THE INFLUENCE OF THE ENVIRONMENT ON THE VOLUME GROWTH, STEM FORM AND DISEASE TOLERANCE OF *EUCALYPTUS GRANDIS* CLONES IN THE SUMMER RAINFALL AREAS OF SOUTH AFRICA

by

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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: Date:

ABSTRACT

A thesis undertaken to quantify genotype-by-environment interaction within *Eucalyptus grandis* clones growing in the eastern portion of South Africa. Thirty one sites were selected to represent the "traditional" *E. grandis* growing areas of South Africa. Eleven common macro- site variables and twelve common micro- site soil variables were recorded at each site. Twenty seven *E. grandis* clones and four *E. grandis* hybrid clones were then evaluated over these 31 sites. An incomplete latin square design was used to evaluate the 31 test clones, and five *E. grandis* controls were incorporated into the trial design to link the 31 sites.

Volume production, stem form, stem defects and survival were assessed at two and five years, as well as the disease infestation of three stem cankers at five years. The analytical methods which were used to evaluate and quantify the GEI portion of the study are the analysis of variance (ANOVA), correlation analysis, and joint regression analysis (JRA) together with the analysis of co-variance (ACOVAR). The growth-site association for volume production, stem form and *Endothia* disease infestation were investigated using factor analysis (FA), and equations derived for the species and for the individual clones using a stepwise multiple regression approach.

GEI, as evaluated through JRA, revealed that an increase in site productivity lead to a positive linear response in productivity on a clonal level, and that there was a diverging or fanning pattern among the regression lines of the clones. This tendency was also observed for both the stem form and the *Endothia* infestation. Hence, no significant changes in the rankings of the clones were found, and only relevant differences between the clones were found to change significantly. Juvenile-mature genetic correlations for volume production and the stem form showed moderate ($r_g = 0,66$ and $r_g = 0,70$) correlations between the two and the five year assessments.

On a species level, rainfall was the main environmental factor responsible for volume production, while latitude was the main influence on stem form and *Endothia* infestation. On an individual clone basis, some micro-site soil factor interaction within the clones was found for the growth-site response models.

Keywords: *Eucalyptus grandis*, genotype environment interaction, clones, site factors, growth-site response, ANOVA, ACOVAR, GEI, FA, JRA,

OPSOMMING

'n Studie is onderneem om die genotipe-omgewingsinteraksie van *Eucalyptus grandis* klone, wat in die oostelike deel van Suid-Afrika groei, te kwantifiseer. Een-en-dertig groeiplekke is geselekteer om die "tradisionele" *E. grandis* groeiplekke in Suid-Afrika te verteenwoordig. Elf gemeenskaplike makro-groeiplek veranderlikes en twaalf gemeenskaplike mikro-groeiplek veranderlikes is by elk van die groei areas opgeteken. Sewe-en-twintig *E. grandis* klone en vier *E. grandis* basterklone is daarna oor hierdie 31 groeiplekke geëvalueer. 'n Onvolledige Latynse roosterontwerp is gebruik om die 31 toetsklone te evalueer en vyf kontroles is gebruik om die groeiplekke gemeenskaplik te verbind.

Volume produksie, stamvorm, stamdefekte en oorlewing is op twee- en vyfjarige ouderdomme geëvalueer terwyl besmetting met drie stamkankers op vyf jaar beoordeel is. Die analitiese metodes wat gebruik was om genotipe-omgewingsinteraksie te evalueer en te kwantifiseer is die variansie analise (ANOVA), korrelasie analise, en gesamentlike regressie analise (JRA) tesame met ko-variansie analise (ACOVAR). Die groeiplek assosiasie vir volume produksie, stamvorm en *Endothia* besmetting is ondersoek deur gebruik te maak van faktor analise (FA), en vergelykings is verkry vir die spesies en individuele klone deur gebruik van 'n stapsgewyse meervoudige regressie benadering.

Genotipe-omgewingsinteraksie, soos geëvalueer deur JRA, wys dat 'n toename in groeiplek produktiwiteit lei tot 'n positiewe lineêre reaksie in produktiwiteit op klonale vlak en dat daar 'n divergerende patroon tussen die regressielyne van die klone is. Hierdie tendens is ook vir beide die stamvorm en *Endothia* besmetting waargeneem. Gevolglik is nie-beduidende veranderings in die rangorde van die klone gevind en slegs reletiewe verskille tussen klone is gevind. Onvolwasse-volwasse genetiese korrelasies vir volume produksie en stamvorm toon matige korrelasies (r_g =0.66 en r_g =0.70) tussen die twee- en vyfjaar metings.

Op 'n spesiesvlak was reënval die oorheersende omgewingsfaktor verantwoordelik vir volume produksie terwyl die breedtegraad ligging stamvorm en *Endothia* besmetting beïnvloed het. Op individuele kloonvlak het sommige mikro-groeiplek interaksie binne klone bygedra tot die groei en groeiplek reaksie modelle.

Sleutelwoorde: *Eucalyptus grandis*, Genotipe-omgewingsinteraksie, klone, groeiplek faktore, groeiplek reaksie, ANOVA, ACOVAR, FA, JRA

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CHAPTER 1

OBJECTIVES AND THESIS OUTLINE

1.1 THE UNDERLYING PROBLEM

Clonal forestry with eucalypts is widespread in numerous countries, particularly Brazil, Columbia, Morroco and South Africa (Endo and Wright, 1993). Commercial clonal forestry, using *Eucalyptus grandis* and *Eucalyptus* hybrids, commenced in South Africa during the mid-1980's. From a slow start and a small beginning, by 1993 an estimated total of 18000 ha was already under clonal planting. (Denison and Kietzka, 1993).

Initially clonal programmes were aimed at producing "specialist" site specific clones, however as the clonal programmes have matured, a greater proportion of clones have become stable "generalists" (Howard, 1997). Most of the initial South African clonal plantings in the mid-1980's were from superior, but untested, individual tree selections (ortets) from open-pollinated progeny trials. The only information on the potential of the selection was from the field performance of the family, the individual ortet's performance, and the nursery rooting performance. The problem attached to this deployment approach was that little was known (and still is not known) about the effects of genotype-by-environmental interaction (GEI) on the clones. Some literature is available on the effects of provenance, family, progeny and fertilizer interactions in forestry, and cultivar interactions in agriculture, but no information is readily available on clone-by-site interactions (Shelbourne, 1972; Matheson and Raymond, 1984; Van Wyk and Falkenhagen, 1984; Zobel and Talbert, 1984; Fakenhagen, 1985).

A clonal breeding and deployment strategy gives the breeder and the grower the opportunity to capture, control and realise the maximum gain from an improvement programme and the practice of clonal forestry is making it relatively easy to capture the maximum amount of genetic gain available in an individual genotype (clone) at any one time (Barnes, 1984). This is possible, as the total variance component is transferred to the clone, and in the late-1990's there can be little doubt that it is the only way forward for both breeding and production.

No large structured GEI studies have been initiated within South Africa, to evaluate and quantify, or even to attempt to understand the magnitude of GEI within a commercial deployment strategy. During the past decade, some of the larger growers in South Africa

have developed some company specific information on clonal deployment. The smaller grower on the other hand is no wiser than a decade previously, and still does not have the resources to evaluate the problem.

1.2 THE RESEARCH OBJECTIVES

The overall objective of this study is to determine the influence of the environment on the growth, stem form and disease tolerance of *E. grandis* clones. To achieve this main objective, a series of site factor based, structured *E. grandis* clonal trials were established and assessed at two and five years of age.

The following five specific objectives were envisaged as possible outcomes of the research:

Through a literature review:

- To determine the influence of environmental factors on the plant growth processes and other response variables
- To gain an understanding of the available methodology to quantify GEI

Through a field experiment:

- To investigate the genotypic adaptability of *E. grandis* clones with respect to growth, stem form and disease resistance when planted on a variety of sites
- To investigate the causes of genotype-by-environment interaction in *E. grandis* by relating site factors to growth performance, and other response variables
- To develop a basis for the selection of *E. grandis* clones for given sites.

A possible future follow-up study, utilising the findings of this initial study, could be a growth factor simulation study. Clones, from this study, showing a positive or a negative growth response to measurable and repeatable environmental growth factors could be used. Growth chambers, utilising a controlled environment, and simulating the growth factors would then be used. This final study could then possibly show the way to the prediction of

GEI at an early age from controlled environment measurements (Isebrands *et al*, 1988; Matheson *et al*, 1995).

1.3 THESIS OUTLINE

The thesis is divided into eight chapters, a bibliography, and ten appendices. The present chapter sketches the background and objectives towards the overall aim of understanding GEI in *E. grandis* in South Africa. Chapter 2 contains a literature study of variation and the plant processes important for growth; the influence of environmental factors on plant growth; and the available methodology used to evaluate plant growth. Chapter 3 contains a final literature section on *E. grandis* as a species, combining both the natural and the exotic environments, and in relationship to the previously mentioned growth factors.

Chapters 4 to 6 contains the research approach, the field experiment, the assessment procedures and field sampling, as well as the statistical methods. Chapter 7 details the results of the research, together with the discussion of these results. Firstly the GEI analysis: analysis of variance (ANOVA); correlations between growth and site variables and age to age genetic correlations, and finally joint- regression analysis (JRA) and analysis of covariance (ACOVAR). Secondly, growth-site models including factor analysis (FA) and multiple regression analysis. The final conclusions and recommendations following the research are given in chapter 8.

A bibliography of references, and ten appendices are included showing and listing the experimental design, the physiographical and soils details, the control seed groups, the assessment procedures, the summary statistics, the correlation matrices, the ANOVA tables, the ACOVAR tables, the factor analysis, and the multiple regression analysis.

CHAPTER 2

LITERATURE REVIEW

2.1 VARIATION

The visible (phenotypic) differences among plants are basically the result of sources of variation: the differing environments in which the plants are growing, the genetic differences among plants, and the interactions between the plant genotypes and the environments in which they grow (Zobel and Talbert, 1984). Variation in plants can therefore be broadly divided into three distinct categories:

- variation due to the environment (E)
- variation due to heredity (G)
- variation due to an interaction between the genotype and the environment (GE)

2.1.1. Environmental variation

Environmental variation can be classified as "predictable" or "unpredictable", and can then be further subdivided into "natural"or "cultural" variation in studying forest trees. Natural variation is typically the variation in climate, soil and biotic factors, while cultural variation is the variation that has been imposed by man by management or silvicultural practices (Shelbourne, 1972).

Predictable cultural variation would be the thinning regime, the pruning regime, the spacing or the type of planting stock. Unpredictable cultural variation would therefore be factors associated with inconsistent silvicultural practices (Shelbourne, 1972).

Unpredictable natural variation is mostly the year to year fluctuations in rainfall, temperature, or even wind (Allard and Bradshaw, 1964; Shelbourne, 1972). Predictable natural variation could typically be used to define the planting range for a species or the breeding region for a landrace. Typically, predictable natural variation is the variation most commonly associated with GEI. Within natural stands of forest tree species, the observed variation can be sub-divided into following categories (Zobel and Talbert, 1984):

- geographic (provenance)
- sites within provenances
- stands within sites
- individuals within stands, and
- within trees.

2.1.1.1 Geographic and site variation

Geographic differences are often large, especially for traits related to adaptability. Most forest tree species have distinct geographic races, related to an altitudinal range, a climatic zone or a soil type (Zobel and Talbert, 1984). Within the natural populations of forest tree species, primary (or clinal) variation generally occurs along the three primary axes of latitude, longitude and altitude, reflecting various changes in photoperiod, thermoperiod and precipitation. However, secondary (or non-clinal) variation may also occur, along these three primary axes, most commonly in response to site factors (Perry, 1978). Clinal growth variation has been reported within many *Eucalyptus* species (Pederick, 1976).

2.1.1.2 Individual tree variation

Individual tree variation can be described as both the variation between trees or the variation within trees. Individual trees of a given species usually display variation from one another even when growing in the same geographic area or forest stand. Differences in wood properties between pith and outer wood are usually cited as the main within tree variation. Geographic and individual tree variation, account for 90 percent of all the variation in trees (Zobel and Talbert, 1984).

2.1.2 Hereditary variation

As the name implies, hereditary variations result from heritable causes and are transmitted to the tree's progeny. The heritable variations are expressed again in the progenies of the tree, although the intensity with which they are expressed will vary with the environment. Qualitative characteristics are simply inherited, discrete, and are easily identifiable even in a variable environment. On the other hand, quantitative characteristics have a complex

inheritance, are easily modified by the environment, and are expressed in a continuous range of variations (Poehlman and Sleper, 1995). To determine whether the extent of observed differences among trees are genetic, environmental or a combination of both, structured field tests are required (Zobel and Talbert, 1984).

2.1.3 Quantifying variation

Methods for estimating heritability are based on partitioning observed variation of a quantitative characteristic into genetically and environmentally controlled components. The statistic that is important here is the variance (V). The variance calculated from the observed variations in the quantitative characteristic constitutes the phenotypic variance (V_P). The phenotypic variance may in turn be divided into three components: genetic variance (V_G), non-genetic or environmental variance (V_E), and variance due to an interaction between genotype and environment (V_{GE}), and can be stated as:

$$V_P = V_G + V_E + V_{GE}$$

The genetic variance V_G is in turn composed of three major components: additive genetic variance (V_A), dominance variance (V_D), and non-allelic interactions or epistasis variance (V_I), and can thus be stated as:

$$V_G = V_A + V_D + V_I$$

If the ratio of the genetic to total variance is high, it indicates a strong genetic control for the trait. Within forest trees, strong genetic control (high heritability) has been commonly observed for bole straightness and wood specific gravity. Traits that are highly influenced by the environment, such as height (strongly influenced by soil fertility and moisture) and diameter (strongly influenced by stand density) are predictably under weaker genetic control and usually have a low heritability (Spurr and Barnes, 1980; Poehlman and Sleper, 1995).

2.2 PHYSIOLOGICAL RESPONSES AND THE ENVIRONMENT

As far back as 1868 it was realised that, "in order to grow plants efficiently it is necessary to understand how plants grow" (Kozlowski *et al*, 1991). The growth of woody plants is

regulated by both their heredity and environment operating through a complex of internal factors and growth processes (Kramer and Kozlowski, 1960; Kozlowski and Pallardy, 1997). A broad understanding of both the genotype and the environment is therefore desirable to implement a study on GEI.

The relative rates of photosynthesis and respiration, together with transpiration and the water balance within a plant, are usually cited as the most important growth processes for the "success" of trees and other plants (Kozlowski and Pallardy, 1997).

2.2.1 Photosynthesis

Photosynthetic capacity varies among species and genotypes, and the photosynthetic rates of closely related species may also differ considerably (Kozlowski and Pallardy, 1997). Genotypic variations in photosynthetic rates in plants, are however often simply reflections of differences in leaf production between early and late initial leaf producers, which in turn is related to the latitudinal and altitudinal differences of the original parent material. Studies within *Populus* clones have shown clonal differences in leaf photosynthesis, integrated whole-tree photosynthesis, stomatal frequency and structure, and leaf area and shape. Leaf photosynthetic capacity and whole leaf photosynthesis have been positively correlated with actual biomass measurements (Isebrands *et al*, 1988). Wide variations have also been found in photosynthetic rates of several species of *Eucalyptus* (Kozlowski and Pallardy, 1997). Studies for photosynthetic efficiency have revealed that photosynthetic rates are however difficult to measure, and are influenced by the growing conditions before and during the measurements (Falkenhagen, 1976).

External environmental factors affecting photosynthesis are light, temperature, CO_2 concentration, water supply, air humidity, soil fertility, salinity, pollutants, applied chemicals, insects, diseases as well as cultural practices that alter the environmental regimes of plants, such as thinnings, prunings, fertilizer and irrigation. Internal factors that influence photosynthesis are those commonly associated with changes in leaf structure (Kozlowski and Pallardy, 1997).

2.2.2 Respiration

Respiration is the process by which the energy stored in reduced carbon compounds during photosynthesis is released by oxidation in a form that can be used by the plant for assimilation and growth (Kozlowski *et al*, 1991). The interaction of several internal and external environmental factors interact to influence the rate of respiration. Important internal factors are the age and the physiological condition of tissues, the amount of oxidizable substrate, and tissue hydration (Kozlowski and Pallardy, 1997). Environmental factors include soil and air temperature; gaseous composition of the soil; available soil moisture; light; injury and mechanical disturbances; and chemicals such as herbicides, fungicides, insecticides, fertilizers and pollutants (Kozlowski *et al*, 1991).

2.2.3 Transpiration and water balance

The growth of plants is more often limited by internal water deficits than by any other single internal factor and it affects almost every internal process within the tree (Kramer and Kozlowski, 1960). The important environmental factors influencing transpiration and water balance are light intensity, vapour concentration gradient between leaf and air, temperature, wind, and soil water supply (Pereira and Kozlowski, 1977; Kozlowski and Pallardy, 1997; Landsberg and Gower, 1997). Transpiration is primarily controlled by the aforementioned physical factors, however, it is also controlled by several plant factors, including leaf area, leaf exposure, canopy structure, stomatal aperture, and the ability of the roots to absorbing surfaces (Kozlowski and Pallardy, 1997; Landsberg and Gower, 1997).

2.3 THE ENVIRONMENT

There is general agreement that certain external factors most often limit the growth of field crops, and this seems to be equally true for woody plants. These factors are light, temperature, water, and nutrient supply (Kozlowski *et al*, 1991).

The following macro- and micro- factors have been consistently mentioned, as important for plant growth:

- Climatic factors: radiation, light and photoperiod, temperature and thermoperiod, water and evapotranspiration, wind.
- Edaphic factors: topography and slope, origin of the soil (parent material), physical properties of the soil, chemical properties of the soil.
- Biotic factors: biotic properties of the soil, fire, cultural practices, pests and diseases, competition (Kramer, 1960; Barbour *et al*, 1987; Kozlowski *et al*, 1991).

2.3.1 Climatic factors

2.3.1.1 Solar radiation

Solar radiation is the principle source of energy in the forest environment, and provides the energy for both photosynthesis and evapotranspiration (Moehring, 1968). Solar radiation varies with atmospheric conditions, as well as with latitude, altitude, and physiographic features (Moehring, 1968; Barbour *et al*, 1987). The effects of solar radiation are however mostly indirect and are seen primarily through differences in growing seasons and temperatures. The optimum temperatures for plant productivity coincide with the 15-25°C optimum range for photosynthesis (Barbour *et al*, 1987).

2.3.1.2 Light and photoperiod

Light intensity has a direct effect on tree growth through its effects on photosynthesis, stomatal opening, and chlorophyll synthesis. Light intensity fluctuates daily and seasonally and is modified by latitude. Isolation received per unit area is greater at higher elevations than at lower ones and in the southern hemisphere, greater on north-facing slopes than on south-facing slopes (Kramer, 1960; Barbour, *et al* 1987; Kozlowski *et al*, 1991). Light is of importance in silviculture, as it can be controlled by cultural activities (Moehring, 1968).

2.3.1.3 Temperature and thermoperiod

Climatic zones are determined largely by temperature variations, usually related to altitude and latitude and altitudinal limits for tree growth are largely determined by low temperatures (Kozlowski, *et al*, 1991). Altitude generally causes a reduction in temperature, however at

any given latitude, local topography, the direction and character of prevailing winds, storm patterns, and location to water bodies will contribute to temperature differences (Griffiths, 1976; Spurr and Barnes, 1980; Barbour *et al*, 1987). Temperature effects upon tree growth are directly related to photosynthesis and respiration and indirectly related to transpiration and tree-water relations (Moehring, 1968). The main influence of temperature however is on evapotranspiration, and forest productivity is limited, at the extremes, by low temperatures and inadequate precipitation (Waring and Schlesinger, 1985).

2.3.1.4 Water and evapotranspiration

The distribution and growth of trees is also controlled by available water. Wherever trees grow, their growth is limited to some degree by too little or too much water (Kozlowski, 1968). Water is further the environmental factor most directly correlated with productivity (Gholz *et al*, 1990). The amount and distribution of rainfall, the temperature extremes, and the length and severity of the dry season, all play an important part in limiting the distribution of commercial forestry (Evans, 1982).

Evapotranspiration is the primary process of water loss in the forest environment, and is the measure of the total amount of water lost by transpiration and evaporation and has high predictive value in productivity studies because it combines the influences of water, light and temperature (Moehring, 1968; Barbour *et al*, 1987).

2.3.1.5 Wind

Wind is an integral part of the environment and has both harmful and beneficial effects on plants. Ecologically, wind is an important agent in increasing transpiration, and influencing morphological development (Moehring, 1968). It causes injury by toppling trees, breaking stems and branches, uprooting trees, causing stem malformations, and injuring leaves (Kozlowski, *et al*, 1991).

2.3.2 Edaphic factors

2.3.2.1 Topography and slope

Topography and soils are closely related to one another. Topographic position affects soil depth, profile development, and the texture and the structure of the surface soil and subsoil (Spurr and Barnes, 1980). The greatest importance of slope is the orienting of the site with regard to the sun and wind. At any given latitude, the hottest and driest sites are those which most nearly face the sun during the middle of the summer day. Steeper slopes receive more isolation and flatter slopes receive less isolation. In the southern hemisphere, south facing slopes receive less sunlight and are therefore invariably cooler and moister, west and east slopes show similar but less extreme variation (Spurr and Barnes, 1980).

2.3.2.2 Parent material (Origin of soil)

Parent material has a large influence on the properties of young soils. These include colour, texture, structure, mineralogy, and pH (Foth, 1990). Abundant plant growth also requires a soil environment that is free of inhibitory factors such as toxic substances, disease organisms, impenetrable layers, extremes in temperature and acidity or basicity, or an excessive salt content (Foth, 1990). The origin of the soil is one of the most important factors influencing the supply of nutrients to forest trees (Ellis, 1997).

2.3.2.3 Physical properties of soil

Colour

Colour in itself is of little importance to tree growth. However, it does serve as an indicator of several important soil characteristics. Geological origin, the degree of weathering, the degree of oxidation and reduction, the content of organic material, and the leaching or accumulation of chemicals can all be deduced from soil colour (Pritchett and Fisher, 1979).

Soil classification

In South Africa the binomial soil classification system was used until 1991. It was replaced with a taxonomic system for South Africa . The system is a two tier system, with soil forms as the higher tier and soil families the lower tier. Soil forms are defined in terms of the type and vertical sequence of diagnostic horizons or materials. Soils can be identified in the field based on the differentiation of the horizons, the texture, the colour of the principal materials, and even which horizons are missing. For ease of usage, soil forms are given locality names such as Hutton or Fernwood (MacVicar *et al*, 1977; Soil Classification Working Group, 1991).

Rooting depth

The growth potential of forest trees is largely determined by the rooting volume and the water storage capacity of the soil. Both can easily be assessed by measuring the effective rooting depth (ERD) of the soil, or the distance from the surface to the first obstructing or impeding horizon for the tree's roots (Grey *et al*, 1993).

Soil water

Of the many factors that determine the productivity of a site, soil moisture is probably the most important (May, 1968). The availability of soil moisture is controlled by the rooting volume of a soil, the texture, the structure, and the clay material and organic matter content. Texture is the main factor influencing water storage capacity.

Soil structure

Soil structure is the nature of the arrangement (or aggregation) of the peds. The aeration of the soil is greatly improved through a good soil structure, as is the movement of water and plant roots through the soil. The presence of good structure: granular peds and a high degree of aggregate stability, is especially desirable in the top soil (Barbour *et al*, 1987).

Soil texture

The texture of a forest soil influences its productivity, however this influence may be more of an indirect than a direct effect. Texture per se has little effect on tree growth as long as moisture, nutrients, and aeration are adequate (Pritchett and Fisher, 1979). Textural changes are however detrimental to water movement, as well as air and root penetration. The severity of the restriction depends primarily on the abruptness of the change (Ellis, 1996). Forest soils usually have much higher rates of infiltration and drain more easily than cultivated soils, because they contain more non-capillary pore space (Kozlowski, *et al*, 1991).

2.3.2.4 Chemical properties of soil

Soil chemistry deals primarily with reactive materials, which are the chemicals that are of significance to living things. Soil pH, cation exchange capacity, S value, and the nature of the interface between the solid phase and the liquid phase are all important aspects of soil chemistry (Barbour *et al*, 1987).

Soil pH

The indirect effects of soil pH on plant growth are numerous and significant. An indirect effect of soil pH is its influence on nutrient availability. Soil pH influences the rates of weathering, the availability of nutrients such as nitrogen, phosphorus and sulphur, and the leaching ability of nutrients such as potassium. Changes in the soil pH dramatically influence the availability of nutrients with low solubilities. Most nutrients needed for plant growth require a near-neutral soil pH (Barbour *et al*, 1987). Typical soils have pH values that range from 4 to 8, although some soils may have higher or lower values. Agricultural soils tend to develop a low pH as a result of fertilizer applications that add both nitrogen and sulphur (Barbour *et al*, 1987; Foth, 1990).

Cation exchange capacity

Most nutrients are "retained" in the soil on colloids or humus, known as the CEC of the particular soil (Ellis, 1997). The CEC of the soil is strongly influenced by three factors: its

clay content, the kinds of clay minerals or amorphous colloids it contains, and the humus content (Barbour *et al*, 1987; Foth, 1990). The CEC is one of the most important influences on the supply of nutrients to trees (Ellis, 1997).

S- value

The S-value is defined as the sum of exchangeable Ca, Mg, K and Na in me per 100g soil, and is basically a measure of the leaching status of the soil. Together with the soil parent material, and the CEC, the S-value is one of the most important factors influencing the supply of nutrients to trees (Ellis, 1997).

Nutrients

Major nutrients (macronutrients) are those required by a plant in rather large amounts. Minor nutrients (micronutrients) are those required in only small or trace amounts (Barbour *et al*, 1987). The availability of nitrogen, phosphorus and potassium is of great economic importance because they are the major plant nutrients derived from the soil. Although values of N, P, and K can be determined in a soil, it has not however proved possible to correlate growth to N, P, K concentrations, except for extreme values (Toleman, 1978).

The nutrient requirements for forest growth are not simply fulfilled by the presence of the essential elements in the soil and fertility does not appear to be the limiting factor in tree production in the vast majority of forested areas (Pritchett, 1968; Waring and Schlesinger, 1985). Within South Africa, the nutrient status of soils is generally low, especially with regards to phosphorus (Herbert, 1993).

Ellis (1997) summarized the most important factors influencing the supply of nutrients to trees as:

- the soil parent material,
- the cation exchange capacity (CEC), and
- the leaching status of the soil (S- value)

together with other nutrient availability indicators being:

- the pH of the soil
- the water content of the rooting zone
- the available rooting volume.

Rooting inhibition

Root development depends on chemical properties such as pH, deficiencies in essential minerals, toxic concentrations of elements such as aluminium or manganese, or excessive amounts of salts. Chemical barriers to root penetration occur in the form of excessive acidity (low pH), or high manganese concentrations. In low rainfall, carbonates often accumulate at the deepest point wetted by rain, forming a hardpan layer that is difficult for the roots to penetrate (Foth, 1990; Kozlowski *et al*, 1991).

2.3.3 Biotic factors

2.3.3.1 Fire

Fire destroys forests, modifies site conditions, and alters physiological processes and thereby influences the growth of plants. Fire modifies the site quality by affecting the natural vegetation, soil properties, hydrology, and geomorphic processes. Both physical and biological properties of soils are drastically altered by fire. Fires are responsible for the increase in some fungal diseases and insects. Concentrations (ash beds) of mineral nutrients after a fire tend to be more variable than those before a fire (Kozlowski *et al*, 1991).

2.3.3.2 Cultural practices

Cultural practices are used to improve the regeneration of forest plantations, by optimising the availability of water, mineral nutrients, light, soil oxygen and growing space. Productivity in forest stands is most likely to be increased by cultural practices that reduce the time to canopy closure (Kozlowski *et al*, 1991). Most forestry cultural activities are aimed at having a positive reaction response (Evans, *et al*, 1992; Kozlowski, *et al*, 1991).

2.3.3.3 Pests and diseases

Exotic plantations are generally more susceptible to diseases and pests than are the same species in their natural environment (Heather and Griffin, 1984). Fungal pathogens damage leaves and cause premature shedding, sometimes block the movement of water in the xylem or carbohydrates in the phloem, and produce toxins that adversely affect physiological processes (Kozlowski et al, 1991).

Leaf diseases

Leaf diseases affect tree growth mainly by reducing photosynthetic tissue and by reducing the efficiency of the remaining tissue. Photosynthesis is reduced chiefly by localized destruction of photosynthetic tissue by invading fungi. Injury by fungi to leaves often causes abscission and thereby deprives the tree of carbohydrates the leaves would otherwise produce (Kramer, 1960).

Stem diseases

Bacterial and fungus pathogens located in the outer sapwood interfere with water movement and cause the wilting of the leaves. Cankers vary in size and may be superficial and do little damage, while other cankers may kill trees by girdling them (Kramer, 1960).

Root diseases

Root diseases often destroy parts of the root system and thereby interfere with absorption of water and minerals. Root diseases cause various distortions, cause wood and bark to decay and may eventually cause death. Root diseases sometimes spread to stem diseases (Kramer, 1960).

2.3.3.4 Competition

Young stands, from planting until canopy closure are particularly sensitive to competition

from weeds and pests and highly responsive to management (Nambier, 1990). Diameter growth is highly sensitive to competition from adjoining trees. Increasing competition greatly reduces the rate of diameter growth and wood production (Kozlowski *et al*, 1991). Height growth is however rather insensitive to competition, from both the initial spacing of the trees and from changes in spacing following a thinning (Ford, 1978).

2.3.4 Growth-site response models

"Climatic conditions such as rainfall, length of growing season, and photoperiod, affect the growth of species with very extensive natural ranges, but within moderately broad geographic areas site quality is controlled more by soil than by climatic factors" (Kramer, 1960). A species-site classification should therefore be based on the soil and climatic factors which are the limitations to forest production when compared to the requirements of the species.

Models used in South Africa have shown many diverse factors responsible for growth, as listed below:

- In *Pinus patula* strong relationships were found between tree parameters and rainfall, altitude, soil wetness, exchangeable bases, effective rooting depth (ERD), slope position, and geology (Schutz, 1990).

- 77% of the growth variation in *Pinus radiata* growing in the southern Cape, was accounted for in a combined model, (containing ERD as a principle component) (Louw, 1991).

- More than 90% of the variation in tree growth of *Acacia mearnsii* was explained by soil factors, effective rooting depth being the most influential (Schönau and Aldworth, 1991).

- For *Pinus elliottii* in the southern Cape, two models were developed using effective soil depth (ESD), the natural log of effective soil depth, slope angle, terrain position and rainfall (Schafer, 1988*a*).

- Effective soil depth (ESD), which reflects soil moisture availability was the most useful parameter for predicting *Pinus pinaster* growth performance and the natural log

of ESD the most convenient application (Schafer, 1988*b*).

A few studies have been undertaken on eucalypts in South Africa.

- A study of the growth of *Eucalyptus grandis* in the Mpumalanga escarpment area revealed that growth is mainly influenced by factors controlling available soil moisture, together with the organic carbon content of the topsoil (Louw, 1997).

- In KwaZulu-Natal, a study of the growth of *Eucalyptus grandis* on sandy textured soils found the major soil component best related to growth was organic carbon content (Noble *et al*, 1991).

- A further study of the growth of *Eucalyptus grandis* at Frankfort, in Mpumalanga, found ERD, terrain position and the mean annual precipitation (MAP) as the most important factors (Louw, 1999).

2.4 THE EVALUATION OF THE INTERACTION COMPONENT

2.4.1 Fundamentals

2.4.1.1 Experimental considerations

The basic requirements for field experiments, for detecting GEI and for selecting genotypes for stability are:

- many genotypes repeated over many sites
- common treatments on more than one site
- replication within sites.

Environments can consist of different locations, years or even management prescriptions (Shelbourne, 1972; Matheson and Raymond, 1984, 1986; Zobel and Talbert, 1984; Matheson, 1988).

The statistical model should include the effects of genotypes, environments, GEI, and error as

well as terms such as replications within sites and interactions with environments. The simplest model for a phenotype can then basically be described (Matheson and Raymond, 1984, 1986; Skrøppa, 1984) as:

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

where:

P	=	the phenotypic value
μ	=	the population mean
G	=	the genotype effect
E	=	the environment effect
GE	=	the interaction between the genotype and the environment effect
ε	=	the random error.

2.4.1.2 Experiment size

The ideal field experiment would be to test all genotypes on all sites. However, if all genotypes are to be tested on all sites, forestry field experiments would be inclined to become large, mostly owing to the plot and replication sizes. To overcome this problem, a core group of genotypes may be selected to be tested at all sites in order to provide information about GEI, while a peripheral group of genotypes maybe tested only a certain sites (Matheson, 1988).

2.4.1.3 Random and fixed effects

If the aim of the experiment is to rank the genotypes overall, then we may treat the sites as random and the genotypes as fixed. If the purpose is to investigate GEI then the genotype effect will be treated as both random and fixed. Forestry experiments are rarely interested in sites that are not fixed or represent some chosen range of environments (Matheson, 1988).

2.4.2 Statistical methods

An appropriate statistical method to analyse experiments planted on multiple sites must be employed (Cochran and Cox, 1950). Various univariate and multivariate techniques are available for detecting and evaluating GEI interactions (Shelbourne, 1972, Barnes *et al*, 1983, Skrøppa, 1984, Falkenhagen, 1985).

The following five methods, plus various modifications, are the most commonly and successfully applied univariate methods used to measure GEI in both agriculture and forestry (Finlay and Wilkinson, 1963; Shelbourne, 1972; Freeman, 1973; Barnes *et al* 1983; Skrøppa, 1984; Falkenhagen, 1985; Matheson and Raymond, 1986; Becker and Léon, 1988; Burdon, 1991; Garnier-Géré *et al* 1995):

- Ranking of means
- Analysis of variance (ANOVA)
- Linear regression techniques (JRA)
- Stability analysis
- Simple and genetic correlations.

