



# INTERNATIONAL TROPICAL TIMBER ORGANIZATION

Project PD 162/91 - Papua New Guinea

Intensification of growth and yield studies in previously logged forest

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## The ITTO permanent sample plots in Papua New Guinea : Some results of analysis

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### Abstract

The 417 species and genera on the ITTO plots in PNG are grouped by typical size in 21 model groups. Growth, mortality rates and typical species are presented for these groups. The design of a simple growth model is discussed. It uses group mean increments, modified by a stand density multiplier derived from basal area of trees 10-30 cm dbh, and provincial growth index. Mortality rates average 2.5% for healthy trees and 6.3% for damaged or defective ones. Tree age at 90% of the size distribution ( $D_{90}$ ) is around 100 years for the more common species groups. This is consistently estimated from increment or mortality rate. Mortality rate, increment and typical size are inter-related. Recruitment averages 41 trees  $ha^{-1} yr^{-1}$  over 10 cm. It is weakly density dependent, and is modelled as basal area recruitment as a function of basal area. These functions are discussed as examples of data analysis using standard programs developed for the ITTO plots in FoxPro. They are the basic functions for the PINFORM natural forest growth model.

## Introduction

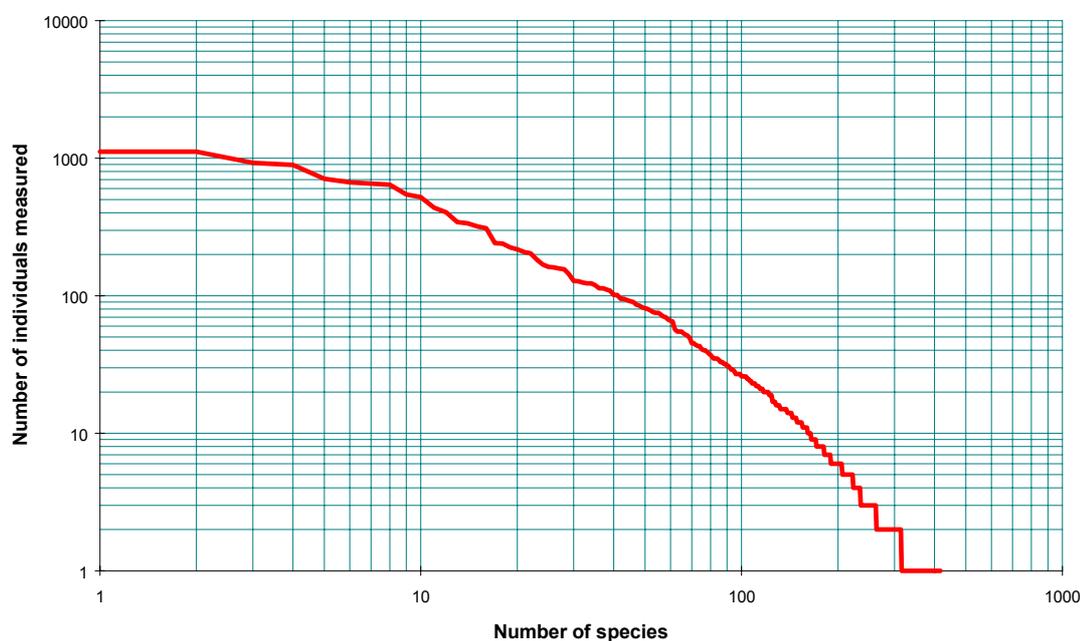
This paper describes the results of some analyses of the ITTO permanent plots in Papua New Guinea. The background and data processing systems for these plots have been described in earlier presentations to this workshop by Oavika (1998) and Yosi (1998). Some of the material in this presentation is taken from the author's earlier reports under the ITTO project, especially Alder (1997b, 1998).

The analyses described here have been directed at developing growth functions for the PINFORM stand growth model. They are based on programs in FoxPro available through the Data Analysis module of the PERSYST program (Romijn, 1994; Alder, 1997a). These programs are designed to generate small summary files from the total dataset of PSPs which can be analysed graphically and statistically using Excel or other programs.

## Species grouping

The PSP data includes some 417 species and genera. Of these, about 40 species are represented by 100 or more trees, whilst over 300 species have less than 30 sample trees, and 100 species have only one or two sample trees. This tendency is illustrated in Figure 1.

Figure 1 : Tree frequency curve for species

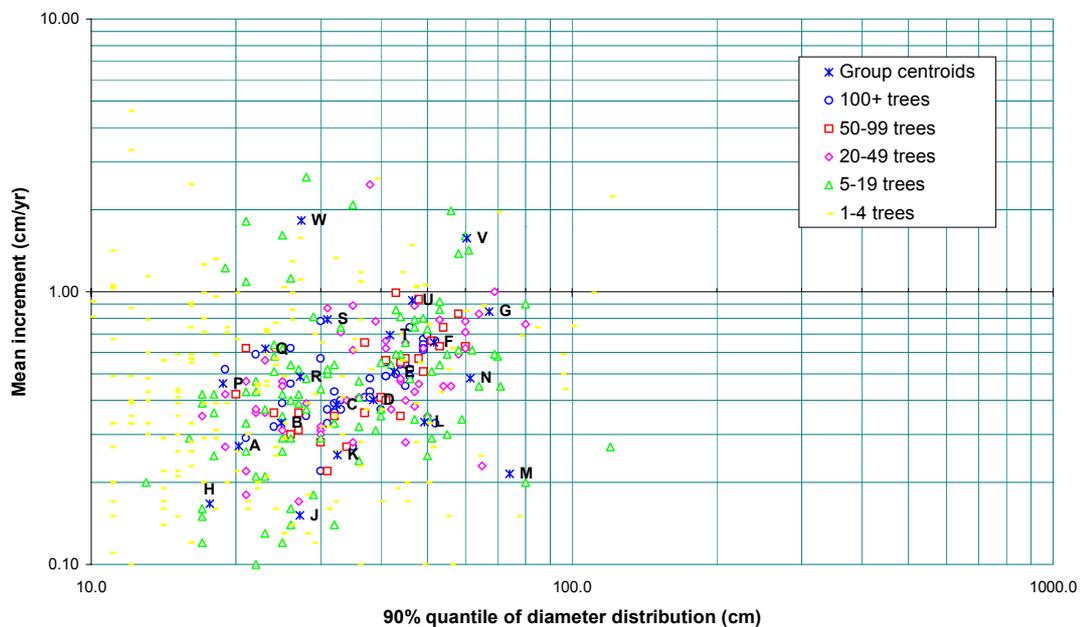


In order to group the many rarer species for analysis of increment and mortality rates, an ordination method was used. Mean increment for each species was plotted against the 90% point of the cumulative diameter distribution (or largest diameter where there were fewer than 10 trees).

