



**Assessment and Analysis of two Pinus kesiya Provenance Trials in Indonesia  
Trial No. 7 (T 72) Aek Nauli, Trial No. 8 (T 70) Habinsaran**

Hansen, Christian Pilegaard; Hansen, Christian Pilegaard; Ræbild, Anders; Saragih, Thomas

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# Assessment and analysis of two *Pinus kesiya* provenance trials in Indonesia

Trial No. 7 (T 72) Aek Nauli

Trial No. 8 (T 70) Habinsaran

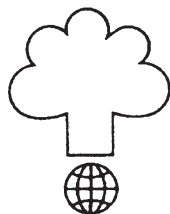
by

Christian Pilegaard Hansen<sup>2</sup>, Anders Ræbild<sup>2</sup> and Thomas Saragih<sup>1</sup>

Research & Development Department,

RGMI Forestry<sup>1</sup>, North Sumatra, Indonesia

Danida Forest Seed Centre<sup>2</sup>, Denmark



**Results and Documentation No. 21**

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Poor branching characteristics; whorls of heavy persistent branches and long internodes have militated against the acceptance of *P. kesiya* as a plantation species. Here Habinsaran trial site, Indonesia. Photo: Christian Pilegaard Hansen

This publication can be requested from:

Danida Forest Seed Centre  
Krogerupvej 21. DK-3050 Humlebaek, Denmark  
Phone: +45-49190500  
Fax: +45-49190258  
Email: [dfsc@sns.dk](mailto:dfsc@sns.dk)  
Web Site: [www.dfsc.dk](http://www.dfsc.dk)

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**Danida Forest Seed Centre (DFSC)** is a Danish non-profit institute which has been working with development and transfer of know-how in management of tree genetic resources since 1969. The development objective of DFSC is to contribute to improve the benefits of growing trees for the well-being of people in developing countries. DFSC's programme is financed by the Danish International Development Assistance (Danida).

# Preface

This report presents the results of a joint assessment of two *Pinus kesiya* provenance trials in Indonesia. The trials were established by RGMI Forestry, Research and Development Division in 1992 as part of an international series of provenance trials of the species.

The joint RGMI/DFSC field assessment took place in September 1999 with participation of Thomas Saragih, Wagiman, Nabil, Parlindungan Panjaitan and Gibson Manurung of RGMI Forestry, R&D. From DFSC participated Anders Ræbild and Christian Pilegaard Hansen.

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# Acronyms

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
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
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 Aek Nauli and Habinsaran trials form 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 given in 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 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, Madagascar, 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 of the seedlots were separated by mother trees to allow testing of individual families.

A status of 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 (Vietnam).



## 2. *P. kesiya* provenance trials in Indonesia

RGMI Forestry, Indonesia, has established two provenance trials of *P. kesiya* in 1992 in North Sumatra, Indonesia. The trials are located at the Aek Nauli and Habinsaran forestry sectors and have trial identification numbers T72 and T70, respectively.

The provenances represented in the trials are shown in the below table.

Remarks about the table:

1. Seedlots 712, 713, 714, 715, 716, 183, 118, 366, i.e. the not *P. kesiya*/*P. yunnanensis* sources, are local controls, and do not form part of the international seed exchange under the international programme.
2. The field assessment revealed that the Doi Inthanon provenance of *P. kesiya* in fact was *P. tecunumanii*. As the seed lot could not be further identified, it has been omitted from the analysis.
3. The Guanaja provenance of *P. caribaea* var. *bondurensis* and the Coto Mines provenance of *P. kesiya* are only in the Aek Nauli trial, not in the Habinsaran one.
4. *Eucalyptus grandis* has been included as a local control in both trials. The Eucalyptus plots in the Aek Nauli trial have been cut down, and hence Eucalyptus is only in the Habinsaran trial. The plots have been assessed, but not included in the statistical analysis.
5. The Simao provenance of *P. kesiya* is only present in the Habinsaran trial, and only in one of the four replicates. This plot has been assessed, but the provenance has not been included in the statistical analysis.

Details of the trial establishment and management are presented in Annex 2 and descriptions of the sites are in Annex 3.

The Aek Nauli trial has a low survival rate. Many trees have reportedly been cut down during weeding operations, probably because weeding operations have been delayed. It is further reported that trees in the trial have suffered from herbicide application. As a result, many plots in the Aek Nauli trial have few trees left, and other plots have been entirely lost (no trees left). This is weakening the statistical analysis of the trial.

The Habinsaran trial, on the other hand, has a much higher and more uniform survival. The growth at the Habinsaran trial also compares favourably to the Aek Nauli trial.

As mentioned above, both trials suffer from misplaced seedling/rows/plots. The problem with seedlot 723 (the Doi Inthanon source of *P. kesiya*) in both trials has been mentioned above, but also in other plots, there are rows, parts of rows or single trees of other origin, i.e. misplaced seedlings. These trees have in all cases been omitted from the assessment.

Local ID	DFSC Acc. No.	Species	Provenance	Country
712	-	<i>P. oocarpa</i>	Mal Paso	Guatemala
713	-	<i>P. tecunumanii</i>	Mt. Pine Ridge	Belize
714	-	<i>P. oocarpa</i>	El Paraiso	Honduras
715	-	<i>P. tecunumanii</i>	San Raphael	Nicaragua
716	-	<i>P. caribaea</i>	Guanaja	Honduras
718	1572/85	<i>P. kesiya</i>	Coto Mines	Philippines
719	1525/85	<i>P. kesiya</i>	Nam Now	Thailand
720	1521/85	<i>P. kesiya</i>	Nong Krating	Thailand
721	1519/85	<i>P. kesiya</i>	Lang Hanh	Vietnam
722	1522/85	<i>P. kesiya</i>	Doi Suthep	Thailand
723	1523/85	<i>P. kesiya</i>	Doi Inthanon	Thailand
724	1639/86	<i>P. kesiya</i>	Simao	China
725	1783/88	<i>P. kesiya</i>	Bodana A8	Madagascar
726	1773/88	<i>P. kesiya</i>	Aungban	Myanmar
727	1633/86	<i>P. yunnanensis</i>	Shangsi	China
183	-	<i>P. merkusii</i>	Indonesia	Indonesia
118	-	<i>P. patula</i>	Zimbabwe landrace	Zimbabwe
366	-	<i>E. grandis</i>	Coff's Harbour	Australia

### 3. Field assessment and data management

The assessment followed the methodology described in DFSC (1998) and included 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. No. of forks;
11. Position of first fork;
12. Foxtail;
13. Flowering and fruiting;
14. Wood density (Pilodyn);

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

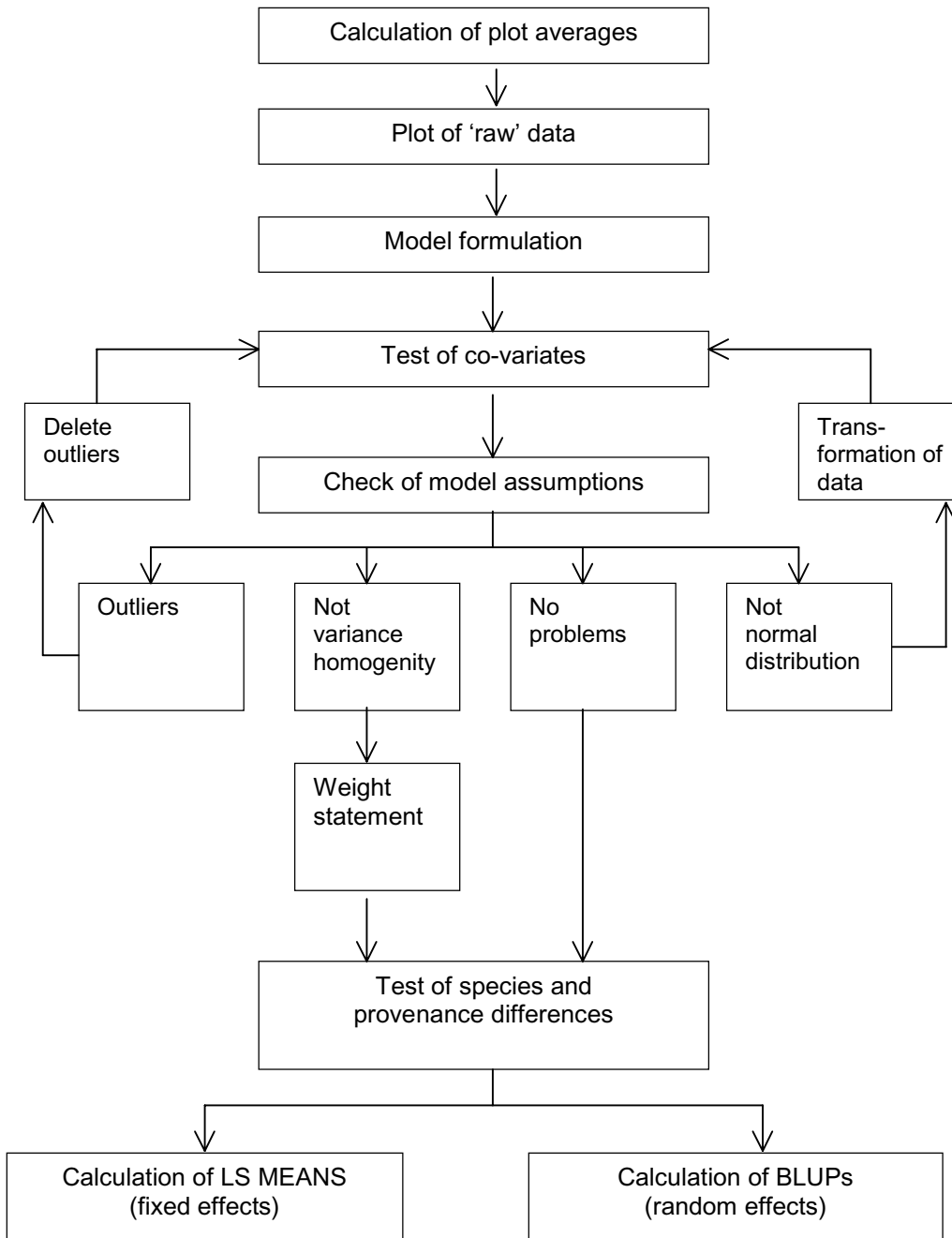
The assessment was a full assessment, i.e. all trees within each plot were included. For the local controls, i.e. seedlots not *P. kesiyá*, the assessment was limited to survival, height, diameter, stemform and pilodyn.

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 spreadsheet, data was later transferred 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  $jk$ ,

$\mu$  is the grand mean,

$\text{provenance}_j$  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),

$\text{block}_k$  is the effect of block  $k$  in the trial, assumed to be a random effect, and

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

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  $\pm 1.96$ . 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  $e_i$  for observation  $ij$  is given by

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

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  $\pm 2$ . 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  $\pm 2.5$  (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 (replica-

tions). 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 species and 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 variables may involve combinations of different mean squares (Skovgård 1994), an approximation called Satterthwaites 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,  $\alpha$  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, cm<sup>2</sup> 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.

