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Aggregating tree species to develop diameter increment equations for tropical rainforests

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ABSTRACT

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Pairwise F-tests provided an efficient approach for aggregating large numbers of species into a manageable number of groups for developing diameter increment functions. The first stage of the two-stage procedure identified the number of groups required and the species defining these groups; the second stage aggregated all the remaining species into the most appropriate group. Although there is no guarantee that this leads to an optimal solution, empirical results suggest that the outcome is near optimal. This approach is readily automated and computationally efficient. An analysis of diameter increments of 237 species from the rainforests of north Queensland indicated 41 species groups, each with increment functions significantly different at $P < 0.01$. These provided a substantially better model than the previous model based on subjectively formed groups.

INTRODUCTION

Tropical rainforests are characterized by large numbers of tree species with diverse growth habits. Although some of these species are widely distributed, others occur infrequently and data from which to develop growth models may be sparse. The rainforests of north Queensland are no exception. Of the 400 tree species recognised on a series of permanent sample plots, the most common 5% of tree species contribute 50% of the available growth data, while the least frequent 50% of species contribute a mere 5% of the data.

It is impractical to develop growth functions for each individual tree species, because of the large number of functions that would be required, and the paucity of data for many species inhibits the development of reliable relationships. Thus, it is desirable to aggregate species into several groups, to reduce the number of functions require to a more manageable number, and to avoid the requirement for specific equations for species with few data.

Previously, five species groups based on subjective criteria, have been employed for growth modelling and yield prediction (Queensland Department of Forestry, 1985; Vanclay, 1988b, 1989a). The present study seeks to develop an objective and automatic procedure to form groups of similar growth habits, without imposing any limit on the number of groups.

DATA

The present study concerns the tropical rainforests of northeast Queensland. These forests have been managed for conservation and timber production for more than 80 years (Just, 1991), and provide a sustained yield of veneer and sawlogs of 60 000 m³ year⁻¹ (Preston and Vanclay, 1988). Management of these forests has been supported by a comprehensive research programme (Queensland Department of Forestry, 1983) which has provided a database of 250 permanent sample plots with a measurement history of up to 40 years. These plots sample virgin, logged and silviculturally treated forests.

Permanent sample plots range in size from 0.04 to 0.5 ha, and have been frequently remeasured. All trees exceeding 10 cm dbh (diameter over bark at breast height (1.3 m) or above buttressing) were uniquely identified and tagged, and were regularly measured for diameter (to the nearest millimetre) using a girth tape. To improve the consistency of diameter measurement, field crews had access to previous records while in the field. Any trees exhibiting defects or bulges at or near the measurement height were noted and so identified on computer. Such trees have not been used in calculating diameter increments, and have only been used in calculating stand basal areas.

Pairs of remeasurements were selected from the database to attain intervals between re-measurements of approximately 5 years, which did not span any logging or silvicultural activity. A data file was created for input to the statistical package GLIM (Payne, 1986), and contained 62,372 observations of diameter increment derived from 28,123 individual trees. The file also contained records of tree species and dbh, and stand variables such as site quality, stand basal area and soil type. Site quality for each plot was estimated using Vanclay's (1989b) eqn. (13), and any plots for which the estimated site quality exceeded the range 0-10, or for which the variance of the estimated site quality exceeded two were rejected, and omitted from the analysis. Valid estimates of site quality were obtained for 212 plots, which provided the present database.

Species identity is recorded in the database as a three-character mnemonic (the Forest Research Branch code) for the great majority of species, but a few trees of indeterminate identity were identified only as miscellaneous. However, correct species identification is often difficult in these forests, and inventory procedures record only the standard trade name (Standards Association of Australia, 1983), using a subset of the mnemonics known as the Harvesting and Marketing (H&M) code. Although the H&M code retains the correct identity of most species, several members of a genus may share a common code, as may members of more than one genus with similar timber characteristics. There are also additional non-commercial species simply labelled miscellaneous. As the present study was to develop diameter increment functions for use in yield prediction, it was appropriate to use the H&M codes, and 300 of the FRB codes in the data were converted into 236 H&M codes for analysis, and the remaining 100 with no H&M equivalent were grouped as miscellaneous.

METHOD

Although the data comprise repeated re-measurements, the present analyses employed ordinary least squares (OLS) rather than generalized least squares (Ferguson and Leech, 1978, 1981; West et al., 1984). OLS offers computational efficiencies, and enables analysis of species restricted to a few plots. The use of OLS should be satisfactory, as for most species, the number of trees was large compared with the number of re-measurements on the same individual, and the regression analysis was a growth rather than a yield function, regressing increment on initial size and avoiding the use of age. However, to avoid inflated estimates of significance, statistical probabilities were computed using degrees of freedom derived from the actual number of trees, rather than from the number of re-measurements.

Vanclay (1989b) presented a diameter increment function which stabilizes variance, provides a good fit, and can be easily fitted using linear regression:

$$\log(DI+\alpha) = \beta_1 + \beta_2 \times D + \beta_3 \times \log(D) + \beta_4 \times \log(D) \times SQ + \beta_5 \times \log(BA) + \beta_6 \times OBA \quad (1)$$

where: *DI* is diameter increment (cm year⁻¹); *D* is dbh (cm); *SQ* is site quality (Vanclay, 1989b); *BA* is stand basal area (m² ha⁻¹) of trees exceeding 10 cm dbh; *OBA* is overtopping basal area (m² ha⁻¹), defined as the basal area of stems the diameter of which exceeds that of the subject tree; and α, β_i are parameters to be estimated.

Parameter *a* should be positive, so that zero increments and small decrements can be included in the analysis. Failure to accommodate these observations may lead to overestimates of diameter increment and timber yields. Vanclay (1989b), investigating the growth of several species, found

that $\alpha = 0.02$ provided both a good fit and a good distribution of residuals, and this convention has been extended to the present study.

It is also logical to expect that the parameters β_2, β_5 and β_6 should be negative (or zero), and that β_4 should be positive. Parameter estimates were examined, and if otherwise, were removed from the regression. This occurred only for those species with few data, and the offending parameter estimates were not significant. Parameters with the appropriate sign were accepted, even if non-significant. The equation was fitted independently to each species, and the residuals were examined and found to be well distributed and free of outliers in every case. However, comparison between species revealed significant heterogeneity of variance for species with fewer observations, which introduced difficulties in comparing and aggregating species.

An obvious approach to aggregating species is to use pairwise F-tests, but the outcome of this approach depends to some extent, upon the order in which comparisons are made. To ensure repeatable results, all possible pairs could be compared, and aggregation commence with the most similar pair. Unfortunately, these will be the species with the fewest data, heterogeneous variance and poor parameter estimates, and thus do not provide a strong basis for comparison. Empirical trials with this approach led to several apparently anomalous groupings, including at least one group comprising a disproportionate number of species.

Leech et al. (1991) considered an alternative approach for aggregating species for developing polynomial volume equations using Hotelling's T^2 and principal coordinate analysis. Their approach is not a panacea, as they caution that their approach should only be used where the order of the polynomial and the sign of the highest order term are the same. The data in the present study appear unsuited to this approach, as many of the species have few data or few sites, and not all of the parameters fl, can be estimated for each species (i.e. some parameters may be aliased for some species).

The present data exhibited homogeneous variance for those species with the most data, and increasing heterogeneity as the numbers of observations decreased. This characteristic suggested an alternative approach entailing pairwise comparisons between those pairs for which the prediction equation could be reliably estimated. Species were ranked by decreasing number of remeasurements, and the 'founding' species of the first group was the species of highest rank (greatest number of observations). Species of lower rank were considered in turn, and pairwise comparisons made with all existing groups. If this incoming species was significantly ($P < 0.01$) different from all existing groups, it became the founding species of a new group; otherwise it was aggregated with the most similar group.

The miscellaneous group comprised 100 taxa from 72 genera, encompassing a variety of life forms, ranging from shrubs to large trees. As this group exhibited significantly greater variance, it was assigned the lowest rank.

Similarity was determined by comparing the residual sum of squares from fitting eqn. (1) to the existing group and the incoming species independently, with that obtained from the pooled data. Three criteria were considered: (1) the change in the residual sum of squares; (2) the F-statistic; (3) the probability of the F-statistic.