Figure 2 shows the result, with different symbols according to the number of sample trees for each species. The bold letters mark the centroids for each group.

Centroids were established arbitrarily, based on inspection of the graph, to cover the range of variation with a reasonable number of groups. More common species were considered as suitable centres for forming groups. The mathematical algorithm, written in Visual Basic for Excel, then calculated Euclidean distance of each species from all possible centroids, and assigned the species to the nearest. The centroids were then re-calculated using the weighted mean values of each provisional group, and the process repeated until centroid values were stable. This scheme has been used by the author elsewhere, and is described in Alder (1995, 1996), for example.

**Figure 2 : Species grouping by mean diameter increment and 90% diameter quantile**



The result was the formation of 21 groups covering a range of mean increments and typical diameters for larger trees of the species. Statistics for each group are shown in Table 1. The most common genera for each group is shown, and other common species listed. The most important groups are A-G, which comprise 78% of the data and 36% of species. Groups H-M are typically slower growing, whilst groups P-V are faster growing. Group X are very fast growing small trees, typically ephemeral pioneers, whilst group V comprises fast growing trees attaining large size, typical of the longer-lived pioneer species.

Table 1 : Typical species and statistics for species groups

Growth Model	Diam <90%	Mean Dinc	No. trees	No. spp.	Principal species	Other common species
<b>A</b>	20.3	0.27	338	29	<b>Timonius</b>	<i>Mammea, Cleistanthus</i>
<b>B</b>	24.8	0.33	1899	22	<b>Myristica</b>	<i>Polyalthia, Medusanthera, Pouteria luzonensis</i>
<b>C</b>	32.3	0.39	2784	20	<b>Horsfieldia</b>	<i>Garcinia, Aglaia, Barringtonia, Chisochiton</i>
<b>D</b>	38.6	0.40	3509	16	<b>Syzygium</b>	<i>Canarium, Planchonella, Dysoxylum</i>
<b>E</b>	42.7	0.51	3778	27	<b>Cryptocarya</b>	<i>Pimeleodendron, Ficus, Calophyllum, Lisea, Celtis</i>
<b>F</b>	51.6	0.65	2091	23	<b>Pometia pinnata</b>	<i>Terminalia, Dillenia, Euodia, Homalium, Sloanea, Intsia</i>
<b>G</b>	67.2	0.84	219	13	<b>Nothofagus</b>	<i>Spondias, Campnosperma, Vitex</i>
<b>H</b>	17.6	0.17	139	35	<b>Zygogynum</b>	<i>Aralia, Ryparosa, Fagraea, Psychotria</i>
<b>J</b>	27.2	0.15	133	21	<b>Cnesmocarpon</b>	<i>Mallotus, Oreocallis</i>
<b>K</b>	32.5	0.25	775	16	<b>Maniltoa</b>	<i>Diospyros, Kibara, Carallia, Parastemon</i>
<b>L</b>	49.3	0.33	325	17	<b>Vatica rassicarpa</b>	<i>Ilex, Gmelina, Schizomeria</i>
<b>M</b>	74.2	0.21	46	8	<b>Alstonia</b>	<i>Decussocarpus</i>
<b>N</b>	61.5	0.48	119	11	<b>Teijsmanniodendron</b>	<i>Neonauclea, Pterygota</i>
<b>P</b>	18.8	0.46	354	43	<b>Gnetum gnemon</b>	<i>Dendrocnide, Melanolepsis</i>
<b>Q</b>	23.0	0.62	576	29	<b>Macaranga</b>	<i>Ziziphus</i>
<b>R</b>	27.2	0.49	596	18	<b>Microcos</b>	<i>Prunus</i>
<b>S</b>	31.0	0.79	218	15	<b>Elaeocarpus</b>	<i>Alphitonia, Neubergia, Duabanga</i>
<b>T</b>	41.8	0.69	412	12	<b>Anisoptera thurifera</b>	<i>Cerbera, Galbulimima, Cananga</i>
<b>U</b>	46.5	0.93	238	15	<b>Anthocephalus</b>	<i>Artocarpus, Tristiropsis</i>
<b>V</b>	60.5	1.57	41	7	<b>Hernandia</b>	<i>Albizia, Ailanthus, Octomeles</i>
<b>X</b>	27.4	1.82	86	20	<b>Trichospermum</b>	<i>Actinodaphne, Lithocarpus, Acacia mangium, Trema</i>

The species ordination and grouping involves the use of two programs. SPPORD.PRG is a FoxPro program that can operate directly on the PERSYST files to generate a list of species with mean increments and 90% diameter quantile in an intermediate file ~SPPORD.DBF. An Excel workbook called SPPORD.XLS contains various macros in Visual Basic to read this file, plot the data graph shown in Figure 2, and perform the ordination analysis.

## Tree and plot increment

Using these 21 species groups, increment and mortality trends could be calculated in various ways, and two FoxPro programs were written, called TREEINC and MORTAL, to do these analyses. These programs produce flexible two-way or multiway tables of increment or mortality classified by diameter, crown position, crown quality, competing basal area, and tree defect codes. The two-way tables can be printed directly from Foxpro; the multi-way tables are designed for regression analysis. The data can be summarised by individual species or the species groups. Figure 3 shows the options screen for the TREEINC program.