<b>Group</b>	<b>Trait description</b>	<b>Analysed trait</b>
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 above bark of trees in plot
	Standing volume per hectare	Volume per hectare
Adaptation	Survival	Survival rate
	Flowering and fruiting	Average score of male flowers
	Foxtailing	Foxtailing percentage
Quality	Stemform	Stemform score (1-9)
	Relative wood density (Pilodyn)	Diameter adjusted pilodyn readings
	Branching	Average branch diameter
	Branching	Average branch/DBH ratio

## 5.1 Survival

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	PLOTY2
Data transformation required	Yes. Arc sin transformation	Yes. Arc sin transformation
Weight statement	Yes	Yes
Outliers	None	None
F-test	6.27 (***)	3.32 (***)

Analysis of survival data at year 7 reflects not only differences in ‘true’ survival rates but is also affected by within-plot competition. For the Aek Nauli trial, irregularities in weeding have resulted in loss of many seedlings, and great care is therefore required in the interpretation of results of this trial.

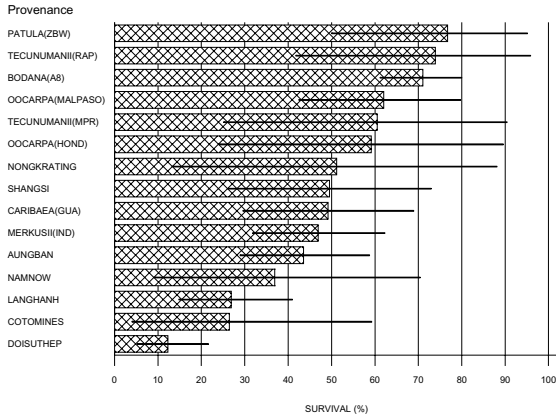
The Habinsaran trial has a much higher survival rate than the Aek Nauli trial. Many of the seed sources have a survival rate above or close to 90 per cent, e.g. *P. oocarpa* (Mal Paso), Lang Hanh (Vietnam), *P. tecunumanii* (Mt. Pine Ridge), and Bodana (Madagascar). There are not statistical significant differences among the top provenances, but it is possible to distinguish between a high and a low survival group. In the latter one we find *P. patula*, Doi Suthep (Thailand) and Aungban (Myanmar).

The ranking in regard to survival is quite different in the Aek Nauli trial, but as mentioned above, these results have to be interpreted with great care, as also indicated by the very wide confidence intervals. The Lang Hanh (Vietnam), Coto Mines (Philippines) and Doi Suthep (Thailand) have very low survival rates. Especially the low survival rate of Lang Hanh is surprising as it is among the highest ranking provenances in the Habinsaran trial. *P. patula*, *P. tecunumanii* (San Raphael) and Bodana (Madagascar) are high ranked at Aek Nauli, whereas only Bodana is among the best at Habinsaran. *P. patula* and *P. tecunumanii* (San Raphael) have below average survival rates.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

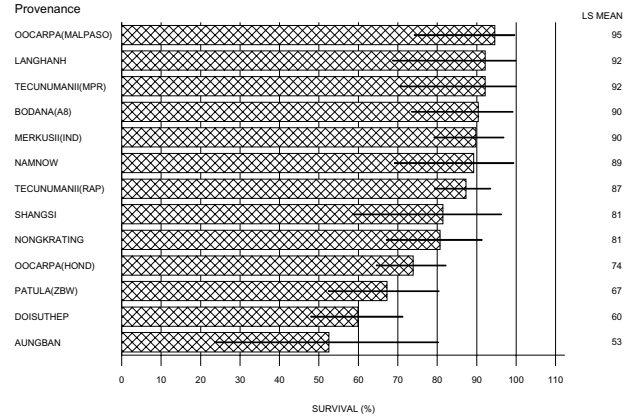
Survival (%)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

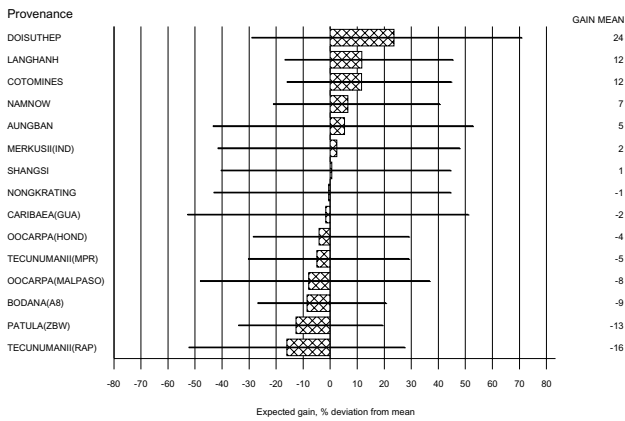
Survival (%)



### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

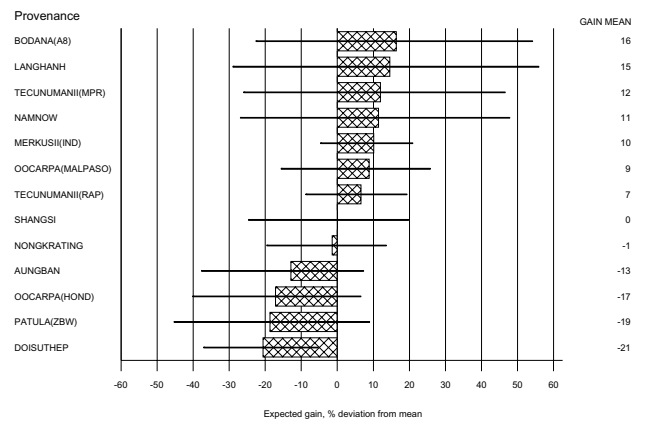
Survival. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

Survival. Best linear un-biased predictors (BLUPs)



## 5.2 Height growth

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	PLOTX and PLOTY2
Data transformation required	No	No
Weight statement	No	Yes
Outliers	Lang Hanh (Block 1)	None
F-test	12.96 (***)	96.18 (***)

The analysis of height growth shows highly significant differences among provenances in both trials. The ranking of provenances is very similar in the two trials. The two *P. tecunumanii* sources are at the top in both trials, although the exact ranking of the two sources are different from the one trial to the other.

The *P. tecunumanii* sources are followed by the two sources of *P. oocarpa*. The best source of *P. kesiya* in the Aek Nauli trial is the Coto Mines provenance (Philippines), which is unfortunately not in the Habinsaran trial. Coto Mines is followed by the provenances Doi Suthep (Thailand), Bodana (Madagascar) and Lang Hanh (Vietnam). There are however no statistically significant differences among these sources. At the bottom end we find Nam Now (Thailand), Nong Krating (Thailand) and Aungban (Myanmar). At the very bottom is the Shangsi provenance of *P. yunnanensis*.

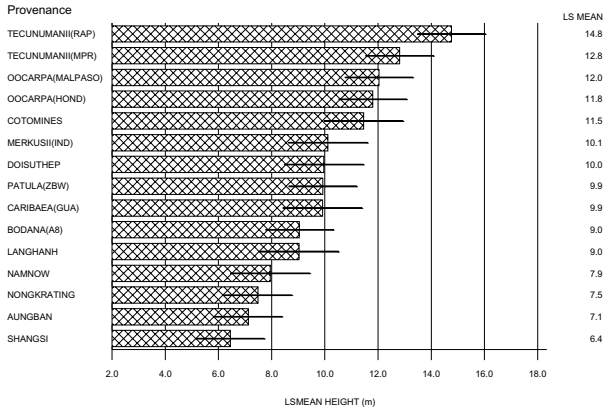
In the Habinsaran trial, again the Lang Hanh, Bodana and Doi Suthep are the most promising *P. kesiya* sources. Nam Now, Nong Krating, Aungban and Shangsi sources are at the bottom.

The local *P. merkusii* source is in both trials ranking below the *P. tecunumanii*/*P. oocarpa* sources but higher than the *P. kesiya* sources. The *P. patula* source (of Zimbabwe origin) does not show much promise. It is intermediately placed in the Aek Nauli trial, but at the very bottom at Habinsaran. The *P. caribaea* source is only in the Aek Nauli trial, where it is showing a (surprisingly) poor growth.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999

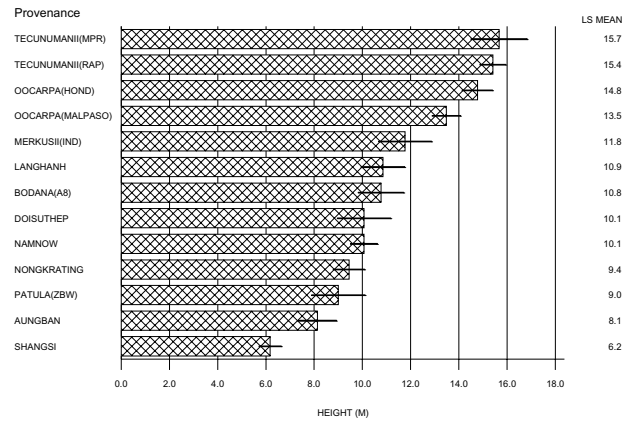
Vertical height (m)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

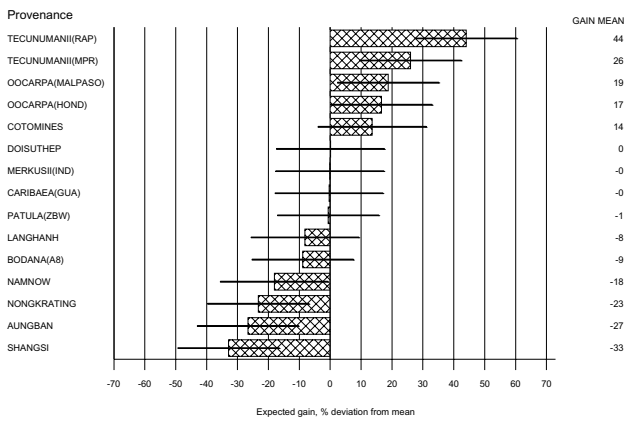
International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999

Height (m)



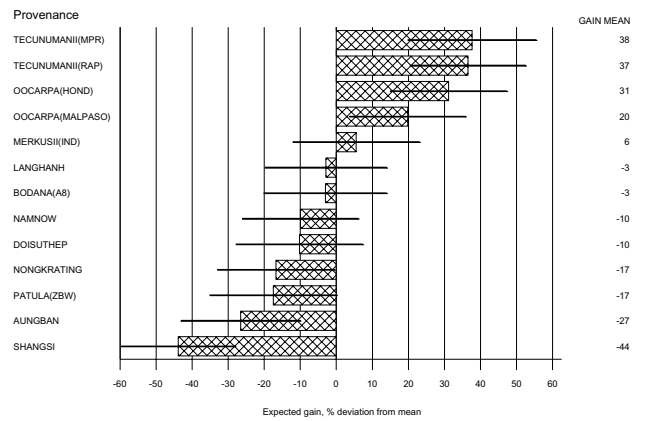
### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999  
 Height gain. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999  
 Height gain. Best linear un-biased predictors (BLUPs)



### 5.3 Diameter growth

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	PLOTX, PLOTY and PLOTY2
Data transformation required	No	No
Weight statement	No	Yes
Outliers	Lang Hanh (Block 1)	None
F-test	6.29 (***)	28.31 (***)

There are highly significant differences in regard to diameter growth in both trials.

