



Assessment and Analysis of two *Pinus kesiya* provenance trials at Cashel, Zimbabwe (PV 144)

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Assessment and analysis of a
Pinus kesiya provenance trial
at Cashel, Zimbabwe (PV 144)

Trial No. 3 in the *Pinus kesiya* series

by

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Cover photo:

Stem defects as basal sweep, butt sweep and sinuosity are common for *P. kesiya*. Here Cashel trial site, Zimbabwe.

Photo: Christian Pilegaard Hansen

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Preface

This report presents the results of a joint assessment of the *Pinus kesiya* provenance trial established at Cashel, Zimbabwe. The trial was established by the Forest Research Centre, Forestry Commission, Zimbabwe in December 1992 as part of an international series of provenance trials of the species.

The joint FRC/DFSC field assessment took place in August 1998 by a team lead by Dr. Isaac Nyoka and Mr. Caleb H. Mhongwe of FRC and Christian Pilegaard Hansen of DFSC.

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Acronyms and abbreviations

BSO	Breeding seed orchard
CAMCORE	Central America and Mexico Coniferous Resources Co-operative, USA
CIEF	Centro de Investigaciones y Experiencias Forestales, Argentina
CSIRO	Commonwealth Scientific and Industrial Research Organisation, Australia
CSO	Clonal seed orchard
Danida	Danish International Development Assistance
DFSC	Danida Forest Seed Centre, Humlebæk, Denmark
EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária, Petrolona, Pernambuco, Brazil
FAO	Food and Agriculture Organization of the United Nations, Rome, Italy
FRC	Forest Research Centre, Forestry Commission, Harare, Zimbabwe
ICFRE	Indian Council of Forestry Research and Education, Dehra Dun, India
IF	Instituto Florestal, São Paulo, Brazil
IPEF	Instituto de Pesquisas e Estudos Florestais, Piracicaba, Brazil
OFI	Oxford Forestry Institute, United Kingdom
RCFTI	Research Centre for Forest Tree Improvement, Forest Science Institute, Vietnam
RFD	Royal Forest Department, Thailand

1. Background

The Cashel trial forms part of an international series of provenance trials of *P. kesiya*.

The objective of the international series is to explore and analyse the genetic variation in growth, quality and adaptive traits among provenances of *P. kesiya* throughout the range of the species. The results will facilitate an informed choice of seed source in planting programmes. Furthermore, the results will be useful when planning conservation activities of the species.

Below the background of the international series is briefly described.

Initial research on inter-population differences in *P. kesiya* was undertaken in Zambia in the 1950s. The test material included provenances from the Philippines, Vietnam and Assam. A comprehensive review of these studies is provided by Armitage and Burley (1980).

During 1969, FAO and the Forest Research Institute of Australia sponsored seed collections of 19 seed sources of *P. kesiya* from the Philippines (17 provenance collections and 2 commercial seedlots). The material was complemented by two Zambian land races (of Philippine and Vietnamese origin, respectively). These collections were used for provenance trials in a large number of countries for which the then Commonwealth Forestry Institute supplied advice and assisted in data processing and interpretation (Burley and Wood 1976). Results from individual trials were reviewed by Gibson and Barnes (1984). They concluded that neither provenance representation nor test site representation warranted an international evaluation. It was recommended that a more comprehensive exploration and analysis of the genetic variation of *P. kesiya* should be undertaken. Recommendations in this regard was also put forward by the Sixth Session of the FAO Panel of Experts on Forest Gene Resources (FAO 1988).

Exploration of provenance variation and collection of seed for field trials took place in the late 1980s in collaboration between national institutions in Brazil, Myanmar, China, Mada-

gascar, Philippines, Thailand, Vietnam, Zambia, Zimbabwe, Oxford Forestry Institute (OFI) and Danida Forest Seed Centre (DFSC). In 1988, seed collections were complete and distribution to collaborating countries could begin (Barnes et al. 1989). Distribution of seed was co-ordinated by OFI and handled by DFSC. During 1989-93, seed of 42 provenances and land races from the above 9 countries were distributed to 20 institutions in 19 countries. Some seedlots were separated by family to allow testing of individual progenies.

A status on seed distribution and established field trials is found in DFSC (1996) and DFSC (1997). Some 30 trials have been established in 17 countries. Trials in Argentina, Brazil, Colombia, Indonesia, South Africa, Swaziland, Vietnam and Zimbabwe are reported with high survival and are in general in good conditions. Status of trials in Burundi, India, Rwanda and Sri Lanka is unknown, as no information has been received from these countries. Trials established in Fiji, Kenya, Nepal, the Philippines and Thailand have been abandoned because of fire damage, drought and browsing.

In a circular letter sent out by OFI and DFSC in 1996, host institutes were asked about their interest in undertaking a joint evaluation and were at the same time asked about the status of the trials (DFSC 1996). Positive responses in regard to the proposal of undertaking a joint assessment and analysis of trials have been received from all countries where existence of trials has been confirmed. The number, distribution and representation of provenances in these trials were considered sufficient to justify an assessment and analysis of the international series. Of special interest is the possibility of an in-depth analysis of provenance x site interactions, thanks to the representation of the same set of provenances at many trial sites.

A manual was elaborated during 1997-98 with a proposal for a set of characters to be assessed in all trials (DFSC 1998). Field assessment of trials commenced in April 1998 in Vietnam.

2. *P. kesiya* provenance trials in Zimbabwe

2.1 Earlier trials

P. kesiya was first introduced into Zimbabwe, probably from the Philippines in 1935 (Mullin *et al.* 1984).

A first provenance trial was established in 1968 at John Meikle Forest Research Station with four seedlots of Philippine, Vietnam, Assam and Burma origin (Mullin *et al.* 1984). In 1970/71 this was followed by trials at nine sites with seed lots of Philippine origin. These trials form part of the first international series of trials as described in Chapter 1. In the early 80's a third series of trials was established at four sites with provenances from Thailand plus four local controls.

Analysis results of the earlier trials are summarized by Mullin *et al.* (1984), and will be briefly discussed in Chapter 6 in connection with the results of the analysis of the present trial.

2.2 Present trial - trial PV144 at Cashel

FRC has established a provenance trial of *P. kesiya* in December 1992 at Cashel. The trial has the identification number PV144.

Information on trial design is in Annex 1 and establishment and site information is in Annex 2 and 3.

The trial forms part of the international series. The 21 seedlots represented in the trial are displayed in the below table together with summary information.

Most of the seedlots in the trial originate from natural forests (collections within the natural distribution range). Morarano (Madagascar) is an example of a land race. The origin of the source is most likely Vietnam. Unfortunately, no seed lot description is available. Two seed lots are from clonal seed orchards, in Zambia and Zimbabwe respectively. The seedlot from the Zimbabwean CSO (1776/88) originates from a single clone according to available information. Seed from all the ramets of this clone in the orchard has been bulked and thus represent half-sibs where the male percentage is (theoretically) a mixture of all the other clones in the seed orchard. The results for this seedlot should be interpreted with great care as it does not provide a fair representation of the seed orchard as such.

Seedlots 1624 (Baoshan), 1632 (Ceheng) and 1633 (Shangsi) are *P. yunnanensis*, whereas all others are *P. kesiya*.

Prov. no.	Acc. no. (DFSC)	Provenance	Country	Latitude	Longitude	Altitude m.a.s.l.	Rainfall mm/year	Temp. °C	No. Coll.
1	01447/84	Mt. Province	Philippines	17 15 N	120 30 E	2300	.	.	83
2	01448/84	Benquet	Philippines	16 35 N	120 30 E	1600	.	.	64
3	01515/8500	Dathien	Vietnam	11 58 N	108 27 E	1550	1769	17.9	45
4	01517/8500	Ho Tien	Vietnam	11 51 N	108 32 E	1500	1769	17.9	11
5	01519/8500	Lang Hanh	Vietnam	11 37 N	108 16 E	950	2059	21.5	22
6	01521/8500	Nong Krating	Thailand	18 05 N	98 35 E	1080	1332	22.2	17
7	01523/8500	Doi Inthanon	Thailand	18 32 N	98 35 E	1000	2084	20	30
8	01525/8500	Nam Now	Thailand	16 40 N	101 33 E	800	1316	.	35
9	01624/86	Baoshan (1)	China	24 51 N	99 12 E	1750	.	.	26
10	01632/86	Ceheng	China	24 24 N	105 34 E	800	.	.	25
11	01633/86	Shangsi	China	21 37 N	107 57 E	530	.	.	25
12	0163686	Jingdung (2)	China	24 28 N	100 51 E	1350	.	.	34
13	01637/86	Jinghong	China	22 25 N	101 10 E	1250	.	.	24
14	01638/86	Lancang	China	22 40 N	104 03 E	1620	2059	21.5	22
15	01772/8800	Zokhua	Burma	22 25 N	93 40 E	1600	2335	15.0	20
16	01773/8800	Aungban	Burma	20 41 N	96 37 E	1350	1303	20.5	61
17	01776/88	John Meikle CSO	Zimbabwe	18 43 S	32 51 E	1268	1725	17.9	1
18	01778/8800	Clonal Seed Orchard	Zambia	13 00 S	28 00 E	1300	.	.	10
19	01786/8800	Morarano	Madagascar	18 40	47 02 E	900	.	.	32
20	01572/8500	Coto Mines	Philippines	15 32 N	120 05 E	800	1000	25.1	9
21	01680/86	Dakha	Vietnam	14 48 N	107 56 E	1200	2684	21.6	40

Note: 'No. coll.' is the number of mother trees represented in the seed lot.

3. Field assessment and data management

The assessment in general followed the methodology described in DFSC (1998) which involves the characters:

1. Survival;
2. Health;
3. Social status (Kraft);
4. Height;
5. Diameter (DBH);
6. Straightness;
7. No. of whorls;
8. No. of branches in whorl;
9. Branch diameter;
10. Crown length;
11. No. of forks;
12. Position of first fork;
13. Foxtail;
14. Flowering and fruiting;
15. Wood density (Pilodyn);

For a detailed description of the assessment methodology, please refer to DFSC (1998).

The assessment of the Cashel trial did not include branch diameter and crown length, because the trial had been recently pruned, making assessment of these traits impossible. Under assessment of health, special attention was paid to assessment of woolly aphid attack and 'leaning trees' (see later description)

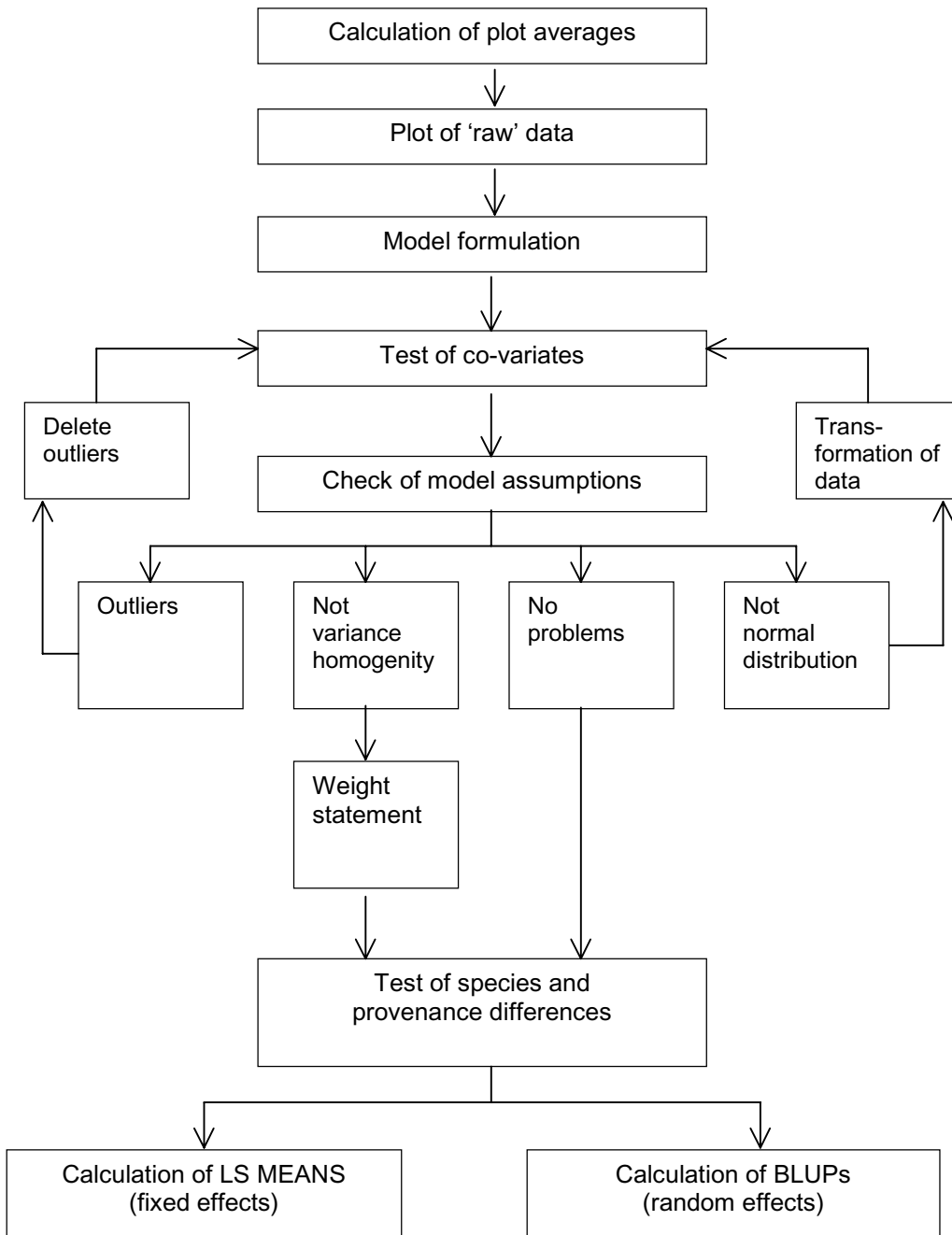
The assessment was a full assessment, i.e. all trees in all plots were included.

Relative wood density was measured with a Pilodyn wood tester with pin diameter 2.0 mm.