Figure 3 : Options screen for the TREEINC program

Species grouping	Classify by	Class definitions
<input type="radio"/> Individual species	<input type="radio"/> Diameter	10,20, 30, 40, 50
<input checked="" type="radio"/> Growth model groups	<input checked="" type="radio"/> Crown illumination	12, 3, 4, 5
	<input type="radio"/> Crown quality	123, 45
	<input type="radio"/> Point basal area	0, 8,16,24,32
	<input type="radio"/> Defect notes	BT,BS,CD,DT,FD,LD,RB,SD,SR,BR

**Output format**

2-way table

N-way regression file

Raw tree data

**Output file**

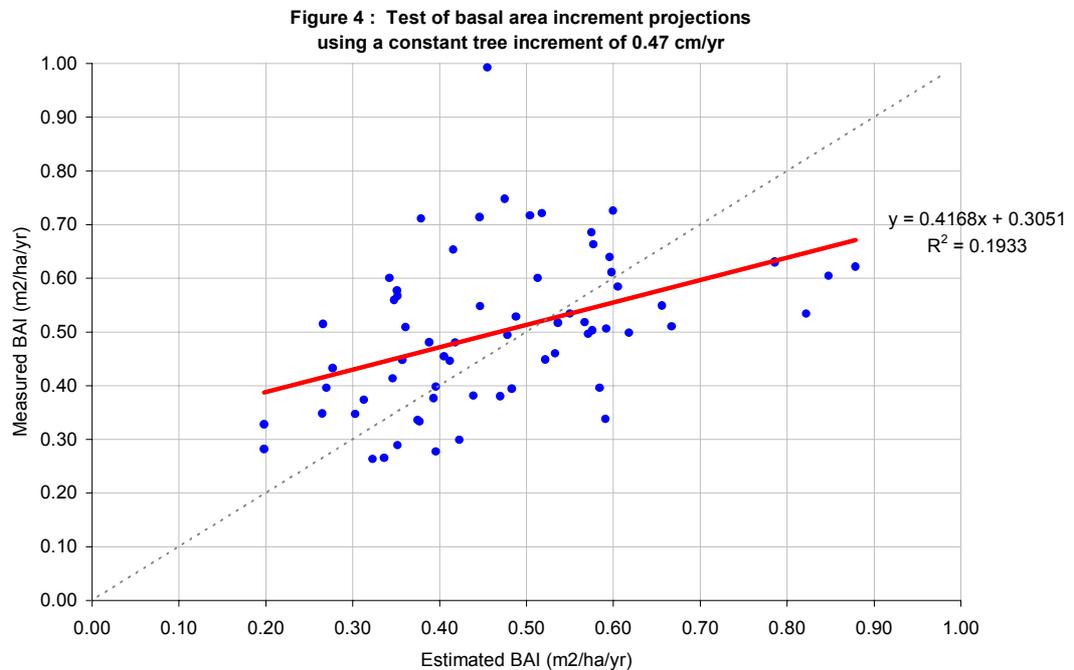
~GXC

Run Edit View Print Notes Exit

It was found that diameter, crown illumination, crown quality, competing basal area and defect status all influence increment. These factors tend to interact. For example, larger trees tend also to have better crown illumination and crown quality. However, it does appear that crown illumination is the primary determinant of increment, with tree vigour, as indicated by crown quality and defect codes, being an important secondary factor.

A test-bed program was designed in FoxPro that would allow various types of growth functions to be compared, in terms of their ability to project overall stand increment. This program uses the species group of each species, and its actual diameter, crown position, defect status, etc. to project growth over the measurement period of the PSP (normally 2-4 years). The total basal area increment for the plot are summarised from (a) the projected increments, and (b) the observed increments. These two statistics are output with plot identity as a simple DBF file which can be analysed using Excel. Various versions of the program were created to test different functions, called MODLTST1, MODLTST2, etc.

Figures 4 to 6 show some results. Figure 4 is the simplest possible model. It uses the overall average increment of 0.47 cm yr<sup>-1</sup> to calculate increment, regardless of species, size, crown position, etc. The graph compares the projected values of basal area increment for each plot with the observed values obtained by direct measurement.



If this type of graph were plotted directly from a regression analysis (ie. Y over estimated Y), then the slope would always be 1 (dotted line on graph), the intercept zero, and the R<sup>2</sup> would be the same as the R<sup>2</sup> of the regression. In this type of graph, therefore, the R<sup>2</sup> can be taken as having a similar meaning as for a regression model (ie. the proportion of total variation accounted for by the model). The slope and intercept should tend to 1 and zero for the best quality model; and can be used as indicators of bias and lack of fit.

This simplest of all possible models (constant increment of 0.47 cm yr<sup>-1</sup>) appears to account for about 20% of variation in plot basal area increment, but is quite biased. BAI tends to be underestimated when actual BAI is low, and overestimated when actual BAI is high.

Figure 5 shows a better result that is obtained when average increments for each species group are used. Here again, there is no consideration of stand density, crown class, tree size, or defect status. The increment calculated for each tree is the species group mean, shown in Table 1. The R<sup>2</sup> in this case has increased to 36%, and the bias or lack of fit is reduced, compared with the estimates based on constant diameter increment.

Several more complicated models were tested, but without exception they gave results that were *worse* than the use of a species group mean increment. An example is shown in Figure 6. This was a model that used regressions for diameter increment based on species group, crown class, and defect status.

