STUDY INTO THE INFLUENCE OF GENETIC IMPROVEMENT OF SECOND LOG BRANCHING OF RADIATA PINE

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Report No. 65   November 1999

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EXECUTIVE SUMMARY

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The development of planning models, which quantify the genetic influence on branch size at the family level, would enable forest managers to make informed decisions regarding the management of improved breeds of radiata pine. This preliminary study explores the genetic influence on branch size at the family level across the "850" multinodal and "870" long internode selection series.

Compartment 905 in Kaingaroa Forest, which contains progeny trials of both the "850" and "870" selection series, was chosen for this study. Second log measurements of branch size and internode length were taken from 210 trees within 30 families across the "850" and "870" selection series. After branch index was adjusted for diameter at breast height, the residuals were plotted successively against mean internode length and branch cluster frequency breeding value at the family level.

Results show that although mean internode length was significantly correlated ($R^2 = 0.34$ for "850" multinodal selection series; $R^2 = 0.60$ for "870" long internode selection series) to branch index residuals within each selection series, it was not correlated to branch index residuals across selection series. Consequently, prediction of the genetic influence on branch index using mean internode length would require the development of separate regression lines for each selection series. In contrast, branch cluster frequency breeding value was moderately correlated ($R^2 = 0.47$) to branch index residuals both within and across the two selection series.

Although this study showed that branch cluster frequency breeding value was correlated to branch index residuals across selection series at the family level, these findings are preliminary. If further research shows the relationship between branch cluster frequency breeding value and branch index holds across other selection series, inclusion of branch cluster frequency breeding value in planning models may enable the genetic influence on branch index to be quantified at a more refined level than previously possible.

OBJECTIVE

To investigate the genetic influence on branch size at the family level, across the "850" multinodal and "870" long internode selection series.

INTRODUCTION

Branch Size Genetic Gains Of Improved Seedlots

Selection Series Comparisons

An early study (Shelbourne, 1970) investigating genetic gains from the breeding programme indicated some improvement in branch size. It was found that the average branch size of 11 year old "850" selection series clones were smaller than the unimproved breeds by 19% in the first log and 10.7 % in the second log.

Shelbourne and Briscoe (1983) compared branch index (BIX) (Figure 1) between 13 year old trees from the "850" and "870" selection series to those from an unselected bulk seedlot. Compared to the "850" selection series, BIX was found to be on average 0.6 cm larger for the "870" selection series. Only marginal differences (0.1 cm) in BIX were noted between the "850" selection series and the unimproved seedlot.
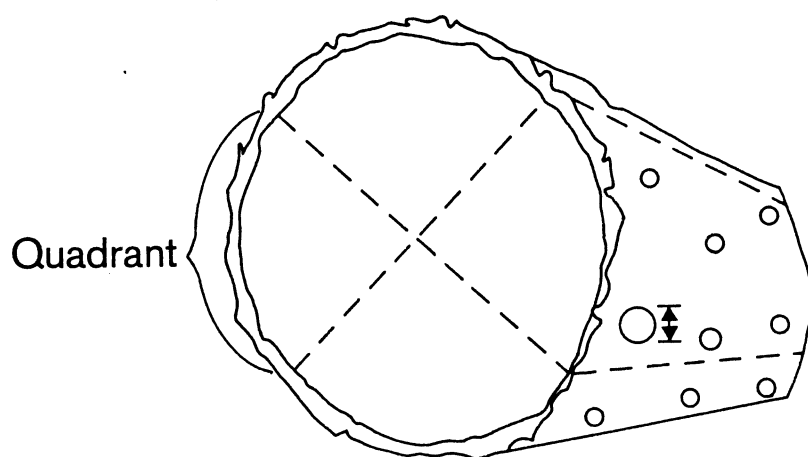

Figure 1 – Branch index (BIX) is the mean of the largest branch in each of four quadrants, for the nominated log length (Source: Inglis and Cleland, 1982).

Inclusion of a genetic effect in branch models.

Using data collected from selected sites throughout the country, an empirical stand level model for predicting BIX was developed by Grace (1989). For the "268" selection series, Grace (1989) recommended half a centimetre be subtracted from the predicted value, while for the "870" selection series, it was suggested that half a centimetre should be added. No adjustment to the model was needed for "850" selection series material.

Knowles and Kimberley (1992) investigated the effect of site fertility, diameter at breast height (dbh), stocking, site index, and genotype on second log branching, using data from 25 direct sawlog stands, from both farm and forest sites. Their findings showed that BIX was significantly related to dbh at age 20, site index and genotype. It was also noted that the effect of stocking and site fertility could be explained by dbh, provided the stand had been managed under a direct sawlog regime.

