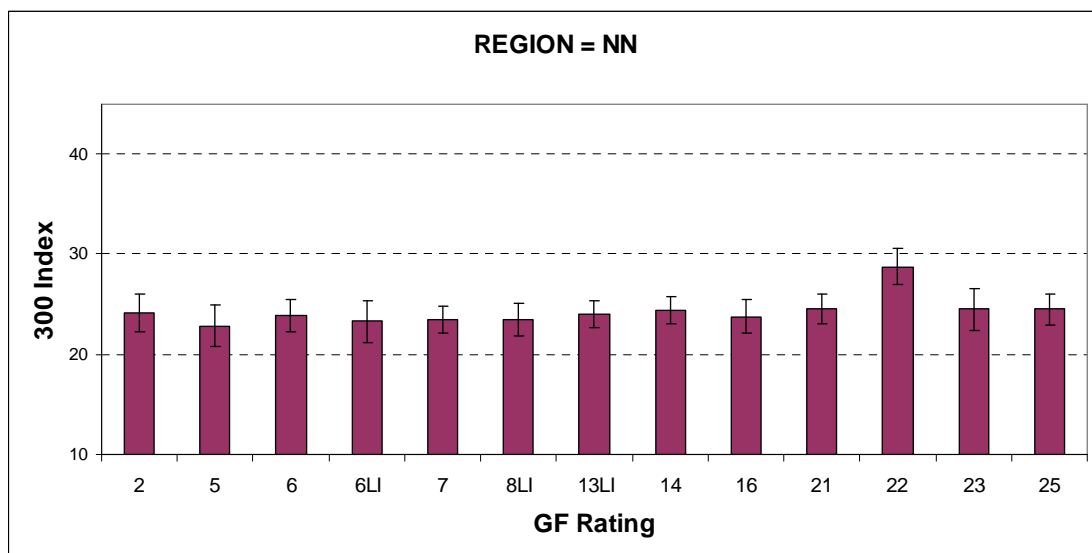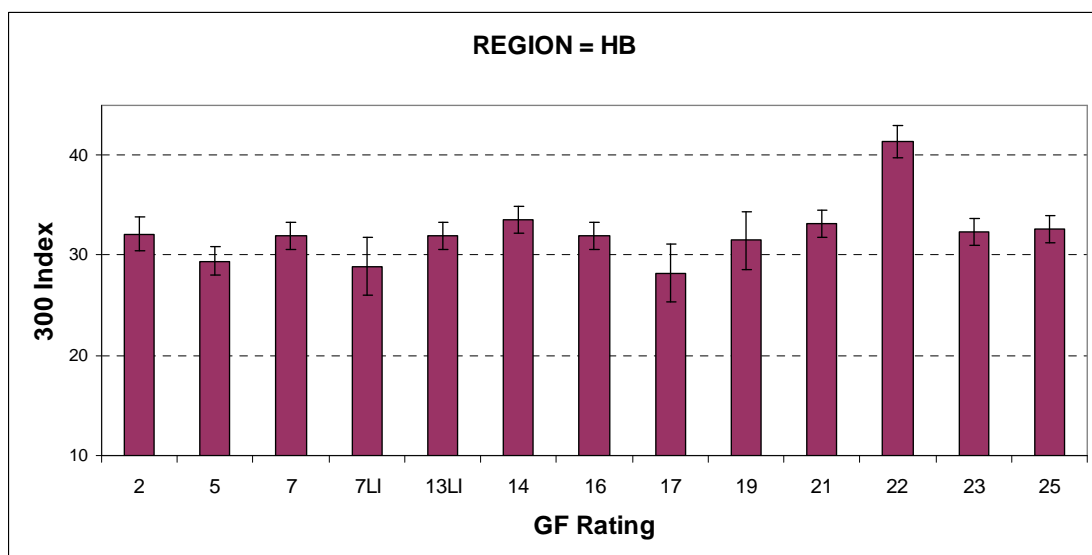
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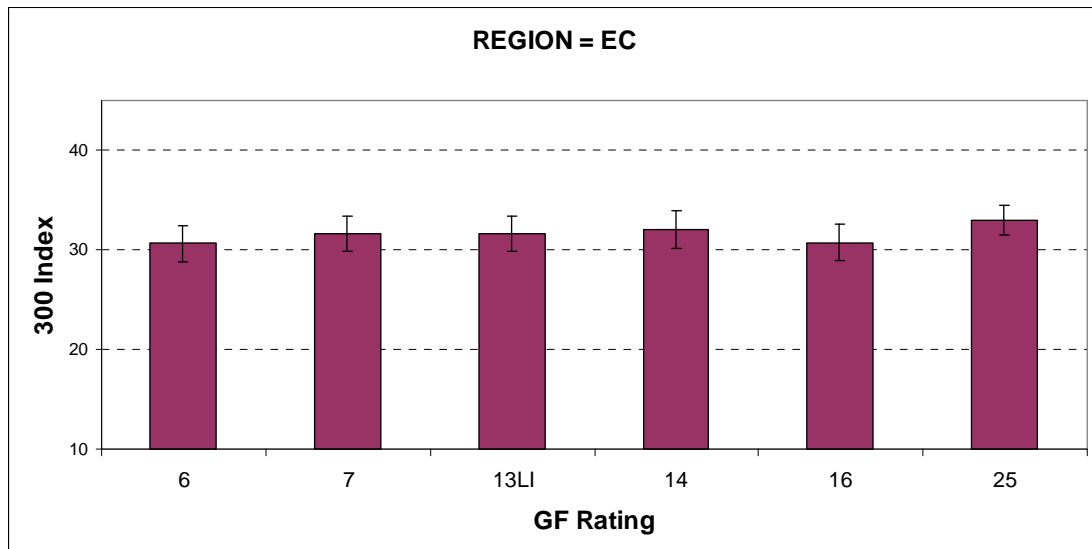
Figure 3 (Cont'd). Mean 300 Index for each GM region by GF rating. The error