Several multivariate statistical techniques are also available for the analysis of many genetic entries over several sites. These methods can group genotypes of similar performance in several environments or classify the environments into groups that minimize the within group interactions (Skrøppa, 1984). Two associated methods have been used with reasonable success in agriculture and limited success in forestry (Skrøppa, 1984; Lin *et al*, 1986; Matheson and Raymond, 1986; Gauch, 1988; James and Schön, 1991; Natchit *et al*, 1992; Garnier-Géré *et al* 1995; Falkenhagen, 1996):

- Principal components analysis (PCA)
- Additive main effects and multiplicative interaction model (AMMI).

Other models have been attempted to measure and quantify GEI in agriculture (and forestry), and include (Skrøppa, 1984; Matheson and Raymond, 1986; Van Eeuwijk, 1992; Garnier-Géré *et al* 1995):

- Multiple regression
- Canonical correlation analysis

- Structuration and Cluster analysis
- Factor analysis (FA)
- Pattern analysis.

2.4.2.1 Ranking of the means

An initial examination of genotype means for each environment can reveal whether changes of ranking occur. If the ranking of the genotypes is consistent between the environments the GEI interaction can be expected to be weak or absent and the genotype effects to be considerable. If a change in rank does occur between different environments, these may be due to GEI, and if the performance is consistent between replications within an environment, GEI interaction can be expected (Shelbourne, 1972). Another aspect of ranking means between sites is that although there is no significant change in the ranking of the genotypes, the relative differences between the genotypes may change (Falkenhagen, 1985).

2.4.2.2 Analysis of variance (ANOVA)

The analysis of variance statistical procedure (ANOVA) compares all differences in the sample means, to the variation within the samples, and judges them statistically significant (or not), through the use of the F-test. The statististical significance of GEI effects can then be determined (Hodge,1996; Ott, 1996).

The first step in the study of interactions is usually an ANOVA over sites using the common treatments. This is done by comparing the interaction mean square with the error mean square. Significant interactions are frequently found but are difficult to interpret (Matheson and Raymond, 1984, 1986).

The ANOVA procedure should normally be used as a basis for all subsequent examinations of data. It allows for the testing of the effects of genotypes, environments and interactions. The calculation of the variance components and expressing the GEI components as a percentage of the total components or as a percentage of the entry component allows some quantitative appreciation of the size of the interaction relative to other effects. If the ratio of the interaction component of variance to the genetic component of variance is greater than 0,5, then the interaction could be serious (Shelbourne, 1972).

The familiar model for ANOVA is (Matheson and Cotterill, 1990):

$$Y_{ijk} = G_i + E_j + GE_{ij} + \varepsilon_{ijk}$$

where:

Y_{ijk} = the *ijk* tree
G_i = the *i*th genotype
E_j = the *j*th environment
GE_{ij} = the interaction between the *i*th genotype and the *j*th environment
ε_{ijk} = the residual variance

OR

In more generalised terms, if Y_{ge} is the measured value, the ANOVA model can be rewritten (Nachit *et al*, 1992) as:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \varrho_{ge}$$

where:

μ = population means
α_g = are the genotype mean deviations
β_e = are the environment mean deviations
ϱ_{ge} = are the residuals (which includes the interaction)

2.4.2.3 Joint regression analysis (JRA)

The most frequently used method to evaluate GEI is that involving regressions (Becker and Léon, 1988). The traditional way in which to quantify environments is by the mean performance of all the genotypes at the environment (Falconer and Mackay, 1996). The genotypic performance can then be plotted against the mean of all genotypes at each site, or against an independant value, or against some external estimator of site quality (Barnes *et al*, 1983). The basic idea with this method is also to express the interaction $(GE)_{ij}$ as a linear function of an environmental index I_j and a deviation σ_{ij} from the regression line.

$$(GE)_{ij} = \beta'_i I_j + \sigma_{ij}$$

In most cases I_j is taken to be the environmental effect E_j and the model becomes

$$Y_{ijk} = \mu + G_i + \beta_i E_j + \sigma_{ij} + B_{jk} + \varepsilon_{ijk}$$

where:

$\beta_i = 1 + \beta'_i$

Usually the environment effects equals the deviation of the site mean from the total means and β_i is estimated as the slope in a regression analysis.

If Y_{ge} is once again the measured value, the equation for the linear regression model can then be given (Nachit *et al*, 1992) as:

$$Y_{ge} = \mu + \alpha_g + \beta_e + K\alpha_g\beta_e + \pi_g\beta_e + \eta_e\alpha_g + \varrho_{ge}$$

where:

μ	=	population means
α_g	=	genotype mean deviations
β_e	=	environmental mean deviations
K	=	joint regression
π	=	genotypic regression
η	=	environmental regression
ϱ_{ge}	=	residual terms.

The regression methods commenced during the early 1960's when a group of related techniques were developed to specifically estimate and correct for GEI effects in agriculture. This pioneering work was done by Finlay and Wilkinson in 1963. Most agricultural data was found to present a distinct triangulation in the plot of regression coefficients against the genotype means. Comparable plots in forestry reveal a consistent difference between this triangulation and the forestry results. Forestry results show an increase in the regression coefficient with an increase in genotype mean (Shelbourne, 1972). The biological explanations for this difference relates to the fundamental difference between the two kinds of plants - annual and multi- year crops (Matheson and Raymond, 1984).

2.4.2.4 Stability analysis

The regression analyses was further developed by Eberhart and Russel (1966) for ranking entries for stability (Hodge, 1996). The authors proposed to supplement the regression coefficient with a second stability parameter, the mean square deviations from the regression line for each individual genetic entry - a low deviation mean square indicating a good fit to the linear model (Shelbourne, 1972 ; Wood, 1976; Skrøppa, 1984). The method was further refined by Perkins and Jinks (1968) by relating the components in the regression analysis to a basic biometrical genetic model. The statistical shortcomings of the previous models were further corrected by Freeman and Perkins (1971). The authors pointed out that if the environment is quantified by the mean of all genotypes growing in it, then regressing the mean of each genotype on this measure of environment leads to statistically invalid regressions. They suggested that the performance of some closely related genotype(s) could be used as a more appropriate measure of the environment rather than the genotypes under test themselves. The invalidity of this method arises from the fact that the sum-of-squares for the joint regression is the same as the total sum-of-squares between environments rather than part of it (Gibson, 1982). Any other physically measurable feature of the environment could also be used, but the implementation of this approach could present some problems (Shelbourne, 1972; Gibson, 1982; Matheson and Raymond, 1984).

Although the applications of the JRA method is now statistically correct, subsequent work regressing genotype means on their environmental means, and on environmental values calculated from an independent though related set of genotypes, has found that all analyses give generally similar values of significance. No techniques have been specifically developed to evaluate GEI in forest trees, and joint regression has been used with good effect in many forest tree experiments (Gibson, 1982; Matheson and Raymond, 1984; Van Wyk *et al*, 1991).

2.4.2.5 Phenotypic and genetic correlations

Working with forest trees, many authors have used simple correlations between genotypic means at pairs of sites for roughly evaluating the extent of GEI and the roles of individual environments. The calculation of the simple correlation coefficients between means at pairs of environments in all possible combinations can provide a matrix of r values that will indicate which environments are out of line with the others. However, equal replication at all environments for all entries is desirable (Burdon, 1977).

Genetic correlations among traits indicate the degree to which one trait will change as a result of change in another trait (Zobel and Talbert, 1984). Genetic correlations have generally been estimated when both traits have been measured on the same individuals. The correlations that have thus been obtained, have been designated Type A genetic correlations. Where the two traits, or even one trait, have been measured on different individuals within genetic groups, the correlation is designated a Type B genetic correlations.

Within forestry, GEI can however often best be studied by characterising the environments rather than genotypes (Burdon, 1977). This can be done by examining the matrix of genetic correlations between pairs of test sites. Using this method it can be found which environments are out of line with the others. The genetic analysis should however be followed by studies of the environmental factors at each site, aiming at determining which sites are well suited and which sites are not suited for selection experiments. This method can then supplement the regression and stability analyses and can explain some interaction but it cannot be used to rank genotypes (Skrøppa, 1984).

Genetic correlations (r_{gxy}) between a pair of environments (sites) *x* and *y*, can be estimated as:

$$r_{gxy} = \sigma_{gxy} / (\sigma_{gx}.\sigma_{gy})$$

where:

σ_{gxy}	=	the covariance for genetic groups between the trait as it is expressed at environments (or age) *x* and *y* respectively
σ^2_{gx} σ^2_{gy}	=	the between-genetic group variances in the respective environments *x* and *y*

The groups can represent clones, full-sib families, half-sib families, as long as the entries within the groups all belong to only one such category (Burdon, 1977; 1991).

This type of analysis is often difficult when using missing or unbalanced data. The sensitivity of Type A correlations has been shown to missing data and the most reliable estimates come from data subsets representing only those individuals without missing values (Burdon, 1991).

Missing or unbalanced data, poses even more problems with Type B correlation estimates. An important situation is where gaps are caused by missing genotypes in certain environments,

such that different subsets of groups will only be common to different pairs of environments. In this situation, the only feasible way of analysis would be to carry out separate ANOVAs on every different subset of groups that is common to a pair of environments. This process is however cumbersome and much good information may be lost in the process (Burdon, 1991).

2.4.2.6 Principal components analysis (PCA)

Principal component analysis consists of finding an orthogonal transformation of the original variables to a new set of uncorrelated variables, called principal components, which are derived in decreasing importance (Chatfield and Collins, 1996). The uncorrelated sets of linear combinations of variables are chosen such that the variance between each observation of all variables is maximized. Principal component analysis could provide linear combinations to maximise the differences between the genotypes, as long as the genotypes and the observations and the measurements at each site are considered to be separate variables (Matheson and Raymond, 1984).

If Y_{ge} is once again the measured value, the equation for the principal component analysis (PCA) can then be written (Nachit *et al*, 1992) as:

$$Y_{ge} = \mu + \sum_{n=1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \varrho_{ge}$$

where:

Y_{ge} is the mean of genotype *g* at environment *e*
μ is the grand mean
N is the number of PCA axes retained within the model
λ_n is the singular value for PCA
γ_{gn} are the genotype eigenvector values for PCA axis n
δ_{en} are the environment eigenvector values for PCA axis n
ϱ_{ge} are the residuals

The first principal component is the compound variable with the largest variance, the second principal component, orthogonal to the first , has the next highest variance etc. PCA can be combined advantageously with other statistical methods (Van Laar, 1987).

The method has not been used much in the analysis of GEI. The method could however be

useful when regression on the environmental mean shows wide deviation from linearity (Freeman, 1973). Principal component analysis of the correlations between genotypic values and environmental variables among two sets of inbred tobacco plants was undertaken by Perkins (1972). She calculated principle components of weather variables and then used functions of the first few components as predictors. Only the environment effects, which had similar effects on all genotypes, were expressed in the first principle component. The second principal component indicated the differing responses of the lines, and she was thus able to characterize the behaviour of varieties in terms of combinations of variables, and concluded that " growth rate must therefore be dependent on a complex interaction of more than one environmental variable" (Matheson and Raymond, 1984).

In the earliest documented case of the use of principle components in a forestry application, the exercise was not very useful owing to a lack of environments and a limited distribution. A disadvantage of this method is that an environmental variable which is of little importance in determining the response of the genotypes may make a big contribution to one or more of the first principle components (Wood, 1976; Matheson and Raymond, 1984).

2.4.2.7 Additive main effect and multiplicative model (AMMI)

The combined model of ANOVA and principal components analyses has however been successful in both agriculture and forestry. The combined model was first proposed in 1971, and then further developed under the name of AMMI (for Additive Main effects and Multiplicative Interaction). The method combines the usual additive analysis of variance with principal component analysis on the GEI term. The model has been very useful in predicting genotypic values. The model has no *a priori* structure given to the interaction component (Garnier-Géré *et al*, 1995).

Although widely used in agriculture, within forestry the AMMI model has not brought any new insight over the three "traditional methods" the ANOVA, the JRA, and graphic representation (Nachit *et al*, 1992; Falgenhagen, 1995). The AMMI model has however been used for demonstration purposes in *Eucalyptus* clonal trials (James and Schön,1991).

The AMMI model sometimes called the "biplot" model equation is as before for measured value Y_{ge} written (James and Schön, 1991; Natchit, *et al*, 1992) as:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n-1}^{N} \lambda_n \gamma_{gn} \delta_{en} + \varrho_{ge}$$

where:

Y_{ge} is the mean of genotype g at environment e

μ is the grand mean

α_g are the genotype mean deviations (means - grand mean)

β_e are the environment mean deviations

N is the number of PCA axes retained within the model

λ_n is the singular value for PCA

γ_{gn} are the genotype eigenvector values for PCA axis *n*

δ_{en} are the environment eigenvector values for PCA axis *n*

ϱ_{ge} are the residuals

The model is obtained in two steps:

Firstly, the additive main effects (genotype and site) are fitted using the standard two way analysis of variance. The variance not captured by this additive model remains in the non-additive residual namely the interaction. Secondly, a principal components analysis (PCA) is applied to the non-additive residual from the additive ANOVA model and not the original data (Gauch, 1988; James and Schön, 1991).

2.4.2.8 Canonical correlation analysis

"Canonical correlation analysis is the multivariate counterpart of the simple correlation analysis. The latter measures the linear relationship between the variables X_i and X_j, assuming that they have a joint bivariate normal distribution. The canonical correlation analysis measures the degree of association between two sets of normally distributed variables" (Van Laar, 1987).

A form of canonical analysis relating genotypic performance to a linear combination of values for environmental variables has also been proposed. The linear combination would be chosen to maximize the correlation with the genotypic values. The method could only work if the critical variable is included in the canonical set, but could be valuable if there is a combination of environmental variables which is causing the interaction (Hardwick and Wood, 1972; Matheson and Raymond, 1984).

2.4.2.9 Multiple regressions

Multiple regression aims at maximizing the multiple correlation coefficient - a measure of the association between a dependent variable and a set of independent variables (Van Eeuwijk, 1992).

The model can be written as follows:

$$Y_{ij} = \mu + \rho_i + \alpha_{i1}x_{j1} + \alpha_{i2}x_{j2} + \ldots + \alpha_{i\rho}x_{j\rho} + e_{ij}$$

where:

μ	=	overall mean
ρ	=	number of environmental variables, indexed by h = 1, ρ
α	=	partial regression coefficient of y_{ij} on x_{jh}, j varying
e_{ij}	=	Normal random variable, mean 0, variance σ^2
x_{jh}	=	measures of the *h*th environmental variable in the *j*th environment

The x's may measure completely different aspects of the environment, or may be terms of a polynomial.

There is some similarity in the multiple regression model and the factor analysis model. The methods are a popular way of interpreting the data in terms of stability and adaptability. The alternative of analysing by regression on environmental variables, the so called factor regression analysis, breaks the GEI into regressions on covariates, which depend on both genotypes or environments. This method can also be used to both explore and confirm the importance of some factors for interpreting GEI (Garnier-Géré *et al*, 1995).

A multiple regression of the genotypic values at each site on a number of environmental variables can be used to determine what the critical factors are in an environment (Hardwick and Wood, 1972). Examples on forest trees, using a multiple regression model have not been successful, presumably because of either too few environments, or the critical factor was not included in the list of independent variables (Matheson and Raymond, 1984).

2.4.2.10 Structuration and cluster analysis

The fundamental aim of cluster analysis is to find natural groupings, if any, in a set of individuals. Cluster analysis aims to allocate a set of individuals into a set of mutually exclusive groups. The individuals within groups would be similar to one another, and the individuals within the other groups would be dissimilar. These sets of groups are called a partition. The groups may be further divided or subdivided, so one eventually ends up with a complete hierarchal structure and tree for a given set of individuals (Chatfield and Collins, 1996).

The structured model deploys classification used for structuring the interaction and produces groups of genotypes showing similar patterns of response to environmental variation. It can be considered as a multivariate extension to the stability analysis methods (Garnier-Géré *et al*, 1995).

Within forestry, these methods can group genotypes performing similarly in several environments or classify the environments into clusters that minimise the within-cluster interaction. Burdon (1977), calculated a matrix of genetic correlation coefficients as a basis for such a grouping. The usefulness of these methods for the grouping of test environments is however doubtful as the number of test sites in forestry in usually low (Skrøppa, 1984).

2.4.2.11 Factor analysis

Factor analysis has similar aims to PCA but is based on a proper statistical model which specifies a given number of underlying variables called factors. The analysis is more about "explaining" the covariance structure of the variables rather than with "explaining" the variances (Chatfield and Collins, 1996). There is also some similarity between the multiple regression and the factor model. In multiple regression the matrix X is observable, while in factor analysis, the common and specific factors are abstract constructs, and are thereby not observable (Van Laar, 1987). The method is widely used in the social sciences, but otherwise little used (Chatfield and Collins, 1996).

2.4.2.12 Pattern analysis

The technique is mostly aimed at simplifying a mass of data which are otherwise difficult to manipulate. Pattern analysis is a numerical method used in the looking for and establishing of patterns and the analyses of patterns in data. The criteria for the establishment of the patterns are usually up to the researcher, and there are many methods for determining patterns (Matheson and Raymond, 1984).

Pattern analysis and the use of numerical classification, to group the environments by their effects on the genotypes has been successfully applied in agriculture. The analyses have mostly been directed towards identifying sites which would best express particular effects on genotypes. Environmental testing could thereby be reduced to only those environments, or groups of environments, which were most likely to provide maximum information on the specific breeding objectives (Byth *et al*, 1976; Shorter *et al*, 1977; Matheson and Raymond, 1984).

CHAPTER 3

EUCALYPTUS GRANDIS : THE SPECIES

3.1 NATURAL HABITAT

3.1.1 Distribution

The natural distribution of *E. grandis* occurs on the north-eastern coastal regions of Australia, limited to a disjunct distribution in north-eastern New South Wales and eastern Queensland. The principal occurrence is on the coastal belt between Newcastle in New South Wales and Bundaberg in Queensland corresponding to a latitude of 25 to 33 °S. It also occurs further north in Queensland in isolated pockets near Mackay (around 21 °S) and on the Atherton Tableland (around 16 to19 °S). The species occurs altitudinally from sea level to 300 m in New South Wales and up to 1100 m in Queensland. The total latitudinal range is from 16 to 33 °S (Poynton, 1979; Boland *et al*, 1984).

3.1.2 Climate

The climate within the natural range of *E. grandis* is subtropical to warmer-temperate, equable and humid throughout this range. In the north, the mean maximum and minimum temperatures for the warmest months are typically in the range of 29 to 32 °C, and for the coolest months from 10 to17 °C. In the south the corresponding ranges are 24 to 30 °C for the warmest months and 3 to 8 °C for the coldest months. The rainfall is mostly during the summer months and averages 1000 to 3500 mm per annum. The heaviest rainfall occurs in the northern part of the species range. During the drier winter months, the monthly rainfall rarely falls below 25 mm. Warm to mildly hot weather conditions prevail in the summer, with some limited mild frost at higher elevations or in valley bottoms. The coastal sites are however mostly frost free. High humidities are present during both summer and winter. (Poynton, 1979; Boland *et al*, 1984)

3.1.3 Site characteristics

In New South Wales, the species usually occurs on moist swampy flats, but further north in Queensland it occurs on fertile valleys as well as on the lower slopes of hills and mountains and ascends to the tablelands. The best development of the species is on deep, moist, well drained, friable, loamy, alluvial deposits mainly derived from basalts. It does however not tolerate waterlogged conditions. The species is typically found in pure, or nearly pure stands (Poynton, 1979; Boland *et al*, 1990).

3.2 EXOTIC HABITAT

3.2.1 Areas planted

As an exotic plantation grown tree *E. grandis* has proved highly successful. It has been planted with great success at intermediate elevations, where it combines rapid growth with excellent stem form (Poynton,1979). Approximately 75% of all the eucalypt plantation area in South Africa is planted with *E. grandis*, where it shows a general adaption to the local soils and climate. A total of 445,612 ha has been planted to the species (and its hybrids) in South Africa, 396,037 (88,9%) are in private hands and 49,575 (11,1%) in the public sector (Forest Owners Association, 1997).

3.2.2 Soil requirements

For optimum growth, it requires a free draining soil with an ERD greater than 100 cm and a minimum ERD of at least 60 cm. The species grows most vigorously on fertile loams or clay-loams (Poynton, 1979; Herbert, 1993). Most South African forestry soils are however suitable, provided they are well-drained and well-weathered. Stonelines, perched water tables and very firm clay-textured or structured subsoils all impede root development. The optimum soils for root development are apedal and friable subsoils or deep (regic) sands, where large quantities of plant-available soil water can be stored. Hydromorphic subsoils have been found to be unsuitable for growth (Herbert, 1993).

3.2.3 Temperature, rainfall, and altitudinal requirements

A mean annual temperature above 16°C, with a upper limit of 22°C and the mean for January of 27°C have been found to be optimum. The mean July temperature should be at least 11°C and the minimum not less than 4°C (Schönau and Schulze, 1984). The aforementioned temperature bands correspond to areas between sea level and 1100 m in southern KwaZulu Natal, 1200 m in Mpumalanga and 1350m in the Northern Province (Herbert, 1993).

E. grandis requires a subtropical or warmer-temperate, humid climate with a summer rainfall never less than 800 mm (Esterhuyse, 1985). A minimum mean annual precipitation of 900 mm in the cooler areas and 1000 mm in the warmer areas has been found to give reasonable growth results (Schönau and Schulze, 1984). Where the rainfall is however lower, the species should be planted on the foot slopes or alluvial plains where additional sources of groundwater could be available (Herbert, 1993).

3.2.4 Pests and diseases

No serious insect pests affect the species, but many fungi attack the species. *Cryphonectria* stem canker, one of the world's most serious diseases of eucalypts, occurs in South Africa, mainly in Zululand. Plantation losses in recent years have however been associated with a second severe pathogen, *Botryosphaeria*. Other severe stem cankers to be found on the species are *Endothia* and *Coniothyrium*, (Wingfield and Kemp, 1993).

CHAPTER 4

EXPERIMENTAL MATERIALS AND METHODS

4.1 RESEARCH APPROACH

Four underlying considerations, relating to the selection of the research material, the selection of the trial sites, the trial design, and the envisaged method of analysis, were considered prior to the planning of the field trial:

- Research material: Thirty unrelated clones, should give a balanced and buffered representative spread of the species, and be a manageable sample size to give reliable growth data.
- Test sites: In order to have enough sites to evaluate the envisaged site growth factors 30 diverse sites should be a reasonable sample.
- Trial design: As a compromise, and to keep the trial series within manageable constraints a balanced but incomplete trial design, with independent controls, should be used.
- Analytical method: The design should be chosen to fully utilise and optimise the use of linear regression or other related analytical procedures.
- Assessments: Two, or more growth assessments should be undertaken on at least two common growth variables to accommodate possible age to age correlations.

These five "assumptions" were in line with the findings, in the previously discussed literature survey on the study of GEI (Barnes and Gibson, 1984; Matheson, 1988; Shelbourne, 1972; Skroppa, 1984).

4.2 EXPERIMENTAL DESIGN

4.2.1 Basic trial design

The design chosen to evaluate all the test clones over all the test sites, was an incomplete latin square design, plan 13.2a (Cochran and Cox, 1957). The design was a compromise design

that would allow 31 test clones to be tested across 31 test sites, but without having to test each of the 31 test clones on all of the 31 test sites. As an incomplete latin square design, each individual test site had only 10 of the 31 test clones, and each individual test clone was only present on 10 of the 31 test sites, as listed and shown in APPENDIX. 1 : Tables 1 and 2.

4.2.2 Complementary trial design

In order to comply with the basic assumption behind regression analysis, of having an independent and a dependent variable, an additional modified design was incorporated into the aforementioned latin square design. At each individual test site, five common among sites controls were randomly incorporated into the modified design. Each individual site was therefore planted with a 15 entry randomised complete block design (RCB), incorporating the 10 test clones and the five common among site controls.

Each site was further expanded and divided into three replications. At all of the sites 4 x 4 tree plots (16 trees) were used for both the test clones and the common controls. All replications, and plots within replications were adjacent to each other, and no internal surrounds were included in the design (Van Wyk, 1987).

4.2.3 Modified design

A shortage of certain test clones, following greenhouse and nursery failures, resulted in a modification of the trial designs of the last sites planted. Only two replications were planted at Ashenden, Gingindlovo, Knogka, Nseleni, Mooiplaas and Richmond. The sites at Eersteling A, B and C, Frankfort, Townlands and Waldeck were limited to only one replication each, as listed in Table 1.

4.3 SITE SELECTION

The 31 test sites, to be incorporated into the experimental design, were selected to represent the widest possible spread of sites within the commercial planted range of *E. grandis* in South Africa, as shown in Table 1 and Figure 1.

4.3.1 Site selection criteria

The sites for trial series were selected primarily based on the measurable site factors mentioned in the literature review and the guidance of Dr D.C. Grey. Sites were selected to cover the following major growth factors:

- Temperature: A range of mean (MAT), minimum (MIN) and maximum (MAX) temperatures to be sampled, though the choice of sites at different latitudes, aspects, and altitudes. Where exact site measurements are not available, latitude, aspect and altitude could serve as surrogates (Grey, 1987*b*).
- Rainfall: Low or high rainfall (MAP) to be evaluated against the mean annual temperature.
- Soil depth: Rooting depth (ERD) in cm to be determined to serve as an indication of shallow or deep sites. Sites with less than 90 cm to a root restricting layer are usually considered shallow, and greater than 90 cm, deep (Grey, 1987*b*).
- Texture: Texture classes to be determined as the percentage sand, silt or clay.
- Slope and aspect: A division between "flat" and steep sites (>5°), and northerly and southerly aspects. Actual slopes and aspects to be recorded in degrees (°).

The sites were selected, using a pre-determined selection matrix to obtain an even spread of the above mentioned site factors. At each site, the latitude (LAT), longitude (LON), altitude (ALT), rainfall (MAP), driest quarter (DRY), mean annual temperature (MAT), minimum temperature (MIN), maximum temperature (MAX), geology, soil form, rooting depth (ERD), slope (SLP) and aspect (ASP) were recorded. The division of the abovementioned growth factors in relationship to the individual trial sites are listed in Table 1 and APPENDIX. 2 : Table 1.

4.3.2 Soil analysis

In addition to the determination of soil texture classes, a number of soil chemical factors that could possibly be important to tree growth were also analysed. The analysis was undertaken

in the analytical laboratory at the Saasveld F.R.C. near George. The following additional analyses were undertaken: Soil acidity in water (pH(H_2O)) and in Potassium chloride (pH(KCl)), soil organic matter (Org.Mat), percentage carbon (C), exchangeable acidity (EA), Aluminium (Al), Nitrogen (N), Phosphorus (P) and the S- value (S-Val), as detailed in APPENDIX 2 : Table 3.

4.4 RESEARCH MATERIAL

4.4.1 Test clones

Thirty one *E. grandis* test clones were preselected from available commercial clones in production or being tested by H.L.& H., Mondi, and Northern Timbers and SAFRI. The clones were selected to represent a diverse genetic make-up and included both half- and full-sib crosses.

The test clones were set and raised at three nurseries: H.L.& H. at Fountains, Mondi in Sabie, and SAFRI at D.R. de Wet FRS. The material was cut from the respective cutting banks at the three nursuries and set during November, 1987. The clones were set and raised using a standard macro-cutting procedure in a controlled environment greenhouse. All clones were raised in a vermiculite and perlite rooting medium and Unigrow 128 containers. Enough cuttings were set to obtain 480 ramets for each test clone.

Unfortunately, due to low rooting percentages, not enough cuttings were available from six of the pre-selected *E. grandis* clones, and clones of four *Eucalyptus* hybrids and two substitute commercial *E. grandis* clones were therefore obtained from the H.L.& H nursery at White River. The hybrid clones were GxC 9/03, GxC16/08, GxT22/02 and MxG25 and the *E. grandis* clones KFT23/33 and KFT81/13/2 as listed in Table 2.

4.4.2 Common controls

Two *E. grandis* seedling mixtures and three *E. grandis* clones were selected to be used as the five common controls. The seedling controls consisted of a clonal seed orchard mixture (38047) and a seedling seed orchard mixture (38046), as listed in Table 3.

Table 1 Location details of trial test sites of GEI clonal trial series

No	Code	Plantation	Company	District	Reps	Planted	Lat (°S)	Long (°E)	Alt (m)
1	FZS	Fransinasrus	Lotzaba	Barberton	3	06-88	25 45	30 52	860
2	RMD	Richmond	SAPPI	Richmond	2	11-88	29 54	30 11	1100
3	TKF2	Tygerskloof 83	H.L.& H.	Vryheid	3	05-88	27 50	31 20	1150
4	AND	Ashenden	H.L.& H.	New Hanover	2	01-89	29 19	30 35	1050
5	TST	Ntenja	SAPPI	KwaMbonambi	3	06-88	28 33	32 10	45
6	NYL2	Nyalasi J9	DWAF	Mtubatuba	3	08-88	28 10	32 20	40
7	SMK	Middagson	H.L.& H.	Soekmekaar	3	09-88	23 27	30 02	1205
8	ESL1	Eersteling A	H.L.& H.	Paulpietersburg	3	11-88	27 34	30 50	1050
9	MPS	Mooiplaas	SAPPI	Melmoth	2	11-88	28 33	31 16	1050
10	NLN	Nseleni	Mondi	Richards Bay	2	10-88	28 41	32 03	50
11	WHB	Waterhoutboom	Mondi	Graskop	3	05-88	24 57	30 55	980
12	TBD	Tidboald	SAPPI	KwaMbonambi	3	06-88	28 38	32 02	80
13	TLD	Townlands	H.L.& H.	Greytown	1	01-89	29 05	30 38	1060
14	TKF1	Tygerskloof 29	H.L.& H.	Vryheid	3	05-88	27 49	31 18	1100
15	UMD	Umsunduze	Mondi	KwaMbonambi	3	08-88	28 30	32 08	45
16	WLD	Waldeck	H.L.& H.	Duiwelskloof	1	12-88	23 44	30 14	910
17	JDM	JDM Keet FRS	DWAF	Tzaneen	3	05-88	23 47	30 07	750
18	ESL3	Eersteling C	H.L.& H.	Paulpietersburg	3	11-88	27 34	30 50	1030
19	ELD	Eldorado	N/Timbers	Duiwelskloof	3	10-88	23 44	30 12	760
20	PDN	Port Durnford	DWAF	Empangeni	3	08-88	28 54	31 48	120
21	ESL2	Eersteling B	H.L.& H.	Vryheid	3	02-88	27 34	30 50	1050
22	SFT	Swartfontein	DWAF	White River	3	06-88	25 16	30 58	1100
23	FRT	Frankfort	DWAF	Sabie	1	10-88	25 02	30 53	980

Table 1 continued

No	Code	Plantation	Company	District	Reps	Planted	Lat (°S)	Long (°E)	Alt (m)
24	FWD	Fernwood	Mondi	Mtubatuba	3	07-88	28 18	32 18	60
25	KGA	Knogka	SAPPI	Highflats	2	11-88	30 15	30 15	975
26	VTM	Venus Timbers	SAPPI	Graskop	3	06-88	24 59	30 53	920
27	CTR	Christinasrust	N/Timbers	Duiwelskloof	3	06-88	23 42	30 06	1350
28	DNL	Doornlaagte	Mondi	Graskop	3	05-88	24 53	30 58	920
29	GLP	Glenthorpe	Lotzaba	Barberton	3	06-88	25 44	30 51	850
30	NYL1	Nyalazi E23	DWAF	Mtubatuba	3	08-88	28 16	32 22	40
31	GNG	Gingindlovo	Shell	Gingindlovo	2	10-88	29 00	31 40	70

The present status of the South African companies involved in the GEI trial series is as follows:

DWAF presently Safcol

H.L.& H. incorporated into Mondi

Lotzaba incorporated into SAPPI

Shell incorporated into Mondi

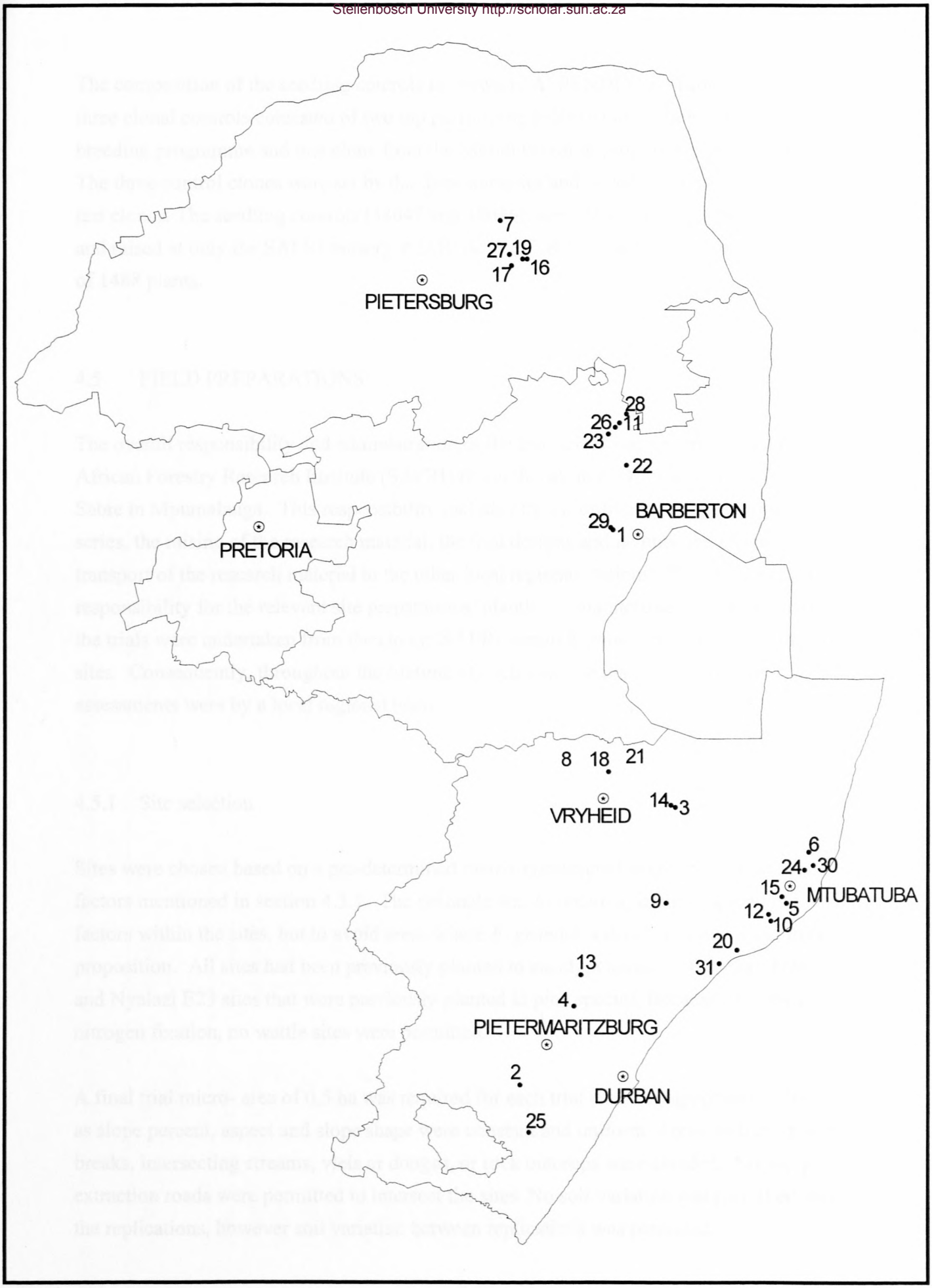

Figure 1. Map of the eastern portion of South Africa showing the locations of the GEI trials

The composition of the seedling controls is shown in APPENDIX. 3 : Tables 1 and 2. The three clonal controls consisted of two top performing half-sib clones from the SAFRI breeding programme and one clone from the Mondi breeding programme, as listed in Table 3. The three control clones were set by the three nurseries and raised concurrently with the 31 test clones. The seedling controls (38047 and 38046) were all sown during November 1987 and raised at only the SAFRI nursery at D.R. de Wet F.R.C.. Each of the controls had a total of 1488 plants.

