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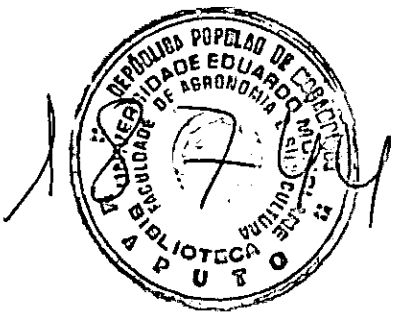

by

ALIMA A.K. ISSUFO

Thesis presented in partial fulfilment of the requirements for the Degree of Master of Science in Forestry at the University of Stellenbosch

Supervisor : Professor Gerrit van Wyk

STELLENBOSCH

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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.

SIGNATURE: A.A.K. Issufo DATE: 15 Feb. 1998.

A.A.K. Issufo

ABSTRACT

A nursery clonal test of 20 clones was established at the University of Stellenbosch on eight soil treatments consisting of combinations of four soil types and two lime levels. One clone was from first-generation and 15 were from second-generation *Eucalyptus grandis* selected in 13 different open pollinated family trials and two full-sib trials. Three hybrid clones were selected from two *E. grandis x E. camaldulensis* and one *E. grandis x E. urophylla* families.

Soil collection was done in four different places in the Western Cape, specifically Lourensford near Somerset West, Pampoenvlei near Malmesbury and Grabouw and Helshoogte near Stellenbosch. The yellowish soil from Grabouw and the reddish soil from Helshoogte were clayey while the black and light soils from Lourensford and Pampoenvlei respectively were sandy soils. Two lime levels, with or without lime application, on these soils generated eight soil treatments.

Results are firstly presented in tables and the delineation of significant differences between the rankings of clones, replications, soil types, soil treatments for selected variables given by Duncan's New Multiple Range Test is included.

Graphical presentations are used to illustrate some of the trends over all the single effects, that is soil types, lime levels and clones. Analysis of variance for the simplified model detected a highly significant difference for soil treatments, which is the combination of different soil types and lime levels. Quite strong correlations between the soil treatments were also evident.

Assessments of height, diameter, root and shoot mass were made at age 12, 18 and 24 weeks. Number of branches was assessed at 24 weeks.

All the single effects were found to be statistically different for most variables at all ages.

The most outstanding on the two-way interactions is the general **in**significance of clone x soil type, clone x lime and soil type x lime interaction, for height and diameter growth but indeed not for shoot mass and root mass. This might mean that height and diameter alone are not sensitive enough but when leaves are included in mass (like a volume) then more expression is obtained justifying the interaction found at 24 weeks for root and shoot mass for all two-way interactions. Generally the three-way interaction seems insignificant. Once again, shoot mass shows some sensitivity being perhaps an indication of "whole tree" response to environment.

Analysis of variance for the simplified model showed that **soil treatment** (soil type x lime), results were highly significant for all the variables studied. When diameter and height means were studied in terms of phenotypic correlations between sites (soil treatments), quite strong correlations were evident between the soil treatments.

Clone x soil treatment interaction, was also detected by means of regression coefficients. Some clones were found to be stable for variable shoot mass, for instance, AG1, AG3-B, AG6, AG12 and AG14. Average stability clones were GU1, GC1 and GC2 while unstable clones were identified as AG5, AG8, AG11, AG13 and AG15.

The magnitude of genotype x environment interaction is low implying that it will not affect broad sense heritability (there are too few clones to reliably estimate) as well as genetic gain. It is noted that genotype x environment interaction tends to disappear for height and diameter over time, while it remains for shoot mass (volume of the tree) and number of branches at age 24 weeks.

The results from this study are encouraging for further research aimed at developing techniques for early prediction of genotype x environment interaction in eucalypt trees.

OPSOMMING

'n Kwekeryproef met 20 verskillende klone is aan die Universiteit van Stellenbosch voltooi. Die proef het uit grondbehandelings bestaan wat verskeie kombinasies van vier verskillende gronde met twee vlakke van kalkbehandeling ingesluit het.

Die gronde is in die Wes-Kaap (Lourensford, naby Somerset Wes) , Pampoenvlei (naby Malmesbury), Grabouw en Helshoogte (naby Stellenbosch) gevind. Die geel gekleurde grond van Grabouw en die rooi gekleurde grond van Helshoogte het beide 'n hoë klei inhoud terwyl die swart en ligte gekleurde gronde van Lourensford en Pampoenvlei 'n sanderige geaardheid het. Twee vlakke van bekalking (met of sonder kalk) het agt verskillende behandelings tot gevolg gehad.

Resultate word eers in getabuleerde vorm aangegee en die afbakening van statistiese rangorde verskille van klone, herhalings, grondsoorte, grondbehandelings word vir verskeie veranderlikes deur Duncan's New Multiple Range Test aangedui.

Grafieke is gebruik om die algemene neiging van die enkelvoudige effekte naamlik gronde, kalkvlakke en klone aan te dui. Analise van variansie vir die vereenvoudige model het baie beduidende statistiese verskille tussen grondbehandelings aangedui wat 'n kombinasie van die verskillende grondsoorte en bekalkingsvlakke is. Sterk korrelasie is tussen die verskillende grondbehandelings waargeneem.

Die meting van hoogte en stamdeurnee en die bepaling van wortel en stam massa, is gemaak op ouderdom 12, 18 en 24 weke. Die aantal takke is op 24 weke getel. Al die enkelvoudige effekte het statisties beduidende verskille vir die meeste van die veranderlikes op alle ouderdomme aangedui.

Die mees opvallende twee rigting interaksie is die algemene **on**beduidenis van die kloon x grondsoort, kloon x bekalking en grondsoort x bekalking interaksies waar hoogte en deursnee as veranderlikes gebruik is. Die effek was egterbeduidend waar stam en wortel massa as veranderlikes gebruik is. Die gebruik van gemiddelde hoogte en deursnee as veranderlikes is egter nie sensitief genoeg nie, maar die gebruik van blaarmassa (as volume) wat by stammassa ingesluit word, gee'n beter aanduiding van interaksie op 24 weke.

Die analise van variansie vir die vereenvoudigde model het getoon dat die grondbehandelings (grondsoort x bekalking) resultate baie beduidend was vir die onderskeie veranderlikes wat gemeet is. By die bestudering van deursnee en hoogte gemiddeldes (in terme van fenotipiese korrelasie tussen grondbehandelings), is sterk korrelasie gevind tussen die verskeie grondbehandelings.

Kloon x grondbehandeling interaksie is opgemerk deur gebruik te maak van regressie koëffisiente. Verskeie klone (AG1, AG3-B, AG6, AG12 en AG14) het stabiliteit getoon ten opsigte van stam massa as veranderlike. Die gemiddelde stabiele klone was GU1, GC1 en GC2 terwyl die onstabiele klone AG5, AG8, AG11, AG13 en AG15 was.

Die grootte van die genotipe x omgewing interaksie was klein en impliseer dat dit nie oorerfbaarheid (daar is te min klone vir betroubare skattings) en genetiese verbetering veel sal beïnvloed nie. Die genotipe x omgewing interaksie neig om onbeduidend te word vir die hoogte en deursnee veranderlikes terwyl dit beduidend bly vir stam massa (boom volume) en aantal takke op 24 weke.

Die resultate van hierdie studie is bemoedigend vir verdere navorsing wat gemik is daarop om tegnieke te ontwikkel vir vroeë voorspelling van genotipe x omgewing interaksie van gombome.

BIOGRAPHY

The author was born January 14, 1967, in Maputo, Mozambique. Third born in a family of five, three boys and two girls, Alima Abdul Kadir Issufo early turned to be distinct from her elder sister on facing the cultural and social barriers.

She did her primary school at Rainha Dª. Leonor in 1976, located in Lourenço Marques. She graduated from the Francisco Manyanga High School in 1985 and entered the University of Eduardo Mondlane where she graduated with an Honours Bachelor of Science, Forestry, in 1992.

In 1992 she was employed by the Mozambican Forestry Research Centre as a tree seed centre manageress. In September 1993 the author's child was born. Then she enrolled at the University of Stellenbosch in February 1995 on a Masters programme in forestry with a minor in Tree Improvement.

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To my daughter Nahida, whose love and presence were the inspiration of my studies, I dedicate this thesis.

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1. INTRODUCTION

1.1 IMPORTANCE OF *EUCALYPTUS*

The genus *Eucalyptus* belongs to the family *Myrtaceae* and it contains a remarkably wide range of tree species in regard to adaptation to sites, types of management systems, and variety of uses, both in natural forests and in plantations. *Eucalyptus* can be grown in most of the tropical and temperate climatic regions of the world between latitude 45 ° S and 40 ° N from wet and fertile to dry and infertile sites, in conditions which accompany degradation such as soil acidity and low fertility following leaching (Brooker and Kleinig 1990; Eldridge *et* al., 1993).

No tree genus has ever been so widely propagated throughout the world as the pungent-smelling, evergreen, emigrant eucalypts with an approximate total area of 6000000 ha planted in 1985 (Zacharian cited by Eldridge *et al.*, 1993). The fast initial growth of the planted genus allows for short rotations which greatly increase its economic value. *Eucalyptus* timber varies appreciably from species to species but different species have proved excellent for papermaking, shipbuilding, and mining timber. Trees are used for firebreaks, shade, windbreaks and their flowers are a good source of nectar and pollen for honey production. Eucalypt wood is a source of domestic fuel, and it produces a good commercial charcoal (Hillis and Brown, 1978).

Eucalypt plantations in the world are expanding so quickly that by the year 2000 they may exceed 10 million ha. The ten most important eucalypts in the world reported by Eldridge *et al.* (1993), in terms of annual increment of wood and frequency of utilisation are the following: *E. grandis*, *E. camaldulensis*, *E. tereticornis*, *E. globulus*, *E. urophylla*, *E. viminalis*, *E. saligna*, *E. deglupta*, *E. exserta* and then either one of *E. citriodora*, *E. paniculata* or *E. robusta.*

1.2 TAXONOMY OF THE GENUS *EUCALYPTUS*

The genus *Eucalyptus* was described and named by the French botanist l'Heritier in 1788; Benthman had named 149 eucalypts by 1860 and in 1943 Blakely and Maiden produced a key to the eucalypts, in which 500 species and 138 varieties were described (Anon., 1979). More research was done by other authors mainly Johnston, Norman, Rosemary, Chippendale, and more recently, 1990, by Brooker and Kleinig (Anon., 1979). Pryor and Johnston's classification divides the genus *Eucalyptus* l' Heritier into seven subgenera. The subgenera are then divided into sections, series, subseries, superspecies, species and subspecies (Anon., 1979).

According to Eldridge *et al.* (1993) it is important to recognise that eucalypts belong to discrete groups based on shared diagnostic morphological characteristics of the constituent species. Two major groups exist, to comprise species with one operculum, *Monocalyptus*, or with two, *Symphyomyrtus*. *Monocalyptus* is also known as *Eucalyptus sensu stricto* because the group of 100 species is based on the type or first-named species, *E. obliqua*. *Symphyomyrtus* includes more than 300 species. The remaining species are classified into six other subgenera.

The transfer of species in the subgenus *Monocalyptus* is unreliable. The group is more difficult to establish in plantations and is often more sensitive to environmental conditions, including pathogens (Turnbull and Pryor, 1978). They point out that the most successful species overseas are in the subgenera *Symphyomyrtus* and *Corymbia*.

Among the nine sections in *Symphyomyrtus* three sections contain nearly all the species which are widely planted as exotics (Eldridge *et al.*, 1993):
Section Transversaria: *E. grandis*, *E. saligna*, *E. urophylla*;
Section Exsertaria (red gums): *E. camaldulensis*, *E. exserta*, *E. tereticornis*;
Section Maidenaria: *E. dalrympleana*, *E. globulus*, *E. gunnii*, *E. maidenii*, *E. nitens*, *E. viminalis*.

Many interspecific hybrids between species within these three sections have been made in recent years to provide foundation stock for clonal forestry. Pairs of species to be crossed are

often chosen for their close - relatedness as indicated by their taxonomic affinities (Martin cited by Eldridge *et al.* 1993).

It is convenient to consider eucalypt species and subspecies as discrete taxa although one has to look at the continuous variation in many characteristics within some species and between some pairs of species. There are several examples of such taxonomic difficulties due to what appears to be continuous variation between the taxa in certain intermediate populations as found on *E. grandis* and *E. saligna*. Results of a taxonomic investigation carried out in 1983 by Burgess and Bell, on 24 populations taken from across the geographic range of the species including core populations clearly assignable to one of the species, showed that the core populations of the species were distinctly different. *E. grandis* W. Hill ex Maiden commonly known as rose gum (or flooded gum) belongs to the subgenus *Symphyomyrtus* as mentioned before (Eldridge *et al.*, 1993).

Species of the genus *Eucalyptus* are commonly known as "eucalypts" throughout the world, although in Australia they are often called 'gum trees' because of the gum that exudes from the trunk of older trees. According to Eldridge *et al.* (1993), the use of correct botanical names is important to growers of eucalypts when they order seed or seek information on appropriate practices in breeding and plantation silviculture. As emphasised by various authors (Anon., 1979; Poynton, 1979; Eldridge *et al.* 1993) use of common names can be useful and confusing. A given example is related to the red gums (*E. camaldulensis* and *E. tereticornis*, and others) which are known as red gums where they occur naturally, but it becomes confusing when *E. tereticornis* is known as red gum in the south of its range and blue gum in the north.

Taxonomic grouping (based on morphological characteristics) is a reasonably good basis for predicting pairs of eucalypt species which have genetic affinity and are readily crossable (Griffin *et al.* cited by Eldridge *et al.* 1993). They also mention the importance of taxonomic grouping for eucalypt growers, and particularly eucalypt breeders, who must know the botanical identity and the exact geographic origin of the seedlot under test in case more seed of the same species and provenances need to be obtained in future.

1.3 NATURAL DISTRIBUTION OF *EUCALYPTUS* SPECIES

The *Eucalyptus* are the dominant feature of the vegetation of Australia. Some are indigenous to New Guinea or to certain islands in the Indonesian Archipelago, including Timor, Wetar, Flores and the Lesser Sunda islands. Two species, *E. deglupta* and *E. urophylla* do not occur on the Australian mainland and tolerate lower latitudes than any of the Australian species, where the northernmost point is 10° 41'S (Anon., 1979 ,1981; Poynton, 1979).

The genus *Eucalyptus* occurs naturally from latitude 7° N to 43° 39' S and longitude 114° to 155° E in the great part of the Australian continent; the altitude varies from 300 to 600 m reaching 2000 m at the Oriental mountain and 2211 m from sea level (Fig. 1.1) (Anon., 1979).

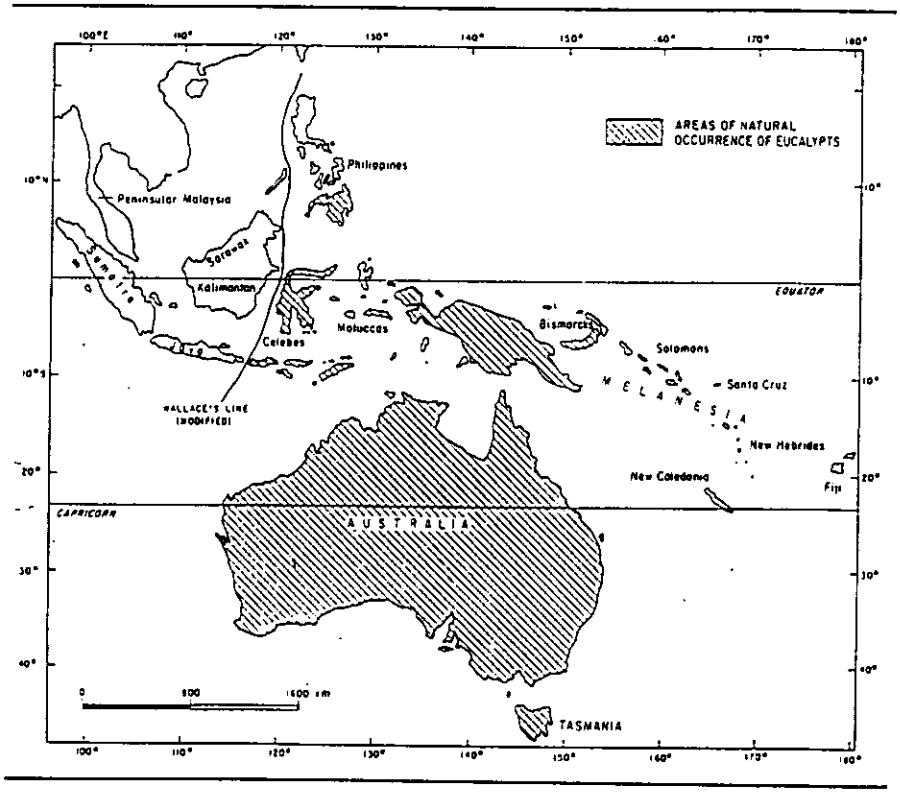


Figure 1.1. Natural distribution of *Eucalyputs*

After: Anon. (1981)

The eucalypts are adapted to a wide range of climates. Thus, different members of the genus are encountered from the tropics to the snow-line; from regions where rain falls only during the warmer months to those in which it is uniformly distributed or confined to the cooler seasons of the year; from humid, forested areas where the precipitation averages 3000 mm or more per annum to semi-arid desert regions in which it is less than one-tenth as much. The mean annual temperatures vary between 6° and 27° C (Penfold and Wills, 1961; Poynton, 1979).

Eucalyptus species are found in variable kinds of soil, from poor to rich, low pH, P and N deficiency, low concentration of Mb, Zn and high levels of Al and Fe; from saline sands (sodium content of 2-3%); to heavy clays; and from waterlogged soils through shallow rocky soils subject to severe drought (Anon., 1981).

This genus has a huge variation. More than 600 species are known (Anon., 1988). A eucalypt may be mature as a low shrub or as a giant tree with top height of 90 m. Species of this genus have a different growth habit. As a generalisation, **forest trees** are single-stemmed and have a crown forming a minor proportion of the tree height; **woodland trees** are single stemmed, although they may branch a short distance above ground level; **mallees** are shrubby, multi-stemmed from ground level, usually less than 10 m in height and it grows in open scrub areas with low annual rainfall (Brooker and Kleinig, 1990).

Eucalyptus grandis and its hybrids are of relevant importance on the present study. This species has its southern limit of distribution at Minmi near Newcastle, New South Wales, at 32° 52'S. Distribution from there is almost continuous up to the New South Wales coast into southern Queensland to latitude 26°S. Most of the natural forest of *E. grandis* in northern New South Wales and southern Queensland are on coastal lowlands and hills with an altitudinal range from sea level to about 600m. Despite the close relationship between *E. grandis* and *E. saligna*, there are no recorded hybrids between them in their natural habitat, although hybrids have been reported from plantations in Florida and South Africa. Hybrids between *E. grandis* and a number of other species have been recorded (Anon., 1981; Eldridge *et al.* 1993).

1.4 INTRODUCTION OF *EUCALYPTUS* SPECIES INTO SOUTHERN AFRICA

From a country relatively poorly endowed with natural forest and timber resources, South Africa has grown into a world leader in plantation forestry. According to Poyton (1979), it all started with a pioneering plantation of *Eucalyptus globulus* "Blue Gum" in the Western Cape established in 1876 to supplement the sparse natural sources of fuel for the early railroads reaching into the interior. Suitable conditions have favoured the establishment of plantations along the southern and eastern mountain ranges. From the Cape the use of eucalypts spreaded rapidly to other parts of Southern Africa. By the end of the nineteenth century the eucalypts plantations reached Angola; several species were introduced into Malawi in or before the first decade of the twentieth century. Rhodesia (now Zimbabwe), Mozambique, Lesotho and Zambia are other countries in the region where eucalypts were introduced before 1930 (Poynton, 1979).

Today, plantations in South Africa cover 1,4 million hectares, 40% of it being covered by *Eucalyptus* species (Anon., 1994). *Eucalyptus grandis* is the most important eucalypt species grown in South Africa with a total area planted for timber production, pulp and paper, oil extraction, fuelwood for industry and energy of 394006 ha. The other eucalypts most commonly grown are *E. cloeziana*, *E. elata*, *E. fastigata*, *E. macarthurii*, *E. nitens* and *E. saligna* (Schönau *et al.*, 1994).

Since the results of the present experimental study will be relevant to Mozambique in future it was deemed necessary to give the background information of the *Eucalyptus* species within that country.

1.4.1 PLANTATIONS OF *EUCALYPTUS* SPECIES IN MOZAMBIQUE

According to Costa (cited by Nuvunga, 1991) the use of exotics in Mozambique started in 1920 with the aim of protection, firewood, materials for construction and others. Eucalypt plantations have been established in Mozambique basically for fuel and charcoal production, to counteract high demand of these products and the over-exploitation of the indigenous forests. A secondary use of eucalypt plantations in Mozambique is the production of honey (Anon., 1979). It was also mentioned that *E. saligna* is used for wood pulp and posts production. The afforested areas per province in Mozambique for *Eucalyptus* species are given in (Table 1.1).

Plantations in Mozambique cover 46000 ha, 52% of it being covered by *Pinus spp*, 40% by *Eucalyptus spp* and 8% by casuarinas and other species (Malleux cited by Issufo, 1992).

Table 1.1. Plantations of *Eucalyptus* species in Mozambique.

Province	**Areas (ha)**
Maputo	3213,3
Gaza	4869,0
Inhambane	166,3
Sofala	1878,0
Manica	3547,0
Zambezia	3935,3
Nampula	490,0
Tete	1,0
Cabo Delgado	-
Niassa	20,0
TOTAL	**18119,9**

After: DNFFB, 1987

1.5 REPRODUCTION

Natural regeneration of *Eucalyptus* is mainly by seed; vegetative propagation is uncommon in nature. The reproductive organs of these plants are flowers which develop into fruits in which seed are formed. The reproductive process takes place in an inflorescence, which is the arrangement of the flower on the stem. Taxonomic classifications and methods of identification of eucalypts are based largely on their reproductive structures. These are important in understanding many aspects of the genus, specially the species identification and timing and methods of seed collection (Boland, *et al.* 1980).

1.5.1 FLOWERING

a. The inflorescence and flower

Eucalyptus belongs to the plant family of *Myrtaceae*, one of many that make up the Angiosperms - the flowering plants. The reproductive organs of these plants are flowers which develop into fruits in which seed are formed. The reproductive process takes place in an inflorescence, which is the arrangement of individual flowers on a stem (Boland *et al.*, 1980).

The unit inflorescence is a single, stalked dichasium commonly referred to as an umbel. Vegetative buds are firstly formed in a season. The umble, which is usually seven-flowered in *E. grandis*, is initially enclosed in six or more bracts, where two are outer bracts and four are inner bracts. The receptacle of the flower bud bears on its rim two independently-shed opercula representing the perianth and numerous stamens. The stamens form a continuous ring and are inflexed, with the anthers arranged at the base of floral cup. The ovary is inferior and there is a single unlobed stigma which is closely enclosed in the tip of the inner operculum (Hodgson, 1976).

At time of flowering the pollen is viable and is immediately shed. The stigmas of the same flower take several days after the onset of flowering before they are receptive to the pollen. This feature ensures that individual flowers are not self-fertilised. The system favours outcrossing but is not a strong mechanism as the pollen from one flower can fertilise the ovules of another on the same tree provided that the flower has opened several days earlier. Flowering on one tree can take place over several weeks (Brooker, 1992).

b. The season of flowering

Eucalypts in their natural environment usually flower within distinct seasons. Some species are known to have regular flower seasons, for instance, *E. marginata* and *E. callophylla* in summer and *E. caesia* in winter. The season of flowering is affected by altitude although the altitude does not affect seed production adversely. Blakely (1955) cites June to August for flowering of *E. grandis* in Australia.

At the lower seed-orchard site (760m) near Tzaneen, South Africa, however, flowering is from February to March, with some clones flowering six-months out -of-season. At 1300 m of altitude, most of the flowering does occur from April to June, with some clones flowering through the year (Hodgson, 1976; Brooker and Kleinig, 1990).

c. Flower bud

An individual flower bud is the smallest unit of an inflorescence. Phenological observations showed the existence of three flower-bud stages, each lasting four to six weeks up to the time of anthesis. The "umbel bud" stage occurs when the flower buds are enclosed in the involucre of bracts; after the bracts are shed the flower buds at first have two opercula, then only the inner petaline operculum remains. The operculum may be free and shed singly, e. g. *E. abbreviata*, or united and shed as an irregularly torn cap, e.g. *E. delegatensis* and *E. kitsoniana* (Hodgson, 1976; Boland et al., 1980).

According to Brooker and Kleinig (1990), the number of buds is usually odd. Through growth and development one or more buds may be aborted although the original number of buds can be deduced from the scars on the summit of the peduncle. It is important to mention that the number of buds is not fixed, for instance in very few species such as *E. rhodantha* the peduncle terminates in a single flower bud while in *E. cosmophylla* and *E. megacarpa* it bears three buds.

1.5.2 FRUIT DEVELOPMENT

After flowering, the stamens fall and the bud (minus operculum and stamens) grows in size and becomes woody. At maturity it becomes the fruit. Inside, the fertilised ovules mature and become the seed. In a very few species the valves remain attached at their tips and the seed shed through gaps between them, e.g. *E. robusta* (Boland *et al.* 1980).

From fertilisation the time taken for the ovule to develop into a viable seed varies from species to species, but the process is complete by the time the fruit has become a brown, woody capsule and sometimes while the capsule is still green. The capsule opens by valves which begin to form before maturity of the ovary. Opening of the valves occurs on drying and is accompanied by widening of the locules and rupture of the locule walls, followed by seed shed (Hodgson 1976; Eldridge *et al.*, 1993).

Valve characters can be important in distinguishing some closely related species. For example, in *E. saligna* the valves are erect and in *E. grandis* they are incurved (Boland *et al.* 1980).

1.5.3 SEED SHED

It is important for the eucalypt breeder to know something of the mechanisms of seed shedding of the particular species to ensure efficient and complete extraction of seed.

Studies done by Cremer (1965) and Bateman (1961) showed that seed shed was accelerated by drought or fire and retarded by wet conditions. It was also concluded that seed shed depends on separation of seed from the placenta, the widening of the chambers, and the opening of the valves on drying of the fruit.

Not all the seed are shed from the fruit at once; in many species some fruit fall with some seed still enclosed. The amount held in this way differs with species and was found to be up to 24% for *E. regnans* and 43% for *E. delegatensis* (Boland *et al.*, 1980).

The time from flowering to the formation of mature fruit (i.e. with viable seed) varies greatly between species. In *E. tessellaris* it may take only a few days while in most species it takes weeks or months (Brooker, 1992). Awareness of the time factor is vital when judging the time to collect fruit for seed after having observed flowering.

The viable seed in eucalypts are formed at the base of the fruit. The seed is always mixed with particles known as chaff, some of which, are derived from unfertilised and infertile ovules. This means that the chaff sheds first, then the seed. In some species the seed may remain jammed in the base of the fruit but complete drying should allow their release (Hodgson, 1976; Brooker, 1992).

1.5.4 CONTROLLED POLLINATION

Due to variation among *Eucalyptus* species, it is necessary when making controlled pollinations to have detailed information on the biology of the particular species of interest. As also referred by Eldridge *et al.*, (1993) it is necessary to be aware of the extent and effects of inbreeding and hybridisation when doing seed collection.

a. E. grandis

For controlled pollination it is important to understand exactly what stage flower development has reached when deciding whether to put pollination bags on or take them off and when to apply pollen; it requires a knowledge of the breeding system , flower phenology, as well as the necessary technical skills to be included in this section. The following is based on the publication describing controlled pollination of *E. grandis* by Van Wyk (1977).

The flower bud consists of a receptacle which carries an operculum on its rim. The operculum covering the pistil and stamens of a bisexual flower falls away when the flower blooms, enabling the stamens to unfold. A distinct ring is visible at the line of junction between the receptacle and the operculum. When the flower reaches maturity, it gradually turns from green to yellow, and a split develops at the junctions of the receptacle and the operculum indicating that the latter is about to drop.

Pollination can be:

a) by anther where the stamens themselves are used to brush pollen onto the stigma. It does not require pollen storage since fresh flowers are used for pollination. The main disadvantage is the need for more pollen flowers than in the case with the brush method.

b) by brush involving the collection of mature, opening flower buds from which pollen is extracted two days after anthesis. This method is appropriate for special purposes, such as experiments requiring mixtures of equal amounts of different pollens or for receptivity tests. The advantage is that it ensures a mixture of pollen, in case enviable pollen is collected from some flowers. Pollen from one flower will be sufficient for 10 female flowers.

Clearly defined stages may be observed in the development of eucalypt flowers and results of such studies are useful in controlled pollination operations, especially if the programme being handled is a large one. The controlled pollination operation requires careful planning and record-keeping. Emasculation (involves cutting through the tissue of the flower cup

slightly below the staminal ring with an emasculation tool) and bagging are done before pollen flowers are isolated to ensure that stigma receptivity and pollen availability coincide.A convenient schedule is emasculation and bagging on Wednesday and Thursday and pollen flower isolation on Friday, leaving the weekend for the development of the pollen and emasculated flower. It is important to cut back the competing branches around the bag one month after controlled pollination because branches with emasculated flowers could be suppressed causing death and loss of seed.

b. Production of interspecific hybrids

Controlled pollination techniques for interspecific hybridization of eucalypts are similar to those described for *E. grandis,* although one has to consider the complementary characteristics, hybrid vigour, taxonomic affinity, reciprocal recurrent selection, and mass propagation before starting the pollinations. The possibility of creating new combinations that are not found in a pure species and heterosis (when the hybrid grows faster than either parent) are the attractions to interspecific hybridization (Eldridge, 1978).

Clones are selected from open and controlled pollinated trial crosses followed by progeny testing. The best trees per species, provenance and families, and with potential for vegetative propagation, are the ones to be selected for continuous breeding programmes.

Outcrossing and propagation of selected F_1 hybrid individuals by seed is likely to produce an unacceptably heterogeneous plantation in the F_2 generation, so F_1 hybrids usually are mass propagated by cuttings. In each generation interspecific F_1 hybrids would be made between selected individuals of different lines. The hybrid progeny would be propagated vegetatively and clone tests conducted before releasing selected clones for mass propagation (Matheson cited by Eldridge, *et al.* 1993).

1.6 GROWTH, VARIABILITY AND DEFECTS

The *Eucalyptus* is one of the genera most widely used in afforestation and reforestation in tropical regions due to the fast growth rate and easy adaptability in different climatic and soil conditions (Van Wyk, 1985; Eldridge *et al.*, 1993). *Eucalyptus* trees pass through several stages of growth, some species develop a single stem which becomes the trunk of the tree right

from the early stages but the majority produce a number of shoots which may persist for some years before one dominates the others, and becomes the erect main stem. The mature stage is characterised by the development of large, persistent branches which determine the shape of the crown (Penfold and Willis, 1961). Stem form varies between species and within the genus *Eucalyptus*. Straight stems, without knots, are the best for the wood processors who select them for different uses (Hillis and Brown, 1978).

The leaves of most species of eucalypt vary, sometimes markedly, from the seedling to the mature tree. The leaves are important aids to identification. The classification system described by Blake in 1953 distinguished the following types of leaves: seedling, juvenile, intermediate, mature, opposite and alternate leaves, reversion shoots (Anon.,1979).

The high ability of colonisation of the majority of eucalypts is related to the high capability of sexual reproduction, coppice and lignotubers, which allow the trees to survive in severe conditions (Poyton, 1979). As the lignotuber develops, it grows down the stem, involving the upper part of the root, and as its size increases, it tends to bury itself in the soil until just a small portion can be seen. Lignotubers are produced by most eucalypts. They are believed to be absent in the marlocks (wiry or effuse shrub, mallee or small tree without distinct erect or oblique stems) and also in *E. grandis*, *E. camaldulensis*, *E. diversicolor*, *E. astringens*, *E. regnans* and *E. gomphocephala* (Penfold and Willis, 1961; Brooker and Kleinig, 1990).

Species of the genus are fast growing with high adaptability to different climatic and edaphic conditions. The reproductive biology as well as the flexibility of using it on hybridisation programmes and clonal forestry are some of the advantages of using the genus *Eucalyptus* for various purposes (Penfold and Willis, 1961).

According to Raulins, cited by Cromer (1990) high quality eucalypt forests in Victoria, regenerated from seed and managed on an 80 year rotation without thinning, has a mean annual increment of about $12m^3$/ha/year. However for better plantations of *E. grandis*, *E. globulus*, *E. nitens* and *E. regnans*, the mean annual increment ranged from 15 to $30m^3$/ha/ year depending on species, site quality and rotation length (Cromer, 1990).

One of the greatest benefits from clonal propagation is volume gain. Experience in Brasil showed that the average production has increased from $33m^3$/ha/yr when improved seedlings were used to about $70m^3$/ha/yr with cuttings from selected trees (Zobel ,1993).

1.7 IMPORTANCE OF GENOTYPE BY ENVIRONMENT INTERACTION

Genotype by environment interactions (GEI) are present if the performance of genotypes relative to each other changes from one environment to another. The reference to genotype includes both individuals, for example eucalypt clones where the genetic makeup of each individual is identical to the other, and families. The environment involves all natural biotic, climatic and edaphic factors and all can interact with genetic effects. Sets of environments are operative in the nursery and in the field that can influence tree growth. The occurrence and significance of GEI has long been recognised in agriculture (Falconer, 1952; Perkins & Jinks, 1968; Allard & Bradshaw, 1962), and many researchers have also documented these interactions in forestry (Shelbourne, 1972; Owino, 1977; Burdon, 1977, Owino *et al.*, 1977; Carson, 1991).

When genotypes are tested at only one location, the interaction of genotypes and the environment is inseparable from genetic effects. If the interaction is large, genetic gain will be overestimated. Randall and Cooper (1973) reported that predicted genotypic gain from cottonwood (*Populus deltoides*) clonal tests showed an overestimate of genetic gains from single sites as excessive only for first-year height.

The implications of GEI in South African forestry has been reported by several researchers (Van Wyk *et al.* 1989, 1991; Falkenhagen, 1985; Darrow, 1983; Robertse, 1989).

The impact of genotype x environment interactions on the Australian *Pinus radiata* breeding programme showed a large loss of potential gain when selections were made at the wrong site. One solution pointed out is to regionalise breeding programmes such that selections grow relatively uniformly within a region (Matheson and Raymond, 1984). On the other hand, they indicate that a better solution to the problem is to omit families which seem to be particularly susceptible to environmental variation.

A large number of hybrid families and clones have been planted on 23 different sites in the summer rainfall area of South Africa. Study of results of families or clones growing on more than one site indicates that a certain degree of genotype x environment interaction exists but that many clones might be very stable in growth on different sites (Van Wyk *et al.*,1989).

Since 1963 a group of related methods have been developed to specify, estimate and correct for GEI effects. These now offer the breeder some prospect of dealing constructively with these effects previously only treated as a source of error and reduced genetic gain (Shelbourne, 1972).

Analysis of variance, ranking of genotypes in different environments, regression and genetic correlation are some of the methodologies used to assess the genotype and environment interaction.

If genotypes can be replicated, and more than one individual of each of several genotypes are reared in different specific environments, then an analysis of variance in a two-way classification of genotype x environments will yield estimates of the variance between genotypes, the variance between the specific environments, and the variance attributable to interaction of genotypes with environments. If there is no interaction, then the best genotype in one environment will be the best in all but if there is much interaction then particular genotypes must be sought for particular environments (Falconer, 1989).

This study follows the basis described by Falconer (1989) that deals with genotype x environment interaction and the difficulties arising from the estimation of environmental variance components. A solution for the study of GEI is the use of clonally propagated plants raised in different environments as done on the present nursery study. Eight different soil treatments constitute the environment and genotypes were represented by 20 clones of *E. grandis*. These clones were randomly assigned to the 8 soil treatments in order to find the best clone for each single environment.

The importance of this study is to detect possible presence of genotype x soil environment interaction and assessing the clones stability at young age, for the possibility of early age selection of clones.

The major objective of this study was to test for the possible presence of different growth responses of *Eucalyptus grandis* clones when grown in different soils in a nursery environment.

The following aspects were investigated:

1. **Comparative growth of *Eucalyptus grandis* clones in the nursery.**
2. **Growth changes in the nursery environment over time.**
3. **Presence and magnitude of genotype x environment interaction (GEI).**

2. LITERATURE REVIEW

2.1 CLONAL FORESTRY WITH *EUCALYPTUS*

Clonal forestry provides more options to the forester than does the planting of unidentified mixtures of improved genotypes as clonal trees of different genotypes can be deployed in different ways, forming forest populations with characteristics that may be different from conventional forests on both the individual and population level (Lindgren, 1993).

Clonal forestry is only as reliable as the clones used for planting. The reliability of clones depends to a substantial degree on the selection criteria used and on the efficiency of testing. One advantage of clonal forestry, sometimes the best of all, is the opportunity to match clones with sites and silvicultural treatment. This is especially true for eucalypt clones, which generally show a strong genotype x environment interaction (GEI) when environments vary considerably (Ahuja and Libby, 1993).

Other clonal forestry advantages are: capture of favourable variation -100% of their additive and nonadditive gene action; use of clones on unusual sites; prevent inbreeds in plantations by using pedigreed clones; control of genetic diversity; use of correlation breakers or trees that are above average in both traits that are found by clonal testing, identified, propagated and entered into production plantations (Libby, 1983; Burdon, 1989).

Cloning not only permits the capture of both additive and nonadditive variance but, if combined with hybridisation, also permits the exploitation of new, favourable genome combinations while retaining uniformity and repeatability in the planting stock (Stettler and Ceulemans, 1993).

Vegetative propagation would play a decisive role in the future application of hybridisation in forestry as recognised by Zobel and Talbert (1984). The strong genotype x environment interaction of *Eucalyptus* clones may create problems as some eucalypts become very sensitive to environmental variation. In such a situation a strong clonal field testing is mandatory to match clones with sites. When using seedlings from improved families, the testing programme

and use of significant genotype x environment interaction of individual trees is not possible because each individual tree has a different genetic make up, making it difficult to compare the genotype performance over all environments (Zobel and Ikemori, 1983). Clones can provide a sensitive means of detecting genotype x environment interactions and evaluating genotypic stability (Clair and Kleinschmit, 1986).

The production of eucalypt cuttings to form clonal plantations has been practised in South Africa since the early 80s (Donald *et al.*, 1994). According to Eldridge *et al.* (1993), outstandingly large straight trees, usually hybrids, are felled and the physiologically juvenile coppice shoots are used to make rooted cuttings. The resulting clones are then selected for their rooting ability.

The general practice in eucalypts is to have cuttings between 2mm and 5mm thick and between 60mm and 100mm long. The length of the cutting is determined by the stem internode lengths, as cuttings cut off just below a stem internode have much better rooting capacity than when they are cut in between internodes (Wignall *et al.* 1991). Two leaves are left on each cutting and each leaf must be halved.

Leaves are left on the cuttings so that photosynthesis can take place and also because it produces rhizocaline, an unidentified rooting co-factor which enhances rooting. The halving of the leaves produces ethylene which stimulates rooting indirectly. Halving of the leaves also reduces transpiration and therefore the drying out of the cutting. It also prevents overlapping of leaves in the tray which encourages fungal infection (Zobel, 1983). Further details of raising eucalypts cuttings are given in section 3.1.1.

2.2 ENVIRONMENT

The influences of environmental factors determine the species best suited to similar conditions of climate and soil. If the environment is inappropriate the trees will die or grow slowly.

The factors of environment can be grouped into those that are climatic, edaphic and biotic. Different sets are operative in the nursery and in the field. Climatic parameters are composed of precipitation, temperature, fire and wind effects; edaphic factors include physical and nutritional characteristics, and biotic influences include the effect of silviculture and competitors (Barnes, 1984).

Separate stages of plant life depend differently on climatic conditions. For instance, germination of seed is commonly affected particularly by temperature while growth is governed by photosynthesis which is too sluggish at lower temperatures. Water, nutrients and oxygen are three essential things that plants absorb from the soil. Soil is a mixture of mineral and organic particles of different sizes and composition in regard to plant growth (Linacre and Hobbs, 1977; Foth, 1990). Soil texture combined with soil pH level represents the different environments on the present study.

Before vegetatively propagated clones are used for operational regeneration, they need to be tested in all the major environments of the proposed planting area. Ultimately, all the potentially good clones need to be tested on each different site. The best clone on a particular site should then be used to reforest the area. Not all the clones will be suitable for all sites. Because of site x genotype interaction, different clones will often be used on different planting sites. Ignoring this aspect leads to huge losses (Zobel and Talbert, 1984).