bars show the standard errors of the means.
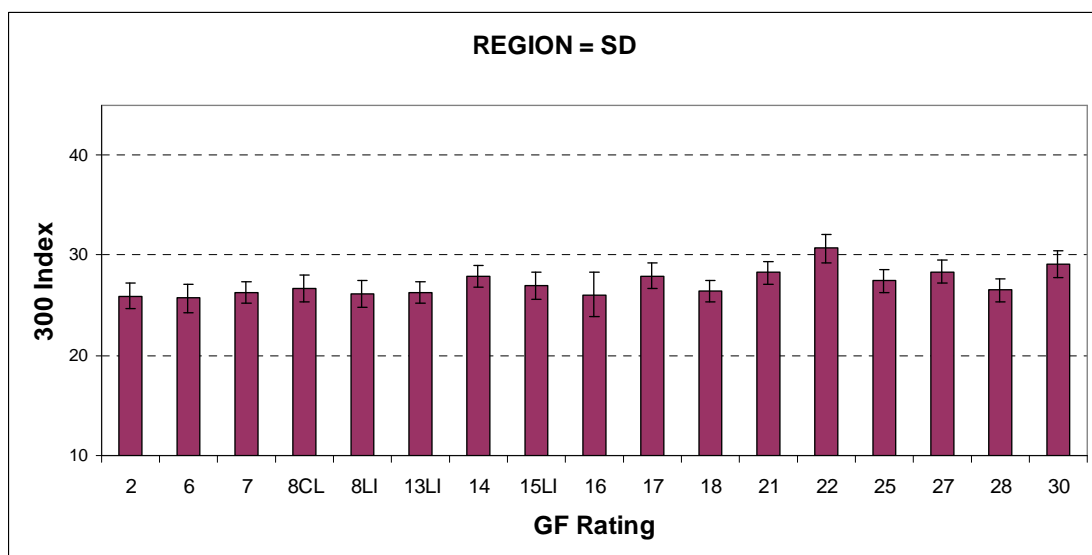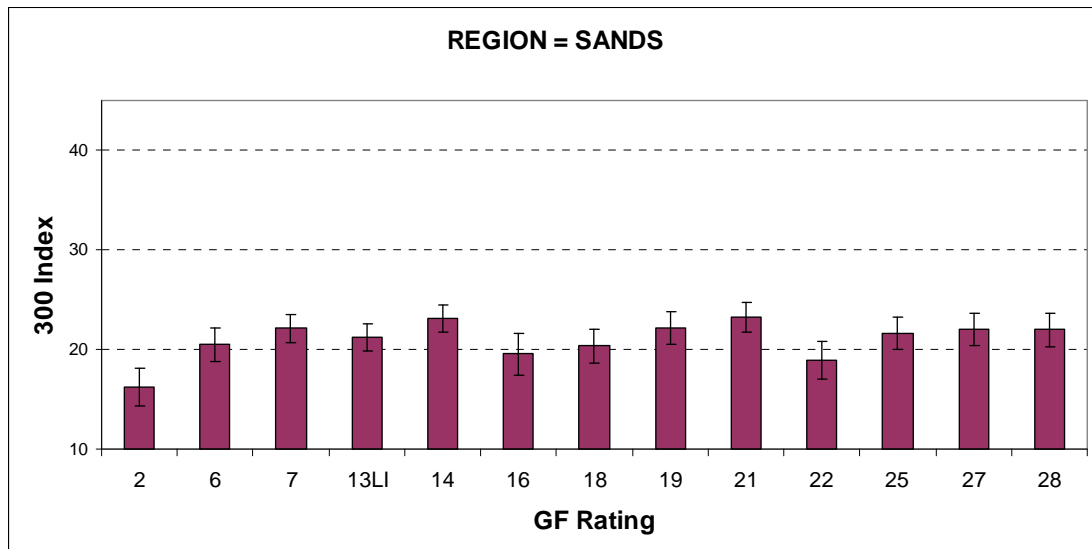
Figure 3 (Cont'd). Mean 300 Index for each GM region by GF rating. The error bars show the standard errors of the means.

