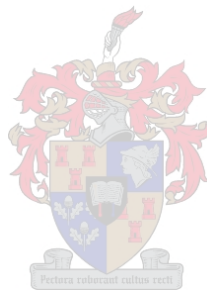


**A SAMPLING STUDY OF BRANCHING CHARACTERISTICS
TOWARDS OBTAINING MORE EFFICIENCY FOR TREE
SELECTION IN BREEDING TRIALS**

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**Thesis presented in partial fulfilment of the requirements for the degree
of Master of Science in Forestry Sciences at the University of
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DECLARATION

I, the undersigned, hereby declare that the work contained in this thesis is my own original work and has not previously in its entirety or in part been submitted at any university for a degree.

ABSTRACT

A total of 125 trees covering a range of tree diameters were selected from a progeny trial of open pollinated progenies of *Pinus patula* for studies on trait assessments and evaluation for branching characteristics. The trees comprised 25 families with each family having five trees. The trial was 36 months old and was located in a relatively high yielding site in Block B at Usutu in Swaziland. The height, diameter, the number of branches and the number of whorls of each tree were recorded. In addition to these objective assessments on individual trees, trees were given scores for branch size, branch angle, stem straightness and crown coarseness. For the detailed branch evaluation study, trees were marked at 20% and 50% of the total tree height and the section between this range was used. On this section the internode length, the internode diameter, the branch diameter and the branch angle were measured. It was observed that the objective assessments correlated strongly with the scoring (subjective) and it was further recommended that a closer look is needed to consider the prospects of employing subjective assessments as a means of reducing costs incurred during objective trait assessments. The branch sampling study revealed that there were prospects of assessing fewer branches on a tree as opposed to assessing all the branches, which could be a major contributor to the high costs in tree breeding. All three methods used to explore this prospect showed some reasonable agreement with each other in this regard. The best sample is to measure all branches in whorl one and two above 20% tree height followed by sampling four branches, two from the first whorl and two from the second whorl. There is a slight difference in these two samples as determined by the coefficients of

determination. The study recommends that four branches can be used in the assessment of the branch angle and the branch diameter on the trees when one considered the cost elements.

UITTREKSEL

In 'n ondersoek na die evaluering van tak-eienskappe van *Pinus patula* is 125 bome in 'n oop-bestuifde nageslags-proef geselekteer. Hierdie bome is gekies met groottes wat strek oor 'n wye verskeidenheid van borshoogtedeursnee. Die ondersoek het 25 families ingesluit met elke familie wat uit 5 bome bestaan. Die proef is 36 maande oud en is gevestig in 'n hoë produksiearea van Blok B, Usutu, in Swaziland. Die hoogte, borshoogtedeurnee, aantal takke en die hoeveelheid takkrans is gemeet en bepaal by elk van die 125 bome. Verder is punte toegeken vir takgrootte, takhoek, graad van stamkromming en kroon grofheid. In die gedetailleerde tak-evaluasie is slegs die stamseksie tussen 20% en 50% van die totale boomhoogte gebruik. Op hierdie seksie van die boomstam is die internodale afstand, die internodale deursnee, die takdeursnee en die tak-hoek gemeet. Uit die gegewens wat versamel is, het dit geblyk dat daar sterk korrelasie tussen die objektiewe evaluasie en die subjektiewe evaluasie (met gebruik van kwalitatiewe eienskappe op 'n tellingbasis) verkry is. Hieruit word aanbeveel dat meer aandag aan subjektiewe evaluasie (as vereenvoudigde evaluasieprosedure) bestee word om kostes te besnoei. Die gedetailleerde tak-evaluasiestudie het aangedui dat die gebruik van slegs 'n paar takke, in teenstelling met al die takke op die boom, voordelig kan wees om verdere kostes van evaluasie te bespaar. Die beste monster is om al die takke in die eerste twee takkrans bo 20% boomhoogte te meet. Daarnaas is die beste monster die eerste twee grootste takke in die eerste en tweede takkrans. Die gebruik van hierdie kleiner monsters vir evaluering het in sekere opsigte nog beter voorspellings gelewer as in die gevalle waar al die takke in die eerste takkrans gebruik is. Die studie b aan dat 'n betroubare monster van vier takke (twee uit elke takkrans bo 20% boomhoogte) geneem kan word om die boom se takeienskappe te beoordeel.

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CHAPTER ONE

1.0 INTRODUCTION

The worldwide increase in timber demands has put the forest industry in ever increasing pressure to seek ways and means of optimizing forest productivity under limited resources. Unlike agriculture, forestry frequently finds itself faced with a problem of finding suitable forest land that could yield the expected increase in productivity as demands for high quality and sustainable timber supply continue to rise. Most countries have established laws which restrict practice of forestry in areas that are better suited for other purposes such as agriculture, which have a competitive advantage over forestry because of better economic returns (Evans, 1992). Consequently, forestry often finds itself in a situation where optimization of forest yields have to be effected even on marginal sites, a condition which requires careful planning to ensure that sustained forest productivity is achievable within justifiable economic returns.

The key aspects of ensuring increased and sustained forest productivity are to practice site specific silviculture and tree breeding. A sound management system in silviculture i.e. species-site matching, site preparation, planting (transplant quality, planting techniques), weed control, thinning, and pruning combined with a dynamic tree breeding programme can together guarantee sustained and improved forest productivity. As Namkoong (1981) puts it, there is no justification for embarking on a tree breeding programme if silvicultural means of triggering genetic improvement have not been exhausted.

It is of paramount importance that cost-effective measures are taken from the inception of a breeding programme, moreso because the correction of mistakes can take generations to correct owing to the long breeding cycles of forest trees. In advanced breeding programmes costs of assessing trials are even higher compared to simple breeding programmes, i.e., mass selection where genetic gains are readily achieved because at that stage the genetic base is still largely diverse to allow for quicker genetic gains. It is often recommended that simpler breeding programmes have to be adopted where resources are limited, without however, sacrificing the broader objective of maintaining a wide genetic base. The multiple population breeding strategy (Namkoong, 1984 *et al*) is a typical strategy where genetic diversity is maintained whilst breeding for different purposes as

required by the market. The long term advantage of this type of breeding strategy is that whilst it is flexible to the ever changing environmental and market demands it is also the most effective way of maintaining a broader genetic base (Namkoong, *et al*, 1981).

In this thesis a review of the literature is carried out to present an overview of selection processes, the criteria of trait selection and methods of trait assessment are given. These processes are essentially the principal tasks of a breeder who then use them to evaluate the genetic parameters that quantify the value of breeding. Relevant studies on these phenomena are discussed in the text and a review of progress being made is presented.

The selection of stem quality traits (i.e. the branching habit and stem straightness) can effect changes in the wood properties. The high costs associated with the selection of intrinsic wood properties (i.e. the fibre length, wood density, and others) are prohibitive when one tries to improve wood quality through their selection. Wood density, for example, requires sophisticated laboratory procedures involving, for example, the use of an X-ray densitometer, which is both difficult and expensive. However, the use of a pilodyn as an alternative to wood density assessment makes wood density a an intrinsic wood property that can be assessed readily without destructive sampling (Cown, 1978; Gough and Barnes, 1984).

The improvement of wood quality through the selection of quality traits (stem form and branching characteristics) provides a better means of improving wood quality traits where costs of selection for intrinsic wood properties can not be met). Selection of quality traits can also be relatively expensive. Efficiency in sampling for the evaluation of branching characteristics can ensure an improvement in wood quality at reasonable costs. This is the focus of the investigations carried out in this study.

In this study trees were selected from a progeny trial at SAPPI-Usutu (set up in compartment B4) for a branch evaluation study. The objectives of the study were as follows:

- 1) To investigate a cost effective method of sampling representative branches on 36 month-old *Pinus patula* trees in order to predict the overall branching characteristics.
- 2) To compare the effectiveness of using objective assessments in the determination of stem quality traits as opposed to subjective assessment.

Both objectives are aimed at finding ways of reducing high costs incurred during trait assessments in a breeding programme. It is important to know whether one should assess the whole tree or just a section in order to reduce costs. For example, how well does the mean of all the branches in one whorl describe the branching characteristics of a specified tree; or could one measure fewer branches (even just one or two) in the relevant whorl to achieve the same objective? The hypothesis thus given is that:

- (i) Fewer branches that are strategically chosen (i.e., from specific whorls) can be used to describe the worth of a tree instead of assessing all branches.
- (ii) Cost-effective objective assessments can be employed with improved accuracy for the assessments of some tree characteristics that are commonly assessed subjectively thereby improving the quality of assessment.

CHAPTER 2

2.0 LITERATURE REVIEW

This chapter presents a brief review of selection. It highlights some key principles employed by the breeder in manipulating this natural phenomenon to mould a population of tree species to achieve desired goals. The choice of tree traits for selection as well as a description of the different methods of trait assessment is reviewed. The importance of controlling cost is cited with examples of relevant work carried out to evaluate possible cost effective procedures. The economic considerations necessary before embarking on a selection and breeding programme are briefly reviewed.

2.1 Selection background

Selection, mutation, migration and genetic drift are the main evolutionary processes which shape up a population (Namkoong, 1981). Together they mold the population structure in certain directions and therefore act as the primary sources of genetic variation and recombination (Wright, 1976). Selection in nature is termed natural selection. In nature, genotypes that are better adapted to the environment reproduce to ensure the survival of a species and thereby avoid its extinction.

The breeder induces these processes through artificial means, i.e., artificial selection, in order to produce strains, varieties and populations that are best suited for set objectives. In animal and plant breeding (mainly for agricultural purposes) a lot of advancement has been made since the beginning of the century. Until recently (past four decades), forest trees remained relatively unexploited in terms of manipulation of the genes to achieve the required objectives. Thus, tree breeders often find themselves in a position where the manipulation of genotypes to achieve the desired goals can be readily accomplished because of the high genetic variation in tree populations (Namkoong, 1981). However, certain precautions have to be made, some of which are mentioned in the text.

Selection is probably the most well understood and more practical method of influencing the evolutionary processes of tree populations used by the tree breeder. Its flexibility can enable the breeder to obtain quick results or even control the accumulation of favourable genotypes

depending on the economic, physical and environmental demands. The tendency of increased fitness through natural and artificial selection is often limited by environmental effects or the genes themselves (Namkoong, 1981). This is due to the fact that phenotypic expressions, used for the estimation of quantitative parameters, are commonly not at par with the genotypes. If the variation is of low heritability then because of slower processes of allelic substitutions more breeding generations may be required for a reasonable gain (Falconer, 1981).

Tree breeders are principally interested in improving the gene pool of the tree populations in order to maximize productivity at the lowest possible costs (Zobel and Talbert, 1984). To achieve this the breeder is expected to conduct a survey of all possible options of improving traits. For example, a breeding programme may not be economically justified if silvicultural practices can be adopted to improve the trait(s) under consideration. However, pioneering work on selection suggests that gains through selection can be achieved for almost all commercial traits (Namkoong, 1981).

An efficient selection and breeding strategy is critical and it must be designed such that conformance to end product uses and sustainability is assured. For the success of selection and breeding there is a great need for a large effective population size to warrant continued realization of gains. Several workers advocate a large effective population for a sustained improvement (Namkoong *et al*, 1980). The reason behind this is that genetic variability can only be maintained in a large population. A small population is vulnerable to genetic drift, which may lead to loss of alleles (Namkoong, 1981). The subject of the importance of a large effective population size is dealt with in most quantitative analysis textbooks (Falconer, 1981; Namkoong, 1981).

The success of trait selection in a tree population largely depends on the presence of sufficient genetic variation in the trait(s) being selected for improvement. Variation in forest trees is enormous. It is said that there is up to two times more variation in forest trees than in plant populations (Zobel and Talbert 1984). In one such argument Barnes (1973) (cited by Warmald 1973), argues that the genetic variation in exotic *Pinus patula* planted in Southern Africa is comparable to that found in its natural range. This is despite the fact that all the plantations are said to have sprung from only a few kilograms of seed introduced to South Africa in the late 40's (Warmald, 1975). In his remarks, Barnes

(1973) suggested that the improvement of traits cannot be deterred by this factor and that selection for continued improvement of traits was possible, and further, that enough genetic variability existed that can ensure a broader genetic base for future breeding purposes. However, this does not rule out the injection of new genetic variants into the breeding population which can trigger more genetic gains especially when correct testing, i.e., provenance trials, has been followed.

In forest trees, tree-to-tree and stand-to-stand variation can be readily noticed. Deviations of individual trees from the norm may be noticed by a more critical observer. The breeder manipulates the genetic variation by analyzing the forces of variation. Estimates of variation and the evaluation of the relative importance of different sources of variable tree behaviour enables the breeder to control the evolutionary processes of trees (Namkoong, 1981).

The subject of genetic variation in forest trees has been extensively studied with variation being observed at provenance level, between sites, between trees and within trees (Libby, 1973; Smith, 1978; Kromhout and Toon, 1978; Bird 1984; Granhof, 1984).

A brief review of some of the essential concepts is now made, simply to highlight the importance of accurate evaluation of genetic variation as a tool for successful trait selection.

Genetic and environmental effects influence tree traits. Tree breeders fix desirable genes as a means of influencing behaviour of tree traits. Silviculturalists may endeavor to control the tree growth behaviour, for example through intensive management but this has limitations as a broader understanding of tree breeding is required for enhanced management through the manipulation of genes (Namkoong *et al*, 1980).

Estimates of genetic and environmental variances enable the breeder to evaluate genetic parameters such as heritability and extended genetic gain. The ability of the breeder to test the performance of the progeny of selected parents using the analysis of variance methods provides an invaluable tool of evaluating tree breeding programmes (Wright, 1976).

The amount of change in the means depends on the degree of genetic variation that exists in the trait being selected. The expression of a trait (phenotype) is influenced by the environment and the genetic constitution as depicted in the following relation;

$$\text{Phenotypic Variance (V}_p\text{)} = \text{Genetic Variance (V}_g\text{)} + \text{Environmental Variance (V}_e\text{)}$$

The Genetic Variance is further split into two components, namely the additive genetic variance plus the non-additive gene effects.

The heritability, H^2 is defined as the ratio of the genetic variance to the phenotypic variance

$$H^2 = V_g/V_p = V_a + V_{na} / V_p \text{ for broad sense heritability, where } V_a \text{ is the additive genetic variance and } V_{na} \text{ is the non-additive genetic variance.}$$

In practical terms the heritability is defined as

$$h^2 = V_a / V_p \text{ for narrow sense heritability.}$$

Provided good experimental designs are employed, estimates of the variances can be made with some degree of accuracy. However, it has been observed that estimates of genetic parameters often lack consistency (Zobel and Talbert, 1984). This can be attributed to, among other factors, assessments carried out while trees are still young, and poor experimentation, varying environmental impacts and smaller numbers.

The heritability of traits varies with age (Namkoong, 1981) and as such caution has to be made when handling results of early tests. It is also, of importance that proper experimentation and efficient selection procedures must be used to obtain a better response to selection through good estimation of the genetic parameters. Studies on experimental design and relative efficiency in the estimation of genetic parameters were initiated by R.A. Fisher and A. Robertson and extended to forest tree breeding by Namkoong, (1981), Van Buijtenen, (1983), Duba *et al*, (1983), Barnes and Gibson, (1984), and Namkoong, (1984).

In what follows, a review on the use of selection and how response to selection is determined will be made. Response to selection involves a knowledge of aspects such as how long the breeding population will continue to respond to selection, and how the gains from the selection for a certain trait affects other traits. For example, breeding for trees with a larger diameter could lead to unacceptable branch quality, i.e., big knots and eclipsed angles.

Change due to selection is a function of fitness of genotypes, and gene frequencies. The greater the differences between genotypic fitness, or in precision and intensity of selection, the greater the change in any one generation (Kearsey and Pooni, 1996). This does not hold entirely where dominance exists because the affects of favourable genes may be masked. Continued selection in the same direction will generally lead to the fixation of favoured alleles (in the absence of migration and mutation) and to elimination of undesired alleles.

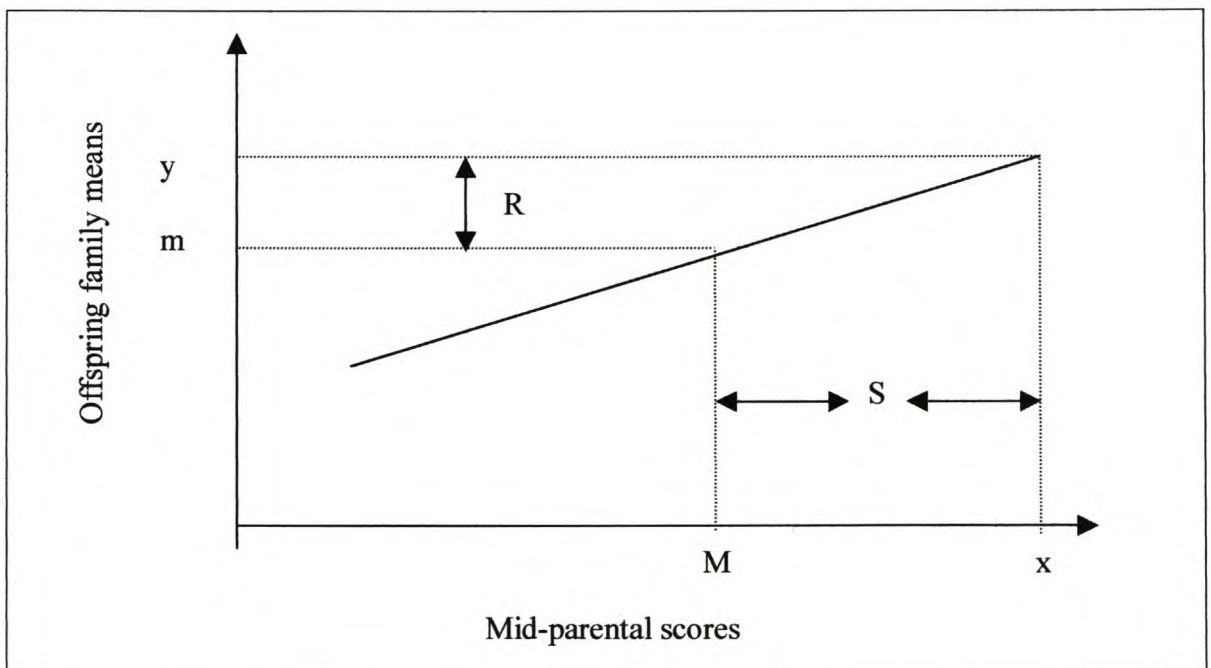


Fig 2.1 Predicting the response to selection. The relationship between the mean of the offspring (m) and that of their mid-parents (M) to illustrate the concept of selection differential (S) and the response to selection (R) (After Kearsey and Pooni, 1996).

The use of selection in tree breeding can be illustrated by considering a classical example of a pair of randomly mating selected parents. The regression of the offspring family means mid-parental values is an estimate of the narrow sense heritability. The resulting model, as illustrated by Kearsley and Pooni, (1996) is as shown in Fig 2.1.

The slope of the regression is the narrow-sense heritability, h^2 . The mean deviation of the selected is the selection differential, S . The predicted response to selection, R , is the deviation of offspring means. Thus if the population mean, the heritability, and the selection differential are known, it is possible to predict the response R .

It can be shown that

$$R=h^2S$$

The most common situation in tree improvement is that a trait is chosen and then scored for its performance, from individuals within a randomly mating population. A more general prediction formula for selection response is obtained using the properties of a normal distribution. Provided the trait is normally distributed, as stated earlier, the selection differential (S) and the point of truncation (t) will vary according to Fig 2.2. Truncation selection means that individuals are selected strictly in order of merit as observed from their phenotypic values and as such all individuals selected (p) will be superior to those left out from the selection (Falconer, 1981). It is clear from Fig 2.2 that the selection differential increases with decrease in the proportion (p) selected, or as the truncation point moves to the right.

For a normal distribution with mean =0 and variance=1, tables can be made from the formula of the curve giving values of the point of truncation (t) and the selection intensity, ($i =S/\sigma$) for given values of p . Thus from the generalized selection response

$$R=h^2S= ih^2\sigma$$

It is therefore possible to predict (R) for any given proportion p provided the heritability and the standard deviation of the trait is known. The truncation point (x) can also be determined from the tables of normal distribution for a given proportion, p , (Falconer, 1981).

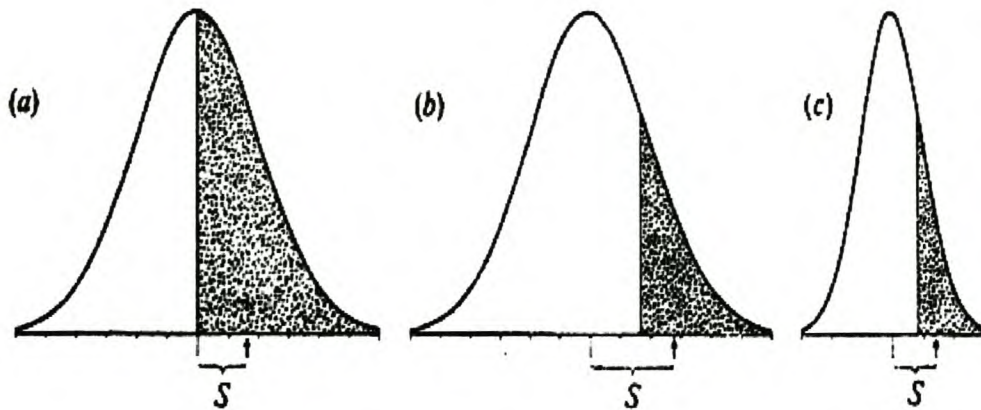


Fig 2.2 Diagrams to show how the selection differential, S depends on the proportion of the population selected and on the variability, of a normally distributed character. All the individuals in the stippled areas, beyond the point of truncation, are selected. (After Falconer, (1981).

As an illustration of these principles, let us use a typical example where tree diameter is measured in a trial. First, a sample estimate is obtained for the mean and the standard deviation for field data. Secondly, the truncation value (t) is read for the proportion (p), which the breeder has decided to select. Thirdly, trees with diameter bigger than mean (\bar{x}) i.e. $\bar{x} + t$ are selected as one proceeds with the measurements.

As summed up in Fig 2.3, it can be noted that the mean of the selected progeny can never exceed that of the selected parents. The tendency will be a regression of the mean of the preceding generation towards that of the base population i.e. in the first generation, F_1 , will tend to have a lower family mean compared to F_2 , and the latter will have a lower family mean than F_3 etc.

Clearly, the mean phenotypic value of the selected parents is bound to be superior to that of their siblings, hence the justification for continued improvement of choice trait(s).

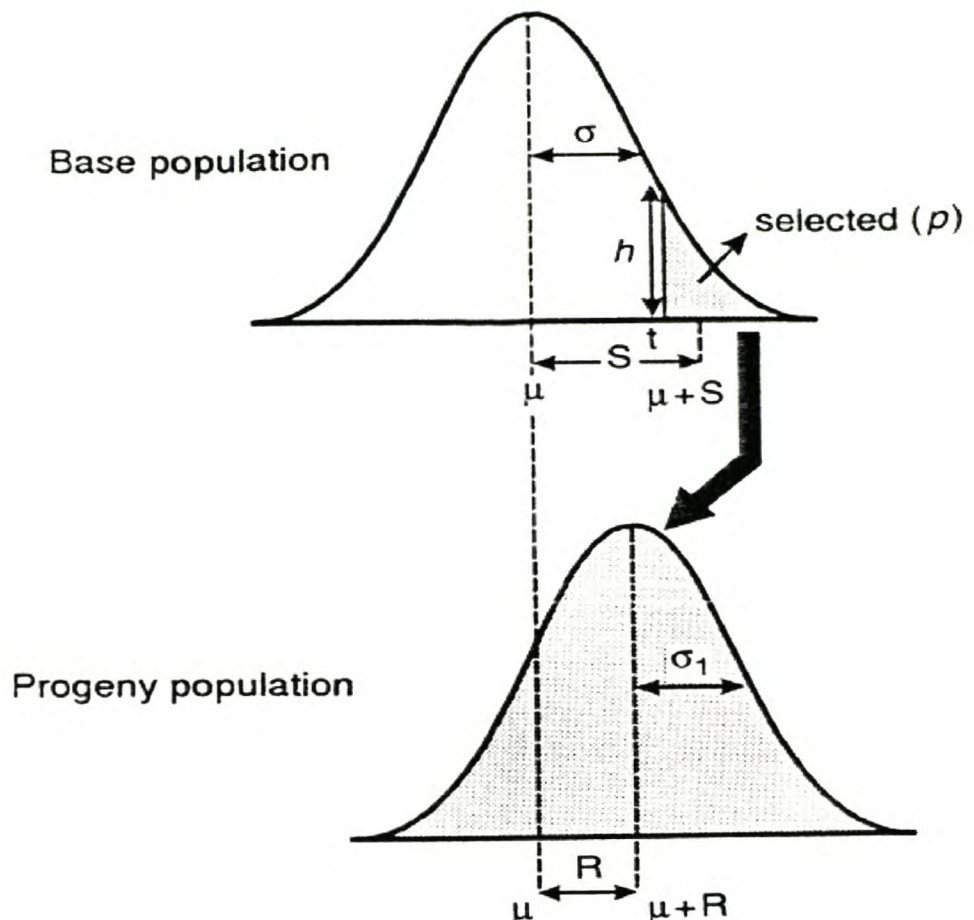


Fig 2.3 Predicting response to mass selection. The mean of the offspring ($\mu+R$) is always less than that of selected parents (p) – a proportion of the best performers (based on trait under consideration). Thus continued selection for a trait can only be expected to show regression towards the mean of the selected parents. Note that μ = mean σ = standard deviation t = point of truncation h = heritability estimate (After Kearsey and Pooni, 1996).

Detailed presentations of procedures and definitions of concepts are found in many standard quantitative genetics textbooks, e.g. Falconer (1981).

Several selection methods are briefly reviewed below, with some highlights of their relative effectiveness in plant breeding.

- 1) Mass (*individual*) selection is often the most widely used method of selection. It involves the selection of individuals from a randomly mating population based on their phenotypic values. Thus, mass selection is only used in the early stages of a

tree breeding programme when pedigree information is not available, e.g., plantations or natural populations (Zobel and Talbert, 1984).

- 2) Sib selection involves choosing parents on the basis of the performance of their offspring and not their own performance (Zobel and Talbert, 1984). The process of sib selection can be illustrated in a flowchart shown (Fig 2.4). Sib-selection is therefore based on the means of the test families. The remnant seed is what is used to continue the cycle. The seed selection for successive generation is dependent on the test family means.

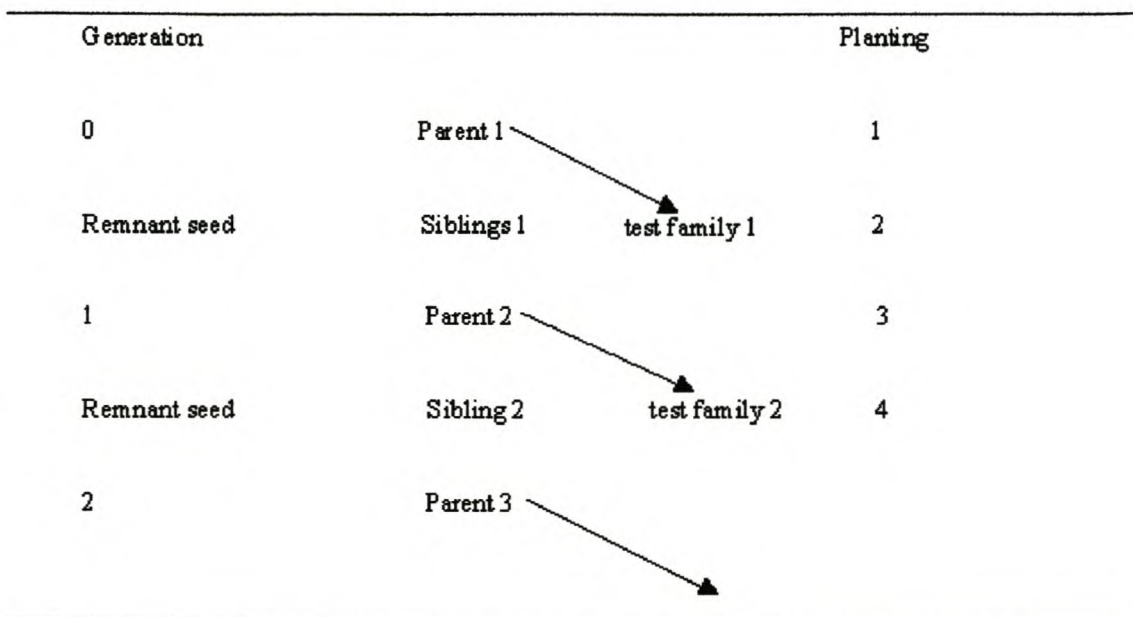


Fig 2.4 A flowchart illustrating the concept of sib selection. The test families may be half- sibs, full sibs, clones or selfs. Seed selection for successive generations is based on family tests.

This selection method is rarely used in forestry though it may be employed in cases where destructive sampling must be used to make measurements (Zobel and Talbert, 1984).

- 3) Family selection involves choosing the entire family based on average phenotypic values of traits under consideration. It is, however, rarely used in forestry (Zobel and Talbert, 1984) though it has some advantages over mass selection especially when the trait being selected has a low heritability. For example, family means tends to have less environmental variance and as such variation is largely genetic which leads to better genetic response, especially when the family size is large, as

illustrated in Fig 2.5. The reason for its lack of popularity is probably because it has a tendency of narrowing the genetic base which causes inbreeding (since the entire family is discarded) (Zobel and Talbert, 1984).

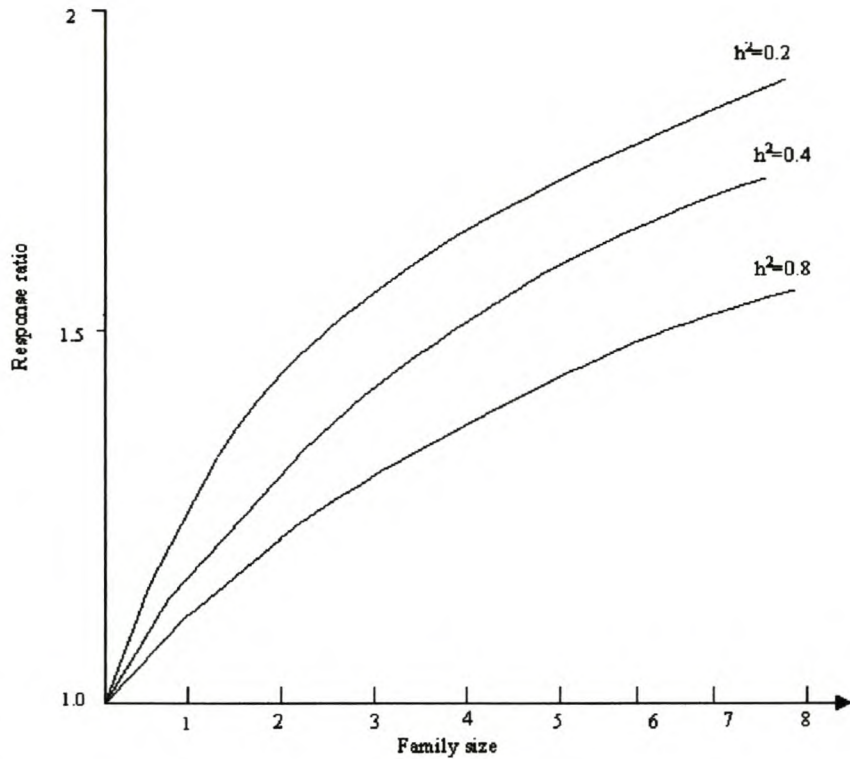


Fig 2.5 A hypothetical example of the response to family selection. Shown here as the ratio of individual selection for traits with different heritability (h^2). Note that the ratio for family size $n=1$ is equivalent to individual selection. More gains are realized when family selection is used compared to individual selection.

- 4) rogeny test selection is a type of selection based on the mean values of an individual's progeny. The means of the progenies are used to judge the breeding value of their parents. Progenies are families, usually half sibs and selection is made between them on the basis of family means (Falconer, 1981). Its advantage is that it gives direct and "precise" estimates of the breeding value of their parents. However, long breeding cycles arising from time of raising and testing of the progeny are a setback in terms of quick delivery of results (Zobel and Talbert, 1984).

- 5) Within family selection is when selection is based on the deviation of each individual from the mean value of the family to which it belongs. Individuals which far exceed their family mean are selected (Falconer, 1981). This method of selection is seldom used in tree improvement (Zobel and Talbert, 1984).
- 6) Family plus within family selection involves a preliminary selection based on the family means followed by selection of individuals within families. Thus, the best of families and best of individuals are selected in this method (Zobel and Talbert, 1984).

Other important types of trait selection are: tandem selection, independent culling, recurrent selection, and index selection. These are described at length in many quantitative analysis textbooks (Falconer, 1981; Namkoong, 1981; Wricke and Weber, 1986; and Bos and Caligari, 1996).

The duration for continued selection for a particular trait is likely to last for several generations provided a large effective population size is maintained and that an optimum selection intensity is used. High selection intensity together with high h^2 may result in an abrupt end to the response to selection, it may occur even in the first generation especially when the population size is small. Kearsey and Pooni (1996) illustrated (Fig 2.6) what may happen in the event of intense and mild selection. The reason for this behaviour is that genes interact and as such selection should be viewed as a holistic affair, with careful observation of negative genetic correlation which can undermine the objectives of the breeding programme.

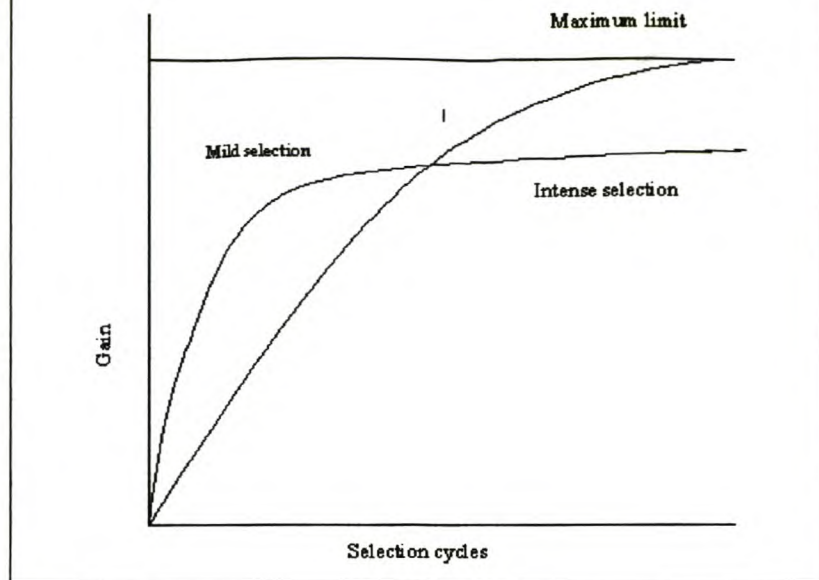


Fig 2.6 The likely long-term effects of intensive versus mild selection. Kearsey and Pooni, (1996).

2.2. Selection of traits for tree improvement

Manipulation of genes for specific objectives can be effected in most traits –e.g. height, diameter, stem form and branch morphology. Expression of wood quality, stem fruiting characteristics, resistance to diseases and insect pests and response to soil and climatic conditions can be altered genetically (Namkoong *et al*, 1971). Important traits for most of the common end uses are similar, although the order of importance differs depending on the needs of the organization concerned. Errors in tree breeding are very costly, correcting them often takes a long time owing to the long breeding cycles. It is therefore important to maintain a high standard from the onset of selection (Namkoong *et al*, 1980).