4.5 FIELD PREPARATIONS

The overall responsibility and administration of the trial series was undertaken from the South African Forestry Research Institute (SAFRI) research station at D.R. de Wet F.R.S., near Sabie in Mpumalanga. This responsibility included the co-ordination of the complete trial series, the raising of the research material, the trial designs and layouts, the pre-packing and transport of the research material to the other local regional stations. The local regional responsibility for the relevant site preparations, plantings, maintenance and assessments of the trials were undertaken from the closest SAFRI research station in proximity to the trial sites. Consequently, throughout the lifetime of each trial, the planting, maintenance and assessments were by a local regional team.

4.5.1 Site selection

Sites were chosen based on a pre-determined matrix constructed to cover the macro- site factors mentioned in section 4.3.1. The rationale was to obtain a balanced spread of the site factors within the sites, but to avoid areas where *E. grandis* was not considered a commercial proposition. All sites had been previously planted to eucalypt species, other than Frankfort and Nyalazi E23 sites that were previously planted to pine species. Because of a possible nitrogen fixation, no wattle sites were permitted.

A final trial micro- area of 0,5 ha was required for each trial site. Topographical features, such as slope percent, aspect and slope shape were constant and uniform. Areas with clear slope breaks, intersecting streams, vleis or dongas, or rock outcrops were avoided. No slip paths or extraction roads were permitted to intersect the sites. No soil variation was permitted within the replications, however soil variation between replications was permitted.

Table 2 Details of the 31 test clones included in the GEI trial series

No	Clone	Other number	Species	Origin of ortet: Company	District	Ortet parentage: Female	Male
1	SGR009	1/08/2	*E. grandis*	SAFRI	Tzaneen	G111	Open pollinated
2	SGR013	1/11/9	*E. grandis*	SAFRI	Tzaneen	G109	Open pollinated
3	SGR041	1/45/8	*E. grandis*	SAFRI	Tzaneen	29154	Open pollinated
4	SGR042	1/45/9	*E. grandis*	SAFRI	Tzaneen	29154	Open pollinated
5	SGR046	1/63/2	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
6	SGR047	1/63/3	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
7	SGR048	1/63/4	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
8	SGR051	1/63/7	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
9	SGR052	1/63/8	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
10	SGR053	1/63/9	*E. grandis*	SAFRI	Tzaneen	G105	Open pollinated
11	SGR054	1/65/9	*E. grandis*	SAFRI	Tzaneen	G163	Open pollinated
12	SGR112	2/39/2	*E. grandis*	SAFRI	Tzaneen	G205	Open pollinated
13	SGR183	3/06/6	*E. grandis*	SAFRI	Tzaneen	G270	Open pollinated
14	SGR192	3/36/5	*E. grandis*	SAFRI	Tzaneen	G299	Open pollinated
15	SGR202	3/54/2	*E. grandis*	SAFRI	Tzaneen	G317	Open pollinated
16	SGR428	71/2	*E. grandis*	SAFRI	Tzaneen	G35	G37
17	SGR438	17/1	*E. grandis*	SAFRI	Tzaneen	G37	G4
18	SGR451	159/4	*E. grandis*	SAFRI	Tzaneen	G44	G4
19	SGR467	203/4	*E. grandis*	SAFRI	Tzaneen	G45	G58
20	SGR470	48/2	*E. grandis*	SAFRI	Tzaneen	G50	G4
21	SGR472	93/2	*E. grandis*	SAFRI	Tzaneen	G50	G4
22	SGR481	58/2	*E. grandis*	SAFRI	Tzaneen	G58	G4
23	SGR482	118/2	*E. grandis*	SAFRI	Tzaneen	G58	G4

Table 2 continued

No	Clone	Other number	Species	Origin of ortet: Company	District	Ortet parentage: Female	Male
24	SGR494	52/2	*E. grandis*	SAFRI	Tzaneen	G66	G39
25	SGR515	37/4	*E. grandis*	SAFRI	Tzaneen	G15	G6
26	KFT23/33		*E. grandis*	H.L.& H.	White River	unknown	unknown
27	KFT81/13/2		*E. grandis*	H.L.& H.	White River	unknown	unknown
28	GXC9/03		*E. grandis* x *E. camaldulensis*	SAFRI	Duiwelskloof	G101	24223
29	GXC16/08		*E. grandis* x *E. camaldulensis*	SAFRI	Duiwelskloof	G101	24223
30	GxT22/02		*E. grandis* x *E. tereticornis*	SAFRI	Duiwelskloof	G15	24322
31	MXG25		*E. macarthurii* x *E. grandis* ?	ICFR	Pietermaritzburg	unknown	unknown

Table 3 Details of the common control clones and seedlots included in the GEI trial series

No	Control	Other	Species	Type	Origin: Company	District	Parentage of ortet/seedlot: Female	Male
1	SGR071	1/92/7	*E. grandis*	clone	SAFRI	Tzaneen	U219	Open pollinated
2	SGR072	1/92/9	*E. grandis*	clone	SAFRI	Tzaneen	U219	Open pollinated
3	TG12		*E. grandis*	clone	Mondi	Panbult	unknown	Open pollinated
4	38046		*E. grandis*	seedlings	SAFRI	Tzaneen	298 families	Open pollinated mixture
5	38047		*E. grandis*	seedlings	SAFRI	Tzaneen	74 clones	Open pollinated mixture

4.5.2. Soil sampling

A soil pit (2 m long x 1 m wide x 1,5 m deep) was dug in the centre of each of the replications. A soil sample from each of the horizons was then collected and the soil classified (form, family and phase). A bulk sample of the A horizons within each replication was also collected from five observation points within each replication (Grey, 1987*a*).

4.5.3 Field preparations

The field preparations for the trial plantings were organised under the supervision of the local regional teams, together with the relevant company plantation staff, as indicated in Table 1. All debris was removed by hand and the coppice material was killed by chemical methods. No burning was undertaken so as to avoid ash bed effects. A pre-planting chemical treatment was undertaken where necessary to ensure a minimum of weeds. An espacement of 2,7 m x 2,7 m was used at all sites. Hand hoed planting pits, measuring 1,0 m wide and 0,5 m deep were made at all sites. Planting lines were laid out between existing stump rows and no destumping was undertaken. For white grub control, 10 grams of Gamma BHC insecticide was applied to each planting pit prior to plant.

4.5.4 Planting operations

The field planting operations commenced in May 1988 at Doornlaagte and was completed in January 1989 at Ashenden, a time lapse of eight months. Planting was undertaken by the relevant local plantation planting crews using the "puddle planting method", each tree receiving 2 litres of water. At the time of planting, one hundred grams of 2.3.2 (22) NPK fertilizer was applied per tree, in a circle 25 cm from each plant.

4.5.5 Post- planting care

Throughout the first twelve months, and where practically and administratively possible, the sites were kept weed free. Frost damage soon after planting resulted in the trials at Eldorado and Frankfort having to be totally replanted after the first winter in October 1988. Severe frost damage during the first winter resulted in the trials at Eersteling B and C being

abandoned. Due to insufficient plants it was not possible to re-establish these two trials. Some frost damage was also recorded during the first winter, in the trials at Richmond, Ashenden, Mooiplaas, Townlands, Knogka and Eersteling A. During October 1989, mild fire scorching occured at the Nyalasi E23 (NYL1) site. The trial at Mooiplaas was severely scorched at age four years in a plantation fire during September 1992. Between the ages of two years and five years, the trials at Richmond and Townlands, were lost due to the theft of the demarcation poles and silvicultural neglect.

CHAPTER 5

ASSESSMENT PROCEDURES AND FIELD SAMPLING

5.1 ASSESSMENTS

To facilitate the objectives of this study, the trials were measured at two and five years. The measurements were however staggered to account for the eight month planting delay between the first trial planted and the last trial planted. All the trials were therefore effectively measured at 26 months, and at 63 months.

5.1.1 Two year growth

After two years, 29 sites were still available for assessment (excluding Eersteling B and C) and these sites were assessed at 26 months for height, diameter at breast height (DBH), stem form and stem defects, as described in APPENDIX 4 : Table 1.

5.1.2 Five year growth

After five years, only 27 sites still remained (excluding Eersteling B and C, Richmond and Townlands). They received a final assessment at 63 months for height, DBH, stem form, stem disease infestation and stem defects, as described in APPENDIX 4 : Table 2.

5.2 MISSING VALUES

5.2.1 Growth data

The Eersteling B and C sites were not assessed at two years and the Richmond, Townlands, Eersteling B and Eersteling C sites were not assessed at five years.

5.2.2 Soils data

Many of the sample numbers from the soil analysis could not be positively identified from the laboratory codings and consequently had to be discarded. These included all nine of the soil samples from the Tidboald and Waldeck sites. There are therefore no soil analysis results available for any of the horizons from these two sites. The site at Gingindlovo and had only a single bulked A and B sample.

Twenty three other soil samples were also either missing or unidentifiable from the laboratory codings. The other missing sites and horizons were as follows: Nyalazi 2, 2A bulk, and 3A bulk; Eersteling A, 1A bulk, 2A bulk, and 3A; Mooiplaas, 1A bulk, 2A bulk, and 3A bulk; Nseleni, 1A bulk, 1B, and 2A bulk; Eersteling C, 3A bulk; Eersteling B, 2A bulk; Swartfontein 3B; Venus Timbers, 3B; Fernwood 2A bulk; Doornlaagte, 1A bulk, 2A bulk, and 3 A bulk; and Nyalazi 1, 1B, 2A bulk and 3A bulk.

5.2.3 Substitute data

With reference to the aforementioned section 5.2.2, and in order to compose a more complete soils data set, the following 18 missing bulk A horizon samples were pooled with the individual soil pit A horizon samples from each respective replication: Nyalazi 2, 2A bulk, and 3A bulk; Eersteling A, 1A bulk, 2A bulk, and 3A; Mooiplaas, 1A bulk, 2A bulk, and 3A bulk; Nseleni, 1A bulk, and 2A bulk; Eersteling C, 3A bulk; Eersteling B, 2A bulk; Fernwood 2A bulk; Doornlaagte, 1A bulk, 2A bulk, and 3 A bulk; and Nyalazi 1, 2A bulk and 3A bulk. This pooling of the 18 bulk samples, from a total of 82 possible bulk A samples (replications), represents a 22% pooled sample for the bulk A horizons.

5.3 ASSESSMENT METHODOLOGY

5.3.1 Height, diameter, and volume assessments

For the two year assessments, tree heights, were measured using height rods, while for the five year assessment a hypsometer was used. All diameter (DBH) measurements were measured using a diameter tape. Measuring units and methodology are described in APPENDIX 4 : Tables 1 and 2.

Stem volumes were calculated from the tree heights in metres and the DBHs in mm, using the formula developed for *E. grandis* by Bredenkamp and Loveday (1984), as described in APPENDIX 4 : Table 5 .

5.3.2 Stem form assessments

Stem form was visually assessed and scored, using an eight point subjective scale of one to eight, where eight is straight and one is malformed, as illustrated in APPENDIX 4 : Table 3.

5.3.3 Disease infestation scores

Stem disease infestation was visually assessed and scored, using a five point subjective scale of 0 to 4, where 0 was no visual infestation and 4 was a chronic visual infestation, as illustrated in APPENDIX 4 : Table 4. The clear bole portion of the tree, up to the live crown, was used for the visual assessment. The three most prevalent stem diseases attacking eucalypts in South Africa, namely *Coniothyrium*, *Cryphonectrea* and *Endothia*, were each assessed separately on the common five point scale,

5.4 ASSESSMENT TEAMS

For practical purposes, the division of work loads, and the vast distances between trial locations, it was deemed necessary to divide the trial assessments between local regional measuring teams. Consequently, for the two year assessments, the trials in Mpumalanga, KwaZulu-Natal, and Northern Province were measured by three local measuring teams, and for the five year assessments, the combined Mpumalanga and Northern Province trials, and the KwaZulu-Natal trials were measured by two local measuring teams.

CHAPTER 6

DATA HANDLING AND ANALYTICAL METHODOLOGY

6.1 DATA HANDLING

All of the field data and assessments, were pre-recorded by pen and paper, on either field soil description forms, laboratory analysis sheets or on pre-prepared coding sheets. The climatic data was downloaded from the site latitude and longitude co-ordinates using the data base generated for South Africa from the South African Atlas of Agrohydrology and -Climatology (Schulze, 1997), and then entered together with the site and soil variables in a common site data set (GEI_SITE) using a Quatro Pro spreadsheet package.

The two and five year growth assessments were entered from the field coding sheets onto a uniformly formatted spreadsheet for each individual site. The individual sites were then merged into two combined data sets, firstly for the two year data (GEI2), and secondly for the five year data (GEI5). All data sets were then transferred from the spreadsheet format into the SAS format where all data verification, editing, and analysis was undertaken using the SAS analyses packages (SAS Institute release 6.11, 1995).

6.2 DATA VERIFICATION

6.2.1 Tests for normality

Tests for normality of the data were undertaken through the calculation of skewness and kurtosis (Gibson, 1982; Ott, 1993). All of these analyses were undertaken utilising the options available in the SAS package. Editing was undertaken by using the proc FREQ and proc SORT procedures, and the tests for normality using the proc UNIVARIATE procedure. For the tree height and DBH distributions, the proc UNIVARIATE procedure showed normality; with no skewness or excess kurtosis following editing. The subjective data scores for stem form and disease infestations did however have some skewness. The stem form data showed positive skewness while the disease scores for *Coniothyrium*, *Cryphonecrea*, and *Endothia* all showed negative skewness. This was however to be expected as most trees would be inclined to have better tree form and little disease infestation.

6.2.2 Summary tables

The growth measurement data was initially analysed as two distinct and separate data sets as described in section 4.2.1. The first unique data set consisted of only the common controls planted on all of the sites, and the second unique data set consisted of the test clones planted on the relevant sites.

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The proc SORT and proc MEANS procedures were then used to construct the site and soil horizon summary data (GEI_SITE) tables as listed in APPENDIX 5 : Tables 1 to 4. This summary data process was repeated for the two year (GEI2) and five year (GEI5) data sets, as listed in APPENDIX 5 : Table 5 and Table 6.

6.3 ANALYTICAL METHODOLOGY

Five analytical methods were employed to analyse the data sets. These methods were chosen (or modified) to suit the incomplete clonal trial design and the RCB common control design, as described in sections 4.2.1, 4.2.2 and 4.2.3. The following five procedures were chosen:

● ANOVA/Newman-Keuls tests	To evaluate and rank the means of the sites and the clones
● Correlation analysis	To determine the correlations between the environmental and the growth variables
● Joint regression analysis (JRA)	To assess the effect of GEI at a clonal level, and to select clones for production
● Factor analysis (FA)	To determine the patterns of association between the environmental factors and the growth variables
● Multiple regression analysis	To construct site-response models, and to link the environmental factors and the growth variables of the clones

Many other possible GEI evaluation methods, such as clone to clone genetic correlations and AMMI, had to be abandoned due to the incomplete design nature of this trial series. The analysis of variance (ANOVA) was undertaken using the proc GLM procedure that is available in SAS. This procedure was deemed more appropriate than using the proc ANOVA

procedure due to the incomplete and unbalanced nature of the data. Delineation of significant differences between sites and between clones, for volume production, stem form, survival percentages, and stem defects was carried out by the Newman-Keuls test (SNK test) that is available within the GLM procedure. The SNK test was used rather than the Duncan or LSD tests for the rankings of both the site and the clone means, as the SNK test results in a more useful resolution. The survival percentages and stem defect percentages were first transformed using an Arcsin transformation. The SNK rankings of the sites was undertaken using only the means of the common controls, while the test clones plus the common controls means were used to rank the treatments. This separation was deemed necessary owing to the trial design and possible bias towards certain clones or sites.

CHAPTER 7

RESULTS AND DISCUSSION

7.1. ANALYSIS OF VARIANCE

A series of ANOVAs was run to test for the effects of genotypes, environments and interactions. This was done for the soils data (GEI_SITE), the two year growth data (GEI2) and the five year growth data (GEI5).

7.1.2 Soils data

As a result of the large proportion of missing samples within the soils data, as mentioned in sections 5.2.2 and 5.2.3, it was initial deemed necessary to investigate the between site, and the within site (replication) variation for each of the soil horizons. For the A horizon, the bulk A horizon, and the B horizon, the ANOVA's revealed highly significant between site differences for every soil variable measured. Further, for replications within sites, utilizing the A horizons (both individual and bulk), highly significant ($p = 0,0001$) within site differences were found for both nitrogen (N) and phosphorus (P), as shown in APPENDIX 7 : Table 1. Due to a lack of sufficient degrees of freedom within the ANOVA, the individual B horizons could not be used on their own to test for a site by replication effect. Therefore, the A and B horizons were pooled to give an indication of the "total bulked site soil sample". This analysis revealed no significant ($p > 0,05$) within site differences other than for phosphorus ($p < 0,05$), but did once again indicate highly significant ($p = 0,0001$) between site differences, as shown in APPENDIX 7 : Table 2. The within site differences for nitrogen and phosphorus must be seen in light of the very large ranges given in APPENDIX 5 : Tables 2, 3 and 4, where the within site ranges are often greater than the between site ranges.

7.1.3 Two year data

Although the main focus of the analysis is to concentrate on the five year data set, the two year set is required for age to age correlations and other possible early indicators of trends within the sites and clones. Consequently the full range of results, including ANOVA tables

and Newman-Keuls groupings, are given in the appendices section of the thesis. The analysis per site, for volume production and stem form, are shown for the common controls in APPENDIX 7 : Tables 3 and 4. The mean survival percentages per sites (using both the common controls and the test clones), are then given in APPENDIX 7 : Table 5. The data was then re-analysed on a treatment basis (common controls plus test clones) and these results are given in APPENDIX 7 : Tables 6 to 9. No summary tables of the two year data are included in the main contents section of the thesis.

The results for the common controls revealed highly significant ($p = 0,0001$) between site differences for mean volume and stem form. The interaction component between sites and controls were also highly significant. The traditionally perceived "good" *E. grandis* sites of KwaZulu-Natal at Port Durnford, and the Mpumalanga area at Doornlaagte, Venus Timbers and Waterhoutboom were the top performing sites for volume production, while the dry Nyalazi 2 site was the poorest performer. Stem form did not however follow the same patterns and no tendency could be seen from the analysis. The mean survival percentage was low at 61%, with a best mean site survival of 78,1% at Swartfontein and the poorest mean site survival of only 25,9% at Ashenden.

The analysis per clone revealed the same highly significant tendencies for all variables. The better clones already had a volume of nearly double the poorer clones and groupings of clones were already present at this early age. The mean stem form scores per clone ranged from 4,2 to 6,7 with a relatively high mean stem form of 5,7. This was however to be expected with this specific range of advanced generation clones. The poorest clone had survival count of 41,8% while the best clone had a survival of 74,3%. The overall mean survival was mediocre at 61%. The mean stem defects for stem forks revealed that 4,3% of all trees had deformed stems. The hybrid clones had a higher percentage of deformed stems with clone MXG25 having 11,1% deformed stems.

7.1.4 Five year data

The analysis of variance and multiple range ranking tests, initially utilising only the common controls over all sites, for volume production, stem form, *Coniothyrium*, *Cryphonectrea*, and *Endothia* infestation, are shown in APPENDIX 7 : Tables 10 to 14. The site mean survival percentages, for all treatments (controls plus test clones), are then given in APPENDIX 7 : Table 15. The data was then re-analysed utilising all treatments (controls plus test clones)

over all the sites, and these results are given in APPENDIX 7 : Tables 16 to 22. The summary tables of the five year data are given in the main contents section of the thesis in Tables 4 to 6.

The same general tendencies, for both the common controls and the test clones, that were observed at two years were repeated at five years for volume production, stem form, survival and stem defects. Venus Timbers, Port Durnford and Waterhoutboom remained the overall better performing sites for volume production. Nyalazi was, as at two years, the poorest performing site. Furthermore, clearly defined Newman-Keuls groupings of the sites were present, the groupings being utilizable for future stratification of possible clonal test zones. The best site now had a common control mean volume ten fold the poorest site. The mean stem form score had declined slightly to 4,85 for both the common controls and test clones combined. The mean survival had remained more or less constant at 60,5%, and the mean stem defects had only become marginally poorer.

The three new variables measured, *Coniothyrium*, *Cryphonectria* and *Endothia* infestation scores all revealed highly significant between sites, between treatments, and interaction differences. The *Coniothyrium* and *Cryphonectrea* infestations were limited to the KwaZulu-Natal sites, but were very low even at the most highly infected sites. The *Endothia* was the mirror image of the previously mentioned diseases with heavier infestation on the Mpumalanga and the Northern Province sites. It must however be pointed out at this point that the disease scores were done by two separate measuring teams across the division between provinces. The overall *Endothia* infestation was higher for all treatments than was the *Coniothyrium* and *Cryphonectrea* infestations. The summary data for all of the variables are given in Table 5 for the clones and in Table 6 for the controls.

Table 4. Means per site of the common controls ($MEAN_{controls}$) for survival, volume, stem form and disease infestation, age 5 years.

Clone	Survival (%)	Volume (m^3)	Stem form	*Coniothyrium*	*Cryphonectrea*	*Endothia*
FZS	66,6	0,0724 (0,0019)	6,0 (0,05)	0,003 (0,000)	0,000	2,217 (0,062)
RMD	-	-	-	-	-	-
TKF2	56,2	0,1090 (0,0058)	3,6 (0,09)	0,000	0,000	0,000
ADN	39,8	0,0921 (0,0055)	4,2 (0,16)	0,000	0,032 (0,022)	0,065 (0,045)
TST	61,0	0,0815 (0,0029)	4,0 (0,07)	0,000	0,000	0,031 (0,023)
NYL2	64,9	0,0212 (0,0008)	4,2 (0,08)	0,009 (0,009)	0,051 (0,022)	0,164 (0,045)
SMK	71,2	0,0429 (0,0013)	5,5 (0,05)	0,000	0,000	1,694 (0,064)
ESL1	61,6	0,0636 (0,0046)	5,7 (0,10)	0,283 (0,068)	0,000	0,000
MPS	67,5	0,0425 (0,0017)	3,4 (0,08)	-	-	-
NLN	61,7	0,0772 (0,0031)	4,0 (0,09)	0,000	0,008 (0,008)	0,056 (0,031)
WHB	52,5	0,1714 (0,0082)	5,9 (0,08)	0,000	0,000	1,392 (0,067)
TBD	56,5	0,0817 (0,0034)	4,3 (0,09)	0,010 (0,010)	0,012 (0,010)	0,021 (0,014)
TLD	-	-	-	-	-	-
TKF1	76,3	0,0637 (0,0019)	3,7 (0,06)	0,000	0,000	0,000
UMD	42,1	0,0617 (0,0026)	4,1 (0,09)	0,000	0,015 (0,011)	0,120 (0,041)
WLD	67,1	0,0948 (0,0072)	5,8 (0,09)	0,000	0,000	1,647 (0,102)
JDM	57,7	0,0626 (0,0028)	5,0 (0,05)	0,000	0,000	2,582 (0,076)
ESL3	-	-	-	-	-	-
ELD	66,7	0,1527 (0,0063)	5,1 (0,06)	0,005 (0,000)	0,000	1,034 (0,036)
PDN	54,6	0,1797 (0,0058)	4,2 (0,10)	0,000	0,000	0,000
ESL2	-	-	-	-	-	-
SFT	67,4	0,0948 (0,0029)	6,0 (0,07)	0,000	0,000	1,524 (0,062)
FRT	59,4	0,1488 (0,0100)	6,1 (0,13)	0,000	0,000	1,555 (0,113)
FWD	63,2	0,1035 (0,0035)	4,3 (0,07)	0,015 (0,015)	0,045 (0,028)	0,075 (0,032)
KGA	68,6	0,0254 (0,0020)	3,1 (0,09)	-	-	-
VTM	56,8	0,2334 (0,0095)	6,0 (0,09)	0,000	0,000	1,712 (0,073)
CTR	59,4	0,1206 (0,0045)	5,2 (0,06)	0,000	0,000	1,767 (0,069)
DNL	61,2	0,1435 (0,0045)	5,9 (0,07)	0,004 (0,000)	0,000	1,863 (0,054)
GLP	62,5	0,0586 (0,0026)	5,9 (0,08)	0,000	0,000	2,562 (0,058)
NYL1	66,1	0,0977 (0,0056)	3,9 (0,11)	0,021 (0,013)	0,026 (0,016)	0,011 (0,011)
GNG	43,9	0,1092 (0,0058)	4,0 (0,10)	0,000	0,000	0,036 (0,026)
mean	60,475	0,0967	4,77	0,0069	0,0085	0,9085

Table 5. Means of the test clones for survival, volume production, stem form, disease infestation and stem defects, age 5 years.

Clone	Survival (%)	Volume (m^3)	Stem form	*Coniothyrium*	*Cryphonectrea*	*Endothia*	Defects (%)
SGR009	51,9	0,1011 (0,0047)	4,73 (0,111)	0,000	0,000	0,346 (0,054)	3,5
SGR013	66,6	0,0750 (0,0024)	5,28 (0,757)	0,000	0,007 (0,007)	0,893 (0,056)	3,1
SGR041	63,0	0,1072 (0,0041)	5,39 (0,081)	0,000	0,000	1,049 (0,059)	4,1
SGR042	61,1	0,0820 (0,0040)	4,56 (0,075)	0,004 (0,004)	0,012 (0,009)	0,717 (0,058)	5,7
SGR046	61,3	0,0754 (0,0037)	5,32 (0,081)	0,008 (0,008)	0,012 (0,009)	0,833 (0,057)	1,0
SGR047	61,2	0,0957 (0,0045)	5,04 (0,078)	0,004 (0,004)	0,000	1,871 (0,066)	7,3
SGR048	54,6	0,0994 (0,0052)	4,51 (0,098)	0,000	0,000	0,791 (0,074)	5,3
SGR051	61,0	0,1366 (0,0053)	5,54 (0,109)	0,699 (0,019)	0,070 (0,019)	1,177 (0,086)	5,3
SGR052	52,7	0,0909 (0,0060)	4,85 (0,130)	0,029 (0,029)	0,000	1,317 (0,102)	1,2
SGR053	63,0	0,0804 (0,0035)	4,67 (0,086)	0,010 (0,010)	0,000	0,756 (0,066)	0,9
SGR054	64,4	0,0936 (0,0040)	4,97 (0,081)	0,000	0,000	0,670 (0,062)	1,0
SGR112	68,9	0,0754 (0,0037)	5,55 (0,077)	0,006 (0,006)	0,019 (0,009)	1,079 (0,062)	3,5
SGR183	62,4	0,1086 (0,0050)	5,21 (0,080)	0,000	0,000	1,402 (0,094)	3,4
SGR192	53,3	0,0801 (0,0035)	4,65 (0,085)	0,005 (0,005)	0,015 (0,011)	0,925 (0,080)	1,3
SGR202	57,7	0,0908 (0,0046)	4,72 (0,077)	0,000	0,000	0,959 (0,078)	2,8
SGR428	57,0	0,1295 (0,0061)	5,12 (0,088)	0,000	0,101 (0,033)	1,244 (0,091)	2,8
SGR438	62,9	0,0914 (0,0041)	4,78 (0,090)	0,060 (0,018)	0,000	0,511 (0,060)	1,6
SGR451	57,6	0,1166 (0,0047)	4,89 (0,090)	0,000	0,000	0,473 (0,052)	1,0
SGR467	49,9	0,0847 (0,0040)	4,76 (0,114)	0,014 (0,014)	0,014 (0,014)	0,824 (0,075)	1,0
SGR470	64,3	0,0863 (0,0052)	3,75 (0,073)	0,000	0,000	0,636 (0,076)	2,4
SGR472	48,5	0,0969 (0,0040)	4,83 (0,092)	0,004 (0,004)	0,025 (0,018)	1,846 (0,092)	0,8
SGR481	60,2	0,1098 (0,0053)	5,76 (0,078)	0,008 (0,008)	0,000	1,825 (0,068)	7,9
SGR482	61,9	0,1241 (0,0045)	5,73 (0,081)	0,115 (0,027)	0,000	1,126 (0,067)	7,2
SGR494	58,3	0,0964 (0,0040)	4,49 (0,079)	0,000	0,047 (0,021)	0,560 (0,063)	2,5
SGR515	56,5	0,0789 (0,0038)	5,40 (0,091)	0,038 (0,013)	0,009 (0,009)	0,701 (0,067)	13,7
KFT23/33	63,5	0,0593 (0,0021)	4,28 (0,076)	0,000	0,008 (0,005)	1,251 (0,087)	3,5
KFT81/13/2	58,7	0,0975 (0,0036)	4,72 (0,082)	0,000	0,029 (0,016)	0,700 (0,054)	3,2
GXC9/03	56,7	0,0583 (0,0025)	5,10 (0,077)	0,142 (0,040)	0,000	0,617 (0,051)	8,3
GXC16/08	72,8	0,0660 (0,0021)	4,90 (0,071)	0,000	0,000	0,839 (0,062)	6,6
GXT22/02	71,3	0,0863 (0,0031)	4,81 (0,081)	0,000	0,000	0,409 (0,035)	6,0
MXG25	65,8	0,0322 (0,0015)	3,61 (0,058)	0,000	0,000	0,480 (0,037)	14,9
mean	60,29	0,08868	4,894	0,0161	0,0113	0,9230	4,28

Standard error (SE) in brackets

Table 6. Means of the controls for survival, volume production, stem form, disease infestation and stem defects, age 5 years.

Control	Survival (%)	Volume (m^3)	Stem form (1 - 8)	*Coniothyrium* (0 - 4)	*Cryphonectrea* (0 - 4)	*Endothia* (0 - 4)	Defects (%)
SGR071	66,6	0,0957 (0,0025)	4,66 (0,044)	0,015 (0,004)	0,001 (0,001)	0,977 (0,041)	3,7
SGR072	56,8	0,0881 (0,0021)	4,51 (0,044)	0,001 (0,001)	0,003 (0,003)	0,768 (0,038)	5,5
TG12	57,1	0,0855 (0,0023)	4,64 (0,045)	0,006 (0,013)	0,010 (0,006)	0,914 (0,045)	6,4
38046	60,0	0,1059 (0,0029)	4,99 (0,050)	0,002 (0,003)	0,022 (0,008)	0,909 (0,040)	4,6
38047	63,6	0,1022 (0,0029)	5,00 (0,052)	0,009 (0,005)	0,008 (0,004)	0,957 (0,040)	6,5
mean	60,82	0,09580	4,766	0,0069	0,0085	0,9085	5,34

Standard error (SE) in brackets

7.2 CORRELATION ANALYSIS

7.2.1 Simple correlations

To investigate the inter-relationships and tendencies between the growth and the site data sets, a series of preliminary correlation matrices were constructed using the proc CORR procedure. APPENDIX 6 : Table 1 and Table 2, shows the correlations between the five year growth data and the site factors. The inter-relationship between the five year growth data and the A, B, and A bulk soil horizons, is listed in APPENDIX 6 : Tables 3 and Table 4.

The following highly significant ($p = 0,0001$) correlations were observed for both the common controls and the test clones:

- Volume and mean annual rainfall ($r = 0,78$ and $r = 0,76$)
- Stem form and latitude ($r = -0,80$ and $r = -0,74$)
- *Endothia* and latitude ($r = -0,87$ and $r = -0,86$); longitude ($r = -0,70$)

Weaker, but significant ($p = 0,05$) correlations were present for volume and aspect ($r = 0,40$); stem form and longitude ($r = -0,49$); stem form and minimum temperature ($r = -0,50$); *Cryphonectrea* and longitude ($r = 0,53$); *Endothia* and altitude ($r = 0,57$); *Endothia* and the driest quarter ($r = -0,65$); and finally, *Endothia* and the minimum temperature ($r = -0,62$). No significant ($p > 0,05$) correlations could be found between any of the soils factors and the growth factors.

7.2.2 Genetic correlations

Additional age to age genetic correlations were undertaken between the two year and five year data sets, using the formula given in section 2.4.2.5. Because of the mixed nature of the genetic material in the common controls, only the test clones were used for the genetic comparisons, as shown in Table 7.