The results of the Aek Nauli trial- again - have to be interpreted with care as differences in survival between plots may have influenced diameter growth. This is reflected in the considerably larger confidence intervals in the Aek Nauli trial compared to the Habinsaran trial.

If we look at the results of the Habinsaran trial first, the ranking of provenances is not very different from what we have seen for height growth. We have the *P. tecunumanii* sources at the top, followed by *P. oocarpa*. Lang Hanh (Vietnam) and Bodana (Madagascar) are again best among the *P. kesiya* sources, although there are only small and statistically insignificant differences among the best *P. kesiya* sources. The *P. yunnanensis* source (Shangsi-China), *P. patula* and Aungban (Myanmar) are at the bottom end and they can be distinguished also statistically from the above mentioned sources.

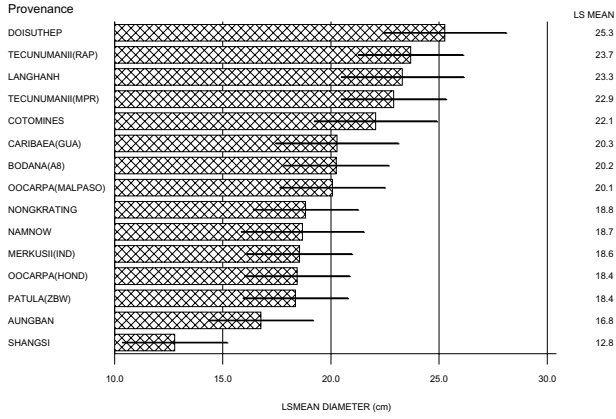
In the Aek Nauli trial the ranking is quite different, which is believed to a large extent due to the differences in survival. Doi Suthep (Thailand) and Lang Hanh (Vietnam) placed in the top together with the two *P. tecunumanii* sources. The two *P. oocarpa* sources are ranked relatively low. In the lower end, the picture is identical to the Habinsaran trial with Shangsi (China), Aungban (Myanmar) and *P. patula* having the poorest diameter growth.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Diameter (cm)

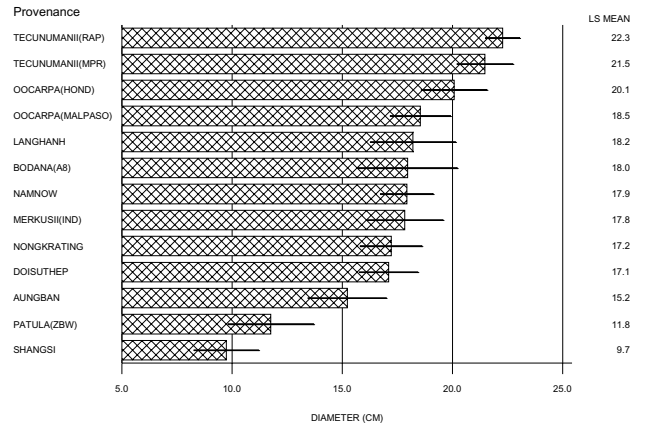


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Diameter (cm)

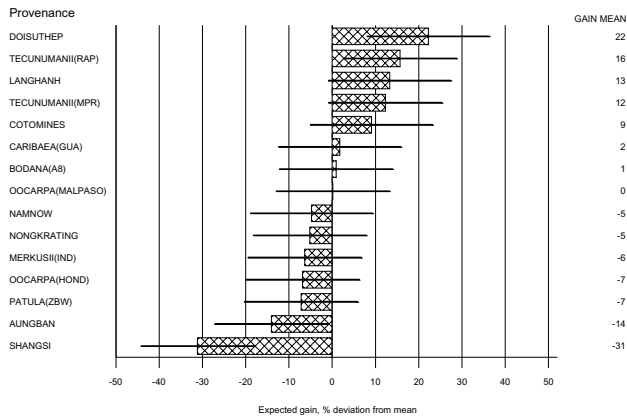


### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Diameter gain. Best linear un-biased predictors (BLUPs)

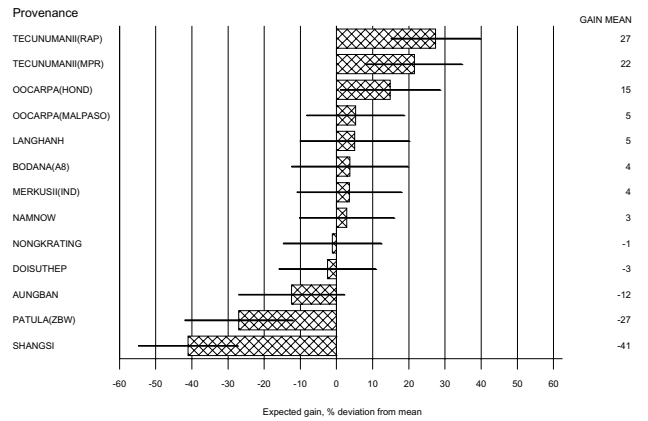


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Diameter gain. Best linear un-biased predictors (BLUPs)





## 5.4 Mean volume of tree

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	PLOTX and PLOTY
Data transformation required	No	No
Weight statement	No	Yes
Outliers	None	None
F-test	6.63 (***)	52.14 (***)

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, the trait thus illustrates a combined effect of height and diameter.

Again, the Aek Nauli results have to be interpreted with care because of the different survival rates and consequently diameter growth.

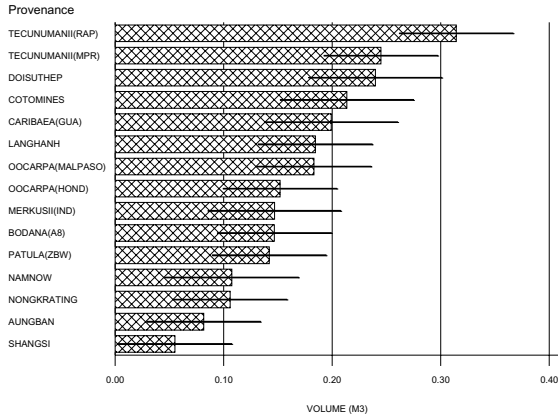
In the Habinsaran trial, the two *P. tecunumanii* seed sources are at the top, followed by the *P. oocarpa* sources. They again are followed by the local *P. merkusii* and only then we find the best *P. kesiya* sources. They are Lang Hanh (Vietnam) and Bodana (Madagascar). *P. patula* and *P. yunnanensis* are at the bottom.

In the Aek Nauli trial, we also have the two *P. tecunumanii* sources at the top, but they are followed closely by Doi Suthep (Thailand) and Coto Mines (Philippines). At the bottom we find, as in the Habinsaran trial, Aungban (Myanmar) and Shangsi (China).

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

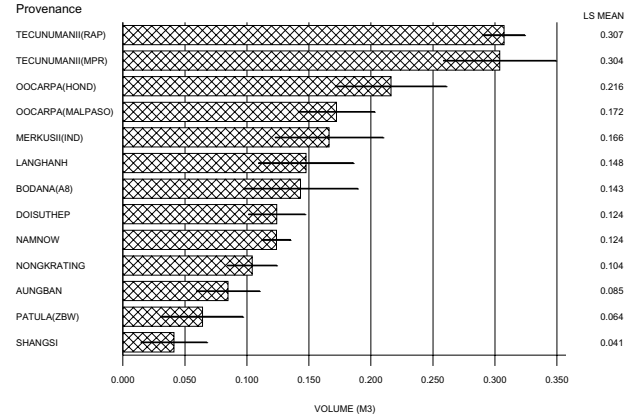
Volume of mean tree (m<sup>3</sup>)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

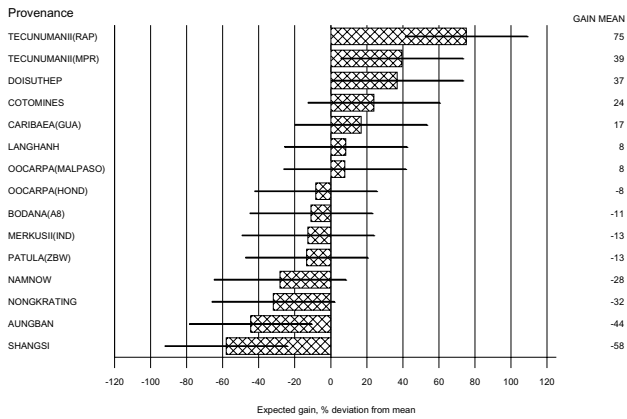
Volume of mean tree (m<sup>3</sup>)



### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

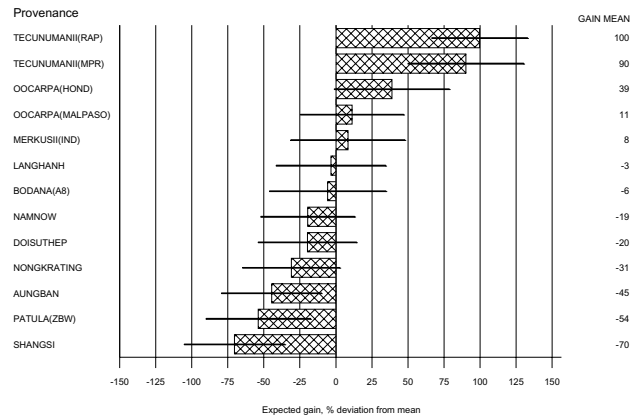
Volume of mean tree. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

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



## 5.5 Total volume per hectare

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	PLOTXY	PLOTX and PLOTY2
Data transformation required	No	No
Weight statement	Yes	Yes
Outliers	None	None
F-test	6.01 (***)	33.88 (***)

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.

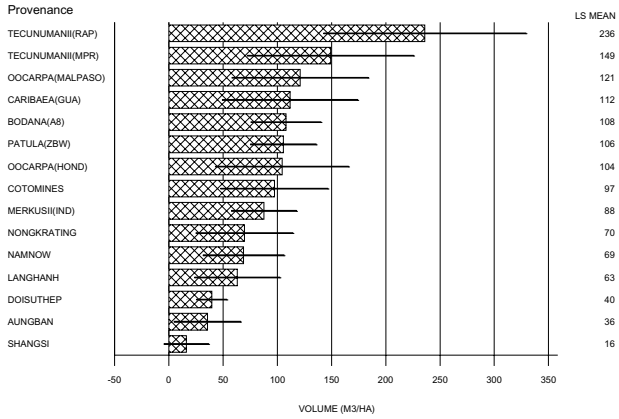
The Habinsaran trial shows a ranking of provenances almost identical to what we have seen for mean volume of tree. The two *P. tecunumanii* sources are by far the most productive, with the San Raphael source slightly better than the Mt. Pine Ridge although the difference is not statistically significant. Following the *P. tecunumanii* sources, but with significantly lower production, we have the two *P. oocarpa* provenances followed by *P. merkusii*. The best sources of *P. kesiya* are again Bodana (Madagascar) and Lang Hanh (Vietnam).