Whereas silviculture tactics can often be altered in the middle of a rotation, tree genes are fixed for life. Reducing breeding cycles and making accurate predictions of genetic gains is one of the breeder's main objectives.

The time delay between grafting and flower induction and the time required for progeny testing contributes to the long breeding cycles (van Buijtenen and Lowe, 1989). Early selection procedures have been applied as a means of reducing high costs associated with field testing in operational breeding programmes. Important mature characteristics, can be

evaluated at a juvenile age and juvenile characteristics that are correlated with an important mature trait are candidates for early testing procedures (van Buijtenen and Lowe, 1989). The determination of optimum ages for selection of traits is also critical if accurate predictions of genetic parameters (Magnussen, 1989) is to be assured, and for it to compliment juvenile trait selection.

The forest tree breeder's principal advantage is that in a situation where forest trees species have not been subjected to heavy selection for fitness in a plantation environment, it is easy to select for genetic gains by almost any method for most traits of commercial importance (Namkoong, 1981).

2.2.1. Traits for tree growth

Genetic, environmental and other effects influence tree growth. Tree breeders fix desirable genes as a means of influencing tree growth behaviour. Silviculturalists may endeavor to control the tree growth behaviour, for example through intensive management but this has limitations. Broader understanding of tree breeding is required for enhanced management through the manipulation of genes.

Fast growing trees provide a quicker return on investment. In large trees the loss in conversion is also reduced (Warmald, 1975). Traits for height and diameter are not necessarily inherited in the same manner. Each may be affected by anatomical or physiological traits (also heritable) such as needle characteristics, rooting habit, or photosynthetic efficiency (Stephenson and Snyder, 1969). Thus, breeding for fast growing trees requires careful planning of matings that will transmit individual traits that promote growth.

A low crown: bole ratio is desirable for tree growth. The crown must be deep, narrow, and conical with apical dominance. The advantage of this feature is that the efficiency of photosynthetic activity enhanced. Consequently, this feature tends to have a positive influence on other i.e. diameter and height (Barnes and Gibson, 1984).

2.2.2. *Stem form and branching habit and its relation to wood quality*

An ideal tree must have no limbs. This is however not practical since the tree limbs carry the leaves which are there to ensure nutrient supply (made available through photosynthetic activity on them) required for tree growth. Clearly, any choice for selecting limb size must not compromise the volume production. The size of limbs and associated knots are the major factors that determine the quality of the resultant timber in most pine species.

The knot size varies with the diameter of the branch and the branch angle in the manner illustrated in Fig 2.7. It can be noted that branches with acute angles tend to cover more knot area as contrasted by (a) and (c) and (b) and (d) in these diagrams. Smaller branches that have an acute angle are however preferred to larger branches that have wider angles. The reason being that the former occupies a smaller surface area compared to the latter. This consideration is well catered for in the method used in this study as it will be observed in the next two chapters where the tree index is calculated on the relation between the tree volume, the branch angle and the branch size. For example, Zobel and van Buijtenen (1989) noted that *Pinus patula*, *P. montezumae*, *P. radiata* and *P. kesiya* whose knots and limbs were large influenced the quality of timber significantly whereas *P. elliotii* and *P. caribaea* with knots finely distributed had minimal influence on timber qualities.

The shape of a tree, its straightness, the arrangement and size of branches, and the size and the number of knots within its trunk all help to determine the tree architecture. These are particularly important when the product is lumber, veneer, poles or piling (Stephenson and Snyder, 1969). Though these traits are affected by the environment there exists an opportunity for the breeder to genetically manipulate them because genetic correlation exists even for traits with average heritability.

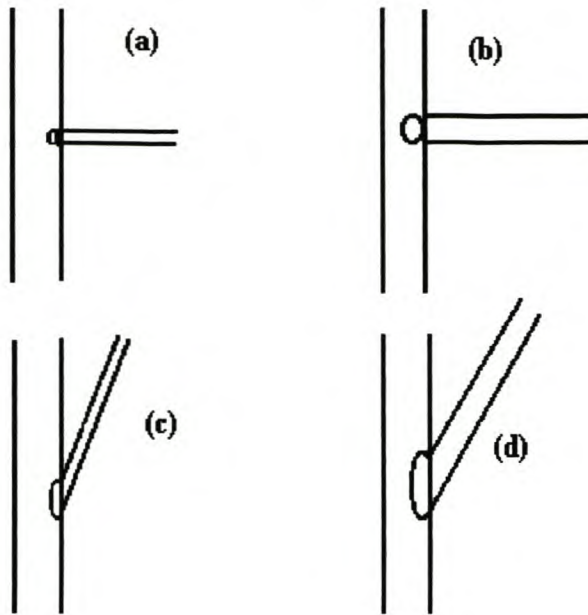


Fig 2.7 An illustration of how the branch angle and the size of the branches can affect the underlying stem quality. It can be noted that smaller and flat branches result in smaller knots (a) and relatively larger knots for same sized branches with steeper angle (c). Large branches with flatter angles are associated with relatively smaller knots compared to large and acute branches as shown in (b) and (d) respectively.

Big limbs are a problem to all the common end uses of timber. They account for high costs incurred during sawing, chipping, and slicing. The quality of timber is largely influenced by the knot size. The knot is a weak point in lumber used where strength is needed. It is characterized by a concentration of undesirable wood that does not suit most purposes, even pulping (Stephenson and Snyder, 1969).

Selecting for smaller limbs without adversely affecting growth might be the most effective strategy. However, the complexity in dealing with tree populations, which is essentially similar to a wild population with highly variable traits, is that when one breeds for a particular trait one does so with the risk of either eliminating desirable alleles or suppressing other valuable traits. For example, Stephenson and Snyder (1969) found that tree limbs are moderately inherited and that selecting for trees with smaller limbs at more or less right angles is ideal for good timber quality.

Stem straightness is also regarded as one of the most important characteristics of trees that affect stem quality. Stem quality has a direct influence on timber quality irrespective of

the end uses (Shelbourne, 1967, 1969). Selecting for stem form was described the most effective way of improving the timber properties in fast growing conifers compared to selecting for the intrinsic wood properties (Shelbourne, 1969) which are difficult (i.e. chemical analysis, determination of fibre length and angle), time consuming and expensive (Birks and Barnes, 1990).

In general stem straightness has a high heritability and, as described by Bannister (1966), it can readily be selected for and its response can be achieved even through simple artificial procedures, such as mass selection. It was also observed that breeding for trees that were predominantly multinodeal or predominantly uninodeal gave rise to trees that had an improved bole. Highly multinodeal trees were found to be associated with trees which had smaller branches and bigger volume whereas in the case of uninodeal trees the branches were larger and stems smaller (Shelbourne et al, 1972).

Studies on variation and heritability for growth characteristics among Sycamore progeny by Jourdain and Olson (1983) on the other hand found that selecting for good crown form could be detrimental to diameter growth, while selecting for diameter lead to trees with larger and more fastigate crowns. An analysis of the relationship between growth rate and crown form by use of phenotypic and genotypic correlation by Jourdain and Olson (1983) showed that a negative relationship existed between live crown characteristics and the diameter growth rate. Genetic correlation indicated that direct selection for diameter growth rate would result in trees with smaller crowns and more acute angles. Selection for flatter branch angles to potentially improve wood quality was not a recommendation due to the reduction in the diameter growth rate. However, selecting for fewer branches appeared to be more favourable for height growth and flatter branch angles.

Tests with pine and sweetgum indicated a wide genetic variation in these characteristics, which suggests that it is likely to breed for them without sacrificing growth (Wilcox, 1970). The branch characteristics on inherent variation in South Mississippi sweetgum suggest that tree form heritability is moderately high. Progenies differed significantly in heritabilities for branch angle, diameter, and length. The branch angle was the most heritable (0.9), diameter had a moderate heritability of 0.38, and the length of branches had a low heritability of 0.2. Again, tree form was found to be under stronger genetic control

than either height or diameter. The high value of the branch angle suggests that genetic improvement through selection was possible.

Subjective assessment of stem and branch quality is now receiving attention because it is cost effective compared to objective assessment which takes a long time when measuring the branching and form traits (Haapanen *et al*, 1997). Subjective assessments were done for straightness, branching and an overall score, whilst the objective assessments included height, diameter, crown width, density, branch diameter, branch angle and branch number. They discovered that subjective assessment tends to cover more traits that are readily scored and incorporated into a selection index. They concluded that the subjective assessments provided an effective means of estimating heritability. Moreover, the scored traits showed favourable relationship with the tree height and stem diameter. These had a close interrelationship with branch diameter. The results also shed some light on the possibility of adopting subjective scoring to ease the high costs of taking the measurements (Haapanen *et al*, 1997). The study also found that all traits related to tree size (i.e. height, diameter, crown width and branch diameter) correlated very positively in *Pinus sylvestris*. The crown form was found to have a strong positive genetic correlation to height and that diameter was moderately correlated. Stem diameter was positively correlated to branch diameter whilst angle was the only trait which showed a negative correlation.

Inheritance of wood properties (i.e. wood specific gravity and fibre length) is very strong and can be readily addressed within the framework of form quality (Zobel and Talbert, 1984). Limb characteristics are more strongly influenced by the environment compared to straightness, but there is enough genetic control to improve these traits through selection. The wood specific gravity or wood density is by far the most important wood quality characteristic for nearly all products (Zobel and Talbert, 1984). Breeding for these characteristics in hardwoods is more complicated than in softwoods because the latter is also largely influenced by additive gene effect and the former is influenced by non-additive gene as well as additive gene effects (van Wyk, 1976).

Branch size, branch angle and stem straightness are the key factors that need to be controlled for better stem quality which impacts directly on the stem quality. Large knot size is associated with reaction wood, which is characterized by abnormal wood formation, which affect the strength of soft boards and plywood. In the pulp industry the reaction

wood is associated with low cellulose and high lignin content, which is unacceptable for pulp production. Reaction wood is the wood that is formed when a tree leans and its function is to help straighten the tree (Zobel and Talbert, 1984). In hardwoods it is referred to as tension wood and in softwoods it is called compression wood.

Tree breeding can effect considerable improvement in morphological characteristics of the tree by simple visual phenotypic selection whereas selection for the intrinsic wood properties is difficult and often depends on the latter (Wilcox, 1978). Stem quality is an important determinant of timber quality whether wood is utilized as lumber or in some reconstituted form such as paper. It is said that breeding for intrinsic properties without due consideration of the stem quality can undermine any progress when breeding for good timber quality (Zobel and Talbert, 1984).

The use of quality traits to improve the wood properties may seem to be the most cost-effective way of improving wood quality through selection. However, some anomalies have been observed whereby a negative correlation was observed between growth traits and wood quality traits (Allen, 1978). While studying genotypic and phenotypic correlations between wood and tree characteristics in *P. elliotii* Allen (1978) observed selecting for height and diameter resulted in undesirable effects on the intrinsic wood properties i.e. spiral grain, microfibrillar angle and latewood content. Selecting for stem form though did not result in any undesirable effects on the wood properties.

2.3 Methods of trait assessment

Assessment of tree traits is either done subjectively or objectively which may lead to qualitative and quantitative data respectively. Whereas objective assessments are simply obtained through measuring and counting or calculation from discretely measured parameters the subjective scores are based on deviations from the ideal tree. As defined by Keiding *et al* (1984) and also Barnes and Gibson (1984) an ideal tree is one that is healthy, vigorously growing with a straight, cylindrical and clean bole, a stem persisting to the top of the crown and light, spreading branches, with angles around 90 degrees. A high score is therefore awarded to a characteric if and only if it conforms to the ideal tree. For example if the score is between 1-6, and the trait under investigation is the branching habit, then 6 points would go to the tree with the small, flat and evenly spread branches.

Barnes and Gibson (1984) suggested five groups for which assessments can be based. These were stem, branches, crown, reproduction, and wood. Where both subjective and objective assessments are employable the assessments will be treated separately in this section.

2.3.1. Stem characteristics

2.3.1.1 Height

Tree height assessment is cumulative and can be measured any time. It can be measured either directly by use of measuring rods or indirectly by use of a hypsometer. It is the most reliable measured parameter (especially when rods are used) though factors such as stem lean may cause some errors (Phillip, 1983). However, it is difficult to employ on larger trees, as this would require climbing. This is a useful trait to measure because, as observed by Shelbourne *et al* (1972), it has a fairly good heritability.

2.3.1.2. Diameter

Like height the diameter is simple to measure and is usually taken at breast height. It is measured with calipers or diameter tapes. Special optical instruments are also in use. It may be measured for yearly growth by use of an increment borer which shows the tree rings. The environment affects diameter at breast height more than it affects height (Barnes and Gibson, 1984).

2.3.1.3. Bark thickness

The bark thickness can be measured readily without damaging the stem e.g. with the Swedish bark gauge (Phillip, 1983). This is variable in tropical trees (especially when trees are still young) and is easily assessed at breast height (Barnes and Gibson, 1984).

2.3.1.4. Forking

Counting the number of times in which the tree forks can be readily done as a means of establishing the frequency of forking. The level of forking can be assessed subjectively,

for example if forking is found at the top, then a higher score is given and a lower score if forking is very low, because this is a deviation from the ideal tree.

Its prevalence in the offspring of certain mating indicates inherited susceptibility to undesirable growth (Stephenson and Snyder, 1969). The frequency and level of bifurcation and multiple stem production is evaluated (Barnes and Gibson, 1984) because they invite breakage by wind, which may lead to insect attack.

2.3.1.5. *Straightness*

Its influence on stem quality, timber quality and wood quality gives it a higher priority in stem form assessment.

a) Objective assessment

Quantitative optical instruments are used, though seldom.

b) Subjective assessment

This type of assessment is most widely used. Barnes and Gibson (1984) noted subjective assessment from one angle with allocation to as few as three classes. Subjective scores used vary; scoring from 1 up to 9 has been used. For example, a 9 point system was used for scoring international provenance trials of *Pinus kesiya* (Lauridsen *etal* 1987,1995) and it has been adopted in this study. The highest score is given to the ideal tree, a perfectly straight tree, and deviations are progressively given lower scores. A tree with excess spiral crooks in two planes, or a crook in one plane that will not allow a line from merchantable top to stump to stay within the confines of the bole is rejected (Zobel and Talbert, 1984).

Assessment is either done on the whole or part of the stem. If carried out on part of the stem it can be an absolute measure related to the utilization value (e.g. the basal six meter log which may contain as much as 90 % of the value of the tree, or a proportional value (e.g. to prune height) (Barnes and Gibson, 1984). The categories of stem straightness may be direct (Shelbourne, 1972) or indirect if some weighting for defect type or position is first applied (Barnes and Gibson, 1984).

2.3.1.6. *Circularity of the stem*

This trait can be assessed subjectively by giving scores or classes as with most of the subjectively assessed traits. This trait may be important because it is usually associated with traits such as small, flatter branches and multinodal branches. This is particularly true in exotic *P. patula* where the stem cylindricity and volume serve as a good guide during intuitive screening of plus-trees.

2.3.1.7. *Lean*

Lean is the angle of inclination from the perpendicular. Severe cyclones and windthrow could cause inclination.

2.3.2. *Branches*

The branch diameter, branch angle, number of branches, branch distribution, branch order, and branch malformation are the common morphological characteristics that are assessed. These features and stem straightness are the main factors that affect stem quality.

Whereas the term wood quality refers to the intrinsic properties of wood sampled in small, clear pieces, stem quality is an important determinant of timber quality whether wood is utilized as lumber or in any reconstituted form such as paper. According to Barnes and Gibson (1984) assessment of branching characteristics should be done early in the tree's life, usually not later than five years, before branch suppression, branch shed and pruning have obscured them. The justification for this is that knot size and distribution of branches are economically most significant on the basal log of the tree.

2.3.2.1. *Branch diameter*

a) Objective assessments

The branch diameter is usually taken at a point about 5 cm from the stem. A caliper is used to measure the diameter with a high degree of reliability. For trees that have a larger canopy, branches with less than 5 mm diameter may be left out as these have a minor

influence on the overall metabolic activity of the tree. Also, these would otherwise be eliminated when editing the data since be outliers.

b) Subjective assessments

Subjective assessment for branch diameter is used. Zobel and Talbert (1984) recommended three classes; these are compared against checks. Average diameter is given 0 points and 1 or 2 points are given to branches smaller than checks. In the current study 6 classes have been used as an assessment for branch size (see chapter 3).

2.3.2.2. *Branch angle*

a) Objective assessments

Several methods have been employed to measure the branch angle, but a large engineering protector may prove efficient. This trait may be measured without employing the more sophisticated devices that some workers have used. In this study, for example a simple 20cm protractor was used and it gave fairly reliable measurement of the branch angle. It is important, of course that the same person takes the measurements.

b) Subjective assessments

Branch angle is also measured subjectively, for example, Zobel and Talbert (1984) suggested three classes; the average branch angle was 0 points, flat branches were given either 1 or 2 points. The classes may be more, depending on the objectives e.g. six have been used in the current study (see section on materials and methods). Subjective assessment of branch angle is very easy especially because deviations from the stem are often similar for branches in the same whorl. For smaller trees there is less variation in the branch angle of the bigger whorls which in any case cover the bulk of the tree, making branch assessment fairly simple.

2.3.2.3. *Number of branches*

a) Objective assessment

A count of the branches is simple for trees at about 3 years of age such as in this study. Branch assessments can be achieved by marking whorls on a defined section of the tree stem.

b) Subjective assessment

Assessment could have five classes. For example, Haapanen, *et al* (1997) used five classes; 1 point was given to very few branches and 5 for very many branches. In this study branch coarseness (which could be likened to this trait) was scored between 1-6, one was given to a tree with highest coarseness tree and 6 was given to the tree with the least coarseness.

2.3.2.4. *Branch distribution*

This is assessed by means of counting the number of branches per whorl and the number of and spacing of whorls.

2.3.2.5. *Branch order*

The order of branching is variable at species and provenance level (Barnes and Gibson, 1984). Assessment is done at 1st, 2nd, 3rd, etc. order at various points in the crown. This trait is seldom included in most studies probably because of the high costs associated with the assessment of branch characteristics. However, an understanding of this trait, like any other trait, is useful to the breeder who can use that information i.e. correlation of traits, to improve other traits which may have economic value.

2.3.2.6. *Branch malformation*

Barnes and Gibson (1984) suggested that an assessment of this trait is necessary because it sometimes affects tropical pines. Indices are constructed and used to indicate the severity

of occurrence. This trait also receives little attention probably for the same reasons as above. However recording the frequency of malformation is useful in identifying possible family variation.

2.3.3. *Crown*

Crown characteristics influence the rate of site capture, photosynthetic efficiency, maximum basal area potential, the ability of the tree to respond to thinning, susceptibility to windthrow and, through shape, they influence the stem form (Barnes and Gibson, 1984).

2.3.3.1. Objective assessments

Measuring from the base of the live crown to the tip of the tree assesses crown depth. Crown width and symmetry becomes more difficult to assess and the measurements themselves become less meaningful when canopy is closed and competition sets in (Barnes and Gibson, 1984). Crown foliage includes counting cotyledon number, number per fascicle and density and needle colour.

2.3.3.2. Subjective assessments

Zobel and Talbert (1984) suggested that the tree being assessed should be compared against checks and scored on the bases of conformation, density of foliage, dominance and crown radius from 0-5 points depending on superiority.

2.4 Management decisions

The manager's decision depends on the value he attaches to wood grown in the improved stand (Namkoong *et al*, 1971). Selection is a key part of applied forest tree improvement programme, (Zobel and Talbert, 1984). Worthy of note is that gains through selection are dependent, from among others, selection intensity. For example, high selection intensity is often required in order to yield more gain from the selection process. However, some workers believe that a high selection intensity could lead to immediate fixing of desired genes at the expense of other mutually beneficial genes whose presence could warrant a sustained improvement over several breeding cycles. Again, a large effective population size is required for a sustained improvement through selection. A high selection intensity would result in low gains immediately after the first generation. Therefore mild selection is recommended for continued and sustained improvement through selection (Namkoong *et al* 1971).

Since selection is the first step of a breeding programme and is associated with huge expenditure most managers often get alarmed about the costs involved (Namkoong, *et al*, 1971). However, Zobel and Talbert (1984) argue that the costs of selection only cover a small fraction of the total costs of running a tree improvement programme.

A breeding programme should not be viewed only as confined to the improvement of traits. For example, a piece of land allocated for tree breeding can also act as an example of a well managed plantation which will ultimately fulfil timber requirements when felled. Another important contribution is that along with the improvement of tree characteristics, improved seed is made available for commercial plantings at a low cost.

Intensive culture (e.g. site preparation, weed control, fertilization, thinning and pruning) should not be undertaken without a sound genetic improvement programme. For example, breeding for pest resistance and survival could induce silvicultural investments in growth improvement (Namkoong, *et al*, 1971). Silvicultural methods of improving traits of some species are documented. For example, Bunn (1966) formulated a proposal of improving *P. radiata* quality traits through silviculture to ensure that tree breeding efforts cater for improvement that can not be achieved through silviculture.

A tree improvement programme must be flexible in order to accommodate changes in the socio-economic and environmental issues. The choice of a breeding programme must, therefore, be tailored to address the needs of individual organizations. The advantage, though, is that traits, which are selected for breeding, are similar for most of the common end uses. They differ only in the way they are prioritized (Namkoong, 1971).

The decision on whether one should choose fewer or many traits to select for in a breeding programme is tricky. It may appear sensible to choose fewer traits, and concentrate on them - provided they meet the requirements of the desired product - because of the advantages i.e. reduced costs and more gain through selection as opposed to covering more traits. As stated by Namkoong *et al* (1971) the addition of poorly chosen traits proportionately reduces the gains to be expected from the useful ones.

However, keeping the list of traits short and consistent in several generations has its own shortcomings. For example, Namkoong *et al*, (1971) noted the following:

- 1) Heritability which is a measure of the probable gains in individual traits per unit of selection effort, are unequal and for most traits unknown,
- 2) Traits are often genetically related. Sometimes, selection for gains in one trait, such as height growth, result in gains in another, such as the ability to withstand competition. It is important that managers must decide on whether to choose fewer traits and concentrate on them in successive generation for better gains or to choose a large number of traits and risk low gains, but with the assurance that no favourable gene combinations will be lost. The latter option will indeed involve extra costs.

2.4.1. Economic impact of stem and branching characteristics on forest productivity

2.4.1.1. Timber harvesting

Timber harvesting constitutes the extraction, loading and transportation of timber. The cost of debranching big limbs is very high because of the difficulty in debranching them. For example, Van Wyk (1977, 1978) noted that big limbs require cutting more than once to enable handling for stacking purposes. He further argues that the cost of delimiting

treetops in heavily branched logs often becomes so high that it can not be justified economically. Smaller branches are readily debranched and often undergo natural pruning by rotation age, which makes debranching even easier and cheaper. This implies that there will be less wear and tear in the case of mechanical debranching and low task rates where manual labour is used. Thus smaller limbs will lead to high productivity and minimal costs.

Stem straightness influences costs of logging. Straight stems allow for quick and easy stacking of logs for transportation and milling.

2.4.1.2. Sawtimber

As noted earlier crooked trees with large limbs are linked with abnormal compression or tension wood formation, which leads to a dramatic decline in the wood quality and productivity. Compression wood leads to distortion during drying and poor dimensional stability of timber used which is caused by longitudinal shrinkage (Shelbourne, 1969).

Large and acute branches lead to a reduced knotwood percentage, which directly impacts on productivity and costs. For example, the relative amount of knot free timber produced tends to decline, whilst the processing of the timber demands more attention.

Swept logs, i.e. logs which have curvature on part or the entire bole, cause a dramatic reduction in the conversion factor (Shelbourne, 1969). Such logs also produce shorter planks, which have a negative effect on the profitability of the forest. However, according to Shelbourne (1969) trees with smaller curvature may not have a pronounced effect on sawmilling processes.

Poor stem quality often leads to log pith wander. There are three main effects of pith wander. It may lead to 1) more timber degradation that occurs due to the presence of a pith. 2) More pieces resulting from a weak corewood. 3) Reduction of timber strength as a result of presence of cross grain (Shelbourne, 1969).

2.4.1.3. Veneer and plywoods

Straight cylindrical logs with an even distribution of annual rings, a straight pith and small knotty core are necessary for peeling, but where relatively short bolts are required, criteria for straightness need not be too strict. Plywood manufacturers will be concerned with compression wood with fluffy grain and high tangential shrinkage (Shelbourne, 1969).

2.4.1.4 Pulpwood

Debarking and chipping of trees with poor stem form is costly. According to Shelbourne (1969) when compression wood is found there is more fragmentation of tracheids which increases the proportion of fines and decreases yields. Compression wood has more serious effects on chemical than mechanical pulping and gives a lower yield of pulp with high lignin content, and poor strength properties because of its fibre dimensions and structure rather than chemical composition (Shelbourne, 1969). There is also a problem of uneven cooking of chips, which arises from the susceptibility of compression wood to acid cooking. The essence of this is that because of a quicker breakdown of the compression wood during acid cooking the resulting pulp will tend to be very weak.

CHAPTER 3

3.0 METHODOLOGY AND DATA ANALYSIS

3.1 Materials and Methods

3.1.1 Trial background

Twenty-five open pollinated families covering a range of tree diameters were selected from thirty-six families in a progeny trial at SAPPI - Usutu, Swaziland. The progeny trial was planted out in April 1995 in a relatively high yielding *Pinus patula* site characterized by relatively high rainfall (1093mm) and altitude (1420m).

Previously designated families selected were as follows:

up138, up136, z17, up143, up159, up172, z51
up146, up137, up156, up153, up165, up149, up142, z44 up155, up189
up175, up190, up186, up184, up154, up141, up144, up152

Each family constituted five randomly selected trees within the family. Thus, a total of 125 trees was used in this investigation.

The assessments were carried out when the trial was 36 months old. Stem form and branching assessments are usually carried out at this age because not only are the trees accessible for taking measurements but also because the trees would have not yet undergone natural pruning.

Trees were assessed subjectively and objectively. The assessment covered either the whole tree or a section. The latter was obtained by marking (using spray paint) the tree at 20% and 50% of the total tree height (Fig 3.1). Whorls that fell on the mark were regarded as part of the marked section, and as such, the corresponding branches and whorls were included in the assessment. Dead branches were not present in this trial owing to the age. Branches less than 5mm were not assessed as these are generally considered to have an insignificant contribution to the metabolic activity of the tree.

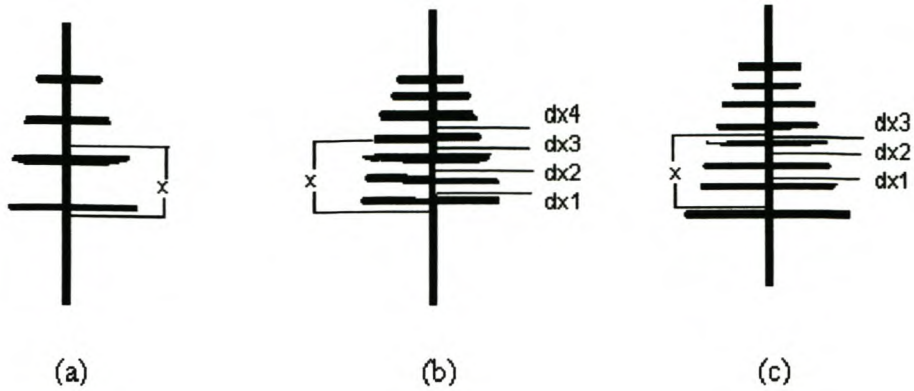


Fig 3.1 A schematic example of how the trees were marked. The section was marked at 20-50% of stem height - labeled x . The internode length measured was strictly above each whorl (b and c). A whorl which fell right on the marks was included in the assessment and the internode above (note that this will be above the mark and not below as illustrated in b and c) measured for length.

3.1.2 Procedures for trait assessment

A summary of traits assessed during this study is presented in Table 3.1. It is important to note that some of the measurements are on whole tree whilst some were taken on a section of the tree as explained in the last paragraph and illustrated in Fig 3.1.

Details of assessment procedures for each trait are given below:

- *Diameter*

This was measured by use of a diameter tape and trees were measured at breast height.

- *Height*

This was measured by use of tree measuring rods. This method is the most reliable and is readily recorded especially when trees are young as in the current study.

Table 3.1 A summary of the traits assessed (× indicates where assessment was done i.e. either on the whole tree or marked section of the tree)

Characteristic and abbreviations used	Assessment covering		Comments
	Whole tree	Section of the tree	
Diameter – DBH (d)	×		Measured in cm
Height(ht)	×		Measured in m
Stem straightness (str)	×		Scored from 1-9
Stem coarseness (coarse)	×		Scored from 1-6
Branch size (bs)	×		Scored from 1-6
Branch angle (ba)	×		Scored from 1-6
Number of branches (nb)	×		Counted
Number of whorls (nw)	×		Counted
Number of whorls (nwx)		×	Counted
Diameter of internodes(dx)		×	Measured in cm
Length of internodes (hx)		×	Measured in cm
Branch diameter (bdx)		×	Measured in mm
Branch angle (bax)		×	Measured using a protractor

- *Straightness*

Straightness was assessed by use of a scoring scale developed by Lauridsen *et al.* 1987 and 1995 (Fig 3.2). The assessment involves cross checking with trees that have already been assessed with new ones to ensure consistency.

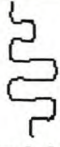








Unacceptable	<p>1 </p> <p>Completely crooked tree with several very serious faults</p>	<p>2 </p> <p>Better than 1</p>	<p>3 </p> <p>Better than 2</p>
Fair	<p>4 </p> <p>In principle almost straight stem, 1-2 serious faults (more serious than 5)</p>	<p>5 </p> <p>In principle almost straight stem, 1-2 serious faults</p>	<p>6 </p> <p>In principle almost straight stem, 1-2 more serious faults (better than 5)</p>
Straight	<p>7 </p> <p>Straight, with minor faults, also at lower stem</p>	<p>8 </p> <p>Straight, with minor faults at the top middle of stem</p>	<p>9 </p> <p>Straight stem, free of any faults</p>

Fig 3.2 Lauridsen stem form (straightness) scale (Lauridsen *et al.* 1987 and 1995).

- *Coarseness*

Coarseness, which describes the degree of “roughness”(size of branches combined with angle) of the branches on the stem was scored from extremely heavily coarse to light branching on each tree. The score is highest for the least coarse tree and decreases progressively as coarseness increases. The score ranges from 1-6. A heavily coarse tree, characterized by heavy branching and irregular internodes, was either given a score of 1 or 2. Moderately coarse trees were those that had an intermediate branching which were either showing regular and longer internodes (scored 4) or less regular and longer internodes (scored 3). A tree that had lighter branching and more regular and shorter internode length (multinodal) is what characterized a less coarse tree and was scored either 5 or 6.

- *Branch size*

This was obtained by scoring for branch size relative to the stem size. Trees that had a large branch to stem ratio were either scored 1 or 2. Branches that had an average branch size were scored 3 or 4. Trees that had a small branch to stem ratio were scored 5 or 6.

- *Branch angle*

Trees that had an acute angle were assigned the lowest score and the highest score was assigned to the flat and perpendicular branches (Fig 3.3).

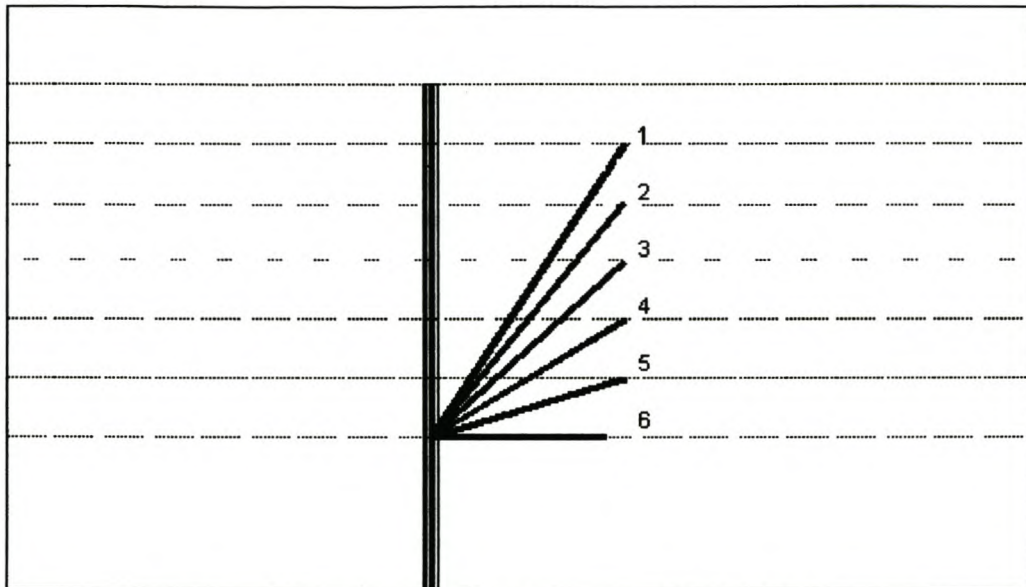


Fig 3.3 Schematic representation of how the branch angle was scored. The highest score was given to a tree which had an average branch angle which is widest and for steep angled trees the least score was given.

- *Number of branches*

All branches on the tree were counted and their number was then recorded. This is also a relatively simple and quick task when dealing with younger trees.

- *Number of whorls*

All whorls were counted on the whole tree and their number recorded. This process is even more readily accomplished than the above as *Pinus patula* has very distinct whorls.

- *Number of whorls on marked section*

Whorls in the marked section of the tree were counted and their number recorded.

- *Diameter of internodes above whorls*

The diameter was measured at the midpoint of every internode above all whorls on the marked section. If the top most whorl fell right on the fifty percent mark then the diameter above this whorl was measured even though it may lie just outside the mark.

- *Length of internodes*

For each whorl the corresponding length of internodes was taken. This is the length between the whorls from which the internode diameter was taken as stated in the last paragraph.

- *Branch diameter*

The diameter was measured for each branch on each whorl on the marked section, starting with the largest and progressing clockwise, giving them numbers. This was done for every whorl (also numbered from the lowest whorl (bottom) to the highest whorl (top) in the marked section (Fig 3.1). A caliper was used to measure the branch diameter (Plate 1).

- *Branch angle*

The angle was measured for each branch on which the diameter was measured ensuring that the branch angle corresponded to the diameter. A protractor was used to measure the angle as illustrated in Plate 2.