Table 1. Lookup table of mean 300 Index by genotype class for all New Zealand and for each GM region.

GF	GM REGIONS								ALL NZ
	CY	CLAYS	CNI	ECOT	HB	NN	SANDS	SD	
2	19.2		26.4		32.1	24.2	16.2	25.9	25.3
5			26.7		29.4	22.8			25.2
6	22.9			30.6		23.9	20.5	25.7	26.7
6LI						23.3			26.3
7	18.0	31.5	27.5	31.6	31.9	23.4	22.1	26.3	26.6
7LI					28.9				26.7
8CL								26.7	26.7
8LI			26.2			23.5		26.1	26.3
9LI	21.1	29.1							26.8
10			26.9						25.8
11			28.8						27.6
13LI	23.5	31.7	27.9	31.6	32.0	24.0	21.2	26.3	27
14	23.0	31.2	28.4	32.0	33.5	24.4	23.1	27.9	27.9
15LI		31.5	28.2					27.0	27.3
16	23.0	30.8	28.5	30.7	32.0	23.8	19.6	26.1	27.1
17	21.5	27.8	28.5		28.2			28.0	26.9
18		31.2	28.2				20.4	26.4	26.8
19					31.5		22.2		28.7
21			28.2		33.2	24.5	23.2	28.3	27.9
22	23.1	30.7	30.2		41.3	28.8	18.9	30.7	29.1
23			29.4		32.4	24.5			27.9
25	24.3	32.5	29.5	32.9	32.6	24.5	21.7	27.4	28.1
27			30.3				22.1	28.4	28.7
28			29.0				22.0	26.5	27.4
30		34.5	30.0					29.1	29.6

* LI = Long Internode and CL = Climbing select

300 Index drift factors

Mean drift factors are plotted in Figures 4-6 and tabulated in Table 2. Drift factors averaged across all regions are generally close to zero for most GF classes (Figure 4) indicating that the 300 Index model at the national level performs well for most GF ratings. Figure 5 shows mean drift factors for the eight GM Regions, and indicates that some regions may benefit from regional adjustment using regional drift factors.
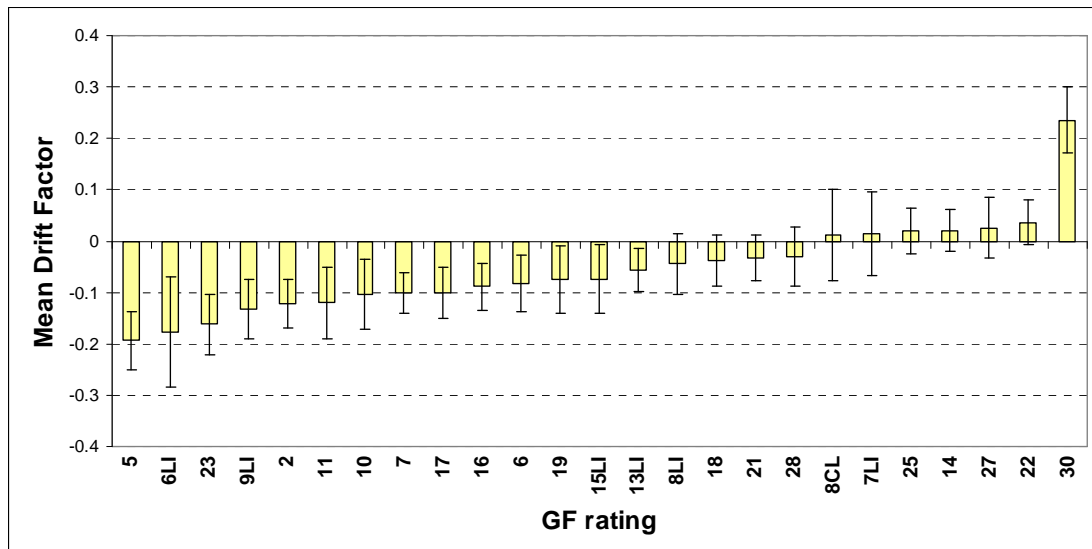
Figure 4. Mean Drift Factor for each GF rating across NZ. The error bars show the standard errors of the means.
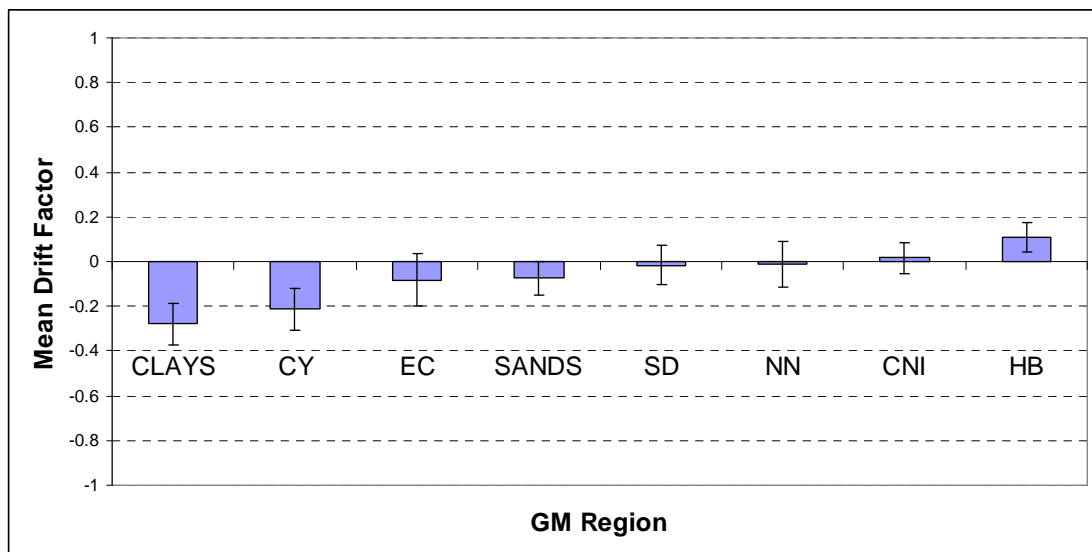