Assessment data was recorded in the field on assessment sheets, see example in DFSC (1998). The data was immediately after the assessment entered to a lap-top computer in spreadsheet format. From the shread-sheet, data was later imported to a SAS-dataset for further analysis.

4. Statistical analysis

Overview of steps involved in the statistical analysis



The objectives of the statistical analysis are:

- to examine statistically significant differences between seedlots (provenances) in adaptability, growth and quality traits. A list of analysed traits is provided in Chapter 5;
- to conclude and recommend on the practical application of the results (species and provenance recommendations);
- to investigate patterns of genetic variation;
- to provide data for an overall analysis of the international series of provenance trials of *Pinus kesiya*, i.e. analysis across sites. This step will await completion of the analysis of individual trials.

Statistical analysis is done on plot values, e.g. plot averages or plot sums. Calculation of plot values is described in Annex 4.

The SAS analytical package has been used for the analysis (SAS, 1990).

The statistical analysis of each trait follows a sequence of steps. They are:

1. Plot of raw data;
2. Formulation of statistical model;
3. Test of co-variates;
4. Check of model assumptions;
5. When model assumptions are not fulfilled: (a) transformation of data; (b) deletion of outliers; (c) weight statement;
6. Test of differences between species and provenances;
7. Calculation of lsmeans (estimated from a model with fixed effects);
8. Calculation of BLUPs (estimated from a model with random effects).

The statistical analysis is illustrated in the above figure and the steps are further described in the below text.

Generally speaking, two different approaches are applied in the statistical analysis: a fixed effect approach and a random effect approach. The fixed effects approach is concerned with the genetic entries (seedlots) actually in the trial, whereas the random effects approach concerns what would happen if the experiment was to be repeated. Following the fixed effect approach, the estimates are calculated as least square means (lsmeans), whereas the random effect approach gives the best linear unbiased predictors (BLUPs). See further explanation below.

4.1 Plot of raw data

The main purpose of the plots is to indicate the scale of the variable along with a first impression of the variation within the trial. Often the visual inspection of the data reveals clear differences between the provenances, or gives hints regarding proper transformations of the data. Obvious

outliers (extreme values) may also be identified already at this stage.

The most useful single plot is probably a plot of the variable against the provenances, marking the values with values identifying the blocks. However, other plots may also be relevant, e.g. plotting the values by block or by the distance along the axis of the trial.

4.2 Statistical model

The test of differences between seedlots (provenances) is based on the model:

$$X_{jk} = \mu + \text{provenance}_j + \text{block}_k + \varepsilon_{jk}$$

where X_{jk} is the value of the trait in question (e.g. height) in plot jk ,

μ is the grand mean,

provenance_j is the effect of seedlot number j and is assumed to be either a fixed or a random effect, according to which approach is used (see later),

block_k is the effect of block k in the trial, assumed to be a random effect, and

ε_{jk} is the residual of plot jk and is assumed to follow a normal distribution $N(0, \sigma_\varepsilon^2)$.

Please note that the controls (seedlots not *Pinus kesiya/P.yunnanensis*) are considered (analysed) together with these sources not considering that they actually are sources of different species.

4.3 Co-variates

In order to reduce the residual variation in trials with heterogeneous trial conditions (e.g. variation in soil, elevation, slope and exposure within trial), a number of co-variates are included in the model. As a standard routine the following four co-variates are tested:

plotx: Horizontal position of plot within trial (see map of trial);

ploty: Vertical position of plot within trial (see map of trial);

To catch non-linear patterns of site variation vertically and horizontally, plotx2 and ploty2 are applied:

$$\text{plotx2: } \text{plotx2} = (\text{plotx} - \text{mean}(\text{plotx}))^2$$

$$\text{ploty2: } \text{ploty2} = (\text{ploty} - \text{mean}(\text{ploty}))^2$$

In addition to the above four co-variates, additional co-variates are considered in some of the trials:

level: Level of plot in relation to a reference plot within the trial (0);

plotxy $\text{plotxy} = \text{plotx} \times \text{ploty}$

In testing the effect of co-variates, we start with a model with all co-variates included. Co-variates

that are not significant are removed successively by removing the least significant co-variate and running the model again until all remaining co-variates in the model are significant ($P < 0.10$).

4.4 Check of model assumptions

The statistical model rests on a number of standard assumptions. Key assumptions are (see e.g. Box *et al.* 1978):

- (i) that the residuals are independent;
- (ii) that the residuals follow a normal distribution;
- (iii) that there is variance homogeneity in effects included in the model.

The model assumptions are checked graphically by producing a number of plots:

1. Student's residuals versus predicted values;
2. Cooks distance versus predicted values;
3. Student's residuals versus provenance;
4. Frequency chart of residuals;
5. Student's residuals versus block;
6. Student's residuals versus plotx;
7. Student's residuals versus ploty;
8. Student's residuals versus level (if level is among the considered co-variates).

The residuals represent variation that can not be accounted for by the model. For each observation, the model calculates a predicted value, taking into account the effects of the model (provenance, block and co-variates). The residual variation is then the difference between the observed value and the predicted value.

Student's residuals (also called 'standardised residuals') are calculated as the residual divided by its standard error. If the assumption of normal distributed residuals is valid, the Student's residuals have the property of a normal distribution with mean 0 and variance 1, meaning that 95% of the values should lie within ± 1.96 . In cases of trials with imbalance, the Student's residuals correct for imprecision due to low sample numbers, and in models with co-variates they compensate for large deviations at extreme values.

The Student's residual e_{ij} for observation ij is given by

$$e_{ij} = \frac{e_{ij}}{s_{ij}} = \frac{X_{ij} - P_{i\bullet} - B_{\bullet j}}{s_{ij}}$$

where e_{ij} is the residual, X_{ij} is the value for observation ij , $P_{i\bullet}$ is the effect of provenance i , $B_{\bullet j}$ is the effect of block j , and s_{ij} is the standard deviation (standard error) of observation ij .

Cooks distance gives a measure of the influence of a single observation (plot) on the model, and gives an indication of possible 'outliers' (see below) (Afifi & Clark 1996). A high value indicates

an observation with a large influence on the outcome of the model.

In the following, a description of the check of the model assumptions is given.

Independence

The assumption of independence means that the residual of one observation is not dependent on the residual of another. This assumption is typically violated when using pseudo-replicates, e.g. when doing more observations on the same experimental unit and treating them as different experimental units. Another example is when two or more plots of the same provenance within the same block are treated as independent observations. In such cases, an average of the values should be used as the block value for the provenance in question.

The graphical check of the residuals does not reveal possible problems with observations dependent upon each other, and there is no easy method to ensure that the condition of independence is fulfilled. Proper design and planning of the experiment result and application of a correct statistical model is the best insurance to obtain independent observations.

The assumption of independence may also be violated if there is a time- or site-dependency in the data. To check for such dependency, residuals are plotted against the horizontal and vertical axis of the trial (plotx and ploty) and where applicable, also the level of plot, to investigate any systematic environmental variation. Usually there is none, as the co-variates (plotx and ploty) account for this.

Normality

The assumption of normality may be checked in various ways, graphically as well as by statistical tests. In this analysis, we use the frequency chart of residuals as a graphical check. In the frequency chart, the frequencies should be more or less bell-shaped with no large tails at the ends. A formal statistical test, the Shapiro-Wilk statistic, is given in the SAS-procedure UNIVARIATE with the option NORMAL (SAS 1988a). This procedure also offers different kinds of plots of the residuals. However, since the test is usually considered to be conservative, rejecting only severe deviations from normality, the test results should be considered with caution (Brockhoff, pers. comm.).

When the number of observations is low, it becomes increasingly difficult to check the assumption of normality. Even though the frequency chart may show a rather odd and irregular distribution, this need not be a sign of non-normality. At small sample sizes it is not unlikely that odd distributions may result from random variation, and unless the test for normality demonstrates that the assumption is violated, there is no need to reject the model. On the other hand, when the number of samples is very large, the test for normality may

become rejected even though the frequency chart of residuals appears to be normal. This is because the power of the test increases with the number of observations, and even small deviations from normality may result in rejection of the hypothesis of normal distributed residuals. In such cases it should be considered whether the frequency chart indicate that the assumption is fulfilled, or the deviations are so large that transformation of data (see later) is required.

Deviations from the assumption of normality may also be interpreted as a distribution with a large number of outliers (see later).

Variance inhomogeneity

Variance inhomogeneity occurs when different experimental units (blocks and provenances) have different variance. A typical example is when the residuals of some provenances appear very clustered in the diagram of Student's residuals versus provenances, whereas the residuals of other provenances are spread out, often with values of Student's residuals exceeding ± 2 . This may result from a simple scale effect (larger provenances have larger variance), in which case the plots of Student's residuals and Cook's distance versus predicted values appear funnel-shaped. It may also be related to the provenance itself (some provenances are more variable than others). In this case, the variance inhomogeneity will be displayed in the plot of student's residuals versus provenance.

Outliers

Outliers are extreme observations that do not follow the trends of the remaining data. Such observations may have a large influence on the estimates and statistical tests of the model and should therefore be considered carefully.

Outliers are detected by inspection of the plots of Student's residuals and of Cook's distance. Observations that have values of Student's residuals exceeding ± 2.5 (rule of thumb), and observations with large values of Cook's distance, are possible outliers and should be investigated further. Outliers may be due to errors in the recording or typing of data, or due to mislabelling of the seedlots in the nursery or in the field. Poor survival in the plot, leaving only a few trees to use in the calculation of plot means is another source of outliers. However, it also happens that the outliers are due to some unexplained variation, perhaps in soil conditions or other environmental variation. Finally it should be mentioned that a large number of outliers might indicate that the distribution of residuals is not normal, and hence that a transformation of data is required (see later).

When outliers occur as a result of errors, the dataset should of course be corrected, which will solve the problem. It is less obvious what to do in the cases where there are no easy explanations. Outliers should only be excluded if it can be justified, i.e. an explanation can be given. In a

few cases, however, explanations were not found, and observations were excluded alone on basis of the extreme nature of the value. Great care is required in the decision to exclude plot values, as it will have great importance for the result of the analysis, especially with few blocks (replications). Running the analysis again without the outlier(s) gives an indication of the sensitivity of the analysis in regard to the outliers, and assist in deciding whether to keep or delete the extreme observation(s).

In the interpretation of the statistical analysis in this report, it is always mentioned if one or more extreme values have been considered as outliers and omitted from the analysis, and on what grounds.

4.5 What to do when model assumptions are not fulfilled?

In many cases one or more of the model assumptions are not fulfilled. In the below, procedures for correction are described.

Independence

Apart from making sure that the statistical design and the model is correct there is not much to do about dependence between observations. If some clear variation can be observed in the residuals, other co-variates than the ones mentioned above could be considered.

Deviations from normality

Usually deviations from normality are handled by transformation of data. Snedecor & Cochran (1980) and Afifi & Clark (1996) provide guidance on data transformations:

1. Counts (of rare events) often follow a Poisson distribution and are transformed with the square root.
2. Variables having a binomial character (e.g. dead or alive) summarised in a proportion (e.g. living trees in a plot) may be transformed with the arc sine transformation.
3. If the standard deviation varies directly with the mean, a logarithmic transformation may stabilise the variance.

There are theoretical reasons for choosing the above transformations (Snedecor & Cochran 1980), but it follows from Afifi & Clark (1996) that the range of transformations may be seen as a continuum and that various other transformations are available.

None of the variables included in the present assessment have the character of a Poisson distribution, but the square root transformation has nevertheless in some cases been applied.

In many cases the analysis of survival data results in skewed distributions of the residuals, with tails at either the lower or upper end (many trees dead or many trees alive). In such cases an arc sine transformation of data will often prove useful.

The arc sine transformation is given by

$$\arcsin(\textit{proportion}) = \sin^{-1} \sqrt{\textit{proportion}}$$

where proportion is a figure between zero and one (e.g. the surviving fraction of trees). An important property of the transformation is that the variance near zero or one is stretched out, thus facilitating the analysis of variance (Snedecor & Cochran 1980).

For many growth variables, the variance increases directly with tree size, and the proper transformation is thus the logarithm. In most cases, the natural logarithm (ln) has been applied to achieve a normal distribution of residuals.

Variance inhomogeneity

In the cases where the variance varies with the size of the variable, a transformation of data is the proper way to solve the problem (see above). However, in some cases the provenances simply have different variances irrespective of size, and it is necessary to weight the observations with weights proportional to the reciprocals of the error variances to ensure variance homogeneity (SAS 1988b, cf. Afifi & Clark 1996). There may also be cases where different blocks have different variances, but this has not been observed in the present trial(s).

Weighting occurs in the following sequence: An ordinary analysis of variance of the variable is performed. The residuals from this analysis are grouped according to provenance, and the variance of the residuals for each provenance is calculated. The inverse of these variances is then used as weights in an analysis of variance. When calculating the sums of squares in the model, the weights are multiplied with the squared value of the deviance of each observation from the predicted value (SAS 1988b). This has the effect that provenances with small variances have a larger influence on the model than provenances with larger variances. In other words, the more stable the provenance, the more it counts in the analysis. Provenances with large uncertainty on the other hand have less influence.

4.6 Fixed or random effects

A special problem relates to the choice between considering the effects in the statistical model as fixed or random. Statistically speaking, fixed effects are considered as *parameters* (unknown constants). Random effects are considered *stochastic variables* with an expected value of zero and a variance (Skovgård 1994). Fixed effects are used when the individual groups (seedlots) are of interest. Models with random effects are used when interest is in the size of the variation between the groups (described by the variance), including groups that are not represented in the trial. In analysis of random effects it is important that the groups are representative of a larger population of groups, and they should preferably be chosen

by randomisation (Skovgård 1994). In the words of Stonecypher (1992), ‘fixed models address estimating and testing to infer the existence of true differences among means, whereas the random models address estimating and testing to infer the existence of components of variance’.

To choose between a fixed or a random effects model is a choice with no simple answer. Stonecypher (1992) has formulated the following two questions to facilitate a choice:

1. ‘Are the conclusion confined to the things actually studied; to the immediate sources of these things; or extended to apply to more general population?’
2. ‘In complete repetitions of the experiment would the same things be studied again; would new samples be drawn from the same sources; or would new samples be drawn from the general population?’