Table 7. Matrix of age to age genetic correlation coefficients between the two year and five year data sets for the test clones only.

	VOL2	STM2	VOL5	STM5	CON5	CRY5
STM2	0,752					
	0,6877^{NS}					
VOL5	0,661	0,430				
	0,0001***	0,0157*				
STM5	0,202	0,700	0,506			
	0,2748^{NS}	0,0001***	0,0037**			
CON5	0,098	0,347	0,081	0,362		
	0,5997^{NS}	0,0555^{NS}	0,6623^{NS}	0,0451*		
CRY5	0,323	0,278	0,443	0,147	-0,011	
	0,0764^{NS}	0,1294^{NS}	0,0126*	0,4310^{NS}	0,9539^{NS}	
END5	0,201	0,209	0,314	0,418	-0,037	0,163
	0,2773^{NS}	0,2592^{NS}	0,0852^{NS}	0,0191*	0,8396^{NS}	0,3823^{NS}

* Significant at the 0,05 probability level

** Significant at the 0,01 probability level

*** Significant at the 0,001 probability level

NS Non significant

The data showed a moderately strong correlation (r_g = 0,66) between the volume at two years and the volume at five years, as well as (r_g = 0,70) between the stem form at two and the stem form at five years. The stem form and volume showed a weaker, but significant correlation.

7.2.3 Indicators of site means

The first priority, prior to the commencement of the regression analysis, was to find a stable indicator of the site means. To determine the most stable indicator of the site means, a correlation matrix was constructed utilising the volume production summary data in Table 8.

Table 8. Site means for volume production (m^3 / tree) based on the common controls only, the test clones only, the test clones minus the hybrids, and the controls plus the test clones.

SITE	MEAN $_{controls}$	MEAN $_{clones}$	MEAN $_{clones\ less\ hybrids}$	MEAN $_{site}$
FZS	0,0724 (0,0019)	0,0613 (0,0011)	0,0654 (0,0013)	0,0646 (0,0010)
RMD	-	-	-	-
TKF2	0,1090 (0,0058)	0,1317 (0,0048)	0,1470 (0,0055)	0,1246 (0,0038)
ADN	0,0921 (0,0055)	0,1003 (0,0037)	0,1003 (0,0037)	0,0977 (0,0030)
TST	0,0815 (0,0029)	0,0772 (0,0023)	0,0832 (0,0027)	0,0787 (0,0019)
NYL2	0,0212 (0,0008)	0,0228 (0,0009)	0,0201 (0,0008)	0,0223 (0,0006)
SMK	0,0429 (0,0013)	0,0443 (0,0009)	0,0481 (0,0012)	0,0438 (0,0008)
ESL1	0,0636 (0,0046)	0,0671 (0,0028)	0,0721 (0,0029)	0,0660 (0,0024)
MPS	0,0425 (0,0017)	0,0445 (0,0011)	0,0474 (0,0011)	0,0438 (0,0009)
NLN	0,0772 (0,0031)	0,0712 (0,0026)	0,0679 (0,0027)	0,0733 (0,0020)
WHB	0,1714 (0,0082)	0,1816 (0,0044)	0,1816 (0,0044)	0,1783 (0,0040)
TBD	0,0817 (0,0034)	0,0576 (0,0022)	0,0627 (0,0022)	0,0671 (0,0019)
TLD	-	-	-	-
TKF1	0,0637 (0,0019)	0,0605 (0,0013)	0,0670 (0,0014)	0,0616 (0,0011)
UMD	0,0617 (0,0026)	0,0620 (0,0024)	0,0618 (0,0028)	0,0612 (0,0018)
WLD	0,0948 (0,0072)	0,0850 (0,0046)	0,0826 (0,0049)	0,0883 (0,0039)
JDM	0,0626 (0,0028)	0,0545 (0,0016)	0,0564 (0,0018)	0,0570 (0,0014)
ESL3	-	-	-	-
ELD	0,1575 (0,0063)	0,1432 (0,0041)	0,1658 (0,0041)	0,1480 (0,0035)
PDN	0,1797 (0,0058)	0,1543 (0,0052)	0,1668 (0,0052)	0,1640 (0,0039)
ESL2	-	-	-	-
SFT	0,0948 (0,0029)	0,0820 (0,0015)	0,0820 (0,0015)	0,0858 (0,0014)
FRT	0,1488 (0,0100)	0,1439 (0,0086)	0,1525 (0,0092)	0,1457 (0,0066)
FWD	0,1035 (0,0035)	0,0990 (0,0025)	0,1069 (0,0025)	0,1006 (0,0020)
KGA	0,0254 (0,0020)	0,0334 (0,0013)	0,0338 (0,0013)	0,0310 (0,0011)
VTM	0,2334 (0,0095)	0,1492 (0,0039)	0,1711 (0,0047)	0,1706 (0,0041)
CTR	0,1206 (0,0045)	0,1034 (0,0031)	0,1148 (0,0033)	0,1091 (0,0026)
DNL	0,1435 (0,0046)	0,1411 (0,0036)	0,1462 (0,0038)	0,1420 (0,0028)
GLP	0,0586 (0,0026)	0,0552 (0,0015)	0,0593 (0,0017)	0,0562 (0,0013)
NYL1	0,0977 (0,0056)	0,0927 (0,0037)	0,1002 (0,0042)	0,0943 (0,0031)
GNG	0,1092 (0,0058)	0,1324 (0,0064)	0,1306 (0,0068)	0,1219 (0,0044)
Mean	0,0967	0,0907	0,0968	0,0925

Standard error (SE) in brackets

The matrix of the correlation coefficients for volume production, between the four site means $MEAN_{site}$, $MEAN_{controls}$, $MEAN_{clones}$, and $MEAN_{clones\ less\ hybrids}$ is shown in Table 9. All of the correlations were highly significant ($p = 0,0001$) and had a $r > 0,92$. The matrix indicating that any of the site means could serve as a reliable estimate of the total site means. However, for statistical correctness, all further analyses would be based on the means of the controls only, as indicated in the literature as being statistically correct (Gibson, 1982). A site summary table for all of the five year data, based on the common controls was then constructed, as previously shown in Table 4.

Table 9. Matrix of correlation coefficients for volume production, among the four sets of means used for comparing the validity of the basic site indicators.

	$MEAN_{site}$	$MEAN_{clones}$	$MEAN_{controls}$
$MEAN_{clones}$	0,991***		
	0,0001		
$MEAN_{controls}$	0,965***	0,924***	
	0,0001	0,0001	
$MEAN_{clones\ less\ hybrids}$	0,992***	0,991***	0,942***
	0,0001	0,0001	0,0001

*** Significant at the 0,001 probability level

7.3 JOINT REGRESSION ANALYSIS (JRA)

The regression analysis was undertaken using a JRA approach, and done separately for volume production, stem form and *Endothia* infestation, utilising the *E. grandis* test clones regressed on the site means of the controls. An analysis of covariance was then run to test the homogeneity of the regression intercepts and slopes.

7.3.1 Joint regressions

7.3.1.1 Volume production

An overall indication for five year volume production, of all the *E. grandis* test clones (pooled) as regressed on the site means of the controls gave the following parameters: $Y = 0,0066 + 0,9375(X)$ and ($R^2 = 0,75$; $p = 0,0001$). The high coefficient of determination

indicates the linear relationship of the *E. grandis* clonal response to environmental influences. This same tendency was found in the two year data, and was further the general trend for all of individual clones included in this study (Van Wyk *et al*, 1991).

The volume β-coefficients in Table 10 show the large variation in response to the site differences that are obtained among individual *E. grandis* (and *E. grandis* hybrid) clones. The five controls showed volume β-coefficients around unity, thereby indicating the overall stability of these common controls, although a bias exists in these analyses due to the individual control values being included in the control means.

Three of the clones, SGR009, SGR467 and SGR472, originally had lower R^2 for both volume production and stem form. However, following the plotting of the value of each clone over the10 sites on which the clone was present, the resultant graphs revealed that SGR009 had an outlier site at Gingindlovo, and that SGR467 and SGR472 had an outlier site at Port Durnford. These outlier sites could only be explained by the fact that at time of planting too few ramets existed to plant the full plot, and seedlings were used in all cases to "fill" the empty holes. The ratio of ramets to seedlings being 5 ramets :11 seedlings for the 16 tree plots. This high seedling to ramet ratio within these plots was the logical reason for the outliers, as the seedlings were either suppressing the ramets, or were changing the ramets growth patterns. For these three clones the sites were then deleted, thereby dramatically increasing the R^2. This cultural adjustment was in line with the findings within the two year data (S. Verryn personal communication).

All of the test clones show regressions with high coefficients of determination ($0,98 > R^2 > 0,65$), other than two hybrid clones ($R^2 = 0,16$ and $0,41$). These high coefficients of determination, imply a good fit for the models, and that the model explains a high proportion of the observed variation. Graphical presentation of the regression lines for volume production of the *E. grandis* test clones are shown in Figure 2.

7.3.1.2 Stem form

An overall indication for individual stem form, of all the *E. grandis* test clones regressed on the site mean stem form of the controls gave the following parameters: $Y = - 0,0691 + 1,0297(X)$ and ($R^2 = 0,80$; $p = 0,0001$). The high coefficient of determination once again confirm the linear relationship of the *E. grandis* clones.

The stem form β-coefficients are listed in Table 10, and show the response of the clones to the environment. Other than one *E. grandis* clone ($R^2 = 0,42$), all of the clones (including the hybrids) have high coefficients of determination ($0,96 > R^2 > 0,59$). Graphical representation for stem form of the *E. grandis* test clones regression lines are shown in Figure 3.

7.3.1.3 *Coniothyrium*, *Cryphonectrea* and *Endothia* infestation

An overall indication for disease infestation, of all the *E. grandis* test clones regressed on the site means of the controls gave the following parameters:

Coniothyrium : $Y = -0,0004 + 1,5264(X)$ and ($R^2 = 0,34$; $p = 0,0001$)
Cryphonectrea: $Y = 0,0035 + 1,1322(X)$ and ($R^2 = 0,06$; $p = 0,0001$)
Endothia: $Y = 0,0137 + 0,9931(X)$ and ($R^2 = 0,89$; $p = 0,0001$).

Due to the limited distribution, on the lower altitude and more southernly KwaZulu-Natal sites, of the *Coniothyrium* and the *Cryphonectrea* infestation, no meaningful significant models could be constructed. The models are however given for comparative purposes in Table 11.

The *Endothia* infestation distribution could be assumed to be normal, and the high coefficients of determination ($0,99 > R^2 > 0,62$) for *Endothia* infestation, suggest a linear relationship between the clonal response to the environmental influences on disease infestation, as shown in Table 12.

Graphical representation of the regression lines of the *E. grandis* test clones for *Endothia* infestation are shown in Figure 4.

Table 10. Regression coefficients for mean tree volume production and mean stem form of the individual test clones (and controls), regressed against the site mean values of the common controls ($MEAN_{controls}$).

Treatment	Volume: □ - coeff.	Volume: □ - coeff.	Model: Pr > F	R^2	Stem: □ - coeff.	Stem: □ - coeff.	Model Pr > F	R^2
SGR009+	0,0370	0,7350	***	0,87	0,5897	1,2081	**	0,91
SGR013	0,0177	0,5204	**	0,85	1,3580	0,7753	**	0,81
SGR041	0,0141	0,7499	**	0,81	-1,1107	1,2533	***	0,93
SGR042	0,0066	0,8999	***	0,96	0,4462	0,8859	***	0,95
SGR046	0,0174	0,6583	**	0,78	1,6050	0,7192	NS	0,42
SGR047	-0,0030	0,9038	**	0,86	-0,0265	0,9759	**	0,88
SGR048	0,0055	0,7875	**	0,86	-0,1836	0,9989	***	0,94
SGR051	-0,0536	1,5889	**	0,83	-1,7870	1,4563	***	0,96
SGR052	0,0156	0,7575	**	0,90	-1,3789	1,2388	**	0,92
SGR053	0,0062	1,0951	**	0,65	-0,2033	1,1066	**	0,87
SGR054	-0,0131	1,0005	***	0,92	0,5520	0,9352	**	0,87
SGR112	-0,0176	1,1692	***	0,94	0,0570	1,0609	***	0,94
SGR183	-0,0008	1,4180	**	0,81	1,3443	0,8399	**	0,66
SGR192	-0,0278	1,2553	**	0,70	0,0227	1,0164	**	0,80
SGR202	0,0009	0,8579	***	0,96	-0,5067	1,0690	**	0,88
SGR428	-0,0138	1,3136	**	0,87	-0,1931	1,0683	***	0,96
SGR438	-0,0006	1,1125	**	0,85	0,3920	0,9766	***	0,92
SGR451	-0,0512	1,4737	**	0,87	-1,1292	1,2878	**	0,76
SGR467+	-0,0108	1,0158	*	0,70	-0,8282	1,2443	*	0,63
SGR470	0,0008	1,0149	***	0,98	-0,1185	0,9100	**	0,92
SGR472+	0,0219	1,0330	*	0,66	-3,0899	1,4740	**	0,80
SGR481	-0,0153	1,4565	***	0,97	0,3812	0,9767	**	0,85
SGR482	-0,0097	1,3315	**	0,83	1,3665	0,8629	**	0,75
SGR494	-0,0255	1,5216	**	0,87	0,1777	0,9780	**	0,72
SGR515	-0,0006	0,9665	**	0,88	1,7067	0,7373	*	0,63
KFT23/33	-0,0157	1,0935	**	0,66	-0,0309	0,9800	***	0,95
KFT81/13/2	0,0062	0,8809	***	0,93	-0,5129	1,1116	***	0,92
GXC9/03	0,0287	0,4396	NS	0,16	1,2878	0,7771	*	0,59
GXC16/08	0,0249	0,4252	**	0,66	-0,1045	1,0520	**	0,78
GXT22/02	0,0367	0,4832	**	0,76	1,0611	0,7853	**	0,77
MXG25	0,0127	0,1731	*	0,41	-0,4647	0,8180	**	0,71
SGR071	-0,0121	1,1300	***	0,93	-0,6064	1,0898	***	0,96
SGR072	0,0001	0,9360	***	0,83	-0,0275	0,9687	***	0,91
TG12	-0,0033	0,9438	***	0,85	-0,2773	1,0530	**	0,92
38046	0,0045	1,0748	***	0,88	0,5461	0,9289	***	0,94
38047	0,0100	0,9901	***	0,88	0,4015	0,9629	***	0,94

\+ Corrected for the Gingindlovo and the Port Durnford sites
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001 probability level
NS Non significant

Table 11. Regression coefficients for mean *Coniothyrium* and *Cryphonectrea* infestation of the individual test clones (and controls), regressed against the site mean values of the common controls ($MEAN_{controls}$).

Treatment	*Con.* α	*Con.* β	Model: Pr > F	R^2	*Cry.* α	*Cry.* β	Model: Pr > F	R^2
SGR009+	-	-	-	-	-	-	-	-
SGR013	-	-	-	-	-0,0013	0,8589	**	0,71
SGR041	-	-	-	-	-	-	-	-
SGR042	0,0019	0,3302	NS	0,08	-0,0042	0,9846	**	0,56
SGR046	-0,0004	2,8431	*	0,48	-0,0034	1,0304	*	0,67
SGR047	-	-	-	-	-	-	-	-
SGR048	-	-	-	-	-	-	-	-
SGR051	-0,0059	3,5502	***	0,99	0,1667	16,250	NS	0,03
SGR052	0,0421	-0,1488	NS	0,04	-	-	-	-
SGR053	0,0025	1,6359	NS	0,22	-	-	-	-
SGR054	-	-	-	-	-	-	-	-
SGR112	0,0178	-0,8169	NS	0,04	0,0118	1,0223	NS	0,26
SGR183	-	-	-	-	-	-	-	-
SGR192	0,0037	-0,2126	NS	0,04	0,0142	0,1634	NS	0,00
SGR202	-	-	-	-	-	-	-	-
SGR428	-	-	-	-	-	-	-	-
SGR438	-	-	-	-	-	-	-	-
SGR451	-	-	-	-	-	-	-	-
SGR467+	0,0142	-1,4534	NS	0,04	-0,0071	2,4368	***	0,89
SGR470	-	-	-	-	-	-	-	-
SGR472+	-0,0010	0,8860	***	0,99	-0,0095	4,1517	**	0,68
SGR481	-	-	-	-	-	-	-	-
SGR482	-0,0155	7,0861	***	0,99	-	-	-	-
SGR494	-	-	-	-	0,0055	2,5249	*	0,64
SGR515	-0,0112	2,8586	***	0,99	0,0007	0,4349	NS	0,34
KFT23/33	-	-	-	-	-0,0020	0,6995	*	0,60
KFT81/13/2	-	-	-	-	0,0279	0,8242	NS	0,02
GXC9/03	-	-	-	-	-	-	-	-
GXC16/08	-	-	-	-	-	-	-	-
GXT22/02	-	-	-	-	-	-	-	-
MXG25	-	-	-	-	-	-	-	-
SGR071	-0,0058	2,6462	***	0,99	-0,0004	0,1852	**	0,37
SGR072	-0,0008	0,3528	***	0,99	0,0010	0,3790	**	0,37
TG12	0,0052	0,0133	NS	0,00	-0,0037	1,3913	**	0,37
38046	-0,0014	0,6415	***	0,99	0,0039	2,0902	***	0,50
38047	0,0070	0,0028	NS	0,00	0,0011	1,0684	***	0,52

\+ Corrected for the Gingindlovo and the Port Durnford sites
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001 probability level
NS Non significant

Table 12. Regression coefficients for mean *Endothia* infestation of the individual test clones (and controls), regressed against the site mean values of the common controls ($MEAN_{controls}$).

Treatment	*Endothia* α - coefficient	*Endothia* β - coefficient	Model: Pr > F	R^2
SGR009+	-0,0149	0,7248	***	0,99
SGR013	-0,1747	0,8318	**	0,83
SGR041	0,0868	0,7470	**	0,83
SGR042	-0,0503	1,2288	**	0,78
SGR046	-0,0633	0,9653	***	0,93
SGR047	0,1954	1,0636	**	0,87
SGR048	-0,0160	0,9092	***	0,97
SGR051	-0,0490	1,3136	***	0,98
SGR052	0,1103	0,8618	**	0,91
SGR053	-0,0088	1,0341	**	0,93
SGR054	-0,0389	0,7425	**	0,80
SGR112	-0,0728	0,9997	***	0,99
SGR183	0,0400	1,1372	**	0,85
SGR192	0,0258	0,9915	***	0,96
SGR202	-0,1308	1,0583	***	0,97
SGR428	0,1165	1,1718	**	0,91
SGR438	-0,0100	0,9030	***	0,95
SGR451	-0,1009	0,7939	**	0,78
SGR467+	0,2276	0,9207	**	0,80
SGR470	-0,0410	0,9694	**	0,98
SGR472+	0,3427	1,1020	**	0,83
SGR481	0,2299	0,9378	*	0,73
SGR482	0,0277	1,0500	**	0,88
SGR494	-0,0064	0,9410	***	0,99
SGR515	-0,0311	0,8903	**	0,93
KFT23/33	-0,0078	1,0872	***	0,99
KFT81/13/2	0,0995	0,8011	**	0,86
GXC9/03	0,0025	0,5116	*	0,62
GXC16/08	-0,1775	0,9891	**	0,87
GXT22/02	-0,0196	0,5486	***	0,97
MXG25	-0,0353	0,6245	***	0,94
SGR071	-0,0280	1,0632	***	0,97
SGR072	-0,0456	0,9529	***	0,91
TG12	0,0394	1,0679	***	0,88
38046	0,0232	0,9706	***	0,97
38047	0,0284	0,9532	***	0,99

\+ Corrected for the Gingindlovo and the Port Durnford sites
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001 probability level
NS Non significant

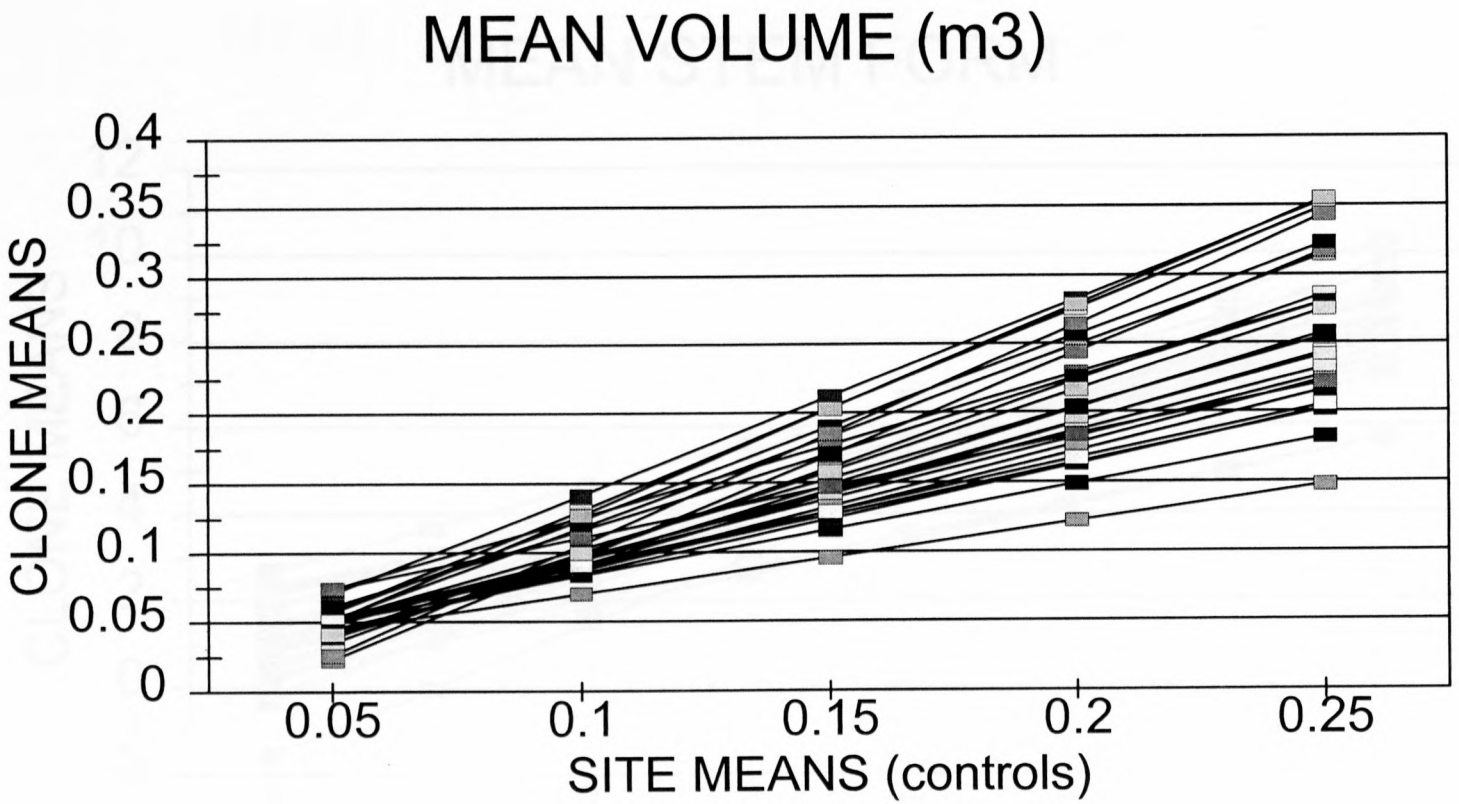

Figure 2. Graphical representation for volume production of the regression lines of the *E. grandis* test clones, age 5 years

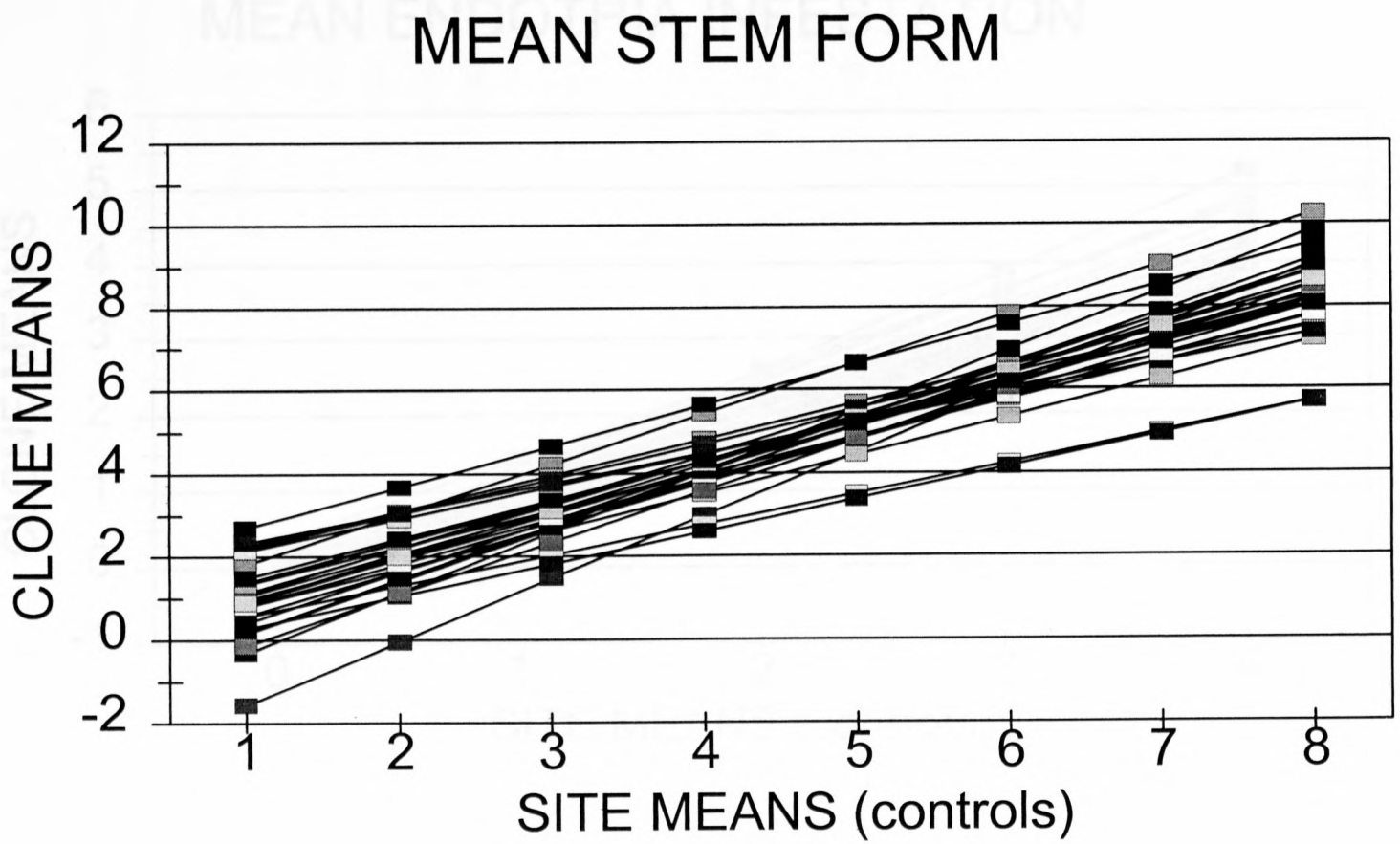

Figure 3. Graphical representation for stem form of the regression lines of the *E. grandis* test clones, age 5 years

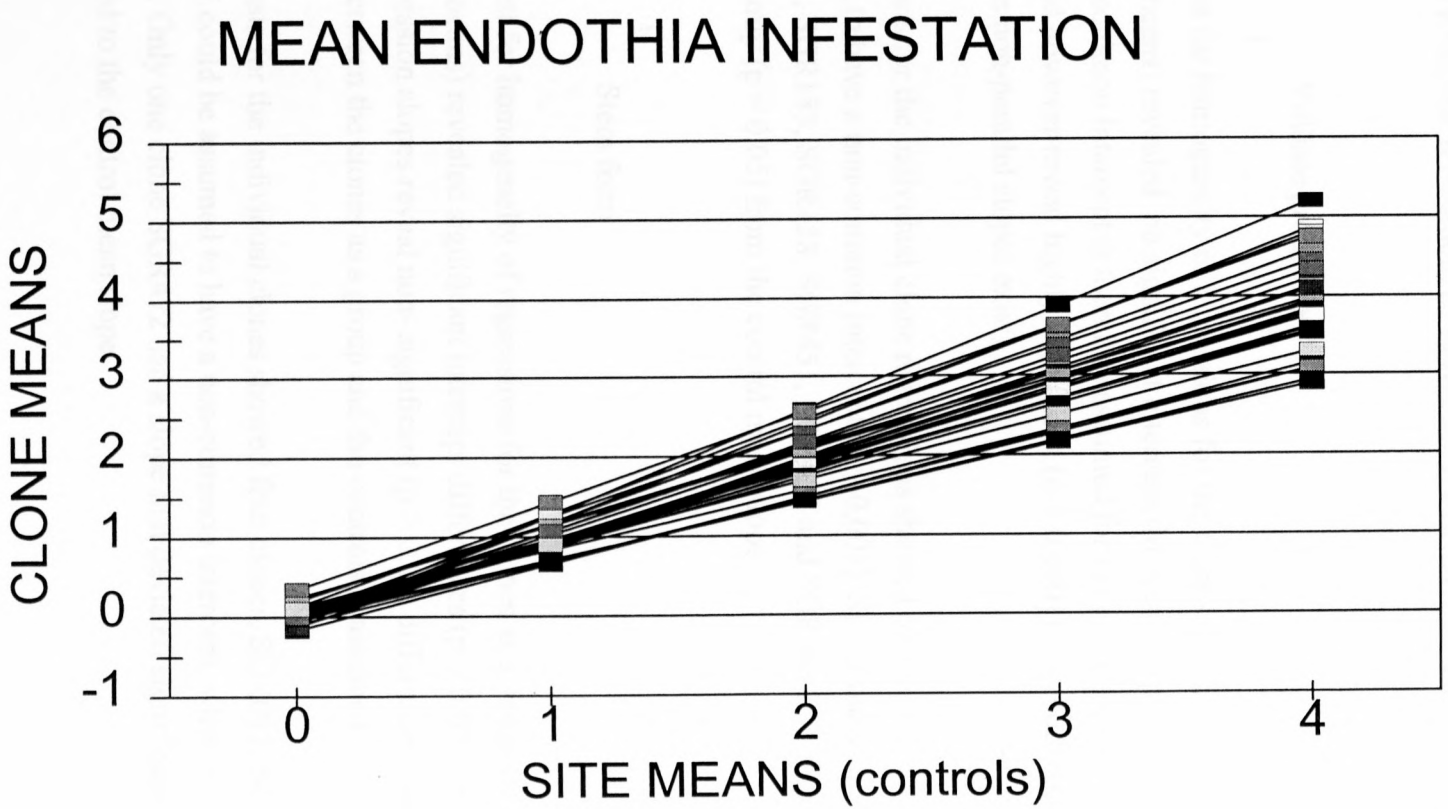

Figure 4. Graphical representation for *Endothia* infestation of the regression lines of the *E. grandis* test clones, age 5 years.

7.3.2 Tests for homogeneity of regression

Tests for homogeneity of regressions were run using a covariance approach (proc GLM) (SAS Institute, 1981; Ott, 1993). The tests were analysed separately for volume production, stem form and *Endothia* infestation, as shown in APPENDIX 8 : Tables 1 to 3.

7.3.2.1 Volume production

The F-test for homogeneity of regressions for the clones as a group (regressed on the common control means) revealed no significant intercept differences ($p > 0,05$) for the regression lines. A common intercept is therefore assumed for the clone regression line. The regression slopes did however reveal highly significant ($p = 0,0001$) slope differences between the clones (ie non-parallel slopes exist).

The T-tests for the individual clone regressions showed only one clone, SGR472 could be assumed to have a non-common intercept ($p = 0,001$). Seven individual clones, SGR013, SGR051, SGR183, SGR428, SGR451, SGR472 and SGR481 had slopes that deviated significantly ($p = 0,05$) from the control mean slope.

7.3.2.2 Stem form

The F-test for homogeneity of regressions for the clones as a group (regressed on the common control means) revealed significant intercept differences ($p = 0,05$) for the regression lines. The regression slopes reveal non- significant ($p > 0,05$) differences, and consequently parallel slopes between the clones as a group and the controls is assumed.

The T-tests for the individual clones showed four clones, SGR013, SGR183, SGR472 and SGR515 could be assumed to have a non-common intercept, when compared to the common controls. Only one clone SGR472 had a slope that deviated significantly ($p = 0,05$) when compared to the control mean slope.

7.3.2.3 *Endothia* infestation

The F-test for homogeneity of regressions for the clones as a group (regressed on the common control means) showed no significant intercept differences ($p > 0,05$) for the regression lines, or the regression slopes.

The T-tests for the individual clones showed all clones could be assumed to have a common intercept. Three clones SGR009, SGR041 and SGR054 had slopes that deviate significantly ($p = 0,05$) when compared to the control mean slope.

7.3.3 Selection of clones

Based on the previously mention regression analysis and the tests for homogeneity of the regressions, and the assumption of a common intercept of the clones for volume production and a linear response to site index (and therefore no rank-changing interaction) the following six clones with the highest □-coefficients in Table 10 can be recommended for commercial production on all sites, SGR051, SGR183, SGR428, SGR451, SGR481 and SGR482. These six clones all have acceptable stem form and disease tolerance. As volume is the main criterea for the selection process no specific stem form or disease selections have been made, but the same procedure can be followed for specific selections.

7.4 FACTOR ANALYSIS

Prior to the analysis of the factors influencing the growth of *E. grandis* and specifically the growth of the clones, a PCA was undertaken using the factor analysis (FA) approach. This procedure was specifically aimed at gaining a better unbiased understanding of the association between the environmental factors influencing the growth, stem form and disease infestation, on both the common controls and the test clones. Three factor analyses were run on the complete data set GEI_SITE, each run containing a separate additional variable, either volume production, or stem form or *Endothia* infestation from the GEI5 data set. The results of the FA are given in APPENDIX 9 : Tables 1 to 6. Five general patterns of the variability and associations within the data were then identified:

- Factor 1 : Temperature
- Factor 2 : Water availability
- Factor 3 : Nutrients
- Factor 4 : Major site factors
- Factor 5 : Minor (other) site factors.