The original dataset (Knowles and Kimberley, 1992) was extended through inclusion of a recently measured stand and used to develop an empirical BIX prediction model for direct sawlog regimes (Kimberley and Knowles, 1993). Using site index, dbh at age 20, growth and form factor (GF) and final thinning mean top height as variables, the model was able to predict 98.5% of the variance in the dataset (Kimberley and Knowles, 1993). It was found that branch indices of GF 14 trees were approximately 1 cm smaller than those of GF 7 trees, although the differences were strongly influenced by dbh at age 20 (Figure 2).
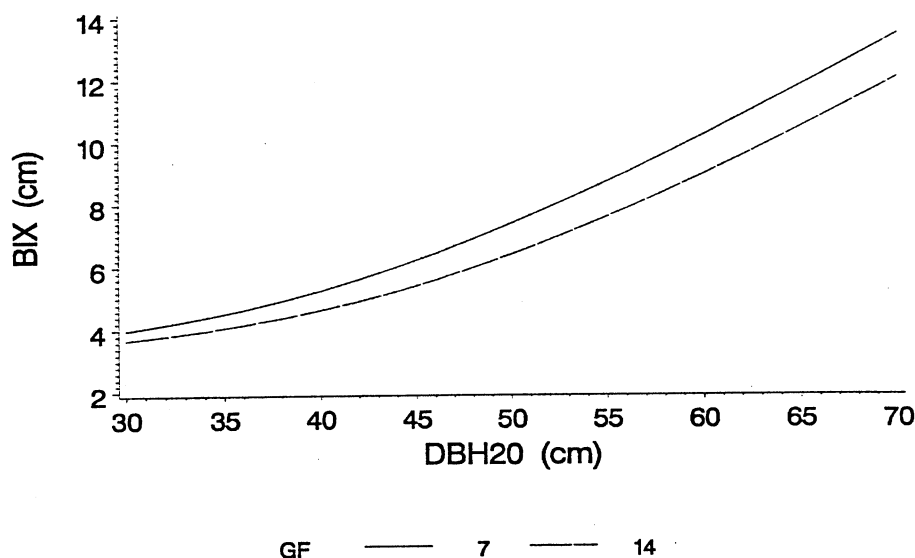

Figure 2 - Relationship of branch index (BIX) to dbh at age 20 for GF14 and GF 7 trees. (Source: Kimberley and Knowles, 1993).

Effect of branch cluster frequency on branch size.

Brown and Carson (1988) compared the size of the largest branch from the diameter over stubs (DOS) whorl within the first log, between trees from the climbing select, "268", "875" and "870" selection series. To remove the effect of dbh, "branch fineness"[1] was used as the dependant variable. Although the analysis indicated a moderate correlation ($R^2 = 0.57$) between the number of branch clusters per log and branch fineness, there were still significant differences between selection series following removal of this factor. Once the effects of dbh and the number of branch clusters per log were removed, it was found that the "870" and climbing select selection series had slightly larger branches than the "875" and "268" selection series (Brown and Carson, 1988).

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1 "Branch fineness" was calculated as the largest branch/dbh.

Quantifying Genetic Gains At The Family Level Across Selection Series

Breeding values have been developed to quantify family level genetic gain across selection series (Carson, 1996). Using subjective measures made at a young age, breeding values have been derived for a range of selection traits, including branch cluster frequency and stem straightness. Breeding values measure the mean amount of gain contributed by each parent, in comparison to the mean of all parents.

The scoring system used to estimate breeding values enables efficient and effective ranking of parents. However, for a number of selection traits including branch cluster frequency, it is not known how well these values quantify absolute differences in target traits, such as mean internode length or branch size.

The aim of this study is to relate objective measures of branch index to branch cluster frequency breeding value (brBV), either directly or indirectly though mean internode length[2] (MIL). It is anticipated that these relationships will be used to produce genetic modifiers, which can then be included in planning models (Carson, 1996). Use of the genetic modifier will allow quantitative measures of the target trait (BIX) to be predicted from the brBV for each family in the breeding programme.