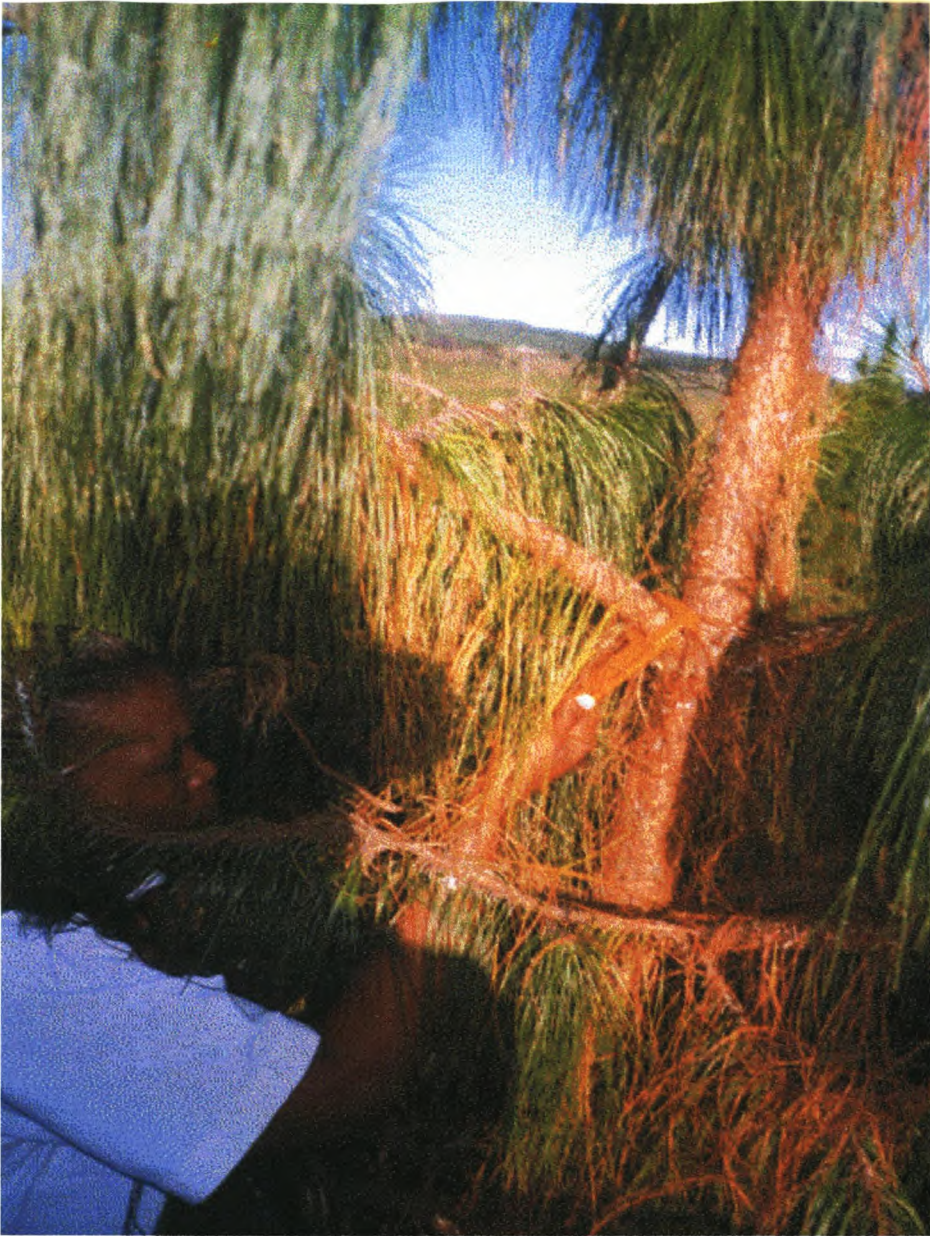


Plate 1. Measuring the diameter using a caliper is readily done in young trees.



Plate 2. Measuring the branch angle can be readily accomplished by use of a protractor. In this study a simple 20 cm protractor was used.

3.2 Data analysis

The bulk of the analysis was carried out using SAS procedures (SAS Institute, 1982 and 1987). In some instances EXCEL (Berk and Carey, 1998) was used, especially in the creation of graphic displays. Three approaches are executed in this step and this involve the following: A) Generation of indices and subsequent correlation and regression analysis, B) Repeatability and regressions , and C) Sample size estimation procedures.

From the raw data means for trees, for whorls, and for whorl and branch combinations were generated. These subsets of means were merged in various combinations and then analysed by the methods illustrated in Fig 3.4 and explained further as follows:

1) The raw data was edited by simply discarding those values of branch diameter that were intuitively regarded as odd. This was done to no more than five branch diameter recordings. These are instances where the branch was either too small or too big when one considers the general trend in the data for individual tree recordings. Simple processes such as eliminating those observations that fell way beyond the standard deviation were not employed though it could probably be effective. Otherwise, the data analysed is based on the assumption that the trees are normal. For example, a very large branch that could be a fork would not have been entered. Incidentally, in this study almost all the trees were normal and devoid of factors such as extremely small branches and/or forking.

2) A branch index was constructed for use in the generation of means (Fig 3.4) taking into account branch diameter and branch angle. The concepts used in the construction of the index are the following:

a) For the same sized tree (volume) with fixed number of branches, an index was required so that the bigger the branch diameter (bd) the smaller the index. Thus

$$\text{Index}_a = \text{Volume (V) / Branch diameter} \dots\dots\dots 1)$$

b) Similarly, for the same sized tree (volume) with fixed number of branches, the bigger the branch angle (ba) the bigger the index should be. Thus

$$\text{Index}_b = \text{Branch Angle / Volume} \dots\dots\dots 2)$$

c) Combining branch diameter and branch angle for a single branch index could be expressed as

$$\text{Index}_c = \text{Volume * ba / bd} \dots\dots\dots 3)$$

d) The combined tree index was calculated from equation

$$\text{Index} = V / \sum(\text{bdx}/\text{bax}) \text{ (Bredenkamp, } \textit{pers comm})$$

where bdx is the branch angle and bdx is the branch diameter of branches on the marked section of the tree.

The volume of the trees was calculated from a general volume formula

$$V = d^2 ht \text{ (Bredenkamp, } \textit{pers comm})$$

where d=DBH and ht=tree height.

The number of branches varies per tree and needs to be standardised. The equation then takes the form

$$\text{Index} = V / \sum((\text{bdx}/\text{bax})/n)$$

The validity of the proposed equation was tested through simulations. A sample of the procedure adopted is presented in Appendix 3. The assumption made was that the number of branches was fixed (24 branches). The simulations involved the calculation of the indices for a range of diameters, heights, branch diameters and branch angles. It can be seen from the interpretation given in Appendix 1 that there is logic in the application of the index formula.

Intermediate entries were made to cover all the likely combinations of volume, branch diameter and angle. It was found that the relationship of the volume, branch diameter and branch angle assumed in this equation, gave consistent indices. For example, an ideal tree with flat branch angles, relatively small branches and a large volume had the highest index, and the lowest index was obtained for a small tree with large branches and acute angles.

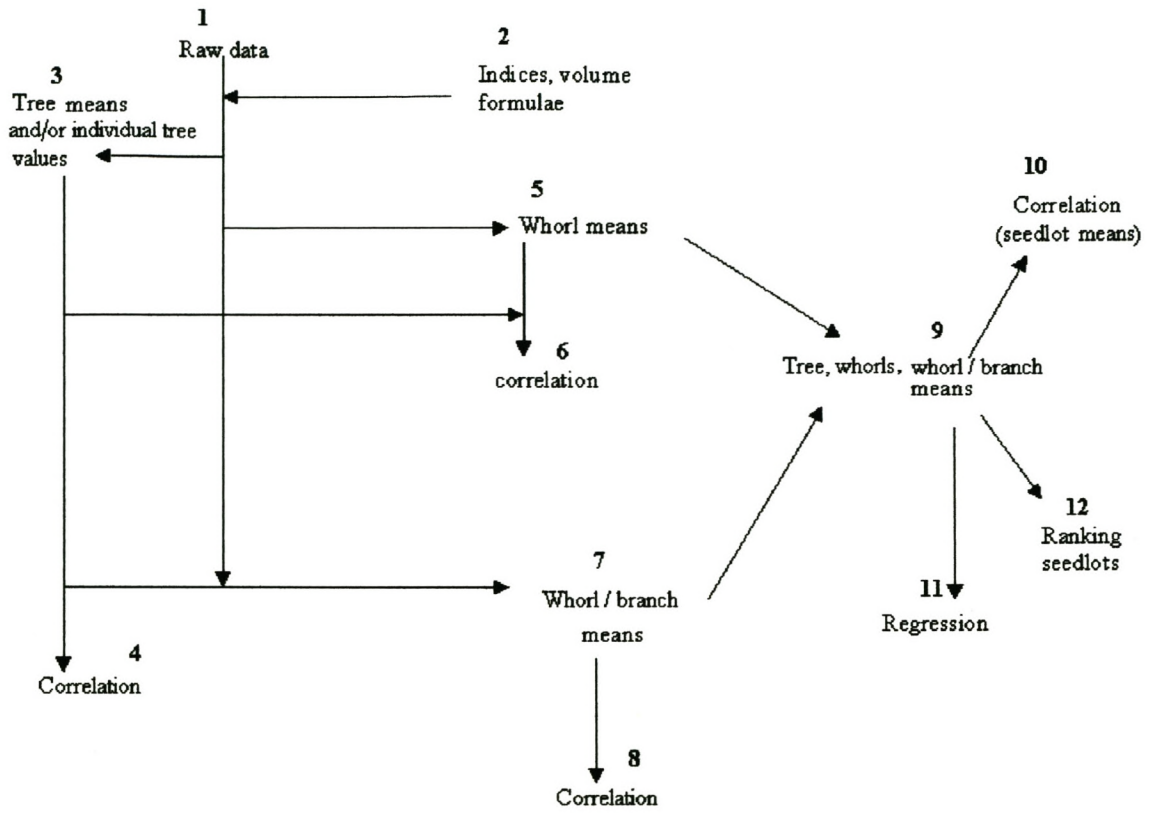


Fig 3.4 Flowchart representing the main processes of data analysis followed in this study.

- 3) Tree means were calculated for;
- number of whorls on the marked section (nwx)
 - internode length (hx)
 - internode diameters (dx)
 - branch diameters (bdx)
 - branch angles (bax)

These were merged with individual tree values for:

- diameter-DBH (d)
- height (ht)
- straightness(strt)
- coarseness score(coarse)
- branch size score (bs)
- branch angle score(ba)
- number of branches (nb)
- number of whorls (nw)
- overall score (score) i.e. the average of the sum of straightness, coarseness, branch size and branch angle
- index = $V / \sum(bdx/bax)/n$.

Note that the divisor in the index formula is calculated as a mean, $\sum(bdx/bax)/n$, to ensure that the assumption of a fixed number of branches (n) used in the simulations, is considered. Again, as will be noted later, the whorl indices and the whorl and branch combination indices can be more logically calculated from means when adopting this formula. It can also be shown that this modification will not affect the trend observed in the simulations made earlier, since this would be equivalent to dividing the indices by twenty-four branches (n).

- 4) A correlation matrix (Pearson correlation) for all the variables listed in the previous step was constructed.
- 5) Whorl means were generated for trees. Variables in this case were

- internode length
- internode diameter
- branch diameter
- branch angle
- and index.

Thus, for whorls 1, 2, 3, and 4 each of the variables just listed were generated. In addition, data from combinations of whorls i.e. avg (whorl 1 +whorl 2), avg (whorl 1 + whorl 2 +whorl 3), avg (whorl 4 +whorl 5 +whorl 6) were generated. A correlation analysis was carried out for the whorl variables.

The whorl variables are abbreviated such that the variable is followed by the whorl number, e.g., for the variable internode length in the 1st whorl the abbreviation hx1 was used. In the event of averages of whorls the whorls involved follow the variable name, e.g., for the variable internode length for whorl 1, 2 and 3 average the abbreviation would be hx123.

- 6) The data generated in step 5 (only the indices) were merged with the tree means indices and correlated. A typical format of the merged data was then as follows:

Tree no.	Tree means	Whorl 1 Means	Whorl 2 means	Whorl 3 means	Avg(whorl1, 2) means

Note that:

- a) A complete table will show whorl 1-4. Whorl averages were calculated for whorl 1 + whorl 2, whorl 1+ whorl 2 + whorl 3 and whorl 4 + whorl 5 + whorl 6. Thus, a complete table would have means for four whorls, and the additional three data combinations.

- b) The means for each tree, whorl, and / or whorl averages would therefore constitute the five variables namely the internode length, diameter of internodes, branch diameter and branch angle and index as listed in step 5.
- c) Whorl indices are abbreviated as follows:

whorl 1, whorl 2 whorl 3 and whorl 4 were abbreviated as index1, index2, index3 and index4, respectively.

Means of whorl 1 and 2, whorl 1, 2 and 3 and whorl 4, 5, 6 were abbreviated as index12, index123 and index456 respectively.

- 7) For whorl and branch combinations, subsets of data generated are shown in the following matrix

	Branch1	Branch 2	Branch3	Branch 4
Whorl1	Index11	Indexb12	Index13	Index14
Whorl2	Index21	Index22	Index23	Index24
Whorl3	Index31	Index32	Index33	Index34
Whorl4	Index41	Index32	Index43	Index44

Note that:

- a) With the exception of whorl 1 branch 2 (where the abbreviation is indexb12), the abbreviation for whorl and branch combinations is given such that the whorl number comes first and is followed by the branch number, e.g., Whorl1 Branch 1 is designated “Index11”. The reason why Whorl 1 Branch 2 was given a different abbreviation is that Index12 was given as an abbreviation for the average index of Whorl 1 and 2 as noted earlier.
- b) As stated in Chapter 3, it must be remembered that the first whorl is the lowest whorl on the marked section of the tree. The first branch is the largest branch in any given whorl. Thus Index11 and Index21 refer to the largest branch in the 1st whorl and the largest branch in the 2nd whorl respectively. Similarly, Index22 and Index 32 is an abbreviation for the 2nd largest branch in the 2nd whorl and the 2nd largest branch in the

3rd whorl respectively. This would be true for all instances *except* in the case cited in (a) above.

Means of the following whorls were also generated in this step and these are:

	(Abbr)
Whorl 1 branch1+2	indexbw
Whorl 1 branch1+2+3	indexbwa
Whorl 1 branch1+2+3 +4	indexbwb
Whorl 2 branch1+2	indexbwc
Whorl 2 branch1+2+3	indexbwd
Whorl1 branch1 and whorl2 branch 1	indexbwe
Whorl1 branch 1+2 and whorl 2 branch 1+2	indexbwf

- 8) Variables generated in step 7 were merged with the tree means and correlated.
- 9) The data sets in steps 5 and 7 were merged.
- 10) A correlation analysis based on seedlot means was conducted for variables generated from step 9.
- 11) A regression analysis was carried out for tree mean values with each of the variables in step 6 and some variables in step 7 and linear models formulated. A summary of the coefficient of determination (R^2) was prepared to identify the best models. In the analysis the assumption of linearity of the model was made. Studentized residuals were used to identify outliers (Appendix 4 and 5). The outliers could also be detected from the scatter plots which can also be effectively used to identify outliers in instances where one or fewer observations are involved (Ott, 1993). To obtain the studentized residuals a SAS programme was first prepared. In the plot of studentized residuals, observations that fell beyond an absolute value greater than two were declared outliers (SAS institute, 1987). In other words a value < -2 or > 2 was deemed an outlier. Such values were then deleted before the regression analysis.

The models used for the regression analysis were as follows:

Model 1	$y = \beta_0 + \beta_1 \text{index1}$
Model 2	$y = \beta_0 + \beta_1 \text{index2}$
Model 3	$y = \beta_0 + \beta_1 \text{index12}$
Model 4	$y = \beta_0 + \beta_1 \text{index11}$
Model 5	$y = \beta_0 + \beta_1 \text{indexb12}$
Model 6	$y = \beta_0 + \beta_1 \text{index13}$
Model 7	$y = \beta_0 + \beta_1 \text{index21}$
Model 8	$y = \beta_0 + \beta_1 \text{index22}$
Model 9	$y = \beta_0 + \beta_1 \text{indexbw}$
Model 10	$y = \beta_0 + \beta_1 \text{indexbwa}$
Model 11	$y = \beta_0 + \beta_1 \text{indexbwb}$
Model 12	$y = \beta_0 + \beta_1 \text{indexbwc}$
Model 13	$y = \beta_0 + \beta_1 \text{indexbwd}$
Model 14	$y = \beta_0 + \beta_1 \text{indexbwe}$
Model 15	$y = \beta_0 + \beta_1 \text{indexbwf}$

Where y = the tree index.

- 12) The seedlot means were ranked using the different indices generated by applying the Student-Newman-Keuls (SNK) procedure for Multiple Means Comparison.

B) Repeatability and regressions

- (i) The second approach of investigating the optimum number of measurements is to apply the following formula:

$$n = ((z_{\sigma/2})^2 \sigma^2) / E^2 \quad \text{Ott and Longnecker, (2001)}$$

where n = sample size (i.e. number of measurements)

$z_{\sigma/2}$ = value for corresponding confidence interval (obtained from Tables)

E = Tolerable error / 2 (i.e. Width (W)/ 2)

σ^2 = the population variance (i.e. the square of the standard deviation)

- (ii) Subsets of means of the branch diameter are generated in the same way as in A) and a selection of subsets are used for a regression analysis. Note that the only difference between this procedure and that in A) is that the measured values (i.e. branch diameter and branch angle) and not the index (based on calculations) are being used in the regressions.

C) Sample size estimation procedures.

The third procedure applied in the data analysis to determine the optimum number of measurements needed for the branch diameter and the branch angle.

$$n = ((z_{\sigma/2})^2 \sigma^2) / E^2$$

where n = sample size (i.e. number of measurements)

$z_{\sigma/2}$ = value for corresponding confidence interval (obtained from Tables)

E = Tolerable error / 2 (i.e. Width (W)/ 2)

σ^2 = the population variance (i.e. the square of the standard deviation)

The assumption used in this study was that the confidence level was 95% in both traits. The tolerable widths chosen for the branch angle and the branch diameter were 20° (i.e. E = W/2 = Mean ± 10 °) and 8mm respectively.

CHAPTER FOUR

4.0 RESULTS

From 4.1 – 4.9 the results are based on approach A) - Generation of indices and subsequent correlation and regression analysis. Sections 4.10 - 4.11 covers results on approach B) - Repeatability and regressions and Section 4.12 covers results on the Sample size estimation procedures.

4.1 Tree means and / or individual tree values.

The overall means and the tree values are presented in Table 4.1 and Table 4.2 respectively. The volume and the indices that are calculated for each tree and / or the overall means for each variable are also included.

Table 4.1 The overall mean, standard deviation and the range of tree variables assessed including those generated from them.

Variable	Units	N (obs)	Mean	Std Deviation	Min	Max	CV(%)
d	cm	125	6.29	1.206	3.5	9.3	19.2
ht	m	125	4.58	0.584	3.4	6	12.7
str	score (1-9)	125	6.63	1.020	2	9	
coarse	score (1-6)	125	2.69	1.130	1	6	
bs	score (1-6)	125	2.84	1.114	1	5	
ba	score (1-6)	125	3.64	1.042	1	6	
nb	counts	125	55.26	9.860	29	78	17.8
nw	counts	125	13.22	2.105	5	18	15.9
nwx	counts	505	4.03	0.860	2	6	21.3
hx	cm	505	30.69	5.711	18.0	46.3	18.0
dx	cm	505	5.29	0.963	2.9	7.9	18.2
bdx	mm	125	14.22	2.576	7.5	20.6	18.1
bax	degrees	125	67.86	6.388	47.1	85.9	9.4
vol	*10 ⁻⁴ m ³	125	194.96	92.422	42.9	486	47.4
score	score	125	3.95	0.752	2	6	
index	-	125	924.53	412.605	222.75	2546.72	44.6

It is evident from Table 4.1 that there is considerable amount of variation in the characteristics covered. The tree index for example, shows a large range with the lowest value at 222.75 and the highest at 2546.72. Similar observations can be made with the rest of the characteristics.

Table 4.2 List of individual tree values and means for all the variables assessed and those calculated from them.

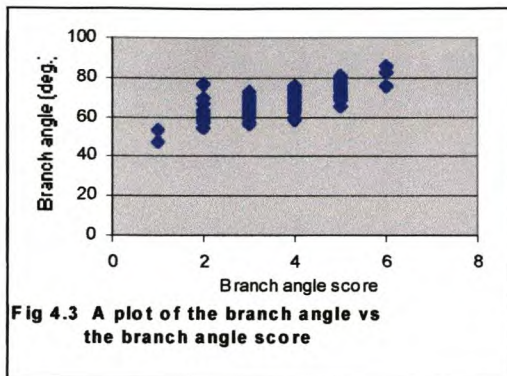
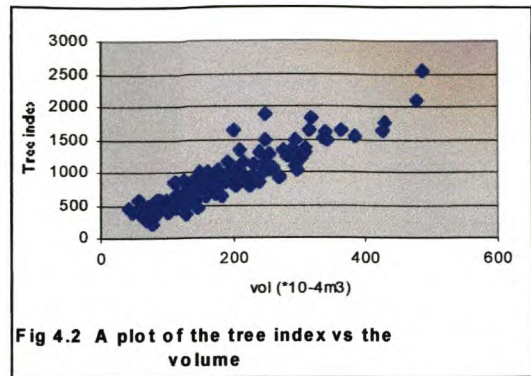
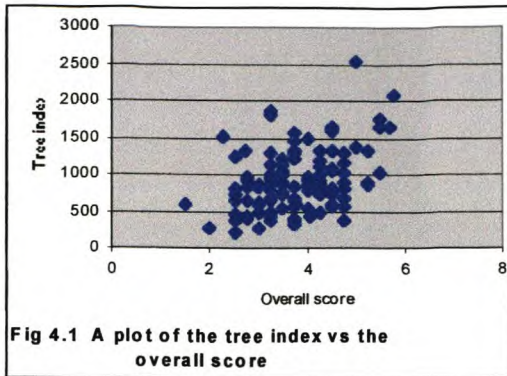
TN	SEEDLOT	INDIVIDUAL TREE VALUES										TREE MEANS				INDIVIDUAL TREE VALUES		
		D(cm)	HT(m)	STRT	COARSE	BS	BA	NB	NW	NWX	HX (cm)	DX (cm)	BDX (mm)	BAX (deg)	VOL (*10 ⁻⁴ m ³)	SCORE	INDEX	
1	up137	4.2	3.5	7	2	3	4	53	12	3	32.3	4.2	12.4	67.6	61.74	3.75	335.4	
2	up137	6.3	4.1	7	3	3	4	52	13	4	29.2	5.2	14.8	70.5	162.7	4	772.6	
3	up137	5.5	4.1	7	2	3	3	56	14	5	21.3	4.8	12.1	65	124	3.75	663.5	
4	up137	5.6	4.5	7	2	3	4	51	17	4	21	4.8	13.8	64	141.1	3.75	651.3	
5	up137	6	4.2	7	3	2	4	51	12	4	32.6	4.6	13.6	65.7	151.2	3.5	726.9	
6	up146	8.9	5.4	7	5	5	4	57	15	4	38.2	6.8	17.7	72.5	427.7	5.5	1752	
7	up146	7.4	5.4	7	3	2	2	55	13	5	34.2	5.9	17.2	60	295.7	3.5	1031	
8	up146	7.5	5.5	8	4	4	4	63	17	5	30.6	6.3	15.7	69.5	309.4	5	1367	
9	up146	6.2	4.1	7	1	2	2	44	15	6	18	5.1	11.4	62.7	157.6	3	863.1	
10	up146	8	5.3	7	3	4	4	52	12	4	39.7	6.5	14.4	68.1	339.2	4.5	1600	
11	up153	6.1	4.6	7	4	3	4	60	14	4	41.2	4.9	13.6	63.4	171.2	4.25	793.3	
12	up153	6.1	4.9	7	4	5	4	51	13	4	37.9	4.8	13.2	65.7	182.3	5.25	901.8	
13	up153	5.4	4.3	7	4	5	4	60	15	5	28	4.7	9.7	67.7	125.4	5.25	874.1	
14	up153	6.4	5.1	7	3	4	4	56	11	3	46.3	4.6	13.1	67.8	208.9	4.5	1078	
15	up153	5.7	5.1	7	4	4	4	59	14	4	40.3	4.7	12.9	63.5	165.7	4.75	812.5	
16	up156	6.9	4.4	7	4	5	5	54	15	4	30.3	5.2	12.3	78.3	209.5	5.25	1331	
17	up156	7	4.4	7	1	3	3	66	16	5	27.6	4.8	12.6	67.3	215.6	3.5	1148	
18	up156	5.5	4.3	7	1	2	4	48	15	4	33.2	5.2	17.4	66.4	130.1	3	496.6	
19	up156	7.3	4.8	7	4	4	4	56	13	3	35.6	5.2	15.8	64.3	255.8	4.75	1037	
20	up156	5.8	4.4	2	2	1	3	53	14	5	25.7	4.6	14.8	60.5	148	1.5	605.1	
21	up149	5.8	4.1	7	3	2	3	53	12	4	40.5	4.1	11.9	65	137.9	3.5	753.4	
22	up149	6.4	4.2	7	4	3	4	57	15	5	24.5	5.1	13	68.1	172	4.25	902.3	
23	up149	5	3.9	7	3	3	4	50	13	5	24.8	4.5	13.7	74.2	97.5	4	528.1	
24	up149	4.9	3.8	7	3	4	5	38	10	4	29.4	3.9	11.2	70	91.24	4.5	570.2	
25	up149	6.5	4.2	7	5	5	5	54	14	4	29.3	5.6	12.9	74	177.5	5.5	1018	
26	up165	6.8	5.3	7	3	4	4	65	13	3	41.7	6.1	15.3	66.4	245.1	4.5	1060	
27	up165	6.8	5.5	7	2	3	3	69	17	5	27.6	5.3	13.6	68.8	254.3	3.75	1287	
28	up165	6.7	5.1	7	2	4	3	58	17	4	33.4	5.3	15.7	64	228.9	4.25	930.3	
29	up165	6.2	5.1	8	2	2	5	60	17	6	30.4	5.6	14.6	74.7	196	3.5	997.8	
30	up165	9	6	7	5	4	5	78	18	6	28.6	7.3	14.7	77.4	486	5	2547	
31	up189	3.6	3.8	7	2	3	3	46	13	3	31.9	3.3	9.1	71	49.25	3.75	384.2	
32	up189	4.7	4.4	7	2	2	2	47	11	3	38.1	4.2	13.1	66.3	97.2	3.25	489.9	
33	up189	6.6	4.8	7	4	4	4	69	17	5	26	4.8	14.4	70.3	209.1	4.75	1020	
34	up189	7.1	4.6	7	2	1	2	54	12	5	29.3	6.2	17.4	63.6	231.9	2.75	847.7	
35	up189	7.2	4.1	5	3	3	4	69	15	5	22.7	6.5	16.1	66	212.5	3.5	868.1	
36	up175	8.6	5.2	5	4	3	5	58	14	5	28.3	6.4	17.6	71.6	384.6	3.75	1560	
37	up175	9.3	5.5	7	6	5	6	61	14	5	28.1	6.9	17.3	76.1	475.7	5.75	2085	
38	up175	7.6	5.1	5	4	4	3	58	13	4	29.5	6.2	16.9	63.1	294.6	4.25	1098	
39	up175	7.5	5.4	7	4	3	3	56	14	5	30.8	5.8	16.7	66	303.8	4.25	1199	
40	up175	5.4	4.8	7	2	3	3	47	12	4	34.3	4.6	13.4	61.6	140	3.75	642	
41	up155	7.8	5.6	5	3	4	4	69	13	4	38.6	6.5	15.8	69.1	340.7	4	1488	
42	up155	7.5	5.2	7	2	3	5	68	17	4	27.9	5.3	15.3	77.1	292.5	3.75	1472	
43	up155	7.3	4.5	7	1	2	3	69	15	4	31.5	6.2	20.1	70.9	239.8	3	844.7	
44	up155	6.5	4.5	7	3	3	4	61	14	4	29.5	5.3	15	67.7	190.1	4	855.9	
45	up155	7.4	5.5	7	2	3	3	71	17	4	29.5	6.2	16.7	67.5	301.2	3.75	1214	
46	up154	7.7	5.3	7	5	5	6	71	15	4	33.2	6.6	15.7	82.6	314.2	5.5	1645	
47	up154	5	3.5	7	4	4	4	51	14	4	24.5	4.3	11.4	74.1	87.5	4.75	568.3	
48	up154	5.5	3.8	7	2	2	2	39	9	3	32.1	3.7	16.3	62.8	115	3.25	441.7	
49	up154	4.3	3.4	7	2	2	3	48	11	3	25.1	3.2	9.7	59.2	62.87	3.25	380.9	
50	up154	5.7	4.3	7	2	2	4	40	10	3	38.5	5	13	73.6	139.7	3.25	785.9	
51	up141	4.8	3.7	5	4	4	4	43	10	3	33.1	4.2	13.5	75.4	85.25	4.25	474.9	
52	up141	6.2	4.7	7	3	4	4	69	14	4	31.8	5.6	15.4	68.9	180.7	4.5	805	
53	up141	4.6	3.8	7	2	2	2	37	10	3	34.5	3.8	11	58.6	80.41	3.25	428.8	
54	up141	7.1	4.1	8	3	4	4	69	14	4	25.5	5.7	16	70	206.7	4.75	904.2	
55	up141	4.5	3.9	7	1	1	1	29	8	3	36.2	4	16.7	47.1	78.98	2.5	222.8	
56	up144	7.2	4.7	5	2	2	2	56	11	4	40.6	6.5	15	60.4	243.6	2.75	978.8	
57	up144	5.9	4.3	7	2	2	4	67	11	4	28.4	4.7	11	74.4	149.7	3.25	1012	
58	up144	7.4	5.3	5	3	3	3	64	16	5	29.4	7.2	15.2	64.5	290.2	3.5	1226	
59	up144	6.5	4.1	7	3	3	5	53	14	3	37.3	5.5	15.5	74	173.2	4	825.2	
60	up144	7	4.6	7	1	1	1	63	13	4	37.5	5.5	15.2	54	225.4	2.5	798.1	
61	up184	7.5	5.2	7	3	4	4	70	15	5	28.3	6.3	16.2	73.1	292.5	4.5	1317	
62	up184	7.3	4.9	7	3	2	5	66	15	5	23.8	6.2	17.4	70.4	261.1	3.5	1052	
63	up184	5.8	4.2	7	2	1	5	46	12	3	28.6	4.8	16.1	75	141.3	2.75	658.2	
64	up184	6.1	5	7	3	3	3	47	11	5	21.3	4.9	13.3	68.1	186.1	4	947.6	
65	up184	6.2	4.5	7	2	2	4	57	13	4	30.4	5.2	17.1	66.3	173	3.25	670.6	
66	up152	7.6	4.7	5	2	2	3	55	13	5	27.6	6	18.2	63.3	271.5	2.75	944.3	
67	up152	7.6	4.8	5	4	4	4	59	12	4	30	5.8	15.8	75.5	277.2	4.25	1321	
68	up152	6.8	5	5	2	2	2	42	13	5	25.4	5.2	16.7	67	231.2	2.75	928.1	

Table 4.2 continued

69	up152	5.6	4.1	7	1	1	3	40	10	4	27	5.1	20.6	60	128.6	2.5	374.5
70	up152	7.5	5	5	1	2	4	57	11	2	38.4	6.2	15.4	67.5	281.3	2.5	1231
71	up172	5.5	4.6	7	3	4	3	65	13	3	29.8	5.1	11.4	62.6	139.2	4.5	764.9
72	up172	6.8	5.2	7	4	4	5	59	14	4	35.9	6.3	13	70	240.4	4.75	1290
73	up172	5.2	3.7	6	4	4	4	40	10	3	34.3	4.7	11.5	67.3	100	4.5	584.1
74	up172	7	5.1	7	3	4	5	54	13	4	33.6	6.1	15.1	65.2	249.9	4.5	1076
75	up172	6.8	5	7	2	2	3	60	13	4	35.7	5.7	13.6	66.6	231.2	3.25	1128
76	up143	5.8	4	5	3	3	3	48	11	3	33.6	4.8	15.6	63	134.6	3.5	543.5
77	up143	8.8	4.7	5	5	4	5	57	14	4	28.1	7.8	15.6	70	364	4.5	1632
78	up143	5.8	4.1	7	2	3	3	38	14	3	30.8	4.8	12.8	61.8	137.9	3.75	665.2
79	up143	6.3	4.6	8	1	1	5	42	13	4	27.9	5.6	19.6	68.3	182.6	2.75	636.2
80	up143	6	4.4	7	1	1	3	46	11	3	35.8	5.1	16.6	67.1	158.4	2.5	639
81	up159	6	4.5	7	4	3	5	44	14	4	28	5.3	12.9	80	162	4.25	1002
82	up159	4	3.5	7	3	1	5	45	11	2	22	3.2	7.5	79	56	3	589.9
83	up159	5.5	4.4	7	1	2	3	50	10	4	25.1	4.2	13	57.8	133.1	3	589.1
84	up159	6	4.3	7	2	3	4	47	13	3	38.8	4	13.8	59.1	154.8	3.75	662.1
85	up159	6.2	5	7	4	4	5	77	15	3	33.8	5	11.9	71.8	192.2	4.75	1157
86	z44	6.5	4.3	7	3	2	5	53	11	5	26	5.7	15.3	74.7	181.7	3.5	887.7
87	z44	8.1	5.1	5	2	1	5	55	12	4	34.2	7	16.6	75.7	334.6	2.27	1524
88	z44	5.6	4.1	4	2	2	4	48	14	4	29.5	5.4	13	73.3	128.6	2.51	722.2
89	z44	4.3	3.8	3	1	2	2	53	12	4	21.6	5	19.1	76.4	70.26	2.01	280.5
90	z44	6.6	4.6	7	6	5	6	71	18	4	21	5.8	10.4	85.8	200.4	5.69	1644
91	up142	4.3	3.7	7	1	2	3	58	17	6	21.4	6.4	17.3	66.3	68.41	3	262.2
92	up142	7.5	4.4	7	2	2	3	47	11	4	23	3	9.6	72.6	247.5	3.25	1866
93	up142	4.2	4.1	7	4	3	4	49	12	3	31.4	4.3	10.1	66.6	72.32	4.25	474.3
94	up142	6.1	4.5	7	4	4	4	64	15	4	26.8	5.4	15.3	63.1	167.4	4.75	688.1
95	up142	4	3.5	7	2	3	4	55	12	4	28.3	2.8	9.6	70.9	56	3.75	412.1
96	z17	5.8	4.3	7	3	3	4	50	13	4	33.2	4.7	10.3	66	144.7	4	923.8
97	z17	7.1	5	7	2	2	3	50	14	3	37.3	6.3	15.4	69.4	252.1	3.25	1135
98	z17	5.5	4.1	6	2	2	2	49	13	5	19	5.4	12.9	63.9	124	3.01	611.8
99	z17	7.5	5.1	8	1	1	2	48	12	5	24.4	5.6	15.1	69.5	286.9	2.72	1320
100	z17	7.5	5.5	7	2	2	3	58	12	4	34.7	6.9	14.8	62.5	309.4	3.26	1302
101	up138	7	5.1	7	3	3	4	70	13	3	33	5.1	11.2	66.6	249.9	4	1488
103	up138	7.9	5.1	7	2	2	3	58	13	4	19.7	5	11.7	67.2	318.3	3.25	1817
104	up138	7.4	5.3	7	2	3	4	77	14	5	25.5	5.6	15.3	70	290.2	3.75	1328
105	up138	8.5	5.9	7	3	4	4	69	13	4	38.1	6.8	15.1	58.5	426.3	4.5	1651
106	up136	5	4.5	8	1	1	3	53	13	4	30.8	4.4	9	68.2	112.5	2.97	847.4
107	up136	5.1	3.5	7	3	3	3	46	12	2	33	4.2	13.3	63.7	91.04	4.06	433.9
108	up136	4.5	4.2	6	3	3	3	53	12	2	38.3	4.1	8.1	56.6	85.05	3.79	590.1
109	up136	6.5	4.8	7	3	3	3	58	15	4	28.7	5.8	15.6	60.5	202.8	4	785.3
110	up136	7	5.5	5	2	2	2	51	14	4	31.1	6.2	17.1	58.1	269.5	2.75	911.4
111	z51	5	4.1	7	2	1	2	41	13	3	40.6	4.7	14.5	57.5	102.5	2.75	406.5
112	z51	7	5.1	7	2	2	4	54	14	4	28.8	6.2	15.6	72	249.9	3.25	1148
113	z51	6.3	4.1	6	3	4	3	58	13	4	27	5.4	12.6	56.5	162.7	4.25	726.8
114	z51	5	4.4	7	2	4	5	45	5	5	24.4	4.6	10.1	79.5	110	4.25	858.4
115	z51	6.3	4.8	7	2	2	4	55	13	4	32.8	5.8	14.4	72.3	190.5	3.25	952.6
116	up190	6.6	4.9	7	3	3	4	66	14	5	22.8	4.6	13.7	63.2	213.4	4	983.2
117	up190	5.2	4.5	4	3	3	4	69	15	5	28.8	4.9	13.6	73.5	121.7	3.25	656.2
118	up190	5.5	5.1	7	3	4	4	59	12	4	39	5.2	14.4	69.5	154.3	4.5	741.3
119	up190	6.3	4.3	7	2	3	2	73	17	6	24	5.6	13.7	66.7	170.7	3.75	831.3
120	up190	5.1	4.4	7	2	2	5	52	12	3	32	5.1	13.5	80	114.4	3.25	675.1
121	up186	3.5	3.5	7	1	1	5	40	11	5	23.7	3.2	7.7	80.5	42.88	2.5	448.4
122	up186	5.3	4.2	7	2	3	3	60	14	4	31.3	4.3	13	63.3	118	3.75	574.8
123	up186	5.7	4.5	7	2	1	2	30	11	4	40.4	4.5	18	54.5	146.2	2.75	440.8
124	up186	4.5	4.1	7	4	4	3	52	13	3	28.5	4	14.1	63.3	83.03	4.75	371.2
125	up186	6.6	4.3	3	4	3	4	61	14	4	29.6	5.8	15.8	72.6	187.3	3.25	858.8

4.1.1 An overview of the individual tree data

- 1) Some scatter plots of the tree index vs the overall score, the tree index vs the volume, and the branch angle score (ba) vs the branch angle (bax) are presented in Figs 4.1, 4.2 and 4.3 respectively. The observed scatter plots do reflect that there is indeed some correlation in these variables as will be pointed out later.