Having species, provenances, families and clones, the expectation is that clones will respond much more to environmental changes because of the genetic makeup. As emphasised by Van Wyk *et al.* (1989), a single genotype (such as a single hybrid clone) may not be genetically buffered against environmental influences as well as is a group of genotypes (e.g. a family), and it might interact with its environment to a much higher degree. A rough model of this is depicted in Fig. 2.1. That is why each hybrid clone should undergo another round of test to evaluate its adaptability and growth to a particular site.

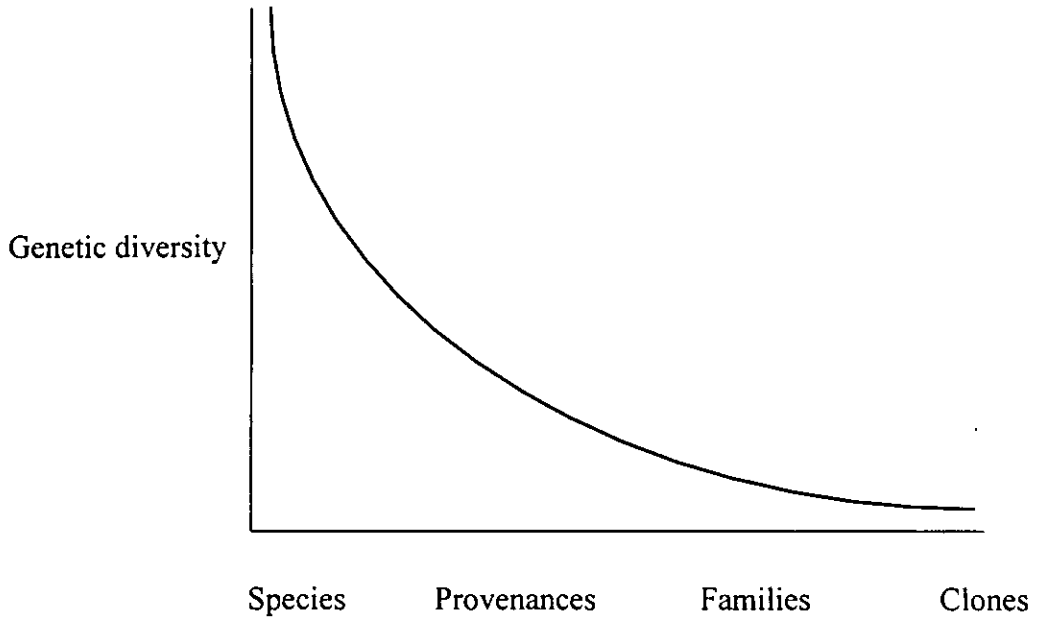


Figure 2.1. A hypothetical model illustrating the decline in genetic diversity when the number of genotypes in a population is reduced with selection (After Van Wyk, personal communication).

2.3 GENOTYPE X ENVIRONMENT INTERACTION

Although genotype x environment interaction (GEI) is a collective term, it is always desirable to declare the factors of interest that distinguish between environments and genotypes. Environment involves all the natural biotic, climatic and edaphic factors that influence tree growth and genotype includes genetic structure at the level of species, provenances, family or individual. In statistical and genetic terms an interaction between two factors (here genotype and environment) can be variously defined as a lack of additivity of their individual effects, or a differential ranking of levels of the first factor at different levels of the second (Barnes, *et al.* 1984 and Ott, 1993).

GEI is present and important at various levels from species to individual genotype in many fast growing species (Barnes, 1984). Different characteristics may have quite different genotype x environment interaction patterns. This has implications for the size and shape of the breeding unit as selection criteria change (Nanson, 1977).

The identification of a highly productive, well adapted, stable provenance for base populations is seen to be an important first step in tree improvement, as stated by Shelbourne (1972). He emphasised that subsequent research should be directed at establishing the causes of interactions by planting families or clones on a wide variety of sites characterised for edaphic and climatic factors. Once this basis for stratification of sites is available, recurrent testing of new genotypes in succeeding cycles of breeding will be necessary on a much more limited range of sites.

Genotype x environment interaction occurs when genotypes perform differently in response to different environments. Such interactions complicate testing and selection in tree improvement programmes, and result in reduced overall genetic gains (Clair and Kleinschmit, 1986; Matheson and Cotterill, 1990). Matheson and Raymond (1984, 1986) introduced the concept regarding the importance of genotype x environment interactions in terms of potential genetic gain which is lost by breeding for general adaptation to a range of sites rather than for specific adaptation. It was also pointed out that loss of potential gain is more meaningful than statistical significance in determining the practical importance of genotype x environment interactions.

There is a distinction between statistical and practical significance which is very important in determining the utility of genotype x environment interactions. Interactions can be statistically significant even though rankings remain the same in different environments.

When evaluating the practical importance of GEI one can estimate the additional cost and benefits of dividing the breeding activities into regions within which GEI is minimal. Also, one can calculate the interaction for certain sites (Barnes, Matheson and Raymond cited by Eldridge *et al.*, 1984).

2.3.1 GENOTYPE X ENVIRONMENT INTERACTION CLASSIFICATION

There are several forms which interaction may take. For example, a specific difference of environment may have a greater effect on some genotypes than on others; or there may be a change in the order of merit of a series of genotypes when measured under different environments. That is to say that genotype A may be superior to genotype B in environment X, but inferior in environment Y (Falconer, 1989).

It is convenient to classify interaction according to the magnitudes of differences between genotypes and between environments. There are four types of interactions as suggested by Dunlop (cited by Matheson and Cotteril, 1990):

a. Type I. Large x Large

These are macro-interactions which occur when the differences between genotypes and between environments are very large. The classical example of type I interactions in forestry is the interaction between species and region. They have been used successfully for such a very long time that they are frequently taken for granted. In the case of exotic pine plantations in eastern Australia, species x region interactions are used in the sense that *P. radiata* dominates Southern plantations (i.e. South of about 28° S), whereas *P. caribaea* is presently the main plantation species in the tropics and sub-tropics of Australia. Type I interactions also include provenance x region effects. There are many provenance trials of *Eucalyptus* species in Australia and around the world and for some species there is evidence of adaptation of provenances to particular regions; e.g. the Northern form of *E. camaldulensis* (particularly Petford and Katherine provenances in Queensland) grows best in areas with a tropical climate, while the provenances from South Australia (e.g. Lake Albacutya) grow best in Mediterranean climates.

b. Type II. Large x Small

In this case, the differences between genotypes are large, such as between species or provenances. The differences between environments are small, such as those of adjacent sites or even those of block replications within an experimental site. Interactions of this type may not be practically important although they are frequently found to be statistically significant.

c. Type III. Small x Large

Here, the genetic differences are small, such as those between families or clones. The environments are large, such as those frequently encountered in fertiliser trials or differences between regions. These type III interactions seem almost universal, examples included are family x fertiliser, clone x fertiliser, family x regions. This experimental study belongs to this type of interaction.

d. Type IV. Small x Small

These include interaction between families or clones and similar sites within a region or even block replications within a site. Type IV effects have been shown in many species, but may not be of great practical importance. However they are often sufficiently large to cause problems in using higher-level type III family x region or family x fertiliser interactions.

2.3.2 CAUSES OF GENOTYPE X ENVIRONMENT INTERACTION

To measure environmental sensitivities, and to see how much of the interaction variance is ascribable to differences of sensitivity, different genotypes are reared or grown in a range of specific environments to be quantified as more or less favourable for expression of the character under study. The only way in which environments can be quantified is by the mean performance of all the genotypes on the site which is called the environmental value. Each genotype has its own mean value in each of the specific environments. The genotype's environmental sensitivity is then the regression of its own value on the environmental value (Falconer, 1989).

The breeder could circumvent interaction by breeding for "broad" genotypes that are high-yielding in a wide range of environments or for many "narrow" genotypes together covering the same range. When looking at the interaction problem on the variety level, that is on a composition of genotypes, the breeder has three principal options. One is to use broad genotypes; the others depend on narrow genotypes used separately or in mixture. As long as the cause of interaction are known it is possible to define a set of environmental conditions in which to screen for the wanted genotypes and naturally it will be easiest to find the narrow genotype. At the same time it will be necessary to develop many more narrow than broad genotypes. If the causes are unknown the screening must be based on the criteria that are supposed to give stability (Gullberg, 1984; Resende *et al*; 1992).

2.3.3 GEI INFLUENCE ON PREDICTION OF GENETIC GAIN

The changes in gene expression with change in environment have long been recognised by plant breeders as an important source of phenotypic variation. The effect of these interactions on breeding programmes is to reduce genetic gain (whether obtained by selection of species,

provenances or individuals) since the GEI appears in the denominator of all heritability estimates and thus reduces heritability and consequent gain. To overcome this heritability gain can be maximised within each environment individually; and this requires the creation of separate breeding populations with consequent problems of cost, management, recording and ancestry control (Shelbourne, 1972; Lindgren, 1984; Namkoong, 1979).

Silvicultural and genetic research, which traditionally have been conducted by different organisations or individuals, must be integrated to determine the optimum genotypes and management system. Each afforestation site requires the integration of genetic and silvicultural research. The level at which genotype x environment interaction effects are important varies with species and trait but ignorance of GEI can cause severe losses of plantation yield through tree death or reduced growth (Barnes *et al.*, 1984).

2.3.4 IMPLICATIONS OF GEI IN TREE BREEDING

The presence of interactions has been regarded as a problem for breeders because it reduces the precision of selection in one environment for use in another. The ability of a breeder to make use of genotype x environment interaction depends on the magnitude of extra gains to be made and the size of the plantation programme in a specific environment. Plant breeders tend to ignore or dispose GEI while geneticists try to explain it in terms of gene action which offers valuable information to be used for breeding strategy. The major problems lie in designing suitable experiments to estimate GEI effects, analysing data appropriately to determine the contributing environments and genotypes, and interpreting the results for use in a breeding strategy (Barnes *et al.*, Matheson and Raymond, 1986).

If genotype x environment interaction is very pronounced, the expenditure of resources for a regionalised tree improvement programme would result in greater realised gain than would a non-regionalised programme. In situations of extremely high GEI, it may be appropriate to operate separate breeding populations in different regions. Less extreme GEI may be handled by producing different commercial seed orchard "breeds" for different regions, with each regional breed comprising a different set of genotypes selected from a single, national, breeding population. If GEI is not large, a non-regionalised programme could yield greater gains for the same expenditure of resources (Carson, 1991).

In forest tree breeding the main attention should be given to the role of environments rather than of genotypes in generating interactions. To some extent this principle is already implicit in the practice of regionalising tree breeding programmes. Forest environments are largely permanent features, since we can do little to change climate, topography, or many of the soil properties. Genotypes, by contrast, are not permanent features in that new ones can be created all the time (Burdon, 1977).

Genotype x environment interactions are likely to prove useful only when the environmental effects are statistically *fixed* and the interactions well-defined and repeatable. When environmental effects are statistically random, interactions with genotypes are not well-defined or repeatable and therefore are unlikely to be of any use to breeders (Matheson and Cotteril, 1990).

If the interactions are non-significant or do not involve appreciable differences in rank among the best families or clones, they may be ignored, in which case selection should be based upon a genotype's average performance at all test sites (Wright, 1976).

2.3.5 METHODS FOR DETECTING AND ASSESSING GENOTYPE x ENVIRONMENT INTERACTION

According to Shelbourne (1972), the basic requirements for detecting genotype x environment interaction and for selecting populations or genotypes for stability are replicated field experiments involving numerous entries (provenance, family, clone), repeated in several environments (combination of soil, climate, year and cultural treatment).The genotype of an individual can be measured only from its phenotype, or that of its parents or relatives. The effects of the genotype and the environment are not independent and thus genotypes differ in their phenotypic response.

The effects of environments can be treated either as random or fixed. If random, the environmental variation in the experiment is an estimate of the true variability between all environments. Where the environmental factors are unknown or unpredictable then sites can be selected at random and the environmental effects are considered as random.

If the environments have been selected to encompass a particular range of possible environments, as the study case discussed in this thesis, then they must be considered as fixed. Inferences about fixed environmental effects can be drawn only from the particular sample involved in the experiment. These differences in statistical inferences also apply to the interactions between genotypes and fixed or random environments.

Regarding the role of environments in generating interactions, Wricke, Morgenstern and Teich, (cited by Shelbourne, 1972), developed a procedure for calculating the contribution to the interaction sum of squares of each environment, its main use being in identifying particular environments which are anomalous.

The principle of orthogonal contrasts can be applied to partitioning the interaction sum of squares so as to identify groups of environments between which the major interactions occur, a refinement of this approach being the use of distance coefficients combined with cluster analysis (Burdon, 1977).

The AMMI method, LR procedure, Ranking of genotypes, ANOVA, the multivariate analyses and the correlation procedure, are the most common methods used for detecting and assessing genotype - environment interaction. A general description of some of the common methods are briefly discussed in this section. Detailed information is given on section 3.7 for the methods applied in this particular study.

a. Additive Main effects and Multivariate Interaction (AMMI)

In general statistical context, the AMMI model, where data are explained by sums of additive and multiplication terms which results from singular value decomposition of the interaction matrix, has been described in the early 1920's. This is one of the methodologies which could come into practical use with the computer advent. The benefit from AMMI will increase with the size of yield trial, that is, with increase on the number of genotypes and number of environments. More data improves the performance of a multivariate analyses like AMMI and this method is particularly useful when a large genotype-environment interaction is present (Gauch and Zobel, 1988; Gauch, 1990).

According to Gauch (1990), the randomized complete block (RCB) is doubtless the most popular experimental design for yield trial. However, blocking is a dubious means of error control in the presence of GEI. In contrast, AMMI frequently provides excellent error control when GEI is present and typical gain in accuracy from AMMI is shown to be much larger than from blocking.

b. Correlations between entry means in pairs of environments

Correlation between genotype and environment is seldom an important complication, and can usually be neglected in experimental populations, where randomization of environment is one of the chief objects of experimental design. When a correlation is present the phenotypic variance is increased by twice the covariance of genotypic values and environmental deviations (Falconer, 1989).

On the other hand, Burdon (1977) pointed out that the concept of genetic correlation between environments has major advantages in research strategy. It is readily directed at the question of the role of environments in generating interactions. As such it can be applied not only in defining the regions or sites categories which warrant separate breeding programmes, but also in defining which sites within a particular grouping are optimal for phenotypic selection or progeny testing. For predicting genetic gain it can be more satisfactory than conventional estimates of genotype-environment interaction variance.

c. Joint regression analysis

The so-called joint regression technique mentioned by Barnes et al (1984), wherein genotypic performance is plotted against the mean of all genotypes in each environment separately, or against some external estimator of site quality. The interaction variance is partitioned into two terms, the heterogeneity of regressions for each genotype and the deviation from regression for each genotype. This methodology has limitations including the assumption of linearity of response and the choice of an environmental mean value biased by the genotype under consideration but it is valuable for determining a genotype's stability over environments.

When plants are tested for genotype x environment interaction, the goal should be estimation of the magnitude as well as the cause of interaction. Regression methods, however, generally only fulfil the first goal, giving little information as to the relationship between interaction and environmental factors (Lundkvist, 1984).

d.Multivariate analyses

Interactions in the two-way table consisting of the performances of many genotypes in several environments can be tested by special tests for non-additivity. The tests are based on a principal component analysis which tries to reduce the dimension of the interactions. This method has not been much used in the analysis of genotype x environment interactions, and it is not quite clear how it can be used in selection experiments to assess stability (Skroppa, 1984).

e. Portions of genetic variance

Genotype environment interactions estimated from the analysis of variance of experiments with families or clones, are composed of the interaction of the environment with differing portions of genetic variance. With half-sib families only 1/4 of the additive genetic variance is present between families to interact with environmental effects; with full-sib families there is 1/2 additive variance plus 3/4 dominance variance, and between clones the total additive, dominance and epistatic genetic variance (plus common physiological origin effects) is present (Shelbourne, 1972).

2.3.6 GENETIC AND ENVIRONMENTAL CORRELATIONS

The two relevant causes of correlation between characters are genetic and environmental. Genetic causes are related to pleiotropy which is the property of a gene whereby it affects two or more characters, so that if the gene is segregating it will cause simultaneous variation in the characters it affects. The correlation resulting from environmental causes is the overall effect of all the environmental factors that vary, some causing positive and others a negative correlation. Environmental causes do not only include the correlation of environmental deviation but also the non-additive genetic deviations (Falconer, 1989).

The genetic correlation expresses the extent to which two measurements reflect what is genetically the same character. This is more important to the breeder because it is the correlation of breeding values. Genetic correlation is based on estimates of genetic covariance between traits from a progeny test (Falconer, 1989; Eldridge, *et al.*, 1993).

According to Falconer (1989), the genetic and environmental causes of correlation combine to give the phenotypic correlation. Phenotypic correlation results from measurements of the two characters in a number of individuals of a certain population. In forest tree breeding, the correlation concept should advantageously replace that of heritability because of its greater generality. If both characters have low heritabilities it implies that the phenotypic correlation is determined by the environmental correlation; if they have high heritabilities, then the genetic correlation is more important.

3. MATERIALS AND METHODS

3.1 GENETIC MATERIAL

The genetic material consists of 19 different *Eucalyptus* clones as listed in Table 3.1. There were 16 pure *E. grandis* clones and three hybrid clones. The list contains 20 entries as one clone, AG3, is split up into two entries, AG3-A and AG3-B. This was because the aim was to have 20 clonal entries but because no more *E. grandis* clones were available Mondi Forests included a duplicate of AG3. It was included in the trial as an "extra" clone.

Table 3.1. *Eucalyptus* clones supplied by Mondi Forests, Natal for the GEI trial.

CLONE NUMBER	SPECIES
AG0001-AG0015	2nd generation *E. grandis*
G0001	1st generation *E. grandis*
GU0001	*E. grandis* x *E. urophylla*
GC0001	*E. grandis* x *E. camaldulensis*
GC0002	*E. grandis* x *camaldulensis*

$F_1 + F_2$ clones were selected by Mondi Forests Ltd. based upon growth performance in five different locations, (Table 3.2.).

The clones at location 1 were assessed at the age of 48 months; 36 months at location 2, 3 and 4 and at various ages at location 5. Height (m) and D.B.H.(cm) were measured and MAI (m^3/ha/yr) was generated (Wex, personal communication). The *E. grandis* 2nd generation ortets were selected in 13 different open pollinated trials and two full-sib trials as shown in Table 3.3. The ortets were propagated in cutting banks at Kwa-Mbonambi.

Table 3.2. Details of the trial locations for the clones used in the genotype x environment interaction study in the nursery at the Faculty of Forestry.

Location	Latitude	Longitude	Altitude M	Rainfall mm	Soil Type	Clones
1. Melmoth 5/17 A	28°30'30"	31°15'30"	1170	-	Clovelly	GC1, GC2, GU1, AG1, AG2, AG3, AG10, AG11, AG12, AG13
2. Louwsburg 5/17 B	29°30'07"	31°20'	0900	-	Cartref	GC1, GC2, GU1, AG1, AG2, AG3, AG10, AG11, AG12, AG13
3. Kwa-Mbonambi 5/19 A	28°41'	32°04'	0040	1250	Pale, dry yellow & red sands	GU1,AG1, AG2, AG3, G1
4. Melmoth 5/19 B	28°34'	31°18'05"	1038	1200	Humic soils	AG9, AG1, G1
5. Kwa-Mbonambi 4/12	28°35'45"	32°05'20"	0080	-	Villafontes, Fernwood, Hutton/oak, Longlands	AG1, AG3, AG4, AG5, AG6, AG7, AG8, AG9, G1

Table 3.3. Pedigrees of *E. grandis* clones and hybrid clones supplied by Mondi Forests for the GEI trial.

	CLONE NUMBER	FEMALE x MALE	
1	AG0001	2407	OP
2	AG0002	G0161	OP
3	AG0003	2411	OP
4	AG0004	G0142	OP
5	AG0005	2407	OP
6	AG0006	2411	OP
7	AG0007	G0211	OP
8	AG0008	G0211	OP
9	AG0009	G0023	OP
10	AG0010	G0050	G0004
11	AG0011	G0050	G0004
12	AG0012	G0347	OP
13	AG0013	G0205	OP
14	AG0014	G0504	OP
15	AG0015	G0456	OP
16	GC1	G45	C24319
17	GC2	G58	C24319
18	GU1	G45	U24198

3.1.1 RAISING OF CUTTINGS

Once the cutting is made and the leaves halved, it is dipped into a fungicide/water mixture (Benlate) for three seconds, shaken and the bottom part of the cutting dipped into a hormone powder (Seradex No.2). It is then firmly placed into a vermiculite rooting medium and sprayed with 30g Multifeed per 15lt. water in a greenhouse environment where no tropical disease exists. In general, the cuttings remain in the greenhouse for a total of 25 days after which they are moved out to the shade-net area. At the Kwa-Mbonambi eucalypt cutting nursery of Mondi Forests, the cuttings trays spend their first 40 days on the ground under 55% shadecloth in the mister section of the nursery. The cuttings receive six seconds of water mist every seven minutes during the initial rooting phase. Once rooted, the cuttings are moved to the grow-out area where they have only 11% shadecloth to protect them. At this stage the plastic cutting-tubes (known as "unigro's" or "inserts") are removed from their original low plastic trays with side walls and placed in wire carriers that are higher to promote aerial pruning of the emerging roots. Cuttings that have failed to root are discarded at this stage. At the grow-out area the cuttings receive 20 minutes water two to three times daily. Halfway through the 42 day grow-out period the cuttings are sorted into small and large size groups. After that the cuttings are ready for planting (Duncan, personal communication).

Cuttings used in the experiment were taken from 1995 shoots harvested after 65 days of growth on the stools and raised by Mondi Clonal Nursery in Kwa-Mbonambi, Kwazulu-Natal.

Early March 1996 the cuttings were received at Stellenbosch. Due to a delay in nursery construction, the cuttings were placed in the Unigro containers in the nursery for several months. This involved watering, topping, weeding and fertilisation with Supranure Plus every second day during March/April 1996 to induce sprouting. At the same period the plants were treated with Benlate, an effective fungicide for diseases control.

In May 1996 the cuttings were treated with Folithion, an insecticide applied against aphids. The cuttings were then transplanted from the unigro's to the soil bags after being labelled. The process took place from Tuesday 11 th till Friday 14 th of June 1996.

3.2 SOIL TREATMENTS

According to Olson (1981) and Smith (1991) soil texture is the most permanent and probably the most important of all soil characteristics influencing soil behaviour. To increase acidity, the hydrogen must be replaced by metallic cations which is commonly done by adding oxides, hydroxides, or carbonates of calcium and magnesium.

The study included eight soil treatments being four soil types with different texture structures and two pH levels. The different soil treatments were based on differences of physical properties, organic carbon content, texture and soil pH. Soil collection was done from November 1995 till January 1996 in 4 different places in the Western Cape, specifically Lourensford near Somerset West; Pampoenvlei near Malmesbury; Helshoogte near Stellenbosch and from Grabouw. The yellowish soil type from Grabouw and the reddish soil type from Helshoogte were clayey (35-45% clay) while the dark and light coloured soil types from Lourensford and Pampoenvlei respectively were sandy soils (26% in clay). Table 3.4. shows the treatment code number for specific soil types.

Table 3.4. Soil type code number

CODE	SOIL TYPE
S1	DARK, SANDY, STRUCTURELESS
S2	RED, CLAYEY,WEAK BLOCKY
S3	YELLOW,CLAYEY,MODERATELY BLOCKY
S4	LIGHT, SANDY, STRUCTURELESS

At the end of January and early February 1996, part of all 4 soil types were limed creating a new pH level, and a new treatment for each soil type. Soil samples were taken to determine the amount of agricultural lime required in grams for pH correction for each soil type as shown in Table 3.5.

Table 3.5. Lime application to the different soils to obtain an approximate pH 7 level in each soil type. See Table 3.6.

Soil type	Location	Amount of lime per Kg of soil type
Dark, Sandy	Somerset West	9 grams
Red, Clayey	Helshoogte	3 grams
Yellow, Clayey	Grabouw	5 grams
Light, Sandy	Pampoenvlei	1 grams

Lime was sieved using a 1,5mm sieve. The mass of the soil was taken and all possible stones removed. After that the lime was added to the soils and mixed very well and watered afterwards. The soil type mixtures were stored in plastic bags for at least a month before being used. Table 3.5 shows the mean of two determinations of pH levels done on 8th of March on the limed and control soil type samples.

Table 3.6. Outcome of pH levels after the liming treatment and a storage period.

Soil Treatment	pH (H2O)
Somerset West limed on 26/1/96	7,03
Somerset West control	5,04
Helshoogte limed on 1/2/96	7,35
Helshoogte control	5,62
Grabouw limed on 31/1/96	7,28
Grabouw control	5,68
Pampoenvlei limed on 2/2/96 (soil 2)	7,34
Pampoenvlei control (soil 2)	5,38
Pampoenvlei limed on 29/1/96	7,14
Somerset West limed on 2/2/96 (soil 2)	7,06

Soil type and lime level combination generated the 8 soil treatments. The soil treatment codes, which are mostly used in data analysis are given in Table 3.7.

Table 3.7. Combinations of soil type with lime levels and respective soil treatment codes.

SOIL TYPE + LIME COMBINATIONS	SOIL TREATMENT CODE
S1L0 = SOMERSET WEST + NO LIME	ST1
S1L1 = SOMERSET WEST + LIME	ST2
S2L0 = HELSHOOGTE + NO LIME	ST3
S2L1 = HELSHOOGTE + LIME	ST4
S3L0 = GRABOUW + NO LIME	ST5
S3L1 = GRABOUW + LIME	ST6
S4L0 = PAMPOENVLEI + NO LIME	ST7
S4L1 = PAMPOENVLEI + LIME	ST8

3.3 TRANSPLANTING

The arrangements for the successful transplanting process involved a previous plant labelling and filling of the soil bags. Each of the 3140 labels contained the clone number and the tree number for all the 20 clones. These where then placed in each and every plant for appropriate identification. Two litre (long shape - dimensions 30 x 10 cm when flat) polythene bags were filled with all 8 soil treatments. For each soil treatment 400 were filled to half the bag length and stored outside the greenhouse for 5 weeks from May 6 to June 10, while the benches were being finished up. After that the half filled bags were then moved to the benches into the greenhouse area and grouped in soil treatments. Between 11 th and 14 th of June the transplanting took place. It consisted of removing the cuttings from the unigro's to the polythene bags and filling the remaining space in each bag with the specific soil treatment. The transplanting was done by clone; 20 cuttings of each clone were planted in each soil treatment before the next clone was started. Five people were involved on this operation and everybody had to plant some cuttings of the same clone in each soil treatment to eliminate possible planting effects of individuals.

The plants were watered by hand, a hosepipe was used for two weeks and from 1st of July the automatic irrigation was established and combined with manual irrigation because the sprays were not 100% efficient . The irrigation time and frequency was changed several times to suit the plant requirements and their response. A growth anomaly was detected on the leaves in middle July 1996, due to a slow night evaporation rate. The leaves had became curly, with light callous spots on them. This anomaly was more evident on Pampoenvlei and Grabouw soil treatments, the two extremes, the very sandy and the very clayey respectively.

A month after transplanting, a 3:2:1(25) granular fertiliser was applied. The fertiliser had to be crushed into very small pieces or powder, with pestle and a mortar before an amount of one gram (equivalent of 20 mg P/ha) was applied to the soil in each of the 3140 bags included in the experiment.

From August 5 till 9 the soil treatments and clones were randomised and applied, as described in section 3.4.

3.4 DESIGN AND LAYOUT

The trial design consisted of an 8 x 20 factorial with eight soil treatments and 20 clones. It was established in June 1996 from 11th to 14th, in a Randomised Complete Block Design with 20 replications and single tree plots. Because of soil shortage, not all the clones were equally represented in all replications. Specifically replications 18, 19 and 20 did not have the limed soil treatment from Grabouw. These three replications had a total number of 140 trees instead of 160 trees as did the other 17 replications. Fig. 3.1. shows the trial layout on four different benches with five replications on each. Soil treatments were randomised in each replication and clones were randomised in each soil treatment within each replication.

REP 1	REP 2	REP 3	REP 4	REP 5
2	3	2	3	2
4	2	3	2	1
3	1	4	4	3
1	4	1	1	4
REP 6	REP 7	REP 8	REP 9	REP 10
2	1	3	1	1
3	3	4	2	2
1	4	2	3	3
4	2	1	4	4
REP 11	REP 12	REP 13	REP 14	REP 15
4	4	1	3	2
1	2	3	2	4
3	3	2	4	1
2	1	4	1	3
REP 16	REP17	REP 18	REP19	REP 20
3	4	1	2	4
2	2	2	4	2
4	1	3*	1	3*
1	3	4	3*	1

Figure 3.1. Trial layout indicating the 4 soil types in each replication. The asterisk (*) indicates that the limed treatment of the Grabouw soil was not included in these replications. See Fig. 3.2. for more detail of each replication.

REPLICATION 15

SOIL 2	S2L0	AG5 AG7	GC1 G1	AG2 GC2	GU1 AG10	AG11 AG13	AG3-A AG1	AG6 AG3-B	AG8 AG9	AG4 AG14	AG12 AG15
	S2L1	AG14 GC1	GC2 AG5	AG15 AG10	AG12 AG11	AG2 AG3-B	AG7 AG9	G1 AG4	AG3-A AG8	AG1 GU1	AG13 AG6
SOIL 4	S4L1	AG14 AG7	AG5 AG4	AG6 AG3-B	AG9 AG3-A	GU1 AG1	AG8 AG13	AG11 GC1	AG10 GC2	AG2 G1	AG15 AG12
	S4L0	AG12 GC2	G1 AG11	AG4 AG6	AG5 AG3-A	AG8 AG7	GU1 AG13	AG14 AG1	AG9 AG2	AG10 AG15	AG3-B GC1
SOIL 1	S1L0	AG3-B AG12	AG10 AG5	AG9 AG6	GU1 GC1	AG2 AG14	AG9 AG13	AG11 AG7	GC2 AG1	AG15 G1	AG4 AG3-A
	S1L1	AG14 AG9	AG8 AG3-B	AG6 AG4	AG10 GU1	GC1 AG5	AG7 AG15	G1 GC2	AG2 AG12	AG11 AG3-A	AG13 AG1
SOIL 3	S3L0	AG14 AG5	GC1 AG9	GU1 AG10	AG3-B AG4	AG12 AG15	GC2 AG6	AG7 AG3-A	AG2 AG13	G1 AG11	AG8 AG1
	S3L1	AG2 AG12	AG7 GC2	AG1 AG3-A	AG1 AG15	AG6 GC1	AG14 AG8	AG10 AG5	GU1 AG3-B	AG13 AG9	AG11 AG4

Figure 3.2. Detail for replication 15, including soil types, soil treatments and 20 clones randomly allocated in each of the eight soil treatments.

3.5 MEASUREMENTS

Measurements were taken before and after transplanting. Two response variables, height and diameter were measured before and after transplanting. Height and diameter, and root and shoot mass were measured at three ages and the number of branches was assessed only at 24 weeks. More detailed information is given in Table 3.8.

3.5.1 BEFORE TRANSPLANTING

The early measurements taken a month after cutting back the plants included height of the shoot measured from the point from where it sprouted at the top of the cutting (the sprouting point) to the last bud, in centimetres, using a measuring tape. Diameter (mm) was measured using a vernier calliper 5 centimetres above the sprouting point. Mass of the whole plant (grams) was taken while plants were wet using a PM 4000 scale.

Table 3.8. Abbreviation used to denote different traits measured before and after transplanting at different ages and replications.

AGE	TRAIT	REP	ABBREVIATION USED IN THE TEXT
BEFORE TRANSPLANTING			
	Mass of the whole plant		M0
	Height		H0
	Diameter		D0
AFTER TRANSPLANTING			
12 weeks	Height	all 20	H12
	Diameter	all 20	D12
	Shoot mass	one: 5	Sm12
	Root mass	one: 5	Rm12
	Ratio: Shoot mass /Root mass	one: 5	R1
18 weeks	Height	all 19	H18
	Diameter	all 19	D18
	Shoot mass	one:16	Sm18
	Root mass	one:16	Rm18
	Ratio: Shoot mass /Root mass	one:16	R18
24 weeks	Height	all 18	H24
	Diameter	all 18	D24
	Number of branches	all 18	Nb24
	Ratio:Number of branches/ height	all 18	B24
	Shoot mass	all 18	Sm24
	Root mass	one:11	Rm24
	Estimated Root mass	all 18	ERm24
	Ratio: Shoot mass /Root mass	one:11	R24

3.5.2 AFTER TRANSPLANTING

Height and diameter measurements were taken at 12 weeks, 18 weeks and 24 weeks and shoot and root mass was determined for one replication only at 12, 18, and 24 weeks. Shoot mass was taken and number of branches were counted on all remaining plants at the last assessment. The height before transplanting and 24 weeks after transplanting was taken with a measuring tape. For the first two assessments, 12 and 18 weeks after transplanting respectively, rulers were used to measure the tree height 5 centimetres above the sprouting point as illustrated in Figs. 3.3 and 3.4.

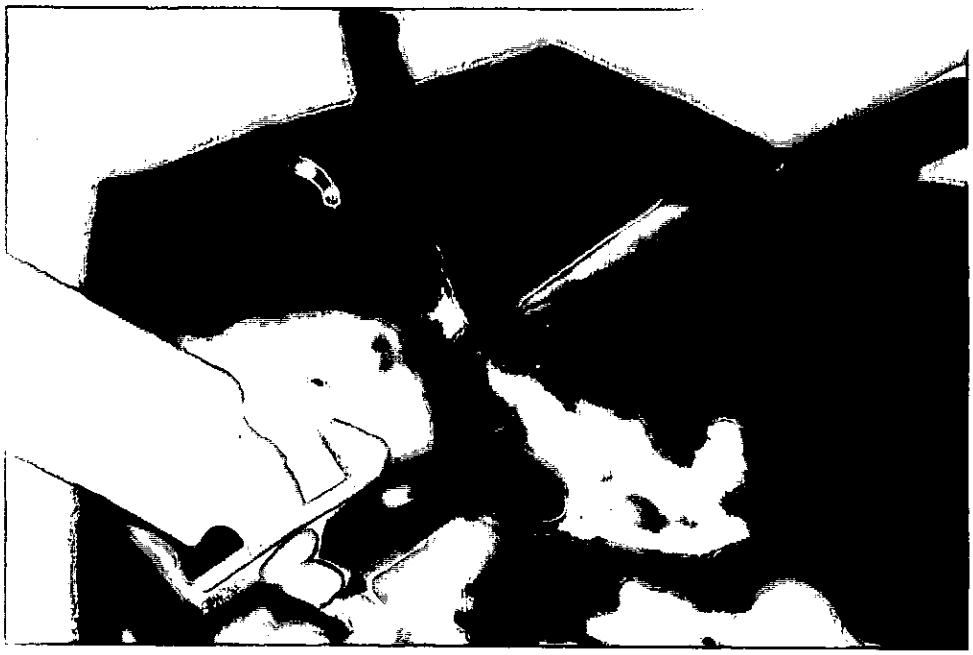


Figure 3.3. The sprouting point indicated by the pencil. Height and diameter measurements were taken 5 cm above this point.

Figure 3.4. Height measurement taken by ruler 5 cm above the sprouting point.

Root mass and shoot mass were taken for replication 5 at 12 weeks; replication 16 at 18 weeks and replication 11 at the last assessment. For the last assessment shoot mass of all trees were taken in the remaining replications.

After cutting down the shoots, they were placed in paper bags, labelled and left in the oven for at least 12 hours at 110 °C. The roots were carefully washed before placing in the oven, also in paper bags. After the materials were dried and cooled down the respective masses were taken on the PM 4000 scale.

3.6 GENERATED VARIABLES

The shoot : root mass ratio at 12, 18 and 24 weeks (R12, R18, R24) was derived from shoot and root mass on an individual using the formula:

$Ratio_i = Sm_i / Rm_i$ where (i = 12,18,24)

These ratios were basically calculated using data from only one replication chosen at random to look at the root system development over time. Root mass taken at 24 weeks on one replication (11) was used to generate regression coefficients for estimation of root mass over all the replications. The shoot mass taken from all remaining replications at the end of the experiment (17), were then used on the predicted root mass equation as shown below:

ERm24 = a + b*Sm24

The number of branches per height unit at 24 weeks was derived using the formula:

B24=No. Branches/ Ht24

Figure 3.5.The roots were carefully washed, labelled and placed in paper bags.

3.7 STATISTICAL PROCEDURES

Data analyses utilised the analysis of variance for a randomised complete block design. All effects were considered to be fixed. Some imbalance occurred in the data sets owing to soil shortage; therefore, a least squares analyses was employed to calculate the sums of squares (Type II sums of squares) (Van Laar, personal communication). Data analyses were performed using the GLM (General Linear Model) procedure (SAS Institute, 1995). Quatro Pro (1987), was initially used for data capture.

The analysis of data from the trial included an initial analysis of variance for all clones and each trait measured on each soil type and lime levels. Data for all 20 clones was used for the comparison of overall performance of clones over soil treatments. The interactions between clones, soil types and lime levels were tested for statistical significance by comparing the mean square with the error mean square. To investigate clone x soil treatment interaction, a linear regression of each mean clone performance on each soil treatment was performed using the trial mean of each soil treatment of the 20 clones as the independent variable for the regressions.

Pearson correlation analysis was also done between traits and for each trait among the different soil treatments. All the calculations were based on individual tree data. The delineation of significant differences between the rankings of clones for each variable was performed using Duncan's New Multiple Range Test.

3.7.1 ANALYSIS OF VARIANCE (MODEL/ANOVA)

Analysis of variance should normally be employed as a basis for all subsequent examination of data. This allows testing the effects of entries, environments and their interaction for significance. Calculation of variance components and expressing the GEI component as a percentage of totalled components or as a percentage of the entry component allows some quantitative appreciation of the size of the interaction relative effects. Estimation of these components however is usually imprecise unless there are large numbers of degrees of freedom for entries and for environments. As an approximate rule of thumb, where the interaction component reaches 50% or more of the entry component of variance then the effects of GEI are likely to be serious on gains from selection and testing (Shelbourne, 1972). The existence of

genotype x environment interaction is usually demonstrated by a significant interaction term in an analyses of variance (Matheson and Raymond, 1984).

The following basic model was used:

$P = \mu + G + E + GE + \varepsilon$

Where:

P = phenotypic value

μ = general mean

G = genotypic effect (= clones)

E = environmental effect (= soil treatments)

GE = genotype x environment interaction effect

ε = random error

To be more specific, if Y_{ijk} is the measured value of the i-th genetic entry in replicate *k* at site *j*, the model can be rewritten as

$$Y_{ijk} = \mu + G_i + E_j + (GE)_{ij} + B_{jk} + \varepsilon_{ijk}$$

where B_{jk} is the effect of replicate *k* at site *j*. This model leads to the familiar analysis of variance (Skrøppa, 1984).

Table 3.9. Analysis of variance table for an a x b factorial experiment with n observations per cell.

Source	**SS**	**df**	**MS**	**EMS**	
				Fixed Effects	Random Effects
A	SSA	a - 1	MSA	$\sigma_\varepsilon^2 + nb\theta_A$	$\sigma_\varepsilon^2 + n\sigma^2_{\alpha\beta} + bn\sigma^2_\alpha$
B	SSB	b - 1	MSB	$\sigma_\varepsilon^2 + na\theta_B$	$\sigma_\varepsilon^2 + n\sigma^2_{\alpha\beta} + an\sigma^2_\beta$
AB	SSAB	$(a - 1)(b - 1)$	MSAB	$\sigma_\varepsilon^2 + n\theta_{AB}$	$\sigma_\varepsilon^2 + n\sigma^2_{\alpha\beta}$
Error	SSE	$ab(n - 1)$	MSE	σ_ε^2	σ_ε^2
Totals	TSS	abn - 1			

After Ott (1993).

In practice the fixed effect situation is often approached (Burdon, 1977). He pointed out that for overall analysis of variance to be strictly valid the residual variation should be reasonably homogeneous among environments.

The data set was analysed for height, diameter and number of branches by fitting the following fixed models:

a) Simple model

$Y_{ijk} = \mu + R_i + S_j + C_k + (SC)_{jk} + \varepsilon_{ijk}$

Where,

Y_{ijk}: is the observation of i^{th} replication and k^{th} clone grown in j^{th} soil treatment.