These criteria were examined both with parameters derived from all species currently assigned to the group, and with only the founding species of each group. Characteristics of the resulting groupings are summarized in Table 1. Three statistics are provided as a guide to the nature of the grouping. While the r^2 statistic is useful in indicating the relative size of the residuals, it does not provide a critical test for the relevance of the aggregation, especially where the amount of data for each group differs greatly. The simple strategy of assigning the 40 species of highest rank to a monospecific group, and aggregating all remaining species into a single group produces an r^2 of 0.445 (Table 1). Thus r^2 should not be used as the only test of aggregation; the maximum number of species in any group, and the minimum number of observations in any group should also be considered.

TABLE 1. Comparison of species groupings, Stage 1

Similarity criterion	Number of groups	Most species in any group	Fewest observations in any group	r ²
All species in group				
Change in Residual Sum of Squares	43	13	26	0.499
F-statistic	44	13	13	0.489
Probability	44	15	81	0.476
Founding species only				
Change in RSS	41	14	16	0.496
F-statistic	41	14	13	0.484
Probability	41	32	182	0.476
For comparison				
Ungrouped	237	1	1	0.507
40 monospecific groups	41	197	394	0.445
One group	1	237	62372	0.327

The six strategies examined produced relatively similar results, with differences generally confined to species with fewer data. However, if similarity is determined by the F-statistic, the approaches using all the species within any group may be biased, as the between-species variance will be incorporated into an inflated estimate of the group variance, and may lead to the inappropriate formation of few all-encompassing groups comprising the majority of the species. This bias may be reduced by the use of probability rather than the F-statistic as the test criterion, as the pooled data contribute additional degrees of freedom. However, empirical trials suggest that probability leads to a sub-optimal grouping (Table 1).

Comparisons based only on the founding species of each group produced slightly fewer groups. This approach is preferred on theoretical grounds, as it is free of any bias caused by between-species variation. Of the three similarity criteria, the smallest change in the residual sum of squares led to the preferred grouping. However, all six approaches examined gave rise to several apparently illogical groupings. These anomalous groupings may be attributed in part to the order of presentation of species. Consider two species of similar growth habit, with the one of higher rank having greater variability and not significantly different from one or more existing groups. The species of lower rank may be significantly different from all existing groups and become the founding species of a new group, but the similarity of the two would not be examined.

A two-stage approach was used to overcome this problem. The first stage identified the number of groups required and their founding species by comparing incoming species with founding species of higher rank, as above. This stage should not be subjectively pre-empted. The present study determined that *Dysoxylum schiffneri* with rank 186 and only 13 increment observations was significantly different from all 40 founding species of higher rank. The second stage involved comparing each non-founding species with each founding species, and grouping the most similar. The order of presentation was irrelevant for comparisons based only on the founding species, but was significant where comparisons were based on all species within a group. Thus comparisons were made both in order of rank, and in order of similarity after comparing all possible pairs and combining the most similar first. Four criteria were examined: (1) the error mean square derived from estimating increments for the incoming species from the existing equation for the group; (2) the change in residual sum of squares, (3) the F-statistic; (4) the probability of the F-statistic.

The analysis aggregating on order of similarity employed the partial residual mean square instead of the residual sum of squares (as in Stage 1) to accommodate incoming species with widely differing numbers of observations, and avoid biased assessment of similarity for groups with many observations. Consider an incoming species with few observations, equally different (i.e. same residual sum of squares (RSS)) from two groups with different numbers of observations. If the RMS (residual mean square) is derived from the total degrees of freedom, rather than adjusted by the number of observations for the incoming species, similarity will be biased towards the group with more observations. Thus the partial RMS was computed as the change in RSS divided by the number of observations for the incoming species, and provides the same outcome as RSS for other approaches to aggregation.

TABLE 2. Comparison of species groupings, Stage 2

Similarity criterion	Number of groups	Fewest species in any group	Fewest observations in any group	r ²
Founding species only				
Error mean square	41	14	13	0.497
Change in Residual Sum Squares	41	197	70	0.441
F-statistic	41	53	70	0.456
Probability	41	58	13	0.455
All species in group-order of rank				
Error mean square	41	16	13	0.497
Change in RSS	41	11	325	0.499
F-statistic	41	12	122	0.494
Probability	41	20	314	0.478
All species in group-reverse order of rank				
Error mean square	41	14	13	0.496
Change in RSS	41	14	220	0.493
F-statistic	41	14	155	0.495
Probability	41	16	218	0.487
All species in group-order of similarity				
Error mean square	41	13	13	0.496
Partial Residual Mean Square	41	22	107	0.498
F-statistic	41	33	84	0.487
Probability	41	11	148	0.489
Ungrouped	237	1	1	0.507

The results of this analysis are summarized in Table 2. One approach was outstanding in respect of all three statistics. This approach used RSS as the criterion and for comparing ungrouped species in order of rank with all species in the group (not just the founding species). It ensured that no group contained more than 11 H&M codes; the smallest group had sufficient data to provide reasonable parameter estimates, and it produced fewer apparently anomalous groupings.

Thus the final approach used to group species involved the following steps.

(1) Ranking species in order of increasing number of observations, with the miscellaneous group assigned lowest rank.

(2) Assigning the species of highest rank the founding species of Group 1.

(3) For each species in decreasing order of rank, conducting pairwise F-tests with the founding species of higher rank. If the incoming species is significantly different ($P < 0.01$) from all existing founding species, it becomes the founding species of a new group. Species not significantly different from all founding species remain ungrouped.

(4) After identifying all founding species, those species remaining ungrouped are compared, in order of rank, with all existing groups, and grouped with the most similar group. Similarity is determined as that grouping which leads to the smallest increase in RSS when the incoming species is amalgamated with the group. These comparisons are made with the whole group, not just the founding species.

(5) Finally, a pairwise comparison of all the resulting groups confirmed that they were all significantly different. It is not necessary that these groups differ significantly. It is possible that the between-species variation inflates the within-group variance more than is compensated for by the increased degrees of freedom, so that not all groups need be significantly different. Despite this, it is probably appropriate that any such groups not be aggregated, as at least one species in each group is known to differ significantly from at least one species in every other group.

This approach overcomes many of the difficulties associated with the alternatives discussed above, and is computationally efficient. Instead of a comparison of all possible pairs, initial comparisons are made between species with many data, reliable parameter estimates and homogeneous variance. Species with few data are only later compared with one of these major groups. It also avoids Leech et al.'s (1991) need to select arbitrarily a subset of the more numerous species to define the groups. This selection is by no means intuitive as in this study the species ranked 186 with only 13 observations initiated a new group.

The present approach provides an objective basis for aggregating species, and empirical trials with subjective assessment of the outcome, suggest that it provides a grouping more sensible than the several alternatives examined. There is, unfortunately, no guarantee that the outcome is optimal.

RESULTS

This analysis produced 41 species groups (see Appendix). Fewer species groups may have been more informative in revealing ecological affinities of tree species, and would have provided a more parsimonious growth model. However, as Stage 1 of the analysis identified 41 species with significantly different increment patterns, any grouping with fewer than 41 groups would aggregate some of these significantly different species into the one group. Fortunately the number of groups does not detract from the utility of the grouping for growth forecasting, as computer-based growth models can readily accommodate any number of growth equations. The final number of groups depends upon the significance level used. Increasing the probability to 0.05 increases the number of groups to 62, while decreasing it to 0.001 decreases the number of groups to 27. The number of parameters in the prediction equation also influences the number of groups; fewer parameters lead to fewer groups.

The group numbering reflects the amount of data available for the founding species of the group, and in no way implies any silvicultural preference or relative growth rate. The resulting groups reflect similarity of diameter increment pattern, and do not necessarily have ecological significance. Pioneer and gap colonizing species are not confined to a single group, but occur in several groups (e.g. *Alphitonia* in Groups 15 and 20, *Macaranga* and *Omalthus* in 22 and *Dendrocnide* in 33). Some groups contain both light demanding and shade-tolerant species (e.g. *Eucalyptus* and *Blepharocarya* in Group 3).

Taxonomy does not provide a good indication of growth pattern. The present analysis assigns 15 different species of *Syzygium* to 13 different groups, and there is not one group which contains more than two species (with differing H&M codes) from the same genus. Groups 15 and 25 both contain the genera *Cryptocarya*, *Planchonella* and *Syzygium*. The size attained by the species at maturity provides little indication of increment pattern (see Appendix). The average growth rate, unless adjusted for tree size, site quality and competition, also provides a poor basis for grouping. Stocker (1983) classified species on the basis of the average annual percentage increase in tree basal area and size at maturity. Three species in the present study fall into his large, fast-growing category, but exhibit quite different increment patterns (Fig. 1) and are assigned to three different groups (see Appendix).