The branch angle score shows some high correlation (Fig 4.3) suggesting that the branch angle can be readily assessed subjectively. The relationship between the index and the volume is linear which suggest that the index is not likely to omit the rather important volume aspects of the tree.

- 2) The evidence shown in the frequency distributions of the characters (Figs 4.4-4.15) suggest that there is high conformance to the assumption that the characteristics are normally distributed. Stem straightness is the only characteristic that shows some exception from this assumption.
- 3) The tree volume largely influences the tree index (Fig 4.2). An increase in volume is complimented by an increase in the tree index. This makes the index particularly suited for a selection of both the branch angle and diameter without sacrificing on volume production e.g. pulpwood production being the end use.

With the volume kept constant (see Table 4.2), e.g. tree nos. 14, 16 & 33 it can be observed that tree no. 16 has the highest index. The reason is that it has relatively flat and smaller branches compared with the rest. Again, consider the indices of tree no 19 and 27. They are more or less similar in volume but latter has flatter branch angles and smaller branches compared to the former.

4) The interpretation of the index is consistent in all the trees.

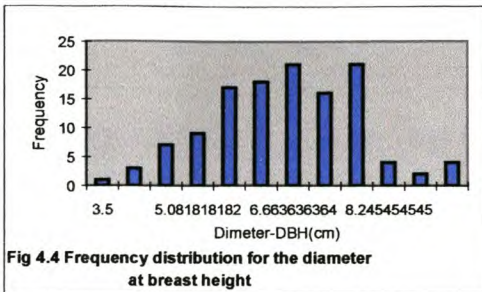


Fig 4.4 Frequency distribution for the diameter at breast height

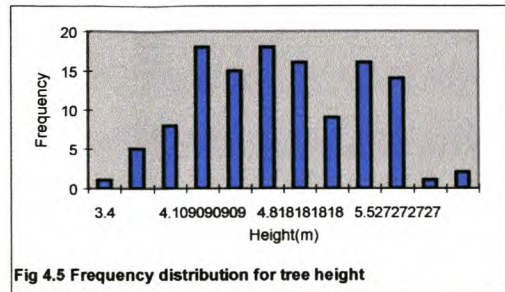


Fig 4.5 Frequency distribution for tree height

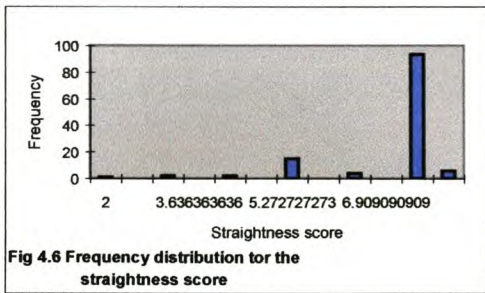


Fig 4.6 Frequency distribution for the straightness score

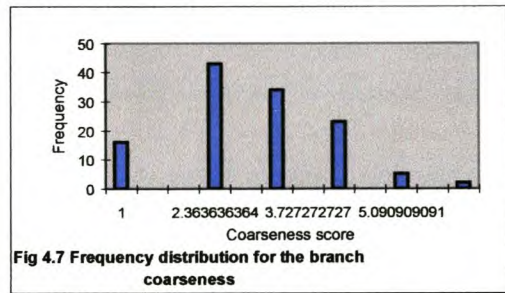


Fig 4.7 Frequency distribution for the branch coarseness

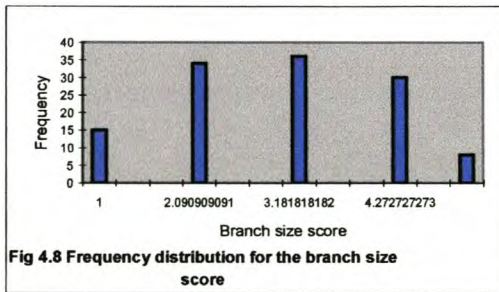


Fig 4.8 Frequency distribution for the branch size score

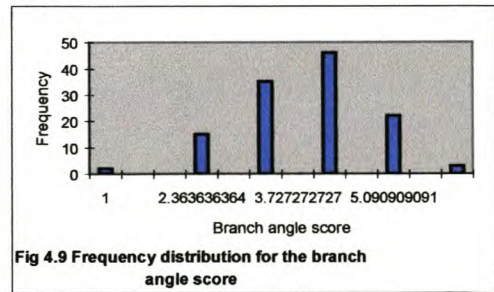


Fig 4.9 Frequency distribution for the branch angle score

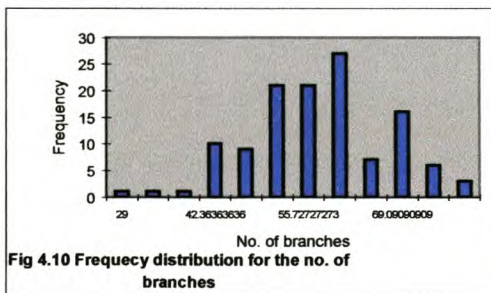


Fig 4.10 Frequency distribution for the no. of branches

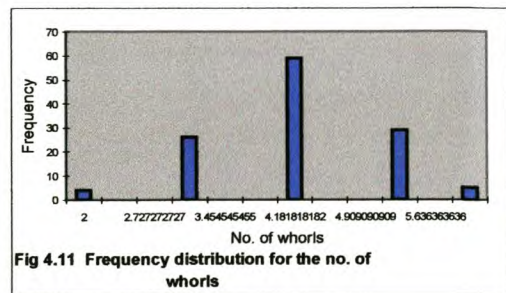
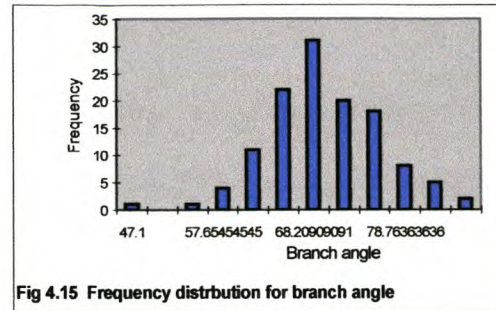
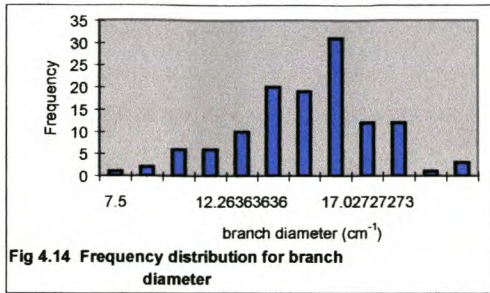
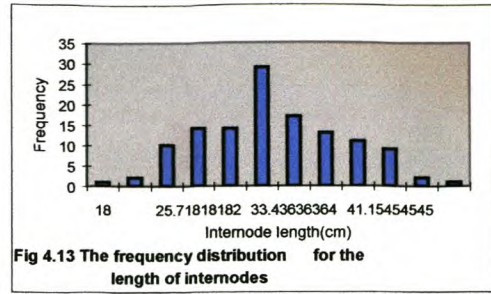
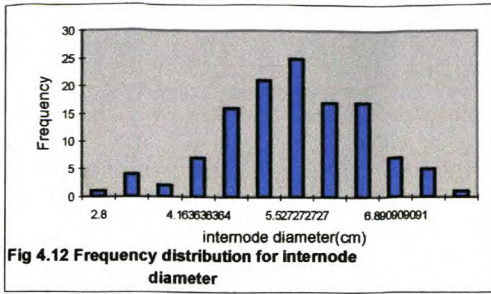


Fig 4.11 Frequency distribution for the no. of whorls



4.1.2. Correlation of tree values

Individual tree values and means of trees as outlined earlier were observed as having the correlations shown in Table 4.3.

Three categories of data are used in the interpretation of the results on correlations.

- i) Tree growth traits (i.e. diameter (d), height (ht) and volume) vs the rest of objectively assessed traits (i.e. the number of branches, number of whorls, number of whorls on the marked section, branch diameter and branch angle).
- ii) Tree growth traits vs subjectively assessed traits (i.e. straightness, coarseness, branch size, branch angle and the overall score).
- iii) Subjective vs the objective traits (an overview).

Table 4.3 A correlation matrix for tree values (tree means/individual values). The second line for corresponding variable is the significance level

	D	HT	STRT	COARSE	BS	BA	NB	NW	NWX	HX	DX	BDX	BAX	VOL	SCORE	INDEX
D	1.00000	0.79641	-0.08292	0.30302	0.23250	0.16852	0.51283	0.37570	0.29684	0.08936	0.80255	0.51225	0.11248	0.96808	0.23186	0.87447
	0.0	0.0001	0.3579	0.0006	0.0091	0.0603	0.0001	0.0001	0.0008	0.3217	0.0001	0.0001	0.2117	0.0001	0.0093	0.0001
HT	0.79641	1.00000	0.03232	0.21760	0.23029	0.11108	0.53019	0.37628	0.27214	0.25159	0.69944	0.40027	0.04684	0.86635	0.23666	0.78083
	0.0001	0.0	0.7205	0.0148	0.0098	0.2175	0.0001	0.0001	0.0021	0.0047	0.0001	0.0001	0.6039	0.0001	0.0079	0.0001
STRT	-0.08292	0.03232	1.00000	-0.05983	0.03973	0.08935	-0.02404	0.04725	-0.03164	0.06421	-0.19041	-0.20948	-0.00155	-0.05906	0.31099	0.02656
	0.3579	0.7205	0.0	0.5075	0.6600	0.3217	0.7902	0.6008	0.7261	0.4768	0.0334	0.0190	0.9863	0.5130	0.0004	0.7688
COARSE	0.30302	0.21760	-0.05983	1.00000	0.76936	0.53590	0.31620	0.26602	0.01867	0.06609	0.25072	-0.08819	0.32149	0.31579	0.83169	0.41288
	0.0006	0.0148	0.5075	0.0	0.0001	0.0001	0.0003	0.0027	0.8363	0.4640	0.0048	0.3281	0.0003	0.0003	0.0001	0.0001
BS	0.23250	0.23029	0.03973	0.76936	1.00000	0.45902	0.42111	0.31009	0.03070	0.07598	0.19522	-0.14203	0.25187	0.25040	0.93775	0.34986
	0.0091	0.0098	0.6600	0.0001	0.0	0.0001	0.0001	0.0004	0.7340	0.3997	0.0291	0.1141	0.0046	0.0049	0.0001	0.0001
BA	0.16852	0.11108	0.08935	0.53590	0.45902	1.00000	0.27210	0.18764	0.01371	-0.07175	0.17694	-0.12447	0.70596	0.17932	0.51381	0.34904
	0.0603	0.2175	0.3217	0.0001	0.0001	0.0	0.0021	0.0361	0.8793	0.4265	0.0484	0.1666	0.0001	0.0454	0.0001	0.0001
NB	0.51283	0.53019	-0.02404	0.31620	0.42111	0.27210	1.00000	0.64271	0.32911	-0.09062	0.50517	0.12799	0.23792	0.51998	0.37985	0.54973
	0.0001	0.0001	0.7902	0.0003	0.0001	0.0021	0.0	0.0001	0.0002	0.3149	0.0001	0.1549	0.0075	0.0001	0.0001	0.0001
NW	0.37570	0.37628	0.04725	0.26602	0.31009	0.18764	0.64271	1.00000	0.43259	-0.22986	0.43667	0.17874	0.17853	0.37056	0.31070	0.37530
	0.0001	0.0001	0.6008	0.0027	0.0004	0.0361	0.0001	0.0	0.0001	0.0099	0.0001	0.0461	0.0464	0.0001	0.0004	0.0001
NWX	0.29684	0.27214	-0.03164	0.01867	0.03070	0.01371	0.32911	0.43259	1.00000	-0.51138	0.34083	0.19802	0.14262	0.29020	0.01710	0.26945
	0.0008	0.0021	0.7261	0.8363	0.7340	0.8793	0.0002	0.0001	0.0	0.0001	0.0001	0.0268	0.1126	0.0010	0.8499	0.0024
HX	0.08936	0.25159	0.06421	0.06609	0.07598	-0.07175	-0.09062	-0.22986	-0.51138	1.00000	0.08476	0.11527	-0.26275	0.12638	0.09248	0.02184
	0.3217	0.0047	0.4768	0.4640	0.3997	0.4265	0.3149	0.0099	0.0001	0.0	0.3473	0.2005	0.0031	0.1602	0.3050	0.8090
DX	0.80255	0.69944	-0.19041	0.25072	0.19522	0.17694	0.50517	0.43667	0.34083	0.08476	1.00000	0.61589	0.13341	0.79490	0.15662	0.63917
	0.0001	0.0001	0.0334	0.0048	0.0291	0.0484	0.0001	0.0001	0.0001	0.3473	0.0	0.0001	0.1380	0.0001	0.0811	0.0001
BDX	0.51225	0.40027	-0.20948	-0.08819	-0.14203	-0.12447	0.12799	0.17874	0.19802	0.11527	0.61589	1.00000	-0.13373	0.47332	-0.18819	0.14420
	0.0001	0.0001	0.0190	0.3281	0.1141	0.1666	0.1549	0.0461	0.0268	0.2005	0.0001	0.0	0.1371	0.0001	0.0356	0.1086
BAX	0.11248	0.04684	-0.00155	0.32149	0.25187	0.70596	0.23792	0.17853	0.14262	-0.26275	0.13341	-0.13373	1.00000	0.13084	0.27579	0.36417
	0.2117	0.6039	0.9863	0.0003	0.0046	0.0001	0.0075	0.0464	0.1126	0.0031	0.1380	0.1371	0.0	0.1458	0.0019	0.0001
VOL	0.96808	0.86635	-0.05906	0.31579	0.25040	0.17932	0.51998	0.37056	0.29020	0.12638	0.79490	0.47332	0.13084	1.00000	0.25535	0.90730
	0.0001	0.0001	0.5130	0.0003	0.0049	0.0454	0.0001	0.0001	0.0010	0.1602	0.0001	0.0001	0.1458	0.0	0.0041	0.0001
SCORE	0.23186	0.23666	0.31099	0.83169	0.93775	0.51381	0.37985	0.31070	0.01710	0.09248	0.15662	-0.18819	0.27579	0.25535	1.00000	0.30023
	0.0093	0.0079	0.0004	0.0001	0.0001	0.0001	0.0001	0.0004	0.8499	0.3050	0.0811	0.0356	0.0019	0.0041	0.0	0.0001
INDEX	0.87447	0.78083	0.02656	0.41288	0.34986	0.34904	0.54973	0.37530	0.26945	0.02184	0.63917	0.14420	0.36417	0.90730	0.38045	1.00000
	0.0001	0.0001	0.7688	0.0001	0.0001	0.0001	0.0001	0.0001	0.0024	0.8090	0.0001	0.1086	0.0001	0.0001	0.0001	0.0

1) Tree growth traits vs objective assessments

Most variables measured or counted showed a significant correlation with the growth parameters. The number of branches and the number of whorls show a good correlation with the diameter and the height. This phenomenon can be expected since a larger surface area in trees can be expected to produce more photosynthates that in turn contribute to the tree size.

2) Tree growth vs subjectively measured traits

The branch size score and the coarseness score were found to be significantly correlated to the tree growth parameters. Stem straightness and branch angle were not correlated with the tree growth parameters.

3) Subjectively measured vs objectively measured traits

The overall score of the tree (score), which is simply the average of all the subjectively measured traits (straightness, coarseness, branch size and branch angle) correlates significantly with the tree indices. This correlation is also found when individual parameters are considered. Straightness, though, still remains the least correlated of all characteristics.

4.2 Whorl means

Individual whorl means of variables measured on the *marked section* of the trees including the tree means are presented in Table 4.4. All the variables indicate a very wide range. The whorl index is particularly the most variable.

There is considerable variation in whorl means as shown in Table 4.5 and Figs 4.15-4.22. The first whorl has generally the largest branch angle, branch diameter and internode diameter. The only exception is in the length of internodes where the opposite is true. These results are fairly consistent with what one would expect in a young *P. patula* stand. The branches tend to be bigger and flatter at the base getting acute along the stem but later getting flatter towards the top part of the stem.

Table 4.4 The overall mean, standard deviation and the range of variables of whorls (length of internodes, diameter of internodes, branch angles and branch diameters) of trees including the indices.

Variable	N	Mean	Std Dev	Minimum	Maximum	Variable	N	Mean	Std Dev	Minimum	Maximum
HX	125	30.6	5.711	18.0	46.39	DX	125	5.2	0.963	2.88	7.8
HX1	125	27.0	8.335	8	50	DX1	125	6.2	1.171	3.4	9
HX2	125	28.6	7.977	8	46	DX2	125	5.5	1.089	2.1	8.3
HX3	121	30.7	9.828	6	66	DX3	121	4.9	1.003	2.8	7.5
HX4	94	33.1	9.273	10	80	DX4	94	4.6	0.921	2.1	7.1
HX5	34	34.2	6.959	19	45	DX5	34	4.5	0.871	2.6	6.8
HX6	5	35.4	13.33	24	58	DX6	5	4.7	0.769	3.8	5.8
HX12	125	27.8	6.504	13.5	46.5	DX12	125	5.8	1.113	3.25	8.6
HX123	125	28.8	6.612	14	46.3	DX123	125	5.5	1.065	3.23	8.27
HXW456	125	29.9	6.419	13	46.3	DX456	125	5.3	0.995	3.02	7.97

Variable	N	Mean	Std Dev	Minimum	Maximum	Variable	N	Mean	Std Dev	Minimum	Maximum
BDX	125	14.2	2.57	7.5	20.6	BAX	125	67.8	6.388	47.14	85.8
BDX1	125	16.2	3.93	6	27.25	BAX1	125	69.7	7.663	50	88
BDX2	125	14.5	3.56	7.5	23.2	BAX2	125	68.3	7.920	47.5	90
BDX3	121	13.2	3.30	5.5	22.66	BAX3	121	66.8	8.644	20	90
BDX4	94	12.4	3.05	5.5	19.5	BAX4	94	67.1	8.629	35	90
BDX5	34	12.9	3.33	6.5	18.66	BAX5	34	67.7	7.938	55	90
BDX6	5	12.2	2.34	8.6	14.75	BAX6	5	66.2	8.004	57.5	77.5
BDX12	125	15.4	3.16	7.5	22.79	BAX12	125	69.0	6.848	53.75	85.47
BDX123	125	14.6	2.77	7.5	22.75	BAX123	125	68.2	6.799	42.5	84.88
BDX456	125	14.1	2.53	7.5	21.16	BAX456	125	67.9	6.719	42.5	86.16

Variable	N	Mean	Std Dev	Minimum	Maximum
INDEX	125	924.5	412.605	222.75	2546.72
INDEX1	125	854.5	404.193	182.01	2091.65
INDEX2	125	926.0	425.180	208.40	2368.16
INDEX3	121	1070.5	717.975	83.131	4818.4
INDEX4	94	1188.8	620.113	244.33	3681.82
INDEX5	34	1158.5	474.927	332.29	2632.5
INDEX6	5	1206.1	802.974	266.69	2467.38
INDEX12	125	890.3	385.783	235.68	2150.37
INDEX123	125	946.6	447.399	218.67	2475.4
INDEX456	125	978.7	462.817	218.67	2603.14

This is supported by the fact that only the first three whorls show an obvious declining trend for the length of internodes and the opposite is true for the rest of the observations.

The gradual decrease in the branch diameter and angle from the first whorl to the last whorl is not conspicuous at the level of seedlot means as shown in Figs 4.15 and 4.16

respectively. However, the length of internodes and the internode diameter show similar trends as observed on Figs 4.17 and 4.18 with zigzagging showing clearly the start of the first whorl and the end of the last whorl for most seedlots Figs 4.20 and 4.21.

Table 4.5 Whorl means of tree for the internode length, diameter of whorl, the branch diameter and the branch angle.

SEEDLOT	WNX	HX	DX	BDX	BAX
up136	1	27.1579	6.04737	14.2105	65.7895
up136	2	32.6316	4.91579	12.6842	60.5263
up136	3	31.5385	5.02308	14.0769	60.0000
up136	4	35.3077	4.63077	12.0769	60.7692
up137	1	26.4348	5.63478	15.3043	66.0870
up137	2	25.0500	5.03500	14.5500	68.5000
up137	3	29.5833	4.43750	12.4583	64.5833
up137	4	28.9412	4.02941	12.2353	65.8824
up137	5	19.0000	4.00000	6.6667	80.0000
up138	1	31.8519	6.83333	15.2593	69.2593
up138	2	26.0385	5.78077	16.3462	65.0000
up138	3	32.8000	5.26000	11.5500	66.5000
up138	4	31.6923	5.07692	11.3846	63.0769
up138	5	40.0000	4.20000	11.3333	66.6667
up141	1	25.7500	5.60500	15.2000	68.5000
up141	2	30.5217	4.78261	14.9565	64.7826
up141	3	35.3333	4.43333	13.3333	62.7778
up141	4	37.6000	4.78000	14.1000	69.0000
up142	1	18.5909	5.73636	17.0000	72.2727
up142	2	25.6500	4.02000	11.5500	70.0000
up142	3	30.0400	4.13600	10.4800	66.8000
up142	4	28.3889	3.45000	10.7778	65.0000
up142	5	23.0000	5.50000	14.0000	68.0000
up142	6	30.0000	5.00000	14.7500	57.5000
up143	1	33.1667	6.58333	20.3750	67.0833
up143	2	28.5000	5.81364	14.6364	66.3636
up143	3	28.7143	5.14286	13.6667	67.1429
up143	4	37.4286	5.31429	16.1429	64.2857
up144	1	28.4444	6.77037	16.9259	64.4444
up144	2	34.2963	6.04444	14.1111	68.5185
up144	3	37.4231	5.80000	13.3462	68.0769
up144	4	37.6087	4.85217	12.3478	60.8696
up144	5	32.0000	6.80000	14.2500	57.5000
up146	1	29.0417	7.18750	16.4583	70.8333
up146	2	26.9615	6.65000	15.1923	67.3077
up146	3	36.1667	6.12083	15.5417	63.3333
up146	4	35.2632	5.47895	14.7368	66.8421
up146	5	37.7273	4.65455	14.5455	62.7273
up146	6	24.0000	3.80000	8.6667	70.0000
up149	1	24.5000	5.50000	14.2917	72.9167
up149	2	26.9000	5.28000	12.0500	70.0000
up149	3	28.2273	4.45909	12.9091	67.2727
up149	4	41.2174	4.03043	11.9565	67.8261
up149	5	22.8889	3.85556	10.5556	77.7778
up152	1	26.8400	6.83600	17.0000	68.4000
up152	2	32.4348	6.05217	18.4348	66.9565
up152	3	20.1667	5.27778	18.7778	62.7778
up152	4	35.2941	4.51765	15.1765	70.0000
up152	5	36.6000	4.22000	17.4000	62.0000
up153	1	33.1250	5.70000	13.0417	70.4167
up153	2	38.5417	5.09167	13.0417	65.8333
up153	3	43.5833	4.40000	13.1250	63.3333
up153	4	41.8947	3.93684	11.2105	62.1053
up153	5	36.0000	3.80000	10.3333	63.3333
up154	1	24.6000	5.62500	14.3000	73.5000
up154	2	31.1538	4.86154	13.8462	71.1538

Table 4.5 Continued

SEEDLOT	WNX	HX	DX	BDX	BAX
up154	3	33.7083	4.03333	12.5833	70.0000
up154	4	33.1111	4.81111	13.2222	75.5556
up155	1	27.6154	6.86923	19.3462	70.0000
up155	2	30.3704	6.22222	16.2963	74.4444
up155	3	32.8750	5.67500	16.5833	67.0833
up155	4	35.9231	5.11538	14.3846	70.3846
up156	1	33.6786	5.91786	16.8214	63.9286
up156	2	29.8000	5.33000	15.3000	67.0000
up156	3	24.5769	4.58462	13.5769	68.8462
up156	4	32.5000	4.28333	11.5833	73.3333
up156	5	33.0000	3.90000	11.2500	66.2500
up159	1	25.9048	4.96667	13.0952	74.2857
up159	2	26.2609	4.41739	12.6957	66.9565
up159	3	37.5294	4.18235	10.4706	68.8235
up159	4	34.5714	4.27143	11.0000	67.1429
up165	1	29.0476	7.00000	16.6667	70.0000
up165	2	29.7200	6.31600	16.9200	70.4000
up165	3	27.9091	5.92727	14.7727	66.8182
up165	4	29.6667	5.46667	11.6111	74.4444
up165	5	35.5714	5.55000	12.9286	76.4286
up165	6	45.7778	5.35556	13.2222	71.1111
up172	1	31.4000	6.58000	15.3600	70.4000
up172	2	31.0000	5.77917	13.1250	65.8333
up172	3	36.9200	5.05600	11.0000	66.0000
up172	4	38.5882	5.23529	12.8824	62.9412
up175	1	26.8333	7.32500	18.7917	71.2500
up175	2	32.2857	6.46071	16.9286	66.7857
up175	3	25.0800	5.67600	16.9200	68.0000
up175	4	30.3333	5.13333	13.2381	67.6190
up175	5	41.7500	5.07500	16.3333	64.1667
up184	1	24.9583	6.59583	18.4167	69.1667
up184	2	21.8750	5.91667	17.6250	70.0000
up184	3	24.9048	5.46667	14.5238	73.8095
up184	4	29.8125	5.23125	14.4375	69.3750
up184	5	35.5714	4.90000	14.7857	70.0000
up186	1	20.9130	5.16087	16.0435	70.0000
up186	2	28.7059	4.59412	11.7647	71.1765
up186	3	33.1765	4.33529	14.2353	65.8824
up186	4	38.8824	3.76471	11.7647	63.5294
up186	5	42.0000	2.60000	8.0000	76.6667
up189	1	27.8750	6.02083	18.0833	67.0833
up189	2	27.9524	5.27143	14.3333	65.7143
up189	3	25.8095	5.10000	13.6190	67.1429
up189	4	29.6000	4.95500	11.4500	71.5000
up189	5	35.0769	4.82308	15.4615	63.8462
up190	1	27.1200	6.26800	15.4000	70.4000
up190	2	27.3846	5.63077	15.4615	70.7692
up190	3	25.8214	5.10357	12.7143	72.8571
up190	4	33.4545	4.47273	13.0000	67.6818
up190	5	32.1429	3.98571	12.3571	67.1429
up190	6	29.0000	4.20000	11.4000	60.0000
z17	1	28.9286	7.02500	16.0714	70.0000
z17	2	26.6296	5.85185	15.7407	65.5556
z17	3	29.6818	5.36364	12.0455	64.0909
z17	4	32.5000	4.80556	9.7222	65.0000
z17	5	31.6250	4.38750	10.2500	62.5000
z44	1	27.3077	7.14231	17.8077	80.7692
z44	2	24.4231	6.02308	17.6154	74.6154
z44	3	27.0556	5.58889	10.8333	80.5556
z44	4	25.8889	4.83333	10.8333	74.4444
z44	5	43.0000	4.00000	14.2000	66.0000
z51	1	24.7143	6.43333	16.1905	69.5238
z51	2	27.9091	5.62273	13.3636	68.6364
z51	3	35.9000	5.04500	12.0000	65.0000
z51	4	30.1176	4.60000	12.1765	66.4706
z51	5	34.0000	3.70000	8.2000	80.0000

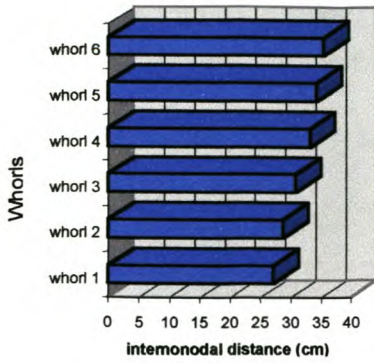


Fig 4.16 The mean length of internodes for individual whorls

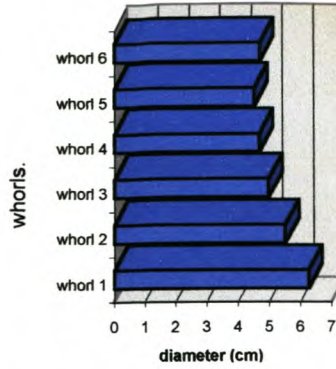


Fig 4.17 The mean internode diameter for individual whorls

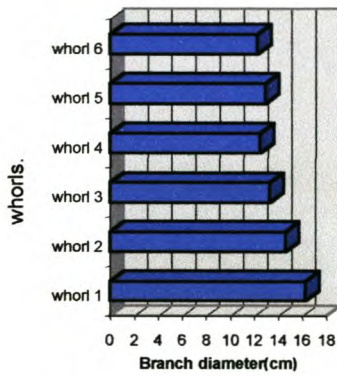


Fig 4.18 The mean branch diameter for individual whorls

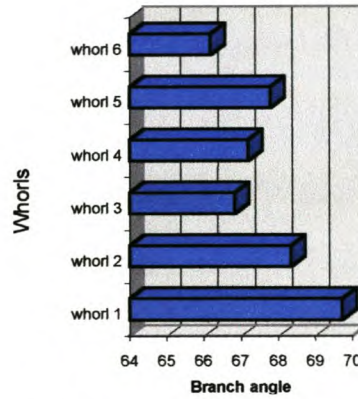


Fig 4.19 The mean branch angle for individual whorls

4.3 Correlation of variable measured on the marked section of the trees

The characteristics measured on the *marked section* of the tree are generally highly correlated (Table 4.6). The following observations are worth noting:

- 1) The internode diameter is negatively correlated to the internode length and has a positive correlation to the branch diameter and the branch angle. In essence this means the internode diameter decreases with longer internodes whilst the opposite is true for the branch diameter and the branch angle.

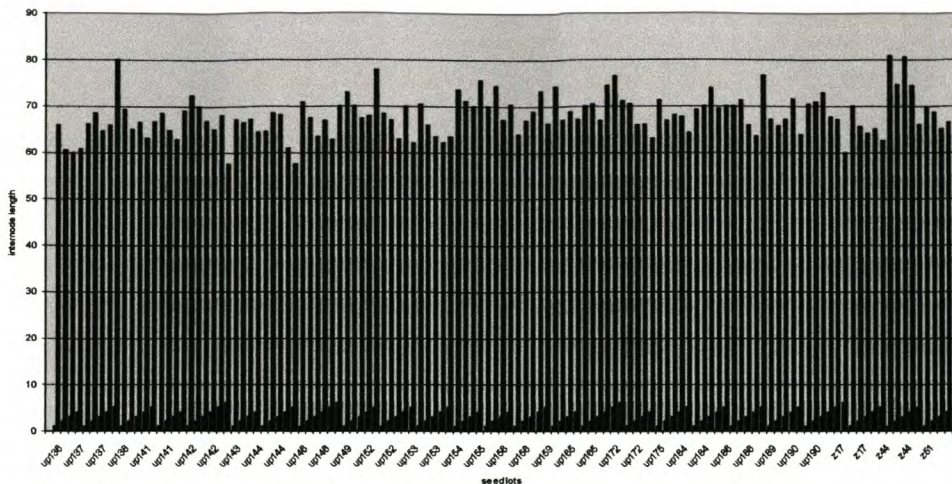


Fig 4.20 The mean internode length for individual seedlot whorls. note that the whorls are shown as the shaded area just above the x-axis

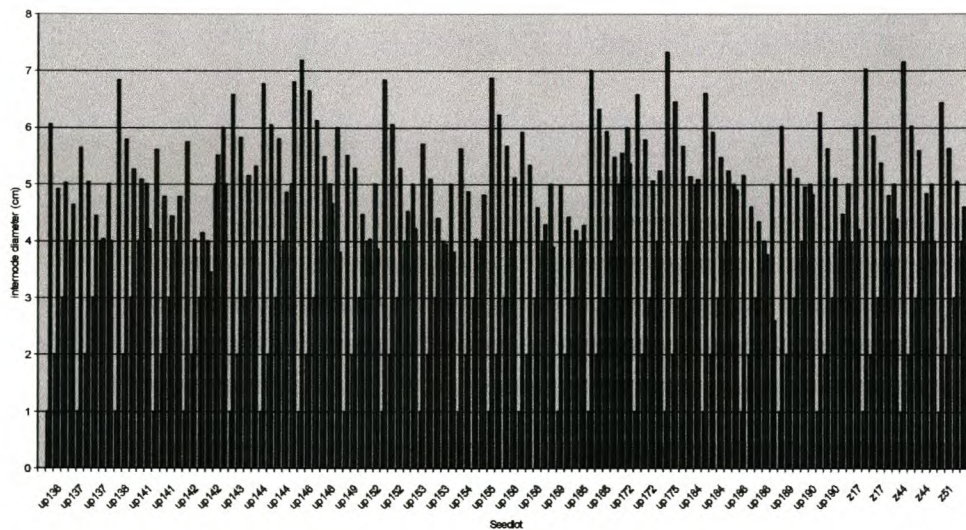


Fig 4.21 The mean internode diameter for seedlot whorls. Note that the whorls are shown as the more regular and thicker bars.