The first factor accounted for the most variability followed by each factor in a decreasing order of importance, as shown in APPENDIX 9 : Tables 1 to 6.

7.4.1 Volume production

For both the common controls and the test clones, volume production was mainly associated with the second factor of the FA (r = 0,77 and r = 0,73). Variables showing the strongest associations > 0,5 with factor 2 were MAP, aspect, S-value, clay content, and pH(H_2O). These variables were the same for both the test clones and the common controls, as shown in APPENDIX 9 : Tables 1 and 4.

7.4.2 Stem form

Stem form was chiefly associated with the fourth factor of the FA (r = -0,70 and r = -0,76) as shown in APPENDIX 9: Tables 2 and 5. The variables showing the strongest associations > 0,5 with factor 4 were latitude, EA and Al.

7.4.3 *Coniothyrium*, *Cryphonectrea* and *Endothia* infestation

Due to the limited occurance of both the *Coniothyrium* and *Cryphonectrea* infestions on the test sites, no FA was undertaken on these two diseases. *Endothia* infestation, was mainly associated with the fourth factor of the FA (r = -0,71 and r = -0,70), as shown in APPENDIX 9: Tables 4 and 6. For both the test clones and the common controls, the strongest association > 0,5 with factor 4 were with latitude, EA and Al.

7.5 MULTIPLE REGRESSION ANALYSIS

Both forwards and backwards stepwise regressions (proc STEPWISE) were used to determine which factors were important for growth, and were possibly influencing stem form, and disease infestations. The complete site factor data set (GEI_SITE), including all soil horizons, and the five year (GEI5) growth data sets were used for the analyses. Firstly, the controls and clones were analysed as two separate "groups", and "general models" for the two "groups'' were produced. Secondly, "individual models" for each individual clone were produced, to indicate which site factors could be affecting each individuals clone's response.

7.5.1 Volume production

Utilising the common controls over all sites, only the following single factor was found to be contributing to an overall model ($\alpha = 0,001$):

$Y = - 0,1603 + 0,0002(X_1)$
with ($R^2 = 0,63$; $p = 0,0001$; $X_1 = MAP$)

In the exploratory analysis the ANOVA tables revealed that individual control and clone mean values were highly significant ($p = 0,0001$). Therefore, by the inclusion of the controls (or clones) means as a new variable within the model, the R^2 was further improved.

Secondly, using only the *E. grandis* test clones ($\alpha = 0,001$):

$Y = -0,2099 + 0,8279(X_1) + 0,0002(X_2)$
with ($R^2 = 0,65$; $p = 0,0001$; X_1 = control means, $X_2 = MAP$).

Thirdly, using only the *E. grandis* test clones and a lower significance level ($\alpha = 0,05$) the following improved model was obtained:

$Y= -0,1464 +0,7126(X_1) + 0,0002(X_2) -0,0057(X_3) + 0,0003(X_4) - 0,0010(X_5)$
with ($R^2 = 0,73$; $p =0,0001$; X_1 = clone means, $X_2 = MAP$, $X_3 = MIN$, $X_4 = ERD$, $X_5 =$ CLAY).

The unbalanced nature of this second set of data must once again be borne in mind when

reviewing the results. As revealed in the correlation analysis and the FA, the MAP was the dominant factor influencing the growth in all of the models, as shown in APPENDIX 10 : Tables 1 and 4.

Analysis of each individual clone was then undertaken, and the results are presented in Table 13. To obtain more degrees of freedom within the stepwise regression analysis, the means of the replications within sites, as opposed to the site means, were used for the calculations. In 23 of the individual models mean annual precipitation (MAP), was the dominant factor determining volume growth ($\alpha = 0,05$).

7.5.2 Stem form

The general models for stem form were more significant than the models for volume production. The model ($\alpha = 0,001$) for the common controls:

$Y = 53,0219 + 0,6894(X_1) - 0,0040(X_2) - 0,0148(X_3) + 0,3161(X_4) - 0,0593(X_5)$
with ($R^2 = 0,89$; $p = 0,0001$ and X_1 = control means, X_2 = LAT, X_3 = LON, X_4 = MAT, X_5 = SLP).

The model ($\alpha = 0,001$) for the test clones showed the following model:

$Y = 56,0187 + 0,5787(X_1) - 0,0034(X_2) - 0,0161(X_3) + 0,3194(X_4) - 0,0568(X_5)$
with ($R^2 = 0,76$; $p = 0,0001$ and X_1 = clone means, X_2 = LAT, X_3 = LON, X_4 = MAT, X_5 = SLP).

No improved fit model for the *E. grandis* test clones could be obtained by lowering the significance level ($\alpha = 0,05$). Latitude (LAT) was the dominant factor influencing the R^2 in all models, as shown in APPENDIX 10 : Tables 2 and 5.

Analysis of each individual clone was then undertaken, and the results are presented in Table 14. As with the previous volume calculations, and to obtain more degrees of freedom, the stepwise regression analysis was undertaken using the means of the replications within sites, as opposed to the site means. In 23 of the individual models latitude (LAT), was the dominant factor determining stem form ($\alpha = 0,05$).

7.5.3 *Coniothyrium*, *Cryphonectrea* and *Endothia* infestation

Due to the limited distribution of the *Coniothyrium* and *Cryphonectrea* infestations, no meaningful, or significant models could be constructed, using the available data. Only from the more widely distributed disease data for the *Endothia* infestation was a meaningful model constructed.

Firstly, using the common controls ($\alpha = 0,001$):

$Y = 16,9417 - 0,0058(X_1) - 0,1831(X_2)$
with ($R^2 = 0,82$; $p = 0,0001$ and X_1 = LAT; X_2 = Org.Mat in A hor)

Secondly, using the *E. grandis* test clones ($\alpha = 0,001$):

$Y = 16,7120 - 0,0058(X_1) - 0,1819(X_2)$
with ($R^2 = 0,77$; $p = 0,0001$ and X_1 = LAT; X_2 = Org.Mat in A hor)

Thirdly, using only the *E. grandis* test clones and a lower significance level ($\alpha = 0,05$) the following complex model was obtained:

$Y = 67,7164 + 0,2253(X_1) - 0,0066(X_2) - 0,0147(X_3) + 0,0028(X_4) - 0,0022(X_5) + 0,0023(X_6) + 0,0171(X_7) + 5,8408(X_8) - 7,7103(X_9) - 7,0157(X_{10}) - 12,6742(X_{11}) + 0,0981(X_{12})$
with ($R^2 = 0,90$, $p = 0,0001$ and X_1 = clones, X_2 = LAT, X_3 = LON, X_4 = ALT, X_5 = MAP, X_6 = DRY, X_7 = ERD, X_8 = Ph(H_2O) in A hor, X_9 = pH(KCl) in A hor, X_{10} = Org.Mat in A hor, X_{11} = C in A hor, X_{12} = P in A hor)

Latitude was the main factor influencing the coefficient of determination, for the intensity of *Endothia* infestation, as shown in APPENDIX 10 : Tables 3, 6 and 9).

The individual clones *Endothia* infestation regressions are given in Table 15. As with the volume and stem form calculations, and in order to obtain more degrees of freedom, the stepwise regression analysis was undertaken using the means of the replications within sites, as opposed to the site means. In 24 of the individual models latitude (LAT), was the dominant factor influencing *Endothia* infestation ($\alpha = 0,001$).

Table 13. Multiple regression coefficients for mean volume production of individual treatments, using treatment per replication within location means, age 5 years.

Treatment	Regression model	Pr > F	R^2
SGR009+	$Y = -0,1262 + 0,0002(X_{MAP})$	**	0,49
SGR013	$Y = -0,1192 + 0,0002(X_{MAP})$	**	0,41
SGR041	$Y = 0,1787 - 0,0027(X_{CLAY})$	***	0,80
SGR042	$Y = 0,1790 - 0,0236(X_{SVAL})$	**	0,62
SGR046	$Y = -0,2675 - 0,00003(X_{ALT}) + 0,0003(X_{MAP})$	***	0,96
SGR047	$Y = 0,0552 + 0,0172(X_{SLP})$	***	0,79
SGR048	$Y = -0,1405 + 0,0002(X_{MAP})$	**	0,53
SGR051	$Y = 1,3731 - 0,0005(X_{LAT}) - 0,0149(X_{P})$	***	0,99
SGR052	$Y = -0,2000 + 0,0002(X_{MAP})$	**	0,70
SGR053	No model ($\alpha = 0,05$).	-	-
SGR054	$Y = -0,1236 + 0,0002(X_{MAP})$	***	0,94
SGR112	$Y = -0,1421 + 0,0002(X_{MAP}) + 0,0003(X_{ERD}) + 0,0010(X_{SILT})$	***	0,90
SGR183	$Y = -0,6216 + 0,1497(X_{pH(H20)})$	***	0,86
SGR192	$Y = -0,2308 + 0,0003(X_{MAP})$	***	0,90
SGR202	$Y = -0,1987 + 0,0002(X_{MAP})$	***	0,79
SGR428	$Y = -0,1597 + 0,0002(X_{MAP})$	***	0,88
SGR438	$Y = -0,1511 + 0,0002(X_{MAP})$	***	0,76
SGR451	$Y = -1,4562 + 0,0569(X_{MAX}) + 0,03141(X_{SLP}) - 0,04777(X_{pH(KCl)}) + 0,0040(X_{SVAL})$	***	0,99
SGR467+	$Y = 1,0111 - 0,04325(X_{MAT}) - 0,0077(X_{SLP})$	***	0,87
SGR470	$Y = -0,1893 + 0,0003(X_{MAP})$	**	0,69
SGR472+	$Y = 1,1603 - 0,0325(X_{MAX}) - 0,0019(X_{SILT})$	***	0,87
SGR481	$Y = -0,3822 + 0,0005(X_{MAP}) - 0,0015(X_{CLAY})$	***	0,91
SGR482	$Y = -0,4645 + 0,0006(X_{MAP}) + 0,0092(X_{SVAL})$	**	0,70
SGR494	$Y = -0,0977 + 0,0017(X_{ERD}) - 0,0051(X_{P})$	***	0,71
SGR515	$Y = 0,4279 - 0,0001(X_{LAT}) + 0,0007(X_{ERD}) - 0,0074(X_{SVAL})$	***	0,95
KFT23/33	$Y = -0,3704 + 0,0004(X_{MAP}) + 0,0055(X_{SLP}) - 0,0010(X_{CLAY})$	***	0,90
KFT81/13/2	$Y = -0,1398 + 0,0002(X_{MAP})$	***	0,59
GXC9/03	$Y = 0,0217 + 0,0009(X_{SAND})$	**	0,50
GXC16/08	$Y = -0,2720 + 0,0002(X_{MAP}) + 0,0064(X_{MAT})$	***	0,86
GXT22/02	$Y = -1,1855 + 0,0003(X_{LON}) + 0,0003(X_{MAP})$	***	0,77
MXG25	$Y = 0,0268 + 0,0044(X_{SLP})$	***	0,68
SGR071	$Y = -0,2580 + 0,0003(X_{MAP})$	***	0,77
SGR072	$Y = -0,2206 + 0,0003(X_{MAP}) - 0,0002(X_{ASP})$	***	0,69
TG12	$Y = -0,2490 + 0,0003(X_{MAP}) -0,0004(X_{DRY})$	***	0,69
38046	$Y = -2,4407 + 0,0008(X_{LON}) + 0,0003(X_{MAP}) -0,0268(X_{MIN}) - 0,0018(X_{CLAY})$	***	0,75
38047	$Y = -0,1642 + 0,0002(X_{MAP}) + 0,0009(X_{SILT}) - 0,0012(X_{CLAY})$	***	0,70

\+ Corrected for the Gingindlovo and the Port Durnford sites
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001 probability level
NS Non significant

Table 14. Multiple regression coefficients for mean stem form of individual treatments, using treatment per replication within location means, age 5 years.

Treatment	Regression model	Pr > F	R^2
SGR009+	$Y = 69,5235 - 0,0052(X_{LAT}) - 0,0139(X_{LON}) - 0,2340(X_{SLP}) - 1,3208(X_{PH(KCL)})$	***	0,93
SGR013	$Y = 8,18529 - 0,3210(X_{MIN})$	***	0,63
SGR041	$Y = -89,1671 - 0,0151(X_{LAT}) + 0,0432(X_{LON})$	***	0,92
SGR042	$Y = 15,1413 - 0,0071(X_{LAT}) - 0,2894(X_{MAX})$	**	0,91
SGR046	$Y = 14,9405 - 0,3404(X_{MAX})$	**	0,67
SGR047	$Y = 23,5311 - 0,0069(X_{LAT}) - 0,3481(X_{C}) + 0,8182(X_{EA})$	***	0,95
SGR048	$Y = 24,3044 - 0,0070(X_{LAT}) - 0,1882(X_{ORG.MAT})$	***	0,88
SGR051	$Y = 27,3940 - 0,0311(X_{ALT}) + 0,0689(X_{ERD}) + 0,2546(X_{CLAY})$	**	0,99
SGR052	$Y = 20,6941 - 0,7629(X_{MAT}) - 0,0587(X_{CLAY}) + 0,6443(X_{ORG.MAT}) - 0,0015(X_{N})$	***	0,96
SGR053	$Y = -6,0803 + 0,3591(X_{MAX})$	*	0,56
SGR054	$Y = 23,3553 - 0,0072(X_{LAT}) - 0,3815(X_{PH(H2O)}) - 0,4040(X_{ORG.MAT})$	***	0,95
SGR112	$Y = 22,9819 - 0,0065(X_{LAT})$	***	0,68
SGR183	$Y = 9,7699 - 0,2386(X_{MIN}) + 0,0360(X_{SILT}) - 1,2018(X_{ORG.MAT})$	***	0,98
SGR192	$Y = -3,1418 + 0,0071(X_{MAP})$	***	0,92
SGR202	$Y = -65,8954 - 0,0081(X_{LAT}) + 0,0313(X_{LON}) - 0,9078(X_{MIN}) + 0,0088(X_{ERD}) - 0,0814(X_{SLP}) + 0,2415(X_{EA})$	***	0,98
SGR428	$Y = 23,3008 - 0,0067(X_{LAT}) - 0,2952(X_{S.VAL})$	***	0,92
SGR438	$Y = 124,4340 - 0,0435(X_{LON}) - 0,8874(X_{MAT})$	***	0,90
SGR451	$Y = 9,2247 - 0,4712(X_{MIN})$	***	0,81
SGR467+	$Y = 76,4449 - 0,01680(X_{LON}) - 3,3888(X_{PH(H2O)})$	***	0,92
SGR470	$Y = 28,1191 - 0,0087(X_{LAT})$	***	0,89
SGR472+	$Y = 33,4304 - 0,0080(X_{LAT}) + 0,0047(X_{ERD}) - 0,6840(X_{PH(KCL)})$	***	0,99
SGR481	$Y = 30,1547 - 0,0077(X_{LAT}) - 0,0042(X_{MAP})$	***	0,79
SGR482	$Y = 4,7235 + 0,3205(X_{P})$	**	0,37
SGR494	$Y = 23,4890 - 0,0069(X_{LAT}) - 0,0426(X_{P}) - 0,1805(X_{S.VAL})$	***	0,92
SGR515	$Y = 5,0870 - 0,0435(X_{CLAY}) + 0,2542(X_{P})$	**	0,64
KFT23/33	$Y = 34,6121 - 0,01298(X_{LAT}) + 0,3451(X_{MIN})$	***	0,94
Kf81/13/2	$Y = 21,8544 - 0,0079(X_{LAT}) + 0,0306(X_{ERD}) + 0,0066(X_{AL})$	***	0,93
GXC9/03	$Y = 21,0983 - 0,0064(X_{LAT}) - 0,0269(X_{SAND})$	**	0,61
GXC16/08	$Y = 4,0685 - 0,0051(X_{LAT}) + 0,3717(X_{MAX}) + 0,3326(X_{SLP}) + 0,04176X_{SAND})$	**	0,96
GXT22/02	$Y = 8,5464 - 0,0049(X_{LAT}) + 0,3187(X_{MAX}) - 0,0059(X_{SAND})$	***	0,84
MXG25	$Y = 9,0835 - 0,0386(X_{ERD}) - 0,0669(X_{CLAY})$	***	0,85
SGR071	$Y = 57,4698 - 0,0044(X_{LAT}) -0,0169(X_{LON}) + 0,4610(X_{MAT}) + 0,1341(X_{MAX}) -0,0065(X_{ERD}) + 0,3360(X_{EA})$	***	0,92
SGR072	$Y = 65,3468 - 0,0089(X_{LAT}) - 0,0110(X_{LON}) - 0,0032(X_{LON}) + 0,0274(X_{DRY})$	***	0,81
TG12	$Y = 68,8330 - 0,0029(X_{LAT}) -0,0201(X_{LON}) - 0,3937(X_{MAT}) - 0,0519(X_{SLP}) - 0,0489(X_{P})$	***	0,87
38046	$Y = 21,3455 - 0,0059(X_{LAT}) - 0,0897(X_{SLP})$	***	0,85
38047	$Y = 22,6459 - 0,0065(X_{LAT}) + 0,0870(X_{SLP}) + 0,0017(X_{ASP})$	***	0,76

\+ Corrected for the Gingindlovo and the Port Durnford sites

* Significant at the 0,05 probability level

** Significant at the 0,01 probability level

*** Significant at the 0,001 probability level

Table 15. Multiple regression coefficients for mean *Endothia* infestation of individual treatments, using treatment per replication within location means, age 5 years.

Treatment	Regression model	Pr > F	R^2
SGR009+	$Y = 14,9519 - 0,0051(X_{LAT}) - 0,0007(X_N)$	**	0,90
SGR013	$Y = 22,6946 - 0,0085(X_{LON}) - 0,0177(X_{DRY}) + (X_{ERD})$	***	0,91
SGR041	$Y = 10,9127 - 0,0038(X_{LAT})$	***	0,77
SGR042	$Y = 17,1209 - 0,0061(X_{LAT})$	***	0,84
SGR046	$Y = 3,6057 - 0,3346(X_{MIN})$	***	0,90
SGR047	$Y = 63,9686 - 0,0200(X_{LON})$	***	0,89
SGR048	$Y = 8,5231 - 0,0016(X_{LAT}) - (X_{ERD})$	***	0,99
SGR051	$Y = 24,6034 - 0,0089(X_{LAT})$	***	0,98
SGR052	No model ($\alpha = 0,001$).	-	-
SGR053	No model ($\alpha = 0,001$).	-	-
SGR054	$Y = 0,0937 + 0,0029(X_{ALT}) - 0,0026(X_{DRY})$	***	0,99
SGR112	$Y = 4,6620 - 0,4413(X_{MIN})$	***	0,88
SGR183	No model ($\alpha = 0,001$).	-	-
SGR192	$Y = -0,0896 + 0,0021(X_{ALT})$	***	0,99
SGR202	$Y = 11,1921 - 0,0040(X_{LAT})$	***	0,88
SGR428	$Y = 21,7070 - 0,0077(X_{LAT}) + 0,1397(X_{MIN}) - 0,0036(X_{ASP})$	***	0,99
SGR438	$Y = 11,9091 - 0,0044(X_{LAT}) + 0,07208(X_{MIN})$	***	0,99
SGR451	$Y = 4,3939 - 0,2929(X_{LAT})$	***	0,95
SGR467+	$Y = 10,4900 - 0,0035(X_{LAT})$	**	0,58
SGR470	$Y = -0,1482 + 0,0023(X_{ALT})$	***	0,96
SGR472+	$Y = 21,4099 - 0,0075(X_{LAT})$	***	0,77
SGR481	$Y = 2,5366 - 0,0255(X_{DRY})$	***	0,78
SGR482	$Y = 16,2011 - 0,0057(X_{LAT})$	***	0,83
SGR494	$Y = 13,2551 - 0,0047(X_{LAT})$	***	0,90
SGR515	$Y = 14,4577 - 0,0051(X_{LAT}) + 0,1563(X_P)$	***	0,95
KFT23/33	$Y = 29,5717 - 0,0103(X_{LAT}) + 0,0066(X_{SAND})$	***	0,99
KFT81/13/2	$Y = 10,4104 - 0,0036(X_{LAT})$	***	0,72
GXC9/03	$Y = 15,5978 - 0,0055(X_{LAT})$	***	0,50
GXC16/08	$Y = 24,9507 - 0,0085(X_{LAT}) - 0,0006(X_N)$	***	0,82
GXT22/02	$Y = 8,5787 - 0,0030(X_{LAT})$	***	0,94
MXG25	$Y = 3,7912 - 0,0250(X_{ERD}) + 0,04176(X_{SLP}) - 0,0118(X_{AL})$	***	0,99
SGR071	$Y = 16,2378 - 0,0057(X_{LAT})$	***	0,75
SGR072	$Y = 15,8851 - 0,0056(X_{LAT})$	***	0,71
TG12	$Y = 14,0695 - 0,0004(X_{LAT})$	***	0,81
38046	$Y = 16,5318 - 0,0057(X_{LAT}) - 0,0680(X_{SLP})$	***	0,82
38047	$Y = 14,6964 - 0,0051(X_{LAT})$	***	0,81

\+ Corrected for the Gingindlovo and the Port Durnford sites
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001 probability level
NS Non significant

CHAPTER 8

CONCLUSIONS AND RECOMMENDATIONS

The literature search revealed that over an extensive range, the growth of trees is primarily controlled by climatic conditions rather than by soil factors. Water is the environmental factor most directly correlated with growth and is the main controlling factor within forest tree site-growth models. Further, the growth potential of a forest is determined by the rooting volume and the water storage capacity in the soil. Latitude and altitude, through temperature extremes, light intensity, and solar radiation also play a part in the distribution and the growth potential of a forest. Low temperature often limits the geographical distribution of trees. Correlations between growth and soil nutrients are often difficult to detect, with significant correlations only being present over extreme values.

The genotypic adaptability of the *Eucalyptus grandis* clones with respect to growth, stem form and disease infestation, was initially investigated using the ANOVA procedure and Newman-Keuls groupings. As early as two years of age significant site and clone differences for all growth variables were present and this tendency was later confirmed with the five year data. The ranking patterns for volume production, of both the clones and the sites, that were observed at two years were also confirmed at five years. For both measurements, there was a 70 percent common sample within the lowest performing and the best performing sites and clones. The age to age genetic correlation between these two measurements confirmed this result with a 0,66 correlation for volume production. The stem form genetic correlation for the clones, revealed a 0,70 correlation between the two and five year measurements. These two correlations indicated that the two year measurement was a little premature to make a final decision on clonal performances, and that the five year measurement would give a more dependable estimate of performances for a short rotation pulpwood regime.

Water availability, measured by the mean annual rainfall was found to be the main driver of *E. grandis* volume production on the *E. grandis* growing sites of South Africa. The correlation analysis showed a 0,77 correlation between volume production and rainfall (MAP), and no other site factors showed tendencies of such magnitude. It must however be stressed that the mean survival of the complete trial was only 60 percent at five years. This was a natural equivalent to a 40 percent commercial thinning at five years, and this factor alone must account for many of the poor correlations that were (or were not) obtained between the other "traditional" water holding capacity indicators and the volume production.

No significant ($p < 0,05$) correlations were found between growth and the soil factors. This is best ascribed to the fact that all of sites were ideal *E. grandis* growing sites, with no shallow soils, all with well distributed high rainfall, and all within the ideal range of temperatures for *E. grandis* (Poynton, 1979; Herbert, 1993).

Stem form and disease infestation showed a definite north/south polarisation between the higher altitude northern sites and the lower altitude southern sites. Consequently, with latitude, stem form showed a -0,76 correlation, and *Endothia* infestation a -0,86 correlation. Basically, the lower the latitude, the better the stem form, and the more *Endothia* infestation. This polarisation corresponds to the better stem form and the more *Endothia* infestation in the Mpumalanga/Northern Province trials as opposed to the KwaZulu-Natal trials . The other two diseases, *Coniothyrium* and *Cryphonectrea*, were limited to KwaZulu-Natal and consequently did not show this tendency. The measuring team effect in both of these correlations could be a confounding factor. The factor analysis (FA) confirmed all of these observed simple correlations: between volume and rainfall; and between stem form/*Endothia* and latitude.

The joint regression analysis component of the study confirmed the tendencies observed in the two year data, that an increasing site productivity showed a linear increasing productivity within the clones and that there was a divergence or fanning pattern within the regression lines (Van Wyk *et al*, 1991). This tendency was repeated for both the stem form and *Endothia* infestation. Using volume production, the tests for homogeneity of the regressions revealed an assumed common point on origin (intercept) and a significant divergence in regression slopes. Stem form showed significant intercept differences and no significant heterogeneity on slopes. For *Endothia* infestation all clones could be assumed to have a common point of origin (intercept), and homogeneity of slopes. Hence, no significant changes in the rankings of the clones were found, and only the relevant differences between the clones changed (so called fanning effect).

The causes of GEI in relation to the site factors were assessed by using a stepwise multiple regression model approach. The best model for the *E. grandis* test clones gave a R^2 of 0,73 by the inclusion of the clone mean effect within the model. This best fit model then included mean annual rainfall, clone effect, minimum temperature, the effective rooting depth and the soil clay content. Likewise, the stem form and the *Endothia* models were improved to a R^2 of 0,76 percent and a R^2 of 0, 90 respectively. The improved stem form model included latitude, clone effect, longitude, mean annual temperature and slope. The *Endothia* model was far

more complex and included 12 variables, with each variable accounting for a very small percentage improvement, however latitude was the most important contributor to the model. The verification of the factors influencing the individual models could now open the way for further testing through nursery or repeat field trials.

The final objective of the research, namely the basis for the selection of clones for given sites, was addressed by using the JRA selections with the highest beta values, and the highest ranking clones within the ANOVA/Newman-Keuls groupings. The top 6 selections for both methods for volume production revealed a 85 percent common selection between the JRA and the ANOVA/Newman-Keuls rankings. A visual elimination process selected the top six clones to plant on any site based on volume production, acceptable stem form and little *Endothia* infestation as SGR051, SGR183, SGR428, SGR451, SGR481 and SGR482.

On the basis of the above, it is recommended that in order to select clones for commercial purposes the JRA method be employed, as used in this study. A more complete and balanced trial design should however allow for other analytical methods better suited to studies of this nature to be employed. The incomplete trial design presented major limitations for the use of other analytical methods such as genetic correlations and AMMI. The selection of *E. grandis* clones would best be undertaken on the more productive sites, mainly as a result of the relevant clone differences being exemplified by the better growth. The process could be further expanded by the utilisation of a number of planting sites. The Newman-Keuls groupings of sites could be used to obtain a representative range of sites.

A summary from this study could be as follows: Water availability is the main environmental influence of growth, while latitude has an effect on the stem form and disease infestation of *E. grandis* within the *E. grandis* growing areas of South Africa. No significant changes in the rankings of clones are present for volume production, stem form or *Endothia* infestation, although the relevant differences between the clones change. This is can be described as a diverging or "fanning type "of GEI effect.

BIBLIOGRAPHY

Ades, P.K. and Garnier-Gere, 1996. Stability analysis for *Pinus radiata* provenances and its implications for genetic resource conservation. In: Dieters, M.J., Matheson, A.C., Nikles, D.G., Harwood, C.E. and Walker, S.M. (Eds.). Tree Improvement for Sustainable Tropical Forestry. Proc. QFRI-IUFRO Conf., Caloundra, Queensland, Australia. 27 October - 1 November 1996: 118-122.

Allard, R.W. and Bradshaw, A. D., 1964. Implication of genotype-environmental interactions in applied plant breeding. *Crop Science* 4: 503-507.

Barbour, M.G., Burk, J.H. and Pitts, W.D., 1987. Terrestrial plant ecology. Second edition. Benjamin/Cummings, California. 634 pp.

Barnes, R.D., 1984. Genotype-environment interaction in the genetic improvement of fast growing plantation trees. In: Grey, D.C., Schönau, A.P.G. and Schutz, C.J., (Eds.). Symposium on site and productivity of fast growing plantations. Proc. IUFRO Conf., Pretoria and Pietermaritzburg, South Africa. 30 April - 11 May 1984: 197-213.

Barnes, R.D. and Gibson, G.L., 1984. Experimental design, management and selection traits in provenance trials of tropical pines. In: Barnes, R.D. and Gibson, G.L., (Eds.). Provenance and genetic improvement strategies in tropical forest trees. Proc. IUFRO Conf., Mutare, Zimbabwe, April, 1984: 8-29.

Barnes, R.D., Burley, J. And Gibson, G.L. and Garcia de Leon, J.P., 1983. Genotype-environment interactions in tropical pines and their effects on the structure of breeding populations. *Silvae Genetica* 33(6): 186-197.

Becker, H.C. and Léon, J., 1988. Stability analysis in plant breeding. *Plant Breeding* 101: 1-23

Byth, D.E., Eisemann, R.L., de Lacy, I.H., 1976. Two-way pattern analysis of a large data set to evaluate genotypic adaption. *Heredity* 37(2): 215-230

Boland, D.J., Brooker, M.I.H., Chippendale, G.M., Hall, N., Hyland, B.P.M., Johnston, R.D., Kleinig, D.A., and Turner, J.D., 1984. Forest trees of Australia. Nelson-CSIRO, Melbourne, Australia

Bredenkamp, B.V. and Loveday, N.C., 1984. Research note. Volume equations for diameter measurements in millimetres. *South African Forestry Journal* 130 (3): 40

Burdon, R.D., 1977. Genetic correlation as a concept for studying genotype-environment interaction in forest breeding. *Silvae Genetica* 26(5-6): 168-175.

Burdon, R.D., 1991. Genetic correlations between environments with genetic groups missing in some environments. *Silvae Genetica* 40(2): 66-67.

Chatfield, C. and Collins, A.J., 1980. Introduction to multivariate analysis. Chapman and Hall, London. 246 pp.

Cochran, W.G., and Cox, G.M., 1950. Experimental Designs. John Wiley, New York, USA. 611 pp.

Denison, N.P., and Kietzka, J.E., 1993. The development and utilisation of vegetative propagation in Mondi for commercial afforestation programmes. *South African Forestry Journal* 166: 53 - 60

Eberhart, S.A. and Russel, W.A., 1966. Stability parameters for comparing varieties. *Crop Science* 6: 36-40.

Ellis, F., 1996. Talking silviculture. Soil properties that restrict plant growth and root development: part 2. *Wood SA/Timber Times*. May, 1996: 6-7.

Ellis, F., 1997. Talking silviculture. Mineral nutrients: introduction. *Wood SA/Timber Times*. August 1997.

Endo, M. and Wright, J., 1993. First year results from interaction of site by clone trials of *Eucalyptus grandis* in the Andes region of Columbia. Investigación Forestal. Smurfit Cartón de Columbia. Columbia.

Esterhuyse, C.J., 1985. Site requirements of the most important commercial trees planted in South Africa. *South African Forestry Journal* 133: 61-66.

Evans, J., 1982. Plantation forestry in the tropics. Clarendon Press, Oxford. 472 pp.

Evans, J., Wood, P.J. and Moutanda, A., 1992. The use of tropical plantations in sustainable forest management. In: Wood, P.J. Vanclay, J.K. and Wan Mohd, W.R. (Eds.). The tropical silviculture workshop at the IUFRO centennial conference in Berlin. Proc. 1 - 3 September, 1992: 32-48.

Falconer, D.S. and Mackay, T.F.C., 1996. Introduction to quantitative genetics. 4th edition. Longman, Essex, England. 464 pp.

Falkenhagen, E.R., 1976. Tree breeding for photosynthetic efficiency. *South African Forestry Journal* 98: 52-56.

Falkenhagen, E.R., 1985. Genotype by environment interactions in South African pine progeny trials: Implications for tree breeding. *South African Forestry Journal* 135: 53-60.

Falkenhagen, E.R., 1996. A comparison of the AMMI method with some classical statistical methods in provenance research: The case of the South African *Pinus radiata* trials. *Forest Genetics* 3(2): 81-87.

Finlay, K.W. and Wilkinson, G.N., 1963. The analysis of adaption in a plant breeding programme. *Australian Journal of Agricultural Research* 14: 742-754.

Forest Owners Association, 1997. Abstract of South African forestry facts for the year 1995/96. Forest Owners Association. Rivonia, South Africa. 7pp.

Ford, E.D., 1978. An ecological basis for predicting the growth and stability of plantation forests. In: Ford, E.D., Malcolm, D.C. and Atterson, J. (Eds.). The ecology of even-aged forest plantations. Proc. IUFRO meeting of division 1. Edinburgh, Scotland, September, 1978: 147-174.

Foth, H.D., 1990. Fundamentals of soil science. Eighth edition. John Wiley, New York. 360 pp.

Freeman, G.H., 1973. Statistical methods for the analysis of genotype-environment interactions. *Heredity* 31(3): 339-354.

Freeman, G.H. and Perkins, J.M., 1971. Environmental and genotype-environmental components of variability. *Heredity* 27: 15-23.

Garnier-Géré, P., Raymond, C.A. and Ades, P.K., 1995. Comparison of models for structuring genotype by environment interaction in *Eucalyptus delegatensis* provenance trials. In : *Eucalyptus* plantations: Improving fibre yield and quality. Proc. IUFRO Conf. Hobart, 19-24 February 1995: 156-162.

Gauch, H.G., 1988. Model selection and validation for yield trials with interaction. *Biometrics* 44: 705-715

Gauch, H.G., 1990. MATMODEL VERSION 2.0: AMMI and relatedanalysis for two way data matrices. Department of Agronomy, Cornell University Ithaca, New York, 69pp

Gholz, H.L., Ewel, K.C. and Teskey, R.O., 1990. Water and forest productivity. *Forest Ecology and Management* 30: 1-18.

Gibson, G.L., 1982. Genotype-Environmental Interaction in *Pinus caribaea*. Department of Forestry. Commonwealth Forestry Institute, Oxford. 112 pp.