**Figure 5 : Test of basal area increment projections using species mean increments**

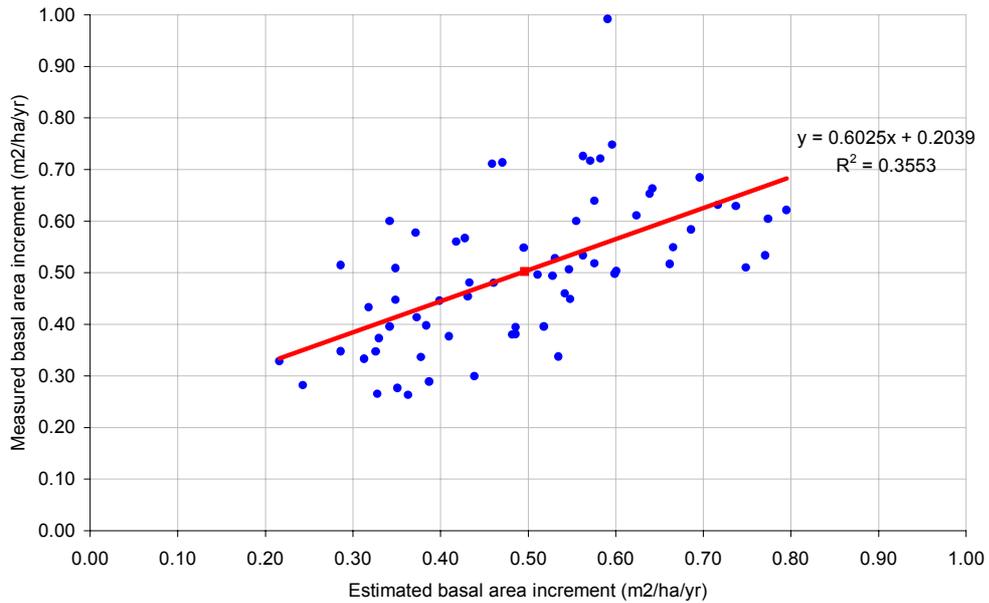
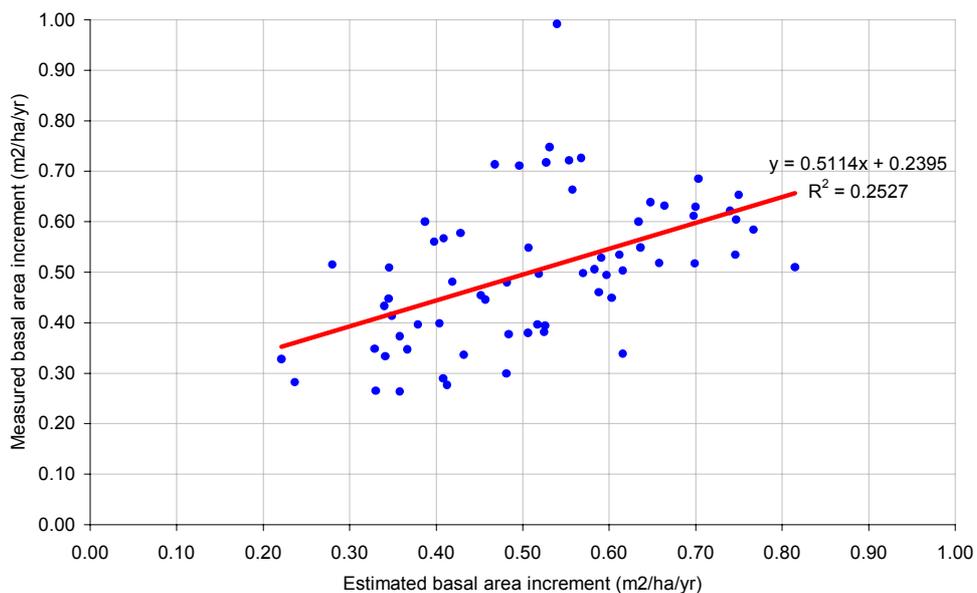


Figure 6 shows projections that in spite of the complexity of the method, are worse than those based on simple species mean increments ( $R^2$  of 25% versus  $R^2$  of 36% for the simpler method). Why is this? I am not sure, but the individual regressions based on crown class and crown quality are very weak, and clearly contribute little useful information.

The conclusion from these analyses is that a simple model for tree increment based on species group means, applied to initial plot measurements, accounts for 36% of the observed variations in plot increments over the project period. As will

**Figure 6 : Test of basal area increment projections using regressions with crown class and crown quality**



be discussed below, this model can be substantially further improved by taking into account stand density and site effects.

## Stand density effects

The ratio of the measured to estimated basal area increments in Figure 5 provides an indicator of error due to the model. By plotting this ratio against various indicators of stand density, and adjustment factor can be determined for stand density effects on growth.

Conventionally in regression analysis errors are analysed using residuals, or the difference between measured and predicted values. In the present case ratios, rather than differences, are used. This allows the resulting adjustment function to be applied directly to tree increments. If errors are analysed conventionally using differences, this is not directly possible.

Various measures of stand density were tested for efficiency, including total basal area of trees over 10 cm dbh, tree numbers over 10 cm, and basal area and tree numbers of various fractions of the stand. Total tree numbers, and basal area of small trees below 30 cm dbh gave the best results. Figure 7 shows the graph of error ratio (observed over estimated increments) versus basal area of small trees. A logarithmic equation explains 28% of the variation in error ratio.

When this stand density correction is applied to projections of plot growth, then there is a further improvement in the accuracy of the model, with the  $R^2$  between measured and estimated BAI's rising to 45%, as shown in Figure 8. It should also be noted in Figure 8 that the slope of combined model is now close to 1 and the intercept close to zero, indicating that there is little residual bias in this model.