μ = is the overall mean

R_i = fixed effect of the i^{th} replicate.

S_j = fixed effect of the j^{th} soil treatment.

C_k = fixed effect of k^{th} clone.

$(SC)_{jk}$ = interaction between the j^{th} soil treatment and k^{th} clone.

ε_{ijk} = experimental error.

b) The dissociation of the soil treatment term in soil types and lime levels generates the following model:

$Y_{ijkl} = \mu + R_i + S_j + L_k + C_l + (SL)_{jk} + (SC)_{jl} + (LC)_{kl} + (SLC)_{jkl} + \varepsilon_{ijkl}$

Where,

Y_{ijkl}: is the observation of i^{th} replication and l^{th} clone grown in j^{th} soil and k^{th} lime level.

μ = is the overall mean

R_i = effect of the i^{th} replicate.

S_j = effect of the j^{th} soil.

L_k = effect of k^{th} lime level.

C_l = effect of l^{th} clone.

$(SL)_{jk}$ = interaction between the j^{th} soil and the k^{th} lime level.

$(SC)_{jl}$ = interaction between the j^{th} soil and l^{th} clone.

$(LC)_{kl}$ = interaction between the k^{th} lime level and the l^{th} clone.

$(SLC)_{jkl}$ = interaction between the j^{th} soil, k^{th} lime level and l^{th} clone.

ε_{ijkl} = experimental error.

For shoot and root mass taken at 12, 18 and 24 weeks for only one replication the analysis was done by fitting the following model:

$Y_{ij} = \mu + C_i + \varepsilon_{ij}$

Where,

Y_{ij} : is the j^{th} observation of i^{th} clone.

μ = is the overall mean

C_i = effect of i^{th} clone.

ε_{ij} = experimental error.

This model applied for a single replication (11) generated the regression coefficients to create a new variable, the estimated root mass (ERm24). Analysis of variance for shoot mass and predicted root mass at 24 weeks was done by fitting both fixed effect models referred to earlier.

3.7.2 REGRESSION OF ENTRY MEANS ON OVERALL ENVIRONMENT MEANS

In order to determine the regression coefficients for each of the 20 clones included on the present study few steps were followed. Firstly, trial means per soil treatment were generated to be used as independent variable (x), known as site index. Secondly, clonal means in each of the eight soil treatments were generated to be used as the regression dependent variable (y). Regressing these two parameters a slope or b_i coefficient, an intercept and a coefficient of determination (R^2) were obtained. The slope is of high value on studying genotype x environment interaction or genotypic stability of different clones.

A linear trend with a slope approaching unity indicates clonal stability but deviation from unity indicates that the clone reacts differently to varying soil treatments (Fig. 3.6). A regression coefficient greater than one indicates that the specific clone has potential for better than average performance on good soil treatments, e.g. Clone I in Fig. 3.6. Conversely, a clone with slope coefficient less than one indicates that such a clone will be adapted to grow better than average on soil treatments with a relatively low fertility level (Clone II). This will hold for clones having regression lines with basically the same intercept. A low slope with a low intercept (Clone III) obviously is poor when compared to another clone with a low slope but higher intercept (Clone II).

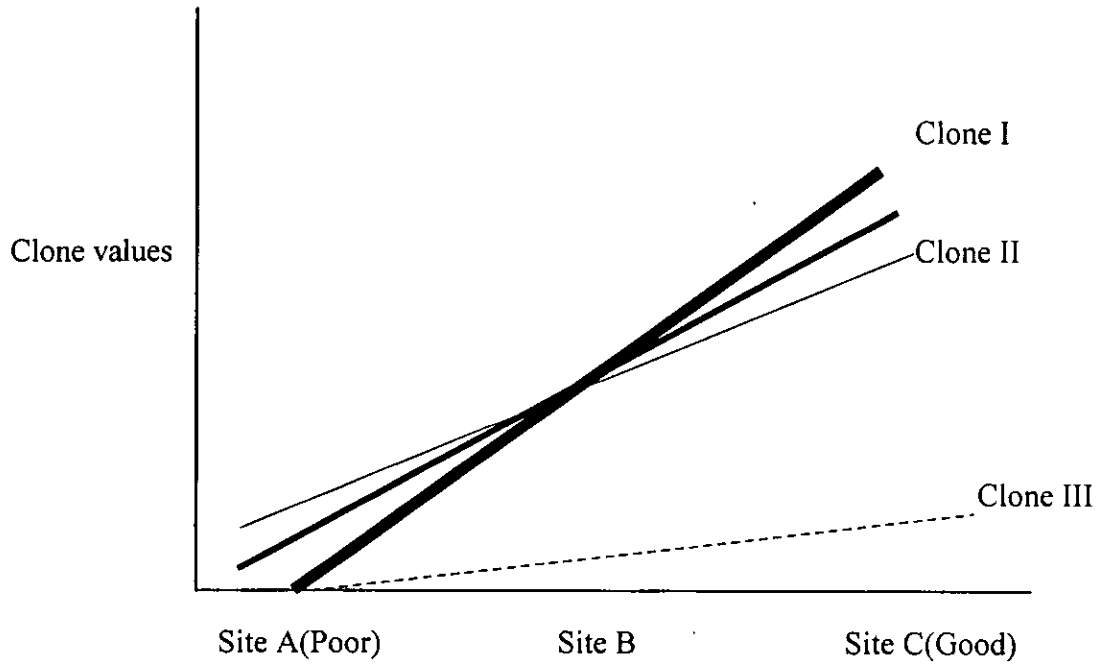


Figure 3.6 Clone mean performance on different sites and corresponding regression lines.

3.7.3 RANKING OF GENOTYPES IN THE DIFFERENT ENVIRONMENTS

Clonal means per soil treatment were firstly generated for variable height and diameter at all ages. These means were then correlated among each other in order to detect a change of ranking of clones on different soils and possible presence of genotype by environment interaction.

According to Shelbourne (1972) when ranking of entries is consistent between environments (soil treatments) GEI can be expected to be weak or absent. When rank changes in different soil treatments occur these may be due to GEI or to experimental error, though if performance is consistent between replicates in an environment, then the effect of genotype is the one exposed.

3.7.4 MAGNITUDE OF VARIANCE COMPONENTS

The VARCOMP procedure (SAS Institute, 1995) is designed to handle models that have random effects. One can specify certain effects as fixed by putting them in the model statement and indicating the number of fixed effect with the fixed options. An intercept is always fitted and assumed as fixed. Except for the effects specified as fixed, all other effects are assumed to be normally distributed and independently distributed. For the purpose of this study the MIVQUE0 method was applied.

This method produces estimates that are invariant with respect to the fixed effects of the model and are locally best quadratic unbiased estimates given that the true ratio of each component to the residual error component is zero.

With VARCOMP method MIVQUE0 results the percentage contribution of variance component for random and fixed effect were obtained by:

$$\text{Random} : \frac{\ldots\ldots C\ldots\ldots}{A+B+C+D} * 100 \qquad \text{Fixed} : \frac{\ldots C\ldots}{C+D} * 100$$

Where,

A = var (clone)

B = var (soil type)

C = var (soil type * clone)

D = var (error)

var = the variance component

The percentage of variance components for fixed model are expected to be greater than for the random model meaning that a study of GEI will be more meaningful if selected clones and environments are included in the investigation.

4. RESULTS AND DISCUSSION

4.1 EXPERIMENTAL DESIGN

The trial design consisted of an 8 x 20 factorial with 8 soil treatments and 20 clones, in a Randomised Complete Block Design with 20 replications and single tree plots. Factorial experiments are aimed at evaluating known or suspected interactions. The factorial experiment is not an experimental design. It is, instead, a way of selecting treatments; given two or more factors each at two or more levels, the treatments are possible combinations of the levels of each factor. Factorial experiments may be conducted in any of the standard designs; randomised block and split plot being the most common for factorial experiments in forest research (Freese,1967).

Table 4.1 illustrates results of analysis of variance for height growth at 12, 18 and 24 weeks. The variation among replications was significant at 12 weeks and this variation increased substantially in older material due to effects caused by different benches in the nursery. Tremendous differences from bench to bench and among replications within benches are obtained. These variations were anticipated and is the reason why 20 replications were included in the experimental design. The interaction between clone and replication within bench is not significant for all the assessments giving weight to inferences that can be made about clonal effects.

The fully fixed model has been used, that is the effects due to replications, clones, soil type and lime levels were all assumed to be fixed. Soil type combinations were regarded as fixed since they were selected to encompass a particular range of possible environments. The positioning of replications may be subject to certain constraints when the experiment is laid out so efforts were made to minimise variation within replications; but by normal convention they are essentially a random sample of all possible ways of arranging the experimental material.

By blocking or having the treatments in replications, the precision of the experiment increases as a result of error control. It is concluded that the design is acceptable, and effective in reducing error variance.

Table 4.1. Summary of analysis of variance for height at 12, 18 and 24 weeks to test for the accuracy of the experimental lay-out.

Source of Variation	Height 12		Height 18		Height 24	
	Df	Mean square	Df	Mean square	Df	Mean square
Bench	3	1209.082***	3	2873.006***	3	7984.021***
Rep(Bench)	16	91.606*	15	442.879***	14	2981.278***
Clone	19	2731.568***	19	2088.335***	19	3459.997***
Clone*Rep(Bench)	361	35.222^{ns}	342	65.301^{ns}	323	207.340^{ns}
Residual	2720	47.031	2557	90.107	2357	248.798

* Significant variance ratio (P<0.05);

** Significant variance ratio (P< 0.01);

*** Significant variance ratio (P< 0.001);

^{ns} non-significant variance ratio.

A test statistic for the null hypothesis that the data values are a random sample from a normal distribution was processed using the univariate D:Normal, test statistic. This procedure, known as Kolmogorov D statistic is applicable if the sample size is greater than 50. The data set is tested against a normal distribution with mean and variance equal to the sample mean and variance (SAS Institute, 1988). Results of the present study showed that the data come from a normal distribution.

The highest number of branches per plant occurred in replication 7, with mean value of 11.9 while the least number of branches occurred on plants located in replication 20, with mean value of 7.8. With trial mean equal to 10.41 and coefficient of variation of 39.4 it is confirmed that high variation between replicates within the trial was present for the variable "number of branches".

The highest shoot mass was registered in replication 11, with mean value of 16.9 while the lowest mass value was found on plants growing in replication 20, with mean of 7.8 grams. The results are as expected as the slower growing trees (lowest height and diameter) more or less occurred in the same replications.

4.2 ROOT AND SHOOT MASS

Linear regression equations were generated for root and shoot mass taken from 160 trees (that is, one replication) at different ages, 12, 18 and 24 weeks. The expected model value for Rm in the model is :

$Rm_i = a + b_i * Sm_i$, where (i = 12,18,24 weeks) and a = intercept, b = slope.

To determine if the 3 regression lines were statistically different, a test of slopes was performed (Ott, 1993). A difference of slopes would indicate that the shoot and root mass growth is differently affected by the age of the tree. For each group of 160 trees a least square regression was done. Next, the 12, 18 and 24 weeks data sets were combined for each variable, root and shoot mass, and another least square analysis was done.

The intercept increases with growth over time while the b- coefficients are more stable.

Table 4.2 illustrates results of regression analysis for shoot and root mass at 12, 18 and 24 weeks.

Table 4.2. Intercept, slope and coefficient of determination for root mass linear regression equations at 3 different ages.

Ages	intercept	b-coefficient	R-square
12 weeks	0.2757	0.4708	0.3844
18 weeks	0.9310	0.4104	0.3028
24 weeks	3.4690	0.5055	0.3293

A model that allows for the possibility that the observation lie on a straight line is $y = \beta_o + \beta_1 + \varepsilon$, where ε represents the difference between a measurement y and a point on the line $\beta_o + \beta_1$. The random error term ε takes into account all unpredictable and unknown factors that are included in the model.

The method of least squares chooses the prediction line that minimises the sum of the squared errors of prediction for all sample points. The regression lines trends are depicted from Fig. 4.1. to 4.3, scatter plots obtained from observed values and regression lines obtained from predicted root mass and respective observed shoot mass are illustrated for each age.

The scatter plot (Fig. 4.1) indicates the existence of three outliers, of which two are influential since its deletion produce substantial different parameter estimates. The influential observations are evaluated on the basis of their leverage on the partial regression coefficients.

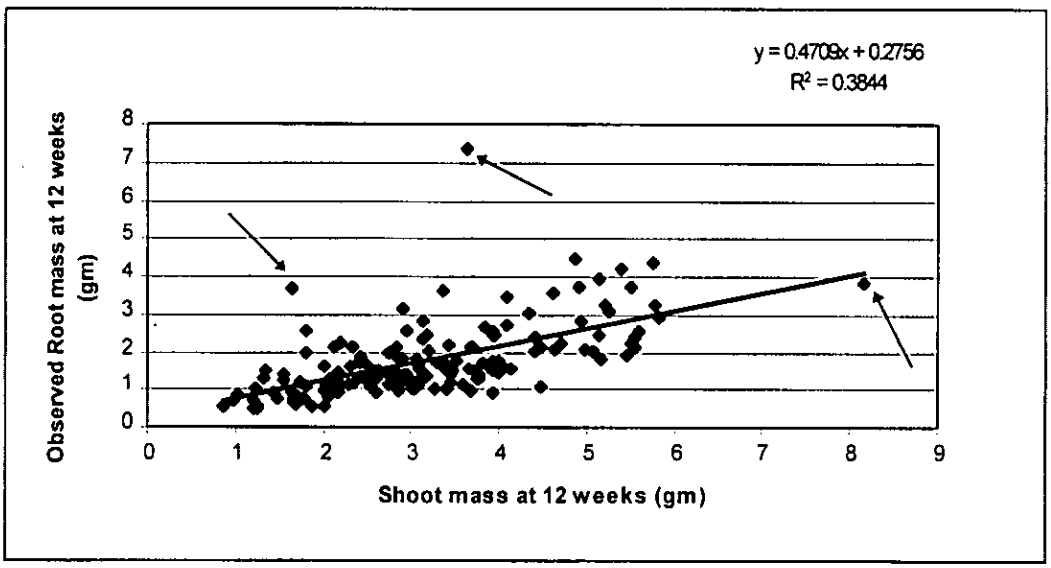


Figure 4.1 Scatter plot and respective fitted regression line of observed root and shoot mass values per plant, at age 12 weeks. Three outliers of which two are influential points are indicated with arrows.

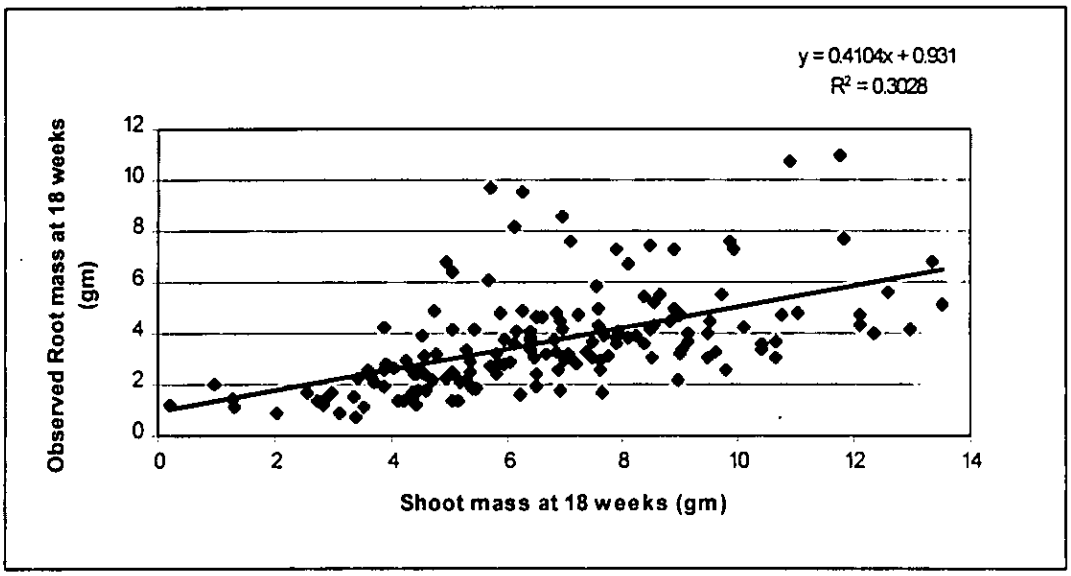


Figure 4.2. Scatter plot and respective fitted regression line of observed root and shoot mass values per plant, at age 18 weeks.

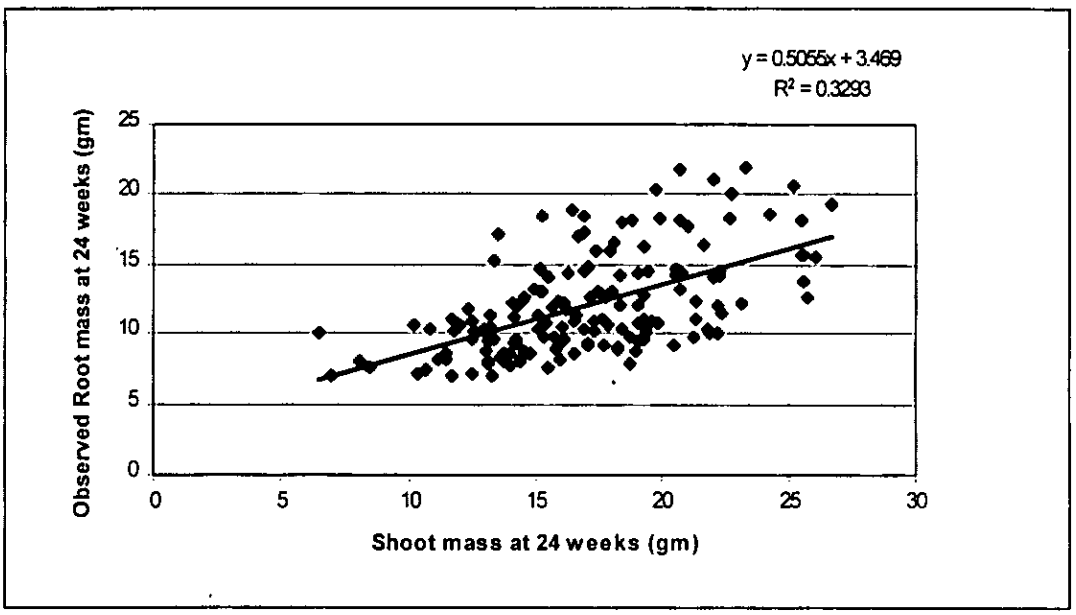


Figure 4.3. Scatter plot and respective fitted regression line of observed root and shoot mass values per plant, at age 24 weeks.

The combined regression yields a fourth equation: Rm = -0.4805 + 0.7055*Sm with $R^2 = 0.8231$. We want to conduct a test of equality of the three slopes. If the hypothesis of equality of slope is not rejected, the three regression are considered to be equivalent implying a similar growth pattern over time. According to Rice and Youngs (1990) an F-test is performed using error sums of squares (SSE) from individual and combined data sets as follows:

$$F = \frac{(SSE_c - SSE_3 - SSE_2 - SSE_1)/4}{(SSE_3 + SSE_2 + SSE_1)/(n + m + l - 8)}$$

where SSE_c is the combined error sum of squares, SSE_3 is the SSE for the last measurement data set, SSE_2 is the SSE for 18 weeks data set and SSE_1 the SSE for 12 weeks data set; l, n, and m are the number of data points in the 12, 18 and 24 weeks data sets respectively. Sums of square and respective number of data points are given in Table 7.1 of Appendix A1.
The $F_{0.01}$ " 19.8 indicates that the null hypothesis (H_0: Slope A = Slope B = Slope C) is rejected therefore it is concluded that the slopes of the three regression equations are statistically different and that the shoot and root mass growth is differently affected by age of the tree.

Table 4.3 illustrates the mean shoot and root mass and respective ratio, per soil treatment for replication 5 at age 12 weeks, replication 16 at 18 weeks and replication 11 at age 24 weeks. Clonal means are given in Tables 7.14 - 7.16 of Appendix C. Shoot mass growth varies with the soil treatment being most evident at age 24 weeks. The same trend has been followed by the root mass although the growth in mass is greater for the shoots. The highest mean growth for shoot and root mass per soil treatment was registered on ST1 (non-limed soil from Somerset West). The shoot growth rate was greater than the one registered for root mass indicating a slower root development compared to shoot. The shoot by root mass ratio changed over time.

The overall trial mean ratio of 1.98 was registered at 12 weeks with an increase at 18 weeks to 2.06 and decreasing from 18 to 24 weeks to the value of 1.46.

Ratio at 12 weeks for soil treatment ST2 and ST4 with standard error of 0.82 and 0.48 (Tab 4.3) respectively show a big deviation from the trial mean (Tab 4.4). At 18 weeks the highest deviation occurred in ST2 with SD of 0.67 followed by ST4 and ST3 with standard error equal to 0.90 and 0.73 respectively. Ratio at 24 weeks had less variation around the mean according to the low standard error value depicted in Table 4.5.

Some clones (Tab 7.4) definitely grow faster roots in sand (GC2 and AG6) than others. AG6 has fast root growth in sand and fast shoot growth in clay whereas AG2 grows shoots fast in all soils. More generally a stable effect of "constant" ratio is obtained at 24 weeks.

So to conclude, shoot and root growth were best in ST1 (non-limed soil from Somerset West) and worst in ST6 (limed soil from Grabouw).

Table 4.3. Mean shoot and root mass (in gm) and respective ratio per soil treatment and respective standard errors for one replication only at 12, 18 and 24 weeks.

TRAITS	SOIL TREATMENTS															
	ST1		ST2		ST3		ST4		ST5		ST6		ST7		ST8	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	SE	Mean	Std Err	Mean	Std Err
Sm12	4.11	1.51	4.59	0.91	3.08	0.97	2.80	0.88	1.99	0.78	2.38	0.67	3.03	0.99	3.19	1.09
Sm18	8.05	3.10	9.13	2.47	5.52	2.09	5.63	1.67	5.75	2.28	5.53	1.72	7.31	2.35	6.74	2.71
Sm24	18.02	3.83	16.32	2.97	14.31	2.94	13.02	2.42	14.24	2.97	12.98	2.63	15.51	3.36	15.24	3.50
Rm12	2.21	1.14	2.43	1.42	1.77	1.02	1.30	0.50	1.455	0.87	1.36	0.53	1.91	0.75	1.62	0.54
Rm18	4.82	2.66	3.36	1.25	2.85	1.24	2.17	1.44	4.144	2.50	4.02	2.25	4.03	1.81	3.45	1.25
Rm24	14.92	3.98	12.91	3.32	10.97	3.26	11.18	2.69	11.966	3.88	10.93	3.03	11.73	3.85	11.86	3.13
R12	2.05	0.57	2.26	0.82	2.05	0.88	2.25	0.48	1.602	0.61	1.94	0.69	1.68	0.45	2.03	0.54
R18	1.87	0.87	2.90	0.67	2.03	0.73	2.33	0.90	1.751	0.85	1.60	0.68	1.96	0.53	2.02	0.59
R24	1.51	0.37	1.52	0.34	1.56	0.43	1.32	0.21	1.509	0.41	1.42	0.34	1.51	0.41	1.38	0.25

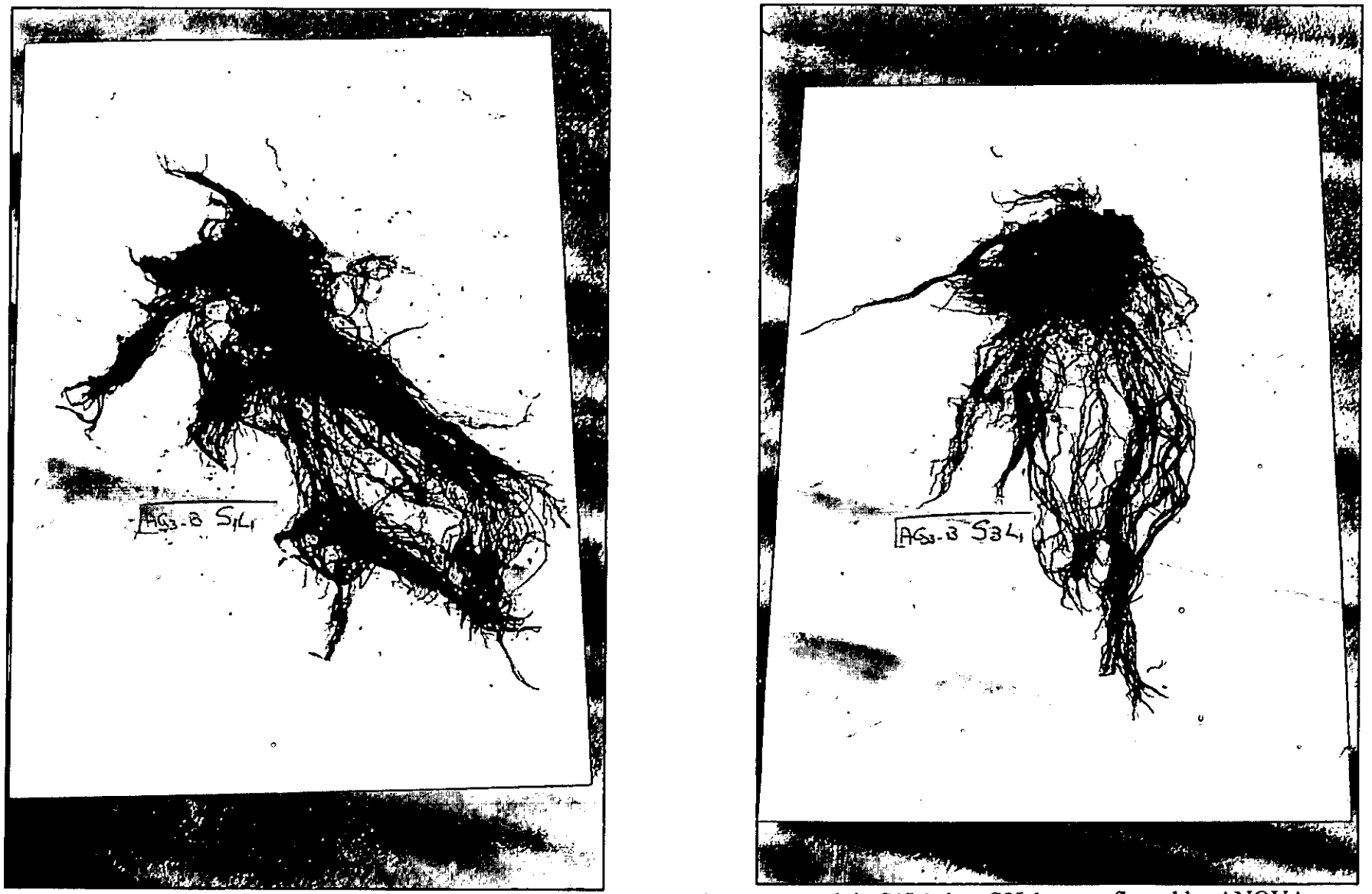


Figure 4.4. Root mass growth for clone AG3-A at 18 weeks. Evidence of better growth in S1L1 than S3L1 as confirmed by ANOVA.

4.3 VARIATION AND MEANS

4.3.1 TRIAL MEANS

Table 4.4 and 4.5 show the trial means and respective standard error and coefficient of variation for all the variables at different ages. The coefficient of variation show higher values for diameter than height at 12 and 18 weeks.

Normally in a forest there is an obvious effect of stand density, since tall trees of all diameter classes are competing for light causing less variation in top height than in diameter growth. This is also true here and at 12 and 18 weeks it is clear that diameter is more sensitive than height growth to competition (Tab. 4.4 and 4.5). The trend is reversed at 24 weeks, maybe because the greenhouse environment does not resemble a closed forest which normally will "force" trees to compete for light. In the greenhouse, due to different benches, there is more opportunity for edge effects than in a normal plantation situation.

The tree growth went through different stages. At the beginning the growth was slightly slow, not only due to weather conditions, winter season, but due to the fact that the plants had been transplanted and they needed some time for adaptation to the new environmental conditions. An irrigation system for an efficient water distribution was installed in the nursery. Comparison between H12/H0 with D12/D0 shows that growth rate was marginally higher for height than diameter with values of 1.39 and 1.36 respectively. The same growth pattern was followed at 18 weeks but diameter growth rate became smaller at 24 weeks with a value equal to 1.31 against 1.38 respectively found for D24/D18 and H24/H18.

The mean height increment per week was 0.825 cm from week zero to 12 opposed to 0.067 mm for mean diameter increment per week. The comparative figures for week 12 to 18 was 2.258 cm for height increment and 0.188 mm for diameter. Figures for the last 6 weeks were 3.069 cm and 0.212 mm for height and diameter respectively. The substantial increasing growth rate from 18 to 24 weeks coincides with the increase of temperatures outside the greenhouse from September to December, i.e., with summer days, when the temperatures inside the greenhouse were not less than 30°C. This is important since different soil types

(i.e. clayey and sandy textured soils), were selected as growth substrate for the purpose of the genotype x environment interaction (GEI).

It was found that trees belonging to different clones grew better in the sandy soil than in the clayey soil. This was probably due to the constant water availability in the nursery environment. In the field, trees could grow better in clayey soils such as the Helshoogte soil because of their high capability of water retention. The poor tree growth registered on both clayey soils is explained by variation in water content experienced within the rooting zone which in the end affected the whole plant system and its functions. It was observed that in the clayey soil treatments many large soil clods occurred in the polythene bags, resulting in either too wet (saturated conditions where the water dammed up) or too dry (where no water infiltration occurred) conditions. This has put an unpredicted type of stress on the plants.

The shoots mostly grew more than the roots, but the highest mass growth difference occurred at 24 weeks, when the root mass was far smaller than the shoot mass, although root development had been progressive over time. This caused the decrease in ratio over time at 12 and 24 weeks. The highest ratio was registered at 18 weeks. The shoots generally produced more dry mass than roots. The mean root mass increment per week was 0.321 gm from week 12 to 18 opposed to 0.592 gm for mean shoot mass increment per week. This gives an "increment ratio" for shoot:root mass of 1.844.

Table 4.4.Trial means, standard error and coefficient of variation, of the nursery trial before transplanting and 12 and 18 weeks after transplanting.

Statistic	H0 (cm)	D0 (cm)	M0 (gm)	H12 (cm)	D12 (mm)	Sm12 (gm)	Rm12 (gm)	R12	H18 (cm)	D18 (mm)	Sm18 (gm)	Rm18 (gm)	R18
Mean	24.929	2.224	42.644	34.829	3.026	3.152	1.759	1.984	48.380	4.160	6.705	3.683	2.058
Standard error	4.636	0.378	4.691	6.108	0.589	1.214	0.883	0.664	8.975	0.809	2.554	1.808	0.801
Coefficient of variation %	18.596	16.987	11.002	17.537	19.467	38.532	50.188	33.462	18.552	19.465	38.094	49.097	38.933

Table 4.5. Trial means, standard error and coefficient of variation, of the nursery trial at 24 weeks.

Statistic	H24 (cm)	D24 (mm)	N.b24	B24	Sm24 a) (gm)	Rm24 a) (gm)	Sm24 b) (gm)	ERm24 (gm)	R24 a)
Mean	66.800	5.433	10.417	0.159	16.956	12.041	15.001	11.052	1.465
Standard error	14.922	0.894	4.108	0.063	3.831	3.387	2.742	1.462	0.332
Coefficient of variation %	22.337	16.454	39.437	39.211	22.591	28.129	18.277	13.224	22.659

a) Rm24, Sm24 and R24 values for replication 11.

b) Sm24 values for all replications.

The comparative figures for week 18 to week 24 was 1.398 for root mass increment and 1.708 for shoot mass increment with a ratio of 1.227. This shows that shoot mass increased more rapidly than root mass over the last 6 weeks compared to the previous 6 weeks of growth meaning that the clonal performance can better be expressed at this later stage related to the favourable temperatures which induce the explosive growth during the last 6 weeks of the trial.

4.3.2 SOIL EFFECTS

Table 4.6 and 4.7 show the summary of analysis of variance for all the variables at different ages. The sources of variation related to soil effects are discussed in detail in this section. Means and respective Duncan grouping are also included.

Table 4.6. Summary of analysis of variance for height and diameter at 12 and 18 weeks.

Source of	Height 12		Diameter 12		Height 18		Diameter 18	
Variation	DF	Mean Square	DF	Mean Square	DF	Mean Square	DF	Mean Square
Replicates	19	250.150***	19	4.719***	18	917.149***	18	5.045***
Soil types	3	7662.707***	3	58.108***	3	6907.577***	3	86.552***
Lime	1	644.864***	1	1.851*	1	445.126*	1	0.753 ns
Clone	19	2732.048***	19	6.685***	19	2122.893***	19	7.783***
Soil type*Lime	3	61.829 ns	3	2.005***	3	120.393 ns	3	0.744 ns
Soil type*Clone	57	48.530 ns	57	0.536**	57	83.536 ns	57	0.732 ns
Lime*Clone	19	107.491 ***	19	0.457 ns	19	97.139 ns	19	0.877 ns
Soil type*Lime*Clone	57	40.767 ns	57	0.498 *	57	58.823 ns	57	0.826 ns
Residual	2961	37.310	2961	0.347	2779	80.559	2776	0.656

* Significant variance ratio (P<0.05);

** Significant variance ratio (P< 0.01);

*** Significant variance ratio (P< 0.001);

ns non-significant variance ratio

Table 4.7. Summary of analysis of variance for height and diameter, number of branches, ratio No. branches/height, shoot mass and respective estimated root mass at 24 weeks.

Source of Variation	Height 24		Diameter 24		No. of Branches		B24=No Branches/Ht24		Shoot mass24		Est. Root mass24	
	DF	Mean Square	DF	Mean Square	DF	Mean Square	DF	Mean Square	DF	Mean Square	DF	Mean Square
Replicates	17	4105.054***	17	21.501***	17	160.033***	17	0.027***	17	132.853***	17	33.948***
Soil type	3	17709.144***	3	96.086***	3	2583.574***	3	0.219***	3	1958.342***	3	500.416***
Lime	1	8655.047***	1	14.323***	1	7.858 ns	1	0.021*	1	934.919***	1	238.900***
Clone	19	3495.344***	19	11.371***	19	791.714***	19	0.242***	19	176.084***	19	44.995***
Soil type*Lime	3	238.338 ns	3	0.244 ns	3	6.769 ns	3	0.001ns	3	61.052***	3	15.600***
Soil type*Clone	57	245.964 ns	57	0.859 ns	57	31.713***	57	0.007**	57	10.308*	57	2.634*
Lime*Clone	19	205.519 ns	19	0.447 ns	19	31.105*	19	0.006*	19	14.826**	19	3.788**
Soil type*Lime*Clone	57	126.913 ns	57	0.988 ns	57	18.066 ns	57	0.005ns	57	11.155*	57	2.850*
Residual	2557	222.653	2558	0.799	2556	16.877	2555	0.004	2516	7.518	2516	1.921

* Significant variance ratio (P<0.05);

** Significant variance ratio (P< 0.01);

*** Significant variance ratio (P< 0.001);

ns non-significant variance ratio.

a. Soil types

The importance of the soil type effect depends upon the trait concerned, and it is underlined by the mean value of all the clones in each soil type. Tables 7.2-7.5. in Appendix A2 include variables root and shoot mass, ratio and number of branches at different ages.

i) Height and diameter

Soil type effect is highly significant for height and diameter at all ages (Tables 4.6 and 4.7). Duncan's NMRT shows a tendency for significant differences between the two clay soils to disappear at 18 and 24 weeks.

The dark sandy soil from Somerset West shows the best growth performance for all the clones, in the nursery environment, followed by light, sandy soil type from Pampoenvlei. On the clayey soil type group, the yellow soil type from Grabouw had better growth rate than the red soil type from Helshoogte for height after 24 weeks (Fig. 4.5). The results are unexpected because the sandy soil types or coarse textured soils are normally well suited for plants which have low requirements for moisture and nutrients while the fine textured or loam and clay soil types support species with high water and nutrient requirements (Wild *et. al.*,1946).

As explained above, the regular watering eliminated the moisture stress that normally occurred on sandy soils in their natural state, while the expected higher cation exchange capacity and excellent physical condition of the dark sandy soil is the reason for the best growth under the trial conditions. The water stress that developed on the clayey soils could be the reason for the below - expected performance on them.

Table 4.8. Mean height and diameter in each soil type at 12,18 and 24 weeks.

Soil type	Ht 12 (cm)	Soil type	Ht 18 (cm)	Soil type	Ht 24 (cm)	Soil type	D 12 (mm)	Soil type	D18 (mm)	Soil type	D24 (mm)
S1	38.8 a*	S1	52.2 a	S1	73.4 a	S1	3.38 a	S1	4.51 a	S1	5.83 a
S4	35.7 b	S4	49.1 b	S4	67.3 b	S4	3.08 b	S4	4.38 b	S4	5.63 b
S2	32.7 c	S2	46.2 c	S3	63.1 c	S2	2.85 c	S2	3.92 c	S2	5.14 c
S3	31.8 d	S3	45.7 c	S2	62.9 c	S3	2.76 d	S3	3.81 d	S3	5.10 c

*Letters indicate grouping according to Duncan's New Multiple Range Test.

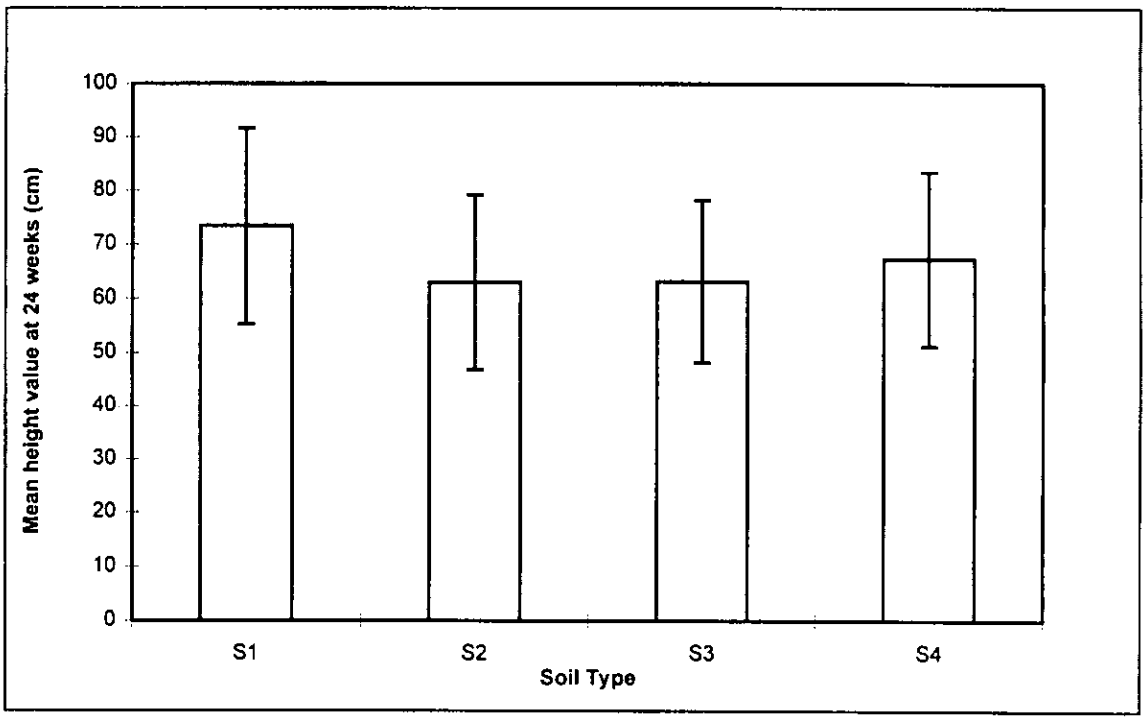


Figure 4.5. Mean height growth at 24 weeks and respective standard error on 4 different soils. Soil codes representation: S1= dark sandy soil from Somerset West; S2= red clayey soil from Helshoogte; S3= yellow clayey soil from Grabouw; S4= light sandy soil from Pampoenvlei.

b. Lime effects

Significant lime effect was detected, by ANOVA, for all traits except diameter at age 18 weeks and number of branches at 24 weeks (Table 4.6 and 4.7).

Duncan groupings for lime effect are depicted in Table 4.9 and 4.10. Trees seem to respond best to lower pH levels. Means for most variable are statistically different over different lime levels but the differences are very small. Number of branches at 24 weeks and diameter at 18 are exceptions indicating that liming might not have any effects.