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[2] Mean internode length = $\dfrac{\sum \text{length (m) of internodes in branched section of log}}{\text{number of internode lengths in branched section of log}}$

METHODOLOGY

Site And Trial Selection

Compartment 905 in Kaingaroa forest, which contains progeny trials of both the "850" multinodal and "870" long internode selection series, was chosen for the study. Stand variables of both progeny trials are summarised in Table 1. The "870" selection series progeny trial is 3 years older than the "850" selection series progeny trial. Both progeny trials have a similar stocking level, and received one thinning at a stand height of 2 to 3 m. As thinning occurred prior to canopy closure, timming of thinning, and differences in initial stocking between the trials will not influence branch size. At the time of branch measurement canopy closure had occurred, therefore all branches measured were dead.

Table 1. Stand variables of the sampled progeny trials.

Selection		Experiment type	Year planted	Stocking (stems/ ha)	Stand ht at thinning
Series	Goal				
"850"	Multinodal	Diallel	1975	400	2 - 3
"870"	Uninodal	Sets in replicates	1972	450	2 - 3

Family Selection

Fifteen families within each progeny trial were selected for sampling. These families cover the range of MIL within the "850" multinodal and "870" long internode selection series. A sample of 7 trees was chosen for each family.

Data Collection

Measurements were taken during the summer of 1999. Only crop trees which had a diameter greater than 30 cm and were free from ramicorns or basket whorls within the second log[3] were sampled. The dbh of each sampled tree was measured, and increment cores were taken to enable calculation of dbh at age 20. Within the second log, the distance from the stump height (0.3 m) to the top and base of each branch cluster (whorl) was measured. Using calipers, the diameter of all branches within the second log were measured to the nearest millimetre. Each branch was allocated to one of four radial quadrants on the second log (Figure 1).

The complete dataset included measurements of 10 576 branches and 1 819 branch clusters from 210 trees within the two trials.

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[3] In this study the second log was defined as the branched zone on the tree from 6.5 m to 12.0 m (with an allowance of 0.3 m. for stump height).

From the data collected, MIL was calculated as the average of all internode lengths greater than 0.05 m, within the second log. As previously described, BIX was calculated as the mean of the largest branch in each of the four quadrants (Figure 1), within the second log. Table 2 shows summary statistics of the measured trees, by selection series.

Table 2. Descriptive statistics of the sampled trees, by selection series

	Mean	SD[4]	Min.	Max.
"850" selection series				
DBH age 20 (cm)	45.7	7.4	30.5	67.5
BIX (cm)	4.90	1.04	3.00	7.90
No. of branch clusters/log	9.4	2.4	4.0	16.0
No. of branches/log	52.3	12.4	20.0	85.0
MIL (m)	0.46	0.20	0.20	1.47
"870" selection series				
DBH age 20 (cm)	41.5	6.9	31.0	61.9
BIX (cm)	5.05	1.07	3.25	7.88
No. of branch clusters/log	7.8	2.4	3.0	12.0
No. of branches/log	48.8	12.3	23.0	82.0
MIL (m)	0.55	0.25	0.25	1.40

Data Analysis

As dbh usually has a large influence on BIX, the effect of this variable was removed before further analysis was undertaken.

Initial analyses, which were undertaken to check findings from previous research (Brown and Carson, 1988), assessed the influence of number of branch clusters per log on the largest branch (adjusted for dbh), at the family level. Further analyses used MIL and brBV, two variables for which values can be easily obtained[5], to estimate BIX. After BIX was adjusted for dbh, the residuals were plotted successively against MIL and brBV, at the family level (Table 3).

Table 3. Branch size models

Model no.	Independent variables included in model				Dependant variable	
	dbh	No. branch clusters/log	MIL	brBV	Largest branch	BIX
1	X	X			X	
2	X		X			X
3	X			X		X

To investigate underlying causes of selection series differences in BIX, within tree spatial distribution of branch clusters was compared between selection series.

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[4] Standard deviation
[5] Values for brBV are available for all families within the breeding program, and MIL can be predicted from brBV at the family level using equations developed by Turner *et al.* (1997).

RESULTS

Removal of the DBH Effect

Previous studies (Kimberley & Knowles, 1993) have identified dbh as having a strong influence on branch size. The relationship between dbh and BIX was, therefore, examined first.

Within each selection series, dbh at age 20 was moderately correlated to BIX. The coefficient of determination (R^2) between BIX and dbh at age 20 was 0.43 for the "870" long internode selection series and 0.55 for the "850" multinodal selection series.