When the objective is to estimate components of variance, the effects should be considered as random. If the objective is to estimate differences among means, the effects should be considered as fixed. In some cases fixed and random effects may be combined in the model (mixed models). This is the case when special designs are applied, such as split-plot or nested designs.

In our model with only provenances and blocks, it is necessary to choose between considering the provenance effect as random or as fixed. If the aim is to compare the specific provenances and the actual production on the site, it is natural to consider the provenance effect as fixed. If, on the other hand, (i) the provenances are assumed to be representatives of a population of provenances; (ii) the aim is to expand the conclusions to this population; (iii) to estimate the production and (iv) should the experiment be repeated, then the provenance effect should be considered as random.

The results of the statistical tests are irrespective of whether the provenance effect is considered a fixed or a random effect. However, there are major differences in the estimates resulting from the two approaches (see below). Since it may be argued that both the fixed and the random approaches are relevant in this analysis, both sets of estimates have been calculated.

4.7 Test of differences between provenances

In our statistical model, differences between provenances for a given trait are tested by an F-test comparing the mean square of provenances with the residual mean square. The hypothesis tested is that there is no difference between the provenances. If the F-test is significant, we reject the hypothesis and conclude that there are significant differences between the provenances.

The testing is done using the GLM procedure in SAS (SAS 1990). Since the testing of random vari-

ables may involve combinations of different mean squares (Skovgård 1994), an approximation called Satterthwaite's approximation is used in the calculation of degrees of freedom (SAS 1988).

4.8 Lsmeans (estimates from the fixed model)

In the fixed model approach, the estimates for the provenances are calculated as the least square means (lsmeans). The main difference between raw means and lsmeans is that lsmeans account for missing values and imbalanced designs. Thus, in completely balanced designs there are no differences between lsmeans and the raw means. It follows that the lsmeans are the best estimates for the given provenance in the trial.

The confidence intervals and limits are calculated from the formula (Skovgård 1994)

$$X \pm t_{1-\alpha/2, (a-1)(b-1)} \sqrt{s^2 / b}$$

where X is the least square mean, α is the confidence level (in this case 0.05, giving a 95% confidence interval), a is the number of provenances and b is the number of replicates (blocks) of each provenance. s^2 is the mean square of the error (MS_e). The confidence limits are calculated directly by SAS in the LSMEANS statement with the CL option.

Since the estimates are calculated individually, different provenances may have different lengths of the confidence intervals (due to different variances). In the cases where the data have been weighted, the confidence intervals are adjusted according to the variance of each provenance and thus are of different lengths.

Special problems arise when the data has been transformed. If the least square means and the confidence limits are calculated on basis of the transformed values, the back-transformed estimates will be geometric means rather than arithmetic means. This implies that the estimates become biased towards lower values, and compared to the real values actually are under-estimates. If on the other hand the estimates are calculated using raw data, the lsmeans will be arithmetic means (comparable to the real mean values), but the confidence limits are based on a faulty distribution and will be wrong. In this analysis we have calculated estimates on the transformed values in order to get a fair representation of the differences between provenances. Usually the figures are presented together with a raw mean to circumvent the problem with under-estimation.

4.9 Best Linear Unbiased Predictors (BLUPs - estimates from the random model)

In the random approach, the provenance effects are seen as coming from a normal distribution with an expected value and a variance. This is in opposition to the fixed effect approach, where the provenance effects are seen as constants. Estimating provenance effects in random models is more complicated than in fixed models, because the observed variation between provenances is contemplated as a mixture between true provenance effects and random error variation (*cf.* White & Hodge 1989). The variation between the provenances is therefore always larger than the true 'genetic' variation, except in cases where the error variation is negligible.

In order to predict the effect of a given provenance, it is necessary to correct the estimates for the part of the variance that is due to random error variation. This is done by calculating the best linear unbiased predictors (BLUPs, White & Hodge 1989). The calculation of BLUPs is cumbersome and only feasible with a suitable software package. In this case, the SAS procedure MIXED has been used. It follows from the above that the predicted values for the provenances fall within a smaller range than the least square means. Often the results are presented as deviations from the mean value to allow for easier comparison between different experiments. The deviations are expressed either in real values (m, cm² etc.) or in % deviation from the mean value. Here deviations are presented as % deviations from the mean values.

The problems with transformed values are the same as described for the least square means above. A further complication arises when calculating the deviations from the mean value in percent. If the mean value is calculated on the base of transformed values, and the deviations are calculated on the basis of this back-transformed mean, the deviations from the mean will not sum to zero. In this analysis, we have therefore chosen to base the deviations from the mean value on values calculated after transformation.

The BLUPs are presented with t -type confidence intervals. However, these should be interpreted with caution since it is probably wrong to assume that the underlying distribution of the estimates is normal because of the limited sample size (Littell et al. 1996). Confidence intervals are presented to give an impression of the variation between the provenances and should not be interpreted with respect to differences between provenances.

5. Results of statistical analysis of individual traits

The below table displays the traits selected for analysis, grouped into growth traits, adaptive traits and quality traits. For a full description of the traits and their calculation, please refer to Annex 4.

Group	Trait description	Analysed trait
Growth	Height growth	Height of tree with diameter corresponding to mean basal area (H_c)
	Diameter growth	Diameter of tree corresponding to mean basal area (D_c)
	Mean volume of tree	Average of volumes of trees in plot
	Standing volume per hectare	Volume per hectare
Adaptation	Survival	Survival percentage
	Cone setting	Average score of old, open cones
	Foxtailing	Foxtailing percentage
	Woolly aphid	Frequency of attack (%)
	'Leaning trees'	Frequency of 'leaning trees' (%)
Quality	Stemform	Stemform score (1-9)
	Relative wood density (Pilodyn)	Diameter adjusted pilodyn readings

5.1 Survival

OVERVIEW OF ANALYSIS	
Co-variates	None
Data transformation required	Yes. Arc sin transformation
Weight statement	Yes
Outliers	None

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	9.97	9.85 (***)	0.0001
Block	5	0.12	0.11	0.99
Error	100	1.01		

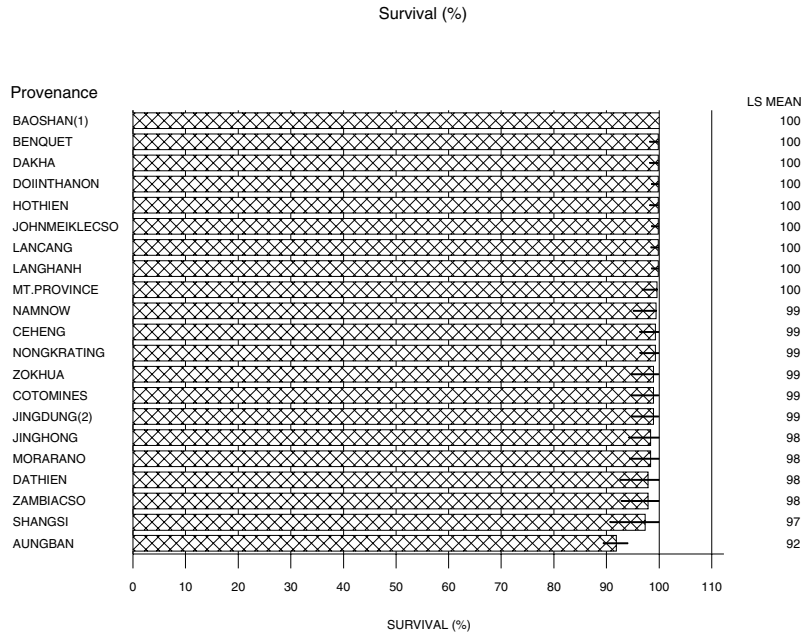
Data has been transformed before analysis using an arc-sin transformation. This has been done to better fulfil the model assumptions as described in Chapter 4.

The survival percentage is high – 100 per cent or close to 100 per cent – for most provenances. The only provenance with a somewhat lower survival (92%) is the Aungban provenance from Myanmar. If this source is left out of the analysis there are not statistically significant differences between provenances.

Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

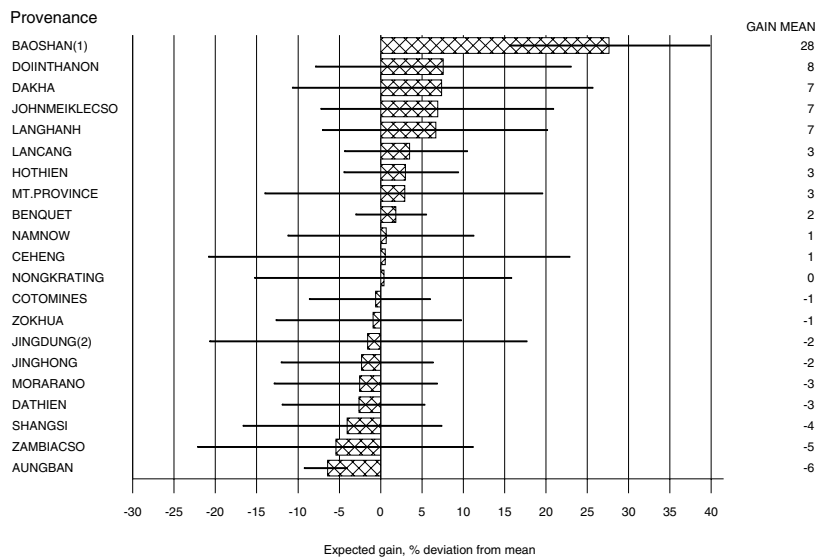


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Survival. Best linear un-biased predictors (BLUPs)



5.2 Height growth

OVERVIEW OF ANALYSIS	
Co-variates	PLOTY
Data transformation required	No
Weight statement	Yes
Outliers	Yes. Shangsi (Block 1)

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	89.95	88.68(***)	<0.0001
Block	5	7.17	7.07	<0.0001
PLOTY	1	7.45	7.34	0.0079
Error	98	1.01		

The height of the Shangsi provenance in Block 1 is very different from the performance of the provenance in the other 5 blocks (much taller in Block 1). An investigation of the assessment data did not reveal any mistakes or data errors which could explain this. It was decided to exclude the plot from the analysis because of its extreme nature.

There are highly significant differences among the provenances in regard to height growth.

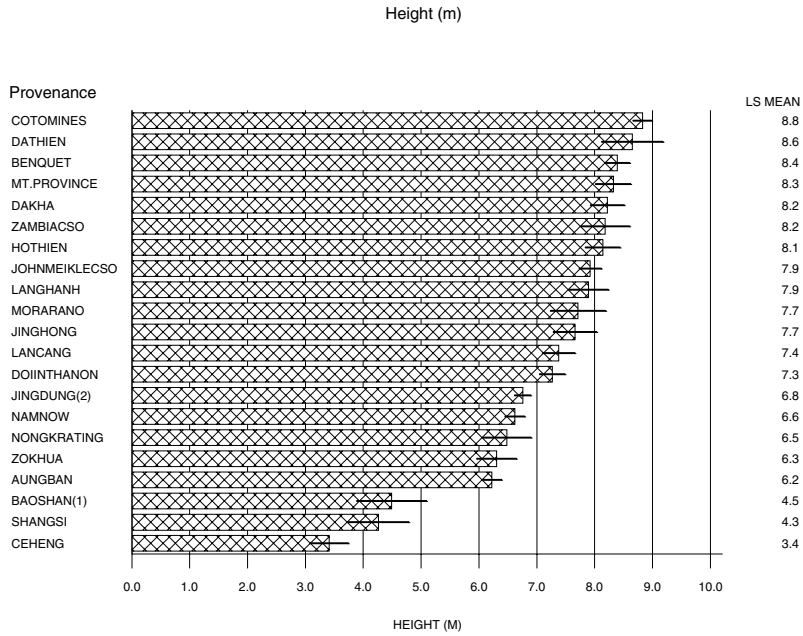
The Philippine sources are ranked at the top, with Coto Mines at the very top, and Benquet and Mt. Province ranked three and four. Also the Vietnamese sources are ranked high in height growth with Da Thien ranked second and Da Kha ranked 5, Ho Thien 7, and Lang Hanh 9. The off-springs from the Zambia CSO, and John Meikle CSO (Zimbabwe) are also doing relatively well, ranked 6 and 8 respectively. There are only small, and statistically not significant differences among many of the top-ranking sources.

The poorest height performers are the *P. yunnanensis* sources Shangsi and Ceheng, the Burmese sources (Zok Hua and Aungban). Thai and Chinese *P. kesiya* sources are intermediate.

Pinus kesiya provenance trial, Cashel, Zimbabwe

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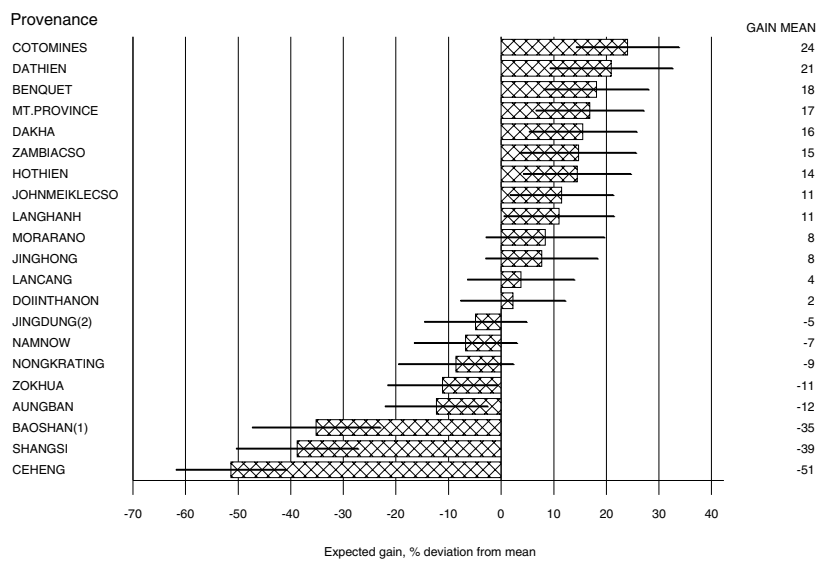


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Height. Best linear un-biased predictors (BLUPs)



5.3 Diameter growth

OVERVIEW OF ANALYSIS	
Co-variates	PLOTY
Data transformation required	No
Weight statement	Yes
Outliers	Yes. Shangsi (Block 1)

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	29.00	27.78(***)	<0.0001
Block	5	12.23	11.72	<0.0001
PLOTY	1	61.21	58.64	<0.0001
Error	98	1.04		

As was the case with the analysis of height growth, Shangsi (Block 1) is identified as 'outlier', and has been excluded from the analysis.