Table 4.9. Mean height and diameter in each lime level at 12, 18 and 24 weeks, and respective grouping according to Duncan NMRT.

Lime	Ht 12 (cm)	Lime	Ht 18 (cm)	Lime	Ht 24 (cm)	Lime	D 12 (mm)	Lime	D18 (mm)	Lime	D24 (mm)
L0	35. 3 a*	L0	48.6 a	L0	68.4 a	L0	3.05 a	L0	4.18 a	L0	5.48 a
L1	34.3 b	L1	48.1 b	L1	65.2 b	L1	3.00 b	L1	4.14 a	L1	5.37 b

* Means identified by different letters indicate statistical difference at the 5% level.

Table 4.10. Mean number of branches, shoot and estimated root mass per lime level at 24 weeks and respective grouping according to Duncan NMRT.

Lime	Nb24	Lime	Sm24 (gm)	Lime	ERm24 (gm)
L0	10.4 a*	L0	15.5 a	L0	11.3 a
L1	10.4 a	L1	14.5 b	L1	10.8 b

* Means identified by different letters indicate statistical difference at the 5% level.

c. Soil type x Lime

i) Height and diameter

When splitting the soil type into two treatments, limed and non-limed it was found that untreated soil types showed the best result, for height at 24 weeks. Soil type x lime effects were statistically highly significant for diameter at 12 weeks but became non-significant at 18 and 24 weeks, with a decreasing of the mean square values. This may indicate a certain

sensitivity of this trait to soil type pH level at early age. The lime effect varies within the soil type being more evident on sandy dark soil from Somerset West and yellow clayey soil type from Grabouw as illustrated in Fig.4.6. The soil type x lime effects were non significant for height growth at all ages.

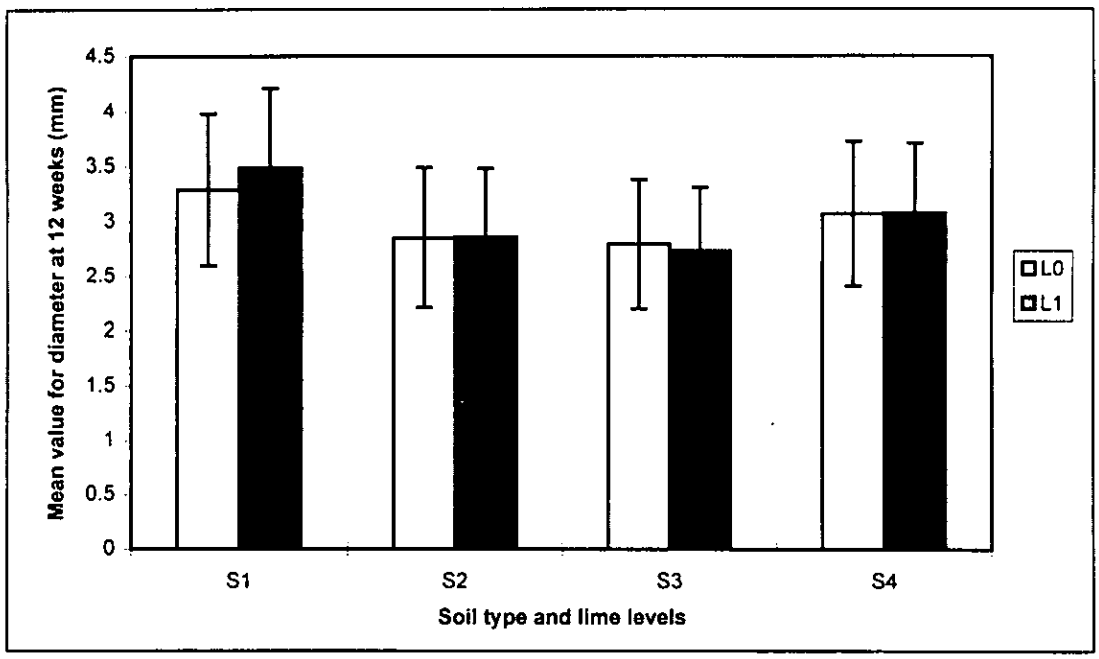


Figure 4.6. Mean diameter growth at 12 weeks and respective standard error on 4 soil types and 2 lime levels.

ii) Root and shoot mass

According to results depicted in Table 4.7. there is a highly significant interaction between soil type and lime at age 24 weeks for estimated root mass and shoot mass, indicating that the potential of root growth and development varied within each soil type and lime combination, which implies selecting appropriate clones for each lime level for a specific soil type.

Shoot mass at 18 weeks is illustrated in Fig.4.7, the effect of lime varies with soil type. Dark sandy soil and red clayey soil show better shoot growth in limed soil types while the yellow clayey and light sandy soils show better shoot growth in non-limed soil types indicating a high sensitivity of these traits to soil types and pH levels.

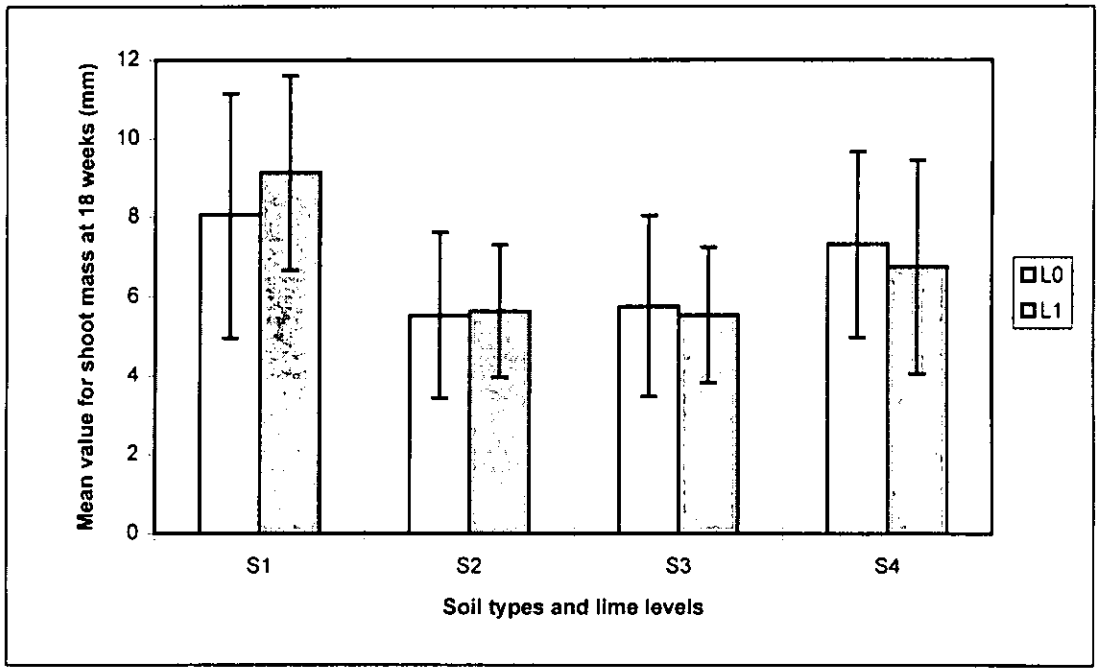


Figure 4.7. Mean shoot mass growth at 18 weeks and respective standard error on 4 soil types and 2 lime levels.

Recall that shoot mass is statistically significant for soil type and lime as single effects as well as when they interact with each other for these particular traits.

d. Soil treatments

i)Height and diameter

There is a high growth variation in the different soil types and soil treatments. The soil type and soil treatment ranking by Duncan's NMRT and the mean values for height and diameter at age 12, 18 and 24 weeks after transplanting are given in Tables 4.8 and 4.11 respectively.

Diameter in each soil treatment was significant (p=0.0001) between the sandy and clayey soil treatments, and also between the Somerset West sandy soil type of differing lime level (ST1 and ST2), at 12 weeks. A similar trend was followed by height at the same age. The clayey soil types with different pH level (ST3, ST4, ST5 and ST6) were in the same Duncan's ranking group indicating a similar growth response of the diameter at 24 weeks. Unlike diameter at 24 weeks, height had a slightly different trend from that found for diameter.

Results show more differences between soil types than between soil treatments indicating that liming can be unnecessary for most of the soils, with more incidence over clayey soils. This is true for 18 and 24 weeks results when all soil treatments are grouped together according to Duncan's NMRT.

ii) Number of branches, shoot mass and estimated root mass

Number of branches in each soil treatment was highly significant (p=0.0001) between the sandy soil types of differing fertility (Somerset West versus Pampoenvlei) but relatively small between the two clayey soil types with different lime levels as depicted in Table 4.12.

Shoot mass in each soil treatment was significant (p<0.01) between the sandy and clayey soil treatments, and also between the Somerset West sandy soil type of differing lime level(ST1 and ST2). The clayey soil types with same pH level (ST3, ST5) and (ST4, ST6) were in the same Duncan group indicating a similar growth response of the shoots when growing in the clayey Helshoogte and Grabouw soil types. The same trend was followed by the estimated root mass.

So, number of branches is more affected by sandy than clayey soil types while shoot and root mass is not only affected by soil types but also by its pH levels indicating that high pH (=7.0) is more beneficial for shoot and root growth development than lower pH levels (=5.0)

Table 4.11. Mean number of branches, shoot mass and estimated root mass per soil type at 24 weeks with their respective Duncan grouping at 5% level.

STreat.	Number of branches	STreat.	Sm24 (gm)	STreat.	ERm24 (gm)
ST1	12.8	ST1	18.0	ST1	12.6
ST2	12.5	ST2	16.3	ST2	11.7
ST7	11.3	ST7	15.5	ST7	11.3
ST8	11.3	ST8	15.2	ST8	11.2
ST6	9.1	ST3	14.3	ST3	10.7
ST5	8.9	ST5	14.2	ST5	10.7
ST4	8.7	ST4	13.0	ST4	10.0
ST3	8.5	ST6	12.9	ST6	10.0

Table 4.12. Mean height and diameter per soil treatment at 12,18 and 24 weeks and their respective Duncan ranking.

Streat.	Ht12 (cm)	STreat.	Ht18 (cm)	Streat.	Ht 24 (cm)	STreat.	D12 (mm)	STreat.	D18 (mm)	STreat	D24 (mm)
ST2	39.6	ST2	52.3	ST1	76.1	ST2	3.49	ST2	4.57	ST1	5.93
ST1	37.9	ST1	52.2	ST2	70.8	ST1	3.39	ST1	4.46	ST2	5.74
ST8	35.9	ST7	49.5	ST7	68.6	ST8	3.08	ST7	4.39	ST7	5.69
ST7	35.6	ST8	48.8	ST8	66.0	ST7	3.08	ST8	4.36	ST8	5.56
ST4	33.1	ST3	46.6	ST3	64.8	ST4	2.86	ST4	3.94	ST3	5.19
ST3	32.3	ST5	46.4	ST5	63.9	ST3	2.85	ST3	3.89	ST5	5.14
ST6	32.2	ST4	45.9	ST6	62.1	ST5	2.79	ST5	3.81	ST4	5.09
ST5	31.5	ST6	44.9	ST4	61.2	ST6	2.73	ST6	3.80	ST6	5.05

At 24 weeks the best growth for all clones was obtained on ST1 (non-limed dark sandy soil from Somerset West) while the worst height growth was registered on ST4 (limed red clayey soil from Helshoogte) for the poorest performer, *E. grandis* G1.

4.3.3 CLONAL VARIATION

Substantial variation is present on growth of all clones included in this study. Recall that such variation is due to growth over different soil types, lime levels and different soil treatments.

The summary of ANOVA for all variables at ages 12, 18 and 24 weeks is given in Tables 4.6 and 4.7. The analysis of variance showed a highly significant difference ($p = 0.0001$) for clones at all ages and for all variables assessed.

a. Height and diameter

Substantial clonal differences were obtained for height and diameter growth in the trial. Clonal mean for height growth ranged from 19.1cm for clone AG10 to 33.8cm for clone AG12 at age 0, before transplanting; from 29.7cm for clone AG10 to 43.1cm for clone AG12 at age 12; from 43.7 cm for clone AG14 to 55.0 cm for AG6 at age 18 weeks and 61.3 cm for clone AG4 to 76.9 cm for clone AG6 at age 24 weeks. Means per clone before transplanting are given in Table 4.13.

The clonal mean for diameter growth ranged from 1.77mm for AG15 to 2.64mm for AG11 at age 0, before transplanting; from 2.69 mm for clones AG3-A and AG14 to 3.31 mm for clone GC2 at 12 weeks; 3.78 mm for clone G1 to 4.57mm for clone AG1 at age 18 and 4.68 mm for clone G1 to 5.84 mm for clone AG1 at age 24 weeks. The clone G1, *E. grandis*, had the poorest growth performance in different soil types and soil treatment as expected being from 1 st super generation, origin.

Table 4.13. Mean mass, height and diameter per clone and respective standard error for measurement before transplanting.

CLONES	TRAITS					
	M0 (gm)		H0 (cm)		D0 (mm)	
	Mean	SE	Mean	SE	Mean	SE
AG1	43.3	4.9	24.5	4.6	2.59	0.41
AG2	41.5	4.7	22.9	3.8	2.11	0.34
AG3-A	39.2	4.1	22.8	4.6	1.97	0.35
AG3-B	45.1	4.0	27.2	4.8	2.31	0.36
AG4	44.3	4.4	24.5	4.7	2.36	0.36
AG5	41.4	6.3	21.3	4.1	2.11	0.38
AG6	41.4	5.4	28.3	5.0	2.27	0.43
AG7	43.8	4.4	24.5	5.1	2.18	0.38
AG8	38.5	4.0	30.6	6.4	2.44	0.41
AG9	44.7	6.4	24.5	3.7	2.19	0.38
AG10	47.8	5.2	19.1	4.2	1.84	0.37
AG11	42.1	3.8	32.6	4.7	2.64	0.37
AG12	41.6	4.2	33.8	5.3	2.52	0.35
AG13	42.4	5.1	23.8	4.4	2.33	0.34
AG14	46.3	4.1	21.4	3.5	1.87	0.32
AG15	43.3	4.1	20.0	3.5	1.77	0.32
G1	40.6	4.0	24.1	3.5	2.18	0.35
GU1	41.6	5.1	20.1	4.8	1.98	0.34
GC1	42.4	4.6	25.2	4.5	2.21	0.38
GC2	41.7	3.4	27.0	6.0	2.55	0.52

One way analysis of variance results are given in Tables 4.14 for height, diameter and mass of the whole plant before transplanting. Highly significant differences ($p<0.001$) were found for clones.

Table 4.14. Summary of analysis of variance for height, diameter and total plant mass before transplanting.

Source of variation	Height 0		Diameter 0		Total mass 0	
	Df	Mean Square	Df	Mean Square	Df	Mean Square
Clone	19	2558.221***	19	10.082***	19	799.367***
Residual	3117	21.475	3117	0.143	3117	22.012

*** Significant variance ratio ($P< 0.001$)

The delineation of significant differences between rankings of clones for some variables and single effects was performed using Duncan's New Multiple Range Test (NMRT) and results are given in Table 4.15 for mean height growth per clone.

Table 4.15. Mean height per clone and respective grouping according to Duncan NMRT at 5% level.

CLONES	Height 12	CLONES	Height 18	CLONES	Height 24
	Mean (cm)		Mean (cm)		Mean (cm)
AG12	43.2	AG6	55.0	AG6	76.9
AG11	40.9	AG8	54.6	GC1	75.3
AG8	40.6	GC1	54.4	GC2	73.2
AG6	40.5	AG12	52.9	AG1	71.4
GC1	39.3	GC2	51.6	AG8	70.5
GC2	38.7	AG11	50.6	AG12	68.2
AG3-B	36.0	AG1	50.4	AG11	67.3
AG7	34.1	AG7	49.2	AG15	66.7
AG4	33.6	AG3-B	48.4	AG10	66.4
AG1	33.5	AG2	47.8	AG13	66.4
AG2	33.2	AG13	46.4	AG3-A	66.3
G1	32.7	AG3-A	46.3	AG7	66.1
AG13	32.6	AG15	46.1	AG2	66.1
AG9	32.6	AG4	45.8	AG5	65.6
AG5	31.6	AG5	45.5	AG3-B	65.4
AG15	31.5	AG9	45.4	AG9	63.4
AG3-A	31.2	AG10	44.9	GU1	62.4
GU1	31.2	G1	44.6	AG4	61.3
AG10	29.6	AG14	43.7	AG14	58.9
AG14	29.6	GU1	43.4	G1	57.1
Trial mean	34.8	Trial mean	48.3	Trial Mean	66.8
St. Error	6.1	St. Error	8.9	St. Error	15.6

The best clone growth at 12 weeks was given by AG12 and the poorest height growth given by AG14. Through time the clone growth position changes slightly, for instance at 18 weeks, AG6 yields the highest height value although it is in the same Duncan NMRT group with AG12, AG8 and hybrid GC1.

b. Root and shoot mass

The standard errors and range of values for shoot and root mass, and respective ratio are given in Table 4.16 and 4.17. There is a visible difference on shoot mass growth from clone to clone being most evident at the last measurement.

The same trend has been followed by the root mass although the growth in mass is greater for the shoots resulting in a smaller value of ratio at 24 weeks. Variation in root regeneration potential after transplanting explains the slow regeneration in the beginning of the experiment and the difference between clones at an early age, but with time root growth increased more than shoot growth.

The shoot mass clonal means ranged from 2.1 gm for clone AG3-A to 4.0 gm for hybrid clones GU1 and GC2 at age 12; from 4.8gm for AG3-A to 8.8gm for clones AG3-B at age 18 weeks and 12.2gm for clone G1 to 16.7 gm for the hybrid GC1 at age 24 weeks. The clone AG3 was split in two, AG3-A and AG3-B, for trial design purpose. Other values also indicate that true differences at age 0 had some kind of lasting influence. This is discussed again later with growth over time.

The root mass clonal means ranged from 1.1gm for clones AG2 and AG7 to 2.7 gm for clone AG1 at 12 weeks; from 2.2 gm for clone AG3-A to 5.7gm for clones AG1 and GC2 at age 18 and from 9.2gm for clone AG2 to 15.8 gm for GC2 at 24 weeks. The coefficient of variation depicted in Table 4.4 and 4.5, also show higher values for root mass than shoot mass although it reduces throughout, meaning that there is a less variation for both variables at age 24 weeks.

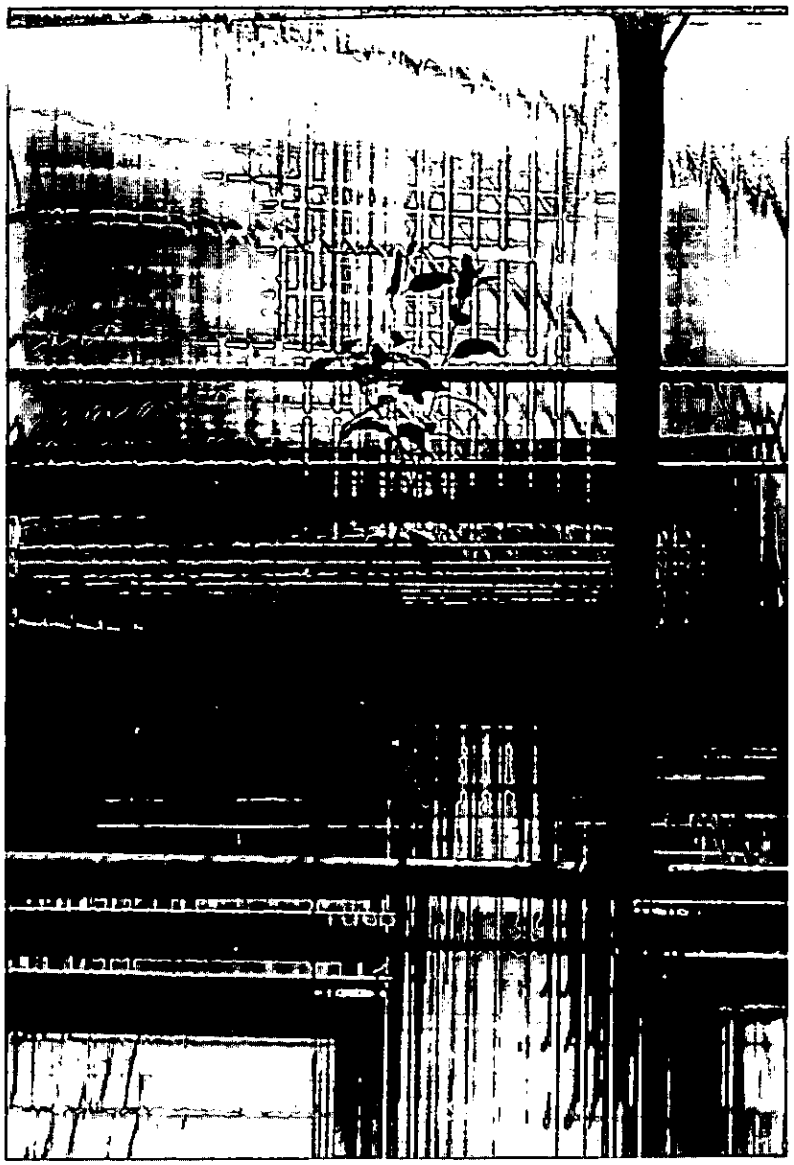
Table 4.16. Mean shoot and root mass (gm) per clone and respective standard error for measurements at 12, 18 and 24 weeks based on one replication at each age.

CLONES	TRAITS											
	SHOOT MASS (gm)						ROOT MASS (gm)					
	Sm12		Sm18		Sm24		Rm12		Rm18		Rm24	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	3.18	1.12	7.66	1.92	16.59	3.68	2.74	1.03	5.76	2.56	13.51	4.56
AG2	2.48	1.03	6.21	1.59	13.68	2.56	1.12	0.56	2.85	0.93	9.22	2.17
AG3-A	2.19	0.89	4.87	2.49	14.92	3.27	1.87	2.23	2.29	1.25	10.94	1.62
AG3-B	3.71	1.51	8.88	2.21	15.87	3.39	1.53	0.57	3.71	1.06	12.04	3.11
AG4	3.43	1.18	6.45	1.26	14.49	3.21	2.04	1.00	3.45	0.79	10.67	2.08
AG5	3.58	1.25	5.47	2.22	14.28	3.12	1.64	0.67	2.82	1.08	12.25	3.28
AG6	2.82	1.34	8.16	2.52	15.95	3.75	1.57	0.81	4.50	1.51	13.99	5.02
AG7	2.21	1.02	6.08	3.30	14.01	3.28	1.09	0.52	3.25	1.96	11.22	3.77
AG8	2.96	0.88	5.86	2.82	14.56	3.42	1.69	0.44	3.07	2.47	11.93	3.48
AG9	3.31	0.85	6.11	3.05	14.58	3.06	1.99	0.43	4.04	2.39	14.76	3.81
AG10	2.85	1.17	6.51	2.48	14.87	3.17	1.43	0.54	3.67	1.54	10.65	2.77
AG11	3.36	1.28	7.69	3.28	15.37	3.53	1.76	0.81	3.55	1.07	13.03	3.40
AG12	3.64	1.38	6.59	2.36	15.44	2.95	1.72	0.61	3.57	2.01	12.86	3.48
AG13	2.61	0.91	6.84	4.11	15.95	3.93	1.79	0.58	2.99	1.14	11.92	2.62
AG14	2.86	1.15	5.44	2.57	13.56	2.74	1.05	0.29	2.77	1.59	11.12	3.88
AG15	2.77	1.18	6.45	1.76	14.41	3.03	1.14	0.41	2.37	1.02	9.79	1.54
G1	2.99	0.93	5.45	2.42	12.24	2.69	1.46	0.33	3.77	3.01	11.22	4.34
GU1	4.05	1.47	8.09	2.29	16.11	3.57	2.31	1.09	4.42	1.27	12.51	4.17
GC1	3.93	1.17	7.84	2.58	16.69	3.65	2.77	1.16	5.03	2.30	11.31	1.92
GC2	4.05	1.96	7.44	2.27	16.15	3.72	2.34	1.22	5.74	2.66	15.89	3.97

The ratios, resulting from dividing Sm (shoot mass) by Rm (root mass), change over time. The ratio trend increases from 1st to 2nd assessment and decreases from age 18 to 24 weeks since at age 18 the shoot grew faster than roots. The same trend is followed by the coefficient of variation, indicating an increasing of variation from 12 to 18 weeks, decreasing from age 18 to 24 weeks.

Table 4.17. Mean shoot and root mass ratio per clone and respective standard errors for measurements, at 12, 18 and 24 weeks based on one replication at each age.

CLONES	TRAITS					
	RATIO					
	R12		R18		R24	
	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	1.25	0.43	1.61	0.79	1.56	0.40
AG2	2.34	0.46	2.37	0.88	1.78	0.19
AG3-A	1.64	0.62	2.48	1.16	1.48	0.45
AG3-B	2.46	0.77	2.45	0.42	1.64	0.33
AG4	1.77	0.33	1.93	0.49	1.41	0.28
AG5	2.24	0.48	2.12	0.94	1.44	0.32
AG6	1.93	0.51	1.91	0.58	1.54	0.35
AG7	2.08	0.61	1.97	0.81	1.38	0.21
AG8	1.81	0.52	2.31	0.76	1.53	0.34
AG9	1.72	0.56	1.69	0.97	1.19	0.50
AG10	2.04	0.47	1.88	0.58	1.43	0.38
AG11	2.08	0.84	2.07	0.55	1.52	0.26
AG12	2.28	0.77	2.20	1.05	1.42	0.30
AG13	1.46	0.28	2.09	0.94	1.49	0.34
AG14	2.63	0.63	2.17	0.78	1.23	0.29
AG15	2.49	0.75	2.99	1.06	1.74	0.44
G1	2.08	0.58	1.78	0.73	1.38	0.28
GU1	1.87	0.55	1.89	0.51	1.43	0.28
GC1	1.51	0.29	1.75	0.57	1.46	0.35
GC2	2.06	1.06	1.47	0.61	1.21	0.23



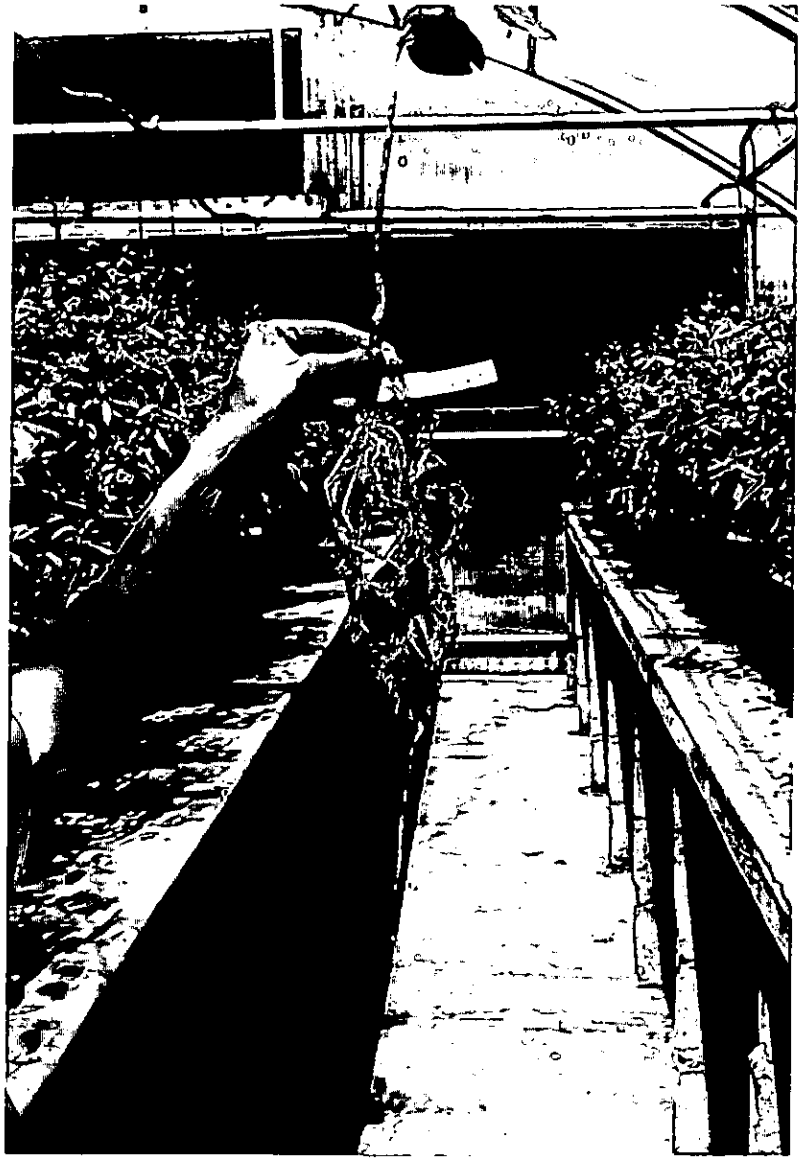


Figure 4.8. Shoot mass growth greater than root mass (left) and an example of root development for clone AG1 (right).

Table 4.18. Summary of the one way analysis of variance for root mass at 12, 18 and 24 weeks based on one replication only at each age.

Source of variation	Shoot mass12		Root mass12		Shoot mass18		Root mass18		Shoot mass24		Root mass24	
	Df	Mean Square	Df	Mean Square	Df	Mean square	Df	Mean square	Df	Mean Square	Df	Mean Square
Clone	19	2.567*	19	1.999***	19	9.449^{ns}	19	7.902**	19	28.264*	19	21.321*
Residual	139	1.475	139	0.799	140	6.525	140	3.269	138	14.673	138	11.471

* Significant variance ratio ($P<0.05$);

** Significant variance ratio ($P< 0.01$);

*** Significant variance ratio ($P< 0.001$);

^{ns} non-significant variance ratio.

One way analysis of variance results are given in Tables 4.18 for shoot and root mass at 12, 18 and 24 weeks after transplanting. The clonal difference for shoot mass was significant at 12 and 24 weeks ($p<0.05$). Shoot growth at 18 weeks was not statistically significant although results showed higher shoot mass growth rate than root mass growth during this period (Fig. 4.8). Refer to section 4.4.

Root mass was found to be statistically significant but the significance level reduced throughout indicating a disappearance of clonal root growth variation with time (Tab 4.18). However it should be noted that these results are based on one replication (160 trees) only.

c) Number of branches

Number of branches varied with clones. In general the pure species (*E. grandis*) have more branches than all the hybrids, although these hybrids had a good growth performance. This might be due to the fact that the few branches observed on hybrid clones are efficient to the plant needs, i.e. on photosynthesis and respiration.

4.4 GROWTH OVER TIME AND CORRELATIONS

a. Growth over time

All soil treatments supported considerable growth over time for all the parameters assessed. The highest growth rate was registered from 18 to 24 weeks. The comparisons were made based on increment per periods. For instance height results calculated as (H18 - H12) / 6 and (H24 - H18)/6 for soil treatment ST1, showed that height, increased more rapidly over the last 6 weeks compared to the previous 6 weeks of growth. Same trend was followed by diameter, root and shoot mass.

Height increment from 12 to 18 weeks was 2.383 cm against 3.983 cm from 18 to 24 weeks. The mean diameter increment per week was 0.195 mm from week 12 to 18 and 0.245 mm from 18 to 24 weeks. Shoot mass increment from 12 to 18 weeks was 0.656 gm and 1.662

gm from 18 to 24 weeks. Root mass also presented a higher increment from 18 to 24 weeks with value of 1.683 gm against 0.435 gm from 12 to 18 weeks. This can be explained considering that at the beginning the root system was still penetrating the soil much slower during the adaptation period and also due to weather changes. June, July and September were cold months in Stellenbosch and this fact reduced the growth rate to a certain extent. From October till December the temperatures were higher resulting in increased growth rate (Table 4.19).

i) Shoot and root mass

Shoot mass growth varies with the soil treatment being most evident at the last measurement. The same trend has been followed by the root mass although the growth in mass is greater for the shoots resulting in a smaller value of ratio at 24 weeks (Fig. 4.9 and 4.10).

The non-limed yellow clayey soil from Grabouw (ST5), had the poorest shoot mass growth at 12 weeks where after an interesting trend developed. At 18 weeks the shoot growth in this soil treatment started to increase with an "explosive" growth up to 24 weeks with the shoot mass greater than ST4 and ST6 at the last assessment. This is explained by the fact that clayey soil from Grabouw had a slow root penetration at the early age (Fig. 4.9).

The root mass shows a progressive growth from 12 to 18 weeks and an explosive growth from 18 to 24 weeks over all soil treatments (Fig. 4.10).

As referred before the ratio trend increases from 1st to 2nd assessment and decreases from 18 to 24 weeks because from then the roots grew faster than roots and shoot masses were higher.

Table 4.19 Growth over time for all traits and for all soil treatments.

TRAITS	SOIL TYPES															
	S1				S2				S3				S4			
	L0		L1		L0		L1		L0		L1		L0		L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
H12	37.9	7.9	39.6	7.5	32.3	7.8	33.1	7.4	31.5	6.7	32.2	7.3	35.6	7.4	35.9	7.5
H18	52.2	10.9	52.3	9.5	46.6	10.7	45.8	9.5	46.4	8.5	44.8	10.5	49.5	9.4	48.7	10.2
H24	76.1	20.2	70.8	15.5	64.7	17.6	61.2	14.3	63.9	14.7	62.1	15.3	68.6	15.9	66.0	19.3
D12	3.29	0.69	3.48	0.72	2.85	0.64	2.86	0.62	2.79	0.59	2.73	0.58	3.07	0.66	3.08	0.63
D18	4.46	0.90	4.57	0.85	3.89	0.89	3.94	0.74	3.81	0.75	3.81	0.85	4.39	0.87	4.36	0.97
D24	5.93	1.03	5.74	0.89	5.18	1.09	5.09	1.06	5.14	0.95	5.05	1.04	5.69	0.93	5.56	1.02
Sm12	4.11	1.51	4.59	0.91	3.08	0.97	2.80	0.88	1.99	0.79	2.38	0.67	3.03	0.99	3.19	1.09
Sm18	8.05	3.10	9.13	2.47	5.52	2.09	5.63	1.67	5.75	2.28	5.53	1.72	7.31	2.35	6.74	2.71
Sm24	18.02	3.83	16.32	2.97	14.31	2.94	13.02	2.42	14.24	2.97	12.98	2.63	15.53	3.36	15.24	3.50
Rm12	2.21	1.14	2.43	1.42	1.77	1.02	1.30	0.50	1.45	0.87	1.36	0.53	1.91	0.75	1.62	0.54
Rm18	4.82	2.66	3.36	1.25	2.85	1.24	2.81	1.44	4.14	2.50	4.02	2.25	4.02	1.81	3.45	1.25
Rm24	14.92	3.98	12.91	3.32	10.97	3.26	11.18	2.69	11.96	3.88	10.93	3.03	11.73	3.85	11.86	3.13
R12	2.05	0.57	2.26	0.82	2.05	0.88	2.26	0.48	1.60	0.61	1.94	0.69	1.68	0.45	2.03	0.54
R18	1.87	0.87	2.90	0.67	2.03	0.73	2.33	0.94	1.75	0.85	1.60	0.68	1.96	0.53	2.02	0.59
R24	1.51	0.37	1.52	0.34	1.56	0.43	1.32	0.21	1.51	0.41	1.42	0.34	1.51	0.41	1.38	0.25

This trend is more evident on limed soils (ST2, ST4, ST6 and ST8), see Fig.4.11. The ratio decreased over time for ST1 (non-limed dark sandy soil from Somerset west), ST3 (non-limed red clayey soil from Helshoogte), ST6 (limed yellow clayey soil from Grabouw) and ST8(limed light sandy soil from Pampoenvlei). Notice that two extremes: very sandy and very clayey from Pampoenvlei and Grabouw respectively, had similar behaviour over limed soils, i.e. soils with higher pH values. The remaining soil treatments (ST2, ST4, ST5 and ST7) show an increase of ratio over time, similar trend followed by the overall mean for ratio.

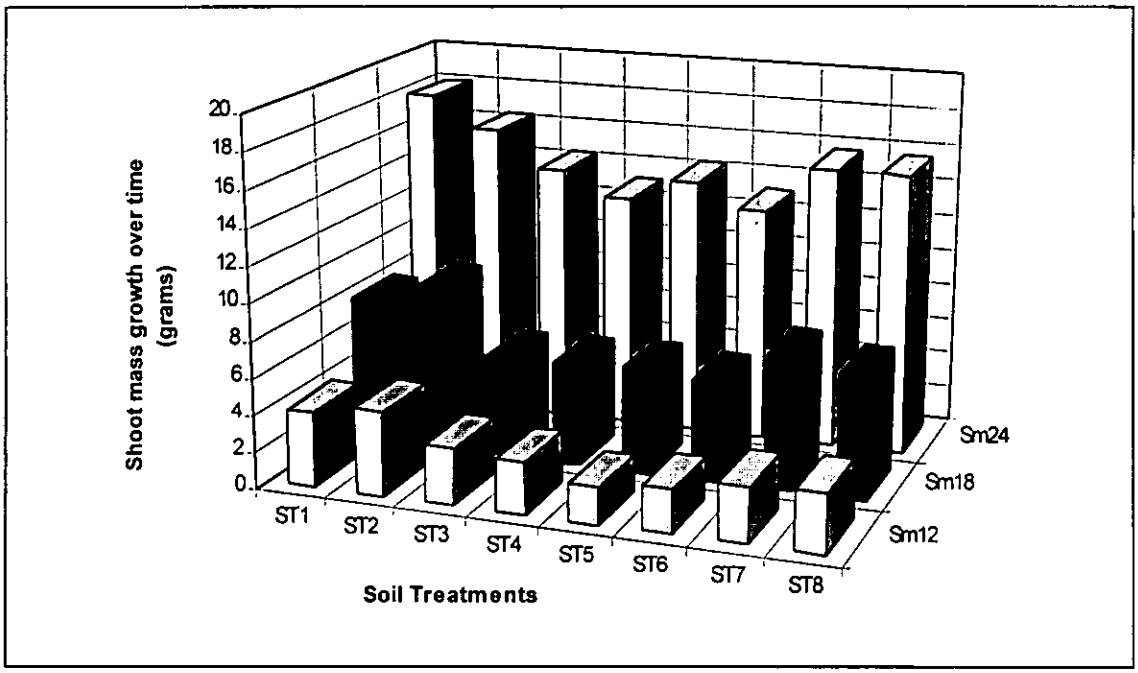


Figure 4.9. Shoot mass over time in all 8 soil treatments.

The hybrids GC1, GC2 and GU1 yielded the highest shoot mass over time showing their potential superiority over most of pure *E. grandis* clones except for AG1, AG6 and AG13 (Fig.4.12).The root mass growth "exploded" for the last 6 weeks of the trial (Fig 4.13). In descending order, GC2, AG9 and AG6 are the clones with the highest root mass growth. Again, one of the hybrids confirmed the hybrids potential over pure *E. grandis.* Recall that root growth is essential to the whole plant development in different climatic and edaphic conditions.

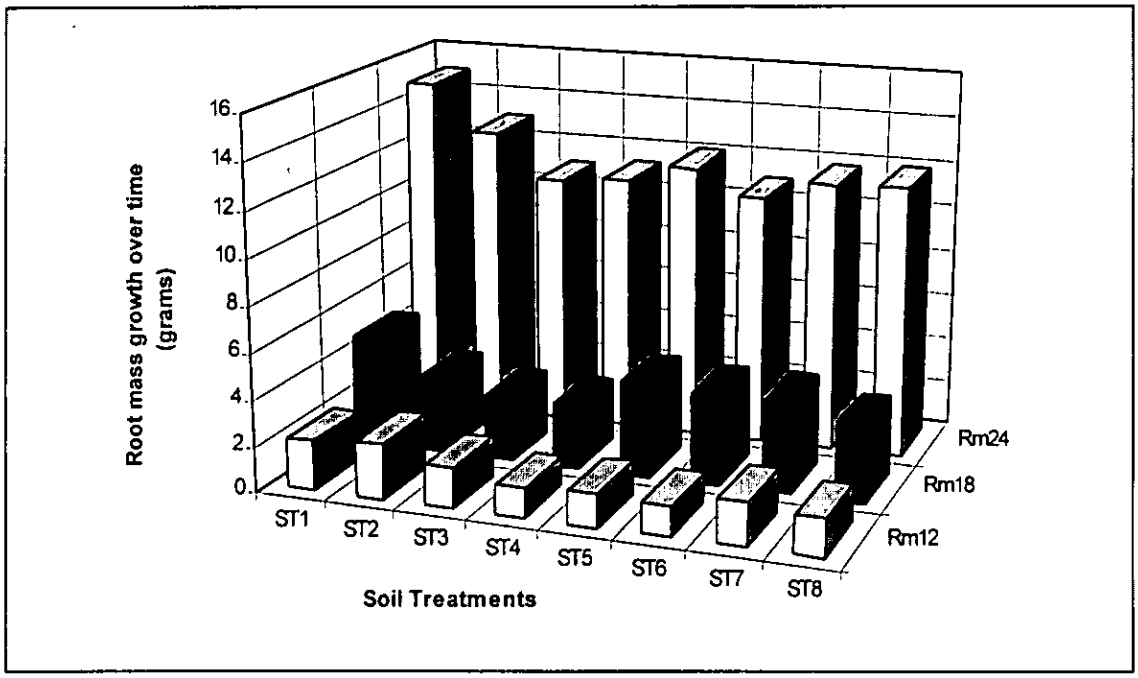


Figure 4.10. Root mass over time in all 8 soil treatments.