In the Aek Nauli trial, we also have the *P. tecunumanii* sources at top, but the ranking underneath is somewhat different to the Habinsaran trial. The Bodana landrace from Madagascar is the best *P. kesiya* source like in the Habinsaran trial, whereas

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

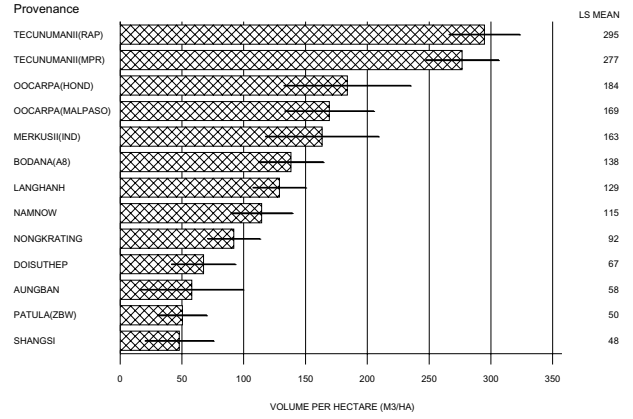
Volume per ha (m3/ha)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

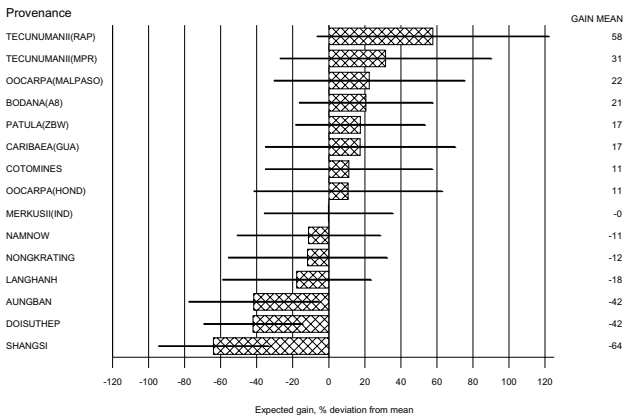
Volume per hectare (m3/ha)



### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
Established November 1992. Assessed September 1999

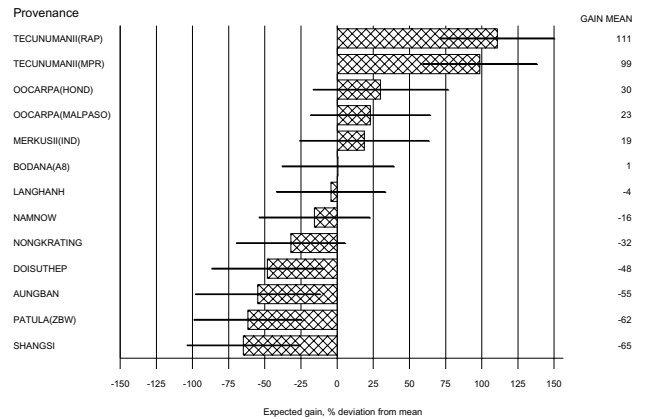
Volume per hectare. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
Established October 1992. Assessed September 1999

Volume gain. Best linear un-biased predictors (BLUPs)



## 5.6 Stemform

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	PLOTY2	None
Data transformation required	Yes. Ln transformation	No
Weight statement	Yes	Yes
Outliers	Nong Krating (Block 2)	None
F-test	8.05 (***)	11.60 (***)

The statistical analysis reveals significant differences among provenances in regard to stemform in both trials.

The *P. merkusii* and the *P. caribaea* source (the latter is only in the Aek Nauli trial) have a considerably poorer stemform than the other sources.

The ranking of provenances is different in the two trials. In the Habinsaran trial, *P. patula* is at the top followed by *P. oocarpa* (Honduras) and the two *P. tecunumanii* sources. The best *P. kesiya* sources are Nong Krating (Thailand), Nam Now (Thailand) and Bodana (Madagascar). Aungban (Myanmar), Lang Hanh (Vietnam), Shangsi (China) and Doi Suthep (Thailand) have the poorest stemform among the *P. kesiya* sources.

At Aek Nauli, Nam Now (Thailand) and Doi Suthep (Thailand) are at the top. This in contrast to the Habinsaran trial where Nam Now is intermediate, and Doi Suthep is in the lower half. Next at Aek Nauli we have the sources of *P. oocarpa*, *P. tecunumanii*, *P. patula* and Bodana (Madagascar) which were at the very top at Habinsaran.

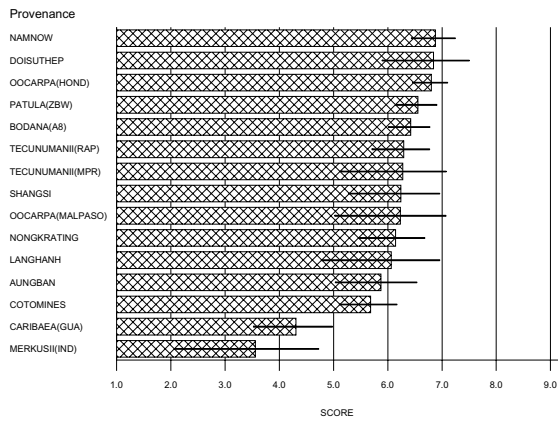
For both trials, there are only small – and not statistically significant – differences among the top ranking seed sources.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Stemform (1-9 score)

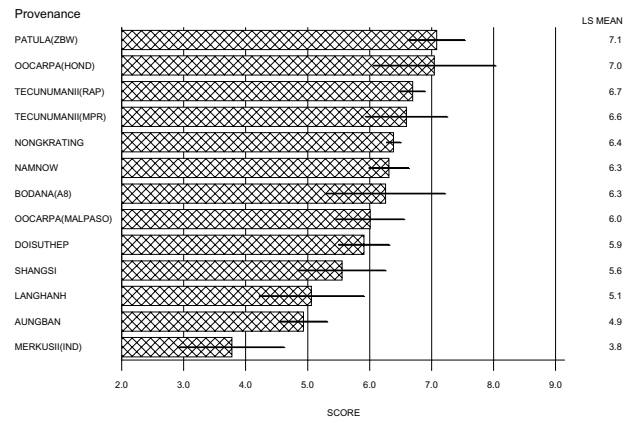


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Stemform (1-9 score)

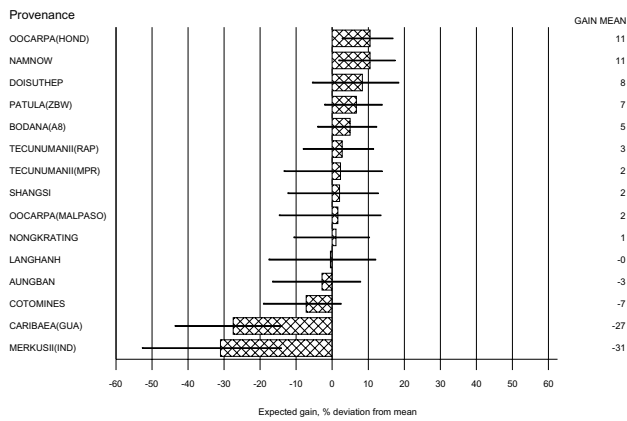


### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Stemform. Best linear un-biased predictors (BLUPs)

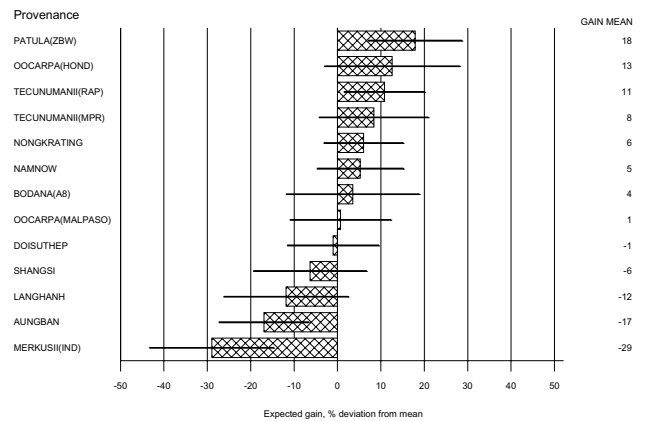


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Stemform. Best linear un-biased predictors (BLUPs)



## 5.7 Wood density (Pilodyn)

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	PLOTY2
Data transformation required	Yes. Square-root transformation	Yes. Ln transformation
Weight statement	No	Yes
Outliers	None	None
F-test	3.71(***)	7.68 (***)

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

Both the Aek Nauli and the Habinsaran trial reveal significant differences between provenances. The ranking of provenances, however, is different in the two trials. As we have seen for most other traits, the confidence intervals in the Aek Nauli trial are much wider than in the Habinsaran trial.

The sources with the fastest growth (diameter and total volume production), i.e. the *P. tecunumanii* and *P. oocarpa* sources, have the highest pilodyn values corresponding to the lowest wood densities. Consequently, the slow growing sources have in general the highest wood densities. This is the general picture, but there are exceptions, and the exact ranking, as mentioned above, is different in the two trials.

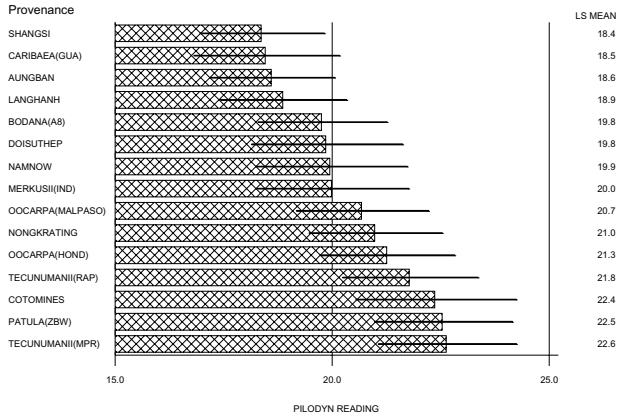
Most remarkable is *P. patula* that is ranked at the top at Habinsaran, but at the bottom end in the Aek Nauli trial. A ranking among the top sources is what would be expected considering the poor growth of *P. patula* in both trials. Also the Aungban (Myanmar) and *P. oocarpa* (Mal Paso) sources have very different rankings in the two trials.