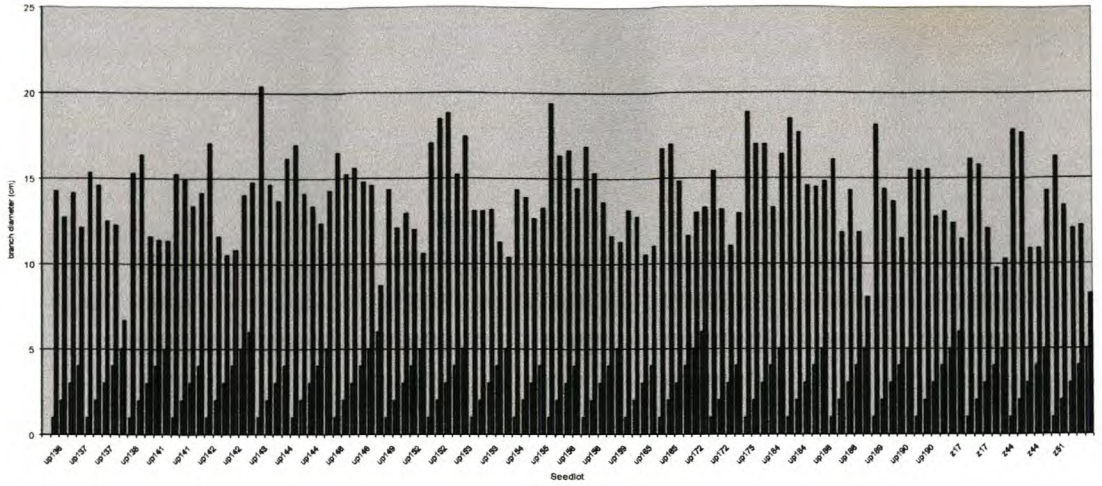


Fig 4.22 The mean branch diameter for seedlot whorls. Note that the whorls are shown as the shaded area just above the x-axis

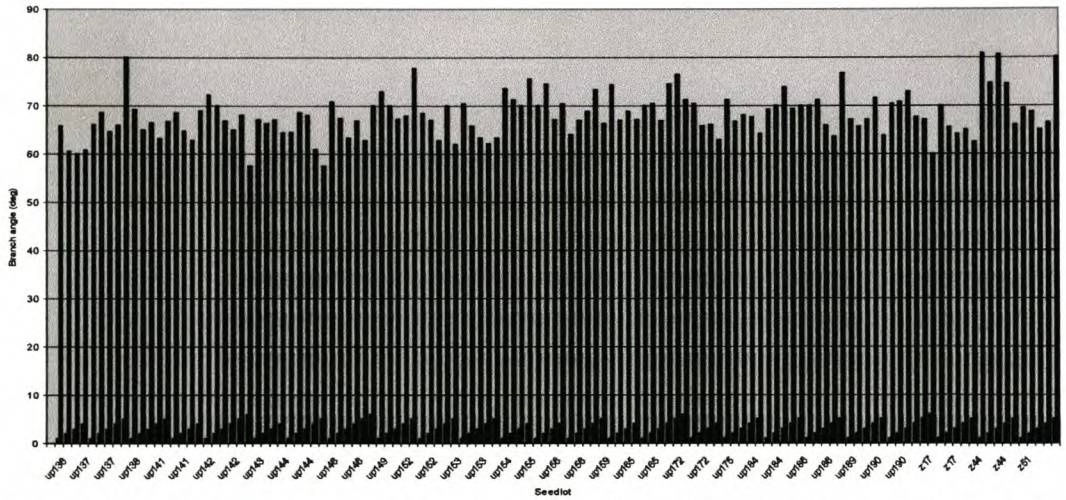


Fig 4.23 The mean branch angle for seedlot whorls. Note that the whorls are shown as the shaded area just above the x-axis

Thus bigger trees may tend to have bigger and acute branches compared to smaller ones. Conversely, these would be trees with shorter internodes. The branch diameter and the internode length are negatively correlated. This suggests that trees with shorter internodes may tend to be associated with larger branches. The branch diameter is also as negatively correlated to the branch angle. Smaller branches will therefore tend to have flatter angles.

- 2) The index is not correlated to the length of the internodes. It however, shows a negative correlation with the branch diameter. The angle and the internode diameter though, are positively correlated to the index. This is no surprise because the index was formulated on the bases of this principle (see index equation in Chapter 3).

Table 4.6 Correlation matrix for whorl mean variables assessed on the trees

	HX ,	DX ,	BDX,	BAX ,	INDEX
HX	1.00000 0.0,	-0.17744 0.0001	-0.00806 0.8567	-0.26288 0.0001	0.01558, 0.7272,
DX	-0.17744 0.0001	1.00000 0.0	0.55978 0.0001	0.17356 0.0001	0.27016, 0.0001,
BDX	-0.00806 0.8567	0.55978 0.0001	1.00000 0.0	-0.25381 0.0001	-0.27750, 0.0001,
BAX	-0.26288 0.0001	0.17356 0.0001	-0.25381 0.0001	1.00000 0.0	0.43164 0.0001
INDEX	0.01558 0.7272	0.27016 0.0001	-0.27750 0.0001	0.43164 0.0001	1.00000 0.0

4.4 Whorl indices and their correlation with the tree mean

Indices for whorl means are presented in Table 4.7. There was generally good correlation between the whorl and the tree means (Table 4.8). The correlation decreases from the first to the third whorl. The rest of the whorls may not be considered because the purported increase is due to the fact that fewer observations are used in the correlation. The index of branch averages of the first two whorls resulted in a better correlation as expected. However, the average of the first three whorls does not increase the correlation any more than that of the first two whorls though it is still much better than individual whorls. Again, the reason is that some trees had less than three branches, which meant that fewer observations were used in the correlations.

Table 4.7 Continued

T n	S E D L O T	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X	I N D E X
84	up159	662.10	580.50	629.69	760.88	605.10	657.03	657.03
85	up159	1157.23	1106.61	1037.27	1333.00	1071.94	1158.96	1158.96
86	z44	887.73	677.15	896.26	1031.73	1816.75	844.40	.	.	786.71	868.38	1105.48
87	z44	1524.45	1404.17	1203.64	4818.40	1191.77	.	.	.	1303.90	2475.40	2154.49
88	z44	722.21	942.89	590.18	665.84	739.75	.	.	.	766.54	732.97	734.67
89	z44	280.52	241.20	230.17	936.83	878.28	.	.	.	235.68	469.40	571.62
90	z44	1643.53	1389.70	1226.18	1929.55	3278.88	.	.	.	1307.94	1515.14	1956.08
91	up142	262.16	182.02	308.96	317.63	244.33	332.29	266.695	.	245.49	269.54	263.24
92	up142	1866.39	1350.00	1767.86	2367.39	2103.75	.	.	.	1558.93	1828.42	1897.25
93	up142	474.26	491.80	474.63	452.03	483.21	472.82	472.82
94	up142	688.13	574.10	813.30	783.21	639.34	.	.	.	693.70	723.54	702.49
95	up142	412.08	305.45	410.00	415.17	546.98	.	.	.	357.73	376.88	419.40
96	z17	923.83	991.13	910.77	754.71	1067.10	.	.	.	950.95	885.54	930.93
97	z17	1135.19	1170.23	990.20	1260.25	1080.21	1140.23	1140.23
98	z17	611.80	413.42	639.50	610.58	992.20	775.16	.	.	526.46	554.50	663.93
99	z17	1320.38	1181.25	891.64	3585.94	2868.75	1687.50	.	.	1036.44	1886.28	2131.89
100	z17	1302.08	1201.46	1278.75	1459.32	1359.38	.	.	.	1240.10	1313.17	1324.72
101	up138	1487.50	1730.08	1466.80	1320.90	1598.44	1505.93	1505.93
102	up138	1584.66	1569.54	1435.88	1786.05	1502.71	1597.16	1597.16
103	up138	1816.66	1591.46	1690.92	3182.91	1701.21	.	.	.	1641.19	2155.10	2041.62
104	up138	1327.84	1263.35	834.64	4221.50	2902.28	1707.22	.	.	1048.99	2106.50	2305.44
105	up138	1651.46	1475.57	1705.10	1750.77	1781.45	.	.	.	1590.33	1643.81	1678.22
106	up136	847.40	912.16	833.33	843.75	807.07	.	.	.	872.75	863.08	849.08
107	up136	433.91	408.09	464.46	436.28	436.28	436.28
108	up136	590.14	600.35	584.72	592.54	592.54	592.54
109	up136	785.28	739.62	786.99	718.25	891.09	.	.	.	763.30	748.29	783.99
110	up136	911.40	959.86	898.33	829.23	1018.11	.	.	.	929.10	895.81	926.38
111	z51	406.47	341.67	471.50	439.29	406.58	417.48	417.48
112	z51	1148.48	932.96	1335.67	1336.67	1101.25	.	.	.	1134.32	1201.77	1176.64
113	z51	726.81	638.56	708.66	828.44	770.82	.	.	.	673.61	725.22	736.62
114	z51	858.41	665.79	664.15	926.32	1000.00	1073.17	.	.	664.97	752.09	814.06
115	z51	952.56	1017.80	1019.64	900.60	810.69	.	.	.	1018.72	979.35	937.18
116	up190	983.21	858.42	868.25	1081.08	1089.00	1067.22	.	.	863.33	935.91	974.19
117	up190	656.22	578.48	501.04	726.92	738.30	718.11	.	.	539.76	602.14	636.18
118	up190	741.26	647.95	672.90	728.52	990.12	.	.	.	660.43	683.13	759.88
119	up190	831.25	903.53	789.11	971.49	640.00	927.54	898.247	.	846.32	888.04	826.03
120	up190	675.06	572.22	624.24	845.12	598.23	680.53	680.53
121	up186	448.39	414.92	470.24	412.26	564.14	410.89	.	.	442.58	432.47	465.39
122	up186	574.76	527.80	842.70	449.44	633.91	.	.	.	685.25	606.65	613.46
123	up186	440.82	394.52	412.37	446.74	503.33	.	.	.	403.45	417.88	439.24
124	up186	371.17	324.00	440.54	383.19	382.27	382.58	382.58
125	up186	858.75	768.44	1060.23	816.47	918.87	.	.	.	914.34	881.72	891.00

Table 4.8 Correlation of single whorl means and whorl averages with the tree mean value.

	INDEX1	INDEX2	INDEX3	INDEX4	INDEX5
INDEX	0.91318	0.85151	0.74955	0.79988	0.83314
	0.0001	0.0001	0.0001	0.0001	0.0001
	125	125	121	94	34
	INDEX6	INDEX12	INDEX123	INDEX456	
INDEX	0.97681	0.94761	0.94390	0.95453	
	0.0042	0.0001	0.0001	0.0001	
	5	125	125	125	

4.5 Whorl and branch combinations indices and their correlation with the tree mean indices

Indices for overall means for whorl and branch combinations as well as individual whorl and branch combination indices for trees are presented in Table 4.9 and Table 4.10 respectively. It can be seen from Table 4.9 that the whorl / branch index generally increases progressively from first in every whorl. The reason is that the first branch is always the largest (have been sorted that way), and as discussed earlier, it can be expected that the bigger branches will tend to be steeper therefore contribute to a low index value.

The correlation of the indices of the tree mean appears to be good (Table 4.11), it compares reasonably with the high correlation found in whorl mean. Again, the correlation increased stronger from the first branch (largest) to the last (smallest). Adding the first three branches results in a much higher correlation ($R=0.92684$) - i.e. indexbwb.

Table 4.9 The means, standard deviation and ranges for whorl and branch combinations

Variable	N	Mean	Std Dev	Minimum	Maximum
INDEX11	125	665.42	313.502	154.480	1767.27
INDEX12	125	774.22	383.875	159.630	2114.2
INDEX13	121	874.08	442.909	159.630	2518.39
INDEX14	109	1026.71	508.455	244.389	2537.04
INDEX15	72	1227.32	584.097	281.048	3182.91
INDEX16	33	1532.81	852.854	295.84	4040.19
INDEX21	125	711.51	322.865	157.95	1706.14
INDEX22	123	827.03	386.071	219.375	2217.98
INDEX23	116	934.35	455.746	185.823	2733.75
INDEX24	110	1130.03	594.835	244.389	3142.26
INDEX25	77	1487.35	865.494	281.048	3816
INDEX26	26	1524.83	810.590	490	3845.92
INDEX31	121	835.46	626.845	83.131	4643.65
INDEX32	117	993.37	721.615	264.6	5019.17
INDEX33	113	1067.92	726.477	284.953	5019.17
INDEX34	98	1288.34	934.863	308.7	6023
INDEX35	69	1561.84	848.697	411.6	4395.34
INDEX36	23	2083.83	1246.5	640	5768.88
INDEXBW	125	719.82	340.329	157.055	1877.73
INDEXBWA	121	770.35	367.168	157.913	2061.82
INDEXBWB	109	834.40	386.781	194.449	2144.77
INDEXBWC	123	763.64	336.540	188.66	1962.06
INDEXBWD	116	821.67	367.319	187.716	2129.52
INDEXBWE	125	688.47	291.173	177.009	1592.39
INDEXBWF	123	744.32	311.339	208.443	1833.24
Variable	N	Mean	Std Dev	Minimum	Maximum
BDX11	125	19.928	4.758	7	32
BDX12	125	17.672	4.536	6	31
BDX13	121	16.26	4.358	5	30
BDX14	109	14.38	4.093	5	26
BDX15	72	13.54	3.917	5	26
BDX16	33	12.27	3.883	7	23
BDX21	125	17.94	4.434	8	36
BDX22	123	15.86	3.980	7	25
BDX23	116	14.60	4.079	6	24
BDX24	110	13.19	4.087	5	23
BDX25	77	12.20	3.954	5	20
BDX26	26	12.53	4.042	6	20
BDX31	121	16.28	3.906	5	26
BDX32	117	14.61	3.745	5	24
BDX33	113	13.24	3.506	5	22
BDX34	98	11.96	3.365	5	21
BDX35	69	10.44	3.341	5	19
BDX36	23	8.86	2.701	5	15
Variable	N	Mean	Std Dev	Minimum	Maximum
BAX11	125	66.9	8.727	50	90
BAX12	125	68.2	9.593	40	90
BAX13	121	69.5	9.949	50	90
BAX14	109	71.4	9.701	40	90
BAX15	72	74.16	9.457	50	90
BAX16	33	72.7	11.798	40	90
BAX21	125	64.8	9.471	40	90
BAX22	123	66.0	9.200	50	90
BAX23	116	66.9	9.799	40	90
BAX24	110	70.2	9.996	50	90
BAX25	77	73.2	9.096	60	90
BAX26	26	73.8	8.978	60	90
BAX31	121	63.3	9.708	20	90
BAX32	117	66.3	9.340	40	90
BAX33	113	65.8	9.703	40	90
BAX34	98	68.5	9.41	50	90
BAX35	69	72.1	8.722	50	90
BAX36	23	75.6	12.367	50	90

Table 4.11 Correlation of mean indices of whorl and branch combinations with the tree mean

	INDEX11	INDEXB12	INDEX13	INDEX14	INDEX15	INDEX16	INDEX21
INDEX	0.89155	0.85233	0.86939	0.77663	0.79708	0.79277	0.78213
	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
	125	125	121	109	72	33	125
	INDEX22	INDEX23	INDEX24	INDEX25	INDEX26	INDEX31	INDEX32
INDEX	0.78296	0.79337	0.72184	0.69459	0.64515	0.65314	0.65735
	0.0001	0.0001	0.0001	0.0001	0.0004	0.0001	0.0001
	123	116	110	77	26	121	117
	INDEX33	INDEX34	INDEX35	INDEX36	INDEXBW	INDEXBWA	INDEXBWB
INDEX	0.73480	0.66937	0.61955	0.70978	0.89133	0.90764	0.92684
	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
	113	98	69	23	125	121	109
	INDEXBWC	INDEXBWD	INDEXBWE	INDEXBWF			
INDEX	0.83951	0.85366	0.91359	0.94111			
	0.0001	0.0001	0.0001	0.0001			
	123	116	125	123			

4.6 Seedlot means and correlations.

The indices selected for a combined correlation analysis based on seedlot means are listed in Table 4.12. It can be observed in the rectangular correlation matrix presented in Table 4.13 that there is very good correlation even within the different indices generated. These, however are not of interest in this presentation except that they demonstrate that the index can be effectively applied in all instances. From Table 4.12 it can be readily observed that the index increases from the first to the last branch for a given whorl. It is not easy to tell the trend in the case of whorls, though, as observed in the correlation analysis (Table 4.13).

The observations made on the mean indices of whorls and whorl and branches combinations, made earlier, apply even in this case of seedlot means.

Table 4.12 Summary for mean indices for whorls and whorl and branch combinations for seedlots

SEEDLOT	INDEX	INDEX1	INDEX2	INDEX12	INDEX11	INDEXB12	INDEX13	INDEX14	INDEX21	INDEX22	INDEXBW	INDEXBWA	INDEXBWB	INDEXBWC	INDEXBWD	INDEXBWE	INDEXBWF
up136	713.63	724.02	713.57	718.79	568.58	657.66	808.74	1226.68	644.10	687.00	613.12	677.23	814.60	665.55	693.40	606.34	639.33
up137	629.94	558.34	747.77	653.06	472.14	489.42	578.19	719.09	682.25	520.50	480.78	513.25	564.71	512.25	543.32	577.20	512.28
up138	1573.62	1526.00	1426.67	1476.33	1189.15	1240.71	1454.23	1706.22	1015.49	1288.96	1214.93	1294.70	1397.58	1152.22	1228.51	1102.32	1183.58
up141	567.14	580.22	574.43	577.33	461.17	541.95	658.80	803.42	463.53	497.96	501.56	573.40	630.91	480.74	388.74	462.35	491.15
up142	740.60	580.67	754.95	667.81	497.43	534.03	603.33	690.15	597.51	722.36	515.73	544.93	581.23	659.93	781.84	547.47	587.83
up143	823.19	717.64	959.60	838.62	581.76	655.78	746.41	887.61	717.14	846.60	618.77	661.31	717.89	781.87	866.85	649.45	700.32
up144	968.07	802.28	1039.24	920.76	668.78	681.30	766.17	897.40	729.31	900.77	675.04	705.42	760.47	815.04	881.75	699.05	745.04
up146	1322.56	1260.91	1321.73	1291.32	1005.33	1183.22	1281.68	1600.81	998.17	1107.91	1094.28	1156.74	1337.90	1053.04	1110.65	1001.75	1073.66
up149	754.38	695.13	814.28	754.70	543.08	586.45	660.07	822.33	565.58	824.00	564.76	596.53	652.98	694.79	791.00	554.33	629.78
up152	959.77	993.90	1040.59	1017.25	752.25	793.72	893.74	1361.55	798.62	1007.05	772.99	813.24	1041.07	902.83	984.75	775.44	837.91
up153	891.94	1110.34	874.31	992.32	927.80	1129.28	1169.43	799.71	678.58	814.06	1028.54	1075.50	779.74	746.32	834.24	803.19	887.43
up154	764.30	743.95	782.34	763.14	587.61	717.43	701.68	938.66	626.07	659.82	652.52	668.91	786.34	642.95	686.43	606.84	647.73
up155	1174.83	1017.36	1249.09	1133.22	767.31	803.75	1075.28	1185.35	1010.28	1081.46	785.53	882.12	957.92	1045.87	1088.52	888.80	915.70
up156	923.56	788.35	943.30	865.83	529.41	690.53	753.95	845.33	744.45	801.55	609.97	657.96	704.81	773.00	883.77	636.93	691.49
up159	800.01	741.99	768.10	755.05	601.92	730.51	848.88	901.87	581.78	749.19	666.22	727.10	798.00	665.49	703.26	591.85	665.85
up165	1364.29	1168.59	1196.32	1182.46	897.90	1057.08	1549.92	1595.70	843.22	1062.38	977.49	1219.39	1360.20	952.80	1053.08	870.56	965.15
up172	968.55	858.09	970.94	914.52	698.80	762.96	838.62	932.89	811.14	871.95	730.88	766.79	808.31	841.54	869.74	754.97	786.21
up175	1316.83	1239.69	1256.06	1247.87	882.49	1167.21	1313.21	1562.21	957.78	1057.67	1024.85	1120.97	1231.28	1007.72	1050.48	920.13	1016.29
up184	928.93	861.88	1012.71	937.30	684.70	928.51	772.86	863.14	833.64	755.18	806.60	702.39	742.58	722.00	756.18	759.17	809.20
up186	538.78	485.94	645.22	565.58	412.03	451.31	478.84	600.94	518.57	562.93	431.67	447.39	495.79	540.75	654.06	465.30	486.21
up189	722.04	555.11	758.65	656.88	408.49	499.16	544.30	659.19	537.00	810.11	453.83	483.98	522.53	673.55	560.45	472.74	563.69
up190	777.40	712.12	691.11	701.61	552.27	626.56	639.77	894.79	589.89	632.83	589.42	606.20	678.35	611.36	620.33	571.08	600.39
z17	1058.66	991.50	942.17	966.83	782.05	898.88	956.58	999.18	656.96	799.19	840.46	879.17	909.17	728.08	780.66	719.51	784.27
z44	1011.69	931.02	829.29	880.16	620.92	863.48	996.39	1252.00	585.47	813.17	742.20	826.93	933.20	699.32	754.43	603.19	720.76
z51	818.55	719.36	839.92	779.64	542.19	664.66	819.92	940.82	601.43	725.51	603.42	675.59	727.25	663.47	765.23	571.81	633.45

Table 4.13 Correlation matrix for indices for whorl means and whorl and branch combination for seedlots. (The second line of each variable represents the significance level)

	INDEX	INDEX1	INDEX2	INDEX12	INDEX11	INDXB12	INDEX13	INDEX14	INDEX21	INDEX22	INDEXBW	INDEXBWA	INDEXBWB	INDEXBWC	INDEBWD	INDEXBWE	INDEXBWF
INDEX	1.00000 0.0	0.94731 0.0001	0.9453 0.000	0.97504 0.0001	0.90709 0.0001	0.88062 0.0001	0.91520 0.0001	0.86910 0.0001	0.86000 0.0001	0.92329 0.0001	0.90391 0.0001	0.92010 0.0001	0.93128 0.0001	0.93115 0.0001	0.89469 0.0001	0.93202 0.0001	0.95684 0.0001
INDEX1	0.94731 0.0001	1.00000 0.0	0.8836 0.000	0.97457 0.0001	0.97882 0.0001	0.96235 0.0001	0.94263 0.0001	0.86555 0.0001	0.81668 0.0001	0.86921 0.0001	0.98202 0.0001	0.97433 0.0001	0.93120 0.0001	0.88135 0.0001	0.84984 0.0001	0.95303 0.0001	0.97813 0.0001
INDEX2	0.94534 0.0001	0.88365 0.0001	1.0000 0.0	0.96608 0.0001	0.86293 0.0001	0.80585 0.0001	0.81961 0.0001	0.79260 0.0001	0.95007 0.0001	0.94131 0.0001	0.84242 0.0001	0.83361 0.0001	0.85599 0.0001	0.96892 0.0001	0.93959 0.0001	0.94910 0.0001	0.94444 0.0001
INDEX12	0.97504 0.0001	0.97457 0.0001	0.9660 0.000	1.00000 0.0	0.95297 0.0001	0.91657 0.0001	0.91228 0.0001	0.85682 0.0001	0.90524 0.0001	0.93002 0.0001	0.94492 0.0001	0.93646 0.0001	0.92339 0.0001	0.94993 0.0001	0.91851 0.0001	0.97999 0.0001	0.99160 0.0001
INDEX11	0.90709 0.0001	0.97882 0.0001	0.8629 0.000	0.95297 0.0001	1.00000 0.0	0.95058 0.0001	0.91768 0.0001	0.80666 0.0001	0.80502 0.0001	0.83800 0.0001	0.98540 0.0001	0.96488 0.0001	0.89541 0.0001	0.85402 0.0001	0.83072 0.0001	0.95977 0.0001	0.96839 0.0001
INDXB12	0.88062 0.0001	0.96235 0.0001	0.8058 0.000	0.91657 0.0001	0.95058 0.0001	1.00000 0.0	0.92526 0.0001	0.79100 0.0001	0.74898 0.0001	0.76293 0.0001	0.98956 0.0001	0.96155 0.0001	0.87716 0.0001	0.78199 0.0001	0.75579 0.0001	0.90464 0.0001	0.94153 0.0001
INDEX13	0.91520 0.0001	0.94263 0.0001	0.8196 0.000	0.91228 0.0001	0.91768 0.0001	0.92526 0.0001	1.00000 0.0	0.87567 0.0001	0.74066 0.0001	0.81271 0.0001	0.93331 0.0001	0.98614 0.0001	0.94013 0.0001	0.81955 0.0001	0.79553 0.0001	0.88166 0.0001	0.91725 0.0001
INDEX14	0.86910 0.0001	0.86555 0.0001	0.7926 0.000	0.85682 0.0001	0.80666 0.0001	0.79100 0.0001	0.87567 0.0001	1.00000 0.0	0.74197 0.0001	0.80026 0.0001	0.80816 0.0001	0.85851 0.0001	0.97086 0.0001	0.81425 0.0001	0.76814 0.0001	0.81803 0.0001	0.84161 0.0001
INDEX21	0.86000 0.0001	0.81668 0.0001	0.9500 0.000	0.90524 0.0001	0.80502 0.0001	0.74898 0.0001	0.74066 0.0001	0.74197 0.0001	1.00000 0.0	0.84208 0.0001	0.78436 0.0001	0.75735 0.0001	0.78577 0.0001	0.91722 0.0001	0.88096 0.0001	0.93921 0.0001	0.89259 0.0001
INDEX22	0.92329 0.0001	0.86921 0.0001	0.9413 0.000	0.93002 0.0001	0.83800 0.0001	0.76293 0.0001	0.81271 0.0001	0.80026 0.0001	0.84208 0.0001	1.00000 0.0	0.80732 0.0001	0.82187 0.0001	0.84602 0.0001	0.98118 0.0001	0.94240 0.0001	0.88356 0.0001	0.91977 0.0001
INDEXBW	0.90391 0.0001	0.98202 0.0001	0.8424 0.000	0.94492 0.0001	0.98540 0.0001	0.98956 0.0001	0.93331 0.0001	0.80816 0.0001	0.78436 0.0001	0.80732 0.0001	1.00000 0.0	0.97512 0.0001	0.89660 0.0001	0.82520 0.0001	0.80002 0.0001	0.94154 0.0001	0.96577 0.0001
INDEXBWA	0.92010 0.0001	0.97433 0.0001	0.8336 0.000	0.93646 0.0001	0.96488 0.0001	0.96155 0.0001	0.98614 0.0001	0.85851 0.0001	0.75735 0.0001	0.82187 0.0001	0.97512 0.0001	1.00000 0.0	0.93704 0.0001	0.83219 0.0001	0.80772 0.0001	0.91688 0.0001	0.94778 0.0001
INDEXBWB	0.93128 0.0001	0.93120 0.0001	0.8559 0.000	0.92339 0.0001	0.89541 0.0001	0.87716 0.0001	0.94013 0.0001	0.97086 0.0001	0.78577 0.0001	0.84602 0.0001	0.89660 0.0001	0.93704 0.0001	1.00000 0.0	0.85925 0.0001	0.82192 0.0001	0.89012 0.0001	0.91488 0.0001
INDEXBWC	0.93115 0.0001	0.88135 0.0001	0.9689 0.000	0.94993 0.0001	0.85402 0.0001	0.78199 0.0001	0.81955 0.0001	0.81425 0.0001	0.91722 0.0001	0.98118 0.0001	0.82520 0.0001	0.83219 0.0001	0.85925 0.0001	1.00000 0.0	0.96173 0.0001	0.92839 0.0001	0.94080 0.0001
INDEBWD	0.89469 0.0001	0.84984 0.0001	0.9395 0.000	0.91851 0.0001	0.83072 0.0001	0.75579 0.0001	0.79553 0.0001	0.76814 0.0001	0.88096 0.0001	0.94240 0.0001	0.80002 0.0001	0.80772 0.0001	0.82192 0.0001	0.96173 0.0001	1.00000 0.0	0.89775 0.0001	0.90773 0.0001
INDEXBWE	0.93202 0.0001	0.95303 0.0001	0.9491 0.000	0.97999 0.0001	0.95977 0.0001	0.90464 0.0001	0.88166 0.0001	0.81803 0.0001	0.93921 0.0001	0.88356 0.0001	0.94154 0.0001	0.91688 0.0001	0.89012 0.0001	0.92839 0.0001	0.89775 0.0001	1.00000 0.0	0.98293 0.0001
INDEXBWF	0.95684 0.0001	0.97813 0.0001	0.9444 0.000	0.99160 0.0001	0.96839 0.0001	0.94153 0.0001	0.91725 0.0001	0.84161 0.0001	0.89259 0.0001	0.91977 0.0001	0.96577 0.0001	0.94778 0.0001	0.91488 0.0001	0.94080 0.0001	0.90773 0.0001	0.98293 0.0001	1.00000 0.0

4.7 Analysis of variance for regression models and their scatter plots.

The linear regression models and analysis of variance (ANOVA) tables for each of the different mean indices for whorls and whorl and branch combinations used in the analysis are presented in Tables 4.14 to 4.28. Scatter plots accompanying each ANOVA table for each model are given in Figs 4.24 to 4.38. It can be observed that all models show some degree of a linear relationship and the coefficients of determination, R^2 , are fairly large for each model. This symbolizes that a large percentage of the variation in the mean tree index can be explained by the changes in each of the whorls and / or whorl and branch combination indices adopted.

The results of the regression analysis indicate that there is an increase in the coefficient of determination (R^2) when whorls or branches are added in the whorls and whorl and branch combination indices (Table 4.29). The response is characteristic of R^2 , which suggest that adding more observations can enhance the precision of the results. It should be noted that R^2 might not increase if this condition is not consistently met. For example, *indexbwb* has a lower R^2 compared to *indexbwa*. The fewer observations conceal the effect of the added branch, otherwise the R^2 for the former should be higher than the latter as illustrated by the trend from index 1 (whorl 1 1st branch), *indexbw* (whorl 1 avg branch 1,2) and *indexwa*.

Based on the R^2 values the five best linear regression models are given by *indexbwf* and / or *index12*, *indexbwe*, *indexbwa*, *indexbw* and *index1* respectively. *Indexbwf* (i.e. the index of average of branches 1 and 2 of both the 1st and 2nd whorl) and *index12* (i.e. the index of the average of whorl 1 and 2) have similar values of R^2 . This suggests that the average of 4 branches (2 largest branches from whorl 1 and 2) can predict the tree index in much the same way as the average of all branches in whorl 1 and 2.

A point worth noting from the scatter plots and studentized residual checks on outliers (appendix 4 and 5) is that mean indices identified as outliers arose from the fact that indices for smaller and flatter branches tend to be extremely high which lead to the inflation of the mean indices. In other words abnormal (smaller – vestigial, bigger- forks) should not be considered when carrying out an assessment of this nature.

Table 4.14 Analysis of Variance for Linear Regression.

Model 1: Tree index = $\beta_0 + \beta_1 \text{index1}$ (i.e. whorl 1)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15353920.768	15353920.768	880.485	0.0001
Error	119	2075124.5635	17438.021542		
C Total	120	17429045.331			
Root MSE		132.05310	R-square	0.8809	
Dep Mean		901.22050	Adj R-sq	0.8799	
C.V.		14.65270			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	114.571011	29.10206072	3.937	0.0001
INDEX1	1	0.952123	0.03208721	29.673	0.0001

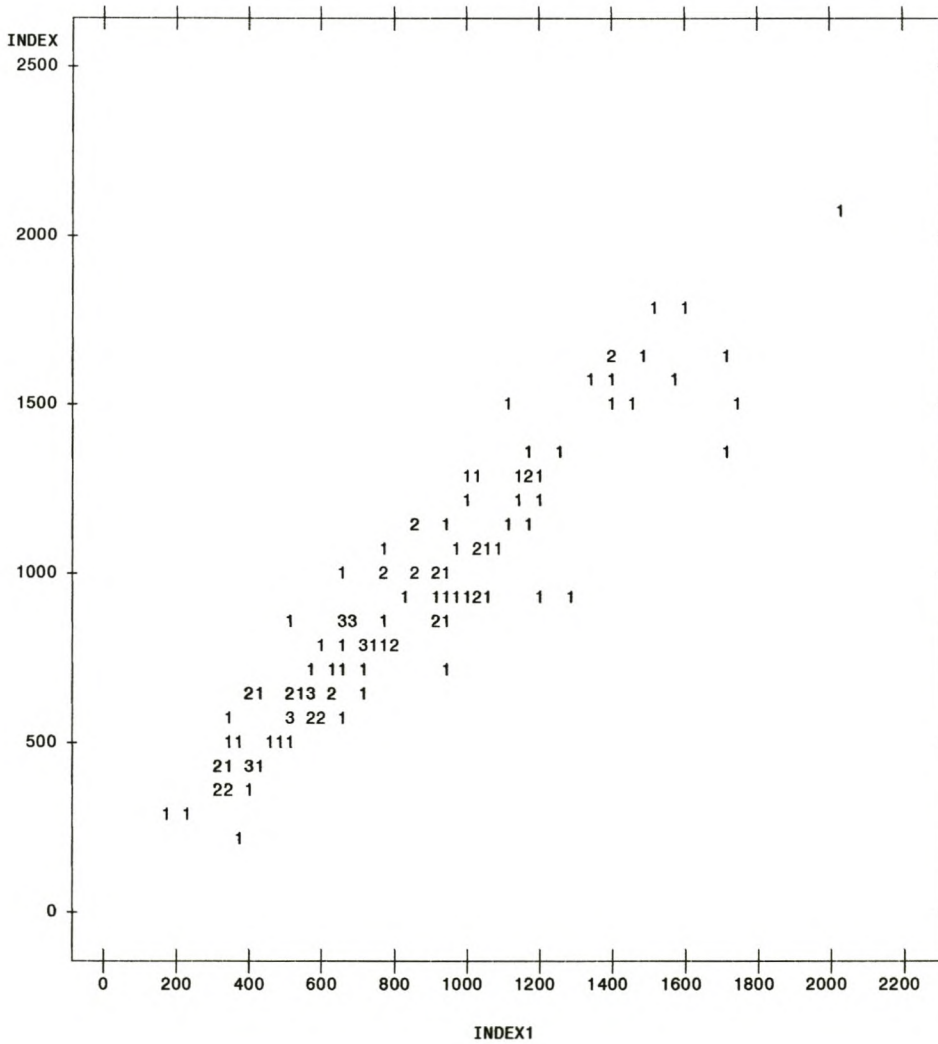


Fig 4.24 A plot of whorl 1 index vs the tree index

Table 4.15 Analysis of Variance for Linear Regression.