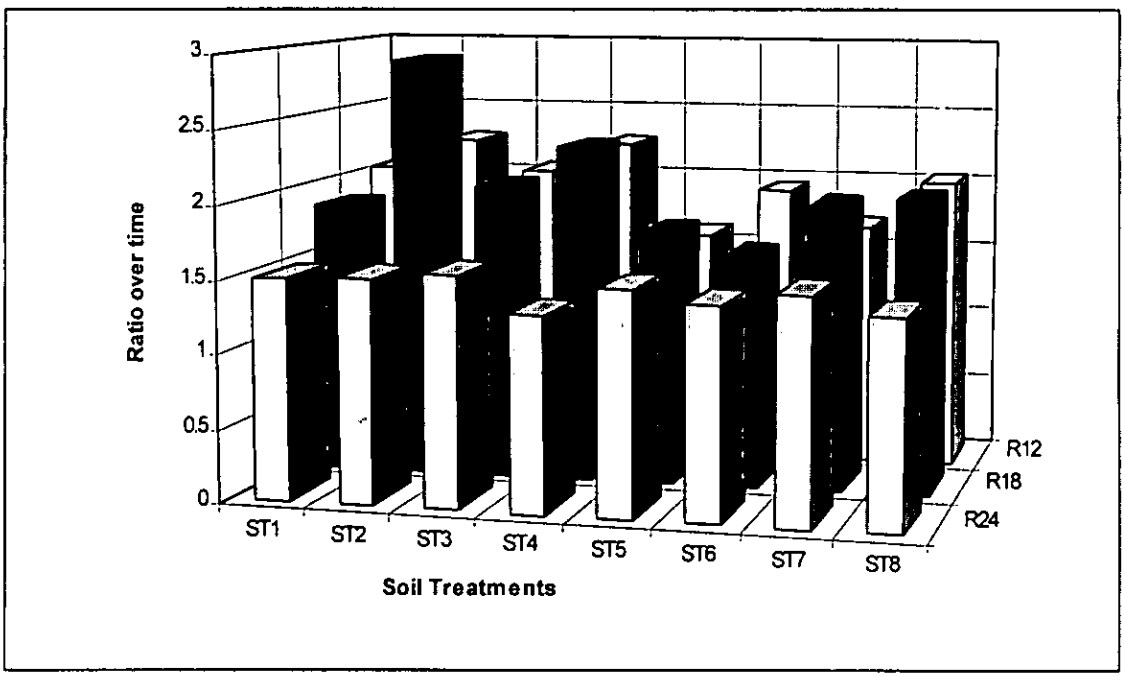


Figure 4.11. Ratio (shoot mass/root mass) over time in all 8 soil treatments.

The ratio per clone indicates that AG15 had the highest ratio at age 18 and 24 weeks indicating a higher growth rate for shoot than root mass for the last 6 weeks of the trial (Tab 4.16 and 4.17). The same trend is followed by AG6, AG1 and AG13. On the other hand, clones with high growth for root mass (GC2, AG9 and AG14) do have the lowest ratio values at age 24 (Figs. 4.13 and 4.14). For illustration purposes, clones with different patterns were selected.

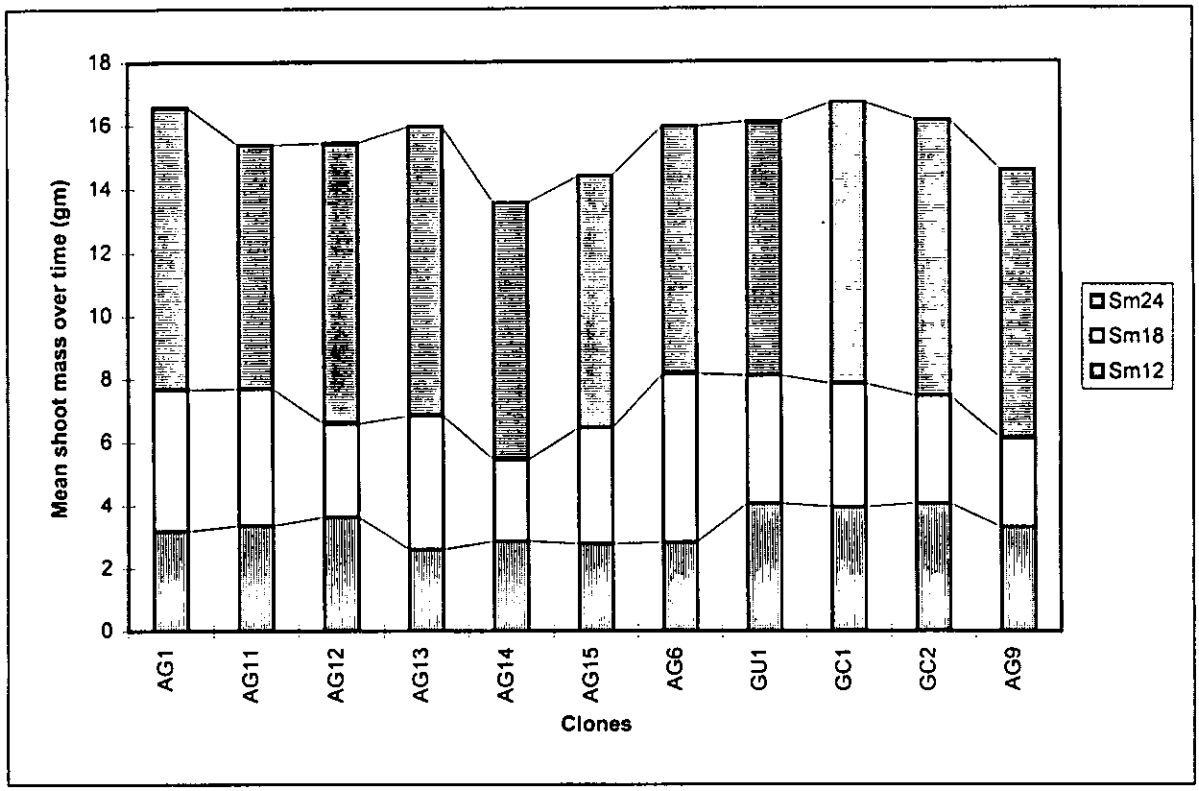


Figure 4.12. Mean shoot mass growth over time for some clones.

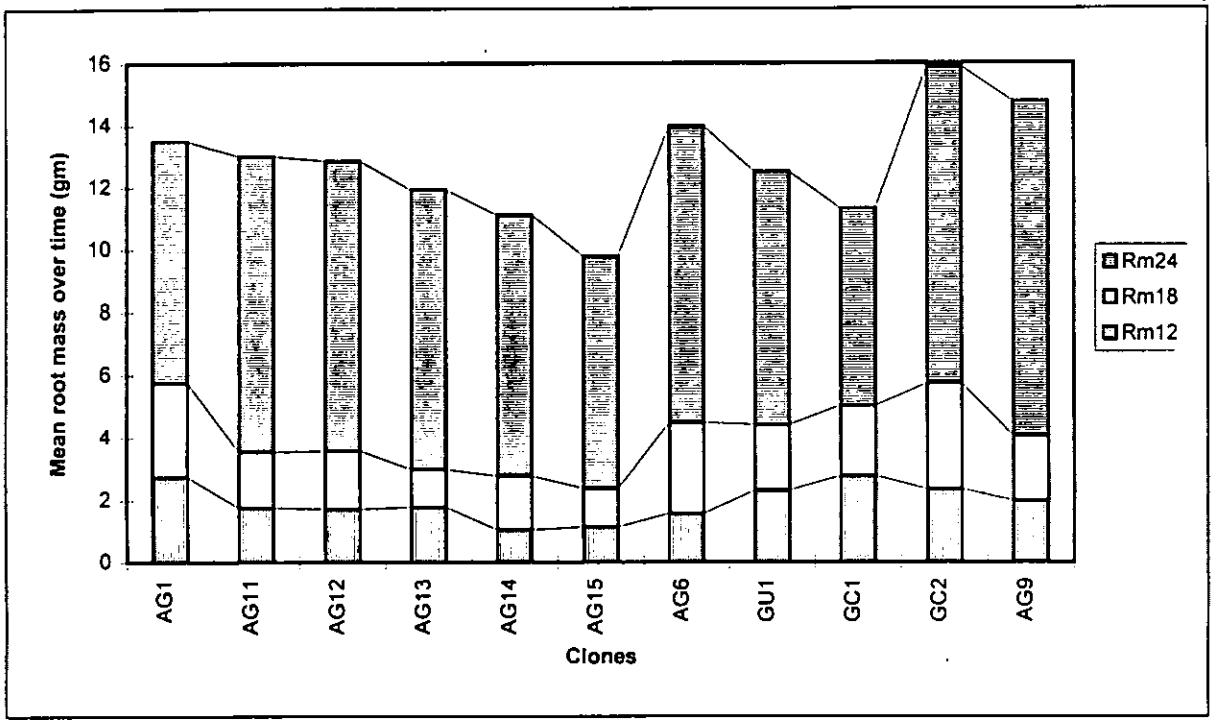


Figure 4.13. Mean root mass growth over time for some clones.

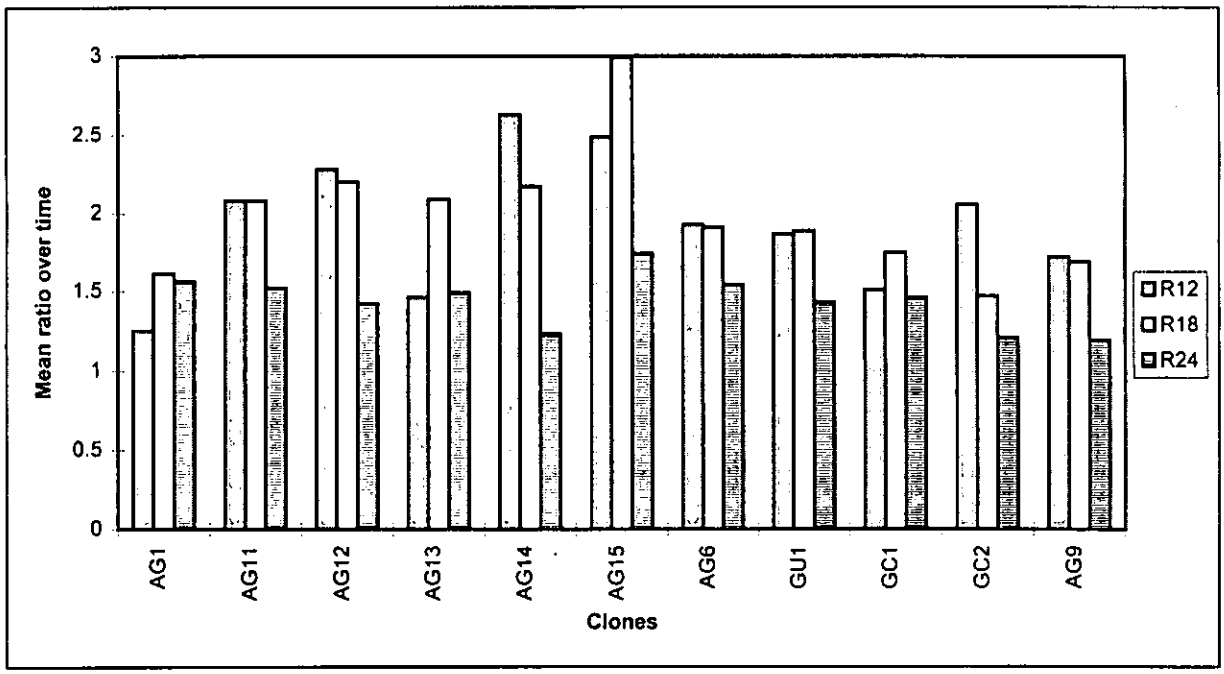


Figure 4.14. Mean ratio over time for some clones.

ii) Height and diameter

Height and diameter have the same growth trend over time. Figs. 4.15 and 4.16 illustrate the height and diameter growth pattern. It is evident that for both treatments of the dark sandy soil from Somerset West and the light sandy soil from Pampoenvlei, respectively, (ST1, ST2, ST7 and ST8), the highest growth rate is obtained at all ages, confirming once again the superiority of these soils in a nursery environment. Clone AG6 showed the best growth in height as illustrated in Fig.4.17 followed by the two *E.grandis* x *E. camaldulensis* crosses, GC1 and GC2, which showed their potential over most of the pure *grandis*.

The clones AG6 have been showing a good performance from the 1st assessment to the end. AG11 and AG12 showed a good growth at the beginning but it slowed down towards the end of the trial while the hybrids GC1 and GC2 had a slow initial growth but their performance became better over time reaching the second best after pure *E. grandis* AG6 at the end of the trial. Diameter followed a similar pattern to height over time (Figs. 4.17 and 4.18). For illustration purposes, clones with different patterns were selected.

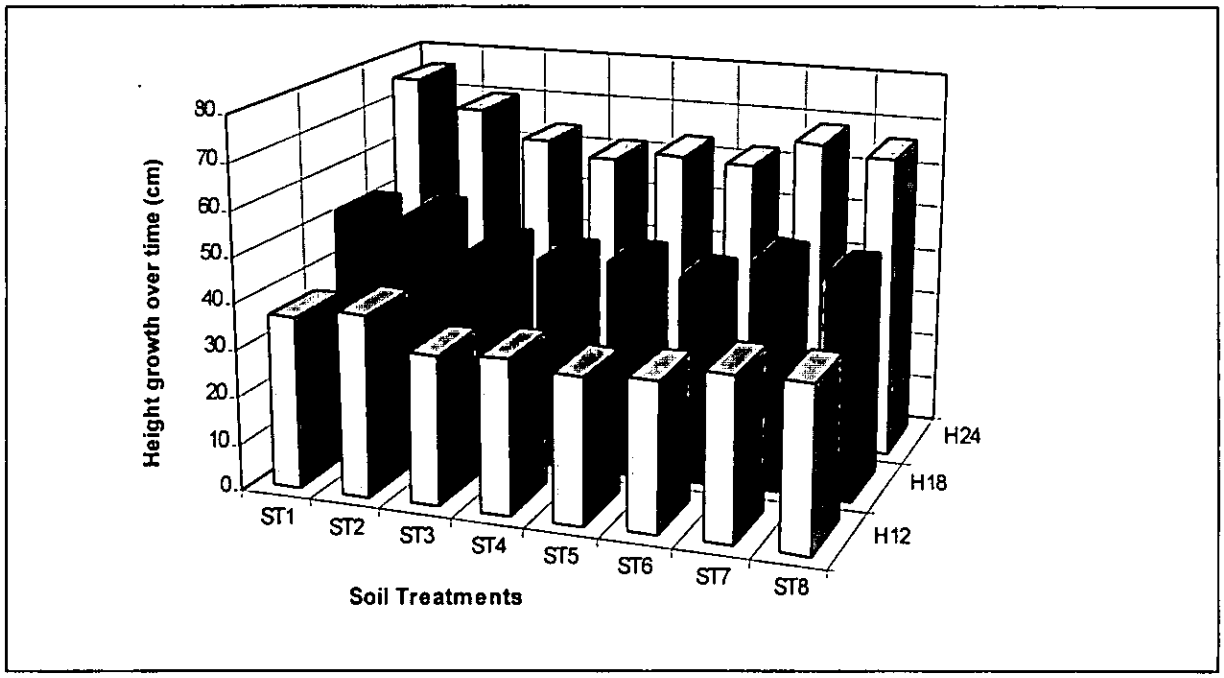


Figure 4.15. Height growth over time for all 8 soil treatments.

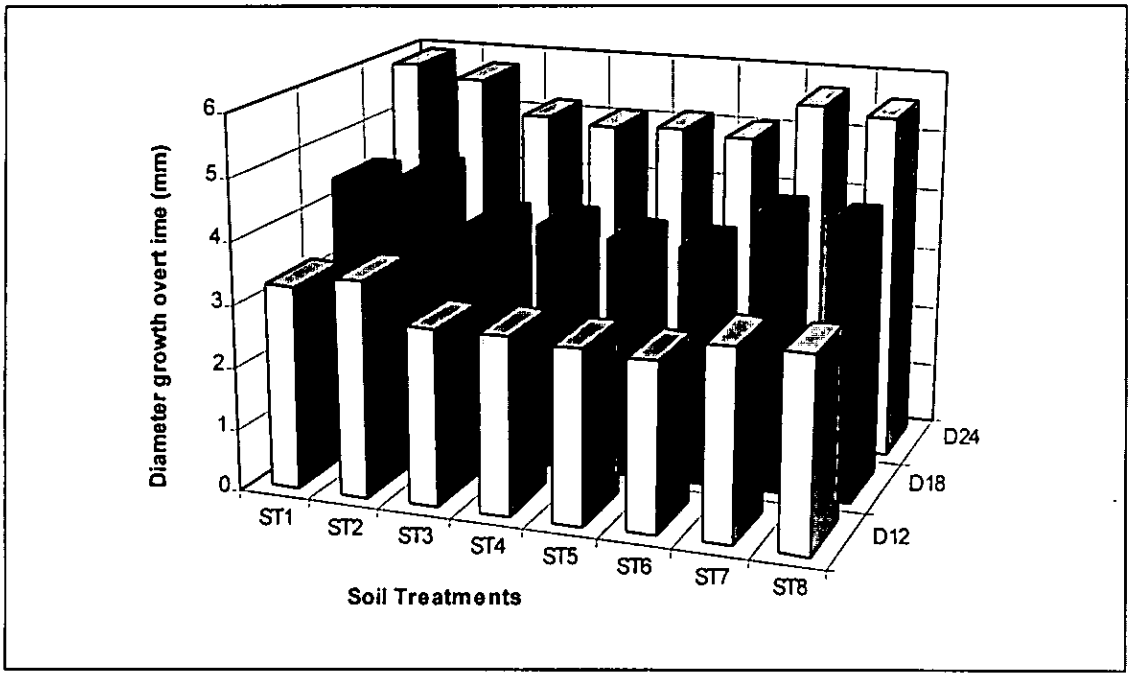


Figure 4.16. Diameter growth over time in all 8 soil treatments.

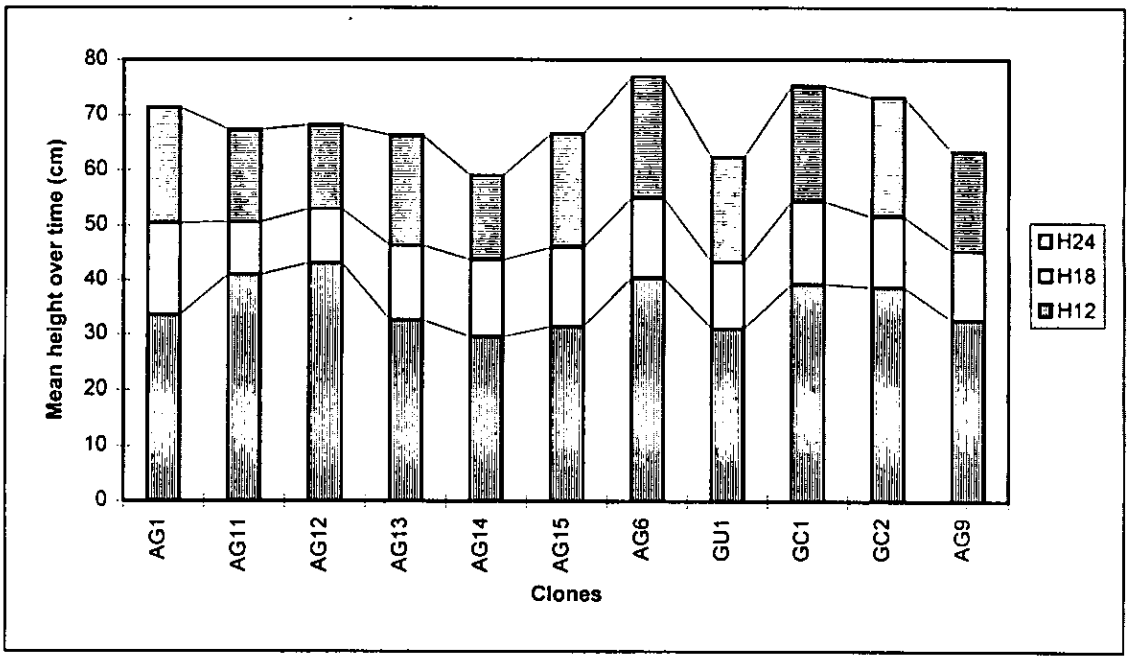


Figure 4.17. Mean height growth over time for some clones.

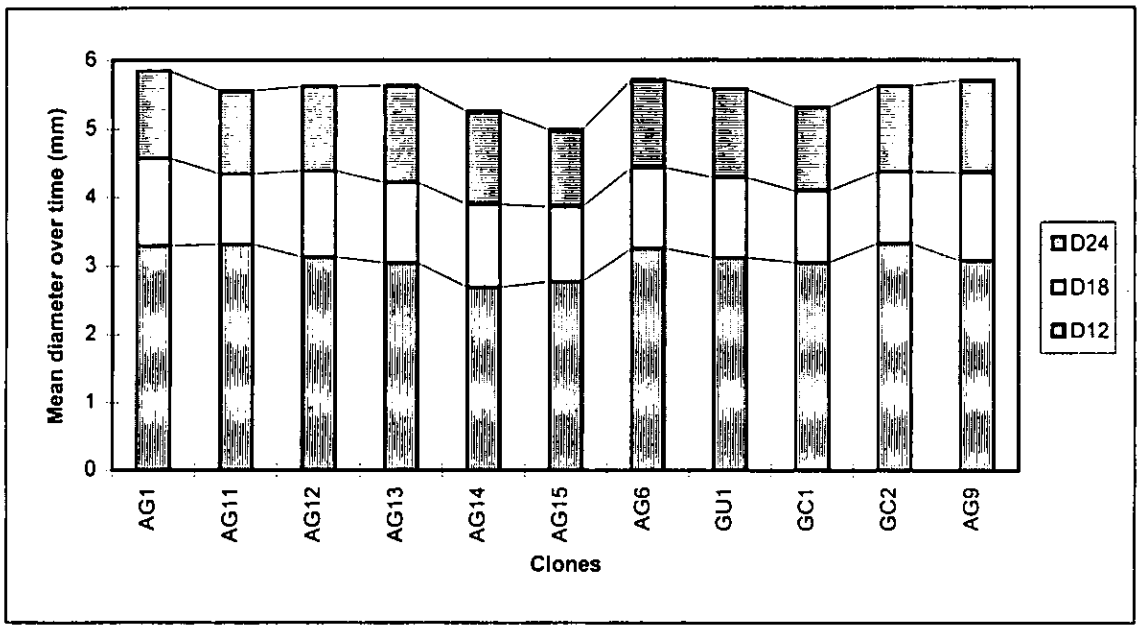


Figure 4.18. Mean diameter growth over time for some clones.

b. Phenotypic correlations

Correlation analysis attempts to measure the strength of the relationship between two variables by means of a correlation coefficient. It is important to remember that the correlation coefficient between two variables is a measure of their linear relationship, and a value of r = 0 implies a lack of linearity (Walpole, 1982).

It should be noted that the phenotypic correlation has both a genetic and environmental component. Genetic and environmental causes of correlations combine together to produce phenotypic correlation (Falconer, 1989).

Phenotypic correlation between two traits is an indication of the correspondence between measurements of two traits. A positive genetic correlation between two traits implies that selection for the one trait will lead to improvement in the other. A strong negative genetic correlation makes improvements in two traits very difficult if not carefully considered.

Juvenile-mature (or age -age) correlations are a special form of trait-trait correlations. Juvenile-mature correlations have important implications for a breeding programme as good correlations

suggest that accurate early selection of desirable clones may be feasible. This in turn has implications for the success of the programme, as it reduces the generation interval between selections and, therefore, increases the rate of genetic gain. Selection is rarely done at rotation age. Good correlations between performance at younger ages and rotation age suggest that a feasible reduction in selection age may be possible.

i) Height and diameter

Table 4.20 lists the Pearsons correlation coefficients for correlations between trait means over the whole experiment. The analyses of the trait means at four soil types and two lime levels produce correlation matrices showing the correlation between measurements of the same trait at 3 different growth ages.

Each tree was cut back proportionally before transplanting. However, the first measurements (H0 and D0) were taken in case an adjustment for early growth differences would be needed for the later measurements. The highly significant positive correlations between H0 and H12, and D0 and D12 were interpreted that the early variation among clones remained relatively constant. Consequently no covariance analysis was considered for interpretation of later growth results.

In this nursery study, the phenotypic correlations generally weakened over time for height and diameter. Although there was a strong correlation between H0 and H12 ($r = 0.93$) the diminishing effect of the height correlation over time means that early prediction on growth performance of different clones is not reliable. The same trend is followed by diameter.

Height growth at age 0 and 12 weeks show stronger correlations with diameter which may be expected from young material in an active growing condition. Strong correlations are obtained among height and diameter at all ages except at 24 weeks.

ii) Number of branches

It is known that the number of branches of a certain tree is proportional to height. The clonal mean values generated on the present study show a high variation among clones for variable height as depicted in Table 4.21. The hybrid GC1 has one of the highest average height values and the lowest number of branches causing the negative correlation (r = -0.416), between height growth and number of branches, which is almost significant at the 5% level (p = 0.068).

To test the effect of hybrids on the negative correlation between height and number of branches at 24 weeks, a correlation analysis without the hybrids was done. The same trend was found showing enough evidence that pure *E. grandis* also have taller trees with few branches.

Table 4.20. Correlation coefficient for height and diameter for clonal means at 12, 18 and 24 weeks.

	H0	H12	H18	H24	D0	D12	D18	D24
H0	1.000	0.927***	0.753***	0.399^{ns}	0.817***	0.699***	0.5611*	0.297^{ns}
H12		1.000	0.898***	0.632***	0.739***	0.741***	0.569***	0.260^{ns}
H18			1.000	0.851***	0.631**	0.657**	0.538*	0.254^{ns}
H24				1.000	0.395^{ns}	0.573**	0.537*	0.401^{ns}
D0					1.000	0.847***	0.725***	0.463*
D12						1.000	0.915***	0.607**
D18							1.000	0.818***
D24								1.000

* Significant correlation (P<0.05);

** Significant correlation (P< 0.01);

*** Significant correlation (P< 0.001);

^{ns} non-significant correlation.

The hybrids do have a strong contribution since the correlation without hybrids is totally non-significant with p= 0.705. Correlation details are given in Table 4.22.

Table 4.21. Clonal means and standard errors for height, diameter and number of branches at 24 weeks.

CLONE	H24 (cm)	Std Err	D24 (mm)	Std Err	NB24	Std Err
AG1	71.4	16.6	5.84	0.9	8	3.8
AG10	66.4	18.6	5.54	1.2	12	4.6
AG11	67.3	14.6	5.56	1.1	11	4.7
AG12	68.2	11.4	5.62	0.8	11	4.4
AG13	66.4	19.1	5.63	1.1	12	4.1
AG14	58.9	14.9	5.26	1.0	13	6.0
AG15	66.7	18.6	4.98	0.9	14	5.5
AG2	66.1	14.0	5.09	0.9	11	4.6
AG3-A	66.3	16.8	5.38	0.9	12	4.8
AG3-B	65.4	16.9	5.68	1.0	13	4.5
AG4	61.3	15.2	5.58	1.1	9	3.5
AG5	65.6	16.6	5.27	1.0	10	6.3
AG6	76.9	17.9	5.72	1.1	11	4.2
AG7	66.1	15.8	5.25	1.1	8	4.9
AG8	70.6	16.3	5.27	1.0	9	4.4
AG9	63.4	15.1	5.71	1.1	13	4.1
G1	57.3	13.6	4.68	0.9	9	4.2
GC1	75.3	17.7	5.31	0.8	4	3.1
GC2	73.2	17.1	5.62	0.9	7	4.3
GU1	62.4	17.3	5.58	0.9	11	4.3

Table 4.22. Correlation coefficients based on clonal means for height, diameter and mean number of branches at 24 weeks with ($Nb24^1$) and without ($Nb24^0$) hybrid clones.

	H24	D24	$Nb24^1$	$Nb24^0$
H24	1.000	0.401^{ns}	-0.416^{ns}	-0.099^{ns}
D24		1.000	0.053^{ns}	0.059^{ns}
Nb24			1.000	1.000

^{ns} non-significant correlation

Table 4.23. Correlation coefficients for height, diameter, shoot and root mass for clonal means for one replication only at 12, 18 and 24 weeks. The mean of each clone is based on the 8 observations obtained in the 8 soil treatments.

	H12	D12	Sm12	Rm12	H18	D18	Sm18	Rm18	H24	D24	Sm24	Rm24
H12	1.000	0.667***	0.555**	0.305^{ns}								
D12		1.000	0.638***	0.413^{ns}								
Sm12			1.000	0.631***								
Rm12				1.000								
H18					1.000	0.263^{ns}	0.325^{ns}	0.318^{ns}				
D18						1.000	0.657***	0.519*				
Sm18							1.000	0.639***				
Rm18								1.000				
H24									1.000	0.394^{ns}	0.816***	0.577***
D24										1.000	0.384^{ns}	0.407^{ns}
Sm24											1.000	0.591***
Rm24												1.000

* Significant correlation (P<0.05);
** Significant correlation (P< 0.01);
*** Significant correlation (P< 0.001);
^{ns} non-significant correlation.

iii) Shoot and root mass

The correlation matrix for root and shoot mass at 12, 18 and 24 weeks is shown in Table 4.23. It should be noted that 160 trees, i.e., one replication, were assessed and included in the analyses. Based on the correlations at age 12 weeks diameter and height are equally good predictors of shoot mass with r = 0.638 and r = 0.555 respectively. At age 18 weeks the diameter turns out to be a better predictor of shoot mass which implies that more variation was present for diameter than height growth as a result of tree to tree competition. Refer to 4.3.1 discussed earlier.

The correlations change over time for the variables included as it was found that height becomes better predictor of shoot and root mass at 24 weeks than does diameter. This change of trait-trait correlations over time shows the importance of following up the growth trend of the trees.

c. Genetic correlations

Correlations can be partitioned into genetic and environmental components. Genetic correlations are more reliable for prediction purposes. However, such correlations were not attempted in this study as the other methods indicated a low tendency for genotype-environment interaction.

4.5 GENOTYPE X ENVIRONMENT INTERACTION

Variation in clonal performance is important. The presence of genotype x environment interaction (GEI) implies that the genotype that shows the best performance on one soil treatment, does not necessarily do so on other soils. GEI may lead to a change in the relative differences between the performance of genotypes.

In this study the clones (different genotypes) are growing in different environments represented by different soil treatments as the main objective is to test for the possible presence of different growth responses of *Eucalyptus grandis* clones when grown in different soils. This will indicate the possible existence and magnitude of genotype x environment interaction.

The results show a different response of clones over soil treatments; GEI is present in a low magnitude and it disappears with time, i.e., the analysis of variance showed a non-significance interaction between clone and soil treatments for height and diameter at age 18 and 24 weeks, although there is a highly significant interaction ($p<0.001$) for number of branches, shoot and estimated root mass at the last assessment as depicted in Table 4.25.

4.5.1 INTERACTION EFFECTS

Results of two and three way interactions for clone and soil effects are given and discussed in this section. Generally significance of these interactions reduces or disappears with time for variable height and diameter although shoot and root mass, as well as number of branches remain significant at 24 weeks. Results are given in Tables 4.24-4.25.

Table 4.24. Summary of analysis of variance for height and diameter at 12 and 18 weeks for the simplified model.

Source of Variation	Height 12		Diameter 12		Height 18		Diameter 18	
	Df	Mean Square	Df	Mean Square	Df	Mean Square	Df	Mean Square
Replicates	19	250.150***	19	4.719***	18	917.149***	18	5.045***
Clone	19	2732.048***	19	6.685***	19	2122.893***	19	7.783***
Soil treatment	7	3428.620***	7	26.027***	7	3056.606***	7	37.647***
Clone*Soil treat.	133	53.548***	133	0.509***	133	74.816^{ns}	133	0.793^{ns}
Residual	2961	37.310	2961	0.347	2779	80.559	2776	0.656

* Significant variance ratio ($P<0.05$);

** Significant variance ratio ($P< 0.01$);

*** Significant variance ratio ($P< 0.001$);

^{ns} non-significant variance ratio.

Table 4.25. Summary of analysis of variance for height and diameter, number of branches, , shoot mass and respective estimated root mass at 24 weeks for the simplified model.

Source of Variation	Height 24		Diameter 24		No. of Branches		Sm24		ERm24	
	Df	Mean Square	Df	Mean Square	Df	Mean Square	Df	Mean Square	Df	Mean Square
Replicates	17	4105.054***	17	21.501***	17	160.033***	17	132.853***	17	33.948***
Clone	19	3495.344***	19	11.371***	19	791.714***	19	176.084***	19	44.994***
Soil treatment	7	8805.575***	7	42.934***	7	1110.009***	7	981.061**	7	250.690***
Clone*Soil treat.	133	189.50^{ns}	133	0.855^{ns}	133	25.793***	133	11.348***	133	2.899***
Residual	2557	222.653	2558	0.799	2556	16.877	2516	7.518	2516	1.921

* Significant variance ratio (P<0.05);

** Significant variance ratio (P< 0.01);

*** Significant variance ratio (P< 0.001);

^{ns} non-significant variance ratio.

a. Clone x soil treatment

There is a high growth variation over all different soil treatments. Appendix C (Tables 7.8-7.16) provides clonal means and details of the standard errors and range of values for each trait at 12, 18 and 24 weeks. Fig. 4.19 illustrates the clonal growth variation over 4 different soil treatments for height at age 24 weeks.

Although the growth rate per clone differs in each soil treatment the clones follow about the same trend in all soil treatments. Clonal trends are much clearer at 12 weeks than at 24 weeks. ST2 (limed dark sandy soil from Somerset West) had the best growth for most of the clones except AG1, G1, AG15 and AG13, which grew better on low pH soil treatment while the worst growth occurred in ST3 (non-limed red clayey soil from Helsghoote), for clone AG10 at 12 weeks.

The significant clone x soil treatment interaction detected at age 12 weeks for height and diameter; number of branches, shoot and estimated root mass at 24 weeks; indicates that clones perform differently between soil treatments. Of greater importance than statistical significance is the importance of the interaction in reducing gains.

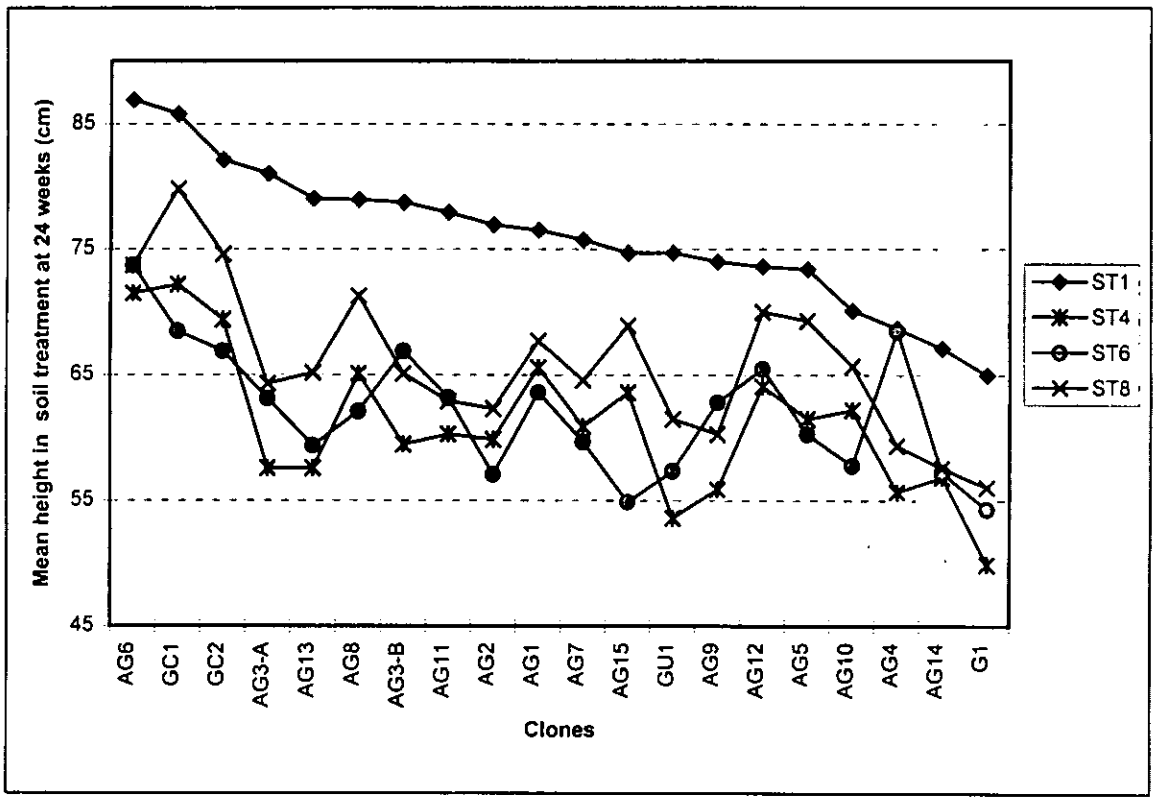


Figure 4.19. Mean height in four soil treatments (ST1, ST4, ST6 and ST8) per clone at 24 weeks. Clonal performance in different soils are illustrated by lines connecting dots, to facilitate following of trends of clonal response to different soils.

Height and shoot mass at 24 weeks were selected for illustration purpose. Clonal means by soil treatment for the selected variables are given in Tables 4.26 and 4.27. Line graphs based on these means are comparing the performance of some clones (AG2, AG6, AG7, AG8 and GC2) across sites (8 different soil treatments), clearly illustrating those clones that may be responsible for causing the GEI. Figures 4.19- 4.22 show that most clones are performing markedly differently on more productive soil treatment for height and shoot mass at 24 weeks (ST1 = non-limed soil type from Somerset West) compared with the less productive soil treatment (ST4 = limed soil type from Helshoogte) when these two soil treatments are compared.

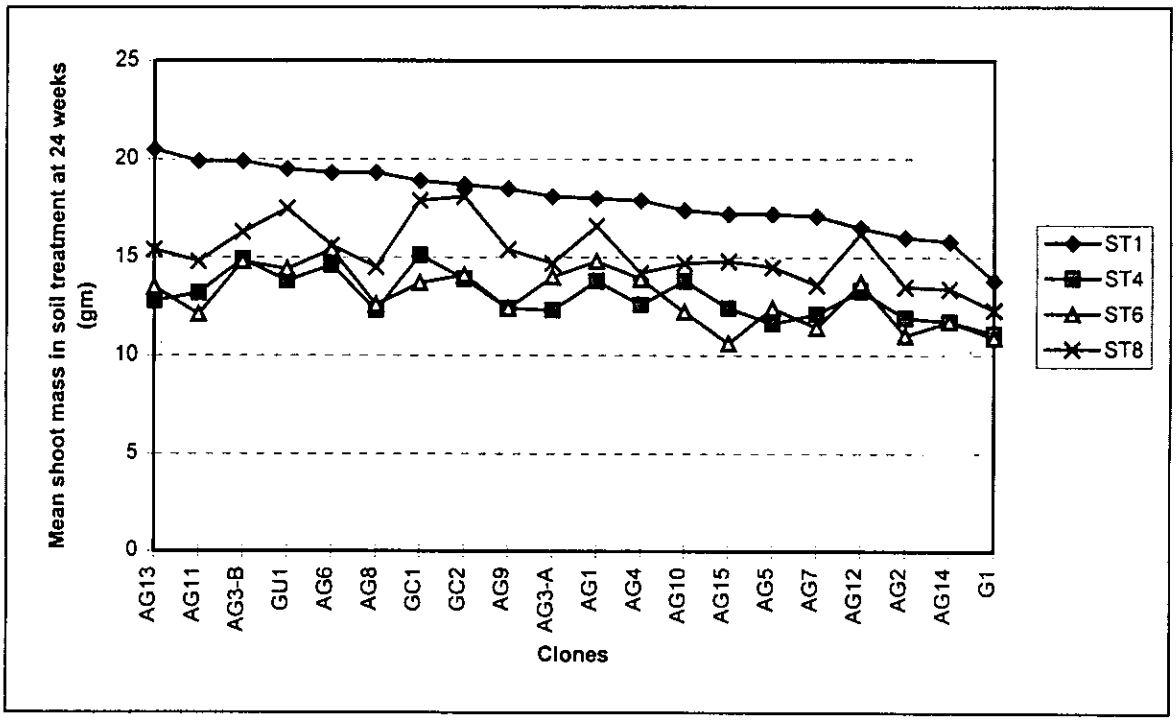


Figure 4.20. Mean shoot mass in four soil treatments (ST1, ST4, ST6 and ST8) per clone at 24 weeks. Clonal performance in different soils are illustrated by lines connecting dots, to facilitate following of trends of clonal response to different soils.