There are highly significant differences between seed lots in regard to diameter growth.

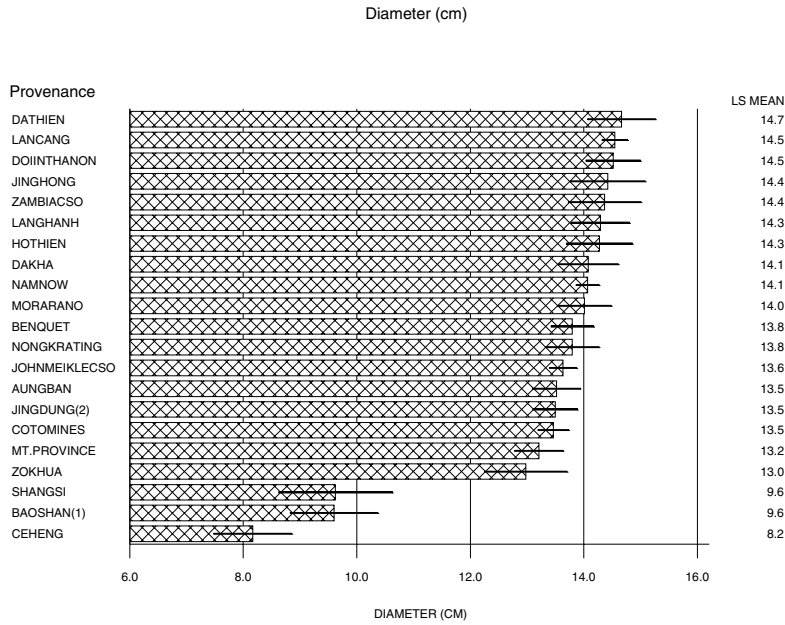
The three *P. yunnanensis* sources, Shangsi, Baoshan and Ceheng, have the poorest diameter growth, as was the case with height growth.

The ranking at the top, however, is quite different to what was seen for height growth. Most notably, the Philippine sources, which were top-ranking in height growth, are ranked low in diameter growth, especially the Coto Mines and Mt. Province. Dathien (Vietnam), which was also ranked high in height growth, has the highest diameter. It is followed by Lancang (China), Doi Inthanon (Thailand) and Jinghong (China), which were intermediate in height growth. The three other Vietnamese sources, Lang Hanh, Ho Thien, Da Kha, and the Zambia CSO are also ranked at the top as was the case with height growth. The Burmese sources Zok Hua and Aungban are among the poorest sources.

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Established December 1992. Assessed August 1998

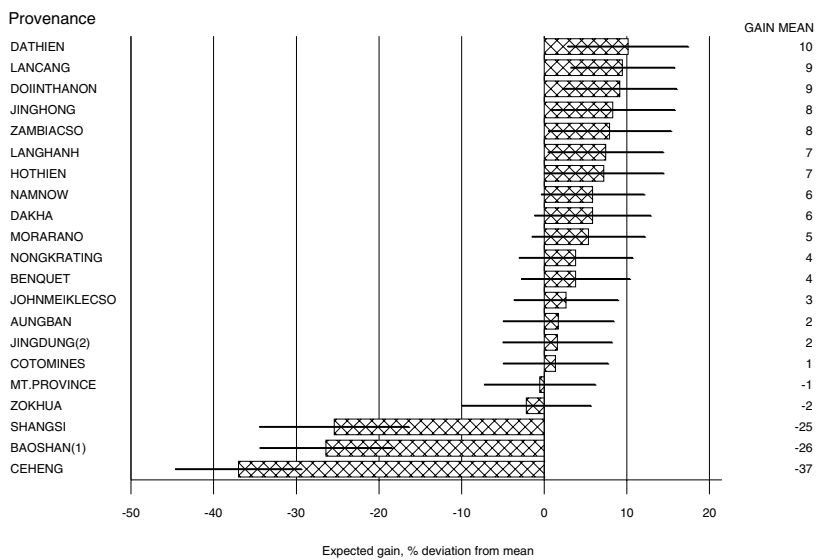


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Diameter. Best linear un-biased predictors (BLUPs)



5.4 Mean volume of tree

OVERVIEW OF ANALYSIS				
Co-variates	PLOTY			
Data transformation required	No			
Weight statement	Yes			
Outliers	Yes. Shangsi (Block 1)			

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	76.51	73.86(***)	<0.0001
Block	5	17.61	17.00	<0.0001
PLOTY	1	91.11	87.95	<0.0001
Error	98	1.04		

Mean volume of tree is calculated as the average of the volumes of individual trees. As both height and diameter are included in the volume formula (see Annex 4), the trait thus illustrates a combined effect of height and diameter.

As for the other growth traits, the Shangsi sources in Block 1 has been omitted from the analysis as it differs very much from the other plots (much taller and bigger trees in this plot than in the other plots). No explanation has been found and the plot is thus omitted from the analysis on the basis of the extremeness of the observation. The omission has little practical importance, as the Shangsi provenance as seen in the previous analysis, is among the poorest growth performers.

The *P. yunnanensis* sources, Baoshan, Shangsi and Ceheng, have very low volumes and are ranked at

the very bottom. Of the *P. kesiya* sources, the Burmese sources Aungban and Zok Hua have the lowest volumes. Slightly better is the sources Jindung (China), Nong Krating and Nam Now (Thailand) and Mt. Province (Philippines).

At the top we find the Vietnamese sources, Dathien, Da Kha, Ho Thien and Lang Hanh. All 4 tested Vietnamese seed sources are among the best five performers, together with the Zambia source (ranked second). Coto Mines of the Philippines is also among the best due to a good height growth. There are only small, and not statistically significant differences, among the top-ranking provenances.

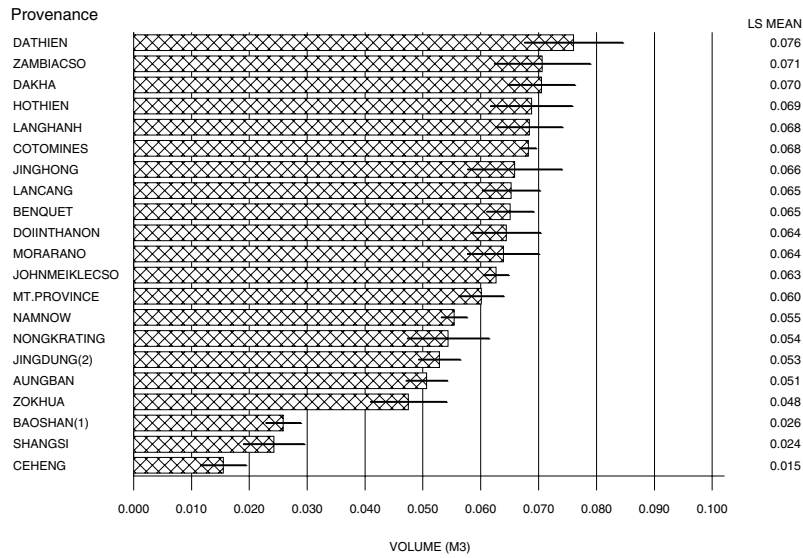
Intermediate growth performers are the Chinese sources Jinghong and Lancang, Benquet (Philippines), Doi Inthanon (Thailand), Morarano (Madagascar), and John Meikle CSO (Zimbabwe).

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Established December 1992. Assessed August 1998

Volume of mean tree (m³)

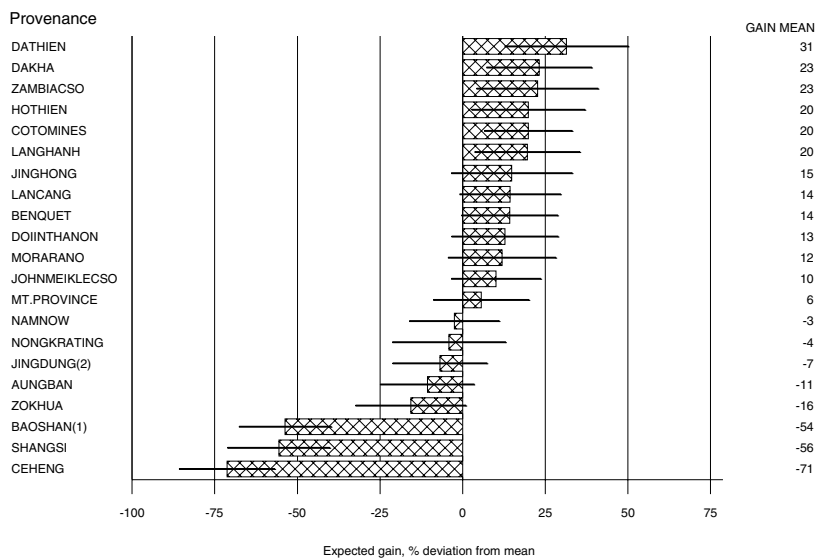


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Volume of mean tree. Best linear un-biased predictors (BLUPs)



5.5 Total volume per hectare

OVERVIEW OF ANALYSIS				
Co-variates			PLOTY	
Data transformation required			No	
Weight statement			Yes	
Outliers			No	

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	50.72	48.25(***)	<0.0001
Block	5	10.71	10.19	<0.0001
PLOTY	1	29.61	28.17	<0.0001
Error	99	1.05		

The analysis of total volume production can be seen as an analysis summarising survival, height growth and diameter growth in one analysis as all three traits are included in the calculation of volume per hectare.

The analysis is performed on the full dataset, i.e. no outliers. Shangsi (Block 1) that has been excluded in the other growth trait analysis is included in the present analysis as the value – even though close to being an outlier – is less extreme than in the other analysis.

The ranking of the provenances is almost identical to what was seen for volume of mean tree; the Vietnamese sources – Dathien, Da Kha, Lang Hanh and Ho Thien are top-ranked together with the seed lot from Zambia. They are followed by Coto Mines (Philippines), Lancang and Jinghong (China), Benquet (Philippines), Doi Inthanon (Thailand) and Morarano (Madagascar). There are no statistical significant differences among the top-ranking provenances.

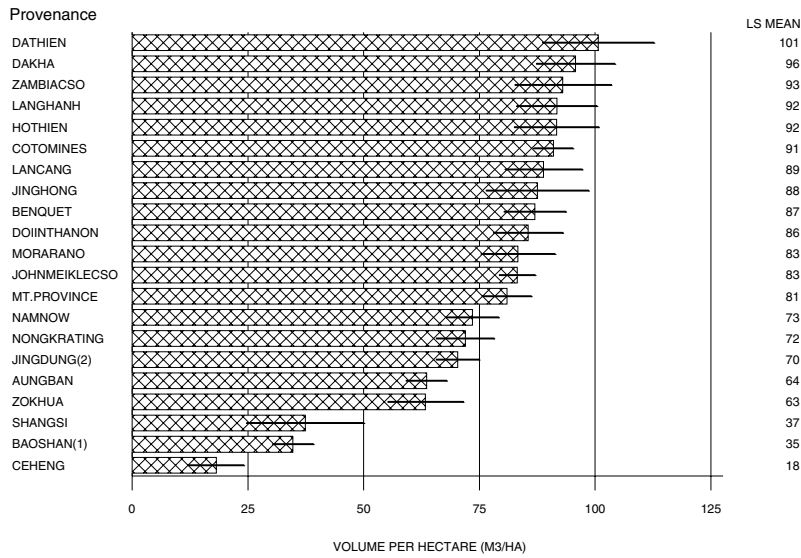
In the bottom end of the ranking, we find – again – the sources of *P. yunnanensis* and the *P. kesiya* sources Aungban and Zok Hua from Myanmar.

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Volume per hectare (m3/ha)

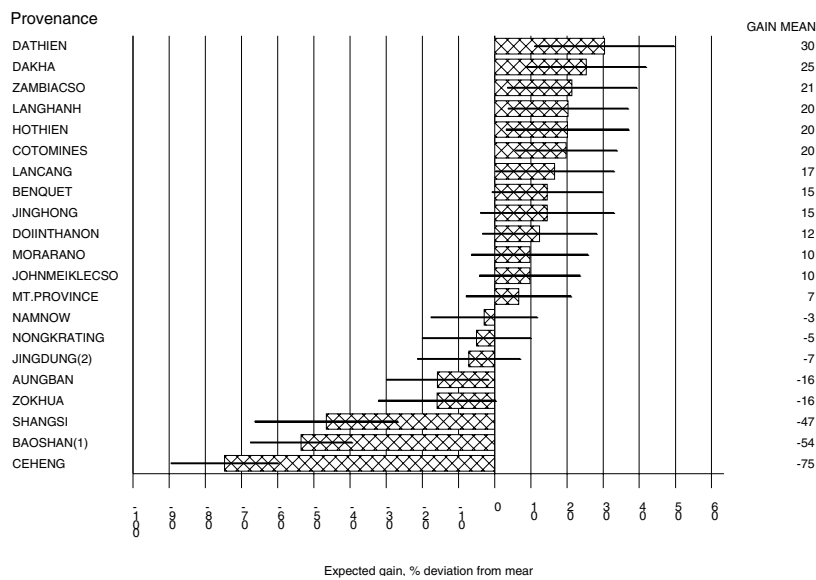


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Volume. Best linear un-biased predictors (BLUPs)



5.6 Stemform

OVERVIEW OF ANALYSIS	
Co-variates	PLOTY
Data transformation required	No
Weight statement	Yes
Outliers	None

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	25.86	24.55 (***)	<0.0001
Block	5	8.01	7.60	<0.0001
PLOTY	1	15.52	14.74	0.0002
Error	99	1.05		

There are highly significant differences between provenances in regard to stemform.

The Zambian seed orchard offspring has the highest stemform score. Lang Hanh and Dathien from Vietnam are next. Then we have John Meikle seed orchard (Zimbabwe) and the Morarano landrace from Madagascar. The seed orchard sources, and especially the Zambia CSO, are ranked high. Improvement of stemform has been a key issue in the selection of plus trees for the orchard, and the results illustrate that this selection has been effective.