Figure 5. Mean drift factor for eight Growth Model regions. The error bars show the standard errors of the means.
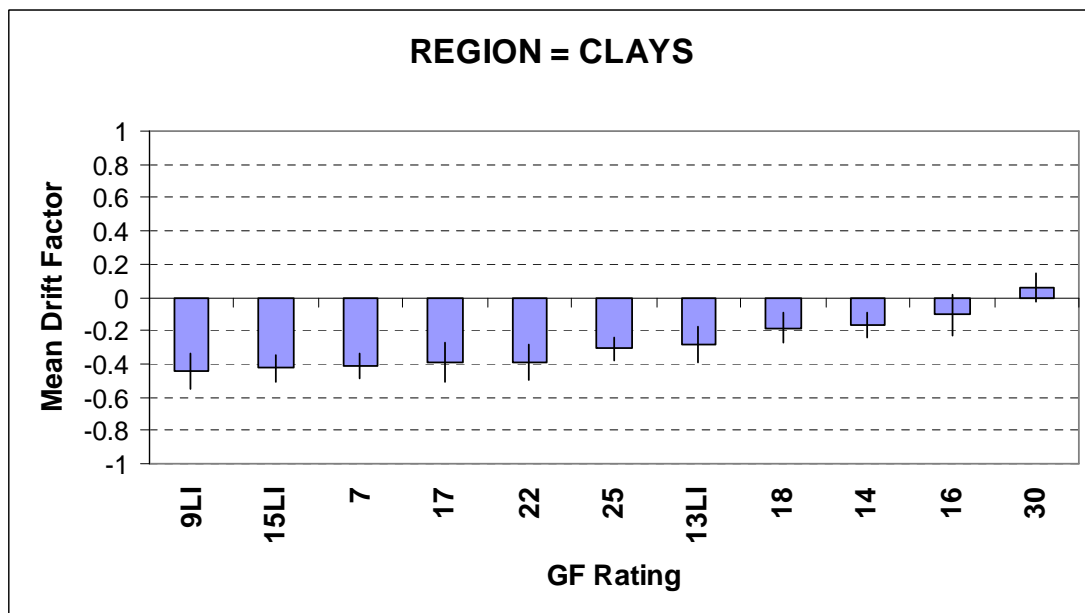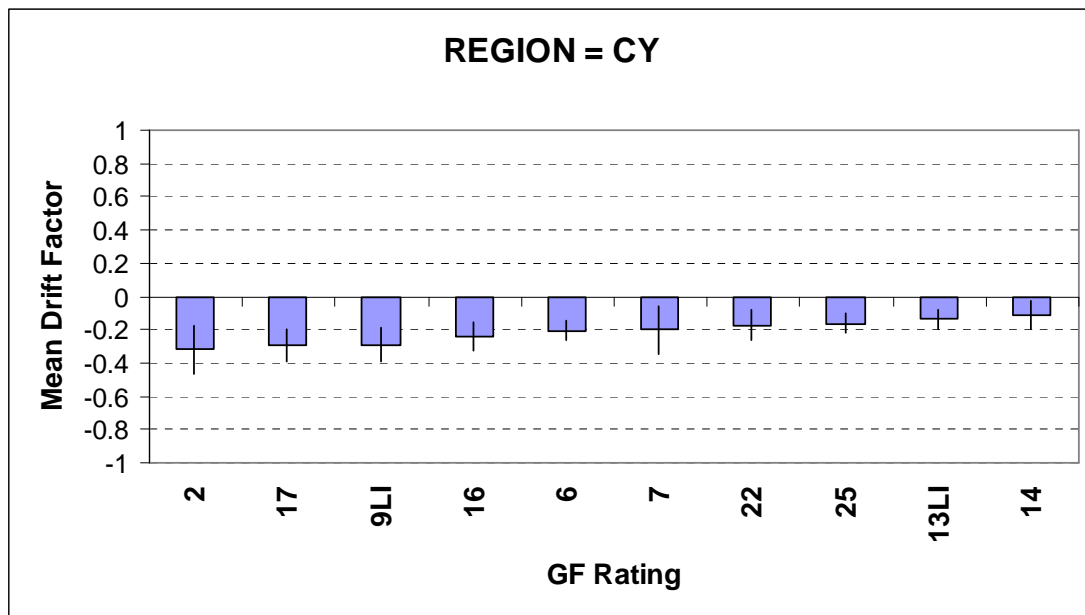
Figure 6. Mean Drift Factor for each GM region by GF rating. The error bars show the standard errors of the means.