Model 2: Index = $\beta_0 + \beta_1$ Index 2 (i.e. whorl 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	13398338.685	13398338.685	474.034	0.0001
Error	117	3306947.1464	28264.505524		
C Total	118	16705285.831			
Root MSE		168.12051	R-square	0.8020	
Dep Mean		904.67134	Adj R-sq	0.8003	
C.V.		18.58360			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	127.527978	38.87911017	3.280	0.0014
INDEX2	1	0.876619	0.04026300	21.772	0.0001

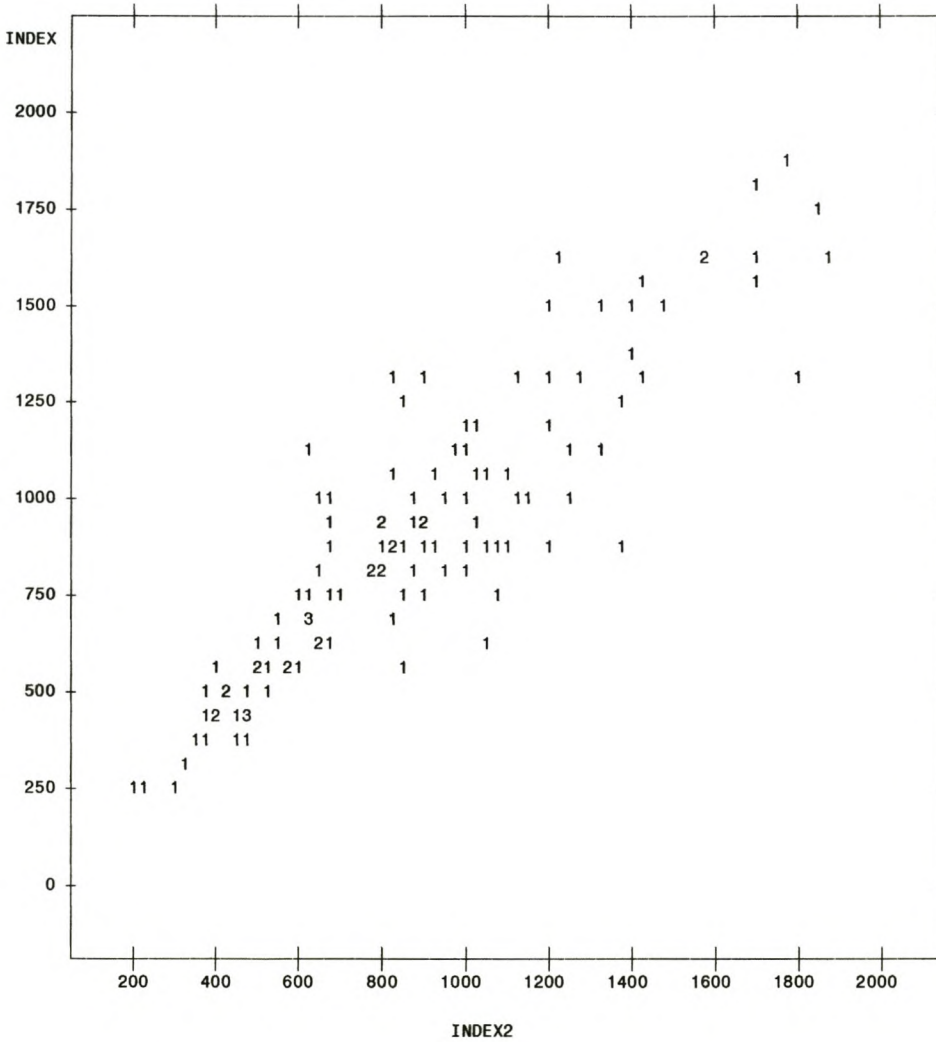


Fig 4.25 A plot of the index of whorl 2 index vs the tree index

Table 4.16 Analysis of Variance for Linear Regression.

Model 3: Index = $\beta_0 + \beta_1$ Index 12 (i.e. the average of whorl 1 and 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15254560.173	15254560.173	1387.239	0.0001
Error	116	1275576.0759	10996.345482		
C Total	117	16530136.249			
Root MSE		104.86346	R-square	0.9228	
Dep Mean		903.83288	Adj R-sq	0.9222	
C.V.		11.60209			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	35.236083	25.23978772	1.396	0.1654
INDEX12	1	1.006684	0.02702823	37.246	0.0001

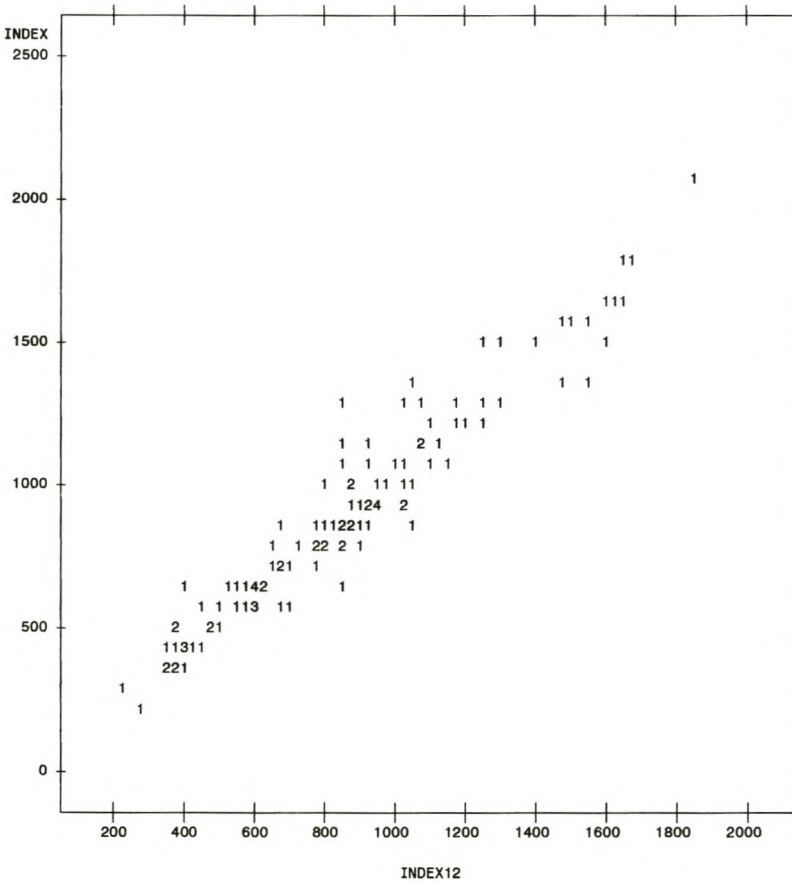


Fig 4.26 A plot of the index of the average of whorl 1 and whorl 2 vs the tree index

Table 4.17 Analysis of Variance for Linear Regression.

Model 4: Index = $\beta_0 + \beta_1$ Index11 (i.e whorl 1 branch 1)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	17448510.1	17448510.1	824.164	0.0001
Error	116	2455854.5061	21171.159535		
C Total	117	19904364.606			
Root MSE	145.50313	R-square	0.8766		
Dep Mean	924.07212	Adj R-sq	0.8756		
C.V.	15.74586				

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	92.154434	31.92429791	2.887	0.0046
INDEX11	1	1.259608	0.04387615	28.708	0.0001

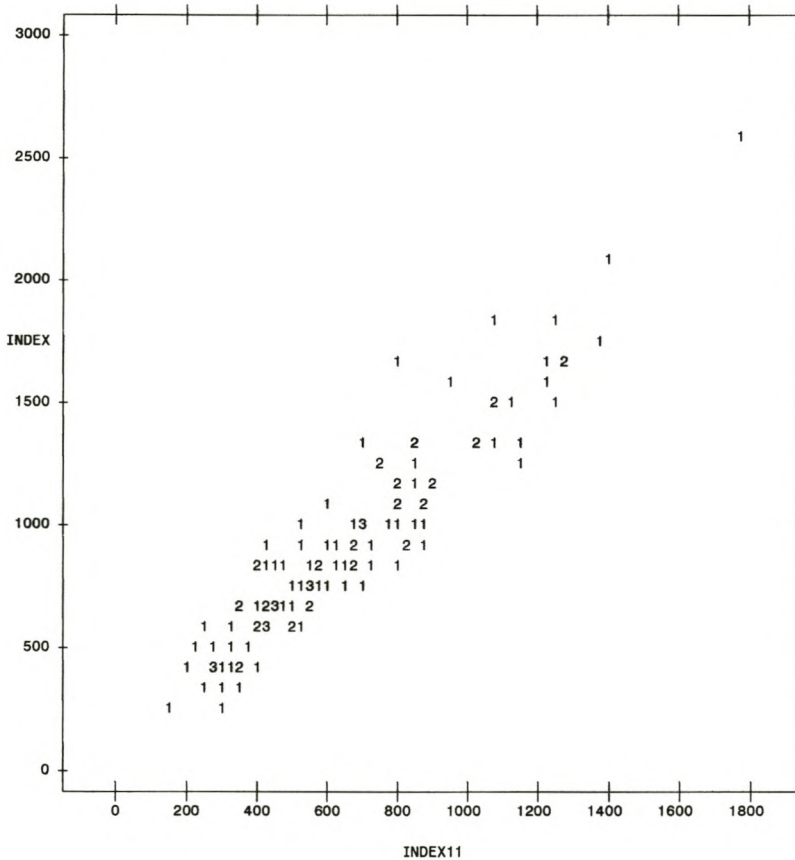


Fig 4.27 A plot of the index of whorl 1 branch 1 vs the tree index

Table 4.18 Analysis of Variance for Linear Regression.

Model 5: Index = $\beta_0 + \beta_1 \text{Indxb12}$ (i.e. whorl 1 branch 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	14770408.353	14770408.353	640.059	0.0001
Error	117	2699966.4751	23076.63654		
C Total	118	17470374.829			
Root MSE		151.90996	R-square	0.8455	
Dep Mean		901.44866	Adj R-sq	0.8441	
C.V.		16.85176			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	136.776330	33.27864202	4.110	0.0001
INDXB12	1	1.040712	0.04113587	25.299	0.0001

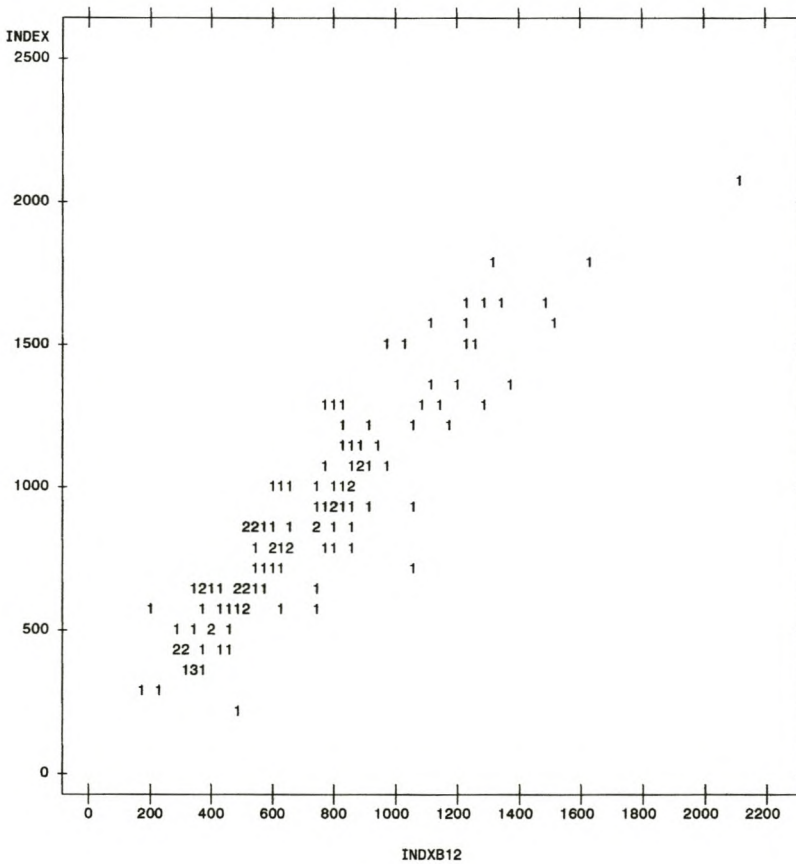


Fig 4.28 A plot of the index of whorl 1 branch 2 vs the tree index

Table 4.19 Analysis of Variance for Linear Regression.

Model 6: Index = $\beta_0 + \beta_1$ Index13 (i.e. whorl 1 branch 3)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15645180.986	15645180.986	523.605	0.0001
Error	100	2987973.8347	29879.738347		
C Total	101	18633154.82			
Root MSE	172.85757	R-square	0.8396		
Dep Mean	968.88335	Adj R-sq	0.8380		
C.V.	17.84091				

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	169.304600	38.90947310	4.351	0.0001
INDEX 13	1	0.896956	0.03919850	22.882	0.0001

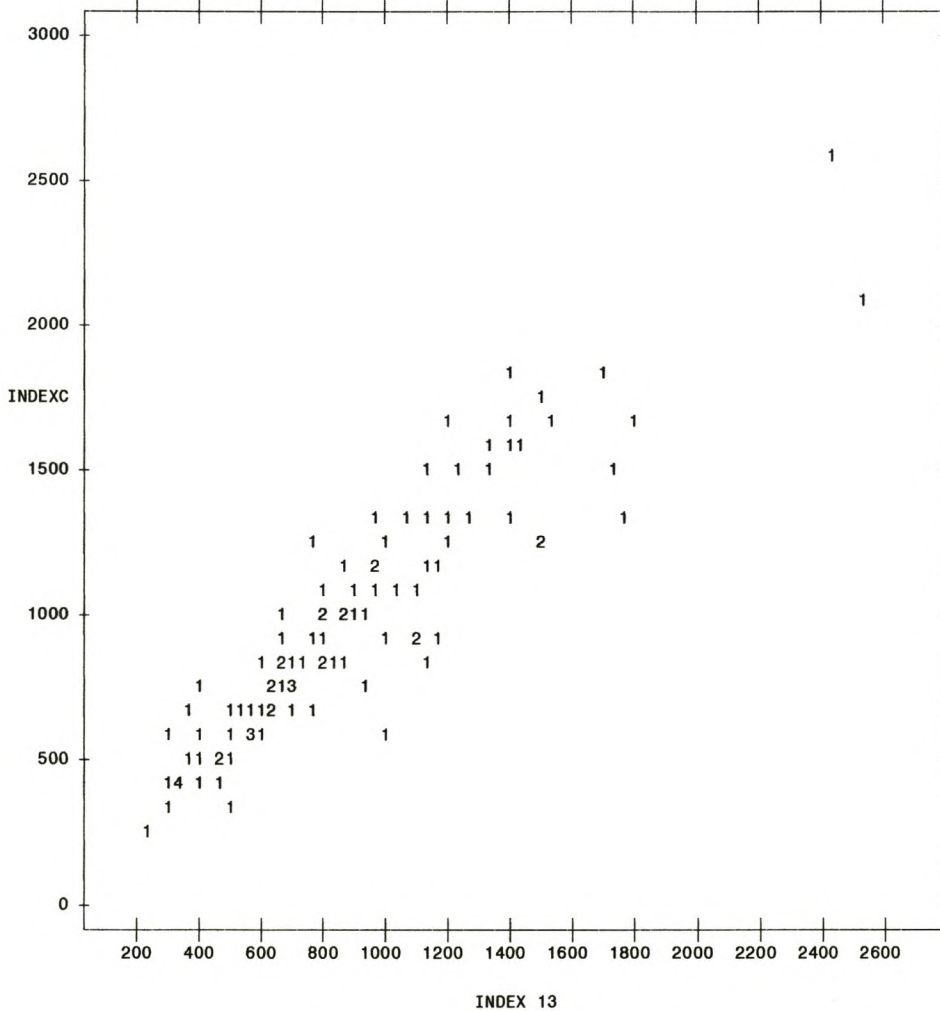


Fig 4.29 A plot of the index of whorl 1 branch 3 index vs the tree index

Table 4.20 Analysis of Variance for Linear Regression.

Model 7: Index = $\beta_0 + \beta_1$ Indexbw (i.e. the average of branch 1 and 2 in the 1st whorl)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15142721.347	15142721.347	1040.831	0.0001
Error	116	1687646.8735	14548.679944		
C Total	117	16830368.22			
Root MSE		120.61791	R-square	0.8997	
Dep Mean		894.06381	Adj R-sq	0.8989	
C.V.		13.49097			

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	91.172628	27.25141232	3.346	0.0011
INDEXBW	1	1.169885	0.03626210	32.262	0.0001

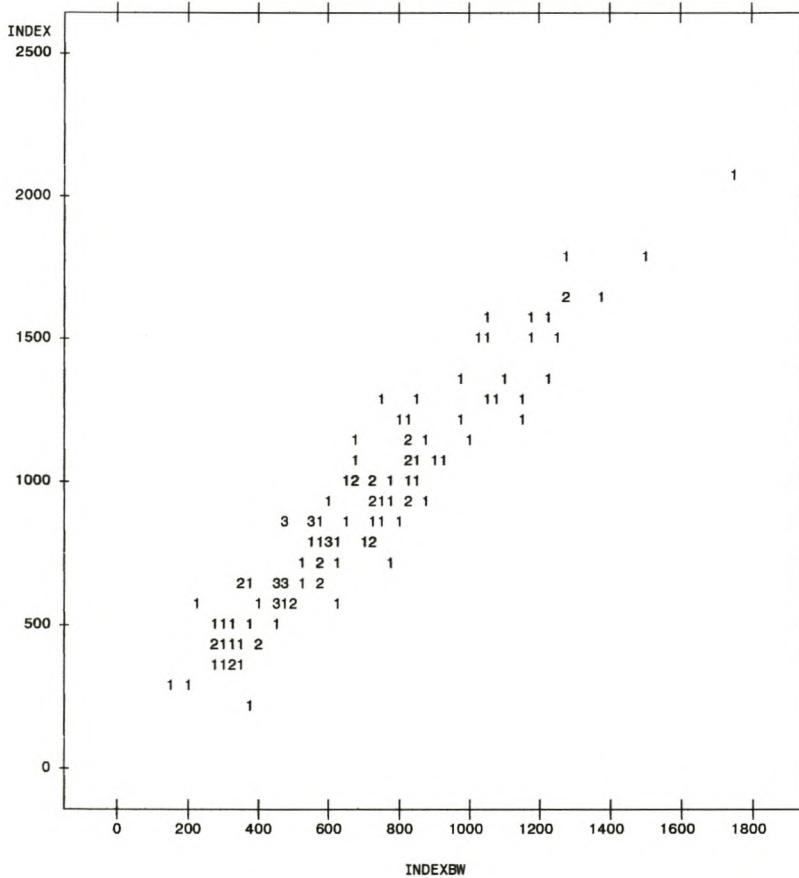


Fig 4.30 A plot of the index of the average of branch1 and2 in the 1st whorl vs the tree index

Table 4.21 Analysis of Variance for Linear Regression.

Model 8: Index = $\beta_0 + \beta_1$ Indexbwa (i.e the average of branches 1, 2 and 3 in the 1st whorl)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	18085173.345	18085173.345	1062.943	0.0001
Error	116	1973652.8176	17014.248427		
C Total	117	20058826.162			
Root MSE		130.43868	R-square	0.9016	
Dep Mean		938.57229	Adj R-sq	0.9008	
C.V.		13.89756			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	90.020376	28.66341311	3.141	0.0021
INDEXBWA	1	1.113298	0.03414731	32.603	0.0001

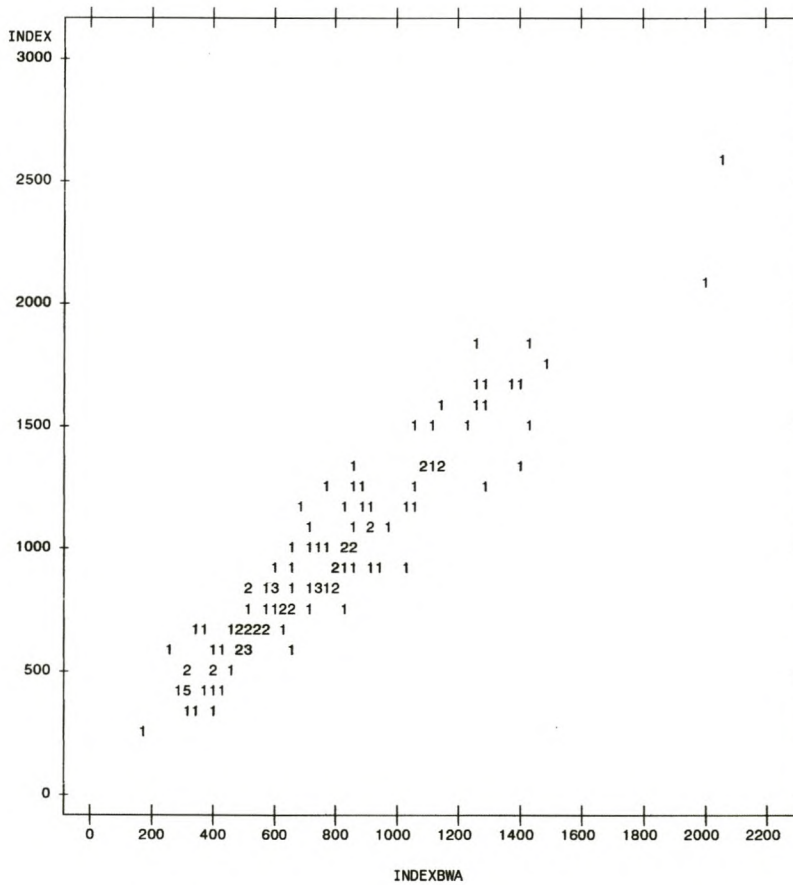


Fig 4.31 A plot of the index of the average of branch 1, 2 and 3 in the 1st whorl vs the tree index

Table 4.22 Analysis of Variance for Linear Regression.

Model 9: Index = $\beta_0 + \beta_1$ Indexbwb (i.e. average of branch 1,2, 3 and 4 on the 1st whorl)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	16634465.594	16634465.594	901.626	0.0001
Error	101	1863389.3827	18449.399829		
C Total	102	18497854.977			
Root MSE		135.82857	R-square	0.8993	
Dep Mean		940.67922	Adj R-sq	0.8983	
C.V.		14.43941			

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	56.913430	32.33232746	1.760	0.0814
INDEXBWB	1	1.095391	0.03648010	30.027	0.0001

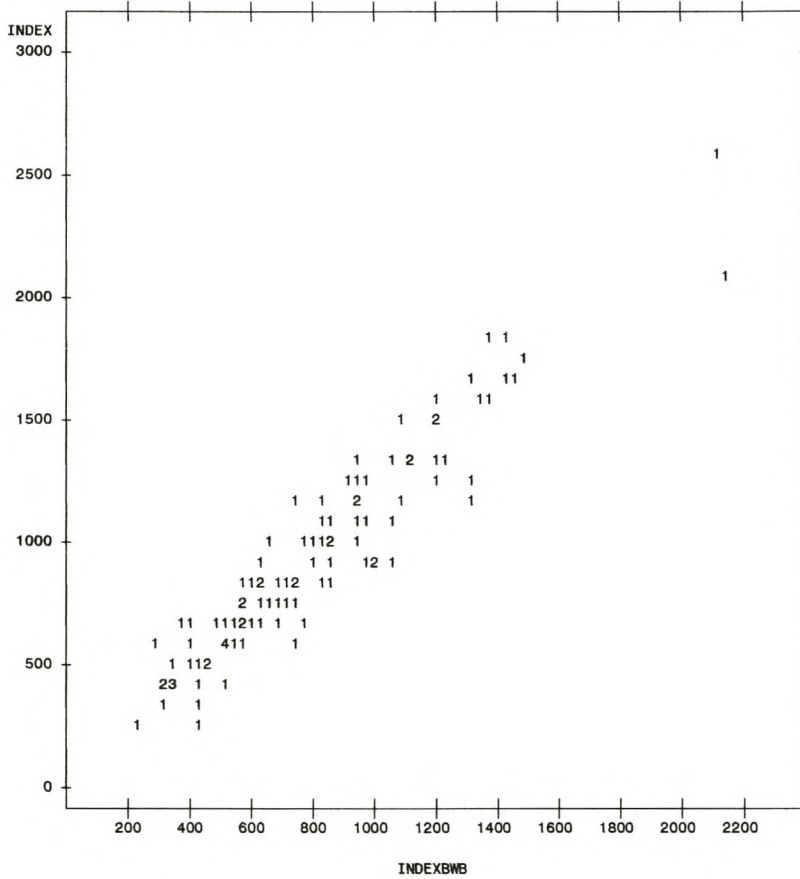


Fig 4.32 A plot of the index of the average of branches 1,2,3 and 4 n the 1st whorl vs the tree index

Table 4.23 Analysis of Variance for Linear Regression.

Model 10: Index = $\beta_0 + \beta_1$ Index21 (i.e. whorl 2 branch 1)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	16007438.422	16007438.422	553.574	0.0001
Error	114	3296484.4757	28916.530489		
C Total	115	19303922.898			
Root MSE	170.04861	R-square	0.8292		
Dep Mean	906.72836	Adj R-sq	0.8277		
C.V.	18.75409				

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	49.979526	39.68933594	1.259	0.2105
INDEX21	1	1.243813	0.05286489	23.528	0.0001

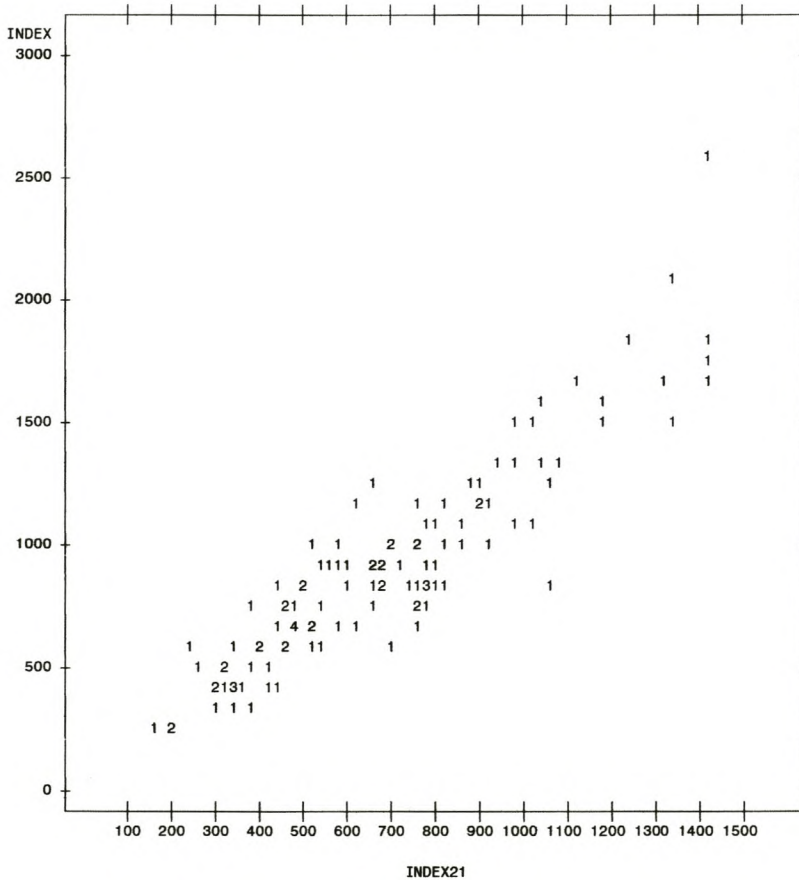


Fig 4.33 A plot of the index of whorl 2 branch 1 vs the tree index

Table 4.24 Analysis of Variance for Linear Regression.

Model 11: $Index = \beta_0 + \beta_1 Index22$ (i.e. whorl 2 branch 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	12991049.71	12991049.71	330.629	0.0001
Error	115	4518565.2309	39291.871573		
C Total	116	17509614.941			
Root MSE		198.22177	R-square	0.7419	
Dep Mean		923.82667	Adj R-sq	0.7397	
C.V.		21.45660			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	107.732171	48.47884629	2.222	0.0282
INDEX22	1	1.030106	0.05665146	18.183	0.0001

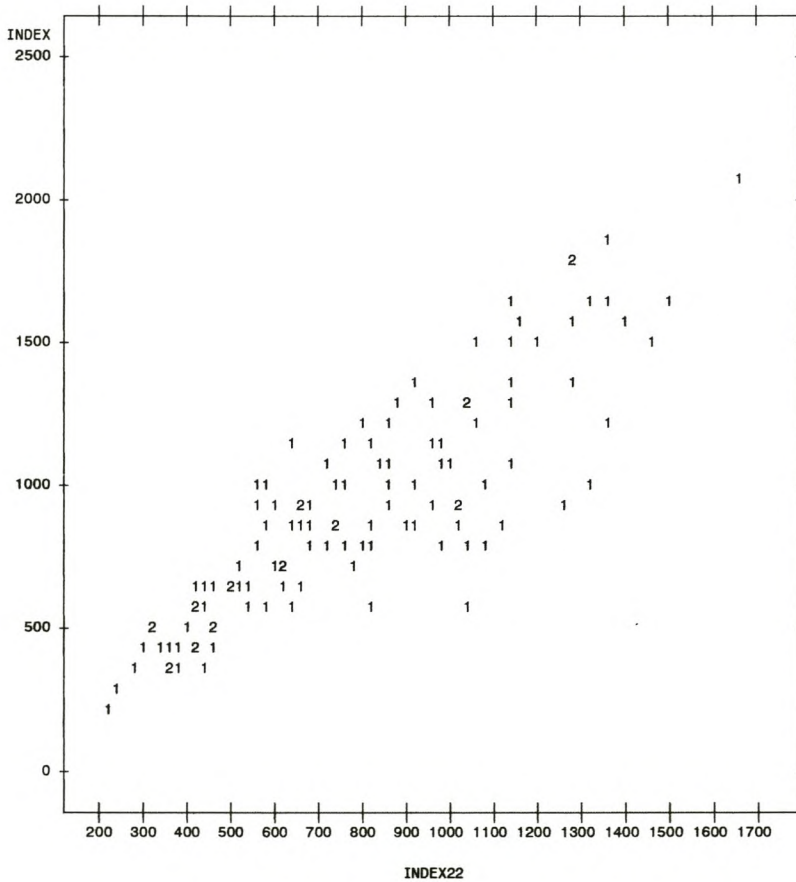


Fig 4.34 A plot of whorl 2 branch 2 index vs the tree index

Table 4.25 Analysis of Variance for Linear Regression.

Model 12: Index = $\beta_0 + \beta_1$ Indexbwc (i.e. the average of branches 1 and 2 in the 2nd whorl)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	13838335.91	13838335.91	486.909	0.0001
Error	113	3211546.5831	28420.766222		
C Total	114	17049882.493			
Root MSE		168.58460	R-square	0.8116	
Dep Mean		905.12365	Adj R-sq	0.8100	
C.V.		18.62559			

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	57.860140	41.49032984	1.395	0.1659
INDEXBWC	1	1.145302	0.05190342	22.066	0.0001

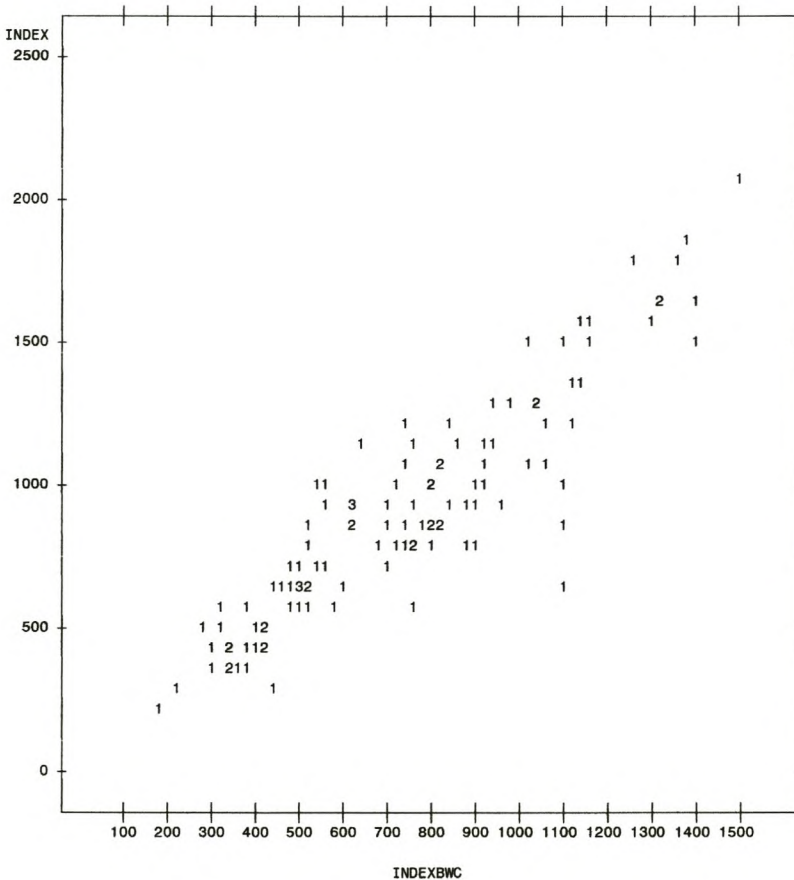


Fig 4.35 A plot of the index of the average of branches 1 and 2 in the 2nd whorl vs the tree index

Table 4.26 Analysis of Variance for Linear Regression.

Model 13: Index = $\beta_0 + \beta_1$ Indexbwd (i.e. the average of branches 1, 2, 3 in the 2nd whorl)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15112163.167	15112163.167	656.620	0.0001
Error	107	2462613.3636	23015.078165		
C Total	108	17574776.531			
Root MSE		151.70721	R-square	0.8599	
Dep Mean		920.21468	Adj R-sq	0.8586	
C.V.		16.48607			

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	53.703157	36.80547680	1.459	0.1475
INDEXBWD	1	1.090145	0.04254292	25.625	0.0001

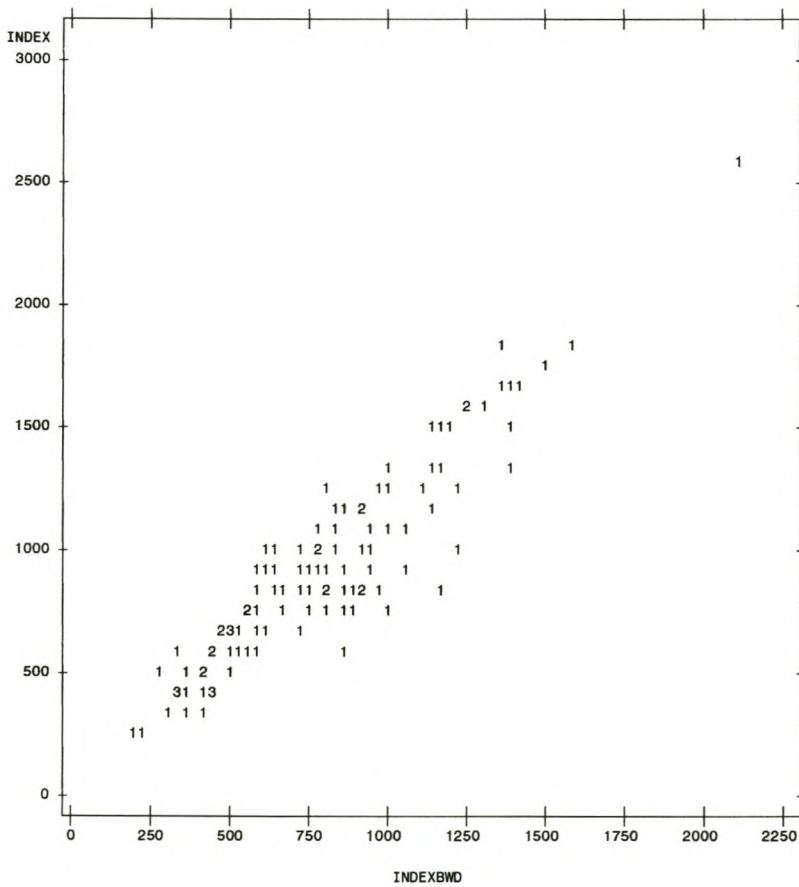


Fig 4.36 A plot of the index of the average of branches 1,2 and 3 in the 2nd whorl vs the tree index

Table 4.27 Analysis of Variance for Linear Regression.