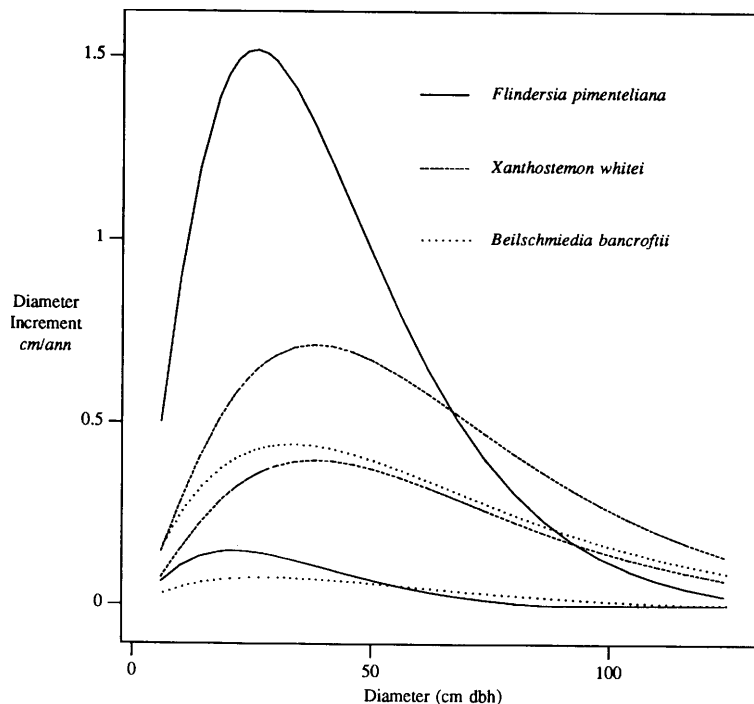


Fig. 1. Increment patterns of 'large fast-growing' species under good (SQ = 7, BA = 20, OBA = 4) and poor (SQ = 4, BA = 40, OBA = 32) conditions.

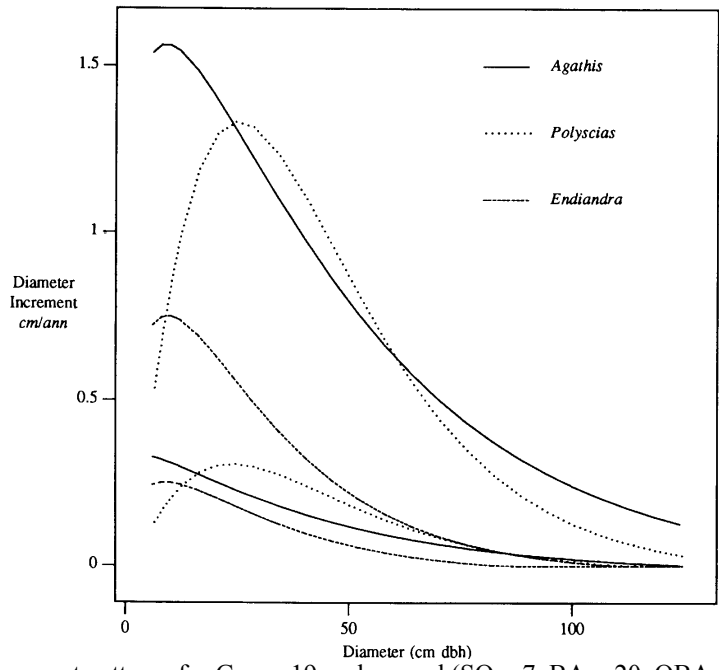


Fig. 2. Diameter increment patterns for Group 19 under good (SQ = 7, BA = 20, OBA = 4) and poor (SQ=4, BA=40, OBA=32) conditions.

Group 19 contains *Agathis*, which commonly occurs as a large emergent tree, and *Polyscias* which is more commonly found as a smaller tree in the understorey. Francis (1981) records that *Agathis* may attain 50 m height and 240 cm dbh, while *Polyscias* attains 30 m height and 75 cm dbh. *Agathis* is well represented in the present database with both understorey seedlings and large emergent trees (dbh range 10-134 cm), while *Polyscias* occurs as small understorey trees (dbh range 10-62 cm, but only three stems exceed 30 cm). However, the specific equations for the species comprising this group are quite similar (Fig. 2) within the range of data available.

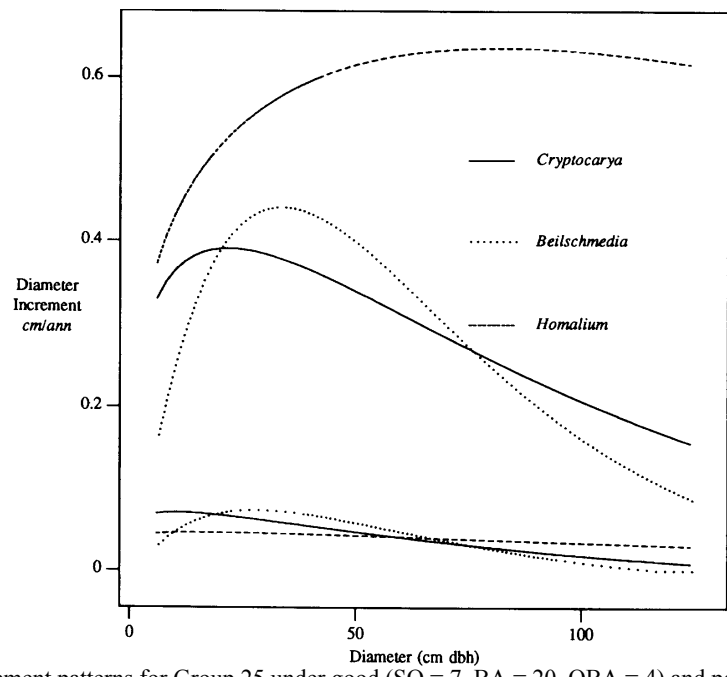


Fig. 3. Diameter increment patterns for Group 25 under good (SQ = 7, BA = 20, OBA = 4) and poor (SQ = 4, BA - 40, OBA= 32) conditions.

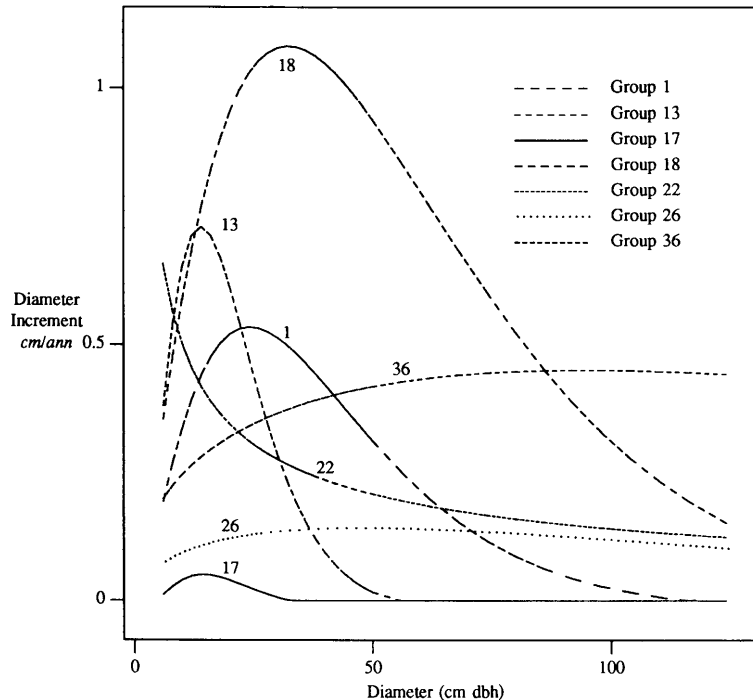


Fig. 4. Diversity of increment patterns for different groups under typical conditions (SQ = 6, BA= 30, OBA=15).

Group 25 contains species classified by Stocker (1983) as large fast-growing and as small slow-growing species, but the specific increment functions are not dissimilar (Fig. 3). Despite such apparent anomalies, the available evidence suggests that the species within any group do, in fact, have indistinguishable diameter increment patterns.