Figure 6 (Cont'd). Mean Drift Factor for each GM region by GF rating. The error bars show the standard errors of the means.

Figure 6 (Cont'd). Mean Drift Factor for each GM region by GF rating. The error bars show the standard errors of the means.

REGION = SANDS

REGION = SD

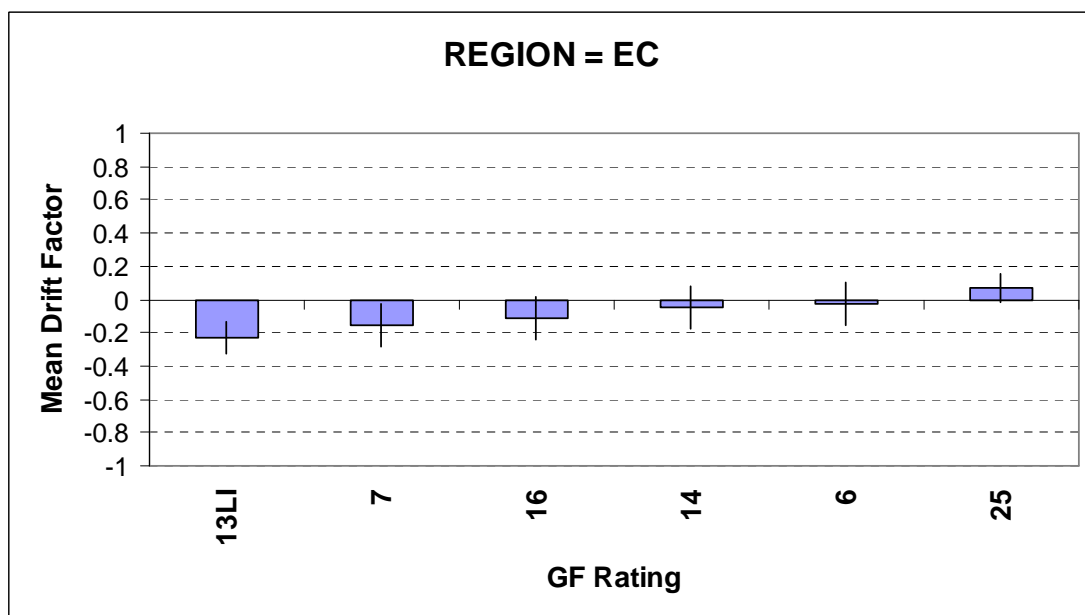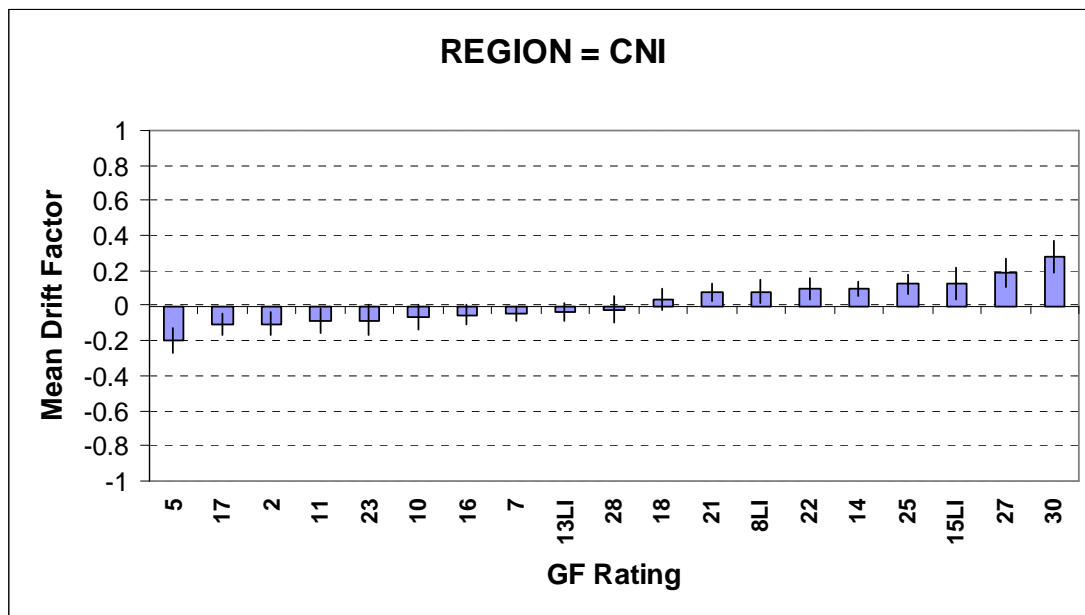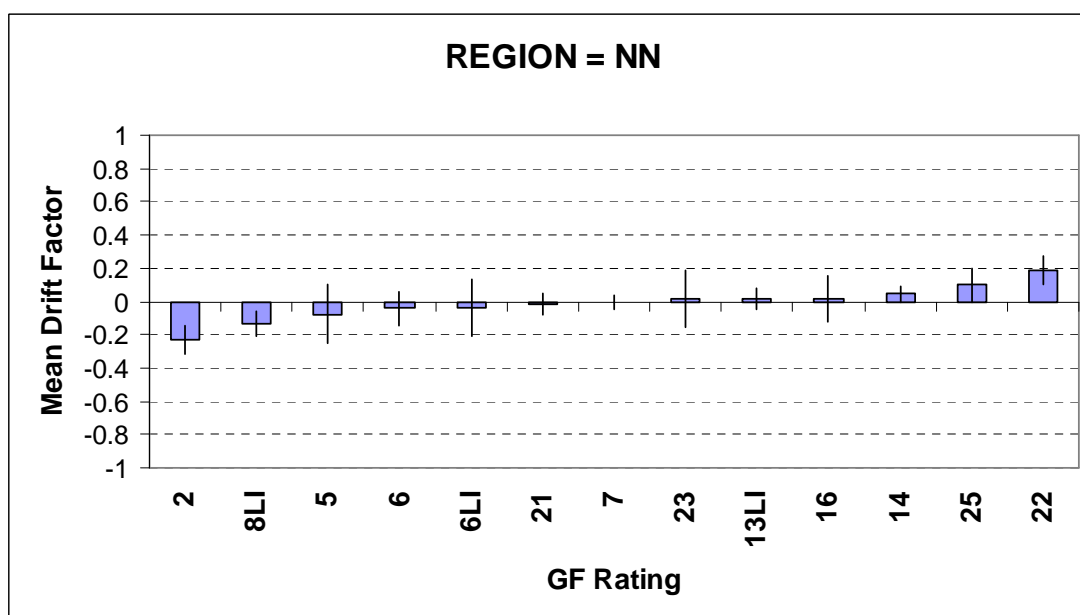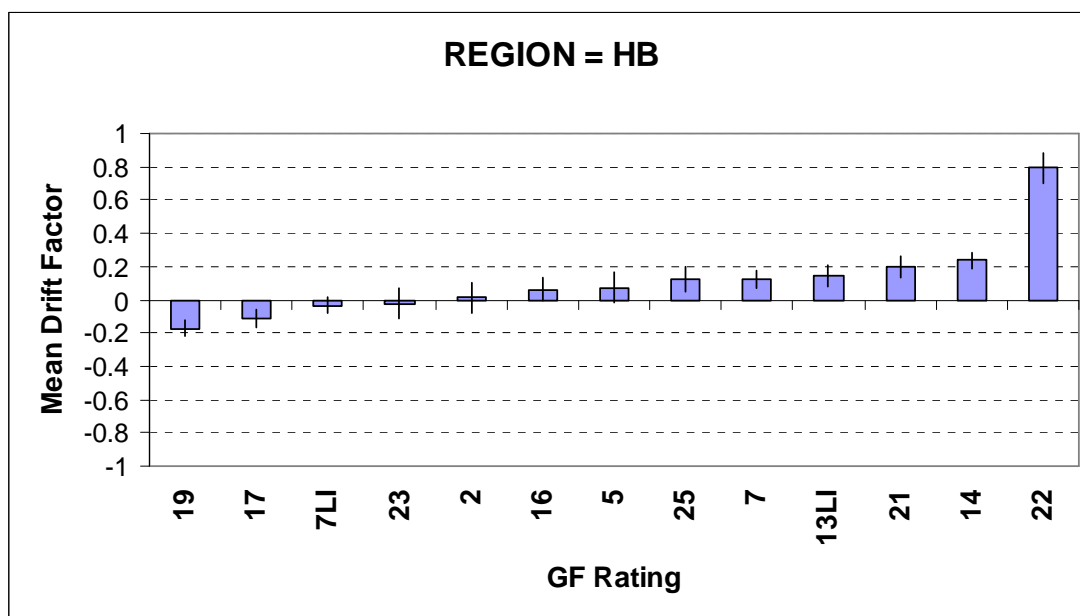