The relationship between BIX and dbh at age 20 differed significantly ($P < 0.01$) between selection series (Figure 3). For a given dbh the "870" long internode series families had a 1 cm larger BIX than the "850" multinodal series families.
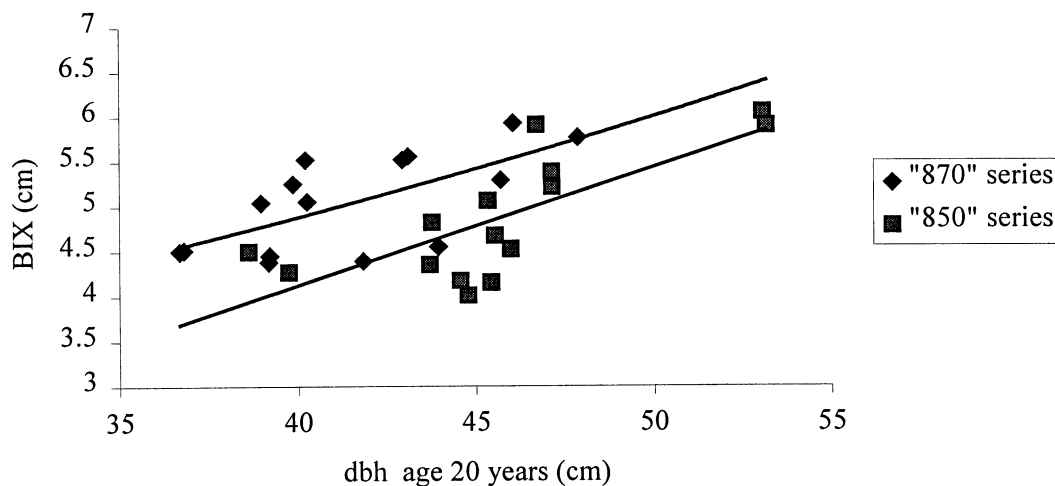

Figure 3 - Relationship between dbh at age 20 and BIX at the family level, by selection series.

Before additional analysis was undertaken, branch size (BIX and largest branch) was adjusted for dbh at age 20.

Influence of Number of Branch Clusters Per Log on Largest Branch (Model 1)

Having removed the effect of tree size (dbh) on branch size the influence of number of branch clusters (whorls) per log on the largest branch was explored following a similar analysis to that used by Brown and Carson (1988).

Addition of number of branch clusters per log was highly significant. No significant differences in slopes between selection series were noted (Table 4). The intercepts of the relationship between residuals of the largest branch (adjusted for dbh at age 20) and the number of branch clusters per log (Figure 4) differed significantly between selection series ($P < 0.05$).
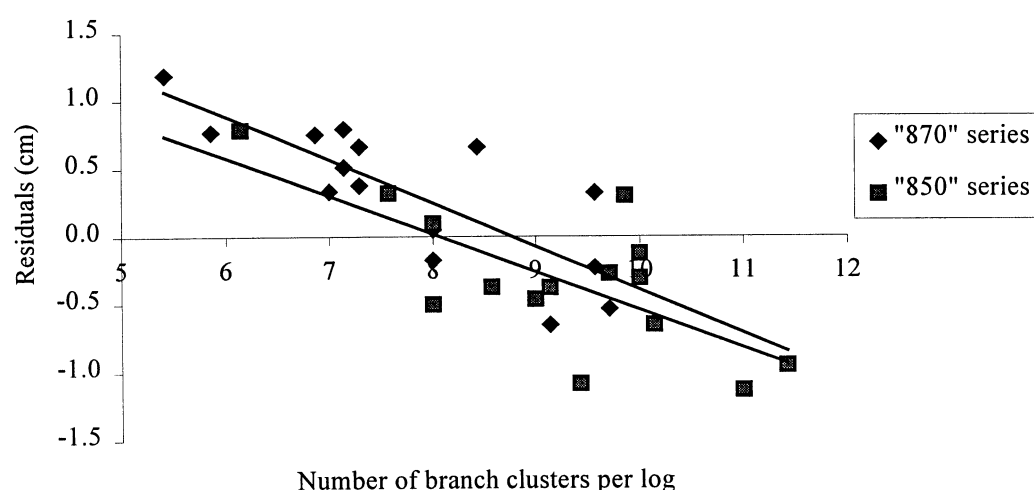

Figure 4 - Relationship between largest branch residuals (adjusted for dbh at age 20) and number of branch clusters per log.

Table 4. Significance of independent variables, series intercepts and slopes (Model 1).