Model 14: $\text{Index} = \beta_0 + \beta_1 \text{Indexbwe}$ (i.e. the average of the largest branches in both of whorl 1 and 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	15790965.895	15790965.895	1139.789	0.0001
Error	115	1593243.5142	13854.291428		
C Total	116	17384209.409			
Root MSE	117.70425	R-square	0.9084		
Dep Mean	900.71521	Adj R-sq	0.9076		
C.V.	13.06787				

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	28.431777	28.03522111	1.014	0.3126
INDEXBWE	1	1.291087	0.03824223	33.761	0.0001

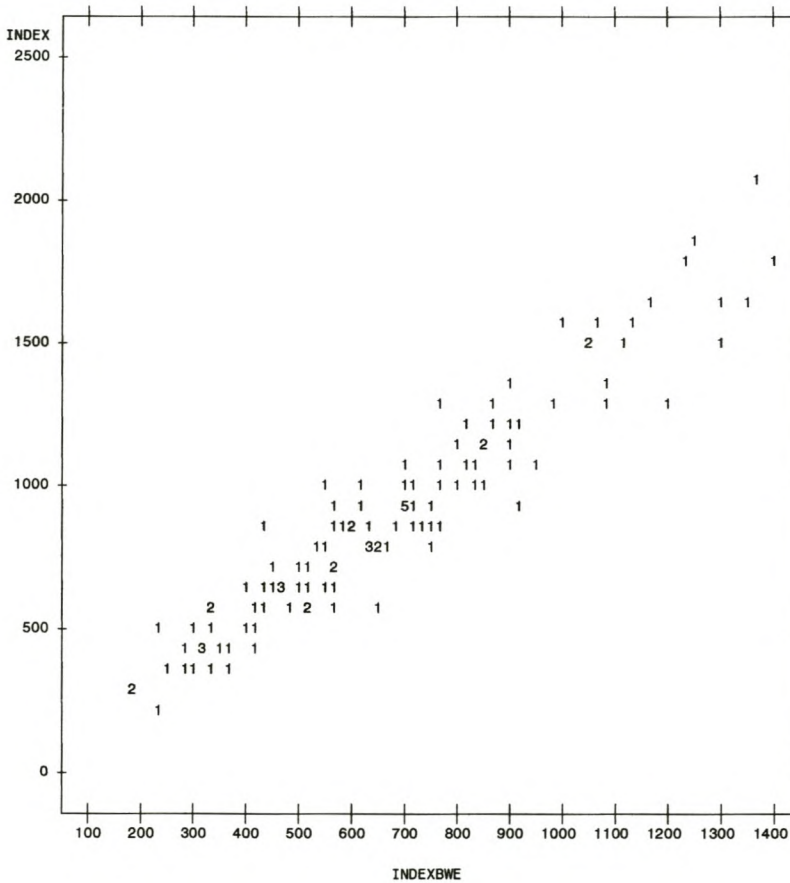


Fig 4.37 A plot of the index of the average of the largest branches in whorl 1 and 2 vs the tree index

Table 4.28 Analysis of Variance for Linear Regression.

Model 15: Index = $\beta_0 + \beta_1$ Indexbwf (i.e. the average of the 2 largest branches in both of whorl 1 and 2)

Source	DF	Sum of Squares	Mean Square	F Value	Prob>F
Model	1	18572247.375	18572247.375	1362.551	0.0001
Error	114	1553876.7056	13630.497417		
C Total	115	20126124.08			
Root MSE		116.74972	R-square	0.9228	
Dep Mean		934.45862	Adj R-sq	0.9221	
C.V.		12.49384			

Parameter Estimates					
Variable	DF	Parameter Estimate	Standard Error	T for H0: Parameter=0	Prob > T
INTERCEP	1	-35.473146	28.42446339	-1.248	0.2146
INDEXBWF	1	1.311282	0.03552382	36.913	0.0001

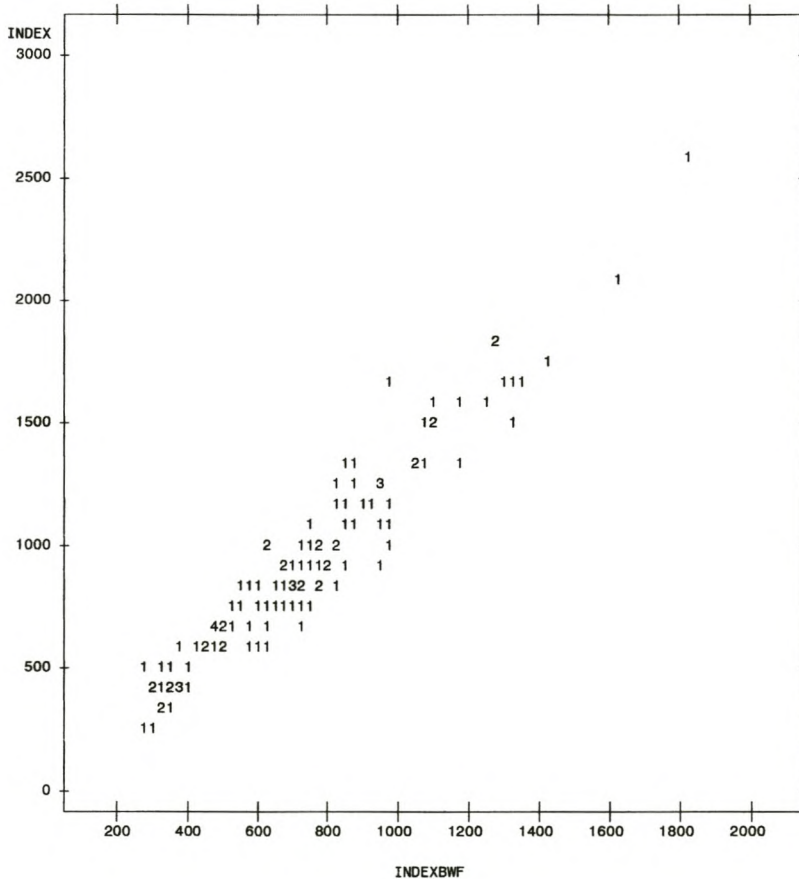


Fig 4.38 A plot of the index of the average of branches 1 and 2 of whorl 1 and 2 vs the tree index

Table 4.29 A summary of the regression analysis for generated whorls data with the tree value

Model	Abbreviation For variable	Variable (means)	R ²	Regression equation y - tree index x - variables
1	Index1	Whorl 1	0.8809	y=11.57+0.95x
2	Index2	Whorl 2	0.8020	Y=127.53+0.88x
3	Index12	Avg (whorl 1, 2)	0.9228	Y=35.24+1.01x
4	Index11	Whorl 1 branch 1	0.8766	Y=92.15+1.26x
5	Indxb12	Whorl 1 branch 2	0.8455	y=136.78+1.04x
6	index13	Whorl 1 branch 3	0.8396	Y=169.30+0.89x
7	Indexbw	Whorl 1 avg(branch 1,2)	0.8997	Y=91.17+1.17x
8	Indexbwa	Whorl 1 avg(branch 1,2,3)	0.9016	y=90.02+1.11x
9	indexbwb	Whorl 1 avg(branch 1,2,3, 4)	0.8983	y=56.91+1.10x
10	Index21	Whorl 2 branch 1	0.8292	Y=49.98+1.24x
11	Index22	Whorl 2 branch 2	0.7419	Y=107.73+1.03x
12	Indexbwc	Whorl 2 avg(branch 1,2)	0.8116	Y=57.86+1.15x
13	Indexbwd	Whorl 2 avg(branch 1,2,3)	0.8599	Y=53.70+1.09x
14	Indexbwe	avg (index11+index21)	0.9084	Y=28.43+1.29x
15	Indexbwf	avg (indexbw+indexbwc)	0.9228	y=-35.4+1.13x

4.8 Ranking of seedlot means

The results of a multiple comparison of means carried out using the Student-Newman-Keuls (SNK) are shown in Table 4.30. The actual means of the seedlots are given in Table 4.31. The interpretation of Table 4.30 is as follows: Families (seedlots) in the three groups (highlighted by the shading) are declared to have means that are significantly different according to the SNK criterion. Thus from the multiple mean comparison of the seedlot indices it can be inferred that up138 (note that the up has been conveniently eliminated in Table 4.30, otherwise all families numbered start with up as listed in Chapter 3.) is significantly different from up142, up189, up136, up137 up141 and up186. Also, all families between up165 and up149 are declared not significantly different. Three groups are therefore, categorized as follows.

Group A	up138
Group B	up165 up146 up175 up155 z17 z44 up172 up144 up152 up184 up 156 up153 up143 z51 up159 up190 up149.
Group C	up 142 up189 up 136 up141 up186

It can be observed that the indices come up with a similar order of rankings (see also Table 4.3). It can be noted that indices that had higher R^2 values gave rankings of seedlots that are more comparable with that of the tree index. Contrary, the index of the whorl 1 branch 3 (index13), which has the lowest R^2 value gave a poor ranking e.g. up138 is not ranked 1st as shown by the rest of the indices.

Table 4.30 The Ranking of the seedlots using different indices. The SNK grouping considered is that of the tree index (index). The rest of the indices are therefore compared in terms of their relative effectiveness in grouping families in the prescribed order.

Indices	Group A										Group B										Group C									
Index	138	165	146	175	155	z17	z44	172	144	152	184	156	153	143	z51	159	190	154	149	142	189	136	137	141	186					
Index1	138	146	175	165	153	155	152	z17	z44	184	172	144	156	154	159	136	z51	143	190	149	142	141	137	189	186					
Index2	138	146	175	155	165	152	144	184	172	143	156	z17	153	z51	z44	149	154	159	189	142	137	136	190	186	141					
Index12	138	146	175	153	165	184	z17	z44	155	152	172	159	154	156	144	z51	136	143	190	149	141	142	189	137	186					
Index11	138	146	153	165	175	z17	155	152	172	184	144	z44	159	154	143	136	190	149	z51	156	142	137	141	186	189					
Indxb12	138	146	175	153	165	184	z17	z44	155	152	172	159	154	156	144	z51	136	143	190	149	141	142	189	137	186					
Index13	165	138	175	146	153	155	z44	z17	152	159	172	z51	136	184	144	156	143	154	149	141	190	142	137	189	186					
Indexbw	138	146	153	175	165	z17	184	155	152	z44	172	144	159	154	143	136	156	z51	190	149	142	141	137	189	186					
Indexbwa	138	165	146	175	153	155	z17	z44	152	172	159	144	184	136	z51	154	143	156	190	149	141	142	137	189	186					
Indexbwb	138	165	146	175	152	155	z44	z17	136	172	159	154	153	144	184	z51	143	156	190	149	141	142	137	189	186					
Index21	138	155	146	175	165	184	172	152	156	144	143	137	153	z17	136	154	z51	142	190	z44	159	149	189	186	141					
Index22	138	146	155	165	175	152	184	172	143	149	153	z44	189	156	z17	184	159	z51	142	136	154	190	186	137	141					
Indexbwc	138	146	155	175	165	152	172	144	143	156	153	z17	184	z44	149	189	136	159	z51	142	154	190	186	137	141					
Indexbwd	138	146	155	165	175	152	156	144	172	143	153	149	142	z17	z51	184	z44	159	136	154	186	190	189	137	141					
Indexbwe	138	146	175	155	165	153	152	184	172	z17	144	143	156	154	136	z44	159	137	z51	190	149	142	189	186	141					
Indexbwf	138	146	175	165	155	153	152	184	172	z17	144	z44	143	156	159	154	136	z51	149	190	142	189	137	141	186					

Table 4.31 Illustration of the ranking of the seedlots using a selection of indices (seven best indices based on R^2 values). Note that the seedlots are replaced by numbers for clarity)

Seedlot	Index	Index1	Index12	Indexbwf	Indexbw	Indexbwa	Index11	Indexbwe
Up138	1	1	1	1	1	1	1	1
Up165	2	4	5	4	5	2	4	5
Up146	3	2	2	2	2	3	2	2
Up175	4	3	3	3	4	4	5	3
Up155	5	6	9	5	8	6	7	4
Z17	6	8	7	10	6	7	6	10
Z44	7	9	8	12	10	8	12	16
Up172	8	11	11	9	11	10	9	9
Up144	9	12	15	11	12	12	11	11
Up152	10	7	10	7	9	9	8	7
Up184	11	10	6	8	7	13	10	8
Up156	12	13	14	14	17	18	20	13
Up153	13	5	4	6	3	5	3	6
Up143	14	18	18	13	15	17	15	12
Z51	15	17	16	18	18	15	19	19
Up159	16	15	12	15	13	11	13	17
Up190	17	19	19	20	19	19	17	20
Up154	18	14	13	16	14	16	14	14
Up149	19	20	20	19	20	20	18	21
Up142	20	21	22	21	21	22	21	22
Up189	21	24	23	22	24	24	25	23
Up136	22	16	17	17	16	14	16	15
Up137	23	23	24	23	23	23	22	18
Up141	24	22	21	24	22	21	23	25
Up186	25	25	25	25	25	25	24	24

The actual summary (Table 4.32) of the seedlot means has been sorted by the mean indices in order to give an overview on the ranking of the seedlots using the conventional parameters namely the diameter, height and the volume. It can be noted that if the seedlots were to be sorted on the bases of the mean diameter, mean height, and mean volume, some changes in the positions of seedlots can occur. The point that is worth noting is that the use of the mean indices can provide a more general method of describing the quality traits of the seedlots i.e. in terms of its conformance to good volume, good branching (flat and small). Thus, it can be said that the ranking of the seedlots on the bases of their diameter, height, and / or volume has some limitations in as far as giving a broader picture on what the tree really looks like. For example, even though seedlot up172 and up143 have similar volumes they are ranked 8th and 14th respectively because up143 (16mm) has much bigger branches than up172 (13mm). However, as noted earlier, it should be appreciated that these changes in rankings do not affect the volume aspect in any considerable way.

Table 4.32 A summary of the mean diameter, height, branch diameter, branch angle and the index for seedlots.

SEEDLOT	D(cm)	HT(m)	BDX(mm)	BAX(deg)	VOL (*10 ⁴ m ³)	INDEX 0 ² m ² deg
up138	7.78	5.4	13.95	66.6	330.4	1574
up165	7.1	5.4	14.83	70.28	282.1	1364
up146	7.6	5.14	15.31	66.6	305.9	1323
up175	7.68	5.2	16.43	67.74	319.7	1317
up155	7.3	5.06	16.62	70.5	272.9	1175
z17	6.68	4.8	13.73	66.28	223.4	1059
z44	6.22	4.38	14.92	77.23	183.1	1012
up172	6.26	4.72	12.96	66.39	192.1	968.6
up144	6.8	4.6	14.42	65.48	216.4	968.1
up152	7.02	4.72	17.36	66.68	237.9	959.8
up184	6.58	4.76	16.06	70.59	210.8	928.9
up156	6.5	4.46	14.61	67.41	191.8	923.6
up153	5.94	4.8	12.56	65.67	170.7	891.9
up143	6.54	4.36	16.06	66.07	195.5	823.2
z51	5.92	4.5	13.5	67.58	163.1	818.6
up159	5.54	4.34	11.86	69.58	139.6	800
up190	5.74	4.64	13.82	70.62	154.9	777.4
up154	5.64	4.06	13.29	70.5	143.9	764.3
up149	5.72	4.04	12.54	70.29	135.2	754.4
up142	5.22	4.04	12.42	67.95	122.3	740.6
up189	5.84	4.34	14.05	67.48	160	722
up136	5.62	4.5	12.69	61.47	152.2	713.6
up137	5.52	4.08	13.4	66.6	128.2	629.9
up141	5.44	4.04	14.55	64.04	126.4	567.1
up186	5.12	4.12	13.76	66.89	115.5	538.8

Table 4.33 has been prepared to demonstrate just how effective the different indices can be compared with the tree index using discriminant analysis (Sadie, *pers comm*). In this analysis the number of seedlots excluded from the tree index based SNK groupings (see table 4.30), are recorded as deviations from the tree index. For example, it can be shown that if index1 is used, up149 will fall in the Group C (instead of Group B) and up136 will falls in the Group B (instead of Group C). Thus, in Table 4.32 these are recorded as deviations (i.e. the number 1 under Group C and the number 1 under Group B that corresponds to index1). Therefore, two seedlots are not in their prescribed position i.e. when the tree index in used as a reference point.

The deviations shown in Table 4.33 are not very convincing because most indices have a percentage of seedlots that were wrongly placed. However some interesting observations are worth mentioning.

- 1) The index of the 3rd branch of the first whorl (index13) appears to be the poorest predictor of the tree index. A total of 6 seedlots (24%) were incorrectly placed. This

evidence is supported by the fact that this index is the only index that failed to place the family up138 as the best entry as shown in Table 4.30.

- 2) The index of the average of the average of the first two branches in the first and second whorl (indexbwf) is proving to be good at predicting the seedlot index.

Table 4.33 Deviations from the tree index. These were seedlots that fell outside the relevant groups as shown in Table 4.30.

Indices	No. of Seedlots inappropriately grouped (SNK method)			Percentage deviations
	Group A	Group B	Group C	
Index	0	0	0	0
Index1	0	1	1	8
Index2	0	1	1	8
Index12	0	1	1	8
Index11	0	1	1	8
Indexb12	0	1	1	8
Index13	0	3	3	24
Indexbw	0	1	1	8
Indexbwa	0	1	1	8
Indexbwb	0	1	1	8
Index21	0	3	3	24
Index22	0	2	2	16
Indexbwc	0	2	2	16
Indexbwd	0	2	2	16
Indexbwe	0	2	2	16
Indexbwf	0	1	1	8

- 3) The second whorl is less accurate in ranking the seedlots, an observation that agrees with R^2 values and other observations cited earlier in the text.

The rank correlation of the the mean indices with the tree index shown in table 4.34 support the preceeding observations on the relative effectiveness of the different indices. The highest correlations are obtained from index 12 and indexbwf which has been earlier identified as the the best indices.

Table 4.34 Rank correlation of mean indices of whorls and whorls and branch combinations with the tree mean

	INDEX1	INDEX2	INDEX12	INDEX11	INDEXB12	INDEX21	INDEX22
INDEX	0.94297	0.89236	0.96576	0.92832	0.93055	0.90200	0.85017
	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
	119	115	116	118	119	116	118
	INDEXBW	INDEXBWA	INDEXBWB	INDEXBWC	INDEXBWD	INDEXBWE	INDEXBWF
INDEX	0.94021	0.92790	0.94533	0.90481	0.90420	0.92521	0.95282
	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
	118	118	104	114	110	116	116

4.9 A comparison of cost effectiveness of different indices

To answer the question of whether one index is cheaper than the other is a very complex exercise and constitutes a study of its own. However, a comparison based on the relation

$$R = \text{Std error (1)} / \text{Std error (2)} \quad (\text{van Laar, pers comms}) \quad \text{where}$$

$$\text{Std Err} = \text{Mse}/n \quad (\text{where Mse is the mean square error and } n \text{ the sample size})$$

could give an idea on how one index relates to the other in terms of its relative effectiveness from a cost perspective.

An illustration of this method is as follows:

Consider all mean indices calculated whose related indices are based on whorl 1 (i.e. index1, index11, indexbw, indexbwa, indexbwb). Suppose one considers measuring a single branch in this whorl (i.e. index11) as opposed to measuring the whole whorl (index1). This suggests that an effort equivalent to 1.62 (982.94/606.86) is required to assess the entire whorl compared to a single branch on the whorl (Table 4.35). Knowing that the R^2 values (Table 4.29) of the index1 and index11 are 0.8809 and 0.8766 respectively one can choose to stick to the latter instead of investing on additional effort with an insignificant improvement in accuracy. Thus, though the R^2 value is known to increase with the sample size one should seek a balance between the additional effort required and the improvement in accuracy achievable. The effort required to evaluate indices: index11, indexbw, indexbwa and indexbwb can be compared in the same way.

This argument can be extended to the second whorl and one can see the justification of a smaller sample size provided the tree is normal and that larger branches are used in the assessment.

Table 4.35 Matrix of standard errors of the mean indices

Variable	index1	index2	index12	index11	indexb12	indexbw	indexbwa	index21	index22	indexbwb	indexbwc	indexbwd	indexbwe	indexbwf	
Std Err	982.94	1313.28	952.49	606.86	948.12	721.84	840.47	787.86	1144.43	1021.49	849.20	1066.45	566.28	649.93	
index1	982.94	1.00	0.75	1.03	1.62	1.04	1.36	1.17	1.25	0.86	0.96	1.16	0.92	1.74	1.51
index2	1313.28		1.00	1.38	2.16	1.39	1.82	1.56	1.67	1.15	1.29	1.55	1.23	2.32	2.02
index12	952.49			1.00	1.57	1.00	1.32	1.13	1.21	0.83	0.93	1.12	0.89	1.68	1.47
index11	606.86				1.00	0.64	0.84	0.72	0.77	0.53	0.59	0.71	0.57	1.07	0.93
indexb12	948.12					1.00	1.31	1.13	1.20	0.83	0.93	1.12	0.89	1.67	1.46
indexbw	721.84						1.00	0.86	0.92	0.63	0.71	0.85	0.68	1.27	1.11
indexbwa	840.47							1.00	1.07	0.73	0.82	0.99	0.79	1.48	1.29
index21	787.86								1.00	0.69	0.77	0.93	0.74	1.39	1.21
index22	1144.43									1.00	1.12	1.35	1.07	2.02	1.76
indexbwb	1021.49										1.00	1.20	0.96	1.80	1.57
indexbwc	849.20											1.00	0.80	1.50	1.31
indexbwd	1066.45												1.00	1.88	1.64
indexbwe	566.28													1.00	0.87
indexbwf	649.93														1.00

Variable	Std Err
index1	982.944
index2	1313.28064
index12	952.488
index11	606.86264
indexb12	948.1248
indexbw	721.8412
indexbwa	840.471074
index21	787.8608
index22	1144.42846
indexbwb	1021.48899
indexbwc	849.200813
indexbwd	1066.45345
indexbwe	566.27592
indexbwf	649.930081

Another way of comparing the efficiency of the indices data would be to look at the intraclass correlations.

The intraclass correlation can be defined as

$$t = \sigma_f^2 / (\sigma_f^2 + \sigma_e^2) \text{ (Falconer, 1980)}$$

where σ_f^2 is the family variance and σ_e^2 is the error variance (Table 4.36). Intra-class correlation is directly related to the heritability (Falconer, 1980).

Inspection of the intraclass coefficients give the following categories:

- a) Index1, index11, indexbwa indexbwb : 0.064, 0.058, 0.061, 0.058 respectively
 b) Index2, index21, indexbwc, indexbwd : 0.020, 0.012, 0.017, 0.017
 c) Index12 indexbwe, indexbwf : 0.049, 0.039, 0.041

It confirms previous observations that sampling fewer branches can describe the branching characteristics of a tree significantly, even for heritability estimates. The cost-saving would be an important trade-off.

Table 4.36 Calculation of intraclass correlations for the mean indices

Treatment	Mean square Error treatment	Error variance(σ^2_e)	Family variance (σ^2_f)	Intraclass correlation (t)
index1	332138.1	122868.6	8370.78	0.063783
Indexbwa	267272.2	101697.5	6622.988	0.061143
Indexbwb	283502.1	111342.3	6886.392	0.058246
index11	191725.7	75857.8	4634.716	0.057579
Indexbw	222464.7	90230.2	5289.38	0.055375
index12	272860.8	119061.1	6151.988	0.049132
indexb12	267547.9	118515.6	5961.292	0.047891
Indexbwf	166312	79941.4	3454.824	0.041427
Indexbwe	143105.9	70784.5	2892.856	0.039264
index2	250022.8	164160.1	3434.508	0.020493
Indexbwd	177447.3	123708.6	2149.548	0.017079
Indexbwc	149226.3	104451.7	1790.984	0.016857
index21	128240	98482.6	1190.296	0.011942
index22	182887.7	140764.7	1684.92	0.011828

4.5 Repeatability and regressions

4.10.1 Calculation of repeatability

SAS was used to generate an ANOVA from which the error (within trees) and between trees variances were obtained in order to calculate the repeatability.

A. The repeatability for the branch angle was calculated as follows:

$$r = (\sigma_w^2 / \sigma_w^2 + \sigma_e^2)$$

$$r = 41.14 / 41.14 + 43.20$$

$$r = 0.49$$

B. The repeatability for the branch diameter was calculated as follows:

$$r = (\sigma_w^2 / \sigma_w^2 + \sigma_e^2)$$

$$r = 18.11 / 18.11 + 4.77$$

$$r = 0.79$$

This result shows that a minimum of 4 – 5 branches can be used for the branch angle measurement (Appendix 5). Branch diameter has a higher repeatability and one can sample even fewer branches (2 branches) without sacrificing substantially on accuracy.

4.10.1 Regressions of different subsets of data on the tree mean (i.e. the branch diameter and the branch angle)

Coefficients of determination (R^2) obtained from regressions of the branch diameter and or branch angle on the tree means for sets of whorls and branches combinations, using the model: $y = \beta_0 + \beta_1 X + \varepsilon$

where

y = tree mean value and X = subset of whorls and branch combinations being regressed on the tree mean, are presented in Table 4.37.

Table 4.37 Summary of R² - values from the regression of subsets of data on the tree mean (i.e. the branch diameter and the branch angle)

Y	X	R ² (bdx)	R ² (bax)
Tree mean	Whorl 1	0.6743	0.6348
Tree mean	Whorl 2	0.5014	0.7401
Tree mean	Whorl 1&2 mean	0.8190	0.8285
Tree mean	Whorl 1 branch 1 (A)	0.5817	0.3689
Tree mean	Whorl 1 branch1 & 2 mean (B)	0.6405	0.3627
Tree mean	Whorl 2 branch 1 (A*)	0.3777	0.3655
Tree mean	Whorl 2 branch1 & 2 mean (B*)	0.6379	0.4928
Tree mean	A & A* mean	0.4446	0.5637
Tree mean	B & B* mean	0.7684	0.7275

The R² values suggest that there is a reasonably good opportunity of determining the tree value based on a mean of fewer branches. As expected the R² value is highest when one performs a regression of the mean of 2 whorls with the tree value. The R² –value for the mean diameter of 2 branches in the second whorl is slightly lower than that of the first whorl.

4.11 Sample size estimation procedures.

The calculation of the optimum number of measurements needed for the branch diameter and the branch angle.

$$n = ((z_{\sigma/2})^2 \sigma^2) / E^2$$

Branch angle

$$z_{\sigma/2} = 1.96$$

$$\sigma^2 = (10.16)^2$$

$$E^2 = (20/2)^2$$

$$n = ((z_{\sigma/2})^2 \sigma^2) / E^2$$

$$n = (1.96)^2 (10.16)^2 / (20/2)^2$$

$$n = 3.97$$

Branch diameter

$$z_{\sigma/2} = 1.96$$

$$\sigma^2 = (4.63)^2$$

$$E^2 = (6/2)^2$$

$$n = ((z_{\sigma/2})^2 \sigma^2) / E^2$$

$$n = (1.96)^2 (4.63)^2 / (8/2)^2 \dots\dots$$

$$n = 5.13$$

This analysis suggests that we can conveniently choose to take either 4 or 5 branches without necessarily sacrificing on quality. The addition of more observations can indeed

improve the accuracy of the estimates of a population at additional cost though. It is therefore of paramount importance that the breeders continue to explore methods of evaluating the upper limits of population sizes.

CHAPTER 5

5.0 Discussion and conclusions

With the exception of stem straightness all characteristics assessed in this study followed a normal distribution. This condition conforms to the underlying assumptions that are made during the evaluation of genetic parameters i.e. genetic variances, heritabilities and the breeding values of an additive trait. The distribution of stem straightness is skewed and lacks all the properties of a normal distribution. Stem straightness was relatively uniform in this material. It should be remembered that the material used came from a first generation i.e. a progeny trial of open pollinated progeny of plus-trees. It is tempting to suggest that the ease of selecting for stem straightness as stated by Shelbourne *et al*, (1972) is demonstrable in this study by the difficulty encountered in discriminating the score for stem straightness. It would appear that the plus - tree selection was probably able to deliver trees which were relatively uniformly straight from the very 1st generation of mass selection. However, this statement can be misleading because no evaluations of genetic parameters were made to support this comment. It can be inferred from the distribution of the stem straightness that stricter scoring should be employed for the distribution to be normal. It is therefore recommended that the scoring for stem straightness should be adapted for, among other factors, different species, cultural practices and ages if it is to be used effectively. It should be pointed out that though stem straightness is under strong genetic influence, its phenotypic expression varies with different environments / sites. For example, it has been found that trees on relatively good sites tend to be more crooked as compared to those on poorer sites (Bunn, 1966).

The correlation of subjective assessment and objective assessments is another important aspect that warrants attention in this study. It has been observed that good correlations exist between the branch angle score and the branch angle (measured). The relationship was almost perfectly linear. Again, the overall score (the average of the subjective scores) was significantly correlated with the tree index (which defined the quality of the tree based on its volume, branch diameter and branch angle). Thus, it can be argued that subjective assessments can be used to describe the stem quality of a tree with reasonable efficiency especially if extra care is given to the scoring (i.e. by ensuring consistency). The observations made in this study agree with observations made by Haapenen *et al* (1996),

who suggested that the use of subjective scores warranted further investigation with the view of adopting it as a replacement to the often costly procedures of objective assessments. However, there were some limitations in the investigation of this aspect. Firstly, the overall score used was somewhat influenced by the inappropriate straightness scoring scale (as discussed earlier). Secondly, The sample size was small for any conclusive evidence to be made. It can only be recommended that more intensive studies should be undertaken to achieve this goal. It is necessary that a review is first made on the scoring procedures, e.g., the investigator might need to compare the overall score with the actual phenotype of the trees whilst still in the field to ensure that consistency is maintained through the scoring exercise. Once the system of scoring is in place it can be envisaged that trees can be assessed readily and at minimal costs.

The indices of whorls and whorl and branch combinations used in this study conform reasonably to the tree index. The reason for some of the deviations in ranking of families when applying the different indices, is that the means of the indices were somewhat inflated by high index values arising from whorls with fewer and / or smaller branches. For example, if a whorl has 2 branches with branch diameters of 8mm and a wide angle (note that branches with this diameter often have an angle of 90°) its index values tend to be very high (see index formula). Thus, the extreme values of the indices are responsible for the rather inaccuracy in the determination of the means of the indices. It would appear that for a more accurate prediction of the tree index the extreme values should be eliminated during editing to guarantee more concise predictions.

The larger branches have been observed to yield better predictions of the tree index. In the example of whorls and branches observations it has been noted that the 1st branch (largest) in every whorl has better correlation with the tree index compared to the successive branches. Again, the index for branches of the 1st whorl was observed as having a better correlation with the tree index compared to all the branches in the 2nd whorl. An important point to note about this is that the 2nd whorl does not necessarily have smaller branches than the 1st whorl. It can be inferred that the 1st whorl would generally give better predictions for the tree index than the 2nd whorl.

Important questions to answer would be: 1) Do the larger branches give better indices than the smaller branches? 2) Does it matter where the measured branches came from i.e.

which whorl the branch came from? 3) What is the optimum number of branches required per whorl for better prediction of the tree index? The first question has been partly answered in the last paragraph. Larger branches (i.e. diameter) in their respective whorls have been found as having better correlations with the tree index. As noted in Chapter 4, the correlation decreases progressively from the first branch to the last branch within each whorl. However, the change in the size of the branches between whorls does not necessarily give the better correlation. The answer to question 2 therefore is that branches of the first whorl tend to be better correlated to the tree index compared to the 2nd whorl. To answer the last question the linear regressions for the coefficients of variation as well as the plots of index12, indexbwa, indexbwc, indexbwbc, indexbwd, indexbwe and indexbwf can be used as an illustration. The highest correlation found was given by indexbwf and index12 ($R^2 = 0.9228$). These indices as stated earlier, was obtained from an average of 4 branches i.e. the 2 largest of the 1st and the 2nd whorl and the mean of branches in the first and second whorl. This suggests that fewer branches can be used to assess a tree with the required efficiency and at low cost. The lowest correlation was found from indexbwc i.e. the index that was calculated from measuring the 1st two branches in whorl 2.

The ranking of the seedlots provided a good tool in the quantification of the effectiveness of the different indices in a more practical environment. It has been observed that some of the indices gave almost a duplicate ranking of seedlots as provided by the tree index. This suggests that sampling procedures outlined earlier, e.g., assessment of two branches in the 1st and 2nd whorl instead of the whole tree, can be applied. Thus, costs can be reduced greatly by taking a smaller sample without affecting the selection process in any negative sense.

The choice of which branches require assessment for an effective determination of the stem quality traits and at reasonable costs remains a prerogative of the individual breeder. For example it can depend on amount of resources available and the degree of accuracy required in the trait assessment. Clearly, a breeder whose interest is to produce trees with larger volume with a lesser emphasis on the knot size e.g. pulpwood production, might find that measuring just the 1st branch in the 1st whorl can provide a good sample. Whereas a breeder whose interest is to produce timber for sawtimber, veneer or plywood might want to measure the first two bigger branches in the 1st and 2nd whorl for a better assessment.

The general consideration is that the different sampling procedures provide different levels of precision in the determination of stem quality characteristics.

Outliers and observations that were influential i.e. smaller branches were eliminated (Van Laar, 1991) in order to improve the regression equations by applying the method of studentized residuals. The editing of the data improved the regression models. Note that the data editing was effected only in this step. Otherwise, unedited data was used to explore the applicability of the index formula in the different subsets of mean indices used. The idea was to highlight the pros and cons of the different indices. For example small, vestigial branches and / or large, fork-like branches were found to impact greatly on the index. It was concluded that only the normal branches gave good predictions of the overall branching characteristic of the tree. Abnormal branches should be excluded in order to warrant better predictions.

A multiple regression model covering the whorls, whorl and branch combinations was not considered in this study. For example, a full model could include the following:

$$Y = \text{index1} + \text{index2} + \dots, \text{index6} + \text{index11} + \dots, \text{index46}$$

Where Y = the tree index. The averages of whorls and whorl and branch combinations could also be included in the full model. Simple linear models replaced this model in order to prevent the problem of multicollinearity that could occur because of the interdependence of the volume, angle and diameter used in the index formula. This phenomenon is very common in forestry studies i.e. wood quality, growth and yield. It requires consideration when describing correlations because it often inflates them (Van Laar, 1991).

There are important points that must be raised regarding the feasibility of employing this type of index in future analyses.

- 1) The index value is influenced by the volume to a large extent. The tree mean index (Table 4.3) correlates rather poorly with mean branch diameter. This is despite the fact that this relationship shows good correlation when one looks at the correlation matrix for whorl means (Table 4.6).

- 2) Standardizing the index formula can improve the accuracy of making predictions in view of the assumptions made in the equation. The use of residuals instead of the true index values can help to correct for correlated effects.
- 3) The most acceptable method to use would still be to employ the Smith-Hazel selection index concept.

The calculation of repeatability and the subsequent regressions gave similar results as those discussed earlier. The procedure for calculating the sample size also supports the concept of reducing the sample to at least four branches in order to reduce costs.

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Appendix 1 A sample of data recorded data. The example is given by seedlot up137 that has five trees from which the abbreviated variables (see appendix 2) were assessed and data entered as shown. Similar data entries were made for the rest of the seedlots.