The best 'un-improved' sources are the Vietnamese sources Lang Hanh, Dathien and Ho Thien and the Morarano landrace from Madagascar. The latter source probably originates also from Vietnam. The Da Kha source from Vietnam is ranked considerably lower than the other Vietnamese sources.

The Philippine sources are of intermediate stemform together with Nam Now (Thailand), Zok Hua (Myanmar) and Shangsi, Jinghong and Lancang from China.

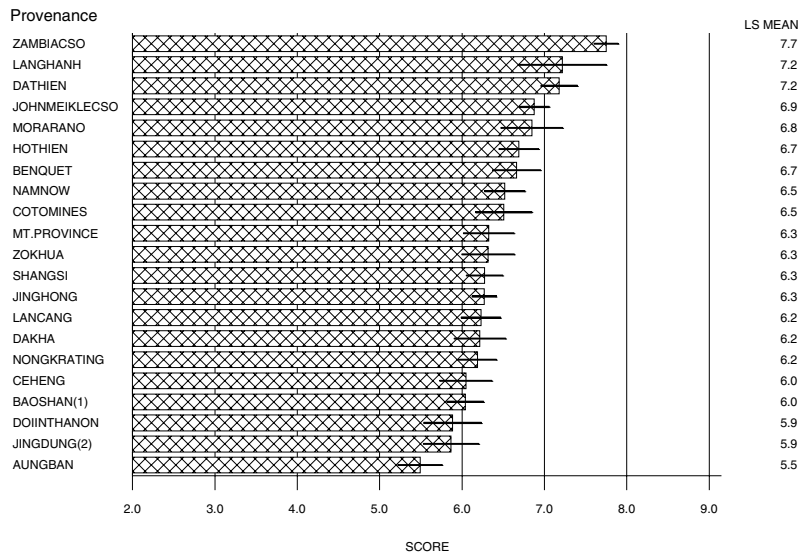
Poorest stemform has Aungban (Burma), Jindung (China) and Doi Inthanon (Thailand).

Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Stemform (1-9 score)

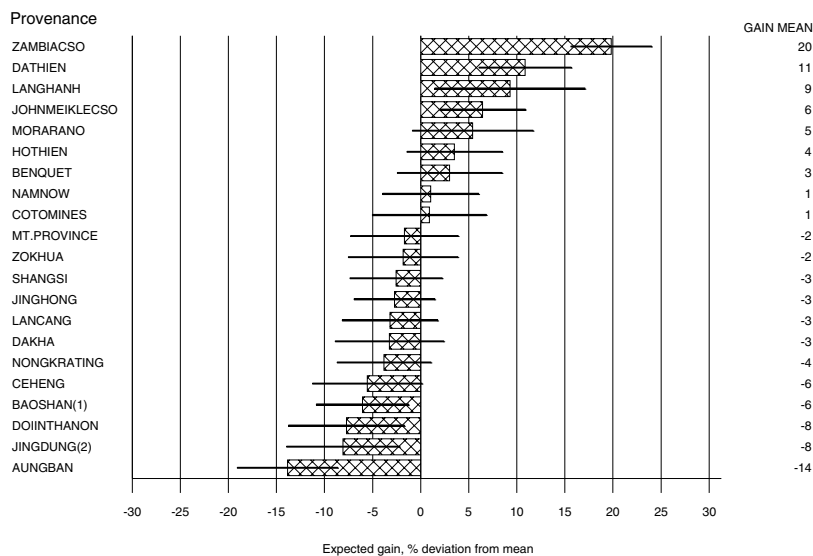


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Stemform. Best linear un-biased predictors (BLUPs)



5.7 Wood density (Pilodyn)

OVERVIEW OF ANALYSIS				
Co-variates	PLOTX, PLOTX2 and PLOTY2			
Data transformation required	No			
Weight statement	Yes			
Outliers	Da Kha (Block 1)			

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	14.46	13.79 (***)	<0.0001
Block	5	22.53	21.48	<0.0001
PLOTX	1	11.02	10.50	0.0017
PLOTX2	1	4.16	3.97	0.0493
PLOTY2	1	12.50	11.92	0.0008
Error	92	1.05		

Diameter adjusted pilodyn readings (ref. Annex 4) are used in the analysis.

The Da Kha source in Block 1 is omitted from the analysis because of the extreme nature of this plot (very high pilodyn reading) compared to other plots. An investigation of assessment data did not reveal anything which could explain the extreme nature of the plot value.

The analysis of variance reveals highly significant differences between provenances.

The Philippine sources, and especially Coto Mines, have the lowest pilodyn readings, corresponding to highest wood densities. The Philippine sources have a relatively slow diameter growth compared to many other sources, and the high wood density may be related to this. Also the Zok Hua source from Myanmar (but not the Aungban source) and John Meikle CSO and Zambia CSO sources have high densities.

The Vietnamese sources have lower wood densities than the top-ranking sources, especially when compared to the Philippine sources Coto Mines and Benquet.

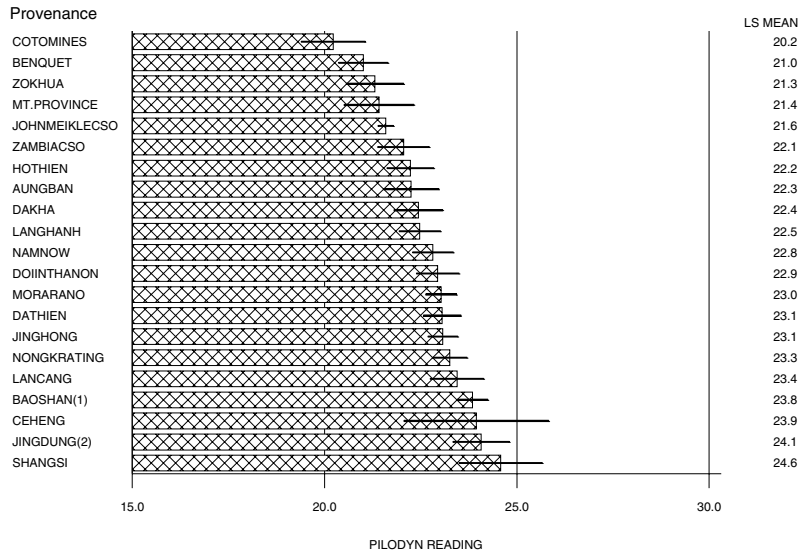
The *P. yunnanensis* sources – Ceheng, Baoshan and Shangsi, have the lowest wood densities. Low densities have also Jingdung and Lancang from China.

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Established December 1992. Assessed August 1998

Pilodyn

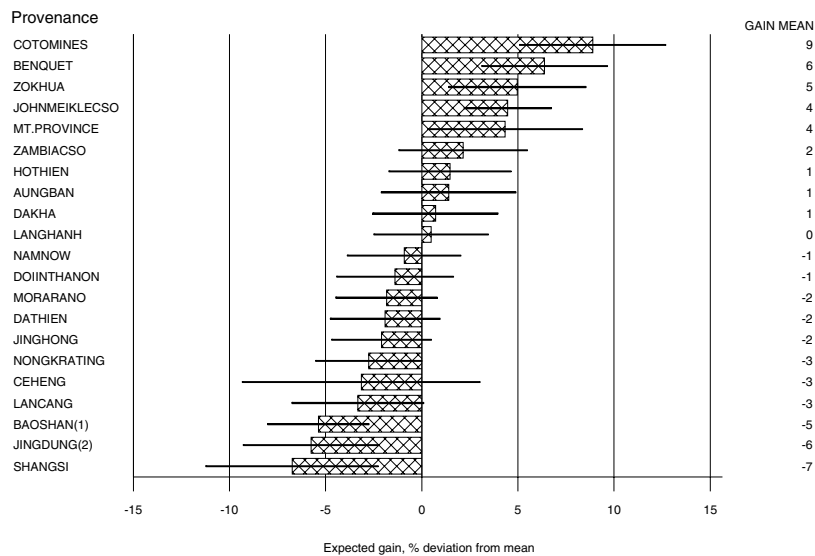


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Pilodyn. Best linear un-biased predictors (BLUPs)



5.8 Foxtailing

OVERVIEW OF ANALYSIS	
Co-variates	None
Data transformation required	No
Weight statement	Yes
Outliers	None

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	9.30	9.67 (***)	<0.0001
Block	5	7.22	7.51	<0.0001
Error	100	0.96		

Analysis of frequency of foxtails gives an indication of the adaptability of the source to site (lower frequency means in general a better adaptation). Moreover, and of great practical importance, foxtails is related to the quality of the tree. Trees with foxtails often have ramicorns, i.e. thick branches from a lower whorl growing (co-evolving) vertically along with the main stem. They are able to develop as there are no whorls on the foxtail to suppress vertical growth of the branches. Trees with coarse branching are thus often a result of foxtails. This means lower quality, especially if timber is the final product. In addition, harvesting operations become more difficult. Apart from leading to coarse branching, foxtails will often result in stem breaks as the wood of the foxtail is of low density.

There are significant differences among seedlots in regard to foxtail percentage.

The Vietnamese sources (Hothien, Dathien, Da Kha and Lang Hanh) have the highest frequencies of foxtails. The Philippine sources (Benquet, Mt. Province and Coto Mines) also have high levels of foxtails, as has the Morarano landrace from Madagascar.

The lowest levels of foxtails are found among the Burmese sources (Aungban and Zok Hua), the *P. yunnanensis* sources (Ceheng, Shangsi and Baoshan), and the Thai sources (Nam Now, Nong Krating and Doi Inthanon). Chinese sources (Jinghong, Jingdung and Lancang) are intermediate, as are the seedlots from John Meikle and Zambia CSOs.

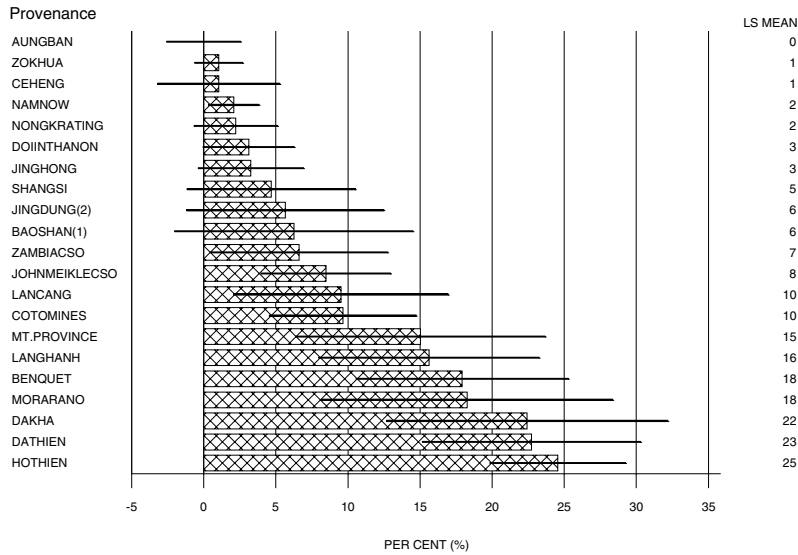
It is important to note the large size of the confidence intervals of many of the seed lots, indicating that there are only significant differences between top and low ranked provenances, whereas many of the differences within these groups are not statistically significant.

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Foxtail percentage (%)

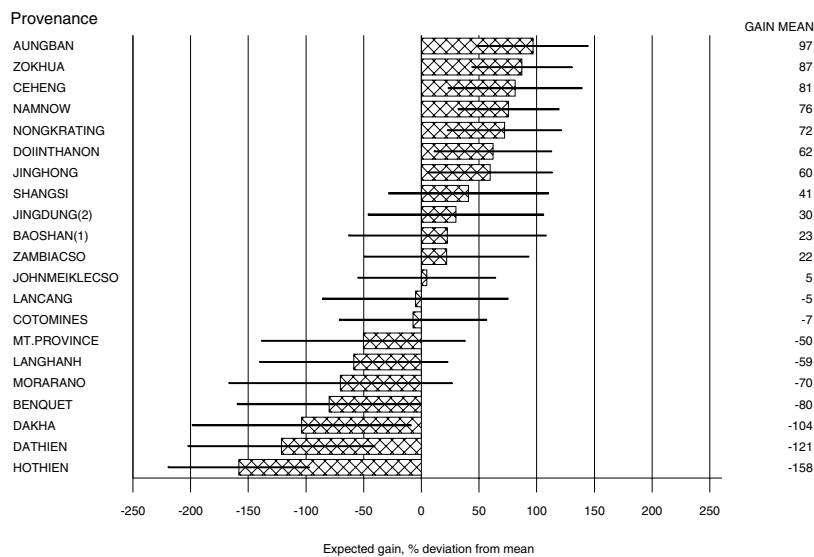


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Foxtailing. Best linear un-biased predictors (BLUPs)



5.9 Cone setting

OVERVIEW OF ANALYSIS	
Co-variates	None
Data transformation required	No
Weight statement	Yes
Outliers	None

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	22.88	22.81 (***)	<0.0001
Block	5	5.98	5.96	<0.0001
Error	100	1.00		

Data on flowering and fruiting provides an indication of the adaptation of the sources to site. Abundant flowering and fruiting is generally interpreted as a sign of good adaptation to the site, and vice versa.

As the trial is still young, only about 6 years of age at the time of assessment, flowering and fruiting may only have just commenced and the tested seedlots do not express their full potential for flowering and fruiting. Consequently, the analysis should be interpreted with care.

The analysed trait is average score of old, open cones. Assessments have been done using a 1-9 scale where score 1 refers to no flowers or cones. More details in DFSC (1998).

The analysis of variance shows highly significant differences among provenances in regard to cone setting.

The most abundant cone setter is the *P. yunnanensis* source of Shangsi, closely followed by the *P. kesija* sources Zok Hua and Aungban from Myanmar. Also the Chinese sources Jindung, Lancang and Jinghong set more cones than the other sources.