Figure 4 shows the diversity of growth patterns predicted for several groups. These figures provide a simplistic view, as it is unrealistic to assume that both small and large trees share the same overtopping basal area. It should be noted that the relativities between groups may change for varying site quality and basal area. The growth of some groups is little influenced by site quality and/ or basal area, while others are strongly influenced.

This analysis combined those species grouped as 'Miscellaneous' with Group 31. Predicted increments for this group are similar to estimates for the pooled non-commercial species. This is desirable, as inventory officers unable to identify a non-commercial tree correctly may record it as miscellaneous. As increment predictions for this group are approximately equal to the average for the non-commercial species, any bias due to mistaken identity will be minimized.

Following grouping, the possible inclusion of additional co-variables in eqn. (1) was investigated. Soil parent material has been an important co-variate in previous equations (Queensland Department of Forestry, 1985; Vanclay, 1988b, 1989a), and was again found to be significant. Although six classes of soil parent material are recognised in the data (alluvial and colluvial, basic volcanic, acid volcanic, coarse grained granite, Tully (fine-grained) granite, and sedimentary and metamorphic), few differed significantly. Unfortunately, no combination of these soil classes applied equally well to all species groups, so soils were combined into two classes for each species groups.

The effect of logging on diameter increment was investigated and found to be short-lived, and with few exceptions, not significant. Although most of the growth stimulus achieved from silvicultural treatment appears to result from a reduction in total stand and overtopping basal areas, a significant effect of silvicultural treatment could be detected for several of the species groups. The treatment response (Fig. 5) was similar to that detected for *Callitris glaucophylla* (Vanclay, 1988a), but lasted longer. Competing basal area is explicitly included in the model, so this response may reflect the improved spacing of trees and absence of climbing vines. A term to account for this largely experimental treatment was incorporated into eqn. (1) to ensure that timber fore casts from the bulk of the estate, which do not receive such treatment, are not overestimated:

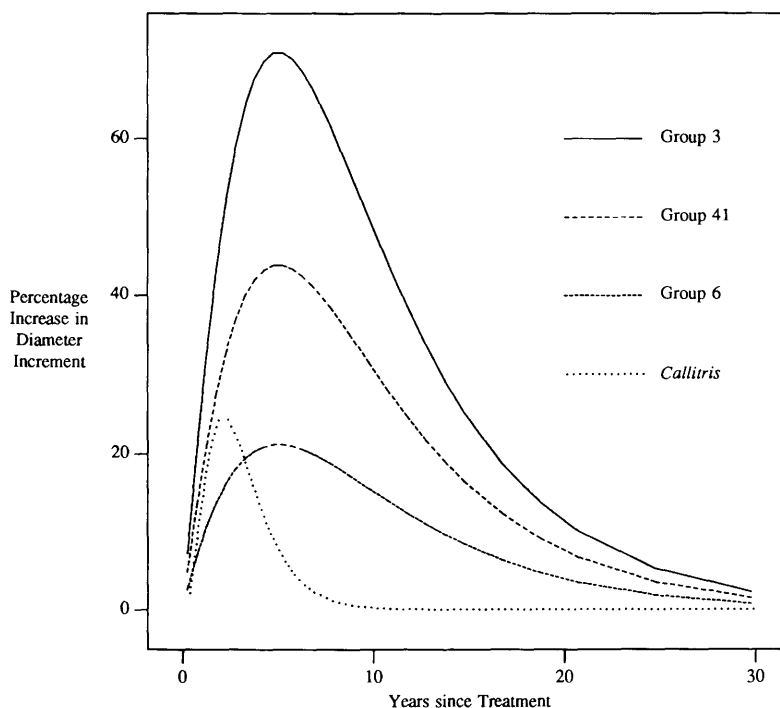


Fig. 5. Response to silvicultural treatment.

$$\log(DI+0.02) = \beta_1 + \beta_2 \times D + \beta_3 \times \log(D) + \beta_4 \times \log(D) \times SQ + \beta_5 \times \log(BA) + \beta_6 \times OBA + \beta_7 \times PS + \beta_8 \times TST \times e^{-TST/5} \quad (2)$$

where TST is time (years) since silvicultural treatment; PS is binary variable which takes the value one if the species is growing on a preferred soil parent material' (Table 3) and zero otherwise; and 13, are parameters to be estimated. The resulting diameter increment equations are presented in Table 3. Because the use of logarithms leads to slightly underestimated predictions, an adjustment to correct this logarithmic transformation discrepancy (Husch et al., 1982) has been computed and added to parameter β_1 . Data exhibiting large decrements in diameter (exceeding - 0.02) were excluded from the regression analyses, but were used in determining this correction, thus ensuring freedom of any bias.

Table 4 compares estimates from the present equations with those previously developed (Queensland Department of Forestry, 1985; Vanclay, 1988b, 1989a). It is evident that the 1985 equations underestimate increments in the present database, and provide no better residuals than a simple average (i.e. notional $r^2 < 0$). This is not unexpected, as the present database comprises many more plots (212 compared with 37 plots in 1985), many of which examine experimental silvicultural treatments with low basal areas and higher increments. A better fit is obtained with eqn. (1), and this improvement may be attributed to the use of a more flexible and more easily estimated equation, and the development of a more reliable measure of site quality (Vanclay, 1989b). Further improvement is obtained by including soil type and treatment history (eqn. 2). The objective formation of 41 groups provides a further substantial improvement in the fit to the data. Clearly, the present model is superior and should contribute more precise yield estimates.

TABLE 3. Parameter estimates for eqn. (2)

Species group	Parameter estimates								Preferred soils ^a
	β_1	β_2	β_3	β_4	β_5	β_6	β_7	β_8	
1	-0.2354	-0.06056	+0.9673	+0.08851	-0.9366	-0.02684	+0.1415		AC AV BV CG TG
2	-1.0762	-0.06005	+1.1948	+0.09639	-1.0247	-0.03662	+0.3514	+0.1477	AV CG SM
3	-1.7553	-0.01541	+0.2361	+0.03350		-0.03282		+0.2916	
4	-0.1422	-0.04298	+0.6487	+0.07254	-0.7847	-0.02368	+0.1274	+0.0691	AC CG SM TG
5	+1.4985	-0.03286	+0.1016	+0.07370	-0.8511	-0.02284		+0.0721	
6	+1.4783	-0.01379	+0.0490	+0.03370	-0.9597	-0.00571		+0.1047	
7	-3.9121	-0.11323	+1.7515	+0.05808	-0.0787	-0.04332	+0.5904		AC BV CG SM
8	-0.1654	-0.02076	+0.4602	+0.04849	-0.7990	-0.01356	+0.4232		BV
9	+3.5094		-0.9398	+0.08594	-0.9896	-0.02194	+0.2035		AC AV BV TG
10	-0.5236	-0.06095	+0.1981	+0.10964	-0.2683	-0.04363	+0.1765		AV BV
11	-0.3824	-0.03038	+0.5254	+0.02626	-0.3946	-0.01897			
12	-0.1463	-0.00386	-0.1948	+0.04810	-0.6117	-0.00410	+0.1819	+0.2117	AC AV BV TG
13	-3.2823	-0.14961	+1.9192	+0.03285		-0.04432	+0.3699		AC BV
14	+0.0250	-0.06610	+1.0530	+0.09348	-1.1435	-0.02350	+0.3051	+0.1619	SM
15	+0.9569	-0.04860	+0.0539	+0.06813	-0.7141	-0.01041	+0.3268		BV CG SM
16	+1.4270	-0.02285	+0.0282	+0.06249	-1.0735		+0.2450	+0.1452	AV BV
17	-5.7585	-0.16820	+2.4223	+0.00194	-0.2680		+0.2725		AV BV SM
18	-0.3342	-0.03988	+1.1840	+0.02680	-0.9318		+0.3218	+0.2065	AC BV SM
19	+0.0514	-0.03515	+0.2965	+0.04438	-0.1758	-0.04689	+0.3562		SM TG
20	-0.8127	-0.10578	+1.6105	+0.07954	-1.1119	-0.00237		+0.5206	
21	-1.0553	-0.08197	+1.9471	+0.07539	-1.5502		+0.3548	+0.1523	AV BV TG
22	+3.1512		-0.9596	+0.08026	-0.7998	-0.02213	+0.5752		BV CG SM
23	+1.1645	-0.01462	-0.3072	+0.03592	-0.7148	-0.00528			
24	+0.0514		-0.6924	+0.03166		-0.03251			~
25	+2.2364	-0.02047	+0.1714	+0.06341	-1.3969	-0.00531			
26	-1.7498	-0.01010	+0.3583	+0.02120	-0.3679	-0.00375		+0.3204	
27	-0.5008	-0.06264	+1.3252	+0.05250	-1.1940	-0.01088	+0.2400		BV
28	+0.5316	-0.02890	+0.0346	+0.03520	-0.2487	-0.04331			
29	+1.2347	-0.00756	+0.6749		-1.3212			+0.3606	
30	-1.4114	-0.08212	+0.9539	+0.10290	-0.7861	-0.02253	+0.7738		BV
31	-0.1781	-0.00798	+0.2320	+0.01937	-0.7603		+0.2974	+0.2749	BV
32	-0.2788	-0.04013	+0.4978	+0.05702	-0.5499	-0.02533		+0.0846	
33	-2.3063	-0.06701	+2.3808	+0.06109	-1.5964				
34	+0.2089	-0.01594	+0.2489	+0.05676	-1.2131		+0.2082		BV CG TG
35	+0.4559	-0.01380	-0.6976	+0.08427	-0.3418	-0.02426			
36	+2.4139	-0.00846	+0.2824	+0.03644	-1.2461	-0.01713	+0.5108		AC CG
37	+0.5576	-0.06552	+0.9285	+0.06729	-1.0462	-0.01147			
38	+0.3451	-0.03725	-0.6649	+0.07957		-0.03231			
39	+0.3235	-0.02976	-0.0491	+0.04685	-0.2219	-0.02190			
40	-1.6960	-0.05239	+0.4479	+0.07968	-0.3640	-0.06019	+1.4954		AV BV CG SM TG
41	-3.3344	-0.06197	+1.6248		-0.4316	-0.00608		+0.1978	