Seedlot	Tree no.	d	ht	strt	coarse	bs	bs	Nb	nw	nwx	hx	dx	wnx	bnx	bdx	Bax
up137	1	4.2	3.5	7	2	3	4	53	12	3	20	5	1	1	15	70
up137	1	4.2	3.5	7	2	3	4	53	12	3	20	5	1	2	13	80
up137	1	4.2	3.5	7	2	3	4	53	12	3	20	5	1	3	11	90
up137	1	4.2	3.5	7	2	3	4	53	12	3	20	5	1	4	9	80
up137	1	4.2	3.5	7	2	3	4	53	12	3	35	4.2	2	1	14	70
up137	1	4.2	3.5	7	2	3	4	53	12	3	35	4.2	2	2	13	60
up137	1	4.2	3.5	7	2	3	4	53	12	3	35	4.2	2	3	13	70
up137	1	4.2	3.5	7	2	3	4	53	12	3	35	4.2	2	4	12	70
up137	1	4.2	3.5	7	2	3	4	53	12	3	40	3.6	3	1	14	50
up137	1	4.2	3.5	7	2	3	4	53	12	3	40	3.6	3	2	14	60
up137	1	4.2	3.5	7	2	3	4	53	12	3	40	3.6	3	3	13	60
up137	1	4.2	3.5	7	2	3	4	53	12	3	40	3.6	3	4	12	60
up137	1	4.2	3.5	7	2	3	4	53	12	3	40	3.6	3	5	9	60
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	6.2	1	1	22	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	6.2	1	2	19	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	6.2	1	3	18	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	6.2	1	4	17	60
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	6.2	1	5	16	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	25	5.7	2	1	15	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	25	5.7	2	2	15	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	25	5.7	2	3	14	80
up137	2	6.3	4.1	7	3	3	4	52	13	4	25	5.7	2	4	13	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	25	5.7	2	5	13	80
up137	2	6.3	4.1	7	3	3	4	52	13	4	28	4.8	3	1	17	60
up137	2	6.3	4.1	7	3	3	4	52	13	4	28	4.8	3	2	17	60
up137	2	6.3	4.1	7	3	3	4	52	13	4	28	4.8	3	3	17	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	28	4.8	3	4	15	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	28	4.8	3	5	7	90
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	4.2	4	1	16	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	4.2	4	2	15	60
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	4.2	4	3	12	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	4.2	4	4	10	70
up137	2	6.3	4.1	7	3	3	4	52	13	4	32	4.2	4	5	9	80
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	1	18	50
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	2	17	50
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	3	17	60
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	4	16	50
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	5	16	50
up137	3	5.5	4.1	7	2	3	3	56	14	5	28	5.5	1	6	12	60
up137	3	5.5	4.1	7	2	3	3	56	14	5	16	5.4	2	1	8	90
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	5.1	3	1	17	60
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	5.1	3	2	10	60
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	5.1	3	3	8	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	5.1	3	4	8	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	5.1	3	5	7	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	18	4.1	4	1	22	40
up137	3	5.5	4.1	7	2	3	3	56	14	5	18	4.1	4	2	16	60

up137	3	5.5	4.1	7	2	3	3	56	14	5	18	4.1	4	3	13	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	18	4.1	4	4	11	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	18	4.1	4	5	7	80
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	4	5	1	9	70
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	4	5	2	6	80
up137	3	5.5	4.1	7	2	3	3	56	14	5	19	4	5	3	5	90
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	5.6	1	1	18	70
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	5.6	1	2	17	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	5.6	1	3	16	70
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	5.6	1	4	11	80
up137	4	5.6	4.5	7	2	3	4	51	17	4	16	5	2	1	18	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	16	5	2	2	17	50
up137	4	5.6	4.5	7	2	3	4	51	17	4	16	5	2	3	17	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	16	5	2	4	14	70
up137	4	5.6	4.5	7	2	3	4	51	17	4	16	5	2	5	14	70
up137	4	5.6	4.5	7	2	3	4	51	17	4	20	4.5	3	1	16	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	20	4.5	3	2	13	50
up137	4	5.6	4.5	7	2	3	4	51	17	4	20	4.5	3	3	10	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	20	4.5	3	4	6	80
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	4	4	1	11	60
up137	4	5.6	4.5	7	2	3	4	51	17	4	26	4	4	2	10	60
up137	5	6	4.2	7	3	2	4	51	12	4	24	5.8	1	1	16	70
up137	5	6	4.2	7	3	2	4	51	12	4	24	5.8	1	2	15	60
up137	5	6	4.2	7	3	2	4	51	12	4	24	5.8	1	3	13	60
up137	5	6	4.2	7	3	2	4	51	12	4	24	5.8	1	4	10	70
up137	5	6	4.2	7	3	2	4	51	12	4	28	5	2	1	19	60
up137	5	6	4.2	7	3	2	4	51	12	4	28	5	2	2	17	70
up137	5	6	4.2	7	3	2	4	51	12	4	28	5	2	3	16	70
up137	5	6	4.2	7	3	2	4	51	12	4	28	5	2	4	15	60
up137	5	6	4.2	7	3	2	4	51	12	4	28	5	2	5	14	70
up137	5	6	4.2	7	3	2	4	51	12	4	39	4.2	3	1	18	60
up137	5	6	4.2	7	3	2	4	51	12	4	39	4.2	3	2	15	70
up137	5	6	4.2	7	3	2	4	51	12	4	39	4.2	3	3	14	70
up137	5	6	4.2	7	3	2	4	51	12	4	39	4.2	3	4	13	60
up137	5	6	4.2	7	3	2	4	51	12	4	39	4.2	3	5	9	70
up137	5	6	4.2	7	3	2	4	51	12	4	38	3.8	4	1	15	70
up137	5	6	4.2	7	3	2	4	51	12	4	38	3.8	4	2	12	70
up137	5	6	4.2	7	3	2	4	51	12	4	38	3.8	4	3	11	60
up137	5	6	4.2	7	3	2	4	51	12	4	38	3.8	4	4	11	60

Appendix 2 A list of abbreviations used in the text.

Abbreviation	Interpretation
D	Diameter
Ht	Height
Strt	Straightness
Coarse	Coarseness of branches
Bs	Branch size score
Ba	Branch angle score
Nb	Number of branches
Nw	Number of whorls
Nwx	Number of whorls on marked section
Hx	Internode length
Dx	Internode diameter
Bdx	Branch diameter
Bax	Branch angle
Index	Tree index
Hx1, hx2..., hx6	Internode length of whorl 1, whorl 2..., whorl 6 respectively
Dx1, dx2..., dx6	Internode diameter of whorl 1, whorl 2..., whorl 6 respectively
Bdx1, bdx2..., bdx6	Branch diameter for whorl 1, whorl 2..., whorl 6 respectively
Bax1, bax2..., bax6	Branch angle for whorl 1, whorl 2..., whorl 6 respectively
Index1, index2..., index6	Index for whorl 1, whorl 2..., whorl 6 respectively
Index12*	Index for the average of whorl 1 and whorl 2
Indx123	Index for the average of whorl 1, whorl 2, and whorl 3 respectively
Indx456	Index for the average of whorl 4, whorl 5, and whorl 6 respectively
Index11, index21..., index46	Index for whorl 1 branch 1, whorl 2 branch 1..., whorl 4 branch 6*
Indexbw	Index for the average of whorl 1 branches 1 and 2
Indexbwa	Index for the average of whorl 1 branches 1, 2 and 3
Indexbwb	Index for the average of whorl 1 branches 1, 2, 3 and 4
Indexbwc	Index for the average of whorl 2 branches 1 and 2
Indexbwd	Index for the average of whorl 2 branches 1, 2 and 3
Indexbwe	Index for the average of branch 1 in whorl 1 and 2
Indexbwf	Index for the average of branches 1, 2 in whorl 1 and 2

*note that because of the confusion that may arise in the abbreviation of index12, it has been chosen that this abbreviation is given to the average of whorl 1 and 2 and indexb12 is the abbreviation for whorl 1 branch 2 index.

Appendix 3 Simulations based on a hypothetical example of eight trees with different conformations (shown below appendix). The index decreases in the order of tree 3, 1, 4, 8, 2, 6, 5 and 7 respectively. This trend together with that of intermediate trees that were included in detailed simulations (not shown here) was considered logical.

Tree no.	diameter	height	whorl no.	branch no.	branch diameter	branch angle	volume	Bdx/bax	$\Sigma(\text{bdx}/\text{bax})$	Index
1	9	6	1	1	2.1	90	486	0.02333	0.56	867.857
1	9	6	1	2	2.1	90	486	0.02333		
1	9	6	1	3	2.1	90	486	0.02333		
1	9	6	1	4	2.1	90	486	0.02333		
1	9	6	1	5	2.1	90	486	0.02333		
1	9	6	1	6	2.1	90	486	0.02333		
1	9	6	2	1	2.1	90	486	0.02333		
1	9	6	2	2	2.1	90	486	0.02333		
1	9	6	2	3	2.1	90	486	0.02333		
1	9	6	2	4	2.1	90	486	0.02333		
1	9	6	2	5	2.1	90	486	0.02333		
1	9	6	2	6	2.1	90	486	0.02333		
1	9	6	3	1	2.1	90	486	0.02333		
1	9	6	3	2	2.1	90	486	0.02333		
1	9	6	3	3	2.1	90	486	0.02333		
1	9	6	3	4	2.1	90	486	0.02333		
1	9	6	3	5	2.1	90	486	0.02333		
1	9	6	3	6	2.1	90	486	0.02333		
1	9	6	4	1	2.1	90	486	0.02333		
1	9	6	4	2	2.1	90	486	0.02333		
1	9	6	4	3	2.1	90	486	0.02333		
1	9	6	4	4	2.1	90	486	0.02333		
1	9	6	4	5	2.1	90	486	0.02333		
1	9	6	4	6	2.1	90	486	0.02333		
2	9	6	1	1	2.1	20	486	0.105	2.52	192.857
2	9	6	1	2	2.1	20	486	0.105		
2	9	6	1	3	2.1	20	486	0.105		
2	9	6	1	4	2.1	20	486	0.105		
2	9	6	1	5	2.1	20	486	0.105		
2	9	6	1	6	2.1	20	486	0.105		
2	9	6	2	1	2.1	20	486	0.105		
2	9	6	2	2	2.1	20	486	0.105		
2	9	6	2	3	2.1	20	486	0.105		
2	9	6	2	4	2.1	20	486	0.105		
2	9	6	2	5	2.1	20	486	0.105		
2	9	6	2	6	2.1	20	486	0.105		
2	9	6	3	1	2.1	20	486	0.105		
2	9	6	3	2	2.1	20	486	0.105		
2	9	6	3	3	2.1	20	486	0.105		
2	9	6	3	4	2.1	20	486	0.105		
2	9	6	3	5	2.1	20	486	0.105		
2	9	6	3	6	2.1	20	486	0.105		
2	9	6	4	1	2.1	20	486	0.105		
2	9	6	4	2	2.1	20	486	0.105		
2	9	6	4	3	2.1	20	486	0.105		
2	9	6	4	4	2.1	20	486	0.105		
2	9	6	4	5	2.1	20	486	0.105		
2	9	6	4	6	2.1	20	486	0.105		
3	9	6	1	1	0.6	90	486	0.00666	0.16	3037.5

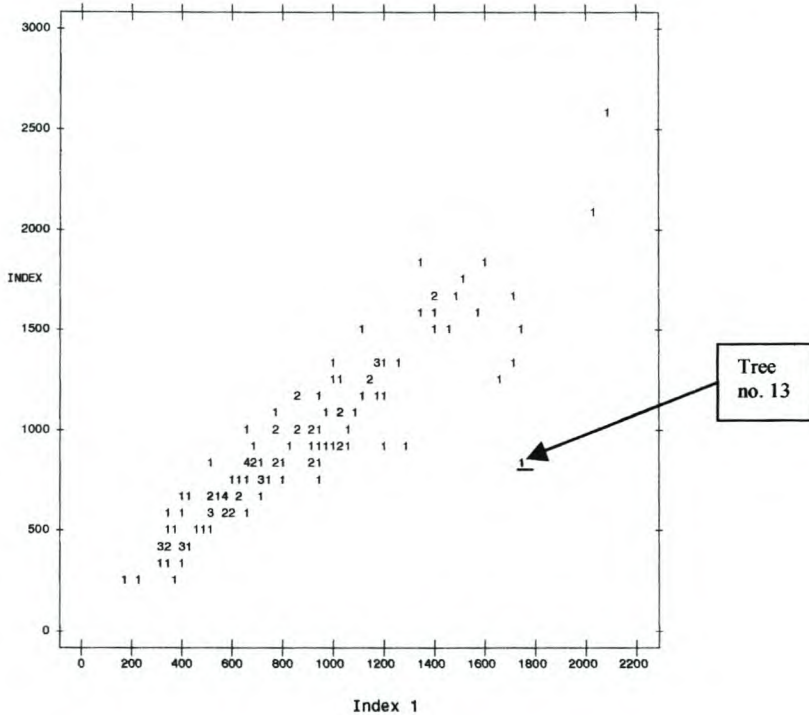
3	9	6	1	2	0.6	90	486	0.00666		
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3	9	6	1	5	0.6	90	486	0.00666		
3	9	6	1	6	0.6	90	486	0.00666		
3	9	6	2	1	0.6	90	486	0.00666		
3	9	6	2	2	0.6	90	486	0.00666		
3	9	6	2	3	0.6	90	486	0.00666		
3	9	6	2	4	0.6	90	486	0.00666		
3	9	6	2	5	0.6	90	486	0.00666		
3	9	6	2	6	0.6	90	486	0.00666		
3	9	6	3	1	0.6	90	486	0.00666		
3	9	6	3	2	0.6	90	486	0.00666		
3	9	6	3	3	0.6	90	486	0.00666		
3	9	6	3	4	0.6	90	486	0.00666		
3	9	6	3	5	0.6	90	486	0.00666		
3	9	6	3	6	0.6	90	486	0.00666		
3	9	6	4	1	0.6	90	486	0.00666		
3	9	6	4	2	0.6	90	486	0.00666		
3	9	6	4	3	0.6	90	486	0.00666		
3	9	6	4	4	0.6	90	486	0.00666		
3	9	6	4	5	0.6	90	486	0.00666		
3	9	6	4	6	0.6	90	486	0.00666		
4	9	6	1	1	0.6	20	486	0.03	0.72	675
4	9	6	1	2	0.6	20	486	0.03		
4	9	6	1	3	0.6	20	486	0.03		
4	9	6	1	4	0.6	20	486	0.03		
4	9	6	1	5	0.6	20	486	0.03		
4	9	6	1	6	0.6	20	486	0.03		
4	9	6	2	1	0.6	20	486	0.03		
4	9	6	2	2	0.6	20	486	0.03		
4	9	6	2	3	0.6	20	486	0.03		
4	9	6	2	4	0.6	20	486	0.03		
4	9	6	2	5	0.6	20	486	0.03		
4	9	6	2	6	0.6	20	486	0.03		
4	9	6	3	1	0.6	20	486	0.03		
4	9	6	3	2	0.6	20	486	0.03		
4	9	6	3	3	0.6	20	486	0.03		
4	9	6	3	4	0.6	20	486	0.03		
4	9	6	3	5	0.6	20	486	0.03		
4	9	6	3	6	0.6	20	486	0.03		
4	9	6	4	1	0.6	20	486	0.03		
4	9	6	4	2	0.6	20	486	0.03		
4	9	6	4	3	0.6	20	486	0.03		
4	9	6	4	4	0.6	20	486	0.03		
4	9	6	4	5	0.6	20	486	0.03		
4	9	6	4	6	0.6	20	486	0.03		
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5	4	3.5	1	3	0.6	20	56	0.03		
5	4	3.5	1	4	0.6	20	56	0.03		
5	4	3.5	1	5	0.6	20	56	0.03		
5	4	3.5	1	6	0.6	20	56	0.03		
5	4	3.5	2	1	0.6	20	56	0.03		
5	4	3.5	2	2	0.6	20	56	0.03		
5	4	3.5	2	3	0.6	20	56	0.03		
5	4	3.5	2	4	0.6	20	56	0.03		
5	4	3.5	2	5	0.6	20	56	0.03		

5	4	3.5	2	6	0.6	20	56	0.03		
5	4	3.5	3	1	0.6	20	56	0.03		
5	4	3.5	3	2	0.6	20	56	0.03		
5	4	3.5	3	3	0.6	20	56	0.03		
5	4	3.5	3	4	0.6	20	56	0.03		
5	4	3.5	3	5	0.6	20	56	0.03		
5	4	3.5	3	6	0.6	20	56	0.03		
5	4	3.5	4	1	0.6	20	56	0.03		
5	4	3.5	4	2	0.6	20	56	0.03		
5	4	3.5	4	3	0.6	20	56	0.03		
5	4	3.5	4	4	0.6	20	56	0.03		
5	4	3.5	4	5	0.6	20	56	0.03		
5	4	3.5	4	6	0.6	20	56	0.03		
6	4	3.5	1	1	2.1	90	56	0.02333	0.56	100
6	4	3.5	1	2	2.1	90	56	0.02333		
6	4	3.5	1	3	2.1	90	56	0.02333		
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6	4	3.5	2	5	2.1	90	56	0.02333		
6	4	3.5	2	6	2.1	90	56	0.02333		
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6	4	3.5	3	4	2.1	90	56	0.02333		
6	4	3.5	3	5	2.1	90	56	0.02333		
6	4	3.5	3	6	2.1	90	56	0.02333		
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6	4	3.5	4	5	2.1	90	56	0.02333		
6	4	3.5	4	6	2.1	90	56	0.02333		
7	4	3.5	1	1	2.1	20	56	0.105	2.52	22.2222
7	4	3.5	1	2	2.1	20	56	0.105		
7	4	3.5	1	3	2.1	20	56	0.105		
7	4	3.5	1	4	2.1	20	56	0.105		
7	4	3.5	1	5	2.1	20	56	0.105		
7	4	3.5	1	6	2.1	20	56	0.105		
7	4	3.5	2	1	2.1	20	56	0.105		
7	4	3.5	2	2	2.1	20	56	0.105		
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7	4	3.5	2	4	2.1	20	56	0.105		
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7	4	3.5	3	1	2.1	20	56	0.105		
7	4	3.5	3	2	2.1	20	56	0.105		
7	4	3.5	3	3	2.1	20	56	0.105		
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7	4	3.5	3	5	2.1	20	56	0.105		
7	4	3.5	3	6	2.1	20	56	0.105		
7	4	3.5	4	1	2.1	20	56	0.105		
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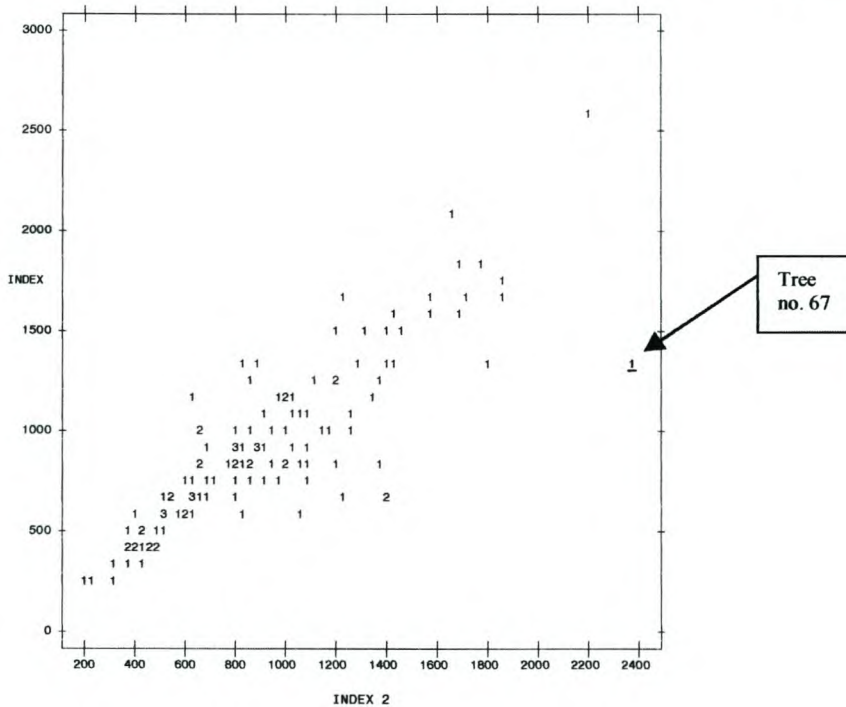
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7	4	3.5	4	5	2.1	20	56	0.105		
7	4	3.5	4	6	2.1	20	56	0.105		
8	4	3.5	1	1	0.6	90	56	0.00667	0.16	350
8	4	3.5	1	2	0.6	90	56	0.00667		
8	4	3.5	1	3	0.6	90	56	0.00667		
8	4	3.5	1	4	0.6	90	56	0.00667		
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8	4	3.5	4	5	0.6	90	56	0.00667		
8	4	3.5	4	6	0.6	90	56	0.00667		

Tree no.	volume	Branch diameter	Branch angle	Index
1	Largest	Largest	Largest	867.8
2	Largest	Largest	Smallest	192.8
3	Largest	Smallest	Largest	3037.5
4	Largest	Smallest	Smallest	675
5	Smallest	Smallest	Smallest	77.7
6	Smallest	Largest	Largest	100
7	Smallest	Largest	Smallest	22.22
8	Smallest	Smallest	Largest	350

81	1001.7	920.1	15.103	890.2	950.0	584.6	1255.7	81.6263	168.168	0.485				0.001
82	589.9	748.7	16.678	715.7	781.7	412.8	1084.5	-158.8	168.019	-0.945	*			0.004
83	589.1	600.6	19.951	561.1	640.1	264.0	937.1	-11.4407	167.662	-0.068				0.000
84	662.1	669.0	18.270	632.9	705.2	332.9	1005.2	-6.9464	167.853	-0.041				0.000
85	1157.2	1159.5	17.817	1124.2	1194.7	823.4	1495.5	-2.2438	167.902	-0.013				0.000
86	887.7	759.1	16.504	726.5	791.8	423.3	1095.0	128.6	168.036	0.765	*			0.003
87	1524.4	1436.9	25.557	1386.3	1487.4	1098.8	1774.9	87.5919	166.899	0.525	*			0.003
88	722.2	1006.9	15.461	976.3	1037.5	671.2	1342.5	-284.6	168.135	-1.693	***			0.012
89	280.5	352.8	27.523	298.3	407.2	14.1227	691.4	-72.2280	166.586	-0.434				0.003
90	1643.5	1423.4	25.121	1373.6	1473.1	1085.5	1761.3	220.2	166.965	1.319	**			0.020
91	262.2	297.6	29.404	239.4	355.8	-41.6644	636.8	-35.4236	166.265	-0.213				0.001
92	1866.4	1386.4	23.947	1339.0	1433.8	1048.8	1723.9	480.0	167.138	2.872	*****			0.085
93	474.3	586.4	20.329	546.1	626.6	249.7	923.0	-112.1	167.616	-0.669	*			0.003
94	688.1	663.1	18.406	626.6	699.5	326.9	999.3	25.0560	167.838	0.149				0.000
95	412.1	412.7	25.542	362.1	463.2	74.6302	750.7	-0.5750	166.902	-0.003				0.000
96	923.8	1051.8	15.947	1020.3	1083.4	716.1	1387.5	-128.0	168.090	-0.761	*			0.003
97	1135.2	1218.8	19.191	1180.8	1256.8	882.4	1555.1	-83.5930	167.751	-0.498				0.002
98	611.8	513.3	22.404	468.9	557.6	176.1	850.4	98.5104	167.352	0.589	*			0.003
99	1320.4	1229.1	19.449	1190.8	1267.5	892.6	1565.5	91.3343	167.721	0.545	*			0.002
100	1302.1	1247.9	19.935	1208.4	1287.3	911.3	1584.4	54.1967	167.664	0.323				0.001
101	1487.5	1740.7	36.149	1669.1	1812.2	1398.9	2082.4	-253.2	164.930	-1.535	***			0.057
102	1584.7	1591.0	30.780	1530.1	1651.9	1251.3	1930.7	-6.3543	166.015	-0.038				0.000
103	1816.7	1611.4	31.499	1549.1	1673.8	1271.5	1951.4	205.2	165.880	1.237	**			0.028
104	1327.8	1305.6	21.522	1263.0	1348.2	968.7	1642.5	22.2621	167.467	0.133				0.000
105	1651.5	1503.4	27.762	1448.5	1558.4	1164.7	1842.1	148.1	166.547	0.889	*			0.011
106	847.4	978.2	15.256	948.0	1008.4	642.6	1313.8	-130.8	168.154	-0.778	*			0.002
107	433.9	508.3	22.552	463.7	553.0	171.1	845.5	-74.4183	167.332	-0.445				0.002
108	590.1	687.5	17.861	652.2	722.9	351.5	1023.6	-97.4064	167.897	-0.580	*			0.002
109	785.3	817.4	15.706	786.3	848.5	481.7	1153.0	-32.0965	168.113	-0.191				0.000
110	911.4	1022.7	15.610	991.8	1053.6	687.0	1358.3	-111.3	168.122	-0.662	*			0.002
111	406.5	446.4	24.460	398.0	494.8	108.7	784.1	-39.9413	167.064	-0.239				0.001
112	1148.5	997.6	15.386	967.1	1028.1	662.0	1333.2	150.9	168.142	0.897	*			0.003
113	726.8	723.2	17.139	689.2	757.1	387.2	1059.1	3.6511	167.973	0.022				0.000
114	858.4	748.5	16.680	715.5	781.6	412.7	1084.4	109.9	168.019	0.654	*			0.002
115	952.6	1076.7	16.296	1044.4	1108.9	740.9	1412.5	-124.1	168.056	-0.739	*			0.003
116	983.2	928.1	15.103	898.2	958.0	592.6	1263.7	55.1005	168.168	0.328				0.000
117	656.2	667.2	18.312	630.9	703.4	331.0	1003.3	-10.9429	167.849	-0.065				0.000
118	741.3	731.9	16.975	698.3	765.5	396.0	1067.8	9.3382	167.989	0.056				0.000
119	831.2	970.2	15.213	940.1	1000.3	634.6	1305.7	-138.9	168.158	-0.826	*			0.003
120	675.1	661.3	18.446	624.8	697.8	325.1	997.5	13.7371	167.834	0.082				0.000
121	448.4	514.7	22.363	470.4	559.0	177.6	851.8	-66.3042	167.357	-0.396				0.001
122	574.8	619.9	19.451	581.4	658.4	283.5	956.3	-45.1487	167.721	-0.269				0.000
123	440.8	495.7	22.933	450.3	541.1	158.4	833.0	-54.8579	167.280	-0.328				0.001
124	371.2	429.9	24.985	380.5	479.4	92.0813	767.8	-58.7677	166.986	-0.352				0.001
125	858.8	844.2	15.444	813.7	874.8	508.6	1179.9	14.5145	168.137	0.086				0.000



86	887.7	899.9	19.477	861.3	938.4	468.2	1331.6	-12.1508	216.350	-0.056			0.000
87	1524.4	1153.9	23.230	1107.9	1199.9	721.4	1586.3	370.6	215.980	1.716	***		0.017
88	722.2	647.0	24.799	597.9	696.1	214.2	1079.7	75.2521	215.805	0.349			0.001
89	280.5	349.5	37.376	275.5	423.5	-86.8294	785.8	-68.9494	213.986	-0.322			0.002
90	1643.5	1172.5	23.813	1125.4	1219.6	739.9	1605.1	471.0	215.916	2.182	****		0.029
91	262.2	414.6	34.339	346.6	482.6	-20.7418	849.9	-152.4	214.494	-0.711	*		0.006
92	1866.4	1620.1	43.232	1534.5	1705.7	1181.7	2058.5	246.3	212.880	1.157	**		0.028
93	474.3	551.5	28.400	495.3	607.7	117.8	985.1	-77.2178	215.361	-0.359			0.001
94	688.1	831.3	20.107	791.5	871.1	399.5	1263.2	-143.2	216.293	-0.662	*		0.002
95	412.1	498.1	30.630	437.4	558.7	63.8340	932.3	-85.9960	215.055	-0.400			0.002
96	923.8	911.9	19.442	873.4	950.4	480.2	1343.6	11.9583	216.353	0.055			0.000
97	1135.2	977.5	19.651	938.6	1016.4	545.8	1409.2	157.7	216.335	0.729	*		0.002
98	611.8	687.7	23.460	641.3	734.2	255.2	1120.2	-75.9141	215.955	-0.352			0.001
99	1320.4	896.1	19.493	857.5	934.6	464.3	1327.8	424.3	216.349	1.961	***		0.016
100	1302.1	1215.9	25.284	1165.9	1266.0	783.1	1648.8	86.1457	215.749	0.399			0.001
101	1487.5	1371.3	31.511	1309.0	1433.7	936.8	1805.8	116.2	214.928	0.541	*		0.003
102	1584.7	1345.8	30.406	1285.6	1406.0	911.6	1780.0	238.9	215.087	1.111	**		0.012
103	1816.7	1556.5	40.110	1477.1	1635.9	1119.3	1993.8	260.1	213.490	1.219	**		0.026
104	1327.8	849.0	19.877	809.6	888.3	417.2	1280.7	478.9	216.314	2.214	****		0.021
105	1651.5	1568.2	40.681	1487.7	1648.8	1130.8	2005.7	83.2233	213.382	0.390			0.003
106	847.4	847.9	19.890	808.5	887.3	416.1	1279.7	-0.4780	216.313	-0.002			0.000
107	433.9	543.1	28.741	486.2	600.0	109.3	976.8	-109.2	215.315	-0.507	*		0.002
108	590.1	642.4	24.956	593.0	691.8	209.6	1075.3	-52.3024	215.787	-0.242			0.000
109	785.3	809.6	20.451	769.1	850.1	377.7	1241.5	-24.3039	216.260	-0.112			0.000
110	911.4	901.6	19.471	863.0	940.1	469.9	1333.3	9.8086	216.351	0.045			0.000
111	406.5	548.9	28.504	492.5	605.3	115.2	982.6	-142.4	215.347	-0.661	*		0.004
112	1148.5	1263.0	27.030	1209.5	1316.5	829.7	1696.3	-114.5	215.537	-0.531	*		0.002
113	726.8	744.9	21.841	701.6	788.1	312.7	1177.0	-18.0459	216.124	-0.083			0.000
114	858.4	708.1	22.846	662.9	753.3	275.7	1140.4	150.3	216.021	0.696	*		0.003
115	952.6	1001.8	19.898	962.4	1041.2	570.0	1433.6	-49.2710	216.312	-0.228			0.000
116	983.2	876.7	19.610	837.9	915.5	445.0	1308.5	106.5	216.338	0.492			0.001
117	656.2	573.3	27.528	518.8	627.8	139.9	1006.7	82.9198	215.474	0.385			0.001
118	741.3	715.3	22.637	670.5	760.1	283.0	1147.6	25.9487	216.042	0.120			0.000
119	831.2	811.3	20.420	770.9	851.8	379.5	1243.2	19.9145	216.263	0.092			0.000
120	675.1	675.1	23.860	627.9	722.3	242.5	1107.7	-0.0411	215.911	-0.000			0.000
121	448.4	547.9	28.547	491.3	604.4	114.2	981.5	-99.4632	215.341	-0.462			0.002
122	574.8	855.6	19.802	816.4	894.8	423.9	1287.4	-280.9	216.321	-1.298	**		0.007
123	440.8	500.0	30.545	439.6	560.5	65.8182	934.2	-59.2133	215.067	-0.275			0.001
124	371.2	523.3	29.560	464.8	581.8	89.3612	957.3	-152.1	215.205	-0.707	*		0.005
125	858.8	1035.4	20.381	995.0	1075.7	603.5	1467.2	-176.6	216.267	-0.817	*		0.003



Appendix 5 Sample of raw data (shown from SAS input Statement): Tree No. 13 and No. 67 have been selected to illustrate the importance of the assumption of a normally branched tree made in this investigation

```
data raw;
  input seedlot $ tn d ht strt coarse bs ba nb nw nrw hx dx wxn brx bdx bax @@;
  vol2=22/7*dx/2*dx/2*ht;
  knot=bdx/bax;
  vol=d*d*ht;
```

```
cards;
up137 5 6.0 4.2 7 3 2 4 51 12 4 24 5.8 1 1 16 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 24 5.8 1 2 15 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 24 5.8 1 3 13 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 24 5.8 1 4 10 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 28 5.0 2 1 19 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 28 5.0 2 2 17 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 28 5.0 2 3 16 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 28 5.0 2 4 15 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 28 5.0 2 5 14 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 39 4.2 3 1 18 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 39 4.2 3 2 15 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 39 4.2 3 3 14 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 39 4.2 3 4 13 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 39 4.2 3 5 9 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 38 3.8 4 1 15 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 38 3.8 4 2 12 70
up137 5 6.0 4.2 7 3 2 4 51 12 4 38 3.8 4 3 11 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 38 3.8 4 4 11 60
up137 5 6.0 4.2 7 3 2 4 51 12 4 38 3.8 4 5 7 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 16 5.8 1 1 7 80
up153 13 5.4 4.3 7 4 5 4 60 15 5 16 5.8 1 2 6 90
up153 13 5.4 4.3 7 4 5 4 60 15 5 16 5.8 1 3 5 80
up153 13 5.4 4.3 7 4 5 4 60 15 5 33 5.4 2 1 15 60
up153 13 5.4 4.3 7 4 5 4 60 15 5 33 5.4 2 2 12 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 33 5.4 2 3 6 80
up153 13 5.4 4.3 7 4 5 4 60 15 5 33 5.4 2 4 5 90
up153 13 5.4 4.3 7 4 5 4 60 15 5 26 4.7 3 1 14 50
up153 13 5.4 4.3 7 4 5 4 60 15 5 26 4.7 3 2 14 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 26 4.7 3 3 12 60
up153 13 5.4 4.3 7 4 5 4 60 15 5 26 4.7 3 4 8 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 28 4.1 4 1 14 60
up153 13 5.4 4.3 7 4 5 4 60 15 5 28 4.1 4 2 10 50
up153 13 5.4 4.3 7 4 5 4 60 15 5 28 4.1 4 3 9 50
up153 13 5.4 4.3 7 4 5 4 60 15 5 28 4.1 4 4 7 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 36 3.8 5 1 14 60
up153 13 5.4 4.3 7 4 5 4 60 15 5 36 3.8 5 2 9 70
up153 13 5.4 4.3 7 4 5 4 60 15 5 36 3.8 5 3 8 60
up152 67 7.6 4.8 5 4 4 4 59 12 4 32 6.6 1 1 28 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 32 6.6 1 2 24 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 32 6.6 1 3 21 90
up152 67 7.6 4.8 5 4 4 4 59 12 4 32 6.6 1 4 18 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 32 6.6 1 5 15 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 25 6.2 2 1 13 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 25 6.2 2 2 10 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 25 6.2 2 3 9 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 25 6.2 2 4 8 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 25 6.2 2 5 8 90
up152 67 7.6 4.8 5 4 4 4 59 12 4 23 5.7 3 1 19 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 23 5.7 3 2 16 60
up152 67 7.6 4.8 5 4 4 4 59 12 4 23 5.7 3 3 15 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 23 5.7 3 4 15 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 23 5.7 3 5 14 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 40 4.8 4 1 23 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 40 4.8 4 2 21 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 40 4.8 4 3 16 70
up152 67 7.6 4.8 5 4 4 4 59 12 4 40 4.8 4 4 13 80
up152 67 7.6 4.8 5 4 4 4 59 12 4 40 4.8 4 5 11 80
```

Whorl 1

These small branches tend to give high indices that offset the mean indices as shown by the outlier (tree no. 13) in the plot shown in appendi 4.

Whorl 2

This abnormal whorl has quiet a number of very small branches which tend to inflate the index shown as the otlier – Tree No. 67 in the next plot.