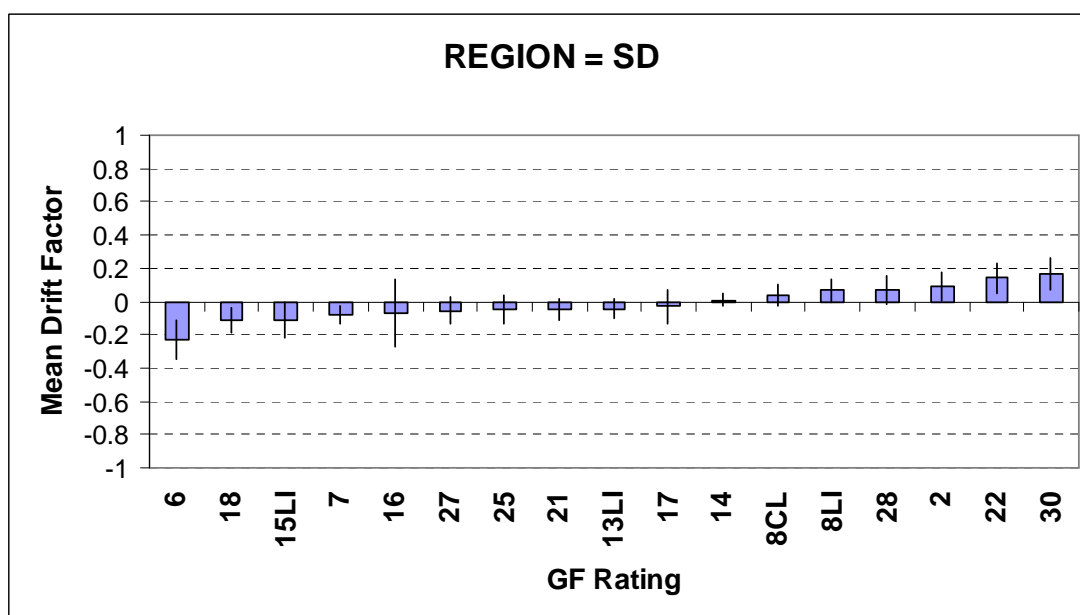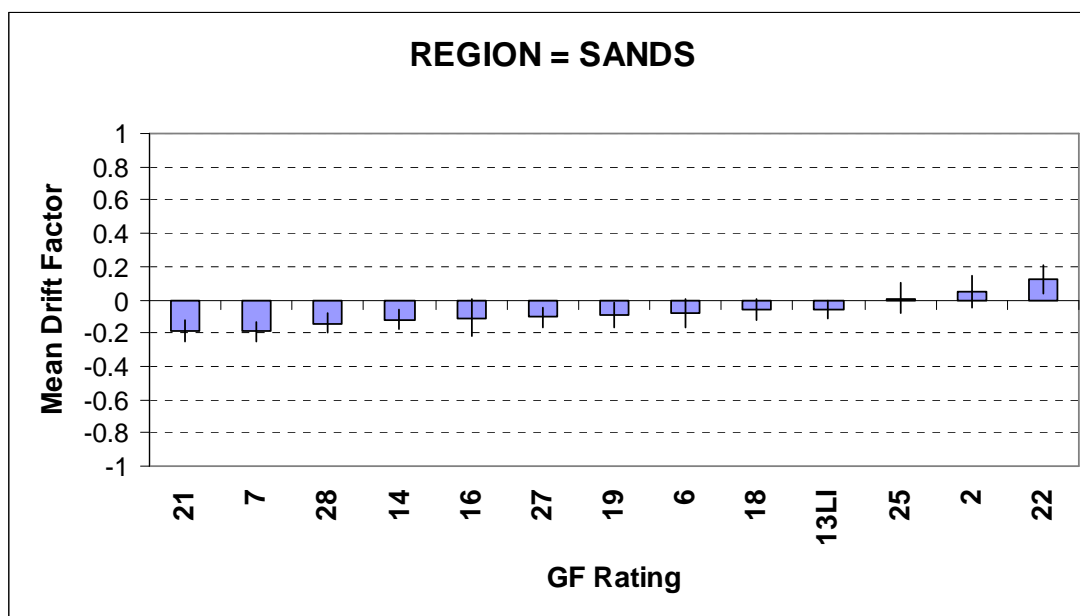**Figure 6 (Cont'd). Mean Drift Factor for each GM region by GF rating. The error bars show the standard errors of the means.**