^a AC, alluvial and colluvial; AV, acid volcanic; BV, basic volcanic; CG, coarse grained granite; SM, sedimentary and metamorphic; TG, Tully (fine grained) granite.

TABLE 4. Comparison of diameter increments models

Source	Mean bias (cm per tree year ⁻¹)	Error mean squared	Notional R ²
Mean increment	0.0	0.1060	0.0
QDF (1985) equations	-0.15	0.1122	-0.06
1985 groups and eqn. (1)	0.0	0.0715	0.33
Present groups and eqn. (1)	0.0	0.0604	0.43
Present groups and eqn. (2)	0.0	0.0579	0.45

CONCLUSION

The two-stage approach using pairwise F-tests provides a simple and robust method of comparing and aggregating species groups. Although there is no guarantee that this approach provides an optimal solution, empirical results confirm that the outcome is near optimal.

However, the success of this depends very much upon the variance associated with each species. If the data exhibit non-homogeneous variance, it may be preferable to rank by increasing variance rather than by decreasing number of observations. In particular, it is critical that the species of highest rank has sufficiently low variance that it differs significantly from at least some other species.

This particular grouping should not be considered final; rather, the analysis should be repeated as more data become available, until the resulting groupings show some stability. The resulting grouping of species is useful for growth and yield studies. The equations derived from species groups are more robust than those for individual species, and the existence of fewer equations leads to a more parsimonious growth model. The equations for the grouped data provide better predictions than those derived from a previous model based on subjectively formed groups.

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APPENDIX: SPECIES GROUPS

The following species groups reflect similarity of diameter increment pattern, and do not necessarily have ecological significance. The group numbering reflects the amount of data available for the founding species of the group, and in no way implies any silvicultural preference or relative growth rate. In the interests of brevity, varieties and subspecies have been omitted from this list.

The species presented are those actually represented in the data. Some H&M codes are also applied to other species not present in the database.

The 'Stocker Code' refers to a classification by Stocker (1983) based on his observations in the glasshouse and research plots, of: (1) primary method of dispersal (B is bird, T is bat, W is wind, G is gravity); (2) glasshouse germination rate (R is rapid, completed within 6 months, I is intermediate, E is extended, not complete within 24 months); (3) average growth rate (F is fast, where the individual's annual basal area increment exceeds 2% of its initial basal area, I is intermediate, S is slow, where increment is less than 1% of its basal area); (4) size at maturity (L is large, exceeding 100 cm dbh, I is intermediate, S is small, less than 40 cm dbh).

The 1985 Group refers to the species grouping previously used (Queensland Department of Forestry, 1985; Vanclay, 1988b, 1989a), where FL indicates species with a fast growth rate and attaining a large size at maturity, SL is slow and large, FS is fast and small at maturity, SS is slow and small, and the remaining species were in the non-commercial group.

H&M code	Botanical name	Common name	Stocker code	1985 Group	No. of obs	No. of sites	Max. dbh observed
Group 1							
MSW	<i>Flindersia pimenteliana</i>	Maple silkwood	WRFL	FL	5045	150	99
RSW	<i>Palaquium galactoxylum</i>	Red silkwood		FL	4	1	38
Group 2							
HCB	<i>Aceratium concinnum</i>	Hard carabeen	BISS		13	4	22
QMP	<i>Flindersia brayleyana</i>	Queensland maple	WRSL	FL	4697	112	93
Group 3							
IWN	<i>Beilschmiedia</i> sp. aff. <i>B. oligandra</i>	Ivory walnut	BRSI		36	8	54
IWN	<i>Beilschmiedia oligandra</i>	Ivory walnut			-	-	-
RBN	<i>Blepharocarya involucrigera</i>	Rose butternut	WRSI	SL	3704	30	76
RSG	<i>Eucalyptus grandis</i>	Rose gum		FL	8	1	93
RBW	<i>Eucalyptus intermedia</i>	Red bloodwood			10	1	68
CDY	<i>Sarcopteryx stipitata</i>	Corduroy			2	1	14
BPN	<i>Xanthostemon chrysanthus</i>	Brown penda	GRSL		21	1	107
Group 4							
ALQ	<i>Elaeocarpus arnhemicus</i>	Arnhem Land quandong	BISS		60	10	55
QSA	<i>Flindersia bourjotiana</i>	Silver ash	WRII	FS	3460	139	83
Group 5							
NSO	<i>Cardwellia sublimis</i>	Northern silky oak	WRSL	SL	1838	151	145
CLO	<i>Carnarvonia araliifolia</i>	Caledonian oak	WRSI		416	39	74
TRQ	<i>Elaeocarpus largiflorens</i>	Tropical quandong	BIFI	FS	312	47	45
EVD	<i>Euodia elleryana</i>	Evodia		FS	180	30	65
FRS	<i>Syzygium suborbiculare</i>	Forest satinash			3	1	13
Group 6							
CTM	<i>Arytera lautererana</i>	Corduroy tamarind	BRFS		66	13	40
NSS	<i>Daphnandra repandula</i>	Sassafras	WRSI	FS	1497	90	128
NSS	<i>Doryphora aromatica</i>	Sassafras	WRSI	FS	-	-	-