Grey, D.C., 1987*a*. Silvicultural prescriptions for G x E trial series. Internal memo, A.23/1/9/3 -2059/2065. Saasveld Forestry Research Centre, George

Grey, D.C., 1987*b*. Site selection for G x E trials. Internal memo, A.23/1/9/3 -2059/2065. Saasveld Forestry Research Centre, George

Grey, D.C., Herbert, M.A., and Ellis, F., 1993. Forest soils and their implications for management. In: Van der Sijde, H.A. (Ed). Forestry Handbook, Southern African Institute of Forestry

Griffiths, J.F., 1976. Climate and the environment: The atmospheric impact on man. Paul Elek, London. 148 pp.

Hardwick, R.C. and Wood, J.T., 1972. Regression methods for studying genotype-environment interactions. *Heredity* 28: 209-222.

Heather, W.A. and Griffin, D.M., 1984. The potential for epidemic disease. In: Hillis, W.E. and Brown, A.G. (Eds). Eucalypts for wood production. Academic press, Sydney

Herbert, M.A., 1993. Site requirements of exotic hardwood species. In: Van der Sijde, H.A. (Ed). Forestry Handbook, Southern African Institute of Forestry

Hodge, G.R., 1996. Marginal gains from regionalisation to utilise genotype x environment interactions variance. In: Dieters, M.J., Matheson, A.C., Nikles, D.G., Harwood, C.E. and Walker, S.M. (Eds.). Tree Improvement for Sustainable Tropical Forestry. Proc. QFRI-IUFRO Conf., Caloundra, Queensland, Australia. 27 October - I November 1996: 307-310.

Howard, M.D., 1997. Site matching and commercial deployment of *Eucalyptus* clones. In: Conferencia IUFRO sobre Silvicultura e Melhoramento de Eucaliptos. Proc. IUFRO Conf. Salvador, Brazil, 24-29 August, 1997: 360-365.

Isebrands, J.G., Ceulemans, R., and Wiard, B., 1988. Genetic variation in photosynthetic traits among *Populus* clones in relation to yield. *Plant Physiol. Biochem.* 26 (4): 427-437.

James, D.J. and Schön, P.P., 1991. Can AMMI be used in clone x site matching? In: Schönau (Ed.). Intensive forestry: The role of eucalypts. Proc. IUFRO Conf., Durban, South Africa. 2-6 September 1991: 371-379.

Kozlowski, T.T., 1968. Soil water and tree growth. In: Linnartz, N.E. (Ed). The ecology of southern forests. 17th annual forestry symposium. Louisiana State University Press. Baton Rouge, USA : 30-57.

Kozlowski, T.T., Kramer, P.J. and Pallardy, S.G., 1991. Physiological ecology of woody plants. Academic Press, New York. 657 pp.

Kozlowski, T.T., and Pallardy, S.G., 1997. Physiology of woody plants. Second edition. Academic Press, New York. 411 pp.

Kramer, P.J. and Kozlowski, T.T., 1960. Physiology of trees. McGraw-Hill, New York. 642 pp.

Landsberg, J.J. and Gower, S.T., 1997. Applications of physiological ecology to forest management. Academic Press, New York. 349 pp.

Lin, C.S., Binns, M.R. and Lefkovitch, L.P., 1986. Stability analysis: Where do we stand. *Crop Science* 26: 894-900

Louw, J.H., 1991. The relationship between site characteristics and *Pinus radiata* growth on the Tsitsikamma plateau, South Africa. *South African Forestry Journal* 158: 37-45.

Louw, J.H., 1997. A site-growth study of *Eucalyptus grandis* in the Mpumalanga escarpment area. *South African Forestry Journal* 180: 1-13.

Louw, J.H., 1999. A review of site-growth studies in South Africa. *South African Forestry Journal* 185: 57-65.

MacVicar, 1977. Soil classification: A binomial system for South Africa. *Memoirs of the Agricultural Natural Resources of South Africa* no 15. Department of Agricultural Development, Pretoria. 150 pp.

Matheson, A.C., 1988. Statistical methods and problems in testing large numbers of genotypes across sites. In: Gibson, G.L., Griffin, A.R. and Matheson, A.C. (Eds.). Breeding tropical trees: Population structure and genetic improvement strategies in clonal and seedling forestry. Proc. IUFRO conf. Pattaya, Thailand. November, 1988: 93-105.

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. Provenance x environment interaction; its detection, practical importance and use with particular reference to tropical forestry. In: Barnes, R.D. and Gibson, G.L., (Eds.). Provenance and genetic improvement strategies in tropical forest trees. Proc. IUFRO Conf., Mutare, Zimbabwe, April, 1984: 81-117.

Matheson, A.C. and Raymond, C.A., 1986. A review of provenance x environmental interaction: Its practical importance and use with particular reference to the tropics. *Commonwealth Forestry Review* 65(4): 283-302.

Matheson, A.C., Spencer, D.J. and Kriedmann, P.E., 1995. Age-age correlation and early selection in radiata pine. I. Family x environmental interactions in plantation and greenhouse. *Australian Forestry* 58(2): 35-43.

May, J.T., 1968. Influence of edaphic and physiographic factors on the forest ecosystem. In: Linnartz, N.E. (Ed). The ecology of southern forests. 17th annual forestry symposium. Louisiana State University Press. Baton Rouge, USA. : 18-29.

Moehring, D.M., 1968. Climatic elements in the Southern Forest environments. In: Linnartz, N.E. (Ed). The ecology of southern forests. 17th annual forestry symposium. Louisiana State University Press. Baton Rouge, USA. : 50-17.

Nachit, M.M., Nachit, G, Ketata, H, Gauch, H.G., and Zobel, R.W., 1992. Use of AMMI and linear regression models to analyze genotype-environment interaction in durum wheat. *Theoretical and Applied Genetics* 83: 597-601

Nambiar, E.K.S., 1990. Interplay between nutrients, water root growth and productivity in young plantations. *Forest Ecology and Management* 30: 213-232.

Ott, R.L., 1993. An introduction to statistical methods and data analysis. 4th edition. Duixbury Press. Belmont, California. 1050 pp.

Noble, A.D., Donkin, M.J. and Smith, C.W., 1991. The importance of soil properties as indicators of site quality for *Eucalyptus grandis* on the Zululand coastal plain. In: Schönau, A.P.G.(Ed.). Intensive forestry: The role of eucalypts. Proc. IUFRO Conf., Durban, South Africa. 2-6 September 1991: 433-443.

Pederick, L.A., 1976. The genetic resources of the Victorian eucalypts. Bulletin no. 22. Forests Commission, Victoria. 31 pp.

Pereira, J.S. and Kozlowski, T.T., 1977. Influence of light intensity, temperature, and leaf area on stomatal aperture and water potential of woody plants. *Canadian Journal of Forestry Research* 7: 145-153.

Perkins, J.M. and Jinks, J.L., 1968. Environmental and genotype-environmental components of variability. *Heredity* 23: 339-356.

Perkins, J.M., 1972. The principle component analysis of genotype-environmental interactions and physical measures of the environment. *Heredity* 29: 51-70.

Perry, D.A., 1978. Variation between and within tree species. In: Ford, E.D., Malcolm, D.C. and Atterson, J. (Eds.). The ecology of even-aged forest plantations. Proc. IUFRO meeting of division I. Edinburgh, Scotland, September, 1978: 71-98.

Phoelman, M.J. and Sleper, D.A., 1995. Breeding field crops. Fourth edition. Iowa State University Press, Ames, Iowa. 494 pp.

Poynton, R.J., 1979. Tree planting in Southern Africa. Volume 2, The Eucalypts. Government printer, Pretoria.

Pritchett, W.L., 1968. Improvement in soil fertility as a means of increasing growth. In: Linnartz, N.E. (Ed). The ecology of southern forests. 17th annual forestry symposium. Louisiana State University Press. Baton Rouge, USA. : 183-198.

Pritchett, W.L. and Fisher, R.F., 1979. Properties and management of forest soils. Second edition. John Wiley, New York. 494 pp.

SAS for linear models: A guide to the ANOVA and GLM procedures, 1981. SAS Institute Inc., SAS Circle, Box 8000, Cary, N.C., USA.

SAS Procedures Guide. Release 6.12, 1996. SAS Institute Inc., SAS Circle, Box 8000, Cary, N.C., USA.

Schönau, A.P.G. and Schulze, R.E., 1984. Climatic and altitudinal criterea for commercial afforestation with special reference to Natal. *South African Forestry Journal* 130: 10-18.

Schönau, A.P.G. and Aldworth, W.J.K., 1991. Site evaluation in Black Wattle with special reference to soil factors. *South African Forestry Journal* 156: 35-43.

Schafer, G.N., 1988*a*. A site growth model for *Pinus elliottii* in the southern Cape. *South African Forestry Journal* 146: 12-17

Schafer, G.N., 1988*b*. A site growth model for *Pinus pinaster* in the southern Cape. *South African Forestry Journal* 146: 18-22

Schulze, R.E., 1997. South African Atlas of Agrrohydrology and -Climatology. Water Research Commission, Pretoria. Report TT82/96

Schutz, C.J., 1990. Site relationships for *Pinus patula* in the eastern Transvaal escarpment. Ph.D thesis, Department of Soil Science and Agrometeorology, University of Natal, Pietermaritzburg. 334 pp.

Shelbourne, C.J.A., 1972. Genotype-environment interaction: Its study and its implications in forest tree improvement. In: Proc. IUFRO Genetics-SABRAO joint symposia, Tokyo B-1(I): 1-28.

Shorter, R., Byth, D.E. and Mungomery, V.E., 1977. Genotype x environment interactions and environmental adaption. II. Assessment of environment contributions. *Australian Journal of Agricultural Research* 28: 223-235.

Skrøppa, T. 1984. A critical evaluation of methods available to estimate the genotype x environmental interaction. Nordic group of forest tree breeders. Proceedings of a conference on genotype x environment interaction, Uppsala, Sweden 23-27 August 1982. *Studia Foresalia Suecica* 166: 3-17.

Soil Classification Working Group, 1991. Soil classification: A taxonomic system for South Africa. *Memoirs of the Agricultural Natural Resources of South Africa* no 15. Department of Agricultural Development, Pretoria. 257 pp.

Spurr, S.H. and Barnes, B.V., 1980. Forest ecology. Third edition. John Wiley, New York. 687 pp.

Tolman, R.D.L., 1978. Ecology of even-aged plantations - site classification. In: Ford, E.D., Malcolm, D.C. and Atterson, J. (Eds.). The ecology of even-aged forest plantations. Proc. IUFRO meeting of division I. Edinburgh, Scotland, September, 1978: 23-37.

Van Eeuwijk, F.A., 1992. Interpreting genotype-by-environment interaction using redundancy analysis. *Theoretical and Applied Genetics* 85: 89-100

Van Laar, A., 1987. Multivariate analysis: A way to better understanding of complexity. *South African Forestry Journal* 141: 34-41.

Van Wyk, G., and Falkenhagen, E.R., 1984. Genotype x environment interaction in South African breeding material. In: Grey, D.C., Schönau, A.P.G., and Schutz, C.J. (Eds.). Symposium on site and productivity of fast growing plantations. Proc. IUFRO Conf., Pretoria and Pietermaritzburg, South Africa. 30 April - 11 May 1984: 251-231.

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: Schönau, A.P.G.(Ed.). Intensive forestry: The role of eucalypts. Proc. IUFRO Conf., Durban, South Africa. 2-6 September 1991: 371-379.

Van Wyk, G., 1987. Project proposal to study clone by site interaction of *E. grandis* clones. SAFRI internal memo.

Waring, R.H. and Schlesinger, W.H., 1985. Forest ecosystems: Concepts and management. Academic Press, New York. 340 pp.

Wingfield, M.J. and Kemp, G.H.J., 1993. Diseases of pines, eucalypts and wattle. In: Van der Sijde, H.A. (Ed). Forestry Handbook, Southern African Institute of Forestry

Wood, J.T., 1976. The use of environmental variables in the interpretation of genotype-environment interaction. *Heredity* 37(1): 1-7.

Wright, A.J., 1976. The significance for breeding of linear regression analysis of genotype-

environment interactions. *Heredity* 37(1): 83-93.

Zobel, B.J. and Talbert, J.T., 1984. Applied forest tree improvement. John Wiley. New York, USA. 505 pp.

APPENDIX 1

EXPERIMENTAL DESIGN

APPENDIX 1 : Table 1. Experimental design - Incomplete latin square

Sites	Clones I	II	III	IV	V	VI	VII	VIII	IX	X
(1)	1	2	4	8	9	11	15	16	18	28
(2)	2	3	12	9	10	17	16	19	5	22
(3)	3	4	20	10	17	13	6	18	11	23
(4)	4	5	7	11	12	21	18	14	19	24
(5)	5	6	1	12	13	8	19	20	15	25
(6)	6	7	13	16	14	9	20	21	2	26
(7)	7	1	15	14	8	10	21	17	3	27
(8)	8	11	17	25	16	23	29	7	26	5
(9)	9	12	24	29	27	18	1	26	17	6
(10)	10	13	18	19	29	25	2	27	28	7
(11)	11	14	22	26	19	20	3	28	29	1
(12)	12	8	27	23	20	29	4	22	21	2
(13)	13	9	29	28	21	15	5	23	24	3
(14)	14	10	25	22	15	16	24	29	6	4
(15)	15	24	26	5	2	27	11	10	30	20
(16)	16	25	6	30	3	28	12	11	27	21
(17)	17	26	28	7	30	22	13	12	4	15
(18)	18	27	23	1	5	30	14	13	22	16
(19)	19	28	30	2	6	14	8	24	23	17
(20)	20	22	8	3	7	24	9	30	25	18
(21)	21	23	10	4	1	26	30	25	9	19
(22)	22	21	11	17	24	1	25	2	31	13
(23)	23	15	3	18	25	2	26	31	12	14
(24)	24	16	19	31	26	3	27	4	13	8
(25)	25	17	14	27	31	4	28	5	20	9
(26)	26	18	5	21	28	31	22	6	8	10
(27)	27	19	31	15	22	6	23	9	7	11
(28)	28	20	16	24	23	7	31	1	10	12
(29)	29	30	2	6	4	5	7	3	1	31
(30)	30	31	9	13	11	12	10	8	14	29
(31)	31	29	21	20	18	19	17	15	16	30

Where: $t = 31, k = 10, r = 10, b = 31, \lambda = 3, E = .93$, Type I

t = number of groups of size k (clones)
r = number of replicates
b = number of blocks (sites)
λ = number of times that two treatments appear in the same row or column
E = Efficiency of the design
Type I = envisaged method of analysis

(Source: Cochran and Cox 1950, plan 13,2a)

APPENDIX 1 : Table 2. Details of allocations of test clones for each of the GEI trial sites

CLONES:	TRIAL LOCATIONS: FZS	RMD	TFK2	ADN	TST	NYL2	SMK	ESL1	MPS	NLN	WHB	TBD	TLD	TKF1	UMD	WLD
SGR009	x	x	x	x	x	x	x	✔	✔	✔	✔	✔	✔	✔	x	x
SGR013	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
SGR041	x	✔	x	x	x	x	x	x	x	x	✔	✔	x	✔	x	x
SGR042	x	x	x	✔	x	✔	✔	x	x	x	✔	x	x	✔	x	x
SGR046	x	x	x	✔	x	✔	✔	x	x	x	x	✔	✔	x	x	✔
SGR047	✔	x	x	x	x	x	x	x	x	✔	✔	x	✔	x	x	✔
SGR048	✔	x	✔	✔	x	x	x	x	✔	✔	x	x	x	x	x	x
SGR051	x	x	✔	x	x	x	x	✔	x	x	x	✔	✔	x	x	x
SGR052	x	✔	x	✔	✔	x	x	✔	x	x	x	x	✔	x	✔	x
SGR053	x	x	x	x	x	x	✔	x	✔	✔	x	✔	x	x	✔	✔
SGR054	x	x	x	x	x	x	x	x	x	x	x	x	x	x	✔	✔
SGR112	✔	✔	x	x	x	✔	x	x	x	✔	x	✔	x	x	✔	x
SGR183	x	✔	✔	x	x	x	✔	✔	✔	x	x	x	x	x	x	x
SGR192	x	✔	x	✔	✔	x	x	x	✔	x	x	✔	x	x	x	✔
SGR202	x	x	x	x	x	✔	x	✔	✔	x	✔	x	x	x	✔	x
SGR428	x	✔	✔	x	x	x	✔	x	x	x	✔	x	✔	x	x	✔
SGR438	x	x	x	x	✔	x	x	✔	x	✔	x	x	x	✔	x	✔
SGR451	x	✔	x	✔	✔	x	x	x	x	✔	✔	x	x	x	x	x
SGR467	x	x	✔	x	✔	✔	x	x	x	x	✔	✔	x	x	✔	x
SGR470	✔	✔	x	x	x	✔	x	x	✔	x	x	x	✔	x	x	x
SGR472	x	x	x	✔	x	✔	✔	✔	x	✔	x	x	x	x	x	x
SGR481	✔	x	x	x	✔	x	✔	x	✔	x	✔	x	x	x	x	x
SGR482	✔	x	✔	✔	x	x	x	✔	x	x	✔	x	x	x	✔	✔
SGR494	x	x	✔	x	✔	✔	x	x	x	✔	x	x	✔	x	x	x
SGR515	✔	✔	x	x	x	✔	x	✔	x	x	x	x	x	✔	x	✔
KFT23/33	✔	x	✔	✔	x	x	x	x	x	x	x	✔	x	✔	x	x
KFT81/13/2	x	x	x	✔	x	x	x	x	✔	x	x	x	✔	✔	✔	✔
GXC9/03	✔	x	x	x	✔	x	✔	x	✔	x	x	x	✔	✔	✔	x
GXC16/08	x	x	✔	x	✔	✔	x	x	x	x	x	x	x	✔	x	x
GxT22/02	x	✔	✔	x	x	x	✔	x	x	✔	x	x	x	✔	✔	x
MXG25	✔	x	x	x	✔	x	✔	✔	x	x	x	✔	x	x	x	x

APPENDIX 1 : Table 2. continued

CLONES:	TRIAL LOCATIONS: JDM	ESL3	ELD	PDN	ESL2	SFT	FRT	FWD	KGA	VTM	CTR	DNL	GLP	NYL1	GNG
SGR009	x	x	x	x	x	x	x	x	x	x	x	x	✔	✔	✔
SGR013	x	x	x	x	x	✔	✔	✔	✔	✔	✔	✔	✔	✔	✔
SGR041	✔	✔	x	✔	x	✔	x	x	x	✔	✔	x	x	x	x
SGR042	x	✔	✔	x	x	x	✔	x	✔	x	x	x	x	✔	x
SGR046	x	x	x	x	✔	✔	x	x	x	✔	x	x	x	x	✔
SGR047	✔	x	✔	x	x	x	x	x	✔	✔	x	✔	x	x	x
SGR048	x	✔	x	✔	x	x	✔	x	x	✔	x	x	x	x	✔
SGR051	x	✔	✔	x	✔	x	✔	x	x	x	✔	✔	x	x	x
SGR052	x	✔	x	x	x	x	x	x	✔	✔	x	x	✔	x	x
SGR053	x	✔	x	x	x	x	x	✔	✔	x	✔	x	x	x	x
SGR054	✔	✔	✔	✔	✔	x	x	x	x	x	x	x	✔	✔	✔
SGR112	x	x	✔	x	x	✔	✔	x	x	x	x	x	✔	x	x
SGR183	✔	x	✔	x	x	✔	x	x	✔	x	x	x	x	x	✔
SGR192	✔	x	x	x	x	x	✔	x	x	x	x	✔	x	✔	x
SGR202	✔	x	x	x	✔	x	✔	✔	x	✔	x	x	x	x	x
SGR428	x	x	x	✔	x	x	✔	✔	x	x	x	x	✔	x	x
SGR438	x	x	x	✔	✔	✔	✔	x	✔	x	x	x	x	x	x
SGR451	x	x	✔	x	✔	x	x	✔	x	x	✔	x	x	x	✔
SGR467	x	x	x	✔	x	x	x	x	✔	x	x	✔	x	x	✔
SGR470	x	x	x	✔	✔	x	x	x	✔	x	✔	x	x	✔	x
SGR472	✔	x	x	✔	x	x	x	x	x	x	✔	✔	✔	x	x
SGR481	x	✔	x	x	✔	✔	x	x	x	x	x	✔	✔	x	x
SGR482	x	x	x	x	x	✔	x	x	x	x	✔	x	x	✔	x
SGR494	✔	✔	x	x	x	✔	x	✔	x	x	x	x	x	✔	x
SGR515	x	✔	x	x	x	x	x	✔	x	x	x	✔	x	x	✔
KFT23/33	✔	x	x	x	✔	x	x	✔	✔	x	x	x	✔	x	x
KFT81/13/2	x	x	✔	✔	x	✔	x	✔	x	x	x	✔	x	x	x
GXC9/03	✔	x	x	x	x	x	✔	x	x	x	✔	x	x	x	✔
GXC16/08	x	x	✔	x	x	x	x	x	x	✔	✔	x	✔	x	x
GxT22/02	x	x	x	x	✔	x	x	x	x	✔	x	✔	x	✔	x
MXG25	x	x	✔	✔	x	x	x	✔	x	✔	x	x	x	✔	x

APPENDIX 2

PHYSIOGRAPHICAL AND SOIL DETAILS

APPENDIX 2 : Table 1 Physiographical details of trial test sites

No	Code	Plantation	Geology*	Soil form**	MAP (mm)	DRY (mm)	MAT (°C)	MAX (°C)	MIN (°C)	ERD (cm)	Slope (°)	Aspect (°)
1	FZS	Fransinasrus	Diabase	Glenrosa	969	8	18,8	28,4	6,1	80	0	85
2	RMD	Richmond	Shale	Oakleaf	1141	37	16,5	25,0	5,6	130	8	50
3	TKF2	Tygerskloof 83	Diabase	Hutton	1050	29	17,4	26,2	6,6	150	11	310
4	ADN	Ashenden	Shale	Oakleaf	1007	32	16,8	25,3	6,0	120	13	200
5	TST	Ntenja	Berea sand	Hutton	1017	100	21,8	30,2	10,3	150	0	0
6	NYL2	Nyalasi J9	Shale	Valsrivier	849	59	22,0	30,6	10,5	80	6	215
7	SMK	Middagson	Granite	Swartland	835	13	19,1	28,8	5,3	65	7	330
8	ESL1	Eersteling A	Granite	Griffin	803	10	17,7	28,0	3,8	100	0	0
9	MPS	Mooiplaas	Granite	Griffin	938	31	17,3	25,8	6,5	120	10	220
10	NLN	Nseleni	Aeolian sand	Fernwood	1038	108	21,7	30,0	10,4	150	1	325
11	WHB	Waterhoutboom	Diabase	Griffin	1210	29	18,3	27,6	5,5	120	8	255
12	TBD	Tidboald	Aeolian sand	Fernwood	974	90	21,7	30,0	10,4	150	0	0
13	TLD	Townlands	Shale	Magwa	861	22	16,9	25,6	6,0	120	7	50
14	TKF1	Tygerskloof 29	Diabase	Hutton	950	23	17,5	26,6	6,1	100	8	95
15	UMD	Umsunduze	Aeolian sand	Clovelly	897	75	21,9	30,6	10,0	150	2	20
16	WLD	Waldeck	Granite	Hutton	917	15	20,6	30,4	6,8	150	10	340
17	JDM	JDM Keet FRS	Granite	Hutton	1072	18	20,1	29,8	6,3	150	9	250
18	ESL3	Eersteling C	Granite	Hutton	803	10	17,7	28,0	3,8	120	5	150
19	ELD	Eldorado	Granite	Hutton	1044	19	20,2	30,0	6,3	135	8	340
20	PDN	Port Durnford	Berea sand	Hutton	1441	166	21,1	28,3	12,3	150	6	330
21	ESL2	Eersteling B	Granite	Hutton	803	10	17,7	28,0	3,8	50	3	155
22	SFT	Swartfontein	Granite	Hutton	1071	18	18,2	27,0	6,5	120	8	175
23	FRT	Frankfort	Granite	Hutton	1467	38	18,2	27,3	6,0	120	5	355

APPENDIX 2 : Table 1. continued

No	Code	Plantation	Geology*	Soil form**	MAP (mm)	DRY (mm)	MAT (°C)	MAX (°C)	MIN (°C)	ERD (cm)	Slope (°)	Aspect (°)
24	FWD	Fernwood	Aeolian sand	Fernwood	1008	80	21,8	30,1	10,6	150	1	360
25	KGA	Knogka	Shale	Cartref	864	37	16,5	24,6	6,0	50	7	180
26	VTM	Venus Timbers	Granite	Hutton	1344	35	18,4	27,4	6,0	120	8	135
27	CTR	Christinasrust	Granite	Oakleaf	1313	23	19,0	27,0	8,6	150	20	300
28	DNL	Doornlaagte	Granite	Hutton	1170	24	19,0	28,3	6,2	120	8	190
29	GLP	Glenthorpe	Granite	Hutton	901	8	18,8	28,6	5,8	150	4	5
30	NYL1	Nyalazi E23	Aeolian sand	Clovelly	1021	91	21,9	30,1	10,9	150	0	0
31	GNG	Gingindlovo	Aeolian sand	Hutton	1181	120	21,0	28,7	11,1	150	6	330

*	International system
**	Local South African system
MAP	Mean annual precipitation
DRY	Mean precipitation in the driest quarter
MAT	Mean annual temperature
MAX	Mean maximum temperature for the hottest month
MIN	Mean minimum temperature for the coldest month
ERD	Effective rooting depth of soil to impeding layer

APPENDIX 2 : Table 2. Summary of physiographical variables, symbols used, and measuring units.

VARIABLE	SYMBOL	UNIT
Latitude	LAT	° ' E
Longitude	LON	° ' S
Altitude	ALT	m
Temperature (Mean annual)	MAT	°C
Temperature (Mean maximum)	MAX	°C
Temperature (Mean minimum)	MIN	°C
Rainfall (Mean Annual)	MAP	mm
Rainfall (Driest Quarter)	DRY	mm
Soil depth	ERD	cm
Slope	SLP	°
Aspect	ASP	0 - 360°

APPENDIX 2 : Table 3. Summary of soil analysis, symbols used, and measuring units

VARIABLE	SYMBOL	UNIT
Soil acidity (Distilled water)	pH (H_2O)	0 - 14
Soil acidity (Potassium chloride)	pH (KCl)	0 - 14
Soil texture: Sand	Sand	%
Soil texture: Silt	Silt	%
Soil texture: Clay	Clay	%
Organic matter content	Org.Mat	%
Percentage Carbon	C	%
Exchangeable acidity	EA	me/100g
Aluminium	Al	mg kg^{-1}
Nitrogen	N	mg kg^{-1}
Phosphorus (Bray no. 2)	P	mg kg^{-1}
Potassium	K	mg kg^{-1}
Calcium	Ca	mg kg^{-1}
Magnesium	Mg	mg kg^{-1}
Sodium	Na	mg kg^{-1}
S-value	SVAL	me/100g

Percentage sand = Total of coarse, medium, fine and very fine grains

Percentage silt = Total of coarse and fine silt

Percentage clay = Total clay

APPENDIX 3

CONTROL SEED GROUPS

APPENDIX 3 : Table 1. Composition of clonal seed orchard mixture, 38047

Stock	Year	Location	Seed orchard	Block
30274	1984	J.D.M. Keet F.R.S.	Clonal seed orchard no 2	Block 2
30283	1985	J.D.M. Keet F.R.S.	Clonal seed orchard no 2	Block 3
30293	1986	J.D.M. Keet F.R.S.	Clonal seed orchard no 2	Block 4
30278	1985	De Hoek.	Clonal seed orchard no 1	Block 2
30289	1986	De Hoek.	Clonal seed orchard no 1	Block 3
38053	1987	J.D.M. Keet F.R.S.	Clonal seed orchard no 2	Block 1

Note:

Open-pollinated mixture from 74 clones

APPENDIX 3 : Table 2. Composition of seedling seed orchard mixture, 38046

Stock	Year	Location	Seed orchard
30261	1983	JDM Keet F.R.S.	Seedling Seed Orchard no 2
30281	1985	JDM Keet F.R.S.	Seedling Seed Orchard no 4
38045	1987	JDM Keet F.R.S.	Seedling Seed Orchard no 5

Note:

Open-pollinated mixture from 298 families

APPENDIX 4

ASSESSMENT PROCEDURES

APPENDIX 4 : Table 1. Two year assessment procedures

Trait	Instrument	Method of assessment	Unit
height	Height rods	from base to tip of tree	dm
DBH	Diameter tape	over bark at 1,3 m from ground level	mm
stem form	Visual	on total bole from base to tip of tree	1 - 8
defects	Visual	broken top dead tree forked tree not planted or seedling filler tree	B D F N

APPENDIX 4 : Table 2. Five year assessment procedures

Trait	Instrument	Method of assessment	Unit
height	Hypsometer	from base to tip of tree	m
DBH	Diameter tape	over bark at 1,3 m from ground level	mm
stem form	Visual	on total bole from base to tip of tree	1 - 8
Coniothyrium	Visual	on total bole from base to live crown	0 - 4
Cryphonectria	Visual	on total bole from base to live crown	0 - 4
Endothia	Visual	on total bole from base to live crown	0 - 4
defects	Visual	broken top dead tree forked tree multi-stemmed tree	B D F M

APPENDIX 4 : Table 3. Stem form assessment procedures

Score	Description	Summary of defects
8	Straight stem - pole quality	STRAIGHT no defects
7	Slight sweep and/or 1 minor bend	NEARLY STRAIGHT 1 - 2 minor defects
6	One slight sweep + >1 minor bend OR More than 1 slight sweep + 1 minor bend OR More than 2 minor bends	VERY SLIGHTLY CROOKED 3 - 4 minor defects
5	Moderate sweep + 1 moderate bend OR Two moderate sweeps + minor defect OR Two moderate bends + minor defect	SLIGHTLY CROOKED 2 moderate defects OR 2 moderate + 1 minor defects
4	Moderate sweep + major bend OR More than two moderate sweeps OR More than two moderate bends OR Two major bends + minor defects	MODERATELY CROOKED 1 moderate + 1 major defect OR > 2 moderate defects OR 2 major + 2 minor defects
3	Obvious sinuosity or major crooks	CROOKED > 2 major defects OR 2 major + 2 moderate defects
2	Presence of multiple severe straightness defects	VERY CROOKED several major and moderate defects
1	Unmerchantable as a short log cork screw)	MALFORMED major defects

APPENDIX 4: Table 4. Stem disease infestation assessment procedures

Score	Description	Summary of infestation
0	No visual sign of any disease infestation	NIL
1	Some visual disease infestation	on 25% STEM COVERAGE
2	Mild visual disease infestation	on 50% STEM COVERAGE
3	Moderate visual disease infestation	on 75% STEM COVERAGE
4	Chronic visual disease infestation	on 100% STEM COVERAGE

Note:

Each disease, *Coniothyrium*, *Cryphonectria*, and *Endothia*, scored separately using the common 5 point disease score.

APPENDIX 4 : Table 5. Volume equation for *Eucalyptus grandis*

Coefficients for estimation of volume, where breast-height diameter is measured in millimetres:

DBH (mm)	b_0	b_1	d	b_2
< 200	-11,162 17	3,651 67	100	1,147 60
200 < DBH < 400	- 4,981 99	1,328 29	- 70	1,178 27
> 400	- 5,390 10	1,414 60	- 60	1,299 11
general	- 5,948 20	1,715 36	- 20	1,107 04

Volume equation based on the Schumacher and Hall model:

$\log V: b_0 + b_1 \log(D+d) + b_2 \log H$

where:

log = common logarithm to the base 10

V = stem volume (m^3), to 75 mm tip diameter

D = breast height diameter (mm)

d = correction factor (mm)

H = tree height (m)

APPENDIX 5

SUMMARY STATISTICS

APPENDIX 5 : Table 1. Summary statistics: Site data

Variable	Sample	Mean	Std Dev	Minimum	Maximum
Latitude	31			23° 27' S	30° 15' E
Longitude	31			30° 07' S	32° 22' E
Altitude (m)	31	732,6	452,22	40	1350
MAT (°C)	31	19,16	1,8779	16,5	22,0
MAX (°C)	31	28,15	1,7576	24,6	30,6
MIN (°C)	31	7,170	2,5338	3,8	12,3
MAP (mm)	31	1015	177,52	803	1467
DRY (mm)	31	44,03	39,999	8	166
ERD (cm)	31	123,4	31,572	40	150
SLP (°)	31	6,132	4,6000	0	25
ASP (°)	31	185,5	127,33	0	360

APPENDIX 5 : Table 2. Summary statistics: Soils data - A Horizons (Soil pit samples)

Variable	Samples	Mean	Std Dev	Minimum	Maximum
pH (H_2O)	79	5,200	0,4181	4,32	6,21
pH (KCl)	79	4,324	0,3575	3,77	5,39
Sand (%)	79	52,00	25,556	8	95
Silt (%)	79	31,66	19,727	4	86
Clay (%)	79	16,34	13,215	0	46
Org.Mat (%)	79	2,782	1,7824	0,1	9,1
C (%)	79	1,633	1,0274	0,3	5,3
EA	79	0,673	0,7549	0	3,1
Al	79	44,27	62,155	0	245
N	57	1123	799,16	172	2874
P	78	3,815	3,6854	0,3	25,8
K	75	62,31	44,547	13	196
Ca	78	248,4	326,00	1	1757
Mg	78	110,8	118,26	6	554
Na	79	27,84	23,045	8	140
S-value	79	2,49	2,5534	0,09	13,93

APPENDIX 5 : Table 3. Summary statistics: Soils data - B Horizons (Soil pit samples)

Variable	Samples	Mean	Std Dev	Minimum	Maximum
pH (H_2O)	75	5,623	0,5636	4,72	7,81
pH (KCl)	75	4,798	0,5993	4,11	6,50
Sand (%)	75	42,67	26,845	8	94
Silt (%)	75	26,43	16,065	5	71
Clay (%)	75	30,90	19,128	0	59
Org.Mat (%)	74	1,182	0,9153	0	5,6
C (%)	74	0,684	0,5341	0	3,3
EA	74	0,320	0,4003	0	1,6
Al	74	21,31	47,356	0	348
N	54	651,8	499,99	115	2690
P	74	1,472	2,1877	0	11,1
K	74	43,92	60,067	2	275
Ca	74	204,9	343,90	1	1565
Mg	74	163,1	432,60	1	2483
Na	74	33,96	53,025	6	366
S-value	74	2,724	5,2556	0,06	29,65

APPENDIX 5 : Table 4. Summary statistics: Soils data - A Horizons (Bulk samples)

Variable	Samples	Mean	Std Dev	Minimum	Maximum
pH (H_2O)	79	5,159	0,4154	4,42	6,21
pH (KCl)	79	4,290	0,3536	3,79	5,22
Sand (%)	79	52,34	25,738	8	95
Silt (%)	79	32,14	19,870	4	86
Clay (%)	79	15,52	13,325	0	44
Org.Mat (%)	79	2,749	1,8544	0,1	8,6
C (%)	79	1,673	1,1757	0,3	6,1
EA	78	0,772	0,7979	0	3,3
Al	78	45,42	57,531	0	243
N	59	1213	797,41	189	2893
P	79	4,047	3,2064	0,3	15,5
K	79	65,68	40,565	13	207
Ca	79	253,7	234,49	1	950
Mg	79	109,0	100,80	7	517
Na	79	28,46	23,411	8	140
S-value	79	2,461	1,9338	0,26	7,89

APPENDIX 5 : Table 5. Summary statistics: Two year measurement data

Variable	Trees	Mean	Std Dev	Minimum	Maximum
Volume (m^3)	12834	0,017	0,0123	0,0002	0,124
Height (m)	12842	8,96	2,437	1,0	15,5
DBH (mm)	12908	78,30	23,030	10	175
Stem form	12811	5,69	1,718	1	8

APPENDIX 5 : Table 6. Summary statistics: Five year measurement data

Variable	Trees	Mean	Std Dev	Minimum	Maximum
Volume (m^3)	11899	0,091	0,0694	0,0004	0,537
Height (m)	11899	17,11	4,227	2	28
DBH (mm)	11961	127,41	36,799	10	273
Stem form	11958	4,85	1,411	1	8
Coniothyrium	11157	0,013	0,1604	0	4
Cryphonectria	11157	0,010	0,1438	0	3
Endothia	11157	0,918	1,1131	0	4

APPENDIX 6

CORRELATION MATRICES

APPENDIX 6 : Table 1. Correlation coefficients between growth and site factors, for common control means and site means, age five years.