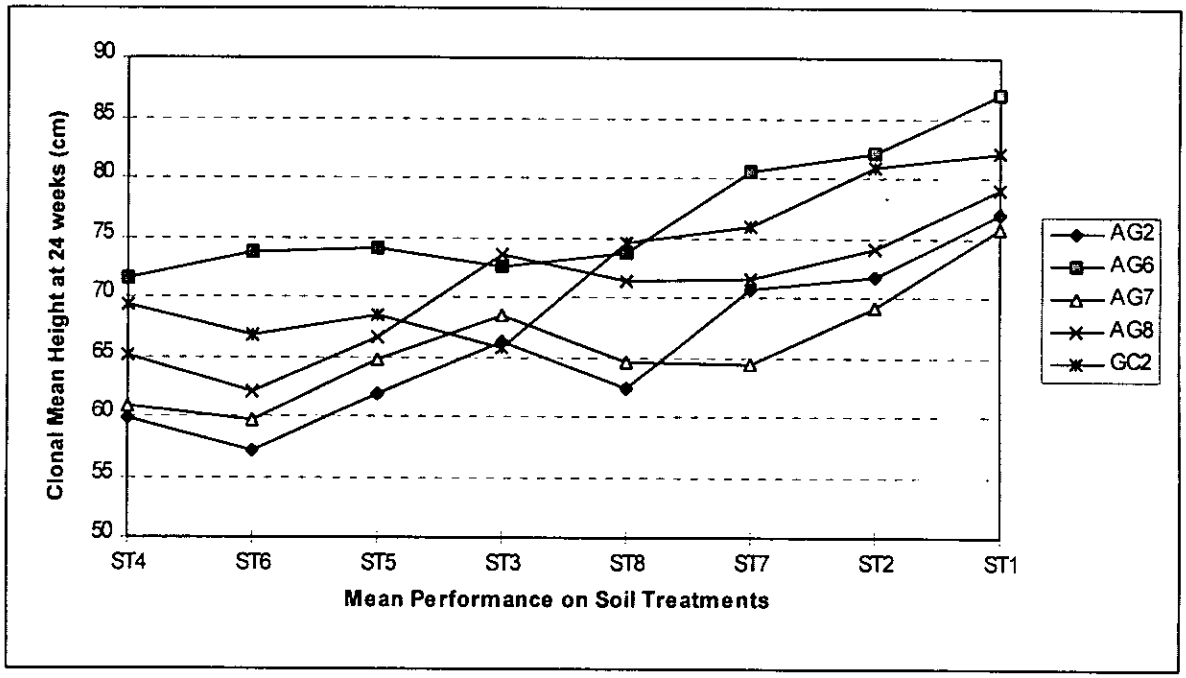


Figure 4.21. Clone mean height against trial mean for each soil treatment for height at 24 weeks. Clonal values in different soils are connected by lines to facilitate following of trends.

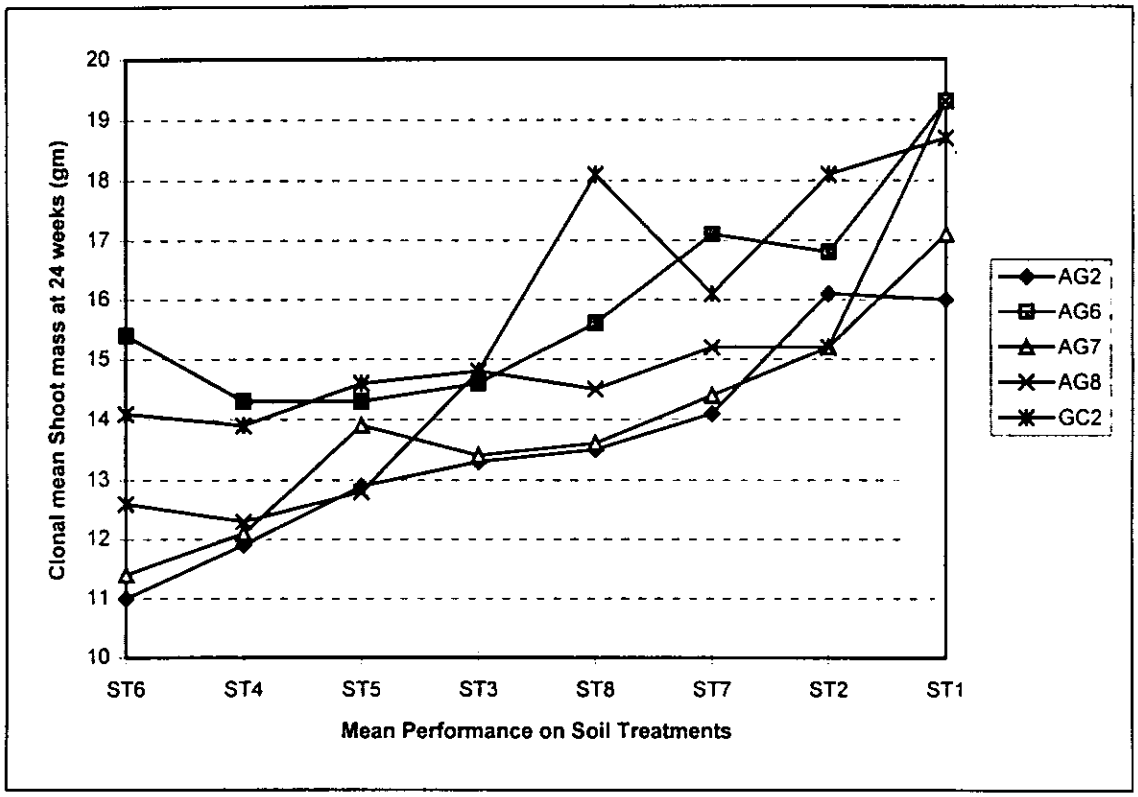


Figure 4.22. Clone mean shoot mass against trial mean for each soil treatment for shoot mass at 24 weeks. Clonal values in different soils are connected by lines to facilitate following of trends.

Table 4.25, show that clone x soil treatment for height at 24 weeks is non-significant although some regression lines still cross each other (Fig. 4.19 and 4.21). This insignificance would be due to relatively large standard errors. For shoot mass at age 24 weeks there is highly significant interaction between clone and soil treatment. ($p<0.001$) and this is emphasized in the rank changes illustrated in (Fig.4.20). These results indicate some possibility of detecting GEI in nursery experiments.

Table 4.26. Clonal mean by soil treatment for height at 24 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN H24 PER SOIL TMTS. (cm)	MEAN H24 PER CLONE (cm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU 1	GC1	GC2
ST1	76.1	76.5	76.9	81.0	78.7	68.7	73.4	86.9	75.7	78.9	74.0	70.1	77.9	73.6	79.0	67.1	74.7	65.0	74.7	85.8	82.1
ST2	70.8	75.4	71.7	70.7	61.0	64.8	71.6	82.1	69.1	74.1	63.1	68.1	74.2	71.9	74.9	61.2	72.7	63.8	64.0	80.8	80.9
ST3	64.8	72.5	66.3	61.9	60.1	56.4	62.6	72.5	68.4	73.6	63.7	66.4	67.1	66.9	61.3	52.8	66.6	56.3	57.3	75.4	65.8
ST4	61.2	65.6	59.9	57.6	59.5	55.7	61.5	71.5	60.9	65.1	55.9	62.2	60.3	64.1	57.6	56.8	63.6	49.8	53.6	72.2	69.4
ST5	63.9	74.6	61.9	64.6	68.9	60.1	59.6	74.1	64.8	66.6	60.7	69.1	64.3	64.4	58.2	59.5	55.5	55.5	62.2	65.5	68.4
ST6	62.1	63.6	57.1	63.1	66.9	68.5	60.3	73.7	59.7	62.1	62.8	57.8	63.2	65.5	59.4	57.3	54.9	54.3	57.4	68.4	66.8
ST7	68.6	73.9	70.7	66.6	63.6	57.5	66.1	80.5	64.4	71.6	66.9	70.6	68.5	68.4	74.8	59.7	73.7	55.7	67.4	73.8	75.9
ST8	66.0	67.7	62.3	64.3	65.1	59.4	69.3	73.7	64.6	71.3	60.3	65.7	62.9	70.0	65.2	57.6	68.8	56.1	61.6	79.8	74.6

Table 4.27. Clonal mean by soil treatment for shoot mass at 24 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN Sm24 PER SOIL TMTS (gm)	MEAN Sm24 PER CLONE (gm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	18.0	18.0	16.0	18.1	19.9	17.9	17.2	19.3	17.1	19.3	18.5	17.4	19.9	16.5	20.5	15.8	17.2	13.8	19.5	18.9	18.7
ST2	16.3	18.3	16.1	15.8	14.6	17.0	16.4	16.8	15.2	15.2	14.7	15.3	17.1	17.0	17.1	14.8	16.3	14.4	16.6	19.4	18.1
ST3	14.3	15.8	13.3	13.6	15.3	13.8	13.5	14.6	13.4	14.8	14.3	14.1	15.5	14.5	14.4	12.8	14.3	11.7	15.1	16.2	14.8
ST4	13.0	13.8	11.9	12.3	14.9	12.6	11.6	14.3	12.1	12.3	12.4	13.9	13.2	13.3	12.8	11.7	12.4	11.1	13.8	15.1	13.9
ST5	14.2	17.9	12.9	15.0	15.2	12.9	13.3	14.3	13.9	12.8	13.7	14.3	13.8	15.6	15.9	13.8	13.9	11.4	14.8	14.7	14.6
ST6	12.9	14.8	11.0	14.0	14.8	13.9	12.4	15.4	11.4	12.6	12.4	12.2	12.1	13.7	13.5	11.7	10.6	10.9	14.4	13.7	14.1
ST7	15.5	17.1	14.1	15.7	15.7	13.4	14.7	17.1	14.4	15.2	14.9	16.3	16.1	16.4	17.5	14.1	15.1	12.2	16.8	17.1	16.1
ST8	15.2	16.6	13.5	14.7	16.3	14.2	14.5	15.6	13.6	14.5	15.4	14.7	14.8	16.3	15.4	13.4	14.8	12.3	17.5	17.9	18.1

b. Clone x soil type

i) Height, diameter and shoot mass

Significant soil type x clone effects were found for diameter measured at 12 weeks and for shoot mass measured at 24 weeks (Table 4.6 and 4.7). Generally, however, it seems as if there was no strong interaction of clones with soil types especially for height at all ages and diameter growth at the later stages. Although the interactions are not statistically different for most of the traits graphical presentation illustrates the change of clonal rankings for shoot mass and the superiority of some clones in the dark sandy soil from Somerset West over the yellow, clayey soil from Grabouw (Fig.4.23).

ii) Number of branches

A strong clone x soil type influence seems to exist for number of branches , even when expressed as a ratio of height growth at 24 weeks. This may clearly illustrate that some clones are more sensitive for the formation of branch biomass on certain soils than other clones.

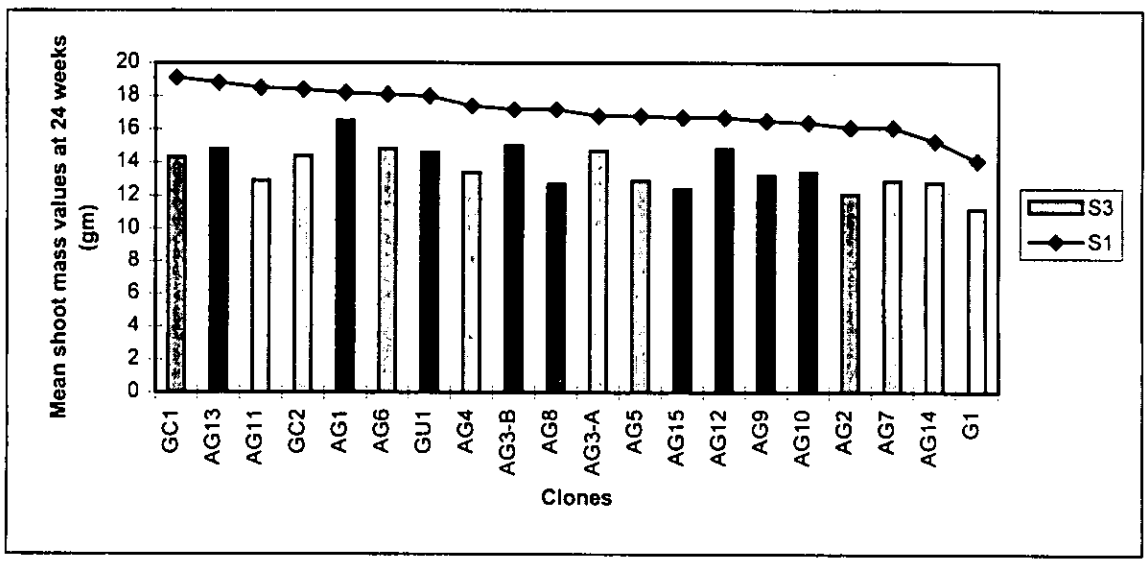


Figure 4.23. Mean shoot mass growth of 20 clones in Somerset West (line) and Grabouw (bars) soil type at 24 weeks. The line connecting values of discrete variables is to facilitate comparison of trends in clonal variation.

c. Clone x lime

Significant clone x lime effects were found for height at 12 weeks, number of branches and its ratio; estimated root mass and shoot mass, which were measured at 24 weeks (Tables 4.6 and 4.7). Generally the trend for all traits are the same as for soil type x clone effects. Means per clone for shoot mass are illustrated in Fig. 4.24.

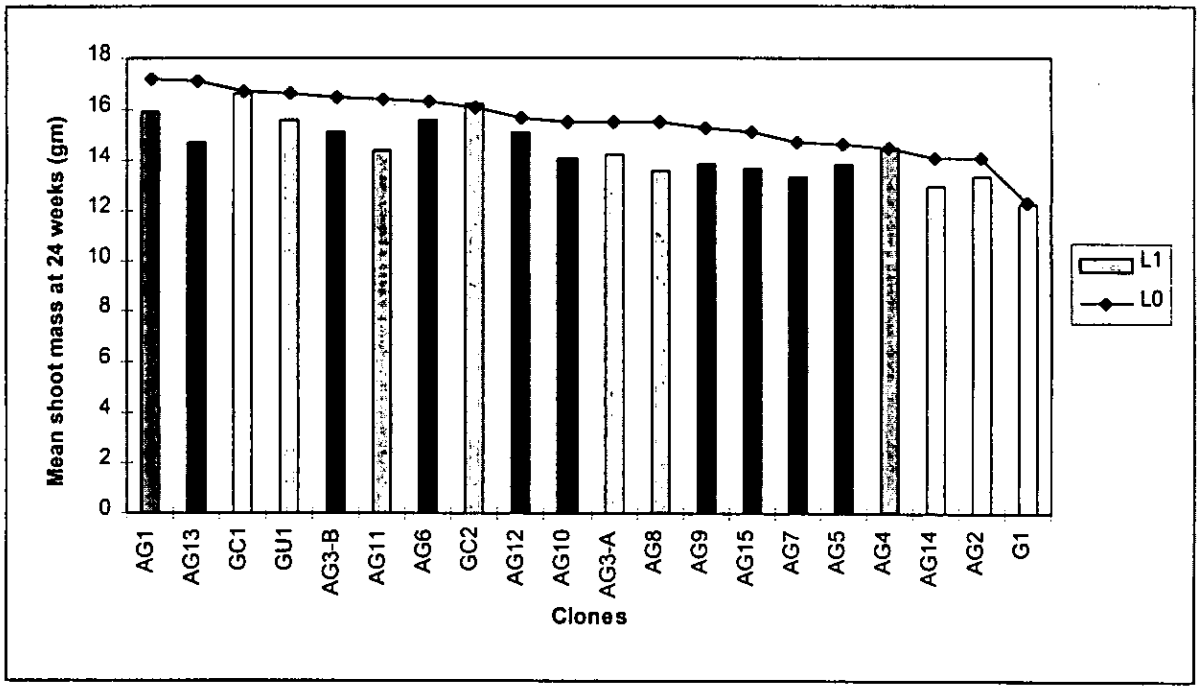


Figure 4.24. Mean shoot mass of 20 clones in non-limed (line) and limed (bars) soil type at 24 weeks. The line connecting values of discrete variables is to facilitate comparison of trends in clonal variation.

According to the results depicted in Table 4.7 there is a significant interaction between clone*lime on the level of 5% indicating that the rank changes in the preceding graphs are of statistical significance.

d. Clone x soil type x lime

The analysis of variance detected non-significant interaction between clone x soil type x lime for all traits in Tables 4.6 and 4.7, with the exception of diameter at 12 weeks, shoot and estimated root mass at 24 weeks.

Although height and diameter at age 12 weeks are strongly correlated, diameter seems to be more sensitive to environment (soil texture and soil pH) at early age.

Shoot growth was affected by the soil characteristic, and the experiment clearly showed a high difference in performance between clones within the different soil treatments. Higher mean values were found on ST1 and ST2, the non-limed and limed soil type from Somerset West, and the lowest values in ST4 and ST6, the limed soil types from Helshoogte an Grabouw respectively. These results may indicate that some clones are more capable of capturing site conditions earlier than others.

4.5.2 MAGNITUDE OF VARIANCE COMPONENT

The existence of genotype x environment interaction is usually demonstrated by a significant interaction term in the analyses of variance as discussed earlier. As an approximate rule of thumb, where the interaction component reaches 50% or more of the total entry components of variance then the effects of genotype x environment interaction (GEI) are likely to be serious on gains from selection and testing (Shelbourne, 1972). Variance components percentage contribution for the simplified model (fixed and random) are given in Table 4.28.

Table 4.28. Percentage contribution of variance components for clone x soil interaction for the simplified, fixed and random, model estimated for height and diameter at age 12, 18 and 24 weeks and for number of branches, shoot and estimated root mass only at age 24 weeks.

VARIANCE COMPONENTS %		
Variables	**Fixed Model**	**Random Model**
H12	2.16	1.21
D12	2.37	1.55
H18	-0.51	-0.45
D18	1.02	0.65
H24	-0.96	-0.59
D24	0.44	0.28
Nb24	2.82	1.77
Sm24	2.97	1.95
ERm24	2.97	1.95

Study of results of clones growing on more than one soil treatment in the nursery indicates that a certain degree of genotype and environment interaction exists although its magnitude is low, implying that gain predictions based on broad sense heritability will not be affected very much on the different soil types.

It must be noted that this is a nursery environment with very young seedlings, a stage where gain predictions normally will not be attempted. The interaction effects might still develop further with age. The results are also somewhat in contrast with what the regression analyses indicate (see below). The latter analyses might also be more sensitive to interaction effects than what is obtained with the analysis of variance.

4.5.3 SITE TO SITE CORRELATIONS

Sensitivity of the clones included in the present study is indicated by the correlation between clones for soil treatments ("sites") for each variable. If the correlation is strong between "sites", could mean there is environmental covariance, and the different clones follow the

same ranking for a specific trait. Low correlation will indicate sensitivity of clones to the soil treatments.

Results depicted in Table 4.29 show that "site to site" correlations reduce with time for variable height meaning that clone sensitivity to soil treatments increases over time. Results for diameter show an irregular pattern, indicating slightly more sensitivity of this variable to different soil characteristics at different ages. Generally, however, the high correlations are in agreement with results obtained from the ANOVA's.

4.5.4 REGRESSION

Regression analysis techniques allow an investigation into the stability and behaviour of genotypes. The regression is especially effective in emphasising the actual trend in the performance of genotype in response to a range of environments. The method of regression analysis performed to test clone adaptability, and hence genotype stability, over soil treatments follows the one used by Shelbourne (1972). The linear relationship of the clone mean performance on the soil treatments means (which can be considered as site index), provides an indication of clonal adaptability. The parameters obtained in these regression analyses are shown in Tables 4.30 and 4.31.

The coefficients of determination R^2 were generally high (>0.7) for fitted regressions although some exceptions were found where this coefficient was found to drop as low as 0.23 as seen for clone AG4 and AG6 at height 24 and 18 respectively. The coefficient of determination describes the variation explained by the regression as a proportion of the variation observed.

High R^2 values can, therefore, be attributed to a clone whose actual performance closely follows the predicted performance. A low R^2 value, however, may indicate a clone whose performance is unexpected on a specific soil treatment rather than over all soil treatments.

Table 4.29 Clonal means per soil treatment correlations for variable height and diameter at ages 12, 18 and 24 weeks.

	Height								Diameter							
	MST1	MST2	MST3	MST4	MST5	MST6	MST7	MST8	MST1	MST2	MST3	MST4	MST5	MST6	MST7	MST8
MST1	1.000	0.804**	0.888	0.820	0.866	0.863	0.872	0.915	1.000	0.420*	0.529	0.618	0.607	0.656	0.521	0.555
		0.826**	0.875	0.823	0.650	0.615	0.769	0.835		0.524	0.633	0.554	0.117*	0.648	0.467	0.600
		0.758**	0.677	0.724	0.560	0.624	0.776	0.763		0.544	0.634	0.605	0.571	0.719	0.401*	0.593
MST2		1.000	0.804	0.882	0.822	0.899	0.858	0.906		1.000	0.568	0.657	0.579	0.657	0.489	0.563
			0.857	0.916	0.665	0.669	0.882	0.919			0.753	0.768	0.346	0.702	0.630	0.726
			0.773	0.831	0.438	0.454	0.833	0.830			0.556	0.673	0.594	0.661	0.539	0.578
MST3			1.000	0.898	0.864	0.818	0.917	0.887			1.000	0.767	0.622	0.749	0.598	0.765
				0.837	0.796	0.682	0.869	0.911				0.792	0.448	0.687	0.616	0.629
				0.831	0.600	0.398	0.744	0.784				0.673	0.684	0.639	0.545	0.852
MST4				1.000	0.815	0.879	0.924	0.907				1.000	0.488	0.737	0.705	0.726
					0.724	0.614	0.845	0.881					0.171*	0.607	0.558	0.631
					0.642	0.590	0.779	0.933					0.658	0.503	0.596	0.549
MST5					1.000	0.829	0.857	0.869					1.000	0.717	0.320*	0.590
						0.673	0.763	0.745						0.265*	0.013*	0.113*
						0.635	0.518	0.506						0.606	0.735	0.723
MST6						1.000	0.816	0.944						1.000	0.608	0.726
							0.567	0.778							0.422*	0.575
							0.336*	0.542							0.552	0.724
MST7							1.000	0.893							1.000	0.704
								0.867								0.594
								0.761								0.668
MST8								1.000								1.000

* the symbol shows non- significant correlations between soil type means.

** different rows indicate values at different ages, the top row for 12 weeks and the bottom row for 24 weeks.

Table 4.30. Parameters obtained through the linear regression (y=bx+c) of clone mean height and diameter (y) on the means of soil treatments (x).

CLONES	AGE	HEIGHT			DIAMETER		
		Intercept	ß	R^2	Intercept	ß	R^2
AG1	12	-5.47	1.12	0.85	1.32	0.65	0.51
	18	-9.68	1.24	0.81	1.14	0.83	0.74
	24	21.30	0.75	0.57	1.57	0.78	0.62
AG2	12	-1.74	1.00	0.90	-0.05	0.96	0.83
	18	-15.39	1.30	0.90	-0.25	1.02	0.75
	24	-20.40	1.29	0.90	0.78	0.79	0.45
AG3-A	12	-7.67	1.12	0.88	-0.58	1.08	0.71
	18	-22.73	1.42	0.72	-1.21	1.20	0.69
	24	-24.40	1.36	0.91	-0.41	1.07	0.75
AG3-B	12	3.46	0.94	0.87	-0.39	1.15	0.82
	18	11.44	0.76	0.77	1.21	0.73	0.52
	24	15.26	0.75	0.35	2.65	0.56	0.32
AG4	12	9.08	0.71	0.63	0.17	0.93	0.70
	18	20.88	0.52	0.32	-1.52	1.34	0.88
	24	27.15	0.51	0.23	-0.34	1.09	0.57
AG5	12	-0.15	0.91	0.54	0.53	0.82	0.50
	18	-3.34	1.01	0.70	1.05	0.71	0.52
	24	1.35	0.96	0.79	-0.51	1.06	0.89
AG6	12	-2.28	1.23	0.85	-0.17	1.13	0.79
	18	37.52	0.36	0.23	2.03	0.58	0.31
	24	5.19	1.07	0.92	0.90	0.83	0.71
AG7	12	-2.74	1.06	0.87	-0.19	1.02	0.97
	18	-7.17	1.16	0.77	1.11	0.69	0.49
	24	4.87	0.92	0.79	-0.98	1.15	0.80
AG8	12	-1.18	1.20	0.78	-0.17	1.13	0.67
	18	19.57	0.73	0.69	-1.75	1.46	0.86
	24	5.08	0.98	0.78	-1.08	1.17	0.89
AG9	12	-3.39	1.04	0.89	-0.71	1.25	0.81
	18	0.64	0.93	0.61	0.68	0.88	0.61
	24	2.12	0.92	0.73	0.97	0.87	0.63
AG10	12	-17.51	1.35	0.81	-1.26	1.34	0.93
	18	13.95	0.64	0.45	-0.65	1.14	0.89
	24	25.45	0.61	0.48	1.38	0.76	0.45
AG11	12	8.53	0.93	0.79	-0.56	1.28	0.82
	18	5.52	0.93	0.78	-0.95	1.27	0.91
	24	- 9.96	1.16	0.90	-1.49	1.29	0.86
AG12	12	11.71	0.90	0.68	0.03	1.05	0.68
	18	14.36	0.79	0.73	-0.42	1.15	0.77
	24	24.27	0.66	0.86	1.41	0.77	0.55
AG13	12	-1.91	0.99	0.90	0.73	0.76	0.72
	18	-14.32	1.26	0.92	0.01	1.01	0.79
	24	-43.47	1.65	0.89	-1.26	1.27	0.88
AG14	12	7.13	0.65	0.64	-0.84	1.16	0.87
	18	9.17	0.71	0.62	0.81	0.74	0.74
	24	13.37	0.68	0.67	-0.36	1.04	0.78
AG15	12	-9.89	1.18	0.87	-0.17	0.97	0.82
	18	-12.79	1.22	0.77	-0.91	1.15	0.79
	24	-14.89	1.22	0.59	-1.18	1.14	0.84
G1	12	1.66	0.89	0.68	0.76	0.69	0.67
	18	-22.16	1.38	0.79	-0.21	0.96	0.79
	24	-4.46	0.92	0.84	-0.63	0.98	0.93
GU1	12	-5.81	1.06	0.83	-0.13	1.07	0.81
	18	-11.79	1.14	0.69	-0.31	1.11	0.78
	24	-20.58	1.24	0.86	-0.38	1.09	0.89
GC1	12	0.81	1.11	0.90	0.98	0.68	0.70
	18	0.14	1.12	0.78	0.85	0.78	0.81
	24	2.16	1.09	0.66	0.47	0.89	0.78
GC2	12	14.24	0.70	0.56	0.16	1.04	0.85
	18	-4.97	1.17	0.76	-0.53	1.18	0.92
	24	-3.41	1.15	0.81	-1.19	1.26	0.92

a) Height and diameter

Many clones had negative intercepts at age 12, 18 and 24 weeks, and this may indicate that the ranking of these clones was inflated merely as result of a very good performance on a good soil treatment. One must look at the performance of these clones over time since if this trend continues, they will not be suitable for poor soils (van Wyk, *et al.*, 1989).

The fitted regression coefficient (ß) reflects that portion of genotypic stability associated with the capacity of genotypes to perform relatively better in unfavourable than in a favourable environment (Hanson cited by Skrøppa, 1984).

A clone with a regression coefficient near to one is considered to be average stability and equally adapted to good and poor soils. A clone with a value greater than unity is of low stability and better adapted to good sites. A clone with a low value has high stability and it can be better adapted to good or poor soils depending on the intercept values (Skrøppa, 1984; Clair and Kleinschmit, 1986).

Clones AG4 and AG14 for variable height and GC1 for diameter, at all ages, are typical examples of relatively stable genotypes because they are better adapted to poor soils. Clone means per soil treatments are given in Tables 7.17-7.21 of Appendix D.

For illustration purposes, two contrasting clones were chosen for variables height at 24 weeks, AG2 and AG14; AG2 with a large negative intercept (-20.40) and high slope (ß = 1.29) has a good performance in good soils but low stability indicating a strong positive reaction to a good site. Rank may not necessarily change depending upon the range in site values (Table 4.30). AG14 with a positive intercept (13.37) and a flat slope (ß = 0.68), indicates that this clone may have the best height growth in poor soils at 24 weeks, especially where "poor soil values" (site index) will be less than 55cm (Fig. 4.25).

Diameter and height, as referred in section 4.4, are strongly correlated at age 12 and 18 weeks but they respond differently on different soil treatments indicating an unequal sensitivity of these two variables to environmental influences. This may lead to conclusion that different degree of genotype x environment interaction is present for variable height and diameter. The poorest growth performance for variable height occurred in limed red clayey soil type from Helshoogte (ST4) while for diameter was in limed yellow clayey soil type from Grabouw (ST6) (Fig. 4.15 and 4.16).

Comparing regression coefficients for diameter at 24 weeks (Table 4.31), of clones AG2 and AG14 one can notice that AG2 with a small positive intercept (0.78) and slope (ß = 0.79) has a good performance in some of the poor soils and AG14 with a negative intercept (-0.36) and a slope close to unity (ß = 1.04) performs better in good soil treatments.

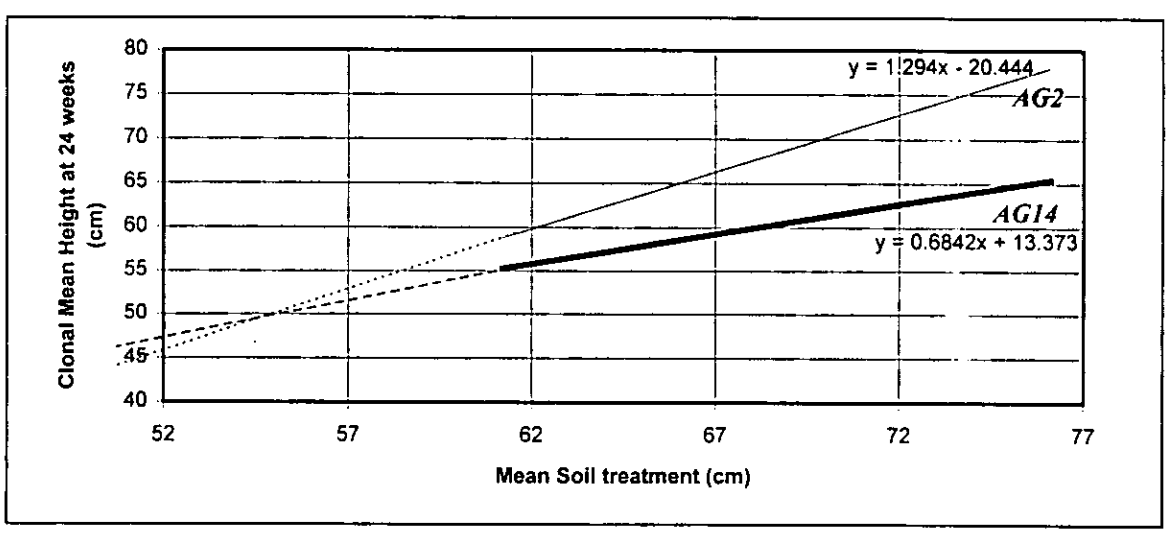


Figure 4.25. Regression lines for clonal mean height for clone AG2 and AG14, produced by the regression of observed clonal mean height in each soil treatment mean height, for data recorded at 24 weeks.

Means per clone and soil treatments for diameter at 12, 18 and 24 weeks, are given in Appendix D, Tables 7.19-7.21 and provide details of growth differences over soil treatments.

The clones are grouped as follows:

1) Clones AG5, AG8, AG11, AG13 and AG15 have negative intercepts and high slopes. Clones belonging to this group should be the most unstable clones with increasing positive response to positive environmental changes.

2) Clones AG1, AG3-B, AG6, AG12, AG14 and G1 with positive intercepts and slopes with value below one indicate that these clones have a tendency for better performance in poor soils, than the "unstable" clones but selection of such clones would depend upon the range of site index values.

3) Clone GU1, GC1 and GC2 with small intercepts and regression coefficients approximating to 1.0 indicate average stability, i.e., responding to soil fertility improvement according to an "expected" linear trend.

5. CONCLUSIONS

Contrary to expectations, nursery environments often are variable. Experimental design and error control therefore, are important. The environmental design used in this study was effective in increasing the precision of the experiment due to the large number of replications that was used.

Amongst the measured or created variables, significant differences were found among clones indicating that there was some measure of quantitative genetic control in nearly every characteristic in the young tree.

The clonal test data from this research illustrates the existence of large genetic variation in *E. grandis* clones and its hybrids when tested in 8 different combinations of soil treatment. The analysis of variance detected highly significant differences between clones, between soil types and its pH levels for all the created and measured variables at all ages. The best growth occurred in the dark sandy soil type from Somerset West and the worst growth in either Grabouw or Helshoogte soil types.

The main sources of variation, **soil types, clones** and **lime levels**, were highly significant for most variables for diameter at age 18 weeks and number of branches at 24 weeks.

Significant positive phenotypic correlations were obtained among all traits. Although the trees were very young, this indicates the possibility of simultaneous improvement of various traits whenever a desired positive correlation between two or more traits is present. This should be confirmed with genetic correlations, which was not attempted in this study.

Height and diameter are highly correlated although the correlations weakened a little bit over time. The strong correlation found between H0 and H12, r =0.93, and the diminishing effect of the height correlation over time might mean that early prediction is not so reliable if one looks at early growth. The same trend was found to be followed by diameter. This may mean that nursery performance would be a poor predictor of field performance at later ages.

Results of correlations between traits based on clonal mean for height, diameter, shoot and root mass showed a change over time indicating that diameter and height are good predictors of shoot mass at 12 weeks; diameter turns out to be a better predictor of shoot mass at 18 weeks. This implies that more variation was present for diameter than for height growth as a result of tree to tree competition for height. At 24 weeks height becomes a better predictor of shoot and root mass.

Branch number decreases with the size of the tree at 24 weeks indicated by the negative and significant correlation found between this trait and height when tested for all the clones. This may be ascribed to the crowded condition of the trees that developed over time. Hybrids were found to have fewer branches than pure *E. grandis* despite their good growth registered over all the trials. The apparent efficiency of eucalypt hybrids despite a low above ground biomass would justify further research.

The analysis of variance detected significant interaction between **clone x soil type** for diameter at 12 weeks, for number of branches and the ratio expressing number of branches relative to height at 24 weeks, and for shoot mass and estimated root mass at 24 weeks. **Clone x lime** interaction is significant for height at 12 weeks, number of branches and its ratio, as well as shoot and estimated root mass, all at age 24 weeks.

Soil type x lime is highly significant for diameter at 12 weeks, shoot and respective estimated root mass at 24 weeks. The interaction between **soil type x lime x clone** for all the traits was found to be statistically non - significant with the exception of diameter at 12 weeks and estimated root mass at 24 weeks. However, significance for more traits were found when combining and analysing the soil type and lime into a **soil treatment** to test its interaction with clones.

The regression method of studying genotype x environment interaction showed a high sensitivity of the clones to a change of soil treatments. Some clones seemed to perform equally well in good and poor soil treatments while others are better adapted to good soil

treatments or poor soil treatments. Genotype x environment interaction exists although its magnitude is low implying that gain predictions based on broad sense heritability will not be affected very much. However, such prediction may be doubtful from a nursery experiment.

The practical implication of the presence of GEI amounts to the fact that the best clone, under field conditions, in one soil type is not necessarily the best in all other soils. If there is no serious or excessive GEI it means that one can select trees on one site and grow them on other sites. In other words, one can easily extrapolate the results from one site to the other, a process known as indirect selection. The early age results from the present study, in general, did not give strong evidence of clones interacting with soils but there was some indication of genotype -environment interaction, for instance for **shoot mass**. This trait, or even total biomass, might be a good indicator for possible prediction of GEI in a nursery environment, especially if the trees are given some time to "mature in the nursery. It should be noted that even though the differences are not statistically significant, we still have to consider that small changes in clonal ranking over environments are of economic importance, simply because small differences are multiplied over large tracts of land. (Testing at 10% significance levels might be more appropraite).

The use of nursery studies for screening of clones could be useful in future research and even in practice. This study indicated that GEI can be detected in a carefully designed nursery experiment. Further studies including a wider range of environments for a longer period and comparison with field results are recommended using the same hybrid clones included in this nursery study.

The results obtained for above ground biomass (i.e. "shoot mass") are encouraging indicating that some index value of total tree response might be useful for early prediction purposes. Understanding of variables in the environment causing interaction will aid in such prediction studies.

6. LIST OF REFERENCES

Ahuja, M.R. and Libby, W.J., (1993). Clonal Forestry II. Conservation and Application. Berlin. Spring-Verlag.240pp.

Allard, R.W., (1961). Relationship between Genetic Diversity and Consistency of Performance in Different Environments. Crop Sci Vol 1. 127-123.

Allard, R.W. and Bradshaw, A.D., (1964). Implications of Genotype x Environmental Interactions in Applied Plant Breeding. Crop Sci. Vol 4. 503-507.

Anon, (1979 -1981). Eucalypts for planting. FAO. Rome. 667pp.

Anon, (1988). The eucalypt dilemma. FAO. Rome.26pp.

Anon, (1988). Mondi's Clonal Nursery. SAF. Jan/Feb.4pp.

Anon, (1994). The South African Forestry. F.O.A.Rivonia. S.A.2pp.

Barnes, R.D.; Burley, J.; Gibson, G.L. and Garcia de Leon, J.P., (1984). Genotype-Environment Interactions in Tropical Pines and their Effects on the Structure of Breeding Populations. Silvae Genetica 33,(1):186-197.

Barnes, R.D. (1984). Genotype- environment interaction in the Genetic Improvement of Fast Growing plantation Trees. In: Proceedings of a Symposium on Site and Productivity of Fast Growing Plantations. Vol. 1. Pretoria and Pietermaritzburg, RSA. 197-213.

Boland, D.J., Brooker, M.I.H. and Turnbull, J.W. (1980). *Eucalyptus* seed. CSIRO. Australia.191 pp.

Brooker, M.I.H. and Kleinig D.A. (1990). Field Guide to Eucalypts. South-Western and Southern Australia. Inkata Press. Sydney.428 pp.

Brooker, M.I.H. (1992). An Introduction to the study of characters in *Eucalyptus*. 118/92: 119-142.

Burdon, R.D., (1977). Genetic Correlation as a Concept for Studying Genotype-Environment Interaction in Forest Tree Breeding. Silvae Genetica 26, 5-6: 168-179.

Burdon, R.D., (1989). Early selection in tree breeding: principals for applying index selection and inferring input parameters. Can.J.For.Res. Vol 19,4: 449-504

Carson, S.D., (1991) Genotype x Environment Interaction and Optimal Number of Progeny Test Sites For Improving *Pinus radiata* in New Zealand. New Zealand Journal of Forestry Science 21(1): 32-49.