DUB	<i>Duboisia myoporoides</i>	Duboisia			27	5	25
QWN	<i>Endiandra palmerstonii</i>	Queensland walnut	B-IL	FL	94	22	113
SNW	<i>Endiandra sankeyana</i>	Sankey's walnut	BRSS		68	15	50
NTG	<i>Myristica insipida</i>	Nutmeg	BRII	FS	337	29	53
HKB	<i>Planchonella euphlebia</i>	Hickory boxwood	BRSI		199	9	70
TRP	<i>Syncarpia glomulifera</i>	Turpentine		SL	3	1	33
YLS	<i>Syzygium canicortex</i>	Yellow satinash		SL	84	14	72
Group 7							
SFW	<i>Endiandra sp.</i>	Saffron walnut			2	1	41
YEV	<i>Euodia bonwickii</i>	Yellow evodia	B-FI	FS	172	27	48
NEV	<i>Euodia vitiflora</i>	Northern evodia	BRII	FS	183	30	54
YEV	<i>Euodia xanthoxyloides</i>	Yellow evodia	B-SS	FS	-	-	-
BWD	<i>Litsea sp. (RFK 599)</i>	Bollywood	BRII	FS	1336	94	66
BWD	<i>Litsea bindoniana</i>	Bollywood	BRSS	FS	-	-	-
BWD	<i>Litsea leefeana</i>	Bollywood	BRFI	FS	-	-	-
Group 8							
PMB	<i>Balanops australiana</i>	Pimplebark	BRSI		11617	96	
STP	<i>Canarium australianum</i>	Scrub turpentine			13131	127	
STP	<i>Canarium muelleri</i>	Scrub turpentine	B-SI		--	-	
STS	<i>Ceratopetalum succirubrum</i>	Satin sycamore	WRIL	SL	116048	109	
SCA	<i>Ganophyllum falcatum</i>	Scaly ash			41	35	
BLD	<i>Hylandia dockrillii</i>	Blushwood	--SS		498	50	
FSO	<i>Neorites kevediana</i>	Fishtail silky oak	WRSS	SL	12015	78	
GCB	<i>Sloanea macbrydei</i>	Grey carabeen	B-SI	FS	31337	136	
RPS	<i>Syzygium endophloium</i>	Rolypoly satinash			48228	105	
RPS	<i>Waterhousea unipunctata</i>	Rolypoly satinash			--	-	
Group 9							
TSR	<i>Archidendron grandiflorum</i>	Tulip siris			304	33	
BMR	<i>Decaspermum humile</i>	Brown myrtle	BRII		92	27	
PRM	<i>Dysoxylum oppositifolium</i>	Pink mahogany	BRSI	SS	8213	57	
NRW	<i>Endriandra cowleyana</i>	Rose walnut	BRII	SS	53937	53	
NRW	<i>Endriandra hypotephra</i>	Rose walnut	BRSS	SS	--	-	
GRD	<i>Gardenia ovularis</i>	Gardenia	--SS		409	39	
TSR	<i>Pararchidendron pruinatum</i>	Tulip siris			--	-	
KRS	<i>Syzygium kuranda</i>	Kuranda satinash	TISI	SS	105479	76	
Group 10							
SPO	<i>Buckinghamia celsissima</i>	Spotted silky oak	WRSI		6311	55	
CRL	<i>Cryptocarya sp. aff. C. corrugata</i>	Corduroy laurel	BRSI		18225	69	
CRL	<i>Cryptocarya corrugata</i>	Corduroy laurel	BRII		-	-	
BRO	<i>Darlingia darlingiana</i>	Brown silky oak	WRSI	SS	99391	59	
CBH	<i>Polyalthia michaeli</i>	Canary beech	BRIS	SS	335	24	
CBH	<i>Polyalthia nitidissima</i>	Canary beech	BRFS	SS	--	-	
Group 11							
RDT	<i>Argyrodendron sp. (RFK 2139)</i>	Red tulip oak		FL	97343	78	
RDT	<i>Argyrodendron sp. aff. A. peralatum</i>	Red tulip oak		FL	--	-	
RDT	<i>Argyrodendron peralatum</i>	Red tulip oak	WRIL	FL	--	-	
BTM	<i>Castanospora alphanthii</i>	Brown tamarind	BRII		7017	65	
SKC	<i>Celtis paniculata</i>	Silk celtis	B-IS		102	37	
HKA	<i>Flindersia iffaiiana</i>	Hickory ash	WRSI	FL	9622	80	
DMN	<i>Terminalia sericocarpa</i>	Damson	BRFS	FS	395	100	
RPN	<i>Xanthostemon whitei</i>	Red penda	GRFL	SL	535	102	
Group 12							
BFC	<i>Aceratium doggrellii</i>	Buff carabeen	BIII		31	14	
PLB	<i>Chrysophyllum sp. (RFK 3144)</i>	Plum boxwood	BRSI		2107	66	
BPM	<i>Erythroxylum ecarinatum</i>	Brown plum			21	13	
MRB	<i>Garcinia sp. aff. G. hunsteinii</i>	Marblewood	BRSI		4017	69	
SHT	<i>Halfordia scleroxyla</i>	Saffronheart	BESI		22533	59	
KML	<i>Mallow mollissimus</i>	Kamala			96843	41	
KML	<i>Mallow philippensis</i>	Kamala	B-IS		--	-	
KML	<i>Mallow polyadenos</i>	Kamala	B-IS		--	-	
PLB	<i>Niemeyera chartacea</i>	Plum boxwood			--	-	
KML	<i>Rockinghamia angustifolia</i>	Kamala	B-SS		--	-	

Group 13

LAN	<i>Acronychia acidula</i>	Lemon aspen	BRIS		900	51	51
TMD	<i>Diploglottis bracteata</i>	Tamarind	BRFS		47	10	33
TMD	<i>Diploglottis cunninghamii</i>	Tamarind			-	-	-
BND	<i>Emmenosperma alphonoioides</i>	Bonewood	BRSS		12	5	25
SSA	<i>Flindersia schottiana</i>	Silver ash	WRII		28	2	37
PBS	<i>Syzygium papyraceum</i>	Paperbark satinash		SS	92	12	49

Group 14

BRQ	<i>Elaeocarpus coorangooloo</i>	Brown quandong	BISS	SL	219	28	77
BRQ	<i>Elaeocarpus ruminatus</i>	Brown quandong	BISS	SL	-	-	-
TST	<i>Franciscodendron laurifolium</i>	Tulip sterculia			824	44	78

Group 15

NRA	<i>Alphitonia whitei</i>	Red ash	BIFI		794	103	57
BLL	<i>Cryptocarya triplinervis</i>	Brown laurel	BRFS		33	13	35
LMO	<i>Lomatia fraxinijolia</i>	Lomatia silky oak	WRFI		127	16	67
STO	<i>Oreocallis wickhamii</i>	Satin oak	WRSI	SS	208	29	66
PKB	<i>Planchonella macrocarpa</i>	Pink boxwood	BRFS		34	7	44
PKB	<i>Planchonella papyracea</i>	Pink boxwood	BRSI		-	-	-
NSR	<i>Synoum muelleri</i>	Scentless rosewood	B-SI	SS	10	3	51
FBS	<i>Syzygium jorte</i>	Flaky-barked satinash	BRSS		4	1	29

Group 16

WCW	<i>Alstonia scholaris</i>	White cheesewood	WRSI	FL	47	9	83
COL	<i>Cryptocarya sp. (RFK 2153)</i>	Coconut laurel	BRII		160	14	46
RLL	<i>Cryptocarya mackinnoniana</i>	Rusty laurel	BRII		657	63	72
KRQ	<i>Elaeocarpus bancroftii</i>	Kuranda quandong	BIII		81	11	69
KRQ	<i>Elaeocarpus johnsonii</i>	Kuranda quandong			-	-	-
HYW	<i>Endiandra pubens</i>	Hairy walnut	B-SI		25	10	35
PAL	<i>Gillbeea adenopetala</i>	Pink alder	WRSI		111	14	72
PTM	<i>Jagera discolor</i>	Pink tamarind	B-SI		370	44	53
PTM	<i>Jagera pseudorhus</i>	Pink tamarind			-	-	-
PTT	<i>Pittosporum sp. (RFK 2369)</i>	Pittosporum	BRSS		25	6	30
PTT	<i>Pittosporum rhombifolium</i>	Pittosporum	BISI		-	-	-
WAL	<i>Polyosma alangiacea</i>	White alder			131	22	54
PTM	<i>Sarcotoechia lanceolata</i>	Pink tamarind			-	-	-
WHZ	<i>Symplocos cochinchinensis</i>	White hazelwood		SS	107	27	61
WES	<i>Syzygium wesa</i>	White Eungella satinash		SL	62	13	152
PTM	<i>Toechima erythrocarpum</i>	Pink tamarind	BRSS		-	-	-
WCW	<i>Wrightia laevis</i>	White cheesewood	WRSI	FL	-	-	-

Group 17

CUW	<i>Antidesma bunius</i>	Currantwood	B-II		123	15	19
CUW	<i>Antidesma erostre</i>	Currantwood	BIIS		-	-	-
BOC	<i>Brackenridgea nitida</i>	Brown ochna	-ISS		611	23	23
NRL	<i>Cryptocarya meisnerana</i>	Northern River's laurel			1	1	10
STB	<i>Levieria acuminata</i>	Straw beech			23	7	17
IBS	<i>Polyscias australiana</i>	Ivory basswood	BISS		486	32	22
WNB	<i>Zygogynum semecarpoides</i>	Winter beech			67	11	20