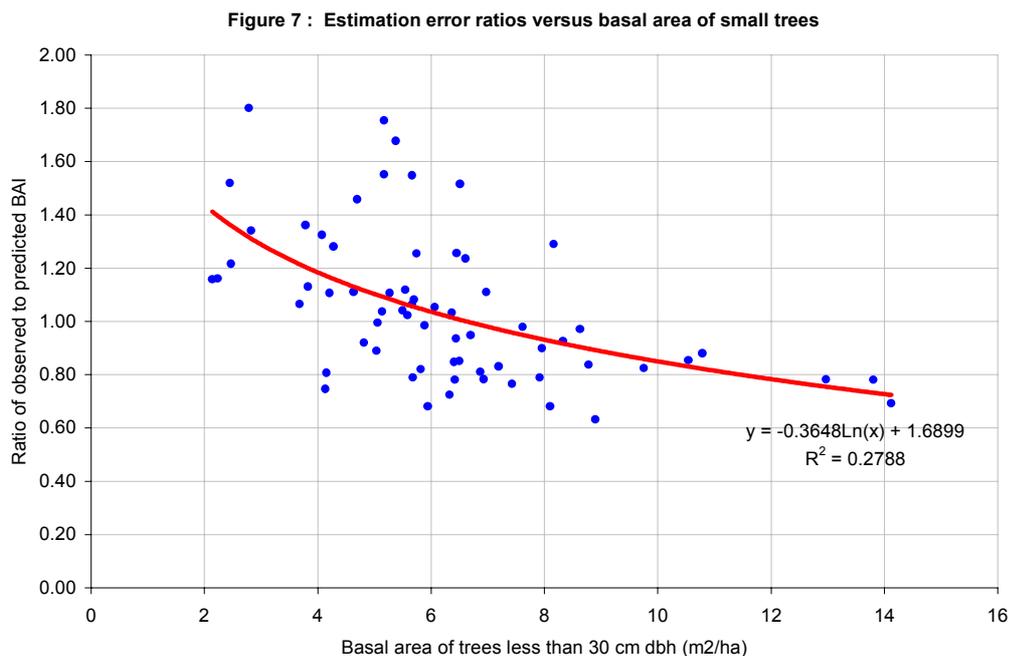
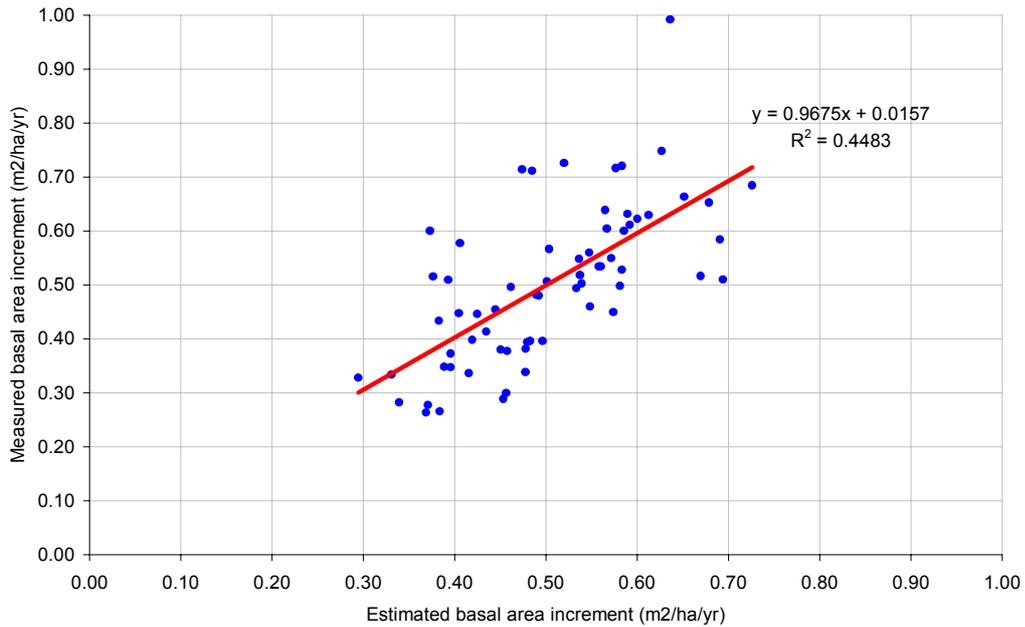


Figure 8 : Estimated BAI after stand density correction



## Site index

The process of examining error ratios can be extended to take account of site factors. The ITTO plots are mostly established in pairs within 1-2 km of each other in widely spaced geographical locations. It was evident from inspection that pairs of plots tended, in Figure 8, to have similar deviations, being either above or below the mean projected value. This implied a site effect.

To analyse this, the mean error ratios were calculated from the combined model shown in Figure 8 (species and stand density) for plots grouped by provinces. These means are shown in Table 2 ranked from highest to lowest.

These site factors are expressed as ratios between the predictions from the basic model and the observed means for the provinces. They can be applied to a final model which includes the province-level site variation. The error analysis from this model is shown in Figure 9. It predicts 77% of the variation in plot basal area, and as indicated by the slope and intercept coefficients of the regression line between measured and estimated values, is very close to being unbiased.

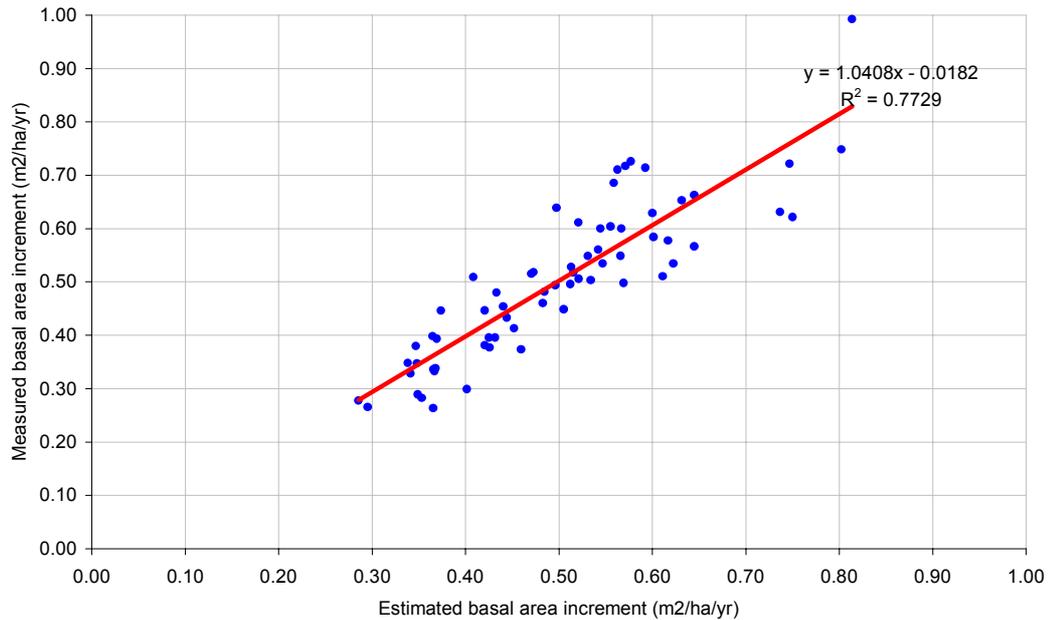
The complete model, including species coefficients, stand density adjustment, and site factors is expressed symbolically in Alder (1997b).

Further research is needed to understand the basis of the site variation, which is probably due to a combination of total rainfall, dry season severity, and soil fertility.

Province	Site
SPKE	1.47
GULF	1.26
MAD	1.26
NI	1.16
CEN	1.13
ORO	1.03
ENB	1.00
WEST	0.99
SPKW	0.92
MAN	0.90
WNB	0.90
BAY	0.86
SH	0.83
MOR	0.76

**Table 2 : Site factors for provinces**

Figure 9 : Estimated BAI after correction for site and stand density



## Volume increments

Plot volume is closely related to basal area, as shown in Figure 10. Bole volume of all trees over 10 cm dbh is slightly over 5 times the basal area to the same diameter limit. The relation becomes weaker for higher diameter limits.