Test	Variable tested	Significance level
Independent variables	dbh age 20	0.0001
	No. of branch clusters/log	0.0001
Series intercepts	Series	0.0137
Series slopes	Series*dbh age 20	0.4227
	Series*No. of branch clusters/log	0.9339

Influence of Mean Internode Length on Branch Index (Model 2)

The next model (Model 2) analysed the influence of mean intenode length (MIL) on branch index (BIX) adjusted for the effect of dbh. Within each selection series, MIL was significantly, positively, correlated to residual BIX. The coefficient of determination (R^2) between residual BIX and MIL was 0.60 for the "870" long internode selection series, and 0.34 for the "850" multinodal selection series. For a given dbh, a 0.1 m increase in MIL led to a 0.25 cm increase in BIX for both the "870" and the "850" selection series.

Although no significant differences in selection series slopes were detected (Table 5), the intercepts of the relationship between residual BIX (adjusted for dbh age 20) and MIL differed significantly ($P < 0.01$) between selection series. For the same dbh and MIL the "870" long internode selection series families had branch indices approximately 0.3 cm larger than those of the "850" multinodal selection series (Figure 5). The significance of the relationship between MIL and residual BIX for the "850" selection series was, however, dependant on one family (circled Figure 5).
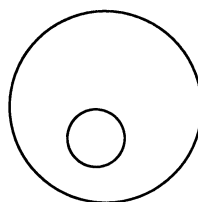

Figure 5 - Relationship between residual BIX (adjusted for dbh age 20) and MIL.

Table 5. Significance of independent variables, series intercepts and slopes (Model 2).

Test	Variable tested	Significance level
Independent variables	dbh age 20	0.0001
	MIL	0.0001
Series intercepts	Series	0.0025
Series slopes	Series*dbh age 20	0.7838
	Series*MIL	0.5718

Influence of Branch Cluster Frequency Breeding Value on Branch Index (Model 3)

The final model (Model 3) analysed the influence of brBV on BIX adjusted for the effect of dbh. This model ineffect tested directly for genetic differences in branch size after the effect of dbh had been removed. Addition of brBV was highly significant (P < 0.01). No significant differences in either slopes or intercepts between selection series were noted (Table 6).

Table 6. Significance of independent variables, series intercepts and slopes (Model 3).

Test	Variable tested	Significance level
Independent variables	dbh age 20	0.0001
	brBV	0.0001
Series intercepts	Series	0.418
Series slopes	Series*dbh age 20	0.217
	Series*brBV	0.826

There was a moderate negative linear correlation (Figure 6) between residual BIX (adjusted for dbh at age 20) and brBV, which had a coefficient of determination (R^2) of 0.47. Therefore, as brBV increases (this corresponds to an increase in branch cluster frequency, or a decrease in internode length) BIX decreases.
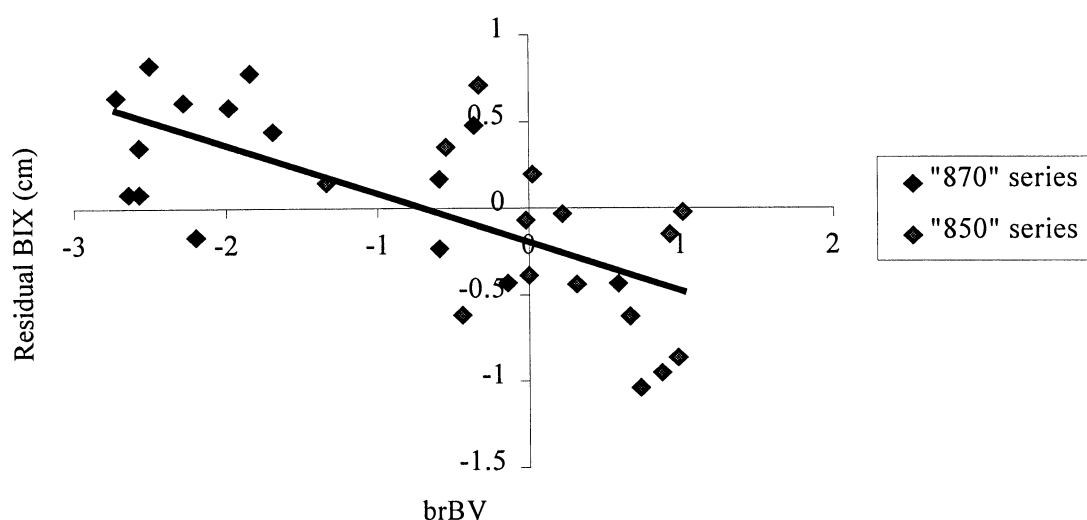

Figure 6 - Relationship between residual BIX (adjusted for dbh age 20) and brBV.