Group 18

BSL	<i>Acacia aulacocarpa</i>	Brown salwood	B-FI	FS	596	51	97
JCD	<i>Bischofia javanica</i>	Java cedar			2	1	16
YBH	<i>Hedycarya loxocarya</i>	Yellow beech	BRSS		1	1	11
WCD	<i>Melia azedarach</i>	White cedar		FS	40	6	26
PCD	<i>Trema orientalis</i>	Peach cedar			11	2	71

Group 19

NKP	<i>Agathis atropurpurea</i>	Queensland kauri pine	WRIL	FL	584	26	134
NKP	<i>Agathis microstachya</i>	Queensland kauri pine		FL	-	-	-
NKP	<i>Agathis robusta</i>	Queensland kauri pine	WRSL	FL	-	-	-
HP-	<i>Araucaria cunninghamii</i>	Hoop pine			241	8	31
SKB	<i>Citronella moorei</i>	Silky beech			5	2	95
BUW	<i>Endiandra sp. (RFK 72)</i>	Buff walnut			36	3	48
BUW	<i>Endiandra longipedicellata</i>	Buff walnut	BRFI		-	-	-
SBS	<i>Polyscias elegans</i>	Silver basswood	BRIS		348	51	62

Group 20

PKA	<i>Alphitonia petriei</i>	Pink ash	BEII	FS	579	49	45
CSO	<i>Musgravea stenostachya</i>	Crater silky oak	WRSI	SL	3	1	18
WBR	<i>Schizomeria whitei</i>	White birch		SS	30	6	51
Group 21							
CNN	<i>Aleurites moluccana</i>	Candlenut	M-SI		510	26	76
RTM	<i>Arytera divaricata</i>	Rose tamarind	BRFS		38	9	24
GMW	<i>Cerbera inflata</i>	Grey milkwood	BRSI		13	4	74
EUQ	<i>Elaeocarpus eumundi</i>	Eumundi quandong	BUS		144	15	58
WBS	<i>Polyscias murrayi</i>	White basswood	BRFS		434	42	54
Group 22							
BLS	<i>Acmena hemilampra</i>	Blush satinash	BRSI		2	1	72
LPS	<i>Acmena smithii</i>	Lilipilli satinash		SS	40	6	65
HMW	<i>Alstonia muellerana</i>	Hard milkwood	WRSI	SS	503	48	61
BTR	<i>Calophyllum sil</i>	Blush touriga	BRII		35	4	48
NNO	<i>Chionanthus ramiflora</i>	Northern olive			2	1	15
CRD	<i>Cordia dichotoma</i>	Cordia	BRSI		6	1	14
MAC	<i>Macaranga tanarius</i>	Macaranga			5	2	16
NBD	<i>Omalanthus populifolius</i>	Native bleedingheart			34	14	21
Group 23							
BUA	<i>Apodytes brachystylis</i>	Buff alder	B-IS		498	34	28
SBN	<i>Archidendron vaillantii</i>	Salmon bean	-RSS	SS	141	32	54
TPW	<i>Harpullia pendula</i>	Tulipwood			10	1	23
BGR	<i>Randia fitzalanii</i>	Brown gardenia	T-IS		60	5	22
UMB	<i>Schefflera actinophylla</i>	Umbrella tree	BRFS		1	1	12
IVW	<i>Siphonodon membranaceus</i>	Ivorywood	B-SS		53	9	45
Group 24							
NSB	<i>Citronella smythii</i>	Silky beech	BRSS		491	39	35
BFB	<i>Irvingbaileya australis</i>	Buff beech	BRSS		105	16	64
SFB	<i>Pouteria castanosperma</i>	Saffron boxwood	BRSS		45	9	30
Group 25							
YWN	<i>Beilschmiedia bancroftii</i>	Yellow walnut	BEFL	SL	388	48	116
NLL	<i>Cryptocarya hypoglauca</i>	Northern laurel	BRSS		479	25	57
NLL	<i>Cryptocarya hypospodia</i>	Northern laurel	BRSS		-	-	-
BRB	<i>Homalium circumpinnatum</i>	Brown boxwood	--II		73	8	49
TTG	<i>Melicope erythrocca</i>	Tingletongue	BRIS		44	2	27
NYB	<i>Planchonella obovoidea</i>	Yellow boxwood	B-FI	SS	58	3	48
SCL	<i>Scolopia braunii</i>	Scolopia	B-FS		17	6	42
RSS	<i>Syzygium johnsonii</i>	Rose satinash	BRII		186	29	48
CHS	<i>Syzygium luehmannii</i>	Cherry satinash	BRFI	SS	257	28	91
Group 26							
BLW	<i>Beilschmiedia sp. aff. B. obtusifolia</i>	Blush walnut	BRII		440	42	75
BLW	<i>Beilschmiedia obtusifolia</i>	Blush walnut	BRII		-	-	-
BRC	<i>Canarium baileyianum</i>	Brown cudgerie	B-SI		365	41	75
CNL	<i>Cryptocarya cunninghamii</i>	Cunningham's laurel	BRFS		4	1	12
BLW	<i>Endiandra sp. (RFK 19)</i>	Blush walnut	BRSI		-	-	-
BLC	<i>Planchonella xerocarpa</i>	Blush coondoo	B-SI		122	20	48
IML	<i>Rhodamnia blairiana</i>	Iron malletwood	BRSS		114	21	59
IML	<i>Rhodamnia sessiliflora</i>	Iron malletwood	B-SS		-	-	-
Group 27							
BRW	<i>Beilschmiedia sp. (RFK 916)</i>	Brown walnut		SL	49	10	80
PPW	<i>Cinnamomum laubatii</i>	Pepperwood	BRII	FS	154	32	57
ILL	<i>Cryptocarya angulata</i>	Ivory laurel	BRSI		360	38	70
BRW	<i>Endiandra acuminata</i>	Brown walnut	BRSS	SL	-	-	-
SSW	<i>Flindersia acuminata</i>	Silver silkwood	WRSI	FS	431	43	67
Group 28							
INW	<i>Anthocarapa nitidula</i>	Incensewood			17	5	56
BBN	<i>Castanaospermum australe</i>	Black bean	MRSL	SL	168	23	88
MWN	<i>Endiandra sp. aff. E. muelleri</i>	Rose walnut	BRSI		165	28	43
FIG	<i>Ficus spp.</i>	Figwood			187	18	180
FIG	<i>Ficus leptoclada</i>	Figwood	BRSS		-	-	-
FIG	<i>Ficus obliqua</i>	Figwood	BRSS		-	-	-
FIG	<i>Ficus watkinsiana</i>	Figwood	BRSL		-	-	-