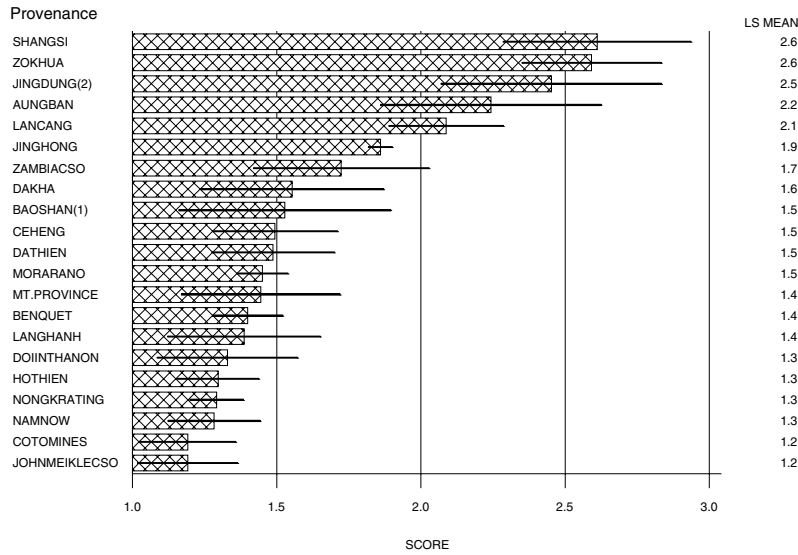
The John Meikle CSO and Coto Mines (Philippines) sources have the lowest cone setting among the tested. Low cone setting is also expressed by the Thai sources (Nam Now, Nong Krating and Doi Inthanon), the Vietnamese sources Ho Thien and Lang Hanh and the two other tested sources from the Philippines (Benquet and Mt. Province).

Pinus kesiya provenance trial, Cashel, Zimbabwe

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Established December 1992. Assessed August 1998

Old, open cones (1-9 score)

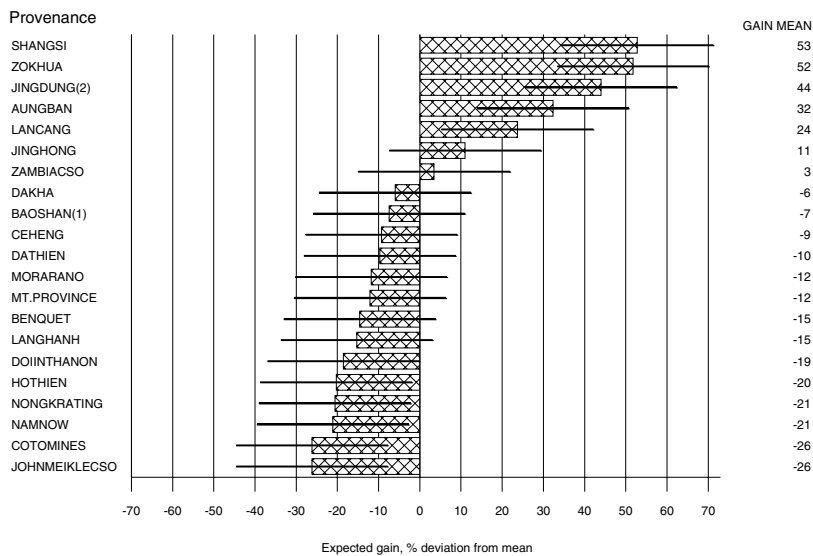


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Old, open cones. Best linear un-biased predictors (BLUPs)



5.10 Aphid attack

OVERVIEW OF ANALYSIS				
Co-variates			PLOTY	
Data transformation required			Yes. Arc sin transformation	
Weight statement			Yes	
Outliers			Aungban, John Meikle, Shangsi and Zokhua in Block 1	

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	3.82	3.69 (***)	<0.0001
Block	5	18.63	18.00	<0.0001
PLOTY	1	4.89	4.72	0.0323
Error	99	1.03		

Attack of the pine woolly aphid, *Pineus pini* (L), has been assessed on all trees. The analyzed trait is the proportion of affected trees to total number of trees in plot.

An arc-sin transformation of data was required to obtain a normal distribution of residuals. Four 'outliers' were identified, all in Block 1. An examination of data did not give any explanation or reveal any errors in data recording or calculations. It was, however, decided to omit them from the analysis because of the extreme nature of the plots.

The analysis of variance reveals statistical significant differences between the tested sources.

The two seed lots originating from seed orchards (John Meikle CSO, Zimbabwe and Zambia CSO) have the lowest frequencies of aphid attack. Resistance to aphid attack has probably been one of the traits considered when selecting for the orchards,

and the analysis results suggest that this selection has been efficient.

In the opposite end of the ranking, we find Zok Hua (Myanmar) having the highest frequency of aphid attack. Also the Philippine sources, especially Coto Mines and Mt. Province show high levels of aphid attack.

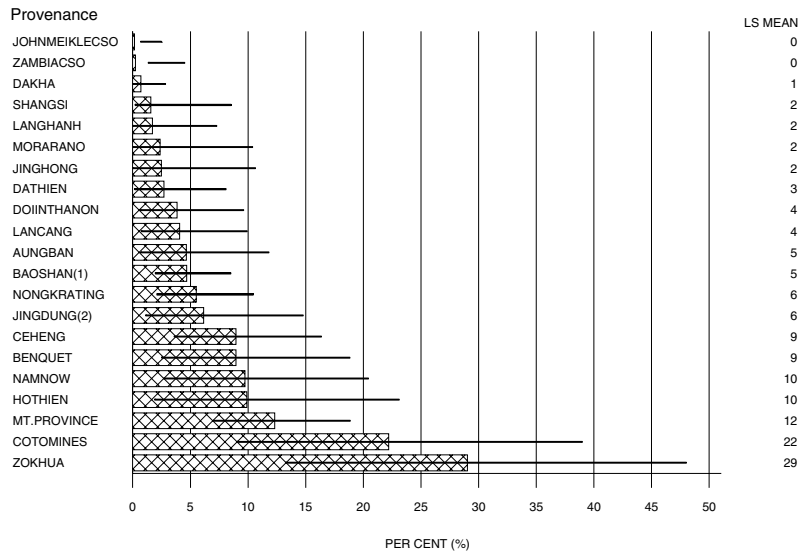
There are no clear patterns of provenance variation, as we have seen for some of the other analyzed traits. As an example, the Vietnamese provenances are spread throughout the ranking, not grouped together as we have seen elsewhere. It is also important to stress that the confidence intervals are extremely large. This is maybe indicating that assessment of woolly aphid has not been consistent. Results should therefore be interpreted with care.

Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Aphid attack (%)

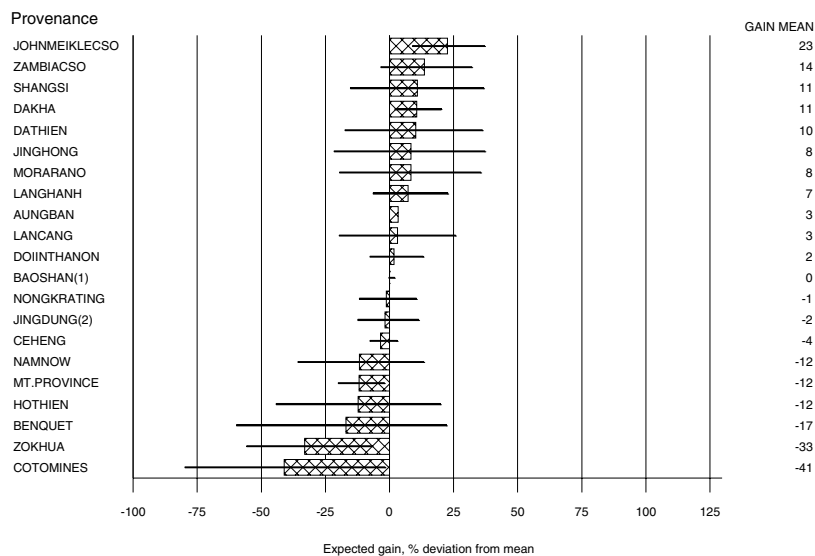


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Aphid attack. Best linear un-biased predictors (BLUPs)



5.11 Frequency of ‘leaning trees’

OVERVIEW OF ANALYSIS				
Co-variates			PLOTX	
Data transformation required			No	
Weight statement			Yes	
Outliers			No	

RESULTS FROM ANALYSIS OF VARIANCE				
Effect	DF	MS	F-value	P-value
Provenance	20	3.39	3.28 (***)	<0.0001
Block	5	4.41	4.27	<0.0015
PLOTX	1	7.37	7.13	0.0089
Error	99	1.03		

A prominent feature of the Cashel trial is a large number of trees with a very peculiar growth habit. They bend to the ground with the crown almost touching the ground. Other trees have collapsed completely and are fallen over. This growth habit has not been observed in any of the other trials and the reason behind it is not known. One explanation could be that the trees are growing in over-luxuriant conditions (former agricultural land) and that this may have caused the strange growth habit of many trees. It has been experienced elsewhere that too favourable site conditions can lead to tree collapse (flop) (Armitage and Burley 1980).

As part of the field assessment, all ‘leaning’ trees were recorded, and the proportion of leaning trees to total number of trees in plot has been analyzed to check for differences among provenances.

The analysis of variance reveals significant differences among provenances.

Ceheng (*P. yunnanensis*) has the lowest percentage of leaning trees, followed by Jinghong (China), Baoshan (*P. yunnanensis*) and Zok Hua (Myanmar). Doi Inthanon (Thailand), John Meikle CSO (Zimbabwe) and Da Kha (Vietnam) have the highest percentages.

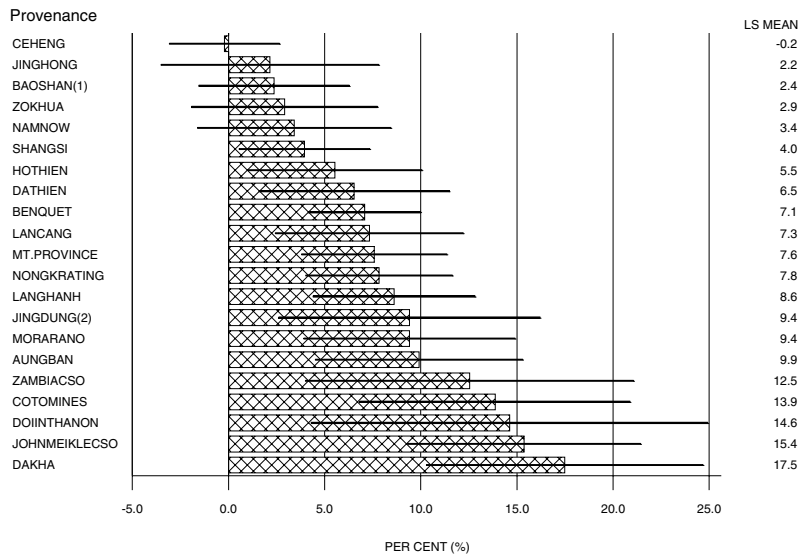
There is a tendency of slow growing sources having fewer problems with ‘leaning’ trees, e.g. the *P. yunnanensis* sources, and fast growing sources having higher frequencies. The picture, however, is not clear, and there are many exceptions. The confidence intervals are also quite wide, and there are not statistically significant differences between many of the provenances, only between the very top and low-ranked sources.

Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Percentage of leaning trees (%)

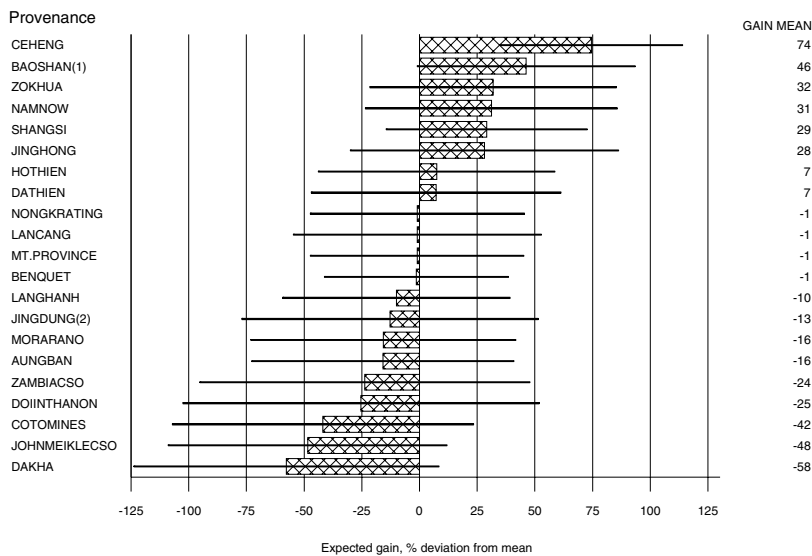


Pinus kesiya provenance trial, Cashel, Zimbabwe

International Series of Pinus kesiya provenance trials, Trial No. 3

Established December 1992. Assessed August 1998

Leaning trees (%). Best linear un-biased predictors (BLUPs)



6. Discussion and conclusions

6.1 Growth

Growth traits should be given key importance in the interpretation of trial results, as wood for pulp has high priority.

The analysis of growth traits (height, diameter, volume of mean tree, total volume per hectare) all indicate that the Vietnamese sources are performing well, especially the Dathien source. The results thus indicate that the Vietnamese sources represent an interesting genetic resource, and that introductions and further exploration of the provenance variation of material from within that region could be an interesting route to follow in the future.

Also the Zambia CSO source has a high volume production at the same level as the Vietnamese sources, and is a good choice of seed source for immediate supply.

Philippine sources (esp. Coto Mines) are also performing relatively well in regard to growth. They have a fast height growth (Coto Mines is the top-ranking provenance in height growth), but a slower diameter growth, making the volume production lower than would be expected based on the height alone.

The Zimbabwean seedlot from John Meikle CSO is not among the top-ranking sources, which is somewhat surprising. As earlier mentioned, the seedlot originates from only one clone in the orchard, and this might explain the somewhat disappointing performance. A 'normal' seedlot, sampling all clones in the orchard, would probably perform better.

The analysis indicates very clearly that *P. yunnanensis* has no potential on sites similar to the trial site. It is performing very poorly both in height and diameter. The same with the Myanmar sources Aungban and Zokhua.