There are significant differences when comparing the top and bottom, but differences among many of the sources ranked in-between are only small, and not statistically significant.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999

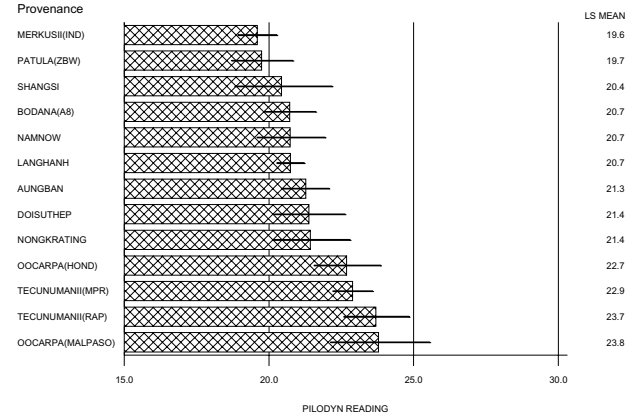
Pilodyn



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999

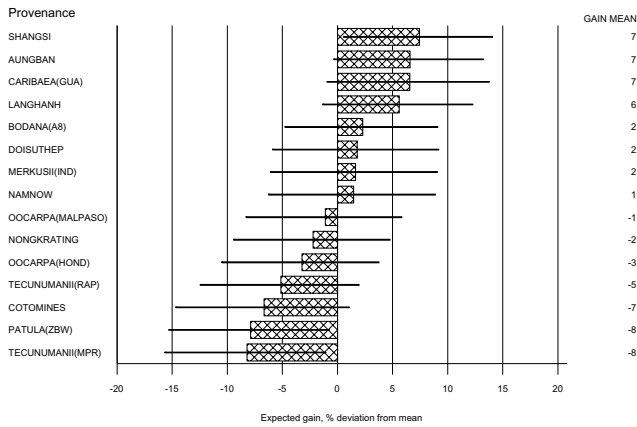
Pilodyn



### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999

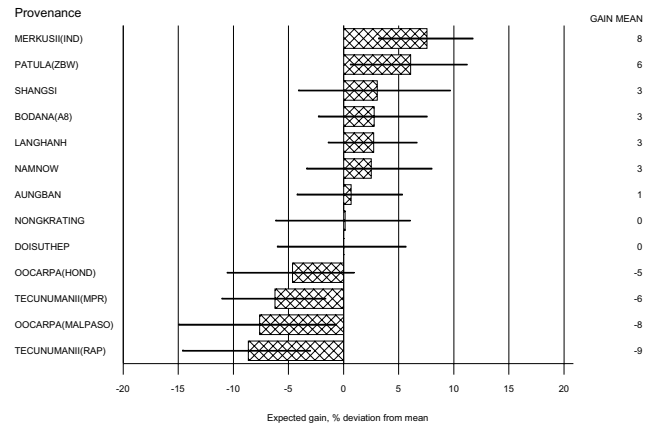
Pilodyn. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999

Pilodyn. Best linear un-biased predictors (BLUPs)





## 5.8 Branching (branch diameter)

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	PLOTX2	PLOTY
Data transformation required	No	No
Weight statement	Yes	Yes
Outliers	None	None
F-test	11.87(***)	4.27 (***)

Branch diameter (largest branch in whorl at 1/10 of tree height) has only been assessed on the *P. kesiya* / *P. yunnanensis* sources, and therefore the analysis is restricted to these sources. The analysis reveals significant differences between provenances in both trials.

In both trials, the Shangsi (*P. yunnanensis*) source has considerably smaller branch diameters than the other sources. The growth potential of this source is very poor, and the small branches are related to this fact.

The results of the Aek Nauli trial, again, have to be interpreted with care as low survival most likely has influenced development of thick branches. This is e.g. the case for Doi Suthep (Thailand) which in the Habinsaran trial is among the provenances with smallest branch diameter but at the very top at Aek Nauli.

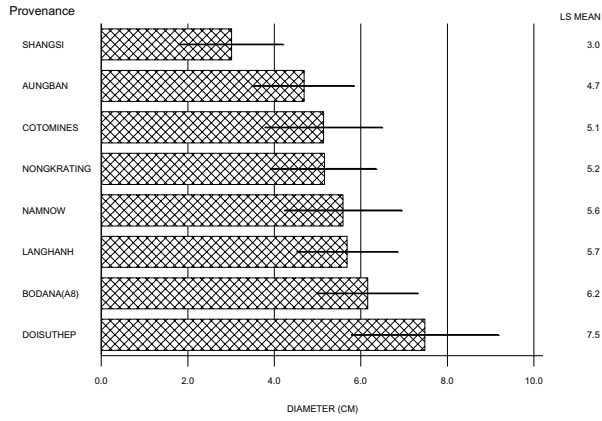
If we leave out Shangsi, there are not great differences among the sources, and differences are not statistically significant. There is maybe a slight tendency to provenances having better growth also having thicker branches.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Branch diameter (cm)

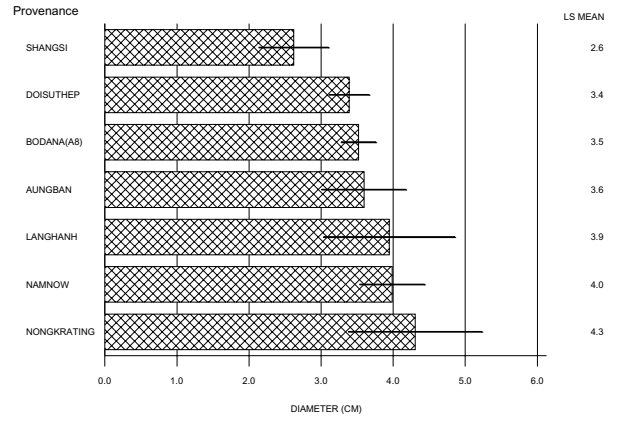


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Branch diameter (cm)

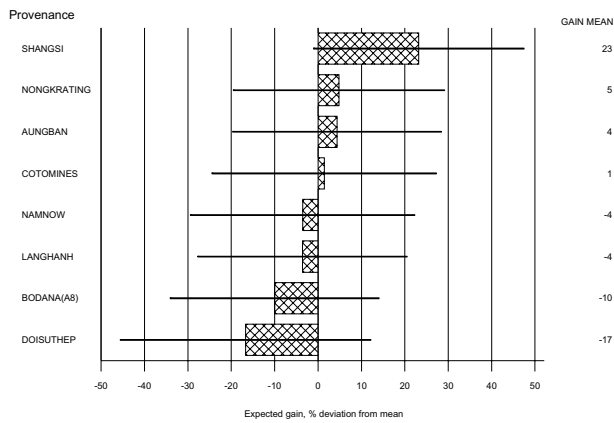


### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Branch diameter. Best linear un-biased predictors (BLUPs)

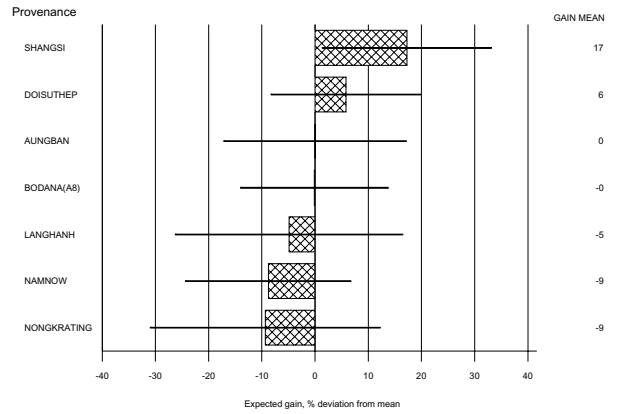


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Branch diameter. Best linear un-biased predictors (BLUPs)



## 5.9 Foxtailing

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	None	None
Data transformation required	No	No
Weight statement	Yes	Yes
Outliers	Block 1: <i>P. tecunumanii</i> (MPR), Lang Hanh and Doi Suthep; Block 2: Nong Krating; Block 3: Doi Suthep and Shangsi; and Block 4: Lang Hanh	None
F-test	1.45(NS)	8.91 (***)

Frequency of foxtails has only been assessed on the *P. kesiya*/*P. yunnanensis* sources.

There are not significant differences among sources in the Aek Nauli trial, whereas in the Habinsaran trial there are significant differences.

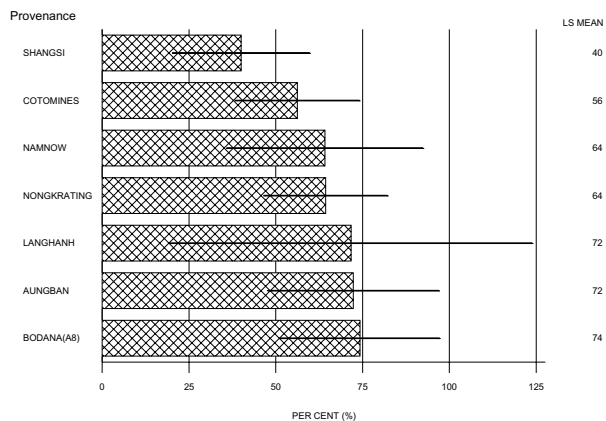
It looks as *P. yunnanensis* (Shangsi) has significantly fewer foxtails than the *P. kesiya* sources. For the *P. kesiya* sources the frequency of foxtails is high; between 55 and 75 percent. There are however not statistically significant differences among provenances. There is a tendency, although not statistically significant, to Thai sources having fewer foxtails than the other sources.

Foxtailing is an important trait to consider. First of all it gives an indication of the adaptability of the source to the site (a low frequency is in general an indication of good adaptation). Moreover, and probably of greater practical importance, foxtails will influence quality. Foxtails will result in ramiflora, i.e. thick branches growing (co-evolving) vertically along with the main stem as there are no branches on the foxtail to suppress this growth. Thick branches mean lower quality, especially if timber is the final products. In addition, harvesting operations become more difficult. Finally, foxtails will often result in broken stems because of the soft wood.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999

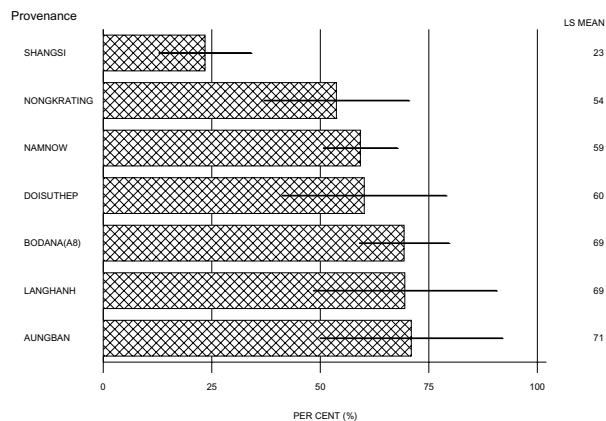
Foxtail percentage (%)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999

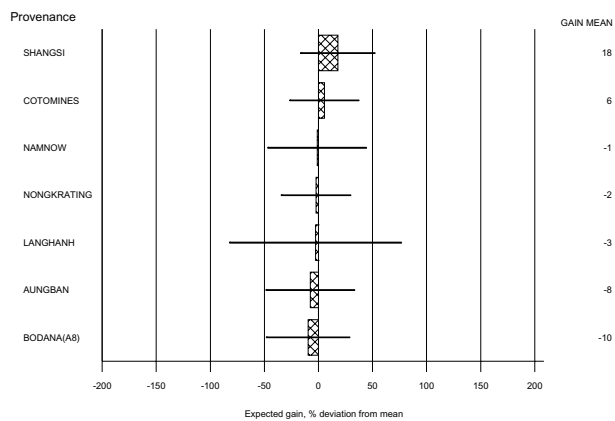
Foxtail percentage (%)



### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7  
 Established November 1992. Assessed September 1999

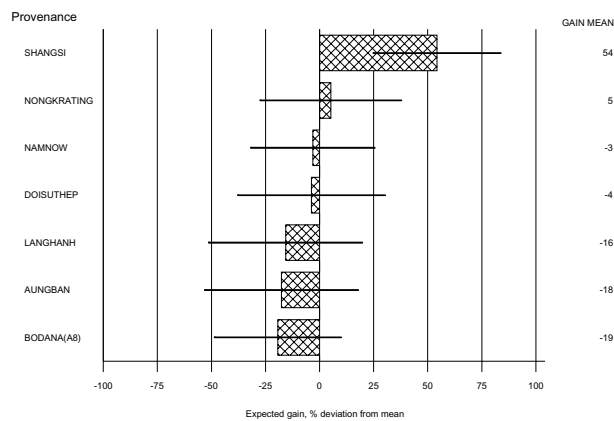
Foxtailing. Best linear un-biased predictors (BLUPs)



### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8  
 Established October 1992. Assessed September 1999

Foxtailing. Best linear un-biased predictors (BLUPs)



## 5.10 Flowering

OVERVIEW OF ANALYSIS		
	Aek Nauli	Habinsaran
Co-variates	LEVEL, PLOTX and PLOTY	None
Data transformation required	No	No
Weight statement	Yes	Yes
Outliers	Block 1: <i>P. tecunumanii</i> (MPR), Lang Hanh and Doi Suthep; Block 2: Nong Krating; Block 3: Doi Suthep and Shangsi; and Block 4: Lang Hanh	None
F-test	3.52(**)	0.70 (NS)

Assessment of flowering has only been done on the *Pinus kesiya*/*P. yunnanensis* sources.