	VOL5	STM5	CON5	CRY5	END5
LAT	-0,326^{NS}	-0,802***	0,135^{NS}	0,481^{NS}	-0,867***
	0,0966	0,0001	0,5215	0,0149	0,0001
LON	-0,086^{NS}	-0,489*	-0,038^{NS}	0,529*	-0,708***
	0,6705	0,0096	0,8562	0,0065	0,0001
ALT	0,067^{NS}	0,427^{NS}	0,111^{NS}	-0,483^{NS}	0,566*
	0,7410	0,0261	0,5978	0,0144	0,0032
MAP	0,782***	0,219^{NS}	-0,293^{NS}	-0,246^{NS}	0,056^{NS}
	0,0001	0,2725	0,1552	0,2353	0,7922
DRY	0,152^{NS}	-0,522*	-0,159^{NS}	0,246^{NS}	-0,651**
	0,4471	0,0053	0,4568	0,2351	0,0004
MAT	-0,020^{NS}	-0,177^{NS}	-0,182^{NS}	0,404^{NS}	-0,355^{NS}
	0,9174	0,3759	0,3813	0,0450	0,0807
MAX	-0,037^{NS}	0,123^{NS}	-0,045^{NS}	0,280^{NS}	-0,061^{NS}
	0,8558	0,5405	0,8298	0,1745	0,7722
MIN	-0,019^{NS}	-0,525*	-0,262^{NS}	0,443^{NS}	-0,615*
	0,9263	0,0049	0,2060	0,0267	0,0011
ERD	0,350^{NS}	-0,087^{NS}	-0,217^{NS}	-0,162^{NS}	0,185^{NS}
	0,073	0,6663	0,2916	0,7701	0,3753
SLP	0,198^{NS}	0,065^{NS}	-0,289^{NS}	-0,178^{NS}	0,322^{NS}
	0,3224	0,7488	0,1609	0,3951	0,1161
ASP	0,289^{NS}	0,034^{NS}	-0,324^{NS}	-0,136^{NS}	0,109^{NS}
	0,1443	0,8662	0,1138	0,9486	0,6026

* Significant at the 0,05 probability level

** Significant at the 0,01 probability level

*** Significant at the 0,001 probability level

NS Non significant

APPENDIX 6 : Table 2. Correlation coefficients between growth and site factors, for test clone means and site means, age five years.

	VOL5	STM5	CON5	CRY5	END5
LAT	-0,245^{NS}	-0,738***	0,218^{NS}	0,330^{NS}	-0,855***
	0,2182	0,0001	0,2947	0,1068	0,0001
LON	-0,070^{NS}	-0,449^{NS}	-0,007^{NS}	0,340^{NS}	-0,704***
	0,7282	0,0189	0,9742	0,0965	0,0001
ALT	0,081^{NS}	0,391*	0,008^{NS}	-0,270^{NS}	0,578**
	0,6892	0,0438	0,9697	0,1916	0,0025
MAP	0,764***	0,180^{NS}	-0,185^{NS}	-0,371^{NS}	0,039^{NS}
	0,0001	0,3689	0,3748	0,0682	0,8527
DRY	0,168^{NS}	-0,502*	0,004^{NS}	0,051^{NS}	-0,651**
	0,4022	0,0076	0,9855	0,8090	0,0004
MAT	-0,066^{NS}	-0,165^{NS}	-0,118^{NS}	0,214^{NS}	-0,368^{NS}
	0,7438	0,4117	0,5733	0,3033	0,0707
MAX	-0,103^{NS}	0,121^{NS}	-0,056^{NS}	0,279^{NS}	-0,071^{NS}
	0,6092	0,5481	0,7902	0,1769	0,7364
MIN	-0,016^{NS}	-0,497*	-0,135^{NS}	0,114^{NS}	-0,621**
	0,9369	0,0084	0,5187	0,5877	0,0009
ERD	0,370^{NS}	-0,081^{NS}	-0,125^{NS}	-0,162^{NS}	0,141^{NS}
	0,0571	0,6889	0,5519	0,4389	0,5008
SLP	0,230^{NS}	0,055^{NS}	-0,247^{NS}	-0,392^{NS}	0,339^{NS}
	0,2484	0,7857	0,2338	0,0525	0,0976
ASP	0,399*	0,071^{NS}	-0,207^{NS}	-0,153^{NS}	0,098^{NS}
	0,0394	0,7248	0,3212	0,4657	0,642

* Significant at the 0,05 probability level

** Significant at the 0,01 probability level

*** Significant at the 0,001 probability level

NS Non significant

APPENDIX 6 : Table 3. Correlation coefficients between growth and soil factors, for the common control means and the soil horizon means, age five years.

	A HORIZON (SOIL PIT SAMPLES):					B HORIZON (SOIL PIT SAMPLES):					A HORIZON (BULK SAMPLES):				
	VOL5	STM5	CON5	CRY5	END5	VOL5	STM5	CON5	CRY5	END5	VOL5	STM5	CON5	CRY5	END5
pH(H_2O)	-0,064	0,082	-0,336	-0,175	0,193	-0,217	-0,025	-0,024	0,349	-0,137	-0,133	0,119	-0,248	-0,104	0,230
	0,7577	0,6961	0,1168	0,4234	0,3758	0,2965	0,9041	0,9112	0,1022	0,5317	0,5259	0,5696	0,2535	0,6369	0,2909
pH(KCl)	-0,431	-0,017	-0,274	-0,159	0,017	0,153	0,126	-0,067	0,160	-0,044	-0,073	0,027	-0,202	-0,129	0,062
	0,8379	0,9373	0,2059	0,4685	0,9369	0,4654	0,547	0,7626	0,4660	0,8416	0,7299	0,8973	0,3554	0,5577	0,7789
Sand	0,064	-0,042	-0,090	0,213	-0,104	0,133	-0,188	-0,124	0,196	-0,238	0,043	-0,040	-0,076	0,208	-0,110
	0,7603	0,8394	0,6821	0,3292	0,6338	0,5251	0,3687	0,5738	0,3712	0,2738	0,8356	0,8494	0,7310	0,3410	0,6154
Silt	0,118	-0,006	0,068	-0,205	-0,007	0,188	0,037	0,035	-0,118	0,043	0,164	0,017	0,029	-0,213	0,0207
	0,5732	0,9760	0,7595	0,3479	0,9740	0,3673	0,8620	0,8742	0,5923	0,8460	0,4348	0,9362	0,8961	0,3293	0,9255
Clay	-0,321	0,099	0,078	-0,112	0,227	-0,359	0,237	0,146	-0,175	0,302	-0,347	0,056	0,109	-0,089	0,192
	0,1168	0,6386	0,7231	0,6121	0,2976	0,0777	0,2540	0,5072	0,4234	0,1616	0,0891	0,7908	0,6220	0,6860	0,3807
Org.Mat	0,073	-0,000	0,064	-0,080	0,032	0,111	0,066	-0,049	-0,222	0,401	0,170	0,088	0,045	-0,115	0,114
	0,7279	0,9960	0,7691	0,7154	0,8846	0,5986	0,7555	0,8242	0,3079	0,0583	0,4176	0,6755	0,8376	0,6001	0,6059
C	0,073	-0,006	0,063	-0,092	0,027	0,113	0,069	-0,056	-0,227	0,408	0,174	0,085	0,043	-0,132	0,111
	0,7294	0,9781	0,7736	0,6734	0,9019	0,5902	0,7445	0,7992	0,2970	0,0531	0,4060	0,6555	0,8450	0,5495	0,6148
EA	-0,084	-0,128	0,057	0,279	-0,140	-0,236	-0,311	-0,031	0,081	-0,193	-0,044	-0,130	0,055	0,165	-0,148
	0,6885	0,5415	0,7946	0,1971	0,5241	0,2571	0,1298	0,8887	0,7123	0,3766	0,8329	0,5361	0,8045	0,4509	0,4991
Al	-0,153	-0,067	0,284	0,281	-0,149	-0,153	-0,237	-0,047	0,235	-0,211	-0,116	-0,124	0,115	0,149	-0,107
	0,4651	0,7495	0,1884	0,1941	0,4986	0,4649	0,2531	0,8327	0,2806	0,3342	0,5812	0,5546	0,5998	0,4983	0,6267
N	0,212	-0,015	0,148	-0,253	-0,016	0,281	0,077	-0,097	-0,167	0,170	0,288	0,033	0,114	-0,254	0,026
	0,3817	0,9522	0,5591	0,310	0,9491	0,2444	0,7526	0,7021	0,5072	0,5002	0,2320	0,8928	0,6527	0,3086	0,9173
P	-0,063	-0,083	-0,095	-0,159	-0,205	0,104	-0,163	-0,112	-0,123	-0,230	-0,030	-0,045	-0,062	-0,210	-0,165
	0,7614	0,6916	0,6660	0,468	0,3480	0,6218	0,4363	0,6078	0,5748	0,2913	0,8853	0,8300	0,7778	0,3356	0,4518
S-value	-0,397	-0,047	0,074	0,259	-0111	-0,418	-0,133	0,020	0,578	-0,190	-0,412	-0,072	0,058	0,303	-0,113
	0,0495	0,8251	0,7377	0,2328	0,6145	0,0375	0,5248	0,9263	0,0039	0,3862	0,0405	0,7309	0,7923	0,1601	0,6090

Probability level below each respective correlation coefficient

APPENDIX 6 : Table 4. Correlation coefficients between growth and soil factors, for the test clone means and the soil horizons means, age five years.

	A HORIZON (SOIL PIT SAMPLES):					B HORIZON (SOIL PIT SAMPLES):					A HORIZON (BULK SAMPLES):				
	VOL5	STM5	CON5	CRY5	END5	VOL5	STM5	CON5	CRY5	END5	VOL5	STM5	CON5	CRY5	END5
$pH(H_2O)$	-0,061	0,135	-0,189	-0,165	0,164	-0,219	0,037	0,009	0,285	-0,152	-0,124	0,185	-0,102	-0,057	0,198
	0,7719	0,5213	0,3873	0,4514	0,4541	0,2936	0,8619	0,9660	0,1882	0,4902	0,5551	0,3750	0,6431	0,7955	0,3643
pH(KCl)	0,021	0,110	-0,001	-0,015	0,005	0,238	0,189	-0,095	0,116	-0,027	-0,016	0,159	0,085	-0,065	0,047
	0,9240	0,5993	0,9981	0,5054	0,9822	0,2526	0,3653	0,6679	0,5983	0,9028	0,9408	0,4484	0,6992	0,7679	0,8319
Sand	0,043	0,019	0,030	0,101	-0,093	0,143	-0,117	0,018	0,034	-0,230	0,026	0,024	0,043	0,107	-0,098
	0,8873	0,9249	0,8920	0,6479	0,6727	0,4955	0,5790	0,9359	0,8785	0,2918	0,9025	0,9093	0,8469	0,6265	0,6555
Silt	0,174	-0,037	-0,027	-0,105	-0,008	0,216	0,002	-0,060	-0,062	0,037	0,215	-0,017	-0,062	-0,135	0,019
	0,4063	0,8595	0,8995	0,6321	0,9721	0,3006	0,9933	0,7850	0,7772	0,8660	0,3012	0,9375	0,7763	0,5363	0,9306
Clay	-0,366	0,018	-0,017	-0,039	0,203	-0,397	0,166	0,027	0,007	0,295	-0,392	-0,023	0,011	-0,005	0,169
	0,0718	0,9316	0,9378	0,8593	0,3517	0,0491	0,4283	0,9010	0,9760	0,1724	0,0528	0,9115	0,9585	0,9819	0,4407
Org.Mat	0,074	-0,064	-0,043	-0,109	0,025	-0,075	-0,044	-0,144	-0,212	0,361	0,168	0,028	-0,062	-0,138	0,106
	0,7235	0,7597	0,8456	0,6196	0,9104	0,7192	0,8324	0,5135	0,3305	0,0903	0,4229	0,8947	0,7779	0,5301	0,6302
C	0,082	-0,059	-0,021	-0,117	0,020	-0,072	-0,041	-0,144	-0,227	0,370	0,180	0,036	-0,041	-0,149	0,104
	0,6962	0,7785	0,9236	0,5960	0,9271	0,7309	0,8441	0,5110	0,2978	0,0823	0,3891	0,8650	0,8538	0,4971	0,6373
EA	-0,058	-0,155	0,013	-0,024	-0,122	-0,266	-0,377	-0,071	-0,130	-0,170	-0,017	-0,169	0,007	-0,078	-0,121
	0,7823	0,4580	0,9536	0,9141	0,5781	0,1985	0,0631	0,7473	0,5558	0,4391	0,9332	0,4206	0,9741	0,7248	0,5813
Al	-0,139	-0,095	0,194	0,145	-0,133	-0,131	-0,286	-0,075	-0,137	-0,190	-0,117	-0,179	0,026	-0,033	-0,082
	0,5075	0,6510	0,3745	0,5091	0,5460	0,5340	0,1656	0,7333	0,5317	0,3856	0,5765	0,3926	0,9046	0,8799	0,7107
N	0,199	-0,054	0,101	-0,049	-0,035	0,101	-0,029	-0,167	-0,166	0,128	0,2617	-0,013	0,062	-0,065	0,007
	0,4148	0,8247	0,6906	0,8481	0,8918	0,6816	0,9050	0,5082	0,5107	0,6133	0,2790	0,9595	0,8083	0,7975	0,9787
P	-0,059	0,021	0,165	-0,132	-0,202	0,145	-0,063	0,235	-0,179	-0,232	-0,034	0,007	0,173	-0,135	-0,156
	0,7810	0,9219	0,4515	0,5474	0,3543	0,4900	0,7639	0,2801	0,4132	0,2870	0,8735	0,9743	0,4303	0,5380	0,4759
S-value	-0,381	-0,002	0,087	0,234	-0,144	-0,460	-0,112	-0,025	0,394	-0,213	-0,406	-0,029	0,078	0,239	-0,148
	0,0605	0,9927	0,6912	0,2823	0,511	0,0208	0,5938	0,9075	0,0623	0,3289	0,0439	0,8889	0,7249	0,2729	0,4991

Probability level below each respective correlation coefficient

APPENDIX 7

ANALYSIS OF VARIANCE TABLES

NEWMAN-KEULS RANGE TESTS

APPENDIX 7 : Table 1.1 ANOVA for pH(H_2O) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	19,315	0,68985	13,57	0,0001***
Reps in sites	50	4,005	0,08010	1,58	0,0349*
Error	79	4,017	0,05085		
Total	157	27,337			

APPENDIX 7 : Table 1.2 ANOVA for pH(KCl) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	12,723	0,45441	8,08	0,0001***
Reps in sites	50	2,565	0,05131	0,91	$0,6328^{NS}$
Error	79	4,445	0,05627		
Total	157	19,733			

APPENDIX 7 : Table 1.3 ANOVA for percentage sand in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	97198	3471,35	164,24	0,0001***
Reps in sites	50	2063	41,27	1,95	0,0038*
Error	79	1669	21,14		
Total	157	100930			

APPENDIX 7 : Table 1.4 ANOVA for percentage silt in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	58146	2076,67	99,11	0,0001***
Reps in sites	50	1385	27,70	1,32	$0,1320^{NS}$
Error	79	1655	20,95		
Total	157	61186			

APPENDIX 7 : Table 1.5 ANOVA for percentage clay in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	23260	803,74	38,55	0,0001***
Reps in sites	50	1265	25,30	1,17	$0,2586^{NS}$
Error	79	1702	21,55		
Total	157	26227			

APPENDIX 7 : Table 1.6 ANOVA for organic matter (Org.Mat) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	410,96	14,6671	17,14	0,0001***
Reps in sites	50	38,12	0,76259	0,89	0,6671^{NS}
Error	79	67,66	0,85649		
Total	157	516,74			

APPENDIX 7 : Table 1.7 ANOVA for percentage carbon in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	166,05	5,9303	34,45	0,0001***
Reps in sites	50	10,69	0,2139	1,24	0,1920^{NS}
Error	79	13,60	0,1722		
Total	157	190,34			

APPENDIX 7 : Table 1.8 ANOVA for S-value in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	573,44	20,4802	13,61	0,0001***
Reps in sites	50	107,58	2,1516	1,43	0,0767*
Error	79	118,89	1,5050		
Total	157	799,91			

APPENDIX 7 : Table 1.9 ANOVA for exchangeable acidity (EA) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	65,843	2,3515	14,51	0,0001***
Reps in sites	50	14,046	0,2809	1,73	0,0144^{NS}
Error	78	12,645	0,1621		
Total	156	92,534			

APPENDIX 7 : Table 1.10 ANOVA for aluminium (Al) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	345426	12336,6	9,16	0,0001***
Reps in sites	50	97706	1954,1	1,45	0,0695*
Error	78	105102	1347,5		
Total	156	548234			

APPENDIX 7 : Table 1.11 ANOVA for nitrogen (N) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	20	62164485	3108224	58,93	0,0001***
Reps in sites	38	6916429	182011	3,45	0,0001***
Error	57	3006189	52740		
Total	115	72087103			

APPENDIX 7 : Table 1.12 ANOVA for phosphorus (P) in the pooled A soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	202422	7229,37	18,05	0,0001***
Reps in sites	48	42907	893,90	2,23	0,0008**
Error	77	30835	400,45		
Total	153	276164			

SS Type III Sum of squares
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001probability level
NS Non significant

APPENDIX 7 : Table 2.1 ANOVA for pH(H_2O) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	31,518	1,12564	6,85	0,0001***
Reps in sites	50	4,215	0,08429	0,51	0,9964^{NS}
Error	154	25,323	0,16443		
Total	232	61,056			

APPENDIX 7 : Table 2.2 ANOVA for pH(KCl) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	22,964	0,82013	3,87	0,0001***
Reps in sites	50	3,017	0,06035	0,28	1,0000^{NS}
Error	154	32,618	0,21181		
Total	232	58,599			

APPENDIX 7 : Table 2.3 ANOVA for percentage sand in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	146513	5232,61	77,60	0,0001***
Reps in sites	50	2139	42,79	0,63	0,9680^{NS}
Error	154	10384	67,43		
Total	232	159036			

APPENDIX 7 : Table 2.4 ANOVA for percentage silt in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	73410	2621,81	59,08	0,0001***
Reps in sites	50	1160	23,22	0,52	0,9954^{NS}
Error	154	6834	44,38		
Total	232	81404			

APPENDIX 7 : Table 2.5 ANOVA for percentage clay in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	45117	1611,33	13,38	0,0001***
Reps in sites	50	1370	27,41	0,23	1,0000^{NS}
Error	154	18544	120,42		
Total	232	65031			

APPENDIX 7 : Table 2.6 ANOVA for organic matter (Org.Mat) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	359,01	12,8217	6,32	0,0001***
Reps in sites	50	33,69	0,6737	0,33	1,0000^{NS}
Error	153	310,41	2,0288		
Total	231	703,11			

APPENDIX 7 : Table 2.7 ANOVA for percentage carbon in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	140,40	5,0145	7,07	0,0001***
Reps in sites	50	9,17	0,1835	0,26	1,0000^{NS}
Error	153	108,55	0,7095		
Total	231	258,12			

APPENDIX 7 : Table 2.8 ANOVA for S-value in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	1785,13	63,7550	10,68	0,0001***
Reps in sites	50	117,97	2,3593	0,40	0,9999^{NS}
Error	153	913,61	5,9713		
Total	231	2816,71			

APPENDIX 7 : Table 2.9 ANOVA for exchangeable acidity (EA) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	62,800	2,2429	8,48	0,0001***
Reps in sites	50	8,147	0,1629	0,62	0,9753^{NS}
Error	152	40,182	0,2644		
Total	230	111,129			

APPENDIX 7 : Table 2.10 ANOVA for aluminium (Al) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	395771	14134,7	7,52	0,0001***
Reps in sites	50	50726	1014,5	0,54	0,9935^{NS}
Error	152	285522	1878,4		
Total	230	732019			

APPENDIX 7 : Table 2.11 ANOVA for nitrogen (N) in the pooled A and B soil horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	20	65360557	3268027	15,33	0,0001***
Reps in sites	38	6707253	176506	0,53	$0,7427^{NS}$
Error	111	23655503	213112		
Total	167	95723313			

APPENDIX 7 : Table 2.12 ANOVA for phosphorus (P) in the pooled A and B horizons over all sites.

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	306862	10959,38	8,19	0,0001***
Reps in sites	50	100434	2008,69	1,50	0,0326*
Error	149	199502	1338,94		
Total	227	606798			

SS Type III Sum of squares
* Significant at the 0,05 probability level
** Significant at the 0,01 probability level
*** Significant at the 0,001probability level
NS Non significant

APPENDIX 7 : Table 3. ANOVA and Newman-Keuls test of sites, for mean volume production, on the common controls, age 2 years.

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	0,5063	0,01808	272,73	0,0001***
Reps in sites	44	0,0259	0,00059	8,89	0,0001***
Controls	4	0,0070	0,00176	26,53	0,0001***
Controls x sites	110	0,0269	0,00024	3,69	0,0001***
Error	4155	0,2754	0,00006		
Total	4341	0,8415			

NEWMAN-KEULS TEST:

Sites	Trees	Mean Volume (m^3)	Newman-Keuls groupings		
PDN	185	0,055	A		
DNL	200	0,034	B		
VTM	124	0,033	B	C	
WHB	164	0,031		C	
WLD	68	0,026	D		
FWD	205	0,023	E		
TST	198	0,023	E		
NYL1	139	0,022	E	F	
CTR	177	0,021	E	F	
SFT	186	0,020		F	
FZS	178	0,019		F	
MPS	136	0,019		F	
TBD	194	0,016	G		
GNG	140	0,016	G		
ELD	218	0,016	G		
JDM	198	0,015	G		
FRT	63	0,014	G	H	
TKF1	220	0,014	G	H	I
UMD	170	0,014	G	H	I
ADN	38	0,013	G	H	I
NLN	132	0,011	J	H	I
SMK	216	0,011	J	H	I
ESL1	53	0,011	J		I
TKF2	194	0,010	J		
GLP	153	0,008	J	K	
RMD	99	0,006		K	L
KGA	87	0,006		K	L
TLD	28	0,004	M		L
NYL2	179	0,002	M		
Mean		0,0188			
SE		0,00151			
F.Value		272,73***			

Sites connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares
*** Significant at the 0,001 probability level

APPENDIX 7 : Table 4. ANOVA and Newman-Keuls test of sites, for mean stem form, on the common controls, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	5458,3	194,939	130,84	0,0001***
Reps in sites	44	289,2	6,573	4,41	0,0001***
Controls	4	148,6	37,148	24,93	0,0001***
Controls x sites	110	640,9	5,826	3,91	0,0001***
Error	4144	6174,2	1,490		
Total	4330	12711.2			

NEWMAN-KEULS TEST:

Sites	Trees	Mean Stem form	Newman-Keuls groupings		
SMK	217	7,7	A		
ELD	218	7,7	A		
CTR	177	7,6	A		
JDM	198	7,2	B		
TKF1	222	6,6	C		
ADN	38	6,4	C	D	
FRT	63	6,4	C	D	
UMD	171	6,2	C	D	
TBD	194	6,1	C	D	E
NLN	134	6,1		D	E
TKF2	194	6,0		D	E
NYL1	124	5,8		D	E
FWD	200	5,8	F		E
ESL1	53	5,8	F		E
FZS	177	5,7	F		E
VTM	126	5,4	F		E
TLD	28	5,3	F	G	
SFT	186	5,3		G	
WHB	165	5,0		G	H
GLP	153	4,9		G	H
DNL	202	4,7			H
PDN	185	4,7			H
WLD	68	4,6	I		H
MPS	134	4,6	I		H
KGA	87	4,3	I		H
RMD	99	4,3	I	J	
GNG	140	4,3	I	J	
NYL2	179	4,1		J	
TST	199	4,0		J	
Mean		5,78			
SE		0,227			
F.Value		130,84***			

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 5. ANOVA and Newman-Keuls test of sites, for mean percentage survival, on controls and test clones, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	55702,81	1989,39	16,60	0,0001***
Error	403	48294,20	119,84		
Total	431	103997,01			

NEWMAN-KEULS TEST:

Sites	Treatments	Survival percentage	Newman-Keuls groupings					
SFT	15	78,1	A					
SMK	15	74,9	A	B				
TKF1	15	74,4	A	B	C			
FZS	15	73,9	A	B	C			
ELD	15	69,5	A	B	C	D		
GLP	15	69,4	A	B	C	D		
JDM	15	69,0	A	B	C	D		
FWD	15	68,4	A	B	C	D	E	
TKF2	15	67,4	A	B	C	D	E	
WLD	15	66,8	A	B	C	D	E	F
MPS	15	66,6	AG	B	C	D	E	F
NLN	15	64,8	G	B	C	D	E	F
DNL	15	63,6	G	B	C	D	E	F
VTM	15	63,5	G		C	D	E	F
TST	15	62,9	G		C	D	E	F
CTR	15	62,6	G		C	D	E	F
ESL1	15	62,1	G		C	D	E	F
GNG	15	60,7	G	H	C	D	E	F
FRT	15	60,0	G	H	C	D	E	F
WHB	15	59,2	G	H	C	D	E	F
TBD	15	57,2	G	H		D	E	F
RMD	15	56,4	G	H		D	E	F
PDN	15	56,2	G	H		D	E	F
KGA	15	54,3	G	H			E	F
NYL1	15	53,0	G	H				F
NYL2	15	51,8	G	H				
UMD	15	47,9	G	H				
TLD	15	30,8	G		I			
ADN	15	25,9	G		I			
Mean		61,16						
SE		2,0328,						
F.Value		16,60***						

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 6. ANOVA and Newman-Keuls test of controls and test clones for mean volume production, over all sites, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	0,8739	0,03120	619,77	0,0001***
Reps in sites	44	0,0394	0,00090	17,80	0,0001***
Treatments	35	0,0525	0,00150	29,80	0,0001***
Treatments x sites	367	0,1539	0,00041	8,33	0,0001***
Error	12359	0,6223	0,00005		
Total	12833	1,7420			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean volume (m3)	Newman-Keuls groupings					
SGR428	244	0,022	A					
SGR481	300	0,021	A					
38046	898	0,021	A	B				
SGR482	307	0,020	C	B	C			
KFT81/13/2	299	0,020	C	B	C			
SGR052	144	0,019	C	B	C	D		
SGR071	952	0,019	C	B	C	D		
SGR072	751	0,019	C	B	C	D		
38047	935	0,019	C		C	D	E	
SGR041	305	0,018	C		C	D	E	
SGR051	219	0,018	C		C	D	E	F
SGR048	249	0,018	G			D	E	F
SGR451	261	0,018	G			D	E	F
SGR515	244	0,017	G	H		D	E	F
SGR047	280	0,017	G	H			E	F
SGR467	259	0,017	G	H			E	F
SGR009	179	0,017	G	H			E	F
SGR053	259	0,017	G	H			E	F
SGR192	243	0,017	G	H			E	F
SGR470	243	0,017	G	H			E	F
GXT22/02	350	0,017	G	H				F
SGR494	253	0,017	G	H				F
SGR472	265	0,017	G	H				F
SGR438	231	0,017	G	H				F
SGR054	269	0,016	G	H	I			
SGR202	245	0,016		H	I			
TG12	806	0,016		H	I	J		
MXG25	393	0,015			I	J		
GXC9/03	289	0,014				J	K	
SGR183	307	0,014	M				K	L
SGR013	314	0,014	M	N			K	L
GXC16/08	400	0,013	M	N			K	L
SGR046	252	0,013	M	N	O			L
KFT23/33	319	0,012	M	N	O			
SGR112	335	0,012		N	O			
SGR042	235	0,012			O			
Mean		0,0171						
SE		0,00118						
F.Value		29,80***						

Treatments connected by the same letter are not significantly different (α =0,05)

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 7. ANOVA and Newman-Keuls test of controls and test clones for mean stem form, over all sites, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	28	14348,53	512,447	403,05	0,0001***
Reps in sites	44	704,59	16,013	12,59	0,0001***
Treatments	35	1572,12	44,918	35,33	0,0001***
Treatments x sites	367	2616,82	7,130	5,61	0,0001***
Error	12336	15684,40	1,271		
Total	12810	34926,46			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean stem form	Newman-Keuls groupings					
SGR051	219	6,7	A					
SGR482	298	6,2	A					
GXC9/03	294	6,4	B					
SGR183	303	6,1	C					
KFT81/13/2	299	6,1	C					
GXT22/02	351	6,1	C					
SGR053	258	6,1	C	D				
SGR112	335	6,0	C	D	E			
38046	895	6,0	C	D	E			
SGR481	301	6,0	C	D	E	F		
SGR041	305	6,0	C	D	E	F		
TG12	805	5,9	C	D	E	F	G	
38047	936	5,9	C	D	E	F	G	
SGR472	265	5,8	C	D	E	F	G	H
SGR042	236	5,8	C	D	E	F	G	H
SGR428	245	5,8		D	E	F	G	H
SGR467	260	5,8		D	E	F	G	H
SGR451	262	5,7			E	F	G	H
SGR013	302	5,7	I			F	G	H
GXC16/08	400	5,7	I			F	G	H
SGR009	178	5,7	I			F	G	H
SGR494	255	5,7	I			F	G	H
SGR046	252	5,6	I	J			G	H
SGR047	278	5,6	I	J				H
SGR071	948	5,5	I	J				H
SGR054	266	5,5	I	J				H
SGR072	747	5,4	I	J	K			
SGR515	255	5,4		J	K	L		
SGR192	248	5,3			K	L		
SGR202	245	5,3			K	L		
KFT23/33	319	5,2				L	M	
SGR048	250	5,0					M	
SGR052	144	4,7						N
SGR438	231	4,6	O					N
MXG25	396	4,5	O					
SGR470	230	4,2		P				
Mean		5,69						
SE		0,188						
F.Value		35,33***						

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares

APPENDIX 7: Table 8. ANOVA and Newman-Keuls test of controls and test clones, for mean percentage survival, over all sites, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Treatments	35	16387,13	468,20	2,12	0,0003**
Error	396	87609,88	221,24		
Total	431				

NEWMAN-KEULS TEST:

Treatments	Sites	Survival percentage	Newman-Keuls groupings		
GXC16/08	10	74,3	A		
MXG25	10	73,2	A		
GXT22/02	9	70,7	A	B	
SGR481	8	67,8	A	B	
SGR112	10	67,5	A	B	
SGR071	29	67,3	A	B	
SGR013	10	66,2	A	B	C
38047	29	64,5	A	B	C
SGR482	10	64,3	A	B	C
SGR054	8	63,8	A	B	C
38046	29	63,4	A	B	C
SGR183	10	63,4	A	B	C
KFT23/33	9	63,3	A	B	C
SGR438	9	63,0	A	B	C
SGR048	9	62,6	A	B	C
SGR053	9	62,6	A	B	C
SGR051	8	61,9	A	B	C
SGR515	9	61,9	A	B	C
SGR041	9	61,8	A	B	C
TG12	29	60,8	A	B	C
SGR047	10	60,3	A	B	C
GXC9/03	10	59,8	A	B	C
SGR202	9	58,7	A	B	C
SGR046	9	58,7	A	B	C
SGR451	9	58,3	A	B	C
KFT81/13/2	10	57,6	A	B	C
SGR072	28	57,6	A	B	C
SGR042	8	56,7	A	B	C
SGR470	9	56,5	A	B	C
SGR428	10	55,6	A	B	C
SGR192	10	54,2	A	B	C
SGR472	10	54,0	A	B	C
SGR494	9	52,6	A	B	C
SGR467	10	50,1	A	B	C
SGR009	9	46,7		B	C
SGR052	9	41,8			C
Mean		61,16			
SE		2,479			
F.Value		2,12**			