The growth analysis results are in accordance with the results of Mullin *et al.* (1984). They reported, based on results from trial 31 at John Meikle Experimental Station, the Vietnamese source from Dalat and the Philippine source from Benquet to perform considerably better in height growth than Burmese and Assam sources. The Dalat source is close to the seed collection sites of the Hothien, Dathien and Lang Hanh sources in the present series.

Production potential, based on the best performing sources and based on growth in the first 6 years, is 15-17 m³/ha/year.

6.2 Adaptation

Adaptive traits include survival percentage, foxtail frequency, flowering and health (aphid attack and 'leaning' trees).

The survival percentage is high for all prov-

enances, and there are no statistically significant differences among the top-ranking provenances.

Vietnamese and Philippine sources, esp. the Vietnamese sources, have more foxtails than Thai, Myanmar and *P. yunnanensis* sources. Foxtails may also influence the quality of the wood as discussed in section 5.8. The Zambian and Zimbabwean sources are intermediate in regard to foxtails.

The results on cone-setting should not be given too much importance because of the early stage of assessment. The results at this early development stage indicate that the Myanmar and *P. yunnanensis* sources have higher cone-setting than the other sources, and that the Vietnamese, Philippine and Thai sources set fewer cones.

In regard to woolly aphid, John Meikle CSO and Zambia CSO express the lowest levels of infestation. Apart from that, the picture is rather confusing with no clear pattern of geographical variation.

The analysis of 'leaning trees' should be interpreted with care. First of all, the reason for the strange growth habit expressed by many trees in the trial is not known, and it has not been experienced in any other trial in the series. There are significant differences among the tested sources, but no clear pattern of provenance variation. Results may indicate that sources with faster growth have more problems than slower growing sources, but the picture is not evident, and there are exceptions.

6.3 Quality

Analyzed quality parameters are stemform, and wood density (pilodyn). Because of pruning, branching habit (branch diameter) could unfortunately not be assessed and analyzed.

The seedlots from the clonal seed orchards in Zambia and Zimbabwe have the best stemform, suggesting that selection has been effective. The Vietnamese sources also have good stemform, as have the landrace from Madagascar. The Philippine sources have a slightly poorer form, but are still above average.

In regard to wood density, the Philippine sources, esp. Coto Mines, are outstanding. They compare favorable to the seed orchard offspring from Zambia and Zimbabwe. The Vietnamese sources have lower basic density than the Philippine and seed orchard material, and this – together with the relatively high levels of foxtails – may be a constraint for a wider use of these sources.

There is good accordance between the results (straightness and wood density) in the present trial and the results of Mullin *et al.* (1984). They also found the Vietnamese source to have better

straightness than other sources, and with a lower basic density than the Philippine source. They further found a significant negative correlation between basic density and altitude of provenance collection site. The results of the present trial confirm this negative correlation for the Philippine sources (only three sources, though), whereas no such correlation is present in the material as such.

6.4 Conclusion

The trial is only 6 years of age, and it may thus be premature to draw very specific and detailed conclusions based on the present assessment. It is thus recommended that the trial is maintained, and re-assessed later on.

Based on the results of the present assessment, the Vietnamese sources show promise. They are fast-growing and they have a – for *P. kesiyana* – good stemform. They are less favorable in regard to wood density, especially compared to the Philippine sources, and they set many fox-tails. It is con-

cluded, however, that Vietnamese material could be an important genetic resource with a potential in Zimbabwe. The feasibility and possibilities to include this material in seed production and further breeding activities of the species should be further investigated.

In regard to practical recommendations on seed sources for immediate use in plantation establishment, John Meikle CSO would be an obvious choice. The trial results do unfortunately not provide reliable information on the performance of this source, as the seedlot only represent one clone in the orchard. Other seed sources may be available within Zimbabwe, e.g. the BSOs established with material from Zambia and Madagascar in the early 90's, which may soon come into production.

If imports are to be considered, the results from the present trials indicate that material from the CSO in Zambia would be a good choice. It is a good volume producer, and it has an excellent stemform.

7. References

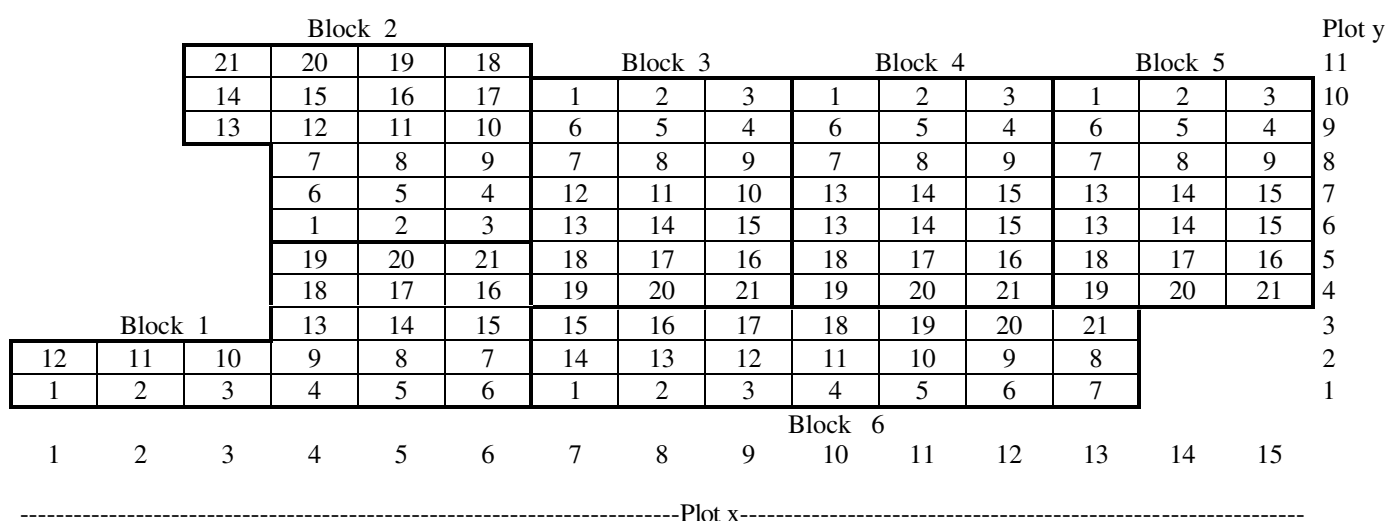
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Annexes

Annex 1. Trial design map



Layout of trial at Cashel. Plot positions are defined by two coordinates (PLOTX, PLOTY).

Randomization

Plot no.	Block 1	Block 2	Block 3	Block 4	Block 5	Block 6
1	01680/86	01632/86	01523/85	01517/85	01773/88	01777/88
2	01517/85	01572/85	01447/84	01772/88	01517/85	01572/85
3	01515/85	01680/86	01777/88	01680/86	01572/85	01517/85
4	01638/86	01773/88	01773/88	01636/86	01515/85	01778/88
5	01773/88	01448/84	01680/86	01572/85	01637/86	01525/85
6	01523/85	01523/85	01448/84	01521/85	01777/88	01773/88
7	01777/88	01624/86	01638/86	01637/86	01448/84	01633/86
8	01624/86	01633/86	01624/86	01523/85	01624/86	01786/88
9	01772/88	01778/88	01519/85	01519/85	01638/86	01680/86
10	01633/86	01521/85	01786/88	01773/88	01633/86	01519/85
11	01572/85	01636/86	01778/88	01624/86	01632/86	01632/86
12	01637/86	01772/88	01772/88	01448/84	01636/86	01638/86
13	01519/85	01637/86	01525/85	01786/88	01778/88	01772/88
14	01632/86	01519/85	01633/86	01515/85	01786/88	01447/84
15	01786/88	01515/85	01517/85	01525/85	01525/85	01636/86
16	01525/85	01447/84	01515/85	01777/88	01519/85	01515/85
17	01448/84	01638/86	01521/85	01633/86	01680/86	01521/85
18	01778/88	01777/88	01636/86	01638/86	01523/85	01523/85
19	01636/86	01517/85	01572/85	01632/86	01447/84	01637/86
20	01521/85	01525/85	01632/86	01447/84	01521/85	01624/86
21	01447/84	01786/88	01637/86	01778/88	01772/88	01448/84

Acc. no. (DFSC)	Provenance	Country	Latitude	Longitude	Altitude m.a.s.l.	Rainfall mm/year	Temp. °C	No. Coll.
01447/84	Mt. Province	Philippines	17 15 N	120 30 E	2300	.	.	83
01448/84	Benquet	Philippines	16 35 N	120 30 E	1600	.	.	64
01515/8500	Dathien	Vietnam	11 58 N	108 27 E	1550	1769	17.9	45
01517/8500	Ho Thien	Vietnam	11 51 N	108 32 E	1500	1769	17.9	11
01519/8500	Lang Hanh	Vietnam	11 37 N	108 16 E	950	2059	21.5	22
01521/8500	Nong Krating	Thailand	18 05 N	98 35 E	1080	1332	22.2	17
01523/8500	Doi Inthanon	Thailand	18 32 N	98 35 E	1000	2084	20	30
01525/8500	Nam Now	Thailand	16 40 N	101 33 E	800	1316	.	35
01624/86	Baoshan (1)	China	24 51 N	99 12 E	1750	.	.	26
01632/86	Ceheng	China	24 24 N	105 34 E	800	.	.	25
01633/86	Shangsi	China	21 37 N	107 57 E	530	.	.	25
0163686	Jingdung (2)	China	24 28 N	100 51 E	1350	.	.	34
01637/86	Jinghong	China	22 25 N	101 10 E	1250	.	.	24
01638/86	Lancang	China	22 40 N	104 03 E	1620	2059	21.5	22
01772/8800	Zokhua	Burma	22 25 N	93 40 E	1600	2335	15.0	20
01773/8800	Aungban	Burma	20 41 N	96 37 E	1350	1303	20.5	61
01776/88	John Meikle CSO	Zimbabwe	18 43 S	32 51 E	1268	1725	17.9	1
01778/8800	Clonal Seed Orchard	Zambia	13 00 S	28 00 E	1300	.	.	10
01786//8800	Moraraho	Madagascar	18 40	47 02 E	900	.	.	32
01572/8500	Coto Mines	Philippines	15 32 N	120 05 E	800	1000	25.1	9
01680/86	Dakha	Vietnam	14 48 N	107 56 E	1200	2684	21.6	40

Trees are assessed starting in lower left corner of plot, going up and down the rows, ending in upper right corner.

Annex 2. Trial description

Cashel, Zimbabwe

TRIAL ESTABLISHMENT AND MANAGEMENT

Year and month of establishment: *December 1992*

Area (ha): *1.0 ha*

Initial spacing (m x m): *2.7 m x 2.7 m*

Soil preparation (time, method/intensity):

Planting method(age of seedlings, type):

Beating up (time, %):

Irrigation (time, amount): *None*

Fertilization (time, type, amount):

Weeding (time, intensity):

Thinning (time, intensity): *None, but pruned in 1998*

Firelines:

TRIAL DESIGN

Statistical design: *Randomized complete block design*

No. of replications (blocks): *6 replications*

No. of treatments (provenances): *21 provenances (see list in Annex 1)*

Plot size (No. of trees in plot): *16 (4 x 4)*

Demarcation (blocks, plots): *Labels, poles in plot corners. Good demarcation*

PROTECTION STATUS

Status (describe any disturbances/damages):

Guarding (permanent, regular, none):

Annex 3. Trial site description

Site description – Cashel, Zimbabwe

LOCATION

Province:
District:
Latitude (degrees and minutes):
Longitude (degrees and minutes):
Altitude (m above sea level): *1450 m above sea level*

Managing office/institution: *Forest Research Centre, Forestry Commission*
Owner: *Forest Research Centre, Forestry Commission*
User(s): *Forest Research Centre, Forestry Commission*

Distance to nearest office responsible for management of the trial (km):
Distance to nearest villages/towns (km):
Number of inhabitants in the nearest villages/towns:

Type of area (e.g. research station, managed forest, etc.): *Research Station*

CLIMATE

Nearest weather station:
Name of the station: *Cashel*
Latitude (degrees and minutes): *19°33'N*
Longitude (degrees and minutes): *32°47'E*
Altitude (m a.s.l.): *1190*

Climatic data ¹	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.	Year
Rainfall (mm)	193.7	165.0	108.7	39.2	17.7	10.4	7.0	12.4	10.8	36.3	94.5	195.0	890.7
Temp. mean (°C)
Temp. mean max. ² (°C)
Temp. mean min. ³ (°C)
Evapotranspiration ⁴ (mm)

¹ Period of observations Unknown ² Average of daily maximum temperatures
³ Average of daily minimum temperatures ⁴ Potential evapotranspiration (ETP) - Penman's formula

Rainy season:

Number/type of seasons: one two even/irregular

Period(s): *Nov. – April* (specify months)

Length of rainy season:

No. of intermediate days: *60* (pre- and posthumid period of the growing season)
No. of wet days: *180* (growing season)

Number of dry months per year (< 50 mm rain/month): *4 months*

Frost (number of days/year):

Prevailing winds (direction, period, speed): *NE (W)*

TOPOGRAPHY (slope) of trial site

Flat/gentle (0-8%) Intermediate (9-30%) Steep (>30%)

GENERAL SOIL DESCRIPTION

Soil texture		Soil depth		Soil drainage/ n		Gravel content, topsoil	
1. Light/sandy		1. Shallow (< 50 cm)		1. Well drained	X	1. None (< 15 %)	
2. Medium/loamy	X	2. Deep (50-100 cm)		2. Seasonal		2. Gravelly (15-35 %)	
3. Heavy/clayey		3. Very deep (> 100 cm)	X	3. Permanent		3. Stony (> 35 %)	

Organic matter content		Reaction (pH)		Soil salinity		Groundwater	
1. Poor (< 2 % DM)	X	1. Acid (pH < 6.5)	X	1. None	X	1. Shallow (< 50 cm)	
2. Medium (2-5 % DM)		2. Neutral (6.5-7.5)		2. Moderate		2. Deep (50 - 150 cm)	
3. Rich (> 5 %)		3. Alkaline (pH> 7.5)		3. High		3. Very deep (>150 cm)	X

Specify soil unit, soil association and phases (subdivisions of soil units) according to the Soil map of the world (FAO-Unesco 1971-1979), if known:

VEGETATION

Natural (original) vegetation type:.