These results indicate that for a given dbh, selection of longer internode genetic material results in an increase in BIX. For the families measured in this study the increase in brBV from −2.72 to +1.02 (corresponding to a change in predicted MIL from 0.80 m to 0.45 m) resulted in a decrease in BIX of 1.05 cm

Comparison of Within Tree Branch Cluster Distribution Between Selection Series

After adjustment had been made for dbh at age 20 and MIL, there were significant (P < 0.01) differences in residual BIX between selection series. To examine possible reasons for these differences, the within tree spatial distribution of branch clusters between selection series were compared.

Within both selection series, trees were classified as either "uninodal" or "binodal[6]". Trees with a MIL greater than 0.6 m were classified as "binodal" if they had 1 or more internodes less than 0.25 m, and "uninodal" if they had no internodes less than 0.25 m. Selection series comparisons indicate that the "binodal" branching habit was more prevalent within the "870" selection series across all MIL categories above 0.6 m (Figure 7).
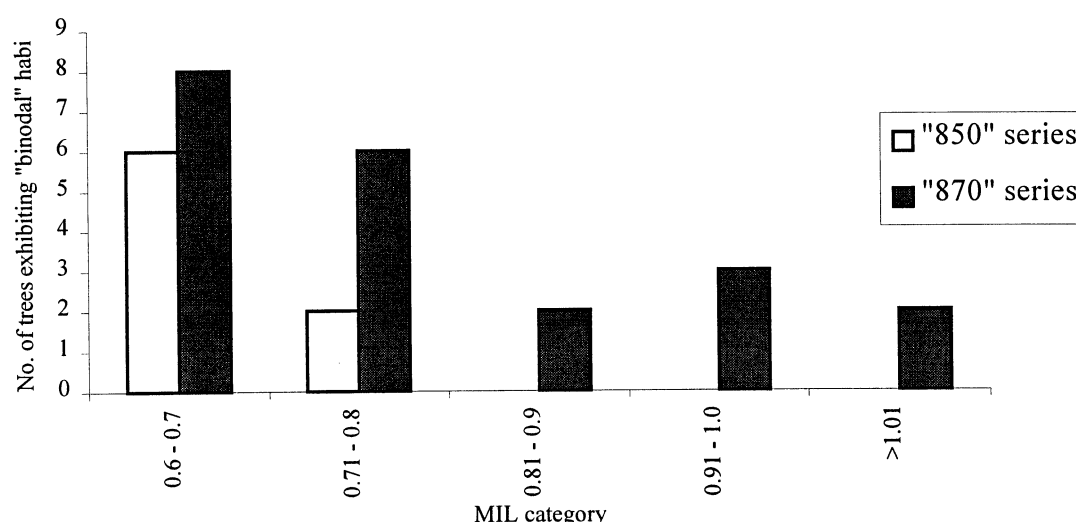

Figure 7 - Number of trees in MIL categories over 0.6 m exhibiting the "binodal" habit, by selection series.

For a given dbh and MIL, "binodal" trees tended to have a larger BIX than "uninodal" trees. After BIX had been adjusted for dbh and MIL at the tree level, the residuals were separated into "binodal" and "uninodal" categories (Figure 8). On average, residual BIX was slightly overpredicted for "uninodal" trees (residual mean = -0.07), and underpredicted for the "binodal" trees (residual mean = 0.33). However, the statistical insignificance of these differences indicated that residual separation was not that pronounced. This may have reflected the limitations of the dataset and analysis to distinguish between the "uninodal" and "binodal" branching habit.

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[6] Binodial trees tend to have two branch clusters (whorls) very close together with a longer internode to the next two branch clusters.
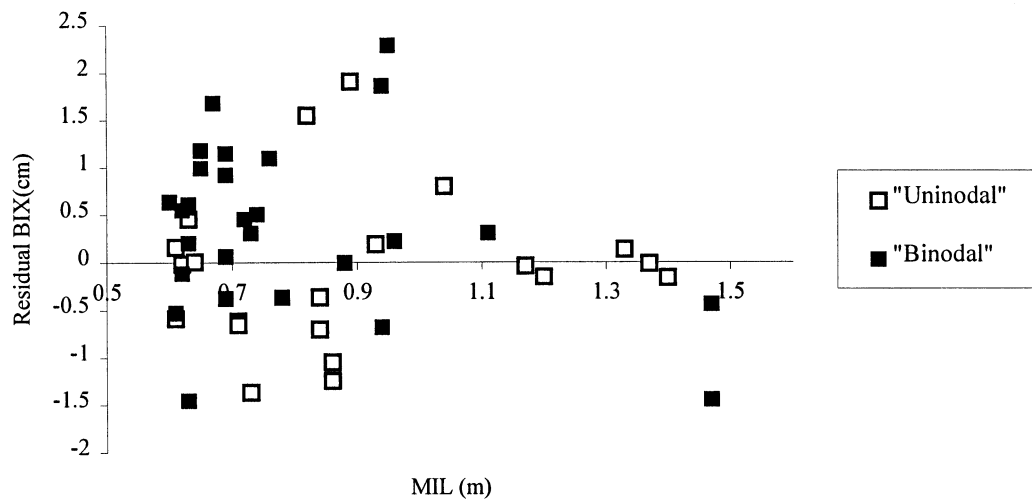
Figure 8 -
Residual BIX (after adjustment for dbh age 20 and MIL) against MIL, by branching habit.