Clair, J.B.S. and Kleinschmit, (1986). Genotype-Environment Interaction and Stability in Ten-Year Height Growth of Norway Spruce Clones (*Picea abies* Karst.). Silvae Genetica 35, 5-6:177-185.

Cromer, R.N. (1990). The role of eucalypt plantation in timber supply and forest conservation in Australia. In: XIX World Congress, IUFRO 2. Canada 10:299-310.

Darrow, W.K., (1983). Provenance type trials of *Eucalyptus grandis* and *Eucalyptus saligna* in South Africa. S.Afr. For. J. No. 126. 30-38.

DNFFB (1987). Vegetação de Moçambique. Maputo.2pp.

Donald, D.G.M.; Goodricke, T.; Young, C.; Leisegang, K.; Herman, B.; Nichol, N. and South, D. (1994). South African Nursery Practice. In: Forestry Handbook. SAIF. Pretoria. 67-93.

Duncan, E. (1997). Personal communication. Mondi Forests, P.O. Box 39. Pietermaritzburg. 3200.

Eldridge, K. ; (1978). Genetic improvement of Eucalypts. Silvae Genetica 27, 5:205-209.

Eldridge, K. ; Davidson, J.; Harwood, C. and Van Wyk, G., (1993). Eucalypt Domestication and Breeding. Clarendon Press. Oxford. 288pp.

Ellis, F. (1997). Personal communication. Faculty of Forestry, University of Stellenboch, Private Bag X1 Matieland, 7602.

Falconer, D.S., (1952). The problem of Environment and Selection. Amer.Nat.Vol 86. No. 830: 293-298.

Falconer, D.S. (1989). Introduction to Quantitative Genetics. Logman. UK. 438pp.

Falkenhagen, E.R. (1985). Genotype by Environment Interaction in South African Pine Progeny trials: Implications for Tree Breeding. SAFJ No. 135. 53-60.

Falkenhagen, E.R., (1989). Relationships between some genetic parameters and test environments in open-pollinated families of *Pinus elliottii* in South Africa. Theor Appl. Genet. Vol. 77: 857-866.

Freese, F. (1967). Elementary Statistical Methods for Foresters. Agriculture Handbook.U.S. Department of Agriculture. 87pp.

Finlay, K.W. and Wilkinson, G.N., (1963). The Analysis of Adaptation in a Plant - Breeding Programme. Austr. J. Agric. Res. Vol.14. 742-754.

Foth, H.D. (1990). Fundamental of Soil Science. 8 E. New York.360pp.

Fowler, D.P. (1976). Genetic Variation Influences Tree Improvement Strategies. Pulp & Paper. Canada.5pp.

Gauch, H.G. and Zobel, R.W. (1988). Predictive and postdictive success of statistical analyses of yield trials. Theor. Appl. Genet. 76, 1-10.

Gauch, H.G. (1990). Full and reduced model for yield trials. Theor. Appl. Genet. 80, 153-160.

Gullberg, U. (1984). Characterising Environments in Swedish Forestry in Order to Minimise the Effects of Genotype x Environment Interaction. In: Proceedings from a conference on genotype x environment interaction, Uppsala. Studia Forestalia Suecia. No. 166. 25-39.

Hillis, W. and Brown, A.G. (1978). Eucalypts for wood production. CSIRO. Australia. 434pp.

Hodgson, L.M. (1976). Some aspects of flowering and reproductive behaviour in *E. grandis* (Hill) Maiden at J.D.M. Keet Forestry Res. Sta. (Formerly Zomerkomst For. Res. Station). 1. Flowering, controlled pollination, pollination and receptivity. S.A.F.J. 18-28.

Hodgson, L.M. (1976). Some aspects of flowering and reproductive behaviour in *E. grandis* (Hill) Maiden at J.D.M. Keet Forestry Res. Sta. (Formerly Zomerkomst For. Res. Station). 2. The fruit, seed, seedling, self fertility, selfing and inbreeding effects. S.A.F.J. 32-43.

Issufo, A.A.K. (1992). Comportamento de espécies e procedências de eucaliptos em Nampula e Maputo. Trabalho de diploma. Faculdade de Agronomia e Engenharia Florestal. Departamento de Florestas. UEM. 56pp.

Linacre, E. and Hobbs, J. (1977). The Australian climatic Environment. Brisbane.354pp.

Lindgren, D. (1993). The Population Biology of Clonal Deployment. In: Clonal Forestry I Conservation and Application. Berlin. Spring-Verlag. 34-49.

Libby, W.J. (1983). What is a safe number of clones. In: Proceedings of the nineteenth meeting Part 2. Symposium on Clonal Forestry: Its impact on tree improvement and our future forests. Toronto. Canadian Forestry Service. 221-222.

Lundkvist, K. (1984). Testing Methods for General and Specific Adaptation in Clonal Forestry. In: Proceedings from a conference on genotype X environment interaction, Uppsala. Studia Forestalia Suecica. No.166. 35-39.

Matheson, A.C. and Cotterill, P.P. (1990). Utility of Genotype x Environment Interactions. Forest Ecology and Management, 30: 159-174.

Matheson, A.C. and Raymond, C.A. (1984). The Impact of Genotype x Environment Interactions on Australian *Pinus radiata* Breeding Programs. Aust. For. Res., 14, 11-25.

Matheson, A.C. and Raymond, C.A. (1986). A Review of performance x environment interaction: Its practical importance and use with particular reference to the tropics. Commonw. For. Rev. 65(4).

Namkoong, G. (1979). Introduction to Quantitative Genetics in Forestry. Technical Bulletin No. 1588. For. Ser. USDA. Washington.342pp.

Nuvunga M., (1991). Eucalypt tree Planting in Mozambique. In: Proceedings of IUFRO. Symposium on Intensive Forestry: The Role of Eucalypts. Durban, South Africa. Vol. II, 1135-1146.

Ott, R. L., (1993). An Introduction to Statistical Methods and Data Analysis. Fourth Edition. Wadsworth. California.1038pp.

Owino, F., (1977). Genotype x Environment Interaction and Genotypic Stability in Loblolly pine. II. Genotypic stability comparisons. Silvae Genetica 26, 5-6:2-26.

Owino, F., Kellison, R.C. and Zobel, B.J. (1977). Genotype x Environment Interaction and Genotypic Stability in Loblolly pine. V. Effects of genotype x environment interaction on genetic variance components estimate and gain prediction. Silvae Genetica 26, 4:131-135.

Park, Y.S. and Fowler, D.P. (1987). Genetic variances among clonally propagated populations of tamarack and the implications for clonal forestry. Can. J. For. Res. Vol 17. 1175-1180.

Penfold, A.R. and Willis, J.L. (1961). The Eucalypts. London. 551pp.

Perkins, J.M. and Jinks, J.L., (1968). Environmental and Genotype- Environmental Components of Variability. III Multiple Lines and Crosses.Heridity Vol 23.339-356.

Poyton, R.J. (1979). Tree planting in South Africa. Vol. II. The Eucalypts. SAFRI. RSA. 882pp.

Quatro Pro, (1987). User's Guide: Superior spreadsheet power. Borland. USA. 794pp.

Randall, W.K. and Cooper, D.T. (1973). Predicted Genotypic Gain from Cottonwood Clonal Tests. Silvae Genetica 22, 5-6.

Resende, M.D.V.; Higa, A.R., Oliveira, J.G. and Campos, W.O. (1992). Environmental Stratification for Breeding *Eucalyptus* spp. Based on Genotype x Environmnet Interaction and Measurements of site Dissimilarities. EMBRAPA. 1-9.

Rice, R.W. and Youngs, R.L. (1990). One and two dimensional moisture profiles in red oak. Virginia Polytechnic Institute and State University. Blacksburg. 328-341.

Robertse, P.J., (1989). The Role of Genotype-Environment Interaction in Adaptability. SAFJ No. 150. 18-19.

SAS Institute Inc., SAS®, (1985). User's Guide: Statistics, Version 5 Edition. Cary, NC:SAS Institute Inc. 956pp.

SAS Institute Inc., SAS®, (1985). User's Guide: Basics, Version 5 Edition. Cary, NC:SAS Institute Inc. 1286pp.

Schönau, A.P.G. (1983). Silvicultural considerations for high productivity of *Eucalyptus grandis.* WRI. Pietermaritzburg.20pp.

Schönau, A.P.G; Stubbings, J.A. and Norris, C. (1994). Silviculture of Eucalypts. In: Forestry Handbook.SAIF. Pretoria.171-185.

Shelbourne, C.J.A. (1972). Genotype x Environment Interaction: Its study and implications in forest tree improvement. IUFRO Genetics - Sabrao Joint Symposia, Tokyo.1-28.

Skrøppa, T. (1984). A Critical Evaluation on Methods Available to Estimate the Genotype x Environment interaction. In: Proceedings from a conference on genotype x environment interaction, Uppsala. Studia Forestalia Suecia. No. 166. 3-13.

Stettler, R.F. and Ceulemans, R.J. (1993). Clonal Material as a Focus for Genetic and Physiological research in Forest Trees. In: Clonal Forestry I Conservation and Application. Berlin. Springer-Verlag. 68-86.

Turnbull, J.W. and Pryor, L.P. (1978). Choice of species and seed sources. In: Eucalypts for wood production. CSIRO. Australia 6-65.

Van Haverbeke, D.F. (1976). Forest Genetics and tree Improvement. In: Shelterbelts on the Great Plains. Proc. Symp.Colorado. 154-159.

Van Wyk, G. (1977). Pollen Handling, Controlled Pollination and Grafting of *Eucalyptus grandis*. SAFJ No. 101. 47-53.

Van Wyk, G. (1985). Tree breeding in support of vegetative propagation of *E. grandis* (Hill) Maiden. SAFJ. Dec. 33-39.

Van Wyk, G.; Schönau, A.P.G. and Schön, P.P. (1989). Growth potential and adaptability of young eucalypt hybrids in South Africa. In: Breeding tropical trees: Population structure and genetic-improvement strategies in clonal and seedling forestry. Proc. IUFRO. Pattaya, Thailand. 325-333.

Van Wyk, G., Pierce, B.T. and Verryn, S.D., (1991). Two Year Results from a site by clone interaction trial series of *Eucalyptus grandis*. In: Proceedings of IUFRO. Symposium on Intensive Forestry: The Role of Eucalypts. Durban, South Africa. Vol 1. 334-344.

Van Wyk, G. (1997). Personal communication. Faculty of Forestry, University of Stellenbosch, Private Bag X1 Matieland, 7602.

Walpole, R.E. (1982). Introduction to Statistics. 3rd edition. New York.521pp.

Wex, Lyndi (1997). Personal communication. Mondi Forests. P.O. Box 39 Pietermaritzburg, 3200.

Wignall, T.A.; Brown, S.N. and Purse, J.G. (1991). The intensive cultivation of *Eucalyptus grandis* clonal stockplants in glasshouses. In: Proceedings of IUFRO. Symposium on Intensive Forestry: The Role of Eucalypts. Durban, South Africa. Vol 1. 162-179.

Wright, J.W., (1976). Introduction to Forest Genetics. AP. New York. 463pp.

Zobel, B.J. and Ikemori, Y.K., (1983). Vegetative Propagation in *Eucalyptus*. In: Proceedings of the nineteenth meeting Part 2. Symposium on Clonal Forestry: Its impact on tree improvement and our future forests. Toronto.Canadian Forestry Service. 136-144.

Zobel, B.J.,Van Wyk, G. and Stahl, P. (1987). Growing exotic forests. John Wiley & Sons. 508pp.

Zobel, B.J. (1993). Clonal Forestry in the Eucalypts. In: Clonal Forestry II. Conservation and Application. Berlin. Springer-Verlag.139-148.

7. APPENDIX

Appendix A1.

F-test performed using error sums of squares (SSE):

$$F = \frac{(SSE_c - SSE_3 - SSE_2 - SSE_1/4)}{(SSE_3 + SSE_2 + SSE_1)/(n + m + l - 8)}$$

Table 7.1. Sums of squares and degrees of freedom for residual calculated from individual and combined data set of root and shoot mass.

SSE	Number of data points
$SSE_c = 2159.77$	477
$SSE_3 = 1333.39$	158
$SSE_2 = 423.76$	160
$SSE_1 = 90.13$	159

Degrees of freedom for the F-test are 4 and 469.

Appendix A2.

SOIL TYPES

Root and shoot mass, ratio and number of branches

Soil means and its standard errors at age 12, 18 and 24 weeks for variables root and shoot mass, ratio and number of branches are given in Tables: 7.2 -7.5.

Table 7.2. Mean and standard error for shoot and root mass per clone over four soil types at 12 weeks.

CLONES	SOILS															
	S1		S2		S3		S4		S1		S2		S3		S4	
	Shoot Mass (grams)								Root Mass (grams)							
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	4.01	1.97	3.13	0.33	2.95	1.62	2.66	0.34	2.73	2.07	2.72	1.30	3.01	0.64	2.51	0.89
AG2	3.75	1.03	1.83	0.81	1.73	0.07	2.61	0.66	1.65	0.70	1.10	0.87	0.69	0.11	1.04	0.11
AG3-A	2.68	1.34	2.64	0.15	1.05	0.26	2.41	0.29	4.27	4.34	1.13	0.03	0.78	0.35	1.31	0.27
AG3-B	4.79	1.08	3.96	0.73	1.88	0.93	4.21	1.92	2.02	0.54	1.24	0.21	0.88	0.23	1.97	0.19
AG4	5.05	0.63	2.84	0.76	2.44	0.04	3.38	0.87	3.65	0.13	1.64	0.07	1.30	0.04	1.59	0.25
AG5	5.35	0.15	3.05	0.64	2.48	0.96	3.43	0.49	2.51	0.86	1.35	0.58	1.23	0.24	1.49	0.11
AG6	3.64	2.77	3.13	0.48	1.85	0.86	2.65	0.66	1.60	1.34	1.47	0.05	1.12	0.82	2.12	1.03
AG7	3.59	0.47	1.78	0.41	1.61	0.57	1.87	1.21	1.41	0.52	0.84	0.12	0.72	0.33	1.43	0.81
AG8	4.06	0.48	2.27	0.11	2.13	0.07	3.39	0.37	1.77	0.35	1.69	0.74	1.35	0.11	1.95	0.55
AG9	4.21	0.29	2.58	1.11	2.81	0.54	3.63	0.29	1.92	0.69	1.75	0.28	1.86	0.23	2.44	0.35
AG10	4.47	0.93	2.12	0.09	1.80	0.34	3.00	0.09	2.07	0.53	0.86	0.08	1.26	0.17	1.52	0.43
AG11	4.85	1.31	3.67	0.38	2.49	1.34	2.42	0.14	2.91	0.47	1.25	0.35	1.19	0.06	1.69	0.62
AG12	4.37	0.99	2.88	0.06	2.07	0.08	5.24	0.38	2.09	0.06	1.30	0.14	1.34	1.12	2.15	0.11
AG13	2.92	1.09	2.26	0.37	1.75	0.60	3.53	0.81	1.66	0.68	1.57	0.03	1.34	0.06	2.63	0.11
AG14	3.95	0.25	2.63	1.36	2.85	.a)	2.02	1.45	1.41	0.19	0.94	0.28	0.95	.a)	0.86	0.21
AG15	4.42	1.06	2.36	0.67	2.65	0.21	1.68	1.64	1.39	0.60	1.00	0.64	1.31	0.11	0.86	0.08
G1	3.87	1.09	2.65	0.52	2.32	1.36	2.32	1.36	1.67	0.55	1.09	0.07	1.62	0.16	1.48	0.19
GU1	5.79	0.05	3.82	0.11	2.14	0.98	4.44	0.71	3.64	1.03	1.44	0.19	1.51	0.86	2.65	0.26
GC1	5.17	0.05	4.41	0.64	2.62	0.79	3.53	1.14	3.60	0.50	3.45	1.42	1.77	0.99	2.25	1.12
GC2	6.04	2.98	4.81	0.14	2.37	1.02	2.96	0.03	2.38	2.06	2.97	1.05	2.67	1.46	1.35	0.08

a) Shoot and root mass and respective ratio were assessed for one replication at the time. The soil clone combination has 2 observations per replication. When only one tree is alive standard error is zero, i.e., the mean value is equal to the value of one observation.

Table 7.3. Mean and standard error for shoot and root mass per clone over four soil types at 18 weeks.

CLONES	SOILS															
	S1		S2		S3		S4		S1		S2		S3		S4	
	Shoot Mass (grams)								Root Mass (grams)							
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	8.99	0.89	6.00	2.19	6.18	0.11	9.45	0.67	4.35	1.51	3.83	2.86	8.88	0.96	6.02	1.82
AG2	7.95	1.45	5.17	0.80	4.69	0.13	7.04	0.77	2.48	1.04	3.20	1.06	2.46	1.03	3.27	1.25
AG3-A	7.37	4.60	3.14	0.36	4.62	1.05	4.35	1.44	2.52	1.66	1.07	0.53	3.35	1.21	2.22	0.93
AG3-B	11.82	1.11	8.05	0.46	8.64	2.48	7.02	0.86	5.21	0.61	3.36	0.35	3.08	0.77	3.21	0.89
AG4	7.18	1.87	6.88	0.12	6.49	0.62	5.25	1.69	3.92	1.20	3.38	0.59	3.66	1.11	2.85	0.32
AG5	7.62	4.29	4.14	0.38	5.29	1.36	4.83	0.64	3.08	0.08	1.56	0.51	3.75	1.55	2.89	0.66
AG6	10.98	3.57	6.51	0.95	8.84	0.42	6.32	1.26	6.31	1.63	2.84	0.01	4.43	1.05	4.45	0.38
AG7	7.34	3.02	6.09	0.42	2.65	2.38	8.26	5.04	2.55	0.70	3.66	0.59	1.87	0.24	4.91	3.92
AG8	8.63	3.51	2.38	0.50	5.59	1.92	6.83	1.95	3.32	0.04	1.13	0.33	4.96	5.05	2.87	1.48
AG9	9.45	0.47	2.13	1.18	7.49	0.56	5.38	2.06	3.29	1.01	1.56	0.13	7.46	0.21	3.83	1.43
AG10	8.34	3.40	4.38	0.97	4.75	0.26	8.56	0.66	4.25	0.64	2.24	0.25	4.61	3.06	3.62	0.37
AG11	10.26	3.79	7.29	0.89	4.34	4.28	8.87	1.71	4.26	0.13	3.67	0.63	2.20	1.56	4.06	0.24
AG12	8.91	0.04	6.98	0.85	4.23	1.59	6.25	3.66	4.75	3.64	4.34	0.86	1.87	1.41	3.36	1.58
AG13	6.15	8.42	6.92	1.36	4.40	1.38	9.91	3.43	2.76	2.19	3.32	0.76	2.04	0.27	3.85	0.25
AG14	6.81	2.47	3.47	1.27	6.99	3.87	4.49	2.32	2.84	2.07	1.58	0.14	4.24	1.82	2.44	1.69
AG15	7.87	2.33	6.41	1.76	4.46	0.03	7.05	0.78	3.07	2.05	1.50	0.23	2.48	0.14	2.43	0.72
G1	7.21	5.21	5.32	0.54	5.13	1.78	4.15	0.79	5.93	6.82	2.48	0.33	2.97	0.59	3.74	1.61
GU1	10.37	2.45	6.57	2.14	6.46	2.02	8.96	0.71	5.15	0.55	4.58	0.99	3.91	0.40	4.05	0.11
GC1	8.91	0.05	6.99	0.06	6.14	0.64	9.32	5.71	4.83	0.14	3.68	0.66	7.15	3.54	4.46	3.29
GC2	9.61	3.04	6.62	0.64	5.35	0.45	8.18	2.37	7.01	5.59	3.58	0.72	6.22	0.21	6.14	2.08

Table 7.4. Mean and standard error for shoot and root mass per clone over four soil types at 24 weeks.

CLONES	SOILS															
	S1		S2		S3		S4		S1		S2		S3		S4	
	Shoot Mass (grams)								Root Mass (grams)							
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	18.17	4.55	14.88	2.47	16.45	3.41	16.88	3.39	18.81	4.45	8.35	0.35	14.59	3.32	12.28	0.56
AG2	16.06	1.76	12.63	1.84	12.06	2.30	13.81	2.51	8.90	0.97	9.04	0.46	8.35	0.77	10.60	5.07
AG3-A	16.87	2.86	12.93	2.70	14.68	2.53	15.21	3.58	11.55	1.70	11.37	1.87	9.66	0.08	11.15	2.74
AG3-B	17.23	3.73	15.12	3.14	15.04	2.78	15.96	3.43	11.29	6.03	13.26	4.61	11.77	2.12	11.85	1.08
AG4	17.45	2.37	13.23	2.94	13.35	2.62	13.81	2.87	12.51	2.22	11.44	1.86	9.57	1.51	9.17	2.21
AG5	16.85	3.03	12.64	2.44	12.89	2.29	14.61	2.71	11.84	3.87	10.05	0.83	11.95	3.25	15.14	4.72
AG6	18.06	4.37	14.49	2.58	14.81	3.57	16.36	3.28	19.83	1.79	9.93	0.62	10.10	0.14	16.11	5.69
AG7	16.13	2.98	12.77	2.68	12.91	2.33	14.02	3.85	16.32	2.57	8.05	0.93	9.04	2.80	11.47	1.59
AG8	17.16	3.43	13.48	3.08	12.72	2.41	14.85	2.99	15.72	5.18	10.01	1.81	9.67	0.13	12.33	2.89
AG9	16.55	3.12	13.36	2.67	13.17	2.78	15.17	2.41	15.62	3.57	16.65	3.24	16.85	2.27	9.91	2.98
AG10	16.41	3.36	14.01	2.83	13.37	2.60	15.59	2.98	11.02	1.85	8.19	1.53	13.46	3.52	9.93	2.54
AG11	18.52	3.36	14.36	2.54	12.95	2.63	15.47	3.05	14.74	1.40	12.79	2.29	7.68	. a)	14.23	4.97
AG12	16.76	3.05	13.90	2.61	14.79	2.50	16.33	2.75	13.53	3.79	15.15	4.08	9.33	0.45	13.445	4.12
AG13	18.86	4.74	13.61	2.73	14.82	2.96	16.44	2.85	12.48	2.51	10.56	0.55	13.23	0.57	11.39	0.11
AG14	15.32	3.21	12.28	2.09	12.85	2.03	13.73	2.49	14.63	1.95	9.50	1.95	12.62	6.46	7.74	1.09
AG15	16.75	2.61	13.31	1.92	12.35	3.40	14.96	2.11	9.63	0.62	9.31	2.37	10.15	2.96	10.09	0.93
G1	14.09	2.71	11.40	2.33	11.17	1.49	12.27	2.98	9.70	. a)	10.58	3.45	9.26	1.33	14.59	8.12
GU1	18.01	3.35	14.48	2.96	14.02	2.05	17.15	4.17	16.35	2.64	13.79	6.33	10.80	3.24	9.12	1.57
GC1	19.14	4.13	15.65	2.54	14.33	2.52	17.54	3.31	13.55	1.66	11.21	0.14	10.47	0.19	10.00	2.84
GC2	18.41	2.88	14.38	2.49	14.42	3.03	17.16	4.46	17.71	4.14	12.30	2.55	18.22	5.06	15.34	4.17

a) Shoot and root mass and respective ratio were assessed for one replication at the time. The soil clone combination has 2 observations per replication. When only one tree is alive standard error is zero, i.e, the mean value is equal to the value of one observation.

Table 7.5. Mean and standard errors for ratio and number of branches per clone over four soils at 24 weeks.

CLONES	SOILS															
	S1		S2		S3		S4		S1		S2		S3		S4	
	Ratio24								Number of Branches24							
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	1.35	0.40	1.78	0.26	1.44	0.64	1.67	0.51	9.28	4.66	6.77	2.93	8.53	3.08	9.11	3.94
AG2	1.88	0.18	1.66	0.24	1.86	0.26	1.73	0.23	13.89	4.58	9.31	3.54	9.39	4.26	11.56	4.63
AG3-A	1.81	0.42	0.89	0.35	1.65	0.04	1.59	0.36	14.50	4.76	9.88	4.83	11.96	3.45	13.27	4.74
AG3-B	1.66	0.01	1.64	0.77	1.72	0.23	1.55	0.27	14.78	4.46	11.77	4.06	12.79	4.85	12.15	4.24
AG4	1.67	0.16	1.34	0.05	1.34	0.55	1.27	0.23	11.08	2.80	7.44	3.02	7.81	3.36	8.58	3.92
AG5	1.74	0.29	1.53	0.21	1.38	0.13	1.09	0.38	11.85	6.31	7.06	5.07	7.12	5.24	12.23	6.67
AG6	1.17	0.18	1.82	0.26	1.81	0.17	1.35	0.31	13.03	4.55	9.50	3.49	9.42	4.01	10.86	3.89
AG7	1.24	0.14	1.55	0.16	1.53	0.09	1.23	0.26	10.86	5.06	6.32	4.85	6.56	3.57	8.24	4.94
AG8	1.45	0.09	1.66	0.70	1.61	0.43	1.39	0.10	10.89	4.53	8.23	4.26	6.57	3.39	10.94	3.93
AG9	1.10	0.09	0.99	0.18	0.89	0.03	1.79	0.85	15.17	3.84	10.64	4.36	11.21	3.15	13.50	3.38
AG10	1.74	0.64	1.64	0.16	1.12	0.03	1.23	0.25	15.17	4.21	10.72	4.76	10.36	3.60	13.26	3.96
AG11	1.74	0.17	1.35	0.13	1.82	.a)	1.31	0.17	14.67	4.01	9.26	4.18	9.26	3.44	11.66	4.97
AG12	1.38	0.28	1.16	0.21	1.70	0.45	1.42	0.14	12.51	4.53	8.81	4.20	10.29	3.52	13.34	4.02
AG13	1.65	0.29	1.33	0.25	1.35	0.54	1.64	0.44	14.34	4.02	9.06	3.96	10.55	3.27	12.25.	3.28
AG14	1.12	0.00	1.43	0.26	1.21	0.59	1.17	0.25	16.62	6.18	8.97	4.52	13.22	5.33	14.33	5.45
AG15	2.21	0.02	1.54	0.68	1.46	0.45	1.73	0.05	16.63	4.51	11.67	4.81	11.00	5.23	16.38	5.08
G1	1.58	.a)	1.27	0.14	1.43	0.28	1.37	0.57	11.03	3.96	8.54	7.97	7.96	3.91	8.21	3.76
GU1	1.28	0.16	1.31	0.31	1.66	0.40	1.49	0.32	12.00	4.82	9.54	3.91	10.24	3.00	11.48	4.69
GC1	1.28	0.16	1.69	0.32	1.46	0.46	1.42	0.59	5.20	2.77	2.42	2.29	2.55	2.38	5.77	3.20
GC2	1.18	0.05	1.17	0.12	0.99	0.06	1.48	0.34	9.97	4.10	5.74	3.77	5.00	3.15	8.78	4.21

Appendix B
LIME

Lime means and its standard errors at age 18 and 24 weeks are given in Tables: 7.6 -7.7.

Table 7.6 Mean value per clone for all measured traits in 2 lime levels at 18weeks.

CLONES	H12 (cm)				D12 (mm)				Sm12 (grams)				Rm12 (grams)				R12			
	L0		L1		L0		L1		L0		L1		L0		L1		L0		L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	51.9	10.0	48.8	10.2	4.45	0.80	4.71	0.93	7.98	1.59	7.33	2.41	6.69	1.29	4.84	3.36	1.24	0.34	1.99	0.98
AG2	48.4	8.5	47.3	8.3	4.07	0.77	3.89	0.66	6.47	1.85	5.96	1.52	2.45	0.61	3.26	1.09	2.64	0.18	2.11	1.26
AG3-A	46.8	11.3	45.8	10.9	3.74	0.91	3.86	1.02	4.06	1.02	5.68	3.43	2.47	1.35	2.11	1.28	1.96	0.88	3.01	1.28
AG3-B	49.2	9.4	47.6	8.3	4.22	0.86	4.29	0.86	9.75	2.23	8.01	2.08	3.86	1.28	3.56	0.97	2.59	0.37	2.29	0.45
AG4	45.1	8.7	46.6	9.8	4.00	0.89	4.26	0.88	5.74	1.22	7.17	0.91	3.31	0.98	3.59	0.66	1.81	0.51	2.05	0.53
AG5	46.3	10.4	44.6	12.1	4.10	0.96	3.92	1.13	4.77	1.04	6.17	3.02	3.08	1.28	2.56	0.95	1.64	0.33	2.59	1.15
AG6	55.3	9.9	54.7	9.6	4.35	0.85	4.53	0.77	7.85	0.75	8.47	3.74	5.05	1.90	3.96	0.96	1.71	0.59	2.12	0.59
AG7	50.5	8.7	47.8	11.4	4.09	0.95	3.91	0.85	6.93	3.36	5.23	3.49	3.87	2.74	2.61	0.62	2.05	0.57	1.89	1.09
AG8	55.1	8.8	54.2	9.8	4.36	0.98	4.25	0.87	5.33	2.75	6.38	3.19	2.37	1.46	3.76	3.29	2.37	0.45	2.23	1.06
AG9	44.7	9.1	46.2	7.6	4.28	0.96	4.45	0.71	6.45	3.65	5.77	2.85	4.05	2.58	4.02	2.58	1.79	1.35	1.59	0.57
AG10	45.5	9.3	44.3	9.9	4.13	0.93	4.04	0.88	5.67	1.86	7.35	3.01	4.13	1.95	3.23	1.08	1.54	0.58	2.24	0.35
AG11	50.4	8.2	50.8	7.9	4.31	0.88	4.39	0.95	5.06	4.95	7.32	0.45	3.40	1.54	3.69	0.53	2.15	0.79	2.00	0.20
AG12	52.6	6.7	53.3	8.1	4.42	0.69	4.36	0.97	6.79	2.73	6.38	2.34	4.10	2.65	3.05	1.29	2.11	1.02	2.28	1.24
AG13	46.8	8.7	45.8	9.7	4.22	0.84	4.22	0.81	4.26	3.18	9.43	3.38	2.47	1.03	3.51	1.13	1.47	0.91	2.71	0.45
AG14	44.6	11.0	42.7	10.4	3.89	0.92	3.87	1.06	5.93	3.75	4.95	0.86	3.19	2.07	2.36	1.11	1.89	0.33	2.44	1.06
AG15	46.0	10.7	46.1	10.7	3.91	0.85	3.81	0.83	7.31	2.08	5.58	0.95	2.93	1.18	1.82	0.45	2.75	1.27	3.24	0.94
G1	46.4	9.7	42.7	8.1	3.77	0.98	3.78	0.81	6.93	2.73	3.98	0.65	5.43	3.66	2.13	0.70	1.49	0.58	2.07	0.83
GU1	42.5	10.2	44.3	8.8	4.13	0.99	4.45	0.79	7.76	1.91	8.42	2.89	3.90	1.27	4.95	1.20	2.04	0.35	1.75	0.66
GC1	53.5	10.6	55.5	9.7	4.02	0.78	4.17	0.65	6.69	1.61	8.98	3.08	5.22	3.18	4.85	1.47	1.64	0.78	1.86	0.32
GC2	51.5	10.2	51.7	9.3	4.33	0.86	4.44	0.89	8.36	2.94	6.52	1.06	7.183	2.90	4.28	1.58	1.20	0.25	1.73	0.78

Table 7.7. Mean value and standard errors per clone for all measured traits in 2 lime levels at 24 weeks.

CLONES	H24 (cm)				D24 (mm)				Sm24 (grams)				Rm24 (grams)				R24			
	L0		L1		L0		L1		L0		L1		L0		L1		L0		L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	74.4	16.1	68.3	16.8	5.87	0.95	5.81	0.94	17.21	4.02	15.96	3.22	13.75	5.84	13.27	3.78	1.74	0.45	1.38	0.30
AG2	68.9	14.9	63.0	12.4	5.18	0.74	4.98	1.20	14.06	2.24	13.29	2.89	8.09	0.98	10.35	2.58	1.78	0.09	1.78	0.29
AG3-A	68.3	19.1	64.0	13.7	5.41	1.07	5.36	0.87	15.55	3.66	14.22	2.65	10.80	1.55	11.07	1.92	1.43	0.61	1.55	0.30
AG3-B	67.8	18.1	62.7	15.4	5.74	1.12	5.62	0.95	16.56	3.66	15.14	2.95	12.47	2.46	11.61	3.99	1.79	0.27	1.49	0.34
AG4	60.7	16.3	61.9	14.0	5.52	1.18	5.66	0.96	14.49	3.55	14.50	2.83	11.27	2.82	10.07	1.09	1.25	0.27	1.56	0.23
AG5	65.4	17.1	65.8	16.2	5.31	0.91	5.23	1.14	14.68	2.96	13.83	3.25	14.48	3.21	10.01	1.22	1.33	0.37	1.54	0.27
AG6	78.4	19.2	75.3	16.4	5.76	1.16	5.68	0.98	16.30	4.19	15.57	3.21	14.55	5.58	13.44	5.18	1.59	0.44	1.48	0.29
AG7	68.4	15.8	63.8	15.6	5.41	1.14	5.09	1.04	14.68	3.47	13.27	2.92	12.29	4.46	10.15	3.19	1.39	0.19	1.37	0.26
AG8	72.7	17.1	68.3	15.3	5.38	1.15	5.15	0.92	15.45	3.85	13.65	2.64	12.04	4.94	11.83	1.99	1.73	0.37	1.33	0.14
AG9	66.3	16.5	60.4	13.1	5.73	0.96	5.68	1.21	15.32	3.28	13.84	2.65	14.57	5.24	14.94	2.53	1.34	0.72	1.06	0.14
AG10	69.0	20.1	63.6	16.5	5.66	1.10	5.42	1.36	15.55	6.16	14.11	3.02	11.12	3.73	10.17	1.85	1.52	0.55	1.34	0.16
AG11	69.6	14.8	65.1	14.1	5.61	1.17	5.50	0.93	16.36	3.66	14.40	3.14	15.96	1.67	10.83	2.49	1.42	0.22	1.59	0.29
AG12	68.3	12.1	68.4	10.6	5.65	0.90	5.59	0.84	15.72	2.99	15.14	2.89	13.46	3.52	12.27	3.88	1.46	0.38	1.38	0.25
AG13	68.5	20.3	64.3	17.6	5.78	1.17	5.47	1.06	17.08	4.31	14.75	3.07	10.57	0.99	13.26	3.19	1.76	0.19	1.23	0.20
AG14	59.7	14.9	58.3	14.8	5.29	1.02	5.24	1.04	14.13	2.76	12.98	2.63	12.58	4.66	9.66	2.78	1.22	0.35	1.25	0.27
AG15	67.8	19.6	65.6	17.5	5.13	0.87	4.85	0.92	15.13	2.82	13.68	3.08	9.13	1.52	10.46	1.43	1.94	0.21	1.53	0.54
G1	58.1	14.1	56.0	13.1	4.68	0.98	4.68	0.93	12.27	2.57	12.21	2.84	10.69	2.13	11.62	5.85	1.39	0.34	1.38	0.30
GU1	65.5	18.9	59.2	14.7	5.59	0.94	5.57	0.95	16.57	3.56	15.62	3.54	13.25	5.77	11.78	2.41	1.54	0.37	1.33	0.15
GC1	75.2	20.2	75.5	14.8	5.31	0.72	5.31	0.72	16.72	3.83	16.66	3.47	10.45	1.85	12.16	1.79	1.47	0.45	1.46	0.29
GC2	73.1	17.9	73.2	16.3	5.65	0.88	5.59	1.02	16.08	3.39	16.23	4.06	16.32	5.72	15.46	1.91	1.28	0.32	1.13	0.08

Appendix C

SOIL X LIME X CLONE

a)Height

Table 7.8. Mean height (cm) and standard errors per clone over 8 soils treatments at 12 weeks.

CLONES	SOIL TREATMENTS													
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	39.1	7.5	37.8	6.1	32.7	5.9	29.7	5.5	29.7	5.1	30.3	6.1	33.9	7.9	34.4	6.7
AG2	34.6	5.1	39.0	3.9	30.8	6.8	31.5	5.0	30.8	3.7	29.3	5.1	34.3	6.7	34.5	4.6
AG3-A	33.9	8.2	36.9	5.3	27.8	7.0	30.9	4.6	28.1	5.2	26.7	6.7	33.5	6.3	31.1	4.2
AG3-B	39.2	8.3	40.3	6.2	31.4	8.3	34.8	7.2	33.8	4.7	34.4	5.9	37.6	6.5	36.5	6.2
AG4	34.8	4.6	38.1	4.6	31.0	7.1	31.7	6.0	30.9	6.4	34.4	6.8	32.0	7.4	36.0	5.1
AG5	38.1	7.1	33.5	7.7	28.2	6.3	26.7	6.5	31.9	4.2	28.4	4.1	32.8	8.2	33.0	4.9
AG6	43.1	11.1	47.9	6.4	37.4	4.3	39.1	4.9	34.6	8.1	39.9	6.8	40.1	5.8	41.3	6.2
AG7	37.8	4.3	40.0	6.4	32.3	6.5	30.5	6.5	31.7	6.6	31.6	5.7	34.8	6.5	33.4	9.1
AG8	45.3	6.8	46.2	8.4	36.3	6.4	38.4	5.2	36.6	6.8	39.6	7.7	38.0	6.4	44.2	6.7
AG9	36.2	5.5	38.4	4.6	29.3	5.5	32.1	5.4	29.2	5.4	30.9	4.4	31.7	5.7	33.0	3.8
AG10	30.7	5.5	38.6	5.4	24.5	5.7	27.1	5.4	27.7	5.2	25.7	5.5	31.3	6.5	31.1	6.6
AG11	42.8	7.8	44.8	6.9	39.3	5.9	40.6	5.8	35.1	7.1	38.9	3.9	43.2	5.1	42.5	6.7
AG12	45.7	6.3	46.4	6.3	43.3	5.5	42.3	7.5	39.1	5.0	37.7	6.6	46.1	4.9	43.9	6.6
AG13	37.0	7.1	36.0	5.3	29.7	4.7	31.4	4.5	28.2	4.5	30.9	6.8	34.1	4.3	34.0	5.5
AG14	32.2	4.9	33.5	3.6	29.0	5.8	26.6	6.7	29.7	7.3	26.9	6.6	28.8	4.4	29.7	7.1
AG15	36.5	5.6	35.6	5.7	29.9	9.4	27.3	5.2	27.5	4.5	27.8	4.3	32.4	4.9	34.2	4.3
G1	36.8	7.8	35.8	4.6	32.9	5.2	31.6	3.4	29.6	4.5	27.3	5.1	34.9	4.3	32.4	5.4
GU1	33.9	8.2	35.7	7.7	27.7	6.5	31.0	5.5	25.1	5.5	30.0	5.3	32.0	5.1	33.1	7.1
GC1	41.4	6.7	45.5	8.1	35.4	7.1	37.3	5.8	35.2	5.3	38.4	5.8	40.6	5.8	40.6	5.8
GC2	39.9	7.9	41.9	8.1	38.0	8.9	41.1	6.1	34.4	8.5	34.7	5.0	39.9	7.31	39.4	8.3

Table 7.9 Mean height (cm) and standard errors per clone over 8 soil treatments at 18 weeks.