Frequency of flowers provides an indication of the adaptation of the sources to site. A good flowering and fruiting will generally be interpreted as a sign of good adaptation to the site, and vice versa.

The two trials are quite young, only about 7 years of age, and flowering and fruiting may have only just commenced. Consequently, male flowers were the only development stage that was present on most trees, and hence the only stage that could be assessed and analysed.

In the Habinsaran trial, there is very sparse flowering, and no statistical differences between the provenances.

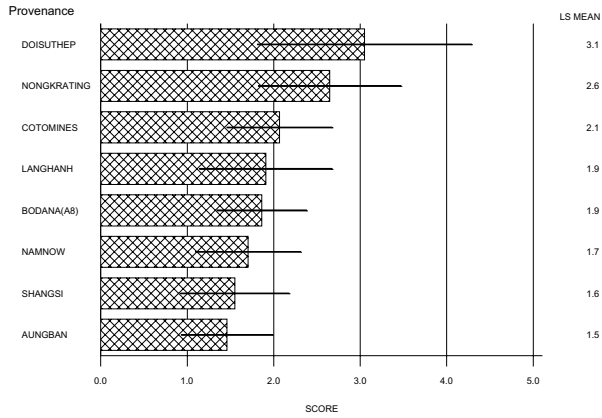
The Aek Nauli trial has more frequent male flowering and there are significant provenance differences. *P. yunnanensis* (Shangsi) and Aungban (Myanmar) have the lowest flowering scores, and Doi Suthep (Thailand) the highest. It is a question if not the uneven survival rates in the Aek Nauli trial have an influence here. The uneven survival rates may have lead to different light conditions in plots which have facilitated flowering to a variable degree. The differences may thus more be because of survival differences than 'true' provenance differences.

### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Male flowers (1-9 score)

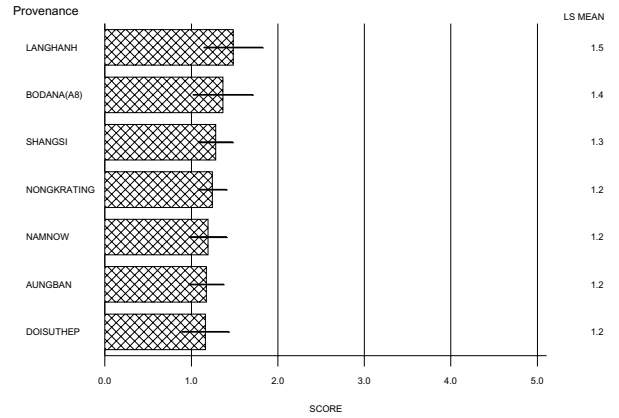


### Pinus kesiya provenance trial, Habinsaran, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 8

Established October 1992. Assessed September 1999

Male flowers (1-9 score)

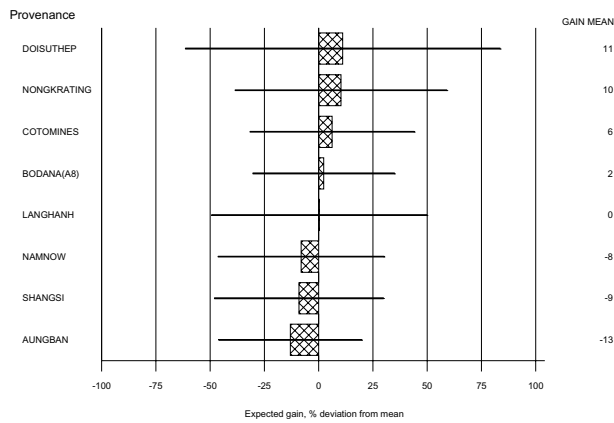


### Pinus kesiya provenance trial, Aek Nauli, Indonesia

International Series of Pinus kesiya provenance trials, Trial No. 7

Established November 1992. Assessed September 1999

Male flowers. Best linear un-biased predictors (BLUPs)



No figure of BLUP-estimates for the Habinsaran trial as there are no statistical differences between provenances.

## 6. Conclusions

Conclusions are to be based mainly on the performance in the Habinsaran trial. This is because of the many lost seedlings in the Aek Nauli trial that has influenced the growth and development. Differences in ranking of seedlots in the two trials are believed to be mainly an effect of this, and not differences caused by different environments at the two sites (i.e. not believed to be genotype x environment interaction).

### 6.1 Growth

Growth traits should be given key importance in the interpretation of trial results, as production of pulpwood has high priority.

The analysis shows not much promise for the tested sources of *P. kesiya* in comparison to the included controls - most of the tested controls have a considerably faster growth than the *P. kesiya* sources.

The two *P. tecunumanii* sources are superior to the other sources in regard to growth in both trials, and is the most promising species at sites similar to the test sites. The San Raphael provenance has a slightly better growth than the Mt. Pine Ridge provenance, but differences are not statistically significant. It would be interesting to test more sources of *P. tecunumanii*, as other sources may have an even greater potential. The company has such trials under way. Mean annual production – based on the results of the Habinsaran trial – is approx. 40 m<sup>3</sup>/ha/year.

Following *P. tecunumanii* we find the two sources of *P. oocarpa*, but growth is considerably slower than that of *P. tecunumanii*. In the Aek Nauli trial the two *P. oocarpa* sources have almost the same growth, whereas at Habinsaran, the Honduran source has the fastest growth.

Next in ranking is the local (Indonesian) *P. merkusii* source, and only then we arrive at the best *P. kesiya* sources.

Lang Hanh (Vietnam) and Bodana (Madagascar) are the best growth performers among the *P. kesiya* sources. It is interesting to note that the Madagascar source (landrace) almost certainly originates from the Central plateau of Vietnam (Armitage & Burley, 1980), i.e. from the same region as the Lang Hanh seedsource. It was introduced from here to Madagascar in the 1920's.

Coto Mines (Philippines) is performing well in the Aek Nauli trial (height growth) but is unfortunately not included at Habinsaran.

Doi Suthep (Thailand) may be mentioned together with the above sources, mainly based on a relatively good growth in the Aek Nauli trial. It seems, however, that this source has a low survival rate.

*P. patula* shows little promise based on the two trials. It is very slow growing, has a low survival rate, and generally looks unhealthy.

The poorest growth performer is the *P. yunnanensis* source that has a volume production less than one fifth of the *P. tecunumanii* sources.

### 6.2 Adaptation

Adaptive traits include survival percentage, foxtail frequency and flowering. The two latter traits have only been assessed on the *P. kesiya*/*P. yunnanensis* sources.

There are no statistical significant differences among top ranking sources in regard to survival. The best *P. kesiya* performers in regard to growth, Lang Hanh (Vietnam) and Bodana (Madagascar), also have a good survival. In the other end of the scale, *P. patula*, Doi Suthep (Thailand) and Aungban (Myanmar) have a low survival rate.

The *P. yunnanensis* source has a considerably lower frequency of foxtails than the *P. kesiya* sources, but the result has little practical value because of the extremely poor growth of this source. The high frequency of foxtails for the *P. kesiya* sources may be another constraint for a more intensive use of the species.

### 6.3 Quality

Quality parameters are stemform, wood density (pilodyn) and branch diameter. The *P. tecunumanii* sources, the *P. oocarpa* ones and *P. patula* have the best stemform. *P. merkusii* has a considerably poorer stemform than the rest of sources, with the *P. kesiya* sources forming an intermediate group. The Bodana (Madagascar) source is again among the best, whereas the Lang Hanh (Vietnam) has a poorer stemform.

The more slow growing sources generally have a better wood density (esp. Shangsi and *P. merkusii*) and thinner branches than the faster growing sources (esp. *P. tecunumanii* and *P. oocarpa*). The Lang Hanh and Bodana sources are again here among the highest ranking sources of *P. kesiya*.

### 6.4 Conclusion

Based on the performance in the two trials, the two sources of *P. tecunumanii* are the most promising. Further testing and investigation of the genetic variation within this species is recommended. The Research & Development Division has trials under way with additional sources of *P. tecunumanii* and these trials will provide valuable information on the most appropriate sources of the species.

*P. kesiya* shows little promise as a plantation species on the tested sites. The growth is much slower than *P. tecunumanii* and *P. oocarpa*, and it also compares less favorable in regard to stemform. *P. kesiya* may have a larger potential on poorer and harsher sites more influenced by fires (Clegg, pers. comm.). If results of the present trials also are applicable under such conditions, the analysis indicates the Lang Hanh source (natural population from the central plateau of Vietnam) and Bodana A8 (offspring from seed orchard in Madagascar, material probably originally from Vietnam) as the most promising sources. The Lang Hanh source may show an even larger potential in subsequent generations as inbreeding depression from the natural population breaks down. Other sources from the Central plateau of Vietnam could also be of potential interest. The same holds for Philippine sources, which are only represented with one provenance and only in the Aek Nauli trial.



## 7. References

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### Personal communication

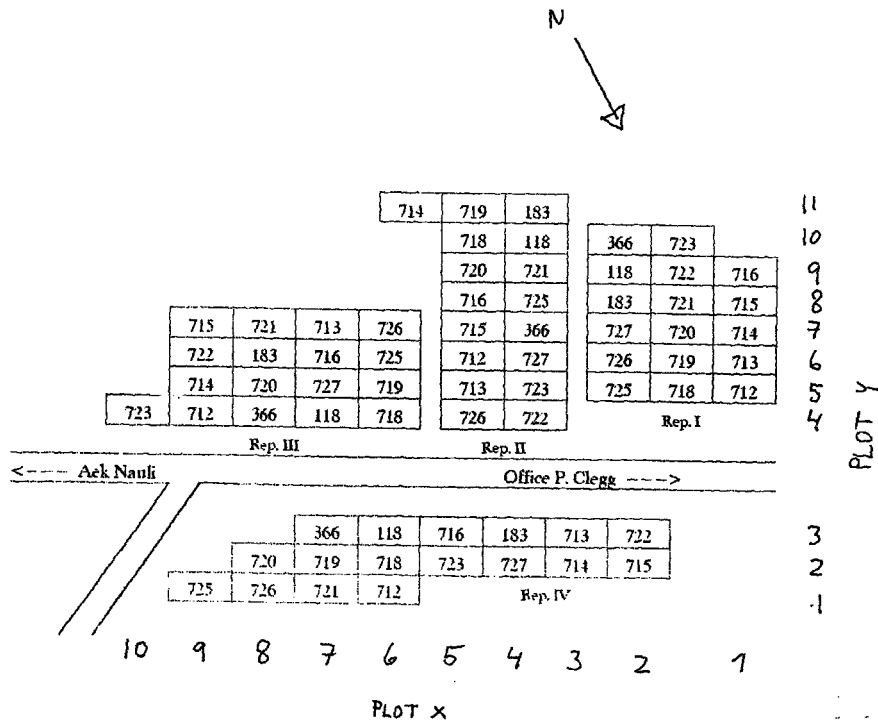
- Brockhoff, P. Lecturer in statistics. The Royal Veterinary and Agricultural University, Copenhagen.
- Clegg, P.A. Research manager, RGMI Forestry, Research & Development Division.