DISCUSSION

Results showed that after the effect of dbh was removed, the "870" long internode selection series had significantly larger branch indices (1 cm) than the "850" multinodal selection series.

After adjustment had been made for dbh and the number of branch clusters per log, the "870" selection series had largest branches with a significantly greater diameter than those of the "850" selection series. These findings were consistent with previous research by Brown and Carson (1988), which showed uninodal selection series had largest branches significantly greater in diameter than multinodal selection series, after adjustment had been made for dbh and number of branch clusters per log.

Although this research was consistent with the work of Brown and Carson (1988), comparisons may be confounded by a number of factors. While both studies compared multinodal and uninodal trees, the multinodal selection series ("875" and "268" selection series) sampled by Brown and Carson (1988) were different to that measured in this study ("850" selection series). Moreover, while this study used largest branch within the second log length as the dependant variable, Brown and Carson (1988) measured the largest branch within the DOS whorl of the first log. Also, in the Brown and Carson (1988) study the branches were measured when they were still alive, therefore the branches had not reached their potential size.

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After the effects of dbh and MIL had been removed, residual plots indicated that families within the "870" selection series had a larger BIX (0.3 cm) than those in the "850" selection series. Results suggest this difference may be due to the greater frequency of "binodal" trees within the "870" selection series (Figure 7), which, on average, had larger branches than "uninodal" trees of the same MIL (Figure 8). While both MIL and brBV incorporated measurements of branch cluster frequency, only brBV included measures of the spatial distribution of branch clusters. It seems likely that, by accounting for the effects of branch cluster distribution on BIX, inclusion of brBV in the model enabled prediction of BIX to be made across selection series.

Correlations of MIL and brBV to BIX may be confounded by differences in stocking between the two trials. The influence of stocking on BIX has been recognised (Grace, 1989). However, recent studies showed that stocking could be excluded without loss of accuracy, if dbh was included as an independent variable (Kimberley and Knowles, 1993; Makinen and Colin, 1998). In accordance with these findings, an assumption underlying this study was that dbh could be used to explain stocking differences both within and between the selection series.

Practical Implications

These results showed that after the influence of dbh (age 20) had been removed, MIL explained a significant amount of variation in BIX within both selection series. Although it was not correlated with BIX across selection series, adjustment for MIL significantly reduced selection series differences from approximately 1.0 cm (Figure 3) to 0.3 cm (Figure 5). These findings suggest that MIL could be a useful variable to include in within selection series predictive models of BIX. However, predictions of the genetic influence on BIX at the family level using MIL would be complicated, as MIL was not correlated to BIX across selection series. Consequently, predictions of the genetic influence on BIX using MIL would require the development of separate regression lines for each selection series.

The results showed that brBV was correlated to BIX, both within and between the two selection series. Although more measurements will need to be taken to confirm whether or not findings hold for other selection series, these preliminary results indicate that inclusion of brBV in branch index models may facilitate the prediction of genetic differences across selection series. If this is the case, inclusion of brBV in predictive models will enable the genetic influence on BIX to be quantified at a more refined level than was previously possible.

FUTURE WORK

Identify Underlying Causes of Selection Series Differences in Branch Index

The underlying causes of selection series differences in BIX need to be explored in greater depth. Although this report suggests that the within tree spatial distribution of branch clusters may influence branch index, more comprehensive research needs to be undertaken to validate these findings.

Investigate the Genetic Influence on Branch Size Across Other Selection Series, Sites and Silvicultural Regimes

Although this study showed that brBV was correlated to BIX across two selection series, the findings were limited in many respects. It is not known if this relationship holds for other selection series, sites or different silvicultural treatments.