CLONES	SOIL TREATMENTS													
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	55.9	12.5	53.5	10.8	51.8	10.2	45.9	8.3	47.1	7.2	44.8	12.4	52.8	8.1	50.3	7.4
AG2	52.5	10.0	53.6	7.1	46.7	7.2	46.2	8.2	45.1	6.9	41.3	7.7	49.2	8.4	47.3	5.7
AG3-A	49.6	13.3	52.4	7.5	43.3	11.6	46.5	6.1	44.4	7.2	36.8	15.1	49.8	11.5	45.6	9.2
AG3-B	53.1	8.8	49.8	7.8	45.7	12.1	45.8	8.3	48.3	8.1	46.3	8.1	49.6	6.9	48.0	8.9
AG4	48.9	8.7	49.4	7.5	45.0	10.3	42.9	10.4	43.8	8.0	47.4	12.1	42.7	6.6	46.7	8.8
AG5	51.5	7.5	48.9	14.5	43.5	10.5	39.9	11.5	45.1	7.5	44.5	7.9	45.2	13.7	45.2	12.0
AG6	54.6	12.8	58.2	8.3	53.3	9.0	51.4	7.4	56.4	8.7	55.3	9.7	56.9	8.9	54.0	12.0
AG7	53.4	9.1	53.4	8.3	49.4	9.8	46.0	9.6	49.4	6.4	41.8	10.8	50.0	9.4	49.3	13.9
AG8	58.1	9.4	57.0	8.9	54.6	8.0	50.2	10.5	52.5	8.8	53.9	6.6	55.2	8.6	55.8	11.6
AG9	50.8	7.5	50.4	7.3	42.1	9.9	43.5	6.2	42.3	8.7	43.8	8.2	43.6	9.7	45.0	7.4
AG10	45.2	11.9	48.1	8.4	42.1	9.7	41.6	10.4	47.4	7.3	41.5	7.7	47.3	7.2	45.6	11.6
AG11	54.0	7.1	54.3	8.9	50.2	8.3	49.7	7.9	45.6	8.8	47.3	7.8	51.9	6.6	51.5	5.6
AG12	55.4	5.7	56.4	6.7	51.9	7.6	53.5	7.4	49.8	7.7	48.5	9.3	53.3	4.7	54.1	7.4
AG13	50.7	10.1	51.4	9.2	44.4	5.8	43.2	8.4	42.6	9.1	42.6	10.5	49.9	7.2	45.9	8.7
AG14	47.8	14.7	45.2	8.6	40.8	9.3	40.6	10.2	45.6	7.4	41.1	10.1	44.4	11.1	43.8	12.6
AG15	48.5	11.3	51.2	8.0	45.2	13.7	41.1	9.8	41.5	8.2	42.4	12.1	49.1	7.7	49.2	10.1
G1	51.8	13.2	47.4	9.6	43.7	9.8	42.2	4.8	43.8	5.8	36.2	5.9	46.0	6.5	44.3	7.3
GU1	47.7	13.4	49.0	7.9	37.6	8.6	40.1	6.2	39.8	5.8	43.4	9.8	44.9	8.8	44.5	9.6
GC1	58.5	11.2	59.7	11.9	51.5	12.5	53.4	9.7	49.8	8.7	51.2	7.5	53.9	7.9	57.2	6.7
GC2	55.2	9.6	56.7	8.7	48.9	11.1	52.6	6. 8	48.4	9.4	45.1	7.7	53.6	9.8	51.7	10.5

Table 7.10 Mean height (cm) and standard errors per clone over 8 soils treatments at 24 weeks.

CLONES	SOIL TREATMENTS															
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	76.2	20.4	75.4	20.0	72.5	16.6	65.6	11.3	74.6	12.7	63.6	18.8	73.9	14.4	67.7	14.7
AG2	76.9	16.1	71.7	11.9	66.3	15.0	59.9	10.3	61.9	13.7	57.1	12.3	70.7	11.5	62.3	10.9
AG3-A	81.0	22.9	70.7	15.4	61.8	17.5	57.6	9.7	64.6	14.2	63.1	13.2	66.6	16.8	64.3	13.2
AG3-B	78.7	18.5	61.0	14.1	60.1	19.3	59.5	17.1	68.9	15.7	66.9	14.4	63.6	13.8	65.1	15.7
AG4	68.7	15.8	64.8	12.9	56.3	17.8	55.7	13.2	60.1	14.4	68.5	15.5	57.5	15.2	59.4	12.6
AG5	73.4	17.9	71.6	19.1	62.6	16.5	61.5	11.7	59.6	12.9	60.3	15.3	66.1	18.7	69.3	16.1
AG6	86.8	25.6	82.1	17.4	72.5	18.7	71.5	14.2	74.1	14.9	73.7	16.2	80.5	14.2	73.7	17.1
AG7	75.7	17.2	69.1	15.7	68.4	19.4	60.9	9.5	64.8	9.7	59.7	17.5	64.4	14.4	64.6	18.2
AG8	78.9	20.9	74.1	11.1	73.6	15.8	65.1	13.8	66.6	13.7	62.1	11.2	71.6	17.0	71.3	20.7
AG9	74.0	17.4	63.1	12.4	63.7	15.8	55.8	13.2	60.7	14.6	62.8	11.9	66.9	16.1	60.3	14.3
AG10	70.1	28.5	68.1	16.9	66.4	19.2	62.2	20.9	69.1	16.4	57.8	12.6	70.6	14.9	65.7	12.4
AG11	77.9	17.4	74.2	10.2	67.1	15.2	60.3	13.9	64.3	11.8	63.2	12.3	68.5	11.2	62.9	15.8
AG12	73.6	13.4	71.9	9.5	66.9	10.0	64.1	9.7	64.4	12.3	65.5	10.4	68.4	11.6	70.0	11.7
AG13	79.0	24.9	74.9	14.2	61.3	16.2	57.6	16.9	58.2	13.3	59.4	16.5	74.8	18.0	65.2	18.6
AG14	67.1	19.1	61.2	15.6	52.8	14.5	56.81	14.3	59.5	11.7	57.3	14.6	59.7	10.0	57.6	15.8
AG15	74.7	19.7	72.6	17.1	66.6	21.2	63.6	15.4	55.5	18.9	54.9	19.7	73.7	13.5	68.8	14.6
G1	65.0	13.9	63.8	13.3	56.3	15.7	49.8	10.7	55.5	12.9	54.3	13.2	55.7	12.7	56.1	12.2
GU1	74.7	22.6	64.0	12.7	57.3	18.1	53.6	11.0	62.2	14.8	57.4	13.1	67.5	16.3	61.5	19.5
GC1	85.8	23.5	80.8	13.6	75.4	16.7	72.2	12.6	65.5	16.4	68.5	14.1	73.8	19.6	79.8	16.5
GC2	82.1	16.4	80.9	13.2	65.8	18.7	69.4	13.2	68.4	15.9	66.8	20.2	75.9	17.2	74.6	16.3

b) Diameter

Table 7.11. Mean diameter (mm) and standard errors per clone over 8 soil treatments at 12 weeks.

CLONES	SOIL TREATMENTS													
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	3.24	0.61	3.76	0.63	3.39	0.56	3.16	0.52	3.04	0.53	3.13	0.47	3.11	0.84	3.48	0.52
AG2	3.09	0.47	3.36	0.55	2.59	0.44	2.89	0.61	2.76	0.49	2.48	0.41	2.89	0.45	2.79	0.61
AG3-A	2.62	0.64	3.38	0.45	2.38	0.65	2.43	0.65	2.59	0.52	2.38	0.71	2.86	0.58	2.82	0.43
AG3-B	3.39	0.73	3.78	0.83	2.84	0.76	2.89	0.56	2.96	0.93	2.87	0.41	2.93	0.65	2.99	0.67
AG4	3.07	0.36	3.51	0.87	2.89	0.51	2.62	0.55	2.94	0.68	2.67	0.42	2.89	0.68	3.24	0.54
AG5	3.55	0.63	3.26	0.92	2.84	0.65	2.52	0.47	3.02	0.48	2.89	0.63	3.01	0.58	2.92	0.72
AG6	3.45	0.76	3.93	1.00	2.98	0.37	3.07	0.57	2.87	0.52	3.19	0.58	3.35	0.63	3.16	0.49
AG7	3.14	0.53	3.34	0.73	2.77	0.37	2.69	0.52	2.61	0.49	2.56	0.49	2.99	0.75	2.86	0.72
AG8	3.93	0.51	3.51	0.71	2.79	0.62	2.99	0.45	3.07	0.63	2.99	0.57	3.21	0.79	3.35	0.69
AG9	3.63	0.62	3.63	0.49	2.85	0.58	3.05	0.61	2.72	0.57	2.77	0.54	2.88	0.57	2.99	0.41
AG10	2.98	0.61	3.53	0.60	2.57	0.79	2.47	0.56	2.59	0.53	2.41	0.58	2.84	0.54	2.91	0.63
AG11	3.60	0.62	3.79	0.66	3.03	0.47	3.23	0.58	2.81	0.64	2.89	0.51	3.68	0.59	3.34	0.54
AG12	3.35	0.67	3.55	0.72	3.04	0.44	3.05	0.56	2.80	0.44	2.77	0.62	3.59	0.61	3.51	0.50
AG13	3.35	0.70	3.26	0.70	3.05	0.84	2.97	0.37	2.64	0.38	2.79	0.49	3.07	0.53	3.19	0.53
AG14	3.04	0.76	3.24	0.57	2.56	0.83	2.48	0.73	2.63	0.61	2.18	0.52	2.69	0.53	2.64	0.52
AG15	3.16	0.74	3.06	0.52	2.66	0.71	2.45	0.56	2.63	0.58	2.37	0.48	2.87	0.53	2.89	0.58
G1	2.95	0.68	3.19	0.67	2.78	0.56	2.79	0.42	2.63	0.67	2.59	0.47	3.10	0.65	2.67	0.56
GU1	3.56	0.82	3.40	0.59	2.86	0.45	3.05	0.55	2.72	0.50	2.76	0.53	3.24	0.58	3.32	0.57
GC1	3.12	0.57	3.39	0.74	2.79	0.53	3.05	0.60	2.78	0.62	2.92	0.57	3.05	0.73	3.26	0.49
GC2	3.57	0.65	3.83	0.78	3.25	0.74	3.32	0.85	3.09	0.66	2.84	0.62	3.24	0.67	3.34	0.76

Table 7.12. Mean diameter (mm) and standard errors per clone over 8 soil treatments at 18 weeks.

CLONES	SOIL TREATMENTS															
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	4.60	0.68	5.05	0.81	4.47	0.75	4.45	0.83	4.06	0.63	4.38	0.66	4.64	1.03	4.91	1.19
AG2	4.45	0.75	4.26	0.59	3.84	0.79	3.92	0.41	3.71	0.59	3.26	0.54	4.27	0.75	4.06	0.67
AG3-A	3.84	0.96	4.51	0.57	3.28	0.71	3.74	0.58	3.72	0.66	3.03	1.27	4.11	1.11	4.01	1.05
AG3-B	4.84	0.77	4.61	0.75	4.03	0.92	4.20	0.82	3.79	0.72	4.22	0.87	4.22	0.67	4.14	0.97
AG4	4.56	0.80	4.73	0.58	3.66	0.70	3.78	0.74	3.47	0.85	3.97	0.93	4.28	0.81	4.52	0.96
AG5	4.38	0.91	4.35	1.45	3.84	1.12	3.39	0.74	4.03	0.73	3.89	0.76	4.16	1.05	4.06	1.19
AG6	4.37	0.88	4.99	0.69	4.29	0.69	4.19	0.63	3.98	0.97	4.67	0.75	4.75	0.72	4.27	0.78
AG7	4.28	0.97	4.39	0.48	3.79	0.82	3.76	0.65	4.20	0.99	3.43	0.84	4.08	1.02	3.98	1.10
AG8	4.93	0.67	4.64	0.96	3.84	0.74	3.86	0.63	3.73	0.78	3.97	0.73	4.93	1.03	4.51	0.89
AG9	4.93	0.78	4.73	0.69	4.08	1.02	4.10	0.66	3.99	0.74	4.24	0.72	4.13	1.00	4.70	0.56
AG10	4.57	1.18	4.39	0.84	3.66	0.77	3.88	0.70	3.82	0.48	3.58	0.59	4.46	0.81	4.25	1.09
AG11	4.73	0.98	4.72	1.24	4.15	0.61	4.09	0.52	3.70	0.93	3.89	0.62	4.63	0.62	4.79	0.92
AG12	4.52	0.78	4.91	0.58	4.38	0.52	4.22	0.79	4.02	0.56	3.61	0.88	4.76	0.70	4.62	1.11
AG13	4.73	0.76	4.51	0.96	4.12	0.68	4.11	0.79	3.57	0.74	3.93	0.72	4.49	0.75	4.32	0.68
AG14	4.05	1.06	4.25	0.81	3.56	0.92	3.57	1.07	3.92	0.64	3.55	0.64	4.03	0.98	4.09	1.42
AG15	4.06	1.02	4.13	0.50	3.59	0.92	3.55	0.77	3.62	0.62	3.21	0.59	4.37	0.53	4.28	0.95
G1	3.92	0.95	4.23	0.80	3.46	1.27	3.77	0.55	3.52	0.69	3.27	0.78	4.22	0.78	3.81	0.84
GU1	4.51	0.81	4.74	0.73	3.78	0.93	4.05	0.73	3.79	1.08	4.17	0.82	4.46	0.97	4.81	0.64
GC1	4.28	0.57	4.30	0.77	3.83	1.08	4.02	0.45	3.64	0.58	3.91	0.58	4.31	0.59	4.42	0.67
GC2	4.56	0.83	4.92	0.94	4.22	0.83	4.16	0.69	3.87	0.59	3.87	0.78	4.65	0.98	4.72	0.81

Table 7.13. Mean diameter (mm) and standard errors per clone over 8 soil treatments at 24 weeks.

CLONES	SOIL TREAMENTS													
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err
AG1	5.91	1.37	6.28	1.03	5.76	0.73	5.29	0.59	5.77	0.72	5.43	0.73	6.05	0.85	6.13	0.96
AG2	5.47	0.63	5.43	0.59	5.00	0.95	5.26	1.85	4.98	0.65	4.21	0.88	5.28	0.62	4.92	0.75
AG3-A	5.86	0.93	5.83	0.79	4.88	1.26	4.77	0.91	5.17	0.86	5.37	0.82	5.76	0.99	5.46	0.58
AG3-B	6.46	1.04	5.45	1.01	5.46	1.24	5.58	1.04	5.44	1.01	5.66	0.98	5.56	0.88	5.83	0.79
AG4	6.30	0.81	6.38	0.81	5.31	1.12	5.13	0.99	5.13	1.27	5.51	0.91	5.32	1.19	5.52	0.74
AG5	5.69	0.88	5.74	1.05	5.01	0.95	4.59	0.98	4.94	0.82	5.17	1.13	5.62	0.77	5.36	1.18
AG6	6.23	1.10	5.94	1.07	5.44	1.04	5.56	0.96	5.17	1.38	5.62	0.78	6.18	0.78	5.61	1.09
AG7	6.09	1.16	5.63	0.75	5.10	1.17	4.74	0.89	5.17	0.83	4.69	0.95	5.28	1.16	5.21	1.27
AG8	5.90	1.12	5.48	0.61	5.21	1.04	4.73	1.01	4.89	1.38	4.79	0.68	5.51	0.79	5.58	0.97
AG9	6.45	0.94	5.72	0.69	5.59	0.83	5.45	0.86	5.18	0.94	5.56	2.11	5.68	0.71	5.97	0.89
AG10	5.83	1.16	5.52	1.03	5.23	1.21	5.65	2.08	5.46	0.98	4.82	0.81	6.13	0.87	5.58	0.97
AG11	6.23	0.86	6.05	0.76	5.05	1.43	5.42	0.94	5.11	1.06	5.06	0.92	6.00	0.85	5.44	0.90
AG12	5.59	0.78	5.89	0.73	5.45	0.85	5.12	0.72	5.39	0.81	5.35	0.77	6.17	0.99	5.96	0.88
AG13	6.20	1.24	5.91	1.01	5.22	1.29	5.06	0.87	5.42	0.94	5.23	1.07	6.27	0.84	5.68	1.15
AG14	5.72	1.13	5.60	1.01	4.61	1.15	4.94	0.85	5.21	0.63	4.95	0.78	5.67	0.71	5.39	1.31
AG15	5.54	0.63	5.12	0.73	4.91	1.12	4.58	0.71	4.73	0.77	4.27	1.21	5.32	0.73	5.29	0.69
G1	5.12	0.81	5.17	0.65	4.36	1.31	4.38	0.76	4.36	0.59	4.41	0.88	4.88	0.94	4.74	1.20
GU1	6.11	1.11	5.88	0.92	5.38	0.95	5.13	0.82	5.17	0.78	5.18	0.58	5.69	0.64	5.99	1.07
GC1	5.59	0.93	5.63	0.71	5.27	0.78	5.11	0.63	4.78	0.77	4.87	0.63	5.56	0.92	5.59	0.68
GC2	6.11	0.80	6.14	0.87	5.35	0.74	5.24	0.73	5.29	0.76	5.00	0.91	5.86	0.98	5.87	1.16

c)Root and shoot mass

Table 7.14. Mean shoot and root mass per clone over 8 soil treatments at 12 weeks for only one replication.

	SOIL TREATMENTS															
	Sm 12 (gm)								Rm12 (gm)							
CLONES	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1
AG1	5.40	2.61	3.36	2.89	4.10	1.81	2.91	2.42	4.20	1.26	3.64	1.80	3.46	2.56	3.14	1.88
AG2	3.03	4.48	2.40	1.25	1.78	1.68	2.12	3.09	1.16	2.15	1.72	0.48	0.77	0.61	0.96	1.12
AG3-A	1.73	3.63	2.74	2.53	1.24	0.87	2.20	2.62	1.20	7.34	1.11	1.15	1.03	0.54	1.12	1.50
AG3-B	4.03	5.56	4.48	3.45	1.22	2.54	2.85	5.56	1.63	2.40	1.09	1.38	0.72	1.05	1.83	2.11
AG4	4.61	5.50	3.38	2.30	2.41	2.46	2.76	4.00	3.55	3.74	1.69	1.59	1.33	1.27	1.41	1.77
AG5	5.25	5.46	3.51	2.60	1.80	3.16	3.08	3.78	3.11	1.90	1.76	0.93	1.06	1.40	1.57	1.41
AG6	1.67	5.60	2.78	3.47	1.25	2.46	3.12	2.19	0.65	2.55	1.44	1.51	0.54	1.70	2.85	1.39
AG7	3.26	3.92	1.49	2.07	1.20	2.02	2.73	1.02	1.04	1.78	0.75	0.92	0.49	0.95	2.00	0.86
AG8	3.72	4.41	2.20	2.35	2.08	2.18	3.13	3.66	1.52	2.02	2.22	1.17	1.27	1.43	2.34	1.56
AG9	4.41	4.00	1.80	3.37	2.43	3.19	3.84	3.42	2.41	1.43	1.95	1.54	1.70	2.03	2.69	2.19
AG10	3.81	5.13	2.05	2.18	2.04	1.56	2.93	3.07	1.70	2.45	0.80	0.92	1.14	1.38	1.21	1.82
AG11	3.92	5.77	3.40	3.94	1.55	3.44	2.32	2.52	2.58	3.24	1.00	1.50	1.24	1.15	2.13	1.26
AG12	3.67	5.07	2.92	2.84	2.13	2.01	5.51	4.97	2.41	2.05	1.40	1.20	2.13	0.54	2.23	2.08
AG13	2.15	3.69	2.00	2.53	1.32	2.17	4.10	2.95	1.18	2.15	1.59	1.55	1.29	1.38	2.70	2.55
AG14	4.13	3.78	3.59	1.67	2.85	.	0.99	3.04	1.55	1.27	1.14	0.74	0.95	.	0.72	1.01
AG15	5.17	3.67	2.84	1.88	2.80	2.50	1.64	1.72	1.82	0.97	1.45	0.55	1.39	1.23	0.92	0.80
G1	3.10	4.64	3.02	2.28	1.35	3.28	3.08	3.18	1.28	2.06	1.04	1.14	1.51	1.73	1.62	1.34
GU1	5.76	5.83	3.89	3.74	1.44	2.84	3.93	4.94	4.36	2.91	1.58	1.30	0.90	2.12	2.47	2.84
GC1	5.21	5.13	4.86	3.95	3.18	2.06	4.33	2.72	3.25	3.96	4.46	2.45	2.48	1.07	3.04	1.46
GC2	8.15	3.93	4.91	4.71	1.65	3.09	2.98	2.94	3.84	0.93	3.71	2.23	3.70	1.64	1.29	1.40

Table 7.15. Mean shoot and root mass per clone over 8 soil treatments at 18 weeks for only one replication.

CLONES	SOIL TREATMENTS															
	Sm 18 (gm)								Rm18 (gm)							
	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1
AG1	8.36	9.62	7.55	4.45	6.11	6.26	9.93	8.98	5.41	3.28	5.85	1.800	8.20	9.56	7.30	4.73
AG2	8.98	6.93	5.80	4.54	4.60	4.78	6.49	7.59	3.22	1.75	2.44	3.960	1.73	3.19	2.39	4.16
AG3-A	4.12	10.63	2.88	3.40	3.87	5.36	5.37	3.34	1.34	3.69	1.45	0.700	4.21	2.50	2.87	1.56
AG3-B	12.60	11.03	8.38	7.73	10.40	6.88	7.62	6.41	5.64	4.78	3.61	3.110	3.63	2.53	2.57	3.84
AG4	5.86	8.51	6.97	6.80	6.06	6.93	4.05	6.45	4.77	3.07	2.96	3.800	2.88	4.45	2.62	3.07
AG5	4.58	10.66	3.87	4.41	6.26	4.33	4.33	5.28	3.14	3.03	1.92	1.200	4.85	2.65	2.42	3.36
AG6	8.46	13.51	7.18	5.83	8.54	9.13	7.21	5.43	7.46	5.15	2.83	2.840	5.17	3.68	4.72	4.17
AG7	5.20	9.47	6.39	5.80	4.34	0.97	11.82	4.70	2.05	3.04	4.08	3.240	1.70	2.04	7.68	2.13
AG8	6.85	10.40	2.03	2.74	4.23	6.95	8.21	5.45	3.29	3.34	0.89	1.360	1.39	8.54	3.92	1.82
AG9	9.78	9.12	1.29	2.96	7.89	7.09	6.84	3.92	2.58	4.01	1.47	1.650	7.31	7.61	4.84	2.82
AG10	5.93	10.74	3.70	5.07	4.94	4.57	8.10	9.03	3.80	4.71	2.06	2.420	6.77	2.44	3.88	3.35
AG11	12.95	7.58	7.92	6.66	1.31	7.37	10.08	7.66	4.17	4.35	4.12	3.220	1.09	3.31	4.23	3.89
AG12	8.88	8.94	6.38	7.58	3.10	5.35	8.83	3.66	7.32	2.17	3.73	4.940	0.97	2.87	4.48	2.24
AG13	10.20	12.11	5.95	7.88	3.42	5.38	7.48	12.33	1.21	4.31	2.78	3.850	2.23	1.84	3.67	4.03
AG14	8.55	5.06	2.57	4.37	9.73	4.25	2.85	6.13	4.31	1.37	1.68	1.480	5.53	2.95	1.24	3.63
AG15	9.52	6.22	7.65	5.16	4.48	4.44	7.60	6.50	4.52	1.62	1.67	1.340	2.58	2.38	2.94	1.92
G1	10.89	3.52	5.70	4.93	6.39	3.87	4.72	3.59	10.75	1.10	2.71	2.250	3.39	2.55	4.87	2.60
GU1	8.64	12.10	5.06	8.09	7.89	5.04	9.46	8.46	5.54	4.76	2.46	6.700	3.62	4.19	3.98	4.13
GC1	8.87	8.94	6.95	7.04	5.69	6.59	5.28	13.35	4.93	4.73	4.15	3.220	9.65	4.64	2.13	6.79
GC2	11.76	7.46	6.17	7.07	5.66	5.03	9.86	6.51	10.96	3.05	4.09	3.070	6.07	6.37	7.61	4.66

Table 7.15a. Mean shoot and respective standard errors per clone over 8 soil treatments at 24 weeks for 18 replications.

	SOIL TREATMENTS															
	SHOOT MASS 24 (gm)															
	S1L0		S1L1		S2L0		S2L1		S3L0		S3L1		S4L0		S4L1	
CLONES	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	Std Err	Mean	td Err
AG1	18.02	5.35	18.31	3.73	15.85	2.10	13.86	2.55	17.96	3.62	14.86	2.36	17.13	4.28	16.6	2.3
AG2	16.02	1.95	16.09	1.61	13.25	2.13	11.98	1.21	12.92	1.92	11.03	2.36	14.11	1.68	13.51	3.15
AG3-A	18.06	3.16	15.82	2.1	13.59	3.22	12.29	1.99	15.03	2.85	14.03	1.73	15.68	4.08	14.69	3.01
AG3-B	19.98	3.08	14.62	2.03	15.31	3.77	14.94	2.45	15.21	3.23	14.85	2.27	15.70	2.27	16.27	4.51
AG4	17.93	2.55	17.00	2.15	13.81	3.02	12.56	2.79	12.91	2.97	13.89	2.09	13.42	3.38	14.19	2.28
AG5	17.21	2.80	16.45	3.30	13.46	2.56	11.65	1.88	13.34	2.28	12.36	2.27	14.68	2.49	14.53	2.99
AG6	19.32	5.05	16.87	3.35	14.64	2.99	14.34	2.18	14.32	3.64	15.44	3.53	17.08	3.05	15.58	3.43
AG7	17.07	3.51	15.24	2.11	13.36	2.88	12.15	2.39	13.97	2.11	11.44	1.81	14.36	4.16	13.65	3.57
AG8	19.27	3.51	15.16	1.79	14.77	3.29	12.28	2.37	12.83	2.84	12.59	1.86	15.17	2.85	14.50	3.19
AG9	18.46	2.99	14.74	1.96	14.29	2.86	12.43	2.17	13.74	2.96	12.44	2.45	14.89	2.08	15.42	2.71
AG10	17.42	2.92	15.34	3.54	14.15	2.50	13.87	3.18	14.30	2.91	12.19	1.54	16.34	3.24	14.75	2.52
AG11	19.99	2.61	17.14	3.47	15.47	2.98	13.25	1.34	13.81	2.91	12.08	2.07	16.08	3.26	14.87	2.79
AG12	16.48	3.32	17.01	2.85	14.51	2.66	13.29	2.48	15.55	2.55	13.74	2.08	16.39	3.22	16.25	2.22
AG13	20.52	5.61	17.11	2.81	14.37	3.08	12.86	2.14	15.92	2.53	13.47	2.96	17.47	2.78	15.40	2.61
AG14	15.82	3.78	14.88	2.62	12.87	2.53	11.69	1.37	13.82	1.78	11.69	1.71	14.09	1.85	13.36	3.03
AG15	17.22	2.89	16.33	2.33	14.29	1.88	12.38	1.48	13.91	3.23	10.57	2.72	15.09	2.06	14.83	2.22
G1	13.81	2.82	14.37	2.64	11.75	2.64	11.05	1.99	11.38	1.39	10.91	1.64	12.24	2.71	12.32	3.33
GU1	19.46	3.76	16.57	2.15	15.14	3.39	13.87	2.43	14.80	2.06	14.36	2.07	16.82	2.98	17.48	5.18
GC1	18.89	4.56	19.39	3.77	16.20	2.74	15.06	2.23	14.76	2.86	13.77	1.94	17.13	3.97	17.99	2.40
GC2	18.75	2.53	18.07	3.23	14.80	2.58	13.97	2.41	14.64	2.98	14.13	3.18	16.14	3.85	18.12	4.88

Table 7.16. Mean root mass for (one replication) and number of branches (18 replications) per clone over 8 soil treatments at 24 weeks.

CLONES	SOIL TREATMENTS															
	Rm 24 (gm)								Number of branches 24							
	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1	S1L0	S1L1	S2L0	S2L1	S3L0	S3L1	S4L0	S4L1
AG1	21.9	15.66	8.11	8.60	12.25	16.94	12.68	11.88	8.2	10.2	6.9	6.5	9.4	7.5	9.7	8.4
AG2	8.2	9.59	9.36	8.71	7.81	8.90	7.01	14.19	14.7	13.0	9.3	9.3	9.8	8.8	11.8	11.2
AG3-A	10.3	12.76	10.05	12.70	9.72	9.60	13.09	9.22	14.4	14.6	9.9	9.8	11.6	12.6	13.1	13.4
AG3-B	15.5	7.03	10.00	16.52	13.27	10.27	11.08	12.62	16.4	13.1	10.3	13.2	11.8	13.9	12.5	11.6
AG4	14.1	10.94	12.75	10.12	10.64	8.50	7.61	10.73	11.1	7.8	6.9	6.7	9.0	7.8	9.2	9.2
AG5	14.5	9.10	10.64	9.47	14.24	9.30	18.48	11.80	10.2	13.6	6.3	7.9	6.0	8.4	11.6	12.8
AG6	18.56	21.10	9.49	10.37	10.00	10.20	20.13	12.08	14.1	12.0	9.7	9.2	9.3	95	11.6	10.0
AG7	18.14	14.50	7.40	2.71	11.02	7.06	12.60	10.35	12.0	9.7	6.9	5.7	7.6	5.1	9.4	7.0
AG8	19.38	12.05	8.73	11.29	9.76	9.58	10.28	14.38	11.0	10.7	9.1	7.3	6.6	6.5	10.5	11.3
AG9	13.09	18.14	18.94	14.36	18.46	15.24	7.80	12.02	16.7	13.6	10.8	10.4	11.2	11.2	12.6	14.2
AG10	9.71	12.33	7.11	9.27	15.95	10.97	11.72	8.13	14.5	15.8	9.7	11.6	10.8	9.7	13.5	13.0
AG11	15.73	13.75	14.41	11.17	.	7.68	17.74	10.71	16.3	13.0	9.0	9.4	9.0	9.5	13.2	10.1
AG12	16.21	10.85	12.27	18.04	9.01	9.65	16.36	10.53	11.5	13.4	9.6	7.9	10.6	9.8	12.9	13.7
AG13	10.71	14.26	10.95	10.17	9.16	17.30	11.47	11.32	13.6	15.1	8.4	9.6	9.9	11.1	12.4	12.1
AG14	16.00	13.25	8.63	10.37	17.19	8.05	8.51	6.96	17.6	15.7	8.7	9.2	13.0	13.4	13.1	15.5
AG15	10.07	9.19	7.63	10.99	8.05	12.24	10.75	9.43	17.2	16.1	11.8	11.5	12.6	9.1	16.1	16.5
G1	.	9.70	13.02	8.14	10.20	8.32	8.85	20.33	10.6	11.4	8.3	8.7	6.5	9.6	8.9	7.3
GU1	18.21	14.48	18.27	9.32	8.51	13.09	8.00	10.23	12.5	11.5	9.3	9.7	10.2	10.2	11.0	11.4
GC1	12.38	14.71	11.11	11.31	10.33	10.61	7.99	12.01	4.8	5.5	2.7	2.0	2.5	2.5	5.5	6.0
GC2	20.63	14.78	10.48	14.12	21.79	14.64	12.39	18.29	9.4	10.5	5.3	6.1	4.5	5.5	8.0	9.5

Appendix D

a) Height

Table 7.17. Clonal mean by soil treatment for height at 12 weeks used to generate regression coefficients.

SOIL TMS	TRIAL MEAN H12 PER SOIL TMTS. (cm)	MEAN H12 PER CLONE (cm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	37.9	39.1	34.6	33.9	39.2	34.8	38.1	43.1	37.8	45.3	36.2	30.7	42.8	45.7	37.0	32.2	36.5	36.8	33.9	41.4	39.9
ST2	39.6	37.8	39.0	36.9	40.3	38.1	33.5	47.9	40.0	46.2	38.4	38.6	44.8	46.4	36.0	33.5	35.6	35.8	35.7	45.5	41.9
ST3	32.3	32.7	30.8	27.8	31.4	31.0	28.2	37.4	32.3	36.3	29.3	24.5	39.3	43.3	29.7	29.0	29.9	32.9	27.7	35.4	38.0
ST4	33.1	29.7	31.5	30.9	34.8	31.7	26.7	39.1	30.4	38.4	32.1	27.1	40.6	42.3	31.4	26.6	27.3	31.6	31.0	37.3	41.1
ST5	31.5	29.7	30.8	28.1	33.8	30.9	31.9	34.6	31.7	36.6	29.2	27.7	35.1	39.1	28.2	29.7	27.5	29.6	25.1	35.2	34.4
ST6	32.2	30.3	29.3	26.7	34.4	34.4	28.4	39.9	31.6	39.6	30.9	25.7	38.9	37.7	30.9	26.9	27.8	27.3	30.0	38.4	34.7
ST7	35.6	33.9	34.3	33.5	37.6	32.0	32.8	40.1	34.8	38.0	31.7	31.3	43.2	46.1	34.1	28.8	32.4	34.9	32.0	40.6	39.9
ST8	35.9	34.4	34.5	31.1	36.5	36.0	33.0	41.3	33.4	44.2	33.0	31.1	42.5	43.9	34.0	29.7	34.2	32.4	33.1	40.7	39.4

Table 7.18. Clonal mean by soil treatment for height at 18 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN H18 PER SOIL TMTS. (cm)	MEAN H18 PER CLONE (cm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	52.2	55.9	52.5	49.6	53.1	48.9	51.5	54.6	53.4	58.1	50.8	45.2	54.0	55.4	50.7	47.8	48.5	51.8	47.7	58.5	55.2
ST2	52.3	53.5	53.6	52.4	49.8	49.4	48.9	58.2	53.4	57.0	50.4	48.1	54.3	56.4	51.4	45.2	51.2	47.4	49.0	59.7	56.7
ST3	46.6	51.8	46.7	43.3	45.7	45.0	43.5	53.3	49.4	54.6	42.1	42.1	50.2	51.9	44.4	40.8	45.2	43.7	37.7	51.5	48.9
ST4	45.8	45.9	46.2	46.5	45.8	42.9	39.9	51.4	46.0	50.2	43.5	41.6	49.7	53.5	43.2	40.6	41.1	42.2	40.1	53.4	52.6
ST5	46.4	47.1	45.1	44.4	48.3	43.8	45.1	56.4	49.4	52.5	42.3	47.4	45.6	49.8	42.6	45.6	41.5	43.8	39.8	49.8	48.4
ST6	44.8	44.8	41.3	36.8	46.3	47.4	44.5	55.3	41.8	53.9	45.8	41.5	47.3	48.5	42.6	41.1	42.3	36.2	43.4	51.2	45.1
ST7	49.5	52.9	48.2	49.8	49.6	42.7	45.2	56.9	50.0	55.2	43.6	47.3	51.9	53.3	49.9	44.4	49.1	46.0	44.9	53.9	53.6
ST8	48.7	50.3	47.3	45.6	48.0	46.7	45.2	54.0	49.3	55.8	45.0	45.6	51.5	54.1	45.9	43.8	49.2	44.3	44.5	57.2	51.7

b) Diameter

Table 7.19. Clonal mean by soil treatments for diameter at 12 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN D12 PER SOIL TMTS (mm)	MEAN D12 PER CLONE (mm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	3.29	3.24	3.09	2.62	3.39	3.07	3.55	3.45	3.14	3.93	3.63	2.98	3.60	3.35	3.35	3.04	3.16	2.95	3.56	3.12	3.57
ST2	3.48	3.76	3.36	3.38	3.78	3.51	3.26	3.93	3.34	3.51	3.63	3.53	3.79	3.55	3.26	3.24	3.06	3.19	3.40	3.39	3.83
ST3	2.85	3.38	2.59	2.38	2.83	2.89	2.84	2.98	2.77	2.79	2.85	2.57	3.03	3.04	3.05	2.56	2.66	2.78	2.86	2.79	3.25
ST4	2.86	3.16	2.89	2.43	2.89	2.62	2.52	3.07	2.69	2.99	3.05	2.47	3.23	3.05	2.97	2.48	2.45	2.79	3.05	3.06	3.32
ST5	2.79	3.04	2.76	2.59	2.96	2.94	3.02	2.87	2.61	3.07	2.72	2.59	2.81	2.80	2.64	2.63	2.63	2.63	2.72	2.78	3.09
ST6	2.73	3.13	2.48	2.38	2.87	2.68	2.89	3.19	2.56	2.99	2.77	2.41	2.89	2.77	2.79	2.18	2.37	2.59	2.76	2.92	2.84
ST7	3.07	3.11	2.89	2.86	2.93	2.89	3.01	3.35	2.99	3.21	2.88	2.84	3.68	3.59	3.07	2.69	2.87	3.10	3.24	3.05	3.23
ST8	3.08	3.48	2.79	2.82	2.99	3.24	2.92	3.16	2.86	3.35	2.99	2.91	3.34	3.51	3.19	2.64	2.89	2.67	3.32	3.26	3.34

Table 7.20. Clonal mean by soil treatment for diameter at 18 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN D18 PER SOIL TMTS (mm)	MEAN D18 PER CLONE (mm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	4.46	4.60	4.45	3.84	4.84	4.56	4.38	4.37	4.28	4.93	4.93	4.57	4.73	4.52	4.73	4.05	4.06	3.92	4.51	4.28	4.56
ST2	4.57	5.05	4.26	4.50	4.60	4.73	4.35	4.99	4.39	4.64	4.73	4.39	4.72	4.91	4.51	4.25	4.13	4.23	4.74	4.30	4.92
ST3	3.89	4.47	3.84	3.28	4.03	3.67	3.84	4.29	3.79	3.84	4.08	3.66	4.15	4.38	4.12	3.57	3.59	3.46	3.78	3.83	4.22
ST4	3.94	4.45	3.92	3.74	4.20	3.78	3.39	4.19	3.76	3.86	4.10	3.88	4.09	4.22	4.11	3.57	3.55	3.77	4.05	4.02	4.16
ST5	3.81	4.06	3.71	3.71	3.79	3.47	4.02	3.98	4.20	3.73	3.99	3.82	3.70	4.01	3.58	3.92	3.62	3.52	3.79	3.64	3.88
ST6	3.80	4.38	3.26	3.03	4.22	3.97	3.89	4.66	3.43	3.97	4.24	3.58	3.89	3.61	3.93	3.55	3.21	3.27	4.17	3.92	3.87
ST7	4.39	4.64	4.27	4.11	4.22	4.28	4.16	4.75	4.08	4.93	4.12	4.46	4.63	4.76	4.49	4.03	4.37	4.21	4.46	4.31	4.65
ST8	4.36	4.91	4.06	4.01	4.14	4.52	4.06	4.27	3.98	4.51	4.70	4.25	4.79	4.62	4.32	4.09	4.28	3.81	4.81	4.42	4.72

Table 7.21. Clonal mean by soil treatment for diameter at 24 weeks used to generate regression coefficients.

SOIL TMTS	TRIAL MEAN D24 PER SOIL TMTS. (mm)	MEAN D24 PER CLONE (mm)																		
		AG1	AG2	AG3-A	AG3-B	AG4	AG5	AG6	AG7	AG8	AG9	AG10	AG11	AG12	AG13	AG14	AG15	G1	GU1	GC1	GC2
ST1	5.92	5.91	5.48	5.86	6.46	6.30	5.69	6.23	6.09	5.90	6.45	5.83	6.23	5.59	6.20	5.72	5.54	5.12	6.11	5.59	6.11
ST2	5.74	6.29	5.43	5.83	5.45	6.38	5.74	5.94	5.63	5.48	5.72	5.52	6.05	5.89	5.91	5.60	5.12	5.17	5.88	5.63	6.14
ST3	5.18	5.76	5.00	4.88	5.46	5.31	5.01	5.44	5.10	5.21	5.59	5.23	5.05	5.45	5.22	4.61	4.91	4.36	5.38	5.27	5.35
ST4	5.09	5.29	5.26	4.77	5.59	5.13	4.59	5.56	4.74	4.73	5.45	5.65	5.42	5.12	5.06	4.94	4.58	4.38	5.13	5.11	5.24
ST5	5.14	5.77	4.98	5.17	5.44	5.13	4.94	5.17	5.17	4.89	5.18	5.46	5.11	5.39	5.41	5.21	4.73	4.36	5.17	4.78	5.29
ST6	5.05	5.43	4.21	5.37	5.66	5.51	5.17	5.62	4.69	4.79	5.56	4.82	5.06	5.34	5.23	4.95	4.27	4.41	5.18	4.87	5.00
ST7	5.69	6.05	5.28	5.77	5.56	5.32	5.62	6.18	5.28	5.51	5.68	6.13	6.00	6.17	6.27	5.67	5.31	4.88	5.69	5.56	5.86
ST8	5.56	6.13	4.92	5.46	5.83	5.52	5.36	5.61	5.21	5.59	5.97	5.59	5.44	5.96	5.68	5.39	5.29	4.74	5.99	5.59	5.99

Appendix E

List of fellow graduate students and other friends who assisted at various stages during the research.

Table 7.22. Names and countries of origin of those who assisted me.

Name	*Country*
Carola Strobach	Namibia
Sarah Bristow	South Africa
Emita van Wyk	South africa
Esther Lusepani	Namibia
Nicky Michelle	South Africa
Frank Wils	Belgium
Lesego Motoma	Botswana
Cori Ham	South Africa
Ben Opperman	South Africa
Njeri Kimani	Kenya
Margaret Vyver	South Africa
Loren Gibbs	South Africa
Cremildo Rungo	Mozambique
Rusta Hangula	Namibia
Senast van Wyk	South Africa
Gerrit van Wyk	South Africa
Basjan van Aardt	South Africa
David Thomas	South Africa
Arnolds Isgaak	South Africa
Abrahams Alie	South Africa
Konrad Buchler	South Africa