# Annexes



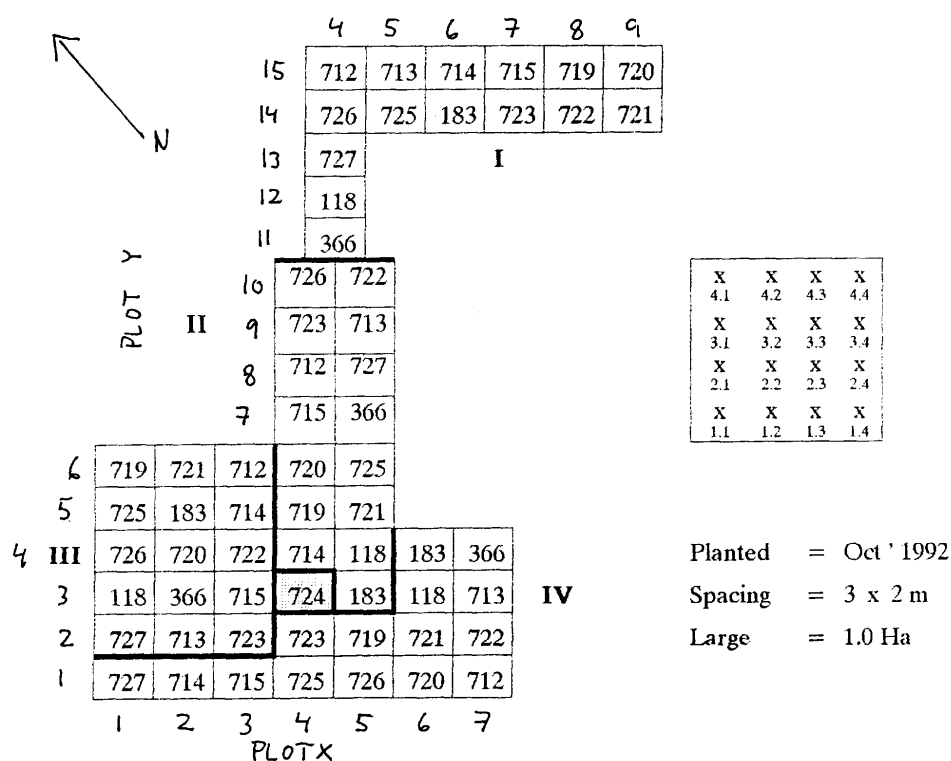
# Annex 1. Maps

## Aek Nauli



Local ID	DFSC Acc. No.	Species	Provenance	Country
712	-	<i>P. oocarpa</i>	Mal Paso	Guatemala
713	-	<i>P. tecunumanii</i>	Mt. Pine Ridge	Belize
714	-	<i>P. oocarpa</i>	El Paraiso	Honduras
715	-	<i>P. tecunumanii</i>	San Raphael	Nicaragua
716	-	<i>P. caribaea</i>	Guanaja	Honduras
718	1572/85	<i>P. kesiya</i>	Coto Mines	Philippines
719	1525/85	<i>P. kesiya</i>	Nam Now	Thailand
720	1521/85	<i>P. kesiya</i>	Nong Krating	Thailand
721	1519/85	<i>P. kesiya</i>	Lang Hanh	Vietnam
722	1522/85	<i>P. kesiya</i>	Doi Suthep	Thailand
723	1523/85	<i>P. kesiya</i>	Doi Inthanon	Thailand
724	1639/86	<i>P. kesiya</i>	Simao	China
725	1783/88	<i>P. kesiya</i>	Bodana A8	Madagascar
726	1773/88	<i>P. kesiya</i>	Aungban	Myanmar
727	1633/86	<i>P. yunnanensis</i>	Shangsi	China
183	-	<i>P. merkusii</i>	Indonesia	Indonesia
118	-	<i>P. patula</i>	Zimbabwe landrace	Zimbabwe
366	-	<i>E. grandis</i>	Coff's Harbour	Australia

# Habinsaran



Local ID	DFSC Acc. No.	Species	Provenance	Country
712	-	<i>P. oocarpa</i>	Mal Paso	Guatemala
713	-	<i>P. tecunumanii</i>	Mt. Pine Ridge	Belize
714	-	<i>P. oocarpa</i>	El Paraiso	Honduras
715	-	<i>P. tecunumanii</i>	San Raphael	Nicaragua
716	-	<i>P. caribaea</i>	Guanaja	Honduras
718	1572/85	<i>P. kesiya</i>	Coto Mines	Philippines
719	1525/85	<i>P. kesiya</i>	Nam Now	Thailand
720	1521/85	<i>P. kesiya</i>	Nong Krating	Thailand
721	1519/85	<i>P. kesiya</i>	Lang Hanh	Vietnam
722	1522/85	<i>P. kesiya</i>	Doi Suthep	Thailand
723	1523/85	<i>P. kesiya</i>	Doi Inthanon	Thailand
724	1639/86	<i>P. kesiya</i>	Simao	China
725	1783/88	<i>P. kesiya</i>	Bodana A8	Madagascar
726	1773/88	<i>P. kesiya</i>	Aungban	Myanmar
727	1633/86	<i>P. yunnanensis</i>	Shangsi	China
183	-	<i>P. merkusii</i>	Indonesia	Indonesia
118	-	<i>P. patula</i>	Zimbabwe landrace	Zimbabwe
366	-	<i>E. grandis</i>	Coff's Harbour	Australia

# Annex 2. Trial descriptions

## Aek Nauli, Indonesia

### TRIAL ESTABLISHMENT AND MANAGEMENT

Year and month of establishment: *November 1992*

Area (ha): *1.0 ha*

Initial spacing (m x m): *3 m x 3 m*

Soil preparation (time, method/intensity): *Site ripper mounded*

Planting method(age of seedlings, type): *Polybags, 6 cm diameter, 10 cm height, seedlings probably 25-30 cm*

Beating up (time, %): *No information*

Irrigation (time, amount): *None*

Fertilization (time, type, amount): *No information*

Weeding (time, intensity): *Irregular, none in 1993-94*

Thinning (time, intensity): *None*

Firelines: *None*

### TRIAL DESIGN

Statistical design: *Randomized complete block design*

No. of replications (blocks): *4 replications*

No. of treatments (provenances): *16 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 . Note problems with identification of seedlot 723 (Doi Inthanon, Thailand)(not kesiya).*

### PROTECTION STATUS

Status (describe any disturbances/damages): *Survival is generally low. Many plots with no surviving trees. Many trees are believed to have been cut by accident when undertaking weeding (irregular weeding). Maybe also by pesticide application...*

Guarding (permanent, regular, none): *Permanent guarding. Trial is close to office and R&D nursery*

# Habinsaran, Indonesia

## TRIAL ESTABLISHMENT AND MANAGEMENT

Year and month of establishment: *October 1992*

Area (ha): *1.0 ha*

Initial spacing (m x m): *3 m x 3 m*

Soil preparation (time, method/intensity): *Site ripper mounded*

Planting method(age of seedlings, type): *Polybags, 6 cm diameter, 10 cm height, seedlings probably 25-30 cm*

Beating up (time, %): *No information*

Irrigation (time, amount): *None*

Fertilization (time, type, amount): *No information*

Weeding (time, intensity): *No information*

Thinning (time, intensity): *None*

Firelines: *None*

## TRIAL DESIGN

Statistical design: *Randomized complete block design*

No. of replications (blocks): *4 replications*

No. of treatments (provenances): *15 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 . Note problems with identification of seedlot 723 (Doi Inthanon, Thailand)(not kesiya).*

## PROTECTION STATUS

Status (describe any disturbances/damages): *Good survival and growth. Problems with proper identification in some plots. Seedlot 723, Doi Inthanon is not P. kesiya but an un-identified source of P. tecunumanii. Problems in other plots identified as well... ..*

Guarding (permanent, regular, none): *Regular guarding. Trial is 2.5 km from sector office*

# Annex 3.

## Site description – Aek Nauli

### LOCATION

Province: *North Sumatra*  
District: *Simalungun*  
Latitude (degrees and minutes): *02°44'04"N*  
Longitude (degrees and minutes): *98°53'39E*  
Altitude (m above sea level): *1250 m above sea level*

Managing office/institution: *PT INTI Indorayon Utama, R&D Department*  
Owner: *do*  
User(s): *do*

Distance to nearest office responsible for management of the trial (km): *70*  
Distance to nearest villages/towns (km): *Ujung Mauli, 2 km*  
Number of inhabitants in the nearest villages/towns: *approx. 200*

Type of area (e.g. research station, managed forest, etc.): *Managed forest plantations, mainly Eucalyptus sp. for pulp*

### CLIMATE

Nearest weather station:

Name of the station: *Aek Nauli base camp (9 km E of trial site)*  
Latitude (degrees and minutes): *see above*  
Longitude (degrees and minutes): *see above*  
Altitude (m a.s.l.): *1200 m above sea level*

Climatic data <sup>1</sup>	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.	Year
Rainfall (mm)	147.5	152.9	174.5	205.9	173.9	143.7	138.9	191.7	173.4	177.6	214.1	220.0	2114.2
Temp. mean (°C)	20.5	20.8	20.9	21.3	21.9	21.9	21.5	21.4	21.1	20.7	20.8	22.8	21.1
Temp. mean max. <sup>2</sup> (°C)	-	-	-	-	-	-	-	-	-	-	-	-	-
Temp. mean min. <sup>3</sup> (°C)	-	-	-	-	-	-	-	-	-	-	-	-	-
Evapotranspiration <sup>4</sup> (mm)	-	-	-	-	-	-	-	-	-	-	-	-	-

<sup>1</sup> Period of observations 1988-98

<sup>2</sup> Average of daily maximum temperatures

<sup>3</sup> Average of daily minimum temperatures <sup>4</sup> Potential evapotranspiration (ETP) - Penman's formula

Rainy season:

Number/type of seasons:  one  two  Even

Period(s): (specify months)

Length of rainy season:

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

No. of wet days: (growing season)

Number of dry months per year (< 50 mm rain/month): *None*

Frost (number of days/year): *None*

Prevailing winds (direction, period, speed): *W to SW very occasionally strong*



Alternative weather station:

Name of the station:

Latitude (degrees and minutes):

Longitude (degrees and minutes):

Altitude (m a.s.l.):

Climatic data <sup>1</sup>	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.	Year
Rainfall (mm)													
Temp. mean (°C)													
Temp. mean max. <sup>2</sup> (°C)													
Temp. mean min. <sup>3</sup> (°C)													
Evapotranspiration <sup>4</sup> (mm)													

<sup>1</sup> Period of observations

<sup>2</sup> Average of daily maximum temperatures

<sup>3</sup> Average of daily minimum temperatures <sup>4</sup> Potential evapotranspiration (ETP) - Penman's formula

Rainy season:

Number/type of seasons:  one  two  even/irregular

Period(s): (specify months)

Length of rainy season:

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

No. of wet days: (growing season)

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

Frost (number of days/year):

Prevailing winds (direction, period, speed):

**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)	X	1. Well drained	X	1. None (< 15 %)	
2. Medium/loamy		2. Deep (50-100 cm)		2. Seasonal		2. Gravelly (15-35 %)	X
3. Heavy/clayey	X	3. Very deep (> 100 cm)		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: *Natural forest*

Dominant natural (original) genera/species: *Many*

Land use history: *Natural forest -> degraded forest/scrub -> pines (+/- 50 years) -> eucalypts (4 yrs)*

## RESULTS OF SOIL SAMPLE

Results of the laboratory analysis of the soil samples taken at the trial site.