Dominant natural (original) genera/species:

Land use history: *Agricultural land (peas)* → *Abandoned for six years* → *Widdringtonia bodflora* → *trial site*

RESULTS OF SOIL SAMPLE

Sample 1: Block 2

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	52.5
Fine silt (2-20 µm)	%	16.6
Coarse silt (20-63 µm)	%	5.9
Fine sand (63-125 µm)	%	4.9
Fine medium sand (125-250 µm)	%	6.1
Coarse medium sand (250-500 µm)	%	5.7
Coarse sand (500-2000 µm)	%	8.5
Org. Mat.	%	1.2
Lime	%	0.0
pH-H ₂ O	-	4.91
P		- 1

Results noted as - 1: Amount not detectable

Sample 2: Block 6

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	24.1
Fine silt (2-20 µm)	%	22.1
Coarse silt (20-63 µm)	%	16.3
Fine sand (63-125 µm)	%	23.7
Fine medium sand (125-250 µm)	%	10.1
Coarse medium sand (250-500 µm)	%	2.4
Coarse sand (500-2000 µm)	%	1.2
Org. Mat.	%	0.6
Lime	%	0.0
pH-H ₂ O	-	5.34
P		- 1

Results noted as - 1: Amount not detectable

Annex 4. Plot data set

Aggregated data set at plot level. This annex describes the variables in the plot dataset, and displays the data. The plot dataset has been prepared from the individual tree dataset and holds the following parameters.

PARAMETER NAME	EXPLANATION
BLOCK	Block No.
SEEDLOT	Seedlot No.
SITE	Name of site
DATEEST	Establishment data of trial (MM/YY)
DATEASS	Date of assessment (MM/YY)
PLOTX	Co-variate
PLOTY	Co-variate
PLOTX2	Co-variate
PLOTY2	Co-variate
PLOTXY	Co-variate
PLOTYX	Co-variate
DBH1	Average of diameters (arithmetic mean)
HEIGHT	Average height (arithmetic mean)
SURV	Survival percentage (%)
GMEAN	Mean basal area per tree (m ²)
GSUM	Total basal area in plot (m ²)
MEANPILO	Mean pilodyn for plot
WHORLS	Average number of whorls
BRANCH	Average number of branches in whorl
DIABRA	Diameter of largest branch (cm)
FORK	Frequency of trees with one or more forks (%)
FOXTAIL	Frequency of foxtails in plot (%)
NO_TOTAL	Number of trees in plot
NO_G	Number of trees in basal area calculation
NOHEIGHT	Number of trees in height-diameter regression
KRAFT1.. KRAFT5	Frequency of individual Kraft scores 1 to 5 (%)
KRAFT	Average Kraft index
STEM	Average stemform
STEM1..STEM9	Frequency of individual stemform scores 1 to 9 (%)
BRARATIO	Branch ratio (not calculated in this trial)
FO_INDEX	Forking index (not calculated in this trial)
INTNODE	Average distance between whorls (m)
CROWNPCT	Crown percentage (not calculated in this trial)
FO_POS	Average position of lower fork (m above ground)
TOP	Percentage of trees with broken top
VTREE	Average volume of tree in plot
MF	Average score of male flowers
FF	Average score of female flowers
CL	Average score of conelets
CC	Average score of closed cones
OC	Average score of old, open cones
LOTH	Percentage of 'leaning trees'
APHID	Percentage of trees with woolly aphid
DG	Diameter corresponding to mean basal area at breast height (cm)
HG	Height for tree with diameter corresponding to mean basal area (m)
PILOCORR	Mean pilodyn reading adjusted for diameter effect
VHA	Volume per ha

DG- Diameter corresponding to mean basal area at breast height (1.3 m)

DG is calculated using the following formula:

$$DG = \sqrt{\frac{\sum_{i=1}^n \pi \times (D_i/2)^2}{n}} \times 2$$

where
 D_i is the diameter at breast height of tree No. i (in cm);
 n is the total number of trees in plot.

GHA - Basal area per hectare

Basal area in m^2 per hectare is calculated using the formula:

$$GHA = \frac{\sum_{i=1}^n \pi \times (D_i/2 \times 100)^2}{n \times sp^2} \times 10000$$

where
 D_i is the diameter at breast height of tree no. i (in cm);
 n is the total number of trees in plot; and
 sp is the spacing in m;

HG- Height of tree with diameter corresponding to mean basal area

A linear regression per plot is prepared using the model:

$$Height = \beta + \alpha \times \ln(DBH1)$$

where
 $DBH1$ is the diameter of stem (first stem if more than one stem) in cm;
 α is the slope of the regression line;
 β is the intercept with y-axis;

For each plot, α and β are estimated using PROC REG (SAS 1990).

HG for the plot is then calculated using the linear regression estimates (α and β) and plot DG (as previously calculated).

PILOCORRR - Correction of pilodyn readings

Tree diameter (ring width) influences the pilodyn reading, i.e. trees with larger diameter (rings) will normally have larger pilodyn readings (deeper penetration of the pilodyn pin) than trees with smaller diameter, all other factors equal (ceteris paribus).

In order to adjust pilodyn readings for the variation in diameter, a correction factor has been introduced. By doing so, we are reducing the variance due to differences in individual tree size, and the provenances are in the subsequent analysis compared assuming that they have the same average tree size. In other words, we compare the level of the trait rather than the actual value.

The adjustment has been made using the GLM procedure in SAS (SAS 1990). The following model is applied:

```
...
PROC GLM;
CLASS plot;
MODEL pilo = plot DBH1;
LSMEANS plot OUT=A;
...
```

Forking index (not used in the analysis of the present trial)

The forking index is calculated using the formula:

$$FO_INDEX = \frac{\sum_{i=1}^n FORK_i / FO_POS_i}{n}$$

where
 $FORK_i$ is the number of forks observed on tree i
 FO_POS_i is position above ground of first fork (in m) on tree i ; and
 n is the total number of trees with forking data in the plot

Branching index (not used in the analysis of the present trial)

The branching index is calculated using the formula:

$$BR_INDEX = \frac{\sum_{i=1}^n BRANCH_i \times DIABRA_i}{n \times 10}$$

where
 $BRANCH_i$ is the number of branches on tree i ;
 $DIABRA_i$ is the branch diameter on tree i ; and
 n is the total number of trees with branching data in the plot.

INTNODE - Average distance between whorls

The INTNODE parameter is calculated using the formula:

$$INTNODE = \frac{\sum_{i=1}^n (HEIGHT_i^{-0.5}) / WHORLS_i}{n}$$

where

HEIGHT_i is the height of tree i
WHORLS_i is the number of whorls on tree i; and
n is the total number of trees with observations on whorls in the plot.

Plot Data Set - Cashel

Plot ID	Address	Suburb	State	Postcode	Lot Area	Frontage	Depth	Area	Volume	Value	Rate	Notes	
1	1292 898	COTOMINES	NSW	2256	99	77	16	12.35	8.14298	0.0013883	0.21924	13.03333	
2	1292 898	BAGSHAN(1)	NSW	2256	77	99	16	4.58225	3.81925	0.00083	0.13163	24.33333	
3	1292 898	CEHENG	NSW	2256	120	120	16	7.266667	3.19375	0.00907	0.091047	24.166667	
4	1292 898	SHANGSI	NSW	2256	120	120	16	9.13125	3.873333	0.00732	0.12371	25.5	
5	1292 898	JINGDANG(2)	NSW	2256	108	84	16	13.0375	6.425	0.014044	0.24706	23.25	
6	1292 898	JINGHONG	NSW	2256	80	80	16	13.186667	7.064286	0.014044	0.24706	23.25	
7	1292 898	JINGHONG	NSW	2256	80	80	16	15.1625	8.169231	0.018404	0.29464	33.2	
8	1292 898	DAKHA	NSW	2256	110	66	16	12.86675	8.4	0.018404	0.29464	33.2	
9	1292 898	ZOKHUA	NSW	2256	110	66	16	10.993333	6.025	0.013533	0.21653	22.3	
10	1292 898	AUNGBAN	NSW	2256	84	108	16	13.093333	6.2077	0.013533	0.21653	22.3	
11	1292 898	JONGHANG	NSW	2256	84	108	16	15.717429	8.941667	0.015049	0.225731	22.1	
12	1292 898	JOHNMEKLECSO	NSW	2256	60	132	16	13.153333	7.4375	0.016963	0.275278	22.428571	
13	1292 898	ZAMBIACSO	NSW	2256	60	100	16	14.76875	8.35714	0.016963	0.275278	22.428571	
14	1292 898	MORARANO	NSW	2256	52	156	16	13.5125	7.966667	0.0151	0.241995	21.3	
15	1292 898	MT-PROVINCE	NSW	2256	104	104	16	12.7875	7.97623	0.013027	0.208428	20.40625	
16	1292 898	BENQUET	NSW	2256	135	105	16	12.7825	8.430769	0.015726	0.251919	21.73333	
17	1292 898	DATHEN	NSW	2256	140	84	16	12.7825	7.62571	0.015726	0.251919	21.73333	
18	1292 898	LANGKAT	NSW	2256	135	105	16	13.266667	7.72727	0.015042	0.22263	20.262071	
19	1292 898	LANGKAT	NSW	2256	135	105	16	14.324125	8.333333	0.015042	0.22263	20.262071	
20	1292 898	DOINTHANON	NSW	2256	65	143	16	13.414125	7.37778	0.015042	0.22263	20.262071	
21	1292 898	NAIHOW	NSW	2256	90	150	16	13.84375	6.653333	0.015181	0.242888	21.96875	
22	1292 898	COTOMINES	NSW	2256	150	90	16	12.58125	7.92957	0.012735	0.203755	18.8	
23	1292 898	BAOSHAN(1)	NSW	2256	112	112	16	8.04666667	3.41225	0.006889	0.09883	11.2	
24	1292 898	CEHENG	NSW	2256	98	126	16	6.75833333	2.62667	0.005209	0.062904	3.8	
25	1292 898	SHANGSI	NSW	2256	105	135	16	7.80714286	3.10625	0.005209	0.062904	3.8	
26	1292 898	JINGDANG(2)	NSW	2256	91	117	16	13.45	6.845455	0.00574	0.09059	24.5	
27	1292 898	JINGHONG	NSW	2256	126	98	16	14.65333333	8.02	0.01482	0.20873	21.966667	
28	1292 898	LANCANG	NSW	2256	120	120	16	14.18125	6.8	0.017006	0.255093	21.966667	
29	1292 898	LANCANG	NSW	2256	70	154	16	13.93125	4.853333	0.016651	0.26422	23.05714	
30	1292 898	DAKHA	NSW	2256	60	180	16	13.3142857	6.20743	0.015623	0.249688	22.357143	
31	1292 898	ZOKHUA	NSW	2256	130	78	16	11.95	5.69009	0.01587	0.23532	20.846154	
32	1292 898	AUNGBAN	NSW	2256	117	91	16	12.85625	7.6	0.012261	0.171654	20.307692	
33	1292 898	JOHNMEKLECSO	NSW	2256	84	130	16	14.70625	8.281618	0.013381	0.214089	20.653846	
34	1292 898	ZAMBIACSO	NSW	2256	140	100	16	14.3142857	8.1	0.01796	0.275134	21.625	
35	1292 898	MT-PROVINCE	NSW	2256	140	100	16	12.9625	8.394515	0.01631	0.23838	22.785714	
36	1292 898	BENQUET	NSW	2256	39	9	16	15.2875	8.05	0.013414	0.21463	21.3	
37	1292 898	DATHEN	NSW	2256	24	24	16	14.726667	7.97623	0.014715	0.235438	20.321429	
38	1292 898	LANGKAT	NSW	2256	27	10	16	15.02625	8.05	0.01712	0.25802	22.32723	
39	1292 898	LANGKAT	NSW	2256	27	10	16	13.7375	6.08	0.018573	0.27162	22.875	
40	1292 898	NONKGRATING	NSW	2256	25	21	16	13.7375	6.08	0.018573	0.27162	22.875	
41	1292 898	DOINTHANON	NSW	2256	20	18	16	14.606667	7.07692	0.015315	0.245641	22.714286	
42	1292 898	DOINTHANON	NSW	2256	20	18	16	13.2875	6.306667	0.014925	0.237194	23.833333	
43	1292 898	NAIHOW	NSW	2256	8	8	16	13.9625	8.871429	0.016112	0.257798	19.84375	
44	1292 898	COTOMINES	NSW	2256	12	16	16	7.85	5.666667	0.009508	0.09924	4	
45	1292 898	BAOSHAN(1)	NSW	2256	12	16	16	9	3.325	0.007567	0.105841	23.392671	
46	1292 898	CEHENG	NSW	2256	30	30	16	8.18571429	3.3	0.005649	0.079081	26.5	
47	1292 898	SHANGSI	NSW	2256	21	27	16	12.54	6.48	0.005649	0.079081	26.5	
48	1292 898	JINGDANG(2)	NSW	2256	21	27	16	14.2625	5.933333	0.014055	0.210821	23.633333	
49	1292 898	JINGHONG	NSW	2256	15	16	16	13.806667	6.815385	0.017799	0.284778	22.366667	
50	1292 898	LANCANG	NSW	2256	18	14	16	14.15	8.00743	0.016673	0.250091	20.869231	
51	1292 898	DAKHA	NSW	2256	24	16	16	14.1875	7.0625	0.016769	0.268296	22.714286	
52	1292 898	ZOKHUA	NSW	2256	24	16	16	12.4175	5.70625	0.012889	0.20569	12.625	
53	1292 898	AUNGBAN	NSW	2256	12	20	16	12.25	5.891667	0.015159	0.212229	22.968333	
54	1292 898	JOHNMEKLECSO	NSW	2256	9	9	16	14.393333	7.92727	0.006442	0.246827	21.5	
55	1292 898	ZAMBIACSO	NSW	2256	6	6	16	15.206667	6.53574	0.018241	0.247458	22.233333	
56	1292 898	MORARANO	NSW	2256	13	2256	26	6	14.16	93.75	0.016577	0.248653	23.1