Volume increment can be calculated in various ways and to different diameter limits. For productivity comparisons with plantations, a 10 cm diameter limit is appropriate. Direct commercial volume increment includes sizes 50 cm and above. Volume increment can be calculated gross, excluding losses from mortality, or net, including mortality loss. The latter represents the real volume increment of the stand over the long term, but for the ITTO plots, established shortly after logging, it gives an unduly pessimistic impression as there are many damaged relict trees which are dying and are irrelevant to the future crop.

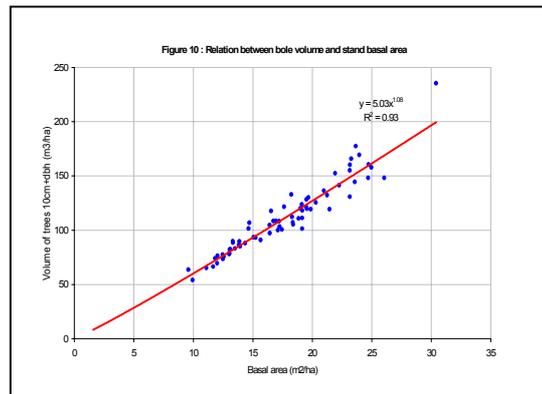
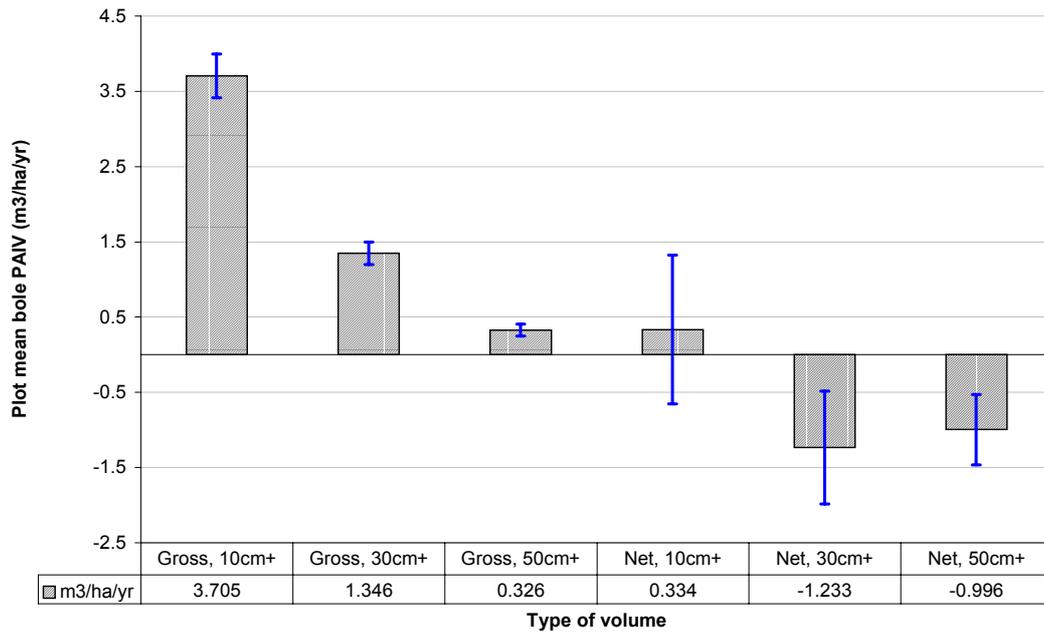


Figure 11 shows these volume figures. The net figures are currently negative, as damaged trees from logging die off. The gross figures for volume increment are 3.7, 1.3 and 0.3  $\text{m}^3 \text{ha}^{-1} \text{yr}^{-1}$  for bole volumes above 10, 30 and 50 cm dbh. These are periodic mean annual increments over the plot measurement period of 2-4 years, and are equivalent to current annual increment.

These figures illustrate why computer models are needed to interpret results from short-term permanent sample plots. They give no real indication of long-term yield or allowable cuts, as they are derived from plots shortly after felling.

Figure 11 : Gross and net volume increments on PSPs



Stand structure in this situation is in a disequilibrium state, with a deficiency of large trees and extensive regeneration. The growth of larger trees is much less than would be observed later in the stand cycle, due to a deficiency in numbers. Net increment, which is the true value required for yield planning, is negative due to the mortality occurring among damaged and physiologically disturbed trees after logging.

The error bars shown on Figure 11 are confidence limits for the plot mean increments.

## Mortality

We have discussed the increment model developed for PINFORM, and have also reviewed actual gross and net volume growth on the plots. It is apparent that mortality is an important factor which can lead to negative volume increment following logging, and which at any time reduces the volume growth available for exploitation.

In PINFORM, three types of mortality are considered:

- Average mortality rates occurring on undamaged trees.
- Mortality rates on more or less severely damaged trees.
- Direct mortality occurring during logging.

Table 3 shows the mortality rates typically observed for the different species groups. This table is produced by the MODELS program directly from the PSP data, and includes here the most recent measurements.

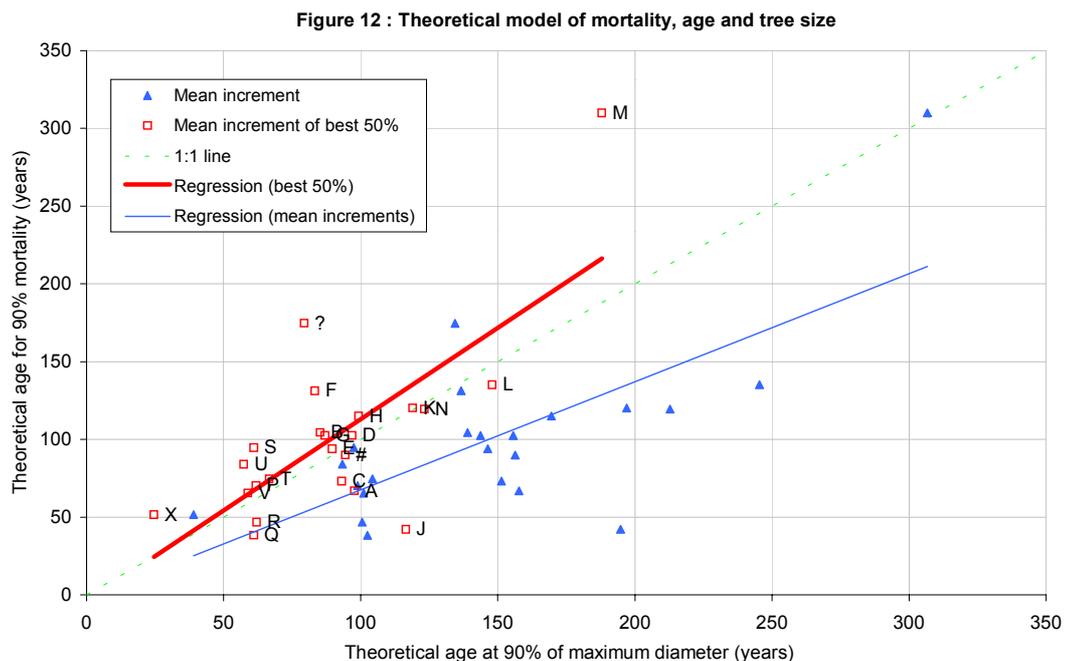
Analysis of mortality rates by crown classes, size classes, tree condition, etc. can be done by the MORTAL program, which has options similar to the TREEINC program shown in Figure 3. However, strong trends with these factors are not apparent except for poor crown quality and defect, which have a clear relation to mortality.