NBM	<i>Geissois biagiana</i>	Brush mahogany	WRSL	SL	5	3	61
BSO	<i>Musgravea heterophylla</i>	Briar silky oak	WRSI	SL	427	40	76
FBH	<i>Sphenostemon lobosporus</i>	Feather beech	B-SI		43	8	32
BKO	<i>Stenocarpus reticulatus</i>	Black silky oak	WRII		80	16	49
Group 29							
WAS	<i>Acronychia acronychioides</i>	White aspen	BRIS		423	36	42
WAS	<i>Acronychia vestita</i>	White aspen	BRSS		-	-	-
JHR	<i>Backhousia bancroftii</i>	Johnstone River hardwood	WRIL	SL	239	1	105
BBL	<i>Cinnamomum baileyanaum</i>	Bollywood	BRFS		15	1	32
SPB	<i>Croton triacros</i>	Spear birch			49	5	32
SMH	<i>Dysoxylum pettigrewianum</i>	Spur mahogany	BRSL	SL	43	7	107
FIO	<i>Grevillea baileyana</i>	Findlay's silky oak			15	1	42
WAS	<i>Medicosma fareana</i>	White aspen			-	-	-
MRR	<i>Pseudoweinmannia lachnocarpa</i>	Mararie	W-SS	SS	7	2	16
PKS	<i>Syzygium sayeri</i>	Pink satinash		SS	13	3	45
Group 30							
BLO	<i>Bleasdalea bleasdalei</i>	Blush silky oak	WRSS	FS	421	51	56
GPN	<i>Diospyros pentamera</i>	Grey persimmon	BRSS		59	8	27
LSO	<i>Helicia lamingtoniana</i>	Lamington's silky oak	BRIS		19	5	15
BLO	<i>Opisthiolepis heterophylla</i>	Blush silky oak	WRII	FS	-	-	-
FCH	<i>Rhodomyrtus macrocarpa</i>	Finger cherry	B-FS		52	8	20
CHB	<i>Ternstroemia cherryi</i>	Cherry beech	BRIS		18	4	18
VTX	<i>Vitex acuminata</i>	Vitex	BRSI		12	7	40
Group 31							
FKJ	<i>Brachychiton acerifolius</i>	Flame kurrajong	BRSI		86	16	42
RSM	<i>Dysoxylum rufum</i>	Rusty mahogany	BRIS		7	6	15
CWN	<i>Endiandra sp. aff. E. glandulosa</i>	Candle walnut	BRSI		6	2	76
COW	<i>Endiandra dichrophylla</i>	Coach walnut	BRSS		368	31	87
COW	<i>Endiandra glauca</i>	Coach walnut			-	-	-
COW	<i>Endiandra montana</i>	Coach walnut	BRSS		-	-	-
COW	<i>Endiandra tooram</i>	Coach walnut	BRSS		-	-	-
YHT	<i>Fagraea gracilipes</i>	Yellowheart	BRII		53	4	31
MIS	Miscellaneous	Miscellaneous			4468	131	99
Group 32							
BRT	<i>Argyrodendron trifoliolatum</i>	Brown tulip oak	WRSI	SS	1036	62	70
BKP	<i>Prumnopitys amara</i>	Black pine		FL	92	22	65
WCB	<i>Sloanea langii</i>	White carabeen	B-SI	FS	347	48	70
Group 33							
CSS	<i>Acmena divaricata</i>	Cassowary satinash	BRSI	SS	3	1	51
YGR	<i>Aidia racemosa</i>	Yellow gardenia			16	4	20
RAL	<i>Caldcluvia australiensis</i>	Rose alder		SL	103	15	71
WTM	<i>Cupaniopsis foveolata</i>	White tamarind	BRFS		10	4	26
SST	<i>Dendrocnide photinophylla</i>	Shining-leaved stinging tree	B-SI		345	25	121
PPL	<i>Euroschinus falcata</i>	Pink poplar	B-FI		18	7	46
YPN	<i>Ristantia pachysperma</i>	Yellow penda		SS	4	1	41
Group 34							
PLM	<i>Archontophoenix alexandrae</i>	Piccabeen palm			329	9	22
CNG	<i>Cananga odorata</i>	Cananga		B-FS	6	2	24
ROS	<i>Casuarina torulosa</i>	Rose sheoak			14	1	46
GEB	<i>Diospyros fasciculosa</i>	Grey ebony			20	3	14
BFM	<i>Dysoxylum klanderi</i>	Buff mahogany	BRSS		82	10	33
PLM	<i>Licuala ramsayi</i>	Licuala palm	BRSS		-	-	-
PLM	<i>Normanbya normanbyi</i>	Black palm	BRSS		-	-	-
SRW	<i>Synoum glandulosum</i>	Scentless rosewood			6	2	35
ONS	<i>Syzygium alliligneum</i>	Onion satinash			1	1	12
MCB	<i>Xanthophyllum octandrum</i>	Macintyre's boxwood	B-SI		895	61	76
Group 35							
BRY	<i>Brombya platynema</i>	Brombya			293	9	20
CRW	<i>Corynocarpus cribbianus</i>	Cribwood	BRSS		31	4	47
YAS	<i>Euodia haplophylla</i>	Yellow aspen	B-SS		34	4	16
RAP	<i>Rapanea achradifolia</i>	Rapanea	B-SS		118	11	21
BML	<i>Rhodamnia rubescens</i>	Brown malletwood			3	1	13

BSH	<i>Syzygium cormiflorum</i>	Bumpy satinash	BRSI		223	30	45
PLS	<i>Syzygium wilsonii</i>	Plum satinash		SS	74	16	44
Group 36							
GHW	<i>Aphananthe philippinensis</i>	Grey handlewood	B-FI		73	2	44
CAN	<i>Canthium odoratum</i>	Canthium	BRII		4	2	20
SLQ	<i>Elaeocarpus grandis</i>	Silver quandong		FL	261	44	81
PFT	<i>Mischocarpus pyriformis</i>	Pear-fruited tamarind	BRSS		19	2	16
RCD	<i>Toona australis</i>	Red cedar	WRFI	FL	672	32	83
Group 37							
BKR	<i>Commersonia bartramia</i>	Brown kurrajong	B-FS		16	5	22
BSW	<i>Cryptocarya oblata</i>	Bolly silkwood	BRSI	FS	62	7	56
SKA	<i>Ehretia acuminata</i>	Silky ash	BRSS		3	1	12
NTQ	<i>Elaeocarpus foveolatus</i>	Northern quandong	BIFI	SS	170	29	86
NHQ	<i>Elaeocarpus sericopetalus</i>	Hard quandong	BIII	FS	179	26	79
ALB	<i>Prunus turneriana</i>	Almond bark	BRII	FS	311	36	57
Group 38							
HAN	<i>Acronychia laevis</i>	Hard aspen	BRSS		6	3	17
CMH	<i>Alangium villosum</i>	Canary muskheart	B-II		142	31	41
SVB	<i>Casearia grayi</i>	Silver birch			33	5	31
CLL	<i>Cryptocarya sp. aff. C. cinnamomifolia</i>	Cinnamon laurel	BRIS		394	25	44
CLL	<i>Cryptocarya cinnamomifolia</i>	Cinnamon laurel	BRSI	SS	-	-	-
RMP	<i>Cryptocarya rigida</i>	Rose maple	BRII		77	14	44
MMH	<i>Dysoxylum muelleri</i>	Miva mahogany		SL	3	3	12
WHO	<i>Stenocarpus sinuatus</i>	White silky oak	WRII		67	16	58
WHW	<i>Streblus pendulinus</i>	White handlewood	BR-S		7	2	16
Group 39							
RES	<i>Acmena resa</i>	Red Eungella satinash		SL	25	8	162
BGT	<i>Barringtonia calypttrata</i>	Barringtonia	TRSI	FS	4	1	77
ROO	<i>Darlingia ferruginea</i>	Rose silky oak		FS	104	29	51
SMP	<i>Flindersia laevis</i>	Scented maple	WRII	SL	132	14	65
HSO	<i>Grevillea hilliania</i>	Hill's silky oak			33	2	58
ROO	<i>Placospermum coriaceum</i>	Rose silky oak	WRSI	FS	-	-	-
PLN	<i>Planchonella chartacea</i>	Planchonella	BRFS		27	5	23
Group 40							
CMO	<i>Athertonia diversifolia</i>	Cream silky oak			18	7	42
MGN	<i>Galbulimima belgraveana</i>	Magnolia	B-SI	SL	35	10	78
BTD	<i>Glochidion ferdinandii</i>	Buttonwood			70	13	52
BTD	<i>Glochidion harveyanum</i>	Buttonwood	B-II		-	-	-
BTD	<i>Glochidion sumatranum</i>	Buttonwood			-	-	-
HAL	<i>Pullea stutzeri</i>	Hard alder			109	18	70
GRS	<i>Syzygium gustavioides</i>	Grey satinash	GRSI	FL	135	12	83
TBH	<i>Tetrasynandra sp. aff. T. laxiflora</i>	Tetra beech			94	22	29
TBH	<i>Tetrasynandra laxiflora</i>	Tetra beech	BRSI		-	-	-
TBH	<i>Tetrasynandra pubescens</i>	Tetra beech	B-IS		-	-	-
Group 41							
SCI	<i>Austromyrtus acmenoides</i>	Scrub ironwood			4	1	13
GBW	<i>Drypetes lasiogyna</i>	Grey boxwood	B-SI		23	6	42
YMH	<i>Dysoxylum schiffneri</i>	Yellow mahogany	BRFS		13	4	15
WBH	<i>Gmelina fasciculiflora</i>	White beech	BRSS	SL	138	38	80
YBW	<i>Planchonella pohlmaniana</i>	Yellow boxwood		SS	39	7	53
BRP	<i>Podocarpus elatus</i>	Brown pine		FS	165	20	56
BRP	<i>Podocarpus grayi</i>	Brown pine		FS	-	-	-
BLA	<i>Sloanea australis</i>	Blush alder	BRSI	SS	295	34	76
SYN	<i>Synima cordierorum</i>	Synima			156	21	64
RBS	<i>Syzygium trachyphloium</i>	Rough-barked satinash		SS	23	6	50
TYW	<i>Zanthoxylum veneficum</i>	Thorny yellowwood	BRII		104	23	19