Table 2. Table of mean 300 Index drift factors by genotype class for all New Zealand and for each GM region.

GF	GM REGIONS								ALL NZ
	CY	CLAYS	CNI	ECOT	HB	NN	SANDS	SD	
2	-0.32		-0.10		0.02	-0.23	0.05	0.09	-0.12
5			-0.20		0.07	-0.08			-0.19
6	-0.20			-0.03		-0.04	-0.08	-0.23	-0.08
6LI						-0.04			-0.18
7	-0.20	-0.41	-0.05	-0.15	0.12	0.00		-0.08	-0.10
7LI					-0.04		-0.19		0.01
8CL								0.04	0.01
8LI			0.08			-0.14		0.07	-0.04
9LI	-0.29	-0.45							-0.13
10			-0.07						-0.10
11			-0.09						-0.12
13LI	-0.14	-0.28	-0.04	-0.23	0.15	0.01	-0.06	-0.04	-0.06
14	-0.11	-0.17	0.10	-0.05	0.24	0.04	-0.12	0.01	0.02
15LI		-0.43	0.13					-0.11	-0.07
16	-0.24	-0.10	-0.05	-0.11	0.06	0.02	-0.11	-0.07	-0.09
17	-0.29	-0.40	-0.11		-0.11			-0.03	-0.10
18		-0.18	0.04				-0.06	-0.11	-0.04
19					-0.17		-0.10		-0.07
21			0.07		0.20	-0.02	-0.19	-0.05	-0.03
22	-0.18	-0.39	0.09		0.79	0.19	0.12	0.14	0.04
23			-0.08		-0.02	0.01			-0.16
25	-0.16	-0.31	0.12	0.07	0.12	0.10	0.01	-0.05	0.02
27			0.19				-0.11	-0.06	0.03
28			-0.02				-0.14	0.07	-0.03
30		0.06	0.28					0.17	0.24

* LI = Long Internode and CL = Climbing select

CONCLUSION

The tabulated values of the 300 Index generally increase with increasing GF rating (Table 1, Figure 1), showing the gradual improvement in growth rate achieved by several decades of selection and tree breeding. Early attempts at selecting for superior performance achieved an immediate increase of 1.3 m³/ha/yr or 5% (GF7 versus GF2) while a further 5% was achieved by the first generation of scientific tree breeding (GF14). Further small increases in growth rate are apparent for higher GF ratings. For example, the mean 300 Index of all seedlots rated GF20 or higher is 0.5 m³/ha/yr higher than the GF14 mean, although this amounts to an increase of only 2%. However, the highest GF rated class, GF30, shows an increase of 6% over GF14. These trends are generally apparent in all GM regions with only a minor GxE interaction apparent in the analysis.

The summary of drift factors (Table 2, Figure 4) gives an indication of how well the 300 Index Growth Model performs for each GF rating. This shows that the model is unbiased for GF14 and for most of the higher GF rated seedlots. For example, the mean drift factor of 0.02 for GF14 implies that on average the model will under-predict the volume MAI, but only by 0.2 m³/ha/yr over a 10-year projection period. This means that when predicting harvest volume for the GF14 seedlots from a mid-rotation inventory, the model will on average across these trial sites, have a bias in predicted harvest volume of less than 1%. This level of bias is nowhere near statistically significant. Similar low levels of bias would be achieved using the model with higher GF rated seedlots. For example, across all seedlots rated higher than GF20, the mean drift factor is also 0.02, identical to that for GF14.

These results imply that the 300 Index model can be used without adjustment for most seedlots rated GF14 and higher when projecting forward from plot measurements. In other words, the plot measurements themselves must adequately account for any level of genetic improvement, and there is no need to make any additional genetic gain adjustment to the growth model.

There may be some exceptions to this general result for some individual seedlots. For GF23, the model apparently over-predicted growth as indicated by its negative mean drift factor, while for GF30 there was a fairly pronounced tendency for under-prediction. However, as both these GF classes were only represented in 3 regions, these results should be treated with caution. The GF22 seedlot '850-55x850-96', which as noted above had an extremely high mean 300 Index, also had an extremely high positive drift factor in the Hawkes Bay region and to a lesser extent in the Nelson, and Southland regions. This indicates that the model under-predicts for this seedlot, especially on more fertile sites. These results suggest that adjustment to the model using drift factors may give improved results for a limited number of specific seedlots.

Of historic interest only, is a clear trend for some of the lower GF ratings to have negative drift factors with GF2 and GF7 having mean drift factors of -0.12 and -0.10 respectively. These values imply that the 300 Index model will tend to slightly over-predict when projecting forward from early measurements for these seedlots. From this we can infer that stem volume growth trajectories for these relatively unimproved breeds have a tendency to flatten out earlier than those of the more improved varieties.

In general the 300 Index Growth Model does not require adjustment when used with higher GF ratings.

ACKNOWLEDGEMENTS

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