The last line of Table 3 shows the weighted mean mortality rates for all species. It is around 2.5% for healthy trees, and 6.3% for trees scored as defective and damaged. Mortality is measured in terms of numbers of trees dying per annum as a percentage of the total population.

There is a relation between mortality rate, growth rate and typical tree size as indicated by the diameter of the 90% point of the cumulative stand table ( $D_{90}$ ). If  $D_{90}$  is divided by mean increment, it gives an estimate of the age to reach this size. Equally, from the mortality rate, an age can be calculated by which a cohort of recruits has been reduced to 90% of its original level. If mortality and growth rates were constant, these figures should be the same. Figure 12 presents an analysis of this. The X axis shows mean age at  $D_{90}$  calculated from the size/increment relation. The Y axis shows age calculated from mortality rate, required to reduce a cohort of recruits by 90%. The triangles show species group mean 'age' at  $D_{90}$  assuming mean increment growth rates. The squares show the same statistic using the mean increment of the best 50% of each group.

This relation is presented for two purposes. It indicates the approximate age for mature trees (*ie.* at  $D_{90}$ ). And it indicates why  $D_{90}$  was used to group species: Because it is a robust index of mortality rate for a species.

Assuming that the larger trees tend to be the faster growing individuals, then it can be seen that the more common species groups (A-G) and the overall mean (#) cluster very closely about 100 years at their typical size ( $D_{90}$ ). If mean increment is used for this calculation then a higher figure closer to 150 years is obtained. The younger figure also equates closely with the estimate obtained from mortality rates.



## Recruitment

*Recruitment* is usually defined as the rate at which trees reach the minimum measurement size, in terms of numbers per year. It is an expression of the natural regeneration occurring in the forest. For the ITTO plots, the minimum size of measurement is 10 cm, and recruitment rates average around 41 trees/year. The figures vary widely and show some tendency to be density dependent.

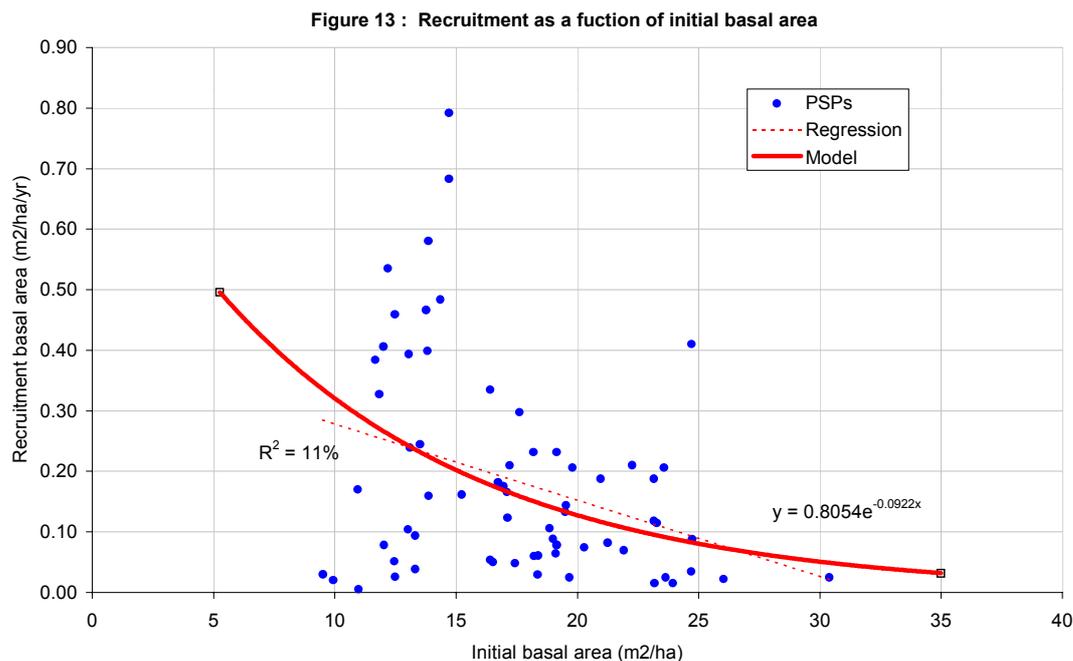
It is also possible to express recruitment in terms of basal area per year. This is more useful for modelling purposes than numbers, in the author's experience, resulting in better relationships and simpler model structure. The two figures can be converted if the typical mean size of recruits is known.

Figure 13 shows the recruitment function used in PINFORM. There is an exponential relationship between stand density at the start of a measurement period, and the average recruitment rate over the period. This is used in the model to determine the total number of recruits.

The data on which Figure 13 is based is calculated by the analysis program BANAL, which calculates basal area changes on plots by various components, including recruitment, and allows the figure shown to be developed very easily using Excel.

In fact a better model of recruitment may exist using only the basal area of smaller sized trees (10-30 cm dbh). However, at the moment this has not been incorporated into PINFORM.

Other aspects of the recruitment model are discussed in Alder (1997b) and Alder (1998). The model takes account of the relative ecological behaviour of species groups, and the existing forest composition when allocating the total calculated recruitment among species groups. This is however a weak aspect of the model



and one which requires further investigation and more longer term data.