Further research will need to be done to investigate the genetic influence on branch size across a wider range of selection series. To ensure site differences do not confound results, measurements of branch size from bulk unselected families should also be taken.

To explore the effect of site on genetic relationships with branch size, measurements of branch size would need to be taken from a wide range of trials throughout New Zealand, encompassing the full range of sites where radiata pine is grown.

Silvicultural influences on the relationship between branch size and genetics would need to be evaluated, through measurement of branch size from a range of thinning trials.

CONCLUSIONS

This study found a moderate degree of correlation between dbh at age 20 and branch index for both the "850" ($R^2 = 0.55$) and "870" ($R^2 = 0.43$) selection series. After the effect of dbh (at age 20) had been removed, families within the "870" selection series had branch indices approximately one centimetre larger than those of the "850" selection series.

Mean internode length was significantly ($R^2 = 0.34$ for "850" selection series; $R^2 = 0.60$ for "870" selection series) correlated to residual branch index within each selection series (adjusted for dbh at age 20). The relationship between residual branch index (adjusted for dbh at age 20) and mean internode length differed significantly between selection series. After adjustment was made for mean internode length, families within the "870" selection series had branch indices approximately 0.3 cm larger than those of the "850" selection series.

Branch cluster frequency breeding value was moderately ($R^2 = 0.47$) correlated to residual branch index (adjusted for dbh age 20). Once the effect of this variable had been removed there were no significant differences in branch index between selection series.

Comparisons of within tree branch cluster distribution between selection series suggested that branch cluster frequency breeding value may be correlated to branch index across selection series, as the variable incorporated spatial measures of branch cluster distribution not included in mean internode length.

ACKNOWLEDGEMENTS

REFERENCES

Brown, J.A.; Carson, M.J. 1988: Comparison of butt-log branching characteristics of improved *Pinus radiata* breeds at Cpt 1218, Kaingaroa. *Management of Improved Radiata Breeds Cooperative Report No. 1*. Forest Research Institute Ltd, Rotorua.

Carson, S.D. 1996: Greater specialisation of improved seedlots in New Zealand : new developments for efficient selection of parents and evaluation of performance. *New Zealand Forestry 41 (1)*: 12-17.

Grace, J.C. 1989: Branch size prediction for radiata pine. *Stand Management Cooperative Report No. 18*. Forest Research Institute, Rotorua, New Zealand.

Inglis, C.S.; Cleland, M.R. 1982: Predicting final branch size in thinned radiata pine stands. *New Zealand Forest Service, FRI Bulletin No.3*.

Kimberley, M.O.; Knowles, R.L. 1993: A model to predict branch index in radiata pine direct sawlog regimes. *Forest and Farm Plantation Management Report No. 1*. Forest Research Institute Ltd, Rotorua, New Zealand.

Knowles, R.L.; Kimberley, M.O. 1992: The effect of site, stocking and genetics on second-log branching in *Pinus radiata. Stand Management Cooperative Report No. 33*. Forest Research Institute Ltd, Rotorua, New Zealand.

Kumar, S.D.; Carson, S.D.; Burger, F.C.; Jefferson, P.A. 1996: Best linear prediction of breeding values for straightness and branch cluster frequency in a *Pinus radiata* improvement programme. *New Zealand Radiata Pine Breeding Cooperative Report No. 42*. Forest Research Institute Ltd, Rotorua, New Zealand.

Makinen, H.; Colin, F. 1998: Predicting branch angle and branch diameter of Scots pine from usual tree measurements and stand structural information. *Canadian Journal of Forest Research 28*: 1686-1696.

Shelbourne, C.J.A. 1970: Genetic improvement in different tree characteristics of *Pinus radiata* and the consequences for silviculture and utilisation. Pp. 44-58 *in* Sutton, W.R.J. (Ed.) "Pruning and thinning practice", Vol.2. Proceedings of New Zealand Forest Service, FRI Symposium No. 12.

Shelbourne, C.J.A.; Briscoe, D. 1983: Gains from selection for branching characteristics in *P.radiata. Production Forestry Division Project Record 314*. Forest Research Institute Ltd, Rotorua, New Zealand.

Turner, J.A.; Carson, S.D.; Manley, B.R. 1997: The relationship of mean internode length to breeding values for branch cluster frequency. *in* Burdon, R. (Ed.) "The Genetics of Radiata Pine" Meeting IUFRO Working Party, S2.02.19 (*Pinus radiata*, provences and breeding) held at Forest Research Institute Ltd, Rotorua, New Zealand, 1-4 December 1997.