The variables are:

Depth:	Soil sample depth
Clay:	Particle size less than 2 µm (0.002 mm) in diameter
Fine silt	Particle size between 2 and 20 µm (0.002 - 0.020 mm) in diameter
Coarse silt	Particle size between 20 and 63 µm (0.020 - 0.063 mm) in diameter
Fine sand	Particle size between 63 and 125 µm (0.063 - 0.125 mm) in diameter
Fine medium sand	Particle size between 125 and 250 µm (0.125 - 0.250 mm) in diameter
Coarse medium sand	Particle size between 250 and 500 µm (0.250 - 0.500 mm) in diameter
Coarse sand	Particle size between 500 and 2000 µm (0.500 - 2.0 mm) in diameter
Gravel	Particle size between 0.2 and 2 cm in diameter
Org. mat.	Organic material in various stages of decomposition
Lime	Lime content
pH-H <sub>2</sub> O	Reaction (pH)
P	Phosphorus content

Sample 1: Block 2, plot 719

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	28.8
Fine silt (2-20 µm)	%	23.1
Coarse silt (20-63 µm)	%	1.4
Fine sand (63-125 µm)	%	3.9
Fine medium sand (125-250 µm)	%	6.5
Coarse medium sand (250-500 µm)	%	10.2
Coarse sand (500-2000 µm)	%	26.1
Org. Mat.	%	1.8
Lime	%	0.0
pH-H <sub>2</sub> O	-	5.4
P		- 1

Results noted as - 1: Amount not detectable

Sample 2: Block 2, plot 183

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	29.4
Fine silt (2-20 µm)	%	24.2
Coarse silt (20-63 µm)	%	3.9
Fine sand (63-125 µm)	%	4.4
Fine medium sand (125-250 µm)	%	6.5
Coarse medium sand (250-500 µm)	%	8.7
Coarse sand (500-2000 µm)	%	22.7
Org. Mat.	%	1.1
Lime	%	0.0
pH-H <sub>2</sub> O	-	5.1
P		- 1

Results noted as - 1: Amount not detectable

# Site description – Habinsaran

## LOCATION

Province: *North Sumatra*

District:

Latitude (degrees and minutes): *02°17'29"N*

Longitude (degrees and minutes): *99°13'42E*

Altitude (m above sea level): *1315 m above sea level*

Managing office/institution: *PT INTI Indorayon Utama, R&D Department*

Owner: *do*

User(s): *do*

Distance to nearest office responsible for management of the trial (km): *30*

Distance to nearest villages/towns (km):

Number of inhabitants in the nearest villages/towns:

Type of area (e.g. research station, managed forest, etc.): *Managed forest plantations, mainly *Eucalyptus* sp. for pulp*

## CLIMATE

Nearest weather station:

Name of the station: *Habinsaran base camp (2 km from trial site)*

Latitude (degrees and minutes): *see above*

Longitude (degrees and minutes): *see above*

Altitude (m a.s.l.): *see above*

Climatic data <sup>1</sup>	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.	Year
Rainfall (mm)	101.1	79.9	163.1	205.9	165.1	84.8	117.2	147.9	217.5	157.8	173.4	150.9	1764.5
Temp. mean (°C)	20.3	20.7	20.6	21.2	21.7	21.4	20.8	20.9	20.6	20.6	20.8	20.4	20.8
Temp. mean max. <sup>2</sup> (°C)	-	-	-	-	-	-	-	-	-	-	-	-	-
Temp. mean min. <sup>3</sup> (°C)	-	-	-	-	-	-	-	-	-	-	-	-	-
Evapotranspiration <sup>4</sup> (mm)	-	-	-	-	-	-	-	-	-	-	-	-	-

<sup>1</sup> Period of observations 1988-98

<sup>2</sup> Average of daily maximum temperatures

<sup>3</sup> Average of daily minimum temperatures <sup>4</sup> Potential evapotranspiration (ETP) - Penman's formula

Rainy season:

Number/type of seasons:  one  two  Even

Period(s): (specify months)

Length of rainy season:

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

No. of wet days: (growing season)

Number of dry months per year (< 50 mm rain/month): *None*

Frost (number of days/year): *None*

Prevailing winds (direction, period, speed): *W to SW very occasionally strong*

Alternative weather station:

Name of the station:

Latitude (degrees and minutes):

Longitude (degrees and minutes):

Altitude (m a.s.l.):

Climatic data <sup>1</sup>	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.	Year
Rainfall (mm)													
Temp. mean (°C)													
Temp. mean max. <sup>2</sup> (°C)													
Temp. mean min. <sup>3</sup> (°C)													
Evapotranspiration <sup>4</sup> (mm)													

<sup>1</sup> Period of observations

<sup>2</sup> Average of daily maximum temperatures

<sup>3</sup> Average of daily minimum temperatures

<sup>4</sup> Potential evapotranspiration (ETP) - Penman's formula

Rainy season:

Number/type of seasons:  one  two  even/irregular

Period(s): (specify months)

Length of rainy season:

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

No. of wet days: (growing season)

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

Frost (number of days/year):

Prevailing winds (direction, period, speed):

**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) X	1. Well drained X	1. None (< 15 %)
2. Medium/loamy X	2. Deep (50-100 cm)	2. Seasonal	2. Gravelly (15-35 %) X
3. Heavy/clayey	3. Very deep (> 100 cm)	3. Permanent	3. Stony (> 35 %)

Organic matter content	Reaction (pH)	Soil salinity	Groundwater
1. Poor (< 2 % DM)	1. Acid (pH < 6.5) X	1. None X	1. Shallow (< 50 cm)
2. Medium (2-5 % DM) X	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: *Natural forest*

Dominant natural (original) genera/species: *Many*

Land use history: *Natural forest -> degraded forest/scrub -> eucalypts*

## RESULTS OF SOIL SAMPLE

Results of the laboratory analysis of the soil samples taken at the trial site.

The variables are:

Depth:	Soil sample depth
Clay:	Particle size less than 2 µm (0.002 mm) in diameter
Fine silt	Particle size between 2 and 20 µm (0.002 - 0.020 mm) in diameter
Coarse silt	Particle size between 20 and 63 µm (0.020 - 0.063 mm) in diameter
Fine sand	Particle size between 63 and 125 µm (0.063 - 0.125 mm) in diameter
Fine medium sand	Particle size between 125 and 250 µm (0.125 - 0.250 mm) in diameter
Coarse medium sand	Particle size between 250 and 500 µm (0.250 - 0.500 mm) in diameter
Coarse sand	Particle size between 500 and 2000 µm (0.500 - 2.0 mm) in diameter
Gravel	Particle size between 0.2 and 2 cm in diameter
Org. mat.	Organic material in various stages of decomposition
Lime	Lime content
pH-H <sub>2</sub> O	Reaction (pH)
P	Phosphorus content

Sample 1: Block 2

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	7.7
Fine silt (2-20 µm)	%	6.3
Coarse silt (20-63 µm)	%	4.9
Fine sand (63-125 µm)	%	9.3
Fine medium sand (125-250 µm)	%	18.4
Coarse medium sand (250-500 µm)	%	22.2
Coarse sand (500-2000 µm)	%	31.2
Org. Mat.	%	3.4
Lime	%	0.0
pH-H <sub>2</sub> O	-	5.7
P		- 1

Results noted as - 1: Amount not detectable

Sample 2: Block 1

Description	Unit	Result
Depth of sample	m	1.2
Clay (<2 µm)	%	23.1
Fine silt (2-20 µm)	%	8.2
Coarse silt (20-63 µm)	%	17.0
Fine sand (63-125 µm)	%	7.4
Fine medium sand (125-250 µm)	%	11.0
Coarse medium sand (250-500 µm)	%	14.9
Coarse sand (500-2000 µm)	%	18.4
Org. Mat.	%	7.5
Lime	%	0.0
pH-H <sub>2</sub> O	-	5.7
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 data set has been prepared from the individual tree dataset and holds the following parameters.

<b>PARAMETER NAME</b>	<b>EXPLANATION</b>
SITE	Name of site
DATEEST	Establishment data of trial (MM/YY)
DATEASS	Date of assessment (MM/YY)
BLOCK	Block No.
PLOT	Plot No.
PLOTX	X- coordinate (see map)
PLOTY	Y-coordinate (see map)
SEEDLOT	Seedlot No.
PROVNAME	Name of provenance
SURV	Survival percentage (%)
DG	Diameter corresponding to mean basal area at breast height (cm)
GHA	Basal area (m <sup>2</sup> /ha)
GMEAN	Mean basal area per tree (m <sup>2</sup> )
HG	Height for tree with diameter corresponding to mean basal area (m)
MEANPILO	Mean pilodyn for plot
PILOCORR	Mean pilodyn reading adjusted for diameter effect
STEM	Average stemform
STEM1..STEM9	Frequency of individual stemform scores 1 to 9 (%)
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 (%)
FO_POS	Average position of lower fork (m above ground)
FO_INDEX	Forking index (m <sup>-1</sup> )
FLOWER	Flowering and fruiting frequency (%)
FOXTAIL	Frequency of foxtails in plot (%)
KRAFT	Average Kraft index
KRAFT1.. KRAFT5	Frequency of individual Kraft scores 1 to 5 (%)
CROWN	Average crown index
CROWN1..CROWN5	Frequency of individual crown index scores 1 to 5 (%)
BR_INDEX	Branching index (cm)
INTNODE	Average distance between whorls (m)
BRARATIO	Ratio between branch diameter and DBH

**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;

$\alpha$  is the slope of the regression line;

$\beta$  is the intercept with y-axis;

For each plot,  $\alpha$  and  $\beta$  are estimated using PROC REG (SAS 1990).

HG for the plot is then calculated using the linear regression estimates ( $\alpha$  and  $\beta$ ) and plot DG (as previously calculated).

**PILOCORR - 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**

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**

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.