## **Conclusions**

This presentation covers a number of issues relating to the analysis of the ITTO plot data in PNG. It shows how the 400 plus species and genera encountered in the data have been grouped using a simple method based on typical size and growth rate. From this 21 growth model groups, designated by letter codes, have been developed.

It discusses design of a tree growth function which is unbiased when applied to projections of forest basal area. The model is quite simple, using average increments for species groups. These are modified by a multiplier for stand density derived from stand basal area in the 10-30 cm size class. The growth rate is further adjusted by a site multiplier which can be applied at a provincial level.

The question of mortality is also discussed. Mortality rate, growth rate, and typical tree size are inter-related. It can be estimated that trees in the more common species groups have ages around 100 years when they attain a diameter that is the 90% quantile of the cumulative diameter distribution. This can be taken as a typical mature size. Mortality rates average around 2.5% for healthy trees, and 6.3% for those recorded as defective or damaged.

The modelling of recruitment is briefly discussed. Recruitment rate depends to some extent on stand density. The species composition of recruits is modelled taking into account existing species composition and the preferences of some groups for greater or less disturbance, as evidenced from the data.

The various analysis programs that have been developed for the ITTO project make the data very accessible. It provides a body of information about stand growth that is already extremely valuable. Further measurements will enhance the usefulness of the plots and improve the quality of the projections and recommendations that can be derived from them.

**Table 3 : Growth models for PINFORM, including mortality rates, based on data to October 1998**

Model	No. trees		Mean increment (cm/yr)		Annual mortality %		Diam.	Typical species, in order of frequency
	Sound	Defect.	Worst 50%	Best 50%	Sound	Defect.		
group							90% freq.	comprising 66% of basal area of group
A	387	22	0.104	0.436	3.4%	5.4%	43	<i>Timonius</i> , <i>Cleistanthus</i> , <i>Lophopetalum torricelliana</i> , <i>Mammea veimaurensis</i>
B	2058	110	0.118	0.521	2.2%	5.6%	44	<i>Myristica</i> , <i>Gonystylus macrophyllus</i> , <i>Polyalthia</i> , <i>Astronidium</i>
C	2405	122	0.132	0.575	3.1%	11.1%	54	<i>Horsfieldia</i> , <i>Garcinia</i> , <i>Aglaia</i> , <i>Chisocheton</i>
D	3829	211	0.151	0.620	2.2%	6.6%	60	<i>Syzygium</i> , <i>Canarium</i> , <i>Dysoxylum</i>
E	4305	232	0.167	0.745	2.4%	5.8%	67	<i>Ficus</i> , <i>Cryptocarya</i> , <i>Pimeleodendron amboinicum</i> , <i>Calophyllum</i> , <i>Celtis</i> , <i>Litsea</i>
F	2678	156	0.210	0.961	1.7%	3.8%	80	<i>Pometia pinnata</i> , <i>Terminalia</i> , <i>Dillenia</i> , <i>Pterocarpus indicus</i> , <i>Euodia</i>
G	342	29	0.256	1.213	2.2%	0.0%	106	<i>Vitex</i> , <i>Spondias cythera</i> , <i>Nothofagus</i> , <i>Terminalia complanata</i>
H	214	20	0.068	0.397	2.0%	1.3%	39	<i>Osmyxylon</i> , <i>Astronidium</i> , <i>Zygogynum</i> , <i>Ficus polyantha</i> , <i>Ryparosa</i> , <i>Diospyros papuana</i>
J	253	22	0.093	0.475	5.3%	18.2%	55	<i>Madhuca leucodermis</i> , <i>Cnesmocarpon discoloroides</i> , <i>Dillenia papuana</i> , <i>Calophyllum microcarpum</i>
K	866	54	0.093	0.449	1.9%	4.4%	53	<i>Maniltoa</i> , <i>Diospyros</i> , <i>Parastemon versteeghii</i> , <i>Carallia brachiata</i>
L	402	12	0.112	0.544	1.7%	2.6%	81	<i>Vatica rassak</i> , <i>Vitex cofassus</i> , <i>Ilex</i> , <i>Gmelina moluccana</i>
M	81	7	0.150	0.665	0.7%	0.0%	125	<i>Alstonia scholaris</i> , <i>Aglaia sapindina</i> , <i>Decussocarpus wallichianus</i>
N	215	9	0.130	0.819	1.9%	0.0%	101	<i>Teijsmanniodendron</i> , <i>Eucalyptopsis papuana</i> , <i>Neonauclea</i> , <i>Endospermum meddulosum</i>
P	497	48	0.165	0.655	3.2%	5.4%	41	<i>Gnetum gnemon</i> , <i>Dendrocnide</i> , <i>Astronia</i> , <i>Polyosma</i> , <i>Erythrospermum</i>
Q	604	52	0.156	0.820	5.8%	11.8%	50	<i>Macaranga</i> , <i>Macaranga aleuritoides</i> , <i>Ziziphus</i> , <i>Syzygium brandar</i>
R	669	29	0.169	0.720	4.8%	10.2%	45	<i>Microcos</i> , <i>Prunus</i>
S	257	10	0.318	1.266	2.4%	4.4%	77	<i>Elaeocarpus</i> , <i>Litsea firma</i> , <i>Duabanga moluccana</i>
T	449	35	0.275	0.985	3.0%	7.3%	66	<i>Anisoptera thurifera</i> , <i>Cerbera floribunda</i> , <i>Canarium indicum</i> , <i>Galbulimima belgraveana</i>
U	276	21	0.293	1.283	2.7%	2.2%	74	<i>Artocarpus</i> , <i>Anthocephalus chinensis</i> , <i>Tristiropsis</i> , <i>Hibiscus</i>
V	68	5	0.336	2.038	3.5%	5.1%	120	<i>Ailanthus integrifolia</i> , <i>Elmerrillia</i> , <i>Hernandia</i> , <i>Albizia</i>
X	156	8	0.540	2.071	4.4%	16.3%	51	<i>Trichospermum burretii</i> , <i>Trichospermum</i> , <i>Polyosma integrifolia</i> , <i>Macaranga tanarius</i>
?	793	63	0.137	0.756	1.3%	3.6%	60	Unknown species
#	21804	1277	0.152	0.731	2.5%	6.3%	69	All species combined

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<sup>1</sup> Copies of unpublished reports by the author may be obtained by e-mail from d-alder@eurobell.co.uk.