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares
** Significant at the 0,01 probability level

APPENDIX 7: Table 9. ANOVA and Newman-Keuls test of controls and test clones, for mean stem defects, over all sites, age 2 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Treatments	35	3442,84	98,366	1,75	0,0062*
Error	399	22384,42	56,101		
Total	434	25827,26			

NEWMAN-KEULS TEST:

Treatments	Sites	Defects percentage	Newman-Keuls groupings
MXG25	10	11,1	A
SGR515	9	10,4	A
SGR013	10	9,6	A
GXT22/02	9	9,5	A
SGR481	8	8,9	A
GXC16/08	10	8,4	A
SGR482	10	7,5	A
SGR048	9	6,4	A
SGR470	9	6,3	A
GXC9/03	10	6,1	A
TG12	29	5,5	A
38047	29	5,3	A
SGR047	10	5,2	A
SGR052	9	5,1	A
SGR041	9	4,9	A
SGR072	29	4,6	A
SGR054	8	4,2	A
SGR071	29	3,9	A
SGR112	10	3,5	A
38046	29	3,2	A
SGR046	9	2,6	A
SGR202	9	2,5	A
SGR183	10	2,5	A
SGR053	9	2,4	A
KFT23/33	9	2,2	A
KFT81/13/2	10	2,0	A
SGR192	10	1,7	A
SGR428	10	1,7	A
SGR494	9	1,6	A
SGR009	10	1,2	A
SGR051	8	1,0	A
SGR438	9	0,9	A
SGR467	10	0,0	A
SGR042	9	0,0	A
SGR472	10	0,0	A
SGR451	9	0,0	A
Mean		4,29	
SE		1,248	
F.Value		1,75*	

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares
* Significant at the 0,05 probability level

APPENDIX 7 : Table 10. ANOVA and Newman-Keuls test of sites, for mean volume, on the common controls only, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	26	9,674	0,37208	141,19	0,0001***
Reps in sites	41	0,543	0,01324	5,03	0,0001***
Controls	4	0,192	0,04806	18,24	0,0001***
Controls x sites	104	1,202	0,01155	4,39	0,0001***
Error	3815	10,054	0,00263		
Total	3990	21,665			

NEWMAN-KEULS TEST:

Sites	Trees	Mean volume (m^3)	Newman-Keuls groupings		
VTM	122	0,233	A		
PDN	179	0,180	B		
WHB	145	0,171	B		
ELD	205	0,157	C		
FRT	63	0,149	C		
DNL	194	0,143	C		
CTR	172	0,121	D		
GNG	110	0,109	D		
TKF2	103	0,109	D	E	
FWD	200	0,103	D	E	
NYL1	189	0,097	F	E	
SFT	169	0,095	F	E	
WLD	68	0,095	F	E	
ADN	62	0,092	F	E	
TBD	195	0,082	F	G	
TST	195	0,082	F	G	
NLN	125	0,077	F	G	H
FZS	170	0,072		G	H
TKF1	149	0,064		G	H
ESL1	53	0,064		G	H
JDM	158	0,063		G	H
UMD	133	0,062		G	H
GLP	153	0,059	I		H
SMK	208	0,043	I		
MPS	135	0,042	I		
KGA	124	0,025	J		
NYL2	212	0,023	J		
Mean		0,0958			
SE		0,00988			
F.Value		141,19***			

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 11. ANOVA and Newman-Keuls test of sites, for mean stem form, on the common controls only, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	26	3145,4	120,980	132,34	0,0001***
Reps in sites	41	131,4	3,204	3,51	0,0001***
Controls	4	100,0	25,006	27,35	0,0001***
Controls x sites	104	258,3	2,484	2,72	0,0001***
Error	3830	3501,4	0,914		
Total	4005	7136,5			

NEWMAN-KEULS TEST:

Sites	Trees	Mean stem form	Newman-Keuls groupings	
FRT	305	6,1	A	
VTM	105	6,0	A	
FZS	415	6,0	A	
SFT	382	6,0	A	
WHB	348	5,9	A	
DNL	120	5,9	A	
GLP	134	5,9	A	
WLD	412	5,8	A	
ESL1	367	5,7	A	
SMK	431	5,5	B	
CTR	133	5,2	C	
ELD	353	5,1	C	
JDM	398	5,0	C	
FWD	351	4,3	D	
TBD	363	4,3	D	
ADN	363	4,2	D	
PDN	194	4,2	D	
NYL2	138	4,2	D	
UMD	402	4,1	D	
NLN	345	4,0	D	E
GNG	99	4,0	D	E
TST	224	4,0	D	E
NYL1	239	3,9	D	E
TKF1	292	3,7	F	E
TKF2	294	3,6	F	
MPS	261	3,4	F	
KGA	284	3,1	G	
Mean		4,77		
SE		0,184		
F.Value		132,34***		

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 12. ANOVA and Newman-Keuls test of sites, for mean *Coniothyrium* infestation, on the common controls only, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	2,043	0,08513	10,41	0,0001***
Reps in sites	39	0,260	0,00667	0,82	0,7850NS
Controls	4	0,294	0,07349	8,99	0,0001***
Controls x sites	96	5,855	0,06099	7,46	0,0001***
Error	3586	29,313	0,00817		
Total	3749	37,765			

NEWMAN-KEULS TEST:

Sites	Trees	Mean score	Newman-Keuls groupings
ESL1	53	0,283	A
NYL1	189	0,021	B
FWD	200	0,015	B
TBD	195	0,010	B
NYL2	214	0,009	B
ELD	205	0,000	B
DNL	197	0,000	B
FZS	175	0,000	B
ADN	62	0,000	B
GNG	110	0,000	B
JDM	158	0,000	B
NLN	125	0,000	B
GLP	153	0,000	B
FRT	63	0,000	B
PDN	179	0,000	B
SFT	170	0,000	B
SMK	209	0,000	B
CTR	172	0,000	B
TKF1	149	0,000	B
TKF2	103	0,000	B
TST	195	0,000	B
UMD	133	0,000	B
VTM	125	0,000	B
WHB	148	0,000	B
WLD	68	0,000	B
Mean		0,0069	
SE		0,01808	
F.Value		10,41***	

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 13. ANOVA and Newman-Keuls test of sites, for mean *Cryphonecrea* infestation, on the common controls only, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	1,050	0,04376	2,75	0,0001***
Reps in sites	39	1,267	0,03249	2,04	0,0002***
Controls	4	1,405	0,03513	2,20	$0,0661^{NS}$
Controls x sites	96	2,194	0,02286	1,43	0,0040**
Error	3586	57,162	0,01594		
Total	3749	63,078			

NEWMAN-KEULS TEST:

Sites	Trees	Mean score	Newman-Keuls groupings
NYL2	214	0,051	A
FWD	200	0,045	A
ADN	62	0,032	A
NYL1	189	0,026	A
UMD	133	0,015	A
TBD	195	0,012	A
NLN	125	0,008	A
DNL	197	0,000	A
GLP	153	0,000	A
FZS	175	0,000	A
JDM	158	0,000	A
ELD	205	0,000	A
ESL1	53	0,000	A
GNG	110	0,000	A
PDN	179	0,000	A
SFT	170	0,000	A
SMK	209	0,000	A
CTR	172	0,000	A
TKF1	149	0,000	A
TKF2	103	0,000	A
TST	195	0,000	A
FRT	63	0,000	A
VTM	125	0,000	A
WHB	148	0,000	A
WLD	68	0,000	A
Mean		0,0085	
SE		0,02525	
F.Value		2,75***	

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

** Significant at the 0,01 probability level

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 14. ANOVA and Newman-Keuls test of sites, for mean *Endothia* infestation, on the common controls only, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	3107,10	129,463	399,63	0,0001***
Reps in sites	39	92,36	2,368	7,31	0,0001***
Controls	4	11,38	2,844	8,78	0,0001***
Controls x sites	96	182,13	1,897	5,86	0,0001***
Error	3586	1161,71	0,324		
Total	3749	4554,.68			

NEWMAN-KEULS TEST:

Sites	Trees	Mean score	Newman-Keuls groupings		
JDM	158	2,582	A		
GLP	153	2,562	A		
FZS	175	2,217	B		
DNL	197	1,863	C		
CTR	172	1,767	C	D	
VTM	125	1,712	C	D	E
SMK	209	1,694	C	D	E
WLD	68	1,647		D	E
FRT	63	1,555	F	D	E
SFT	170	1,524	F		E
WHB	148	1,392	F		
ELD	205	0,034	G		
NYL2	214	0,164	H		
UMD	133	0,120	H		
FWD	200	0,075	H		
ADN	62	0,065	H		
NLN	125	0,056	H		
GNG	110	0,036	H		
TST	195	0,031	H		
TBD	195	0,021	H		
NYL1	189	0,011	H		
TKF1	149	0,000	H		
PDN	179	0,000	H		
TKF2	103	0,000	H		
ESL1	53	0,000	H		
Mean		0,9085			
SE		0,11383			
F.Value		399,63***			

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001 probability level

APPENDIX 7 : Table 15. ANOVA and Newman-Keuls test of sites, for mean survival percentage, of controls and test clones, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	26	28650,82	1101,95	7,74	0,0001***
Error	378	53821,18	142,38		
Total	404	82427,00			

NEWMAN-KEULS TEST:

Sites	Treatments	Survival percentage	Newman-Keuls groupings				
TKF1	15	76,3	A				
SMK	15	71,2	A	B			
KGA	15	68,6	A	B			
MPS	15	67,5	A	B	C		
SFT	15	67,4	A	B	C		
WLD	15	67,1	A	B	C		
ELD	15	66,7	A	B	C		
FZS	15	66,6	A	B	C		
NYL1	15	66,1	A	B	C		
NYL2	15	64,9	A	B	C		
FWD	15	63,2	A	B	C		
GLP	15	62,5	A	B	C		
NLN	15	61,7	A	B	C		
ESL1	15	61,6	A	B	C		
DNL	15	61,2	A	B	C	D	
TST	15	61,0		B	C	D	
FRT	15	59,4		B	C	D	
CTR	15	59,4		B	C	D	
JDM	15	57,7		B	C	D	
VTM	15	56,8		B	C	D	
TBD	15	56,5		B	C	D	
TKF2	15	56,2		B	C	D	
PDN	15	54,6		B	C	D	
WHB	15	52,5			C	D	E
GNG	15	43,9	F			D	E
UMD	15	42,1	F				E
ADN	15	39,8	F				E
Mean		60,475					
SE		2,296					
F.Value		7,74***					

Sites connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

*** Significant at the 0,001probability level

APPENDIX 7 : Table 16. ANOVA and Newman-Keuls test of controls and test clones, for mean volume production, over all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	26	22,228	0,85491	391,63	0,0001***
Reps in sites	41	0,563	0,01372	6,29	0,0001***
Treatments	35	3,433	0,09808	44,93	0,0001***
Treatments x sites	341	4,999	0,01466	6,72	0,0001***
Error	11455	25,006	0,00218		
Total	11898	56,229			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean volume (m^3)	Newman-Keuls groupings					
SGR051	186	0,137	A					
SGR428	217	0,129	A	B				
SGR482	277	0,124	A	B				
SGR451	239	0,117		B	C			
SGR481	257	0,110			C	D		
SGR183	256	0,109			C	D		
SGR041	265	0,107			C	D	E	
38046	787	0,106			C	D	E	F
38047	848	0,102			C	D	E	F
SGR009	191	0,101			C	D	E	F
SGR048	220	0,099			C	D	E	F
KFT81/13/2	270	0,097	J			D	E	F
SGR472	240	0,097	J	K		D	E	F
SGR494	256	0,096	J	K		D	E	F
SGR071	880	0,096	J	K		D	E	F
SGR047	261	0,096	J	K		D	E	F
SGR054	269	0,094	J	K	L	D	E	F
SGR438	213	0,091	J	K	L	D	E	F
SGR052	163	0,091	J	K	L	D	E	F
SGR202	243	0,091	J	K	L	D	E	F
SGR072	743	0,088	J	K	L		E	F
GXT22/02	294	0,086	J	K	L			F
SGR470	239	0,086	J	K	L			F
TG12	733	0,086	J	K	L			
SGR467	249	0,085	J	K	L			
SGR042	271	0,082	J	K	L	M		
SGR053	264	0,080	J	K	L	M		
SGR192	222	0,080	J	K	L	M		
SGR515	208	0,079	J	K	L	M		
SGR112	317	0,077		K	L	M		
SGR046	251	0,075			L	M		
SGR013	335	0,075			L	M		
GXC16/08	357	0,066				M	N	
KFT23/33	287	0,059					N	
GXC9/03	244	0,058					N	
MXG25	347	0,032					O	
Mean		0,0911						
SE		0,0078						
F.Value		44,93***						

Treatments connected by the same letter are not significantly different (α =0,05) and not all subsets are shown
SS Type III Sum of squares

APPENDIX 7 : Table 17. ANOVA and Newman-Keuls test of controls and test clones, for mean stem form, over all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	26	9353,2	359,740	410,17	0,0001***
Reps in sites	41	209,1	5,099	5,81	0,0001***
Treatments	35	1135,7	32,447	37,00	0,0001***
Treatments x sites	341	1528,0	4,481	5,11	0,0001***
Error	11514	10098,3	0,877		
Total	11957	22324,3			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean stem form	Newman-Keuls groupings					
SGR481	270	5,7	A					
SGR482	278	5,7	A					
SGR112	318	5,6	A	B				
SGR051	186	5,5	A	B	C			
SGR515	211	5,4		B	C	D		
SGR041	265	5,4		B	C	D		
SGR046	251	5,3		B	C	D	E	
SGR013	335	5,3		B	C	D	E	
SGR183	259	5,2			C	D	E	F
SGR428	217	5,1	G			D	E	F
GXC9/03	253	5,1	G	H		D	E	F
SGR047	264	5,0	G	H	I		E	F
38047	853	5,0	G	H	I		E	F
38046	792	5,0	G	H	I		E	F
SGR054	269	5,0	G	H	I		E	F
GXC16/08	358	4,9	G	H	I	J		F
SGR451	239	4,9	G	H	I	J		F
SGR052	163	4,9	G	H	I	J	K	F
SGR472	240	4,8	G	H	I	J	K	
GXT22/02	296	4,8	G	H	I	J	K	
SGR438	213	4,8	G	H	I	J	K	
SGR467	249	4,8	G	H	I	J	K	
SGR009	191	4,7		H	I	J	K	
KFT81/13/2	270	4,7		H	I	J	K	
SGR202	243	4,7		H	I	J	K	
SGR053	264	4,7			I	J	K	
SGR071	882	4,7			I	J	K	
SGR192	223	4,6			I	J	K	
TG12	735	4,6			I	J	K	
SGR042	271	4,6	L			J	K	
SGR072	744	4,5	L			J	K	
SGR048	221	4,5	L			J	K	
SGR494	257	4,5	L				K	
KFT23/33	287	4,3	L					
SGR470	241	3,8		M				
MXG25	350	3,6		M				
Mean		4,85						
SE		0,156						
F.Value		37,00***						

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares

APPENDIX 7 : Table 18. ANOVA and Newman-Keuls test of controls and test clones, for mean *Coniothyrium* infestation, on all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	33,750	1,40624	183,83	0,0001***
Reps in sites	39	0,249	0,00639	0,84	0,7556^{NS}
Treatments	35	29,630	0,84658	110,67	0,0001***
Treatments x sites	313	149,005	0,47605	62,23	0,0001***
Error	10745	82,196	0,00765		
Total	11156	294,830			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean score	Newman-Keuls groupings		
GXC9/03	253	0,142	A		
SGR482	278	0,115	A		
SGR051	186	0,070	B		
SGR438	182	0,060	B	C	
SGR515	211	0,039	B	C	D
SGR052	139	0,029		C	D
SGR071	821	0,015			D
SGR467	221	0,014			D
SGR053	209	0,010			D
38047	798	0,009			D
SGR481	246	0,008			D
SGR046	251	0,008			D
SGR112	318	0,006			D
TG12	685	0,006			D
SGR192	200	0,005			D
SGR047	232	0,004			D
SGR472	240	0,004			D
SGR042	244	0,004			D
38046	740	0,002			D
SGR072	706	0,001			D
KFT81/13/2	243	0,000			D
SGR054	269	0,000			D
SGR183	209	0,000			D
SGR013	307	0,000			D
SGR009	159	0,000			D
KFT23/33	259	0,000			D
SGR041	265	0,000			D
SGR428	217	0,000			D
GXT22/02	296	0,000			D
SGR470	184	0,000			D
SGR048	196	0,000			D
MXG25	350	0,000			D
SGR202	217	0,000			D
SGR494	257	0,000			D
GXC16/08	330	0,000			D
SGR451	239	0,000			D
Mean		0,9182			
SE		0,0146			
F.Value		110,67***			

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares

APPENDIX 7 : Table 19. ANOVA and Newman-Keuls test of controls and test clones, for mean *Cryphonectrea* infestation, on all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	4,874	0,20310	11,16	0,0001***
Reps in sites	39	2,185	0,05601	3,08	0,0001***
Treatments	35	4,341	0,12401	6,81	0,0001***
Treatments x sites	313	24,078	0,07693	4,23	0,0001***
Error	10745	195,568	0,01820		
Total	11156	231,046			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean score	Newman-Keuls groupings	
SGR428	217	0,101	A	
SGR051	186	0,070	B	
SGR494	257	0,047	B	C
KFT81/13/2	243	0,029		C
SGR472	240	0,025		C
38046	740	0,022		C
SGR112	318	0,019		C
SGR192	200	0,015		C
SGR467	221	0,014		C
SGR042	244	0,012		C
SGR046	251	0,012		C
TG12	685	0,010		C
SGR515	211	0,009		C
KFT23/33	259	0,008		C
38047	798	0,008		C
SGR013	307	0,007		C
SGR072	706	0,003		C
SGR071	821	0,001		C
SGR041	265	0,000		C
SGR009	159	0,000		C
SGR054	269	0,000		C
SGR052	139	0,000		C
SGR183	209	0,000		C
MXG25	350	0,000		C
SGR202	217	0,000		C
SGR047	232	0,000		C
SGR438	182	0,000		C
SGR451	239	0,000		C
GXT22/02	296	0,000		C
SGR470	184	0,000		C
SGR048	196	0,000		C
SGR481	246	0,000		C
SGR482	278	0,000		C
SGR053	209	0,000		C
GXC16/08	330	0,000		C
GXC9/03	253	0,000		C
Mean		0,0140		
SE		0,0225		
F.Value		6,81***		

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares

APPENDIX 7 : Table 20. ANOVA and Newman-Keuls test of controls and test clones, for mean *Endothia* infestation, over all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Sites	24	7707,2	321,134	1046,92	0,0001***
Reps in sites	39	189,7	4,864	15,86	0,0001***
Treatments	35	316,1	9,030	29,44	0,0001***
Treatments x sites	313	908,9	2,904	9,47	0,0001***
Error	10745	3295,9	0,307		
Total	11156	12417,8			

NEWMAN-KEULS TEST:

Treatments	Trees	Mean score	Newman-Keuls groupings					
SGR047	232	1,871	A					
SGR472	240	1,846	A					
SGR481	246	1,825	A	B				
SGR183	209	1,402		B				
SGR052	139	1,317		B	C			
KFT23/33	259	1,251		B	C	D		
SGR428	217	1,244		B	C	D		
SGR051	186	1,177		B	C	D	E	
SGR482	278	1,126			C	D	E	F
SGR112	318	1,078			C	D	E	F
SGR041	265	1,049			C	D	E	F
SGR071	821	0,977				D	E	F
SGR202	217	0,959					E	F
38047	798	0,957					E	F
SGR192	200	0,925					E	F
TG12	685	0,913					E	F
38046	740	0,909					E	F
SGR013	307	0,893					E	F
GXC16/08	330	0,839		L				F
SGR046	251	0,833		L				F
SGR467	221	0,824		L				F
SGR048	196	0,791		L	M			
SGR072	706	0,768		L	M	N		
SGR053	209	0,756		L	M	N		
SGR042	244	0,717		L	M	N		
SGR515	211	0,701		L	M	N	O	
KFT81/13/2	243	0,700		L	M	N	O	
SGR054	269	0,700		L	M	N	O	
SGR470	184	0,636		L	M	N	O	
GXC9/03	253	0,617		L	M	N	O	P
SGR494	257	0,560		L	M	N	O	P
SGR438	182	0,511			M	N	O	P
MXG25	350	0,480				N	O	P
SGR451	239	0,473				N	O	P
GXT22/02	296	0,408					O	P
SGR009	159	0,345						P
Mean		0,9182						
SE		0,0923						
F.Value		29,44***						

Treatments connected by the same letter are not significantly different (α =0,05) and not all subsets are shown
SS Type III Sum of squares

APPENDIX 7 : Table 21. ANOVA and Newman-Keuls test of controls and test clones, for mean percentage survival, over all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Treatments	35	11227,75	320,793	1,66	0,0125^{NS}
Error	369	71244,25	193,074		
Total	404	82427,00			

NEWMAN-KEULS TEST:

Treatments	Sites	Survival percentage	Newman-Keuls grouping
GXC16/08	10	72,8	A
GXT22/02	8	71,3	A
SGR112	9	68,9	A
SGR013	10	66,6	A
SGR071	27	66,6	A
MXG25	10	65,8	A
SGR054	8	64,4	A
SGR470	7	64,3	A
38047	27	63,6	A
KFT23/33	9	63,5	A
SGR041	8	63,0	A
SGR053	9	63,0	A
SGR438	9	62,9	A
SGR183	9	62,4	A
SGR482	10	61,9	A
SGR046	8	61,3	A
SGR047	9	61,2	A
SGR042	9	61,1	A
SGR051	7	61,0	A
SGR481	8	60,2	A
38046	27	60,0	A
KFT81/13/2	9	58,7	A
SGR494	8	58,3	A
SGR202	9	57,7	A
SGR451	8	57,6	A
TG12	27	57,1	A
SGR428	8	57,0	A
SGR072	27	56,8	A
GXC9/03	9	56,7	A
SGR515	8	56,5	A
SGR048	9	54,6	A
SGR192	9	53,3	A
SGR052	7	52,7	A
SGR009	9	51,9	A
SGR467	10	49,9	A
SGR472	10	48,5	A
Mean		60,475	
SE		2,316	
F.Value		1,66^{NS}	

Treatments connected by the same letter are not significantly different (α =0,05)
SS Type III Sum of squares
NS Non significant

APPENDIX 7 : Table 22. ANOVA and Newman-Keuls test of controls and test clones, for mean percentage stem defects, over all sites, age 5 years

ANOVA:

SOURCE	DF	SS	MS	F value	Pr > F
Treatments	35	3545,22	101,292	1,67	0,0115^{NS}
Error	369	22340,86	60,544		
Total	404	25886,08			

NEWMAN-KEULS TEST:

Treatments	Sites	Defects percentage	Newman-Keuls groupings	
MXG25	10	14,9	A	
SGR515	8	13,7	A	B
GXC9/03	9	8,3	A	B
SGR481	8	7,9	A	B
SGR047	9	7,3	A	B
SGR482	10	7,2	A	B
GXC16/08	10	6,6	A	B
38047	27	6,5	A	B
TG12	27	6,4	A	B
GXT22/02	8	6,0	A	B
SGR042	9	5,7	A	B
SGR072	27	5,5	A	B
SGR051	8	5,3	A	B
SGR048	9	5,3	A	B
38046	27	4,6	A	B
SGR041	8	4,1	A	B
SGR071	27	3,7	A	B
KFT23/33	9	3,5	A	B
SGR009	9	3,5	A	B
SGR112	9	3,5	A	B
SGR183	9	3,4	A	B
KFT81/13/2	9	3,2	A	B
SGR013	10	3,1	A	B
SGR428	8	2,8	A	B
SGR202	9	2,8	A	B
SGR494	8	2,5	A	B
SGR470	7	2,4	A	B
SGR438	9	1,6	A	B
SGR192	9	1,3		B
SGR052	7	1,2		B
SGR046	8	1,0		B
SGR054	8	1,0		B
SGR451	8	1,0		B
SGR467	10	1,0		B
SGR053	9	0.9		B
SGR472	10	0,8		B
Mean		4,68		
SE		1,297		
F.Value		1,67^{NS}		

Treatments connected by the same letter are not significantly different (α =0,05)

SS Type III Sum of squares

Stem defects Sum of stem forks (F) and multi-stemmed trees (M)

NS Non significant

APPENDIX 8

COVARIANCE ANALYSIS

APPENDIX 8 : Table 1. Analysis of covariance: Test for homogeneity of regressions, for mean volume production, over all sites, age 5 years

GLM:

SOURCE	DF	SS	MS	F value	Pr > F
Controls (mean)	1	0,5190	0,51905	1114,70	0,0001
Clones	31	0,0177	0,00057	1,23	0,1938
Controls (mean) x clones	31	0,0394	0,00127	2,73	0,0001
Error	301	0,1402	0,00047		
Total	364	0,2163			

SS Type III Sum of squares

R-square	C.V.	Root MSE	Mean
0,8612	22,279	0,0216	0,0969

TEST:

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Intercept		-0,0033	0,00919	-0,36	0,7197
Control (mean)		0,9438	0,08480	11,13	0,0001
Clones:	38046	0,0078	0,01300	0,60	0,5488
	38047	0,0133	0,01300	1,02	0,3085
	KFT23/33	-0,0124	0,02490	-0,50	0,6187
	KFT81/13/2	0,0095	0,02060	0,46	0,6460
	SGR009	0,0403	0,02065	1,95	0,0520
	SGR013	0,2103	0,01857	1,13	0,2584
	SGR041	0,0174	0,02032	0,86	0,3915
	SGR042	0,0099	0,01681	0,59	0,5569
	SGR046	0,0207	0,01728	1,20	0,2319
	SGR047	0,0002	0,01781	0,01	0,9902
	SGR048	0,0088	0,01943	0,45	0,6509
	SGR051	-0,0503	0,03178	-1,58	0,1147
	SGR052	0,0189	0,01683	1,12	0,2625
	SGR053	0,0095	0,02098	0,45	0,6511
	SGR054	-0,0098	0,02205	-0,45	0,6557
	SGR071	-0,0088	0,01300	-0,67	0,5010
	SGR072	0,0034	0,01300	0,26	0,7934
	SGR112	-0,0143	0,01915	-0,75	0,4555
	SGR183	0,0025	0,01839	0,13	0,8930
	SGR192	-0,0245	0,02392	-1,02	0,3065
	SGR202	0,0042	0,01606	0,26	0,7953
	SGR428	-0,0105	0,02207	-0,48	0,6332
	SGR438	0,0027	0,01911	0,14	0,8864
	SGR451	-0,0479	0,02963	-1,62	0,1068
	SGR467	0,0084	0,01720	0,49	0,6256
	SGR470	0,0041	0,01736	0,24	0,8139
	SGR472	0,0567	0,01714	3,31	0,0010
	SGR481	-0,1200	0,01950	-0,62	0,5388
	SGR482	-0,0064	0,02477	-0,26	0,7975
	SGR494	-0,0222	0,02608	-0,85	0,3944
	SGR515	0,0027	0,02217	0,12	0,9032
	TG12	0,0000			

(Table 1 continued overleaf)

Table 1 (continued)

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Control x clones:	38046	0,1310	0,11992	1,09	0,2755
	38047	0,0463	0,11992	0,39	0,6996
	KFT23/33	0,1497	0,30785	0,49	0,6272
	KFT81/13/2	-0,0629	0,18357	-0,34	0,7319
	SGR009	-0,2088	0,22220	-0,94	0,3481
	SGR013	-0,4234	0,15422	-2,75	0,0064
	SGR041	-0,1939	0,15564	-1,25	0,2137
	SGR042	-0,0439	0,15740	-0,28	0,7806
	SGR046	-0,2855	0,15496	-1,84	0,0664
	SGR047	-0,0400	0,14419	-0,28	0,7819
	SGR048	-0,1563	0,15387	-1,02	0,3107
	SGR051	0,6451	0,26280	2,45	0,0147
	SGR052	-0,1863	0,15577	-1,20	0,2327
	SGR053	0,1513	0,25590	0,59	0,5548
	SGR054	0,0566	0,19939	0,28	0,7765
	SGR071	0,1862	0,11992	1,55	0,1216
	SGR072	-0,0078	0,11992	-0,06	0,9483
	SGR112	0,2255	0,19584	1,15	0,2505
	SGR183	0,4742	0,19973	2,37	0,0182
	SGR192	0,3115	0,23800	1,31	0,1916
	SGR202	-0,0859	0,13834	-0,62	0,5350
	SGR428	0,3698	0,18406	2,01	0,0454
	SGR438	0,1687	0,18472	0,91	0,3617
	SGR451	0,5299	0,25229	2,10	0,0365
	SGR467	-0,1736	0,15556	-1,12	0,2654
	SGR470	0,0711	0,17530	0,41	0,6855
	SGR472	-0,4101	0,17062	-2,40	0,0168
	SGR481	0,5127	0,19380	2,65	0,0086
	SGR482	0,3877	0,24005	1,62	0,1073
	SGR494	0,5778	0,29863	1,93	0,0540
	SGR515	0,02269	0,24472	0,09	0,9262
	TG12	0,0000			

APPENDIX 8 : Table 2. Analysis of covariance: Test for homogeneity of regressions, for mean stem form, over all sites, age 5 years

GLM:

SOURCE	DF	SS	MS	F value	Pr > F
Controls (mean)	1	257,132	257,1320	1443,68	0,0001
Clones	31	8,610	0,0278	4,73	0,0331
Controls (mean) x clones	31	6,745	0,2176	1,22	0,2001
Error	301	53,610	0,1781		
Total	364	326,097			

SS Type III Sum of squares

R-square	C.V.	Root MSE	Mean
0,8782	8,669	0,4220	4,868

TEST:

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Intercept		-0,2773	0,41679	-0,67	0,5063
Control (mean)		1,0530	0,08541	12,33	0,0001
Clones:	38046	0,8234	0,58943	1,40	0,1634
	38047	0,6788	0,58943	1,15	0,2504
	KFT23/33	-0,0317	0,79903	-0,04	0,9684
	KFT81/13/2	-0,2356	0,86466	-0,27	0,7854
	SGR009	-0,3124	0,83279	-0,38	0,7078
	SGR013	1,6354	0,77728	2,10	0,0362
	SGR041	-0,8334	0,98393	-0,85	0,3977
	SGR042	0,7235	0,79705	0,91	0,3647
	SGR046	1,8823	0,97936	1,92	0,0556
	SGR047	0,2508	0,88023	0,28	0,7759
	SGR048	0,0937	0,78900	0,12	0,9055
	SGR051	-1,5097	1,06245	-1,42	0,1564
	SGR052	-1,1016	0,84712	-1,30	0,1944
	SGR053	0,0740	0,85505	0,09	0,9311
	SGR054	0,8293	1,03752	0,80	0,4247
	SGR071	-0,3291	0,58943	-0,56	0,5770
	SGR072	0,2499	0,58943	0,42	0,6719
	SGR112	0,3343	0,92826	0,36	0,7190
	SGR183	1,6216	0,77340	2,10	0,0368
	SGR192	0,3000	0,84393	0,36	0,7224
	SGR202	-0,2294	0,86201	-0,27	0,7903
	SGR428	0,0842	0,94957	0,09	0,9294
	SGR438	0,6693	0,75887	0,88	0,3785
	SGR451	-0,8519	1,10871	-0,77	0,4429
	SGR467	-0,7043	0,80503	-0,87	0,3823
	SGR470	0,1588	0,86348	0,18	0,8542
	SGR472	-2,5617	1,02207	-2,51	0,0127
	SGR481	0,6585	0,94455	0,70	0,4862
	SGR482	1,6438	0,84632	1,94	0,0530
	SGR494	0,4550	1,00075	0,45	0,6497
	SGR515	1,9840	0,99350	2,00	0,0467
	TG12	0,0000			

(Table 2 continued overleaf)

Table 2 (continued)

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Control x clones:	38046	-0,1242	0,12079	-1,03	0,3048
	38047	-0,0901	0,12079	-0,75	0,4563
	KFT23/33	-0,0700	0,17235	-0,42	0,6722
	KFT81/13/2	0,0586	0,18427	0,32	0,7509
	SGR009	0,1551	0,17520	0,89	0,3768
	SGR013	-0,2778	0,15338	-1,81	0,0711
	SGR041	0,2003	0,19417	1,03	0,3031
	SGR042	-0,1672	0,16674	1,00	0,3168
	SGR046	-0,3339	0,19454	-1,72	0,0872
	SGR047	-0,0772	0,16909	-0,46	0,6485
	SGR048	-0,0541	0,16301	-0,33	0,7401
	SGR051	0,4033	0,20675	1,95	0,0520
	SGR052	0,1857	0,17449	1,06	0,2879
	SGR053	0,0536	0,18659	0,29	0,7742
	SGR054	-0,1178	0,21503	-0,55	0,5842
	SGR071	0,0367	0,12079	0,30	0,7613
	SGR072	-0,0843	0,12079	-0,70	0,4856
	SGR112	0,0079	0,18219	0,04	0,9653
	SGR183	-0,2131	0,16232	-1,31	0,1902
	SGR192	-0,3666	0,17437	-0,21	0,8336
	SGR202	0,0160	0,17175	0,09	0,9259
	SGR428	0,0152	0,18417	0,08	0,9341
	SGR438	-0,0764	0,15589	-0,49	0,6244
	SGR451	0,2347	0,23681	0,99	0,3224
	SGR467	0,1913	0,17816	1,07	0,2838
	SGR470	-0,1429	0,19220	-0,74	0,4577
	SGR472	0,4210	0,20433	2,06	0,0402
	SGR481	-0,0763	0,17843	-0,43	0,6694
	SGR482	-0,1902	0,16693	-1,14	0,2556
	SGR494	-0,0750	0,22234	-0,34	0,7360
	SGR515	-0,3157	0,19435	-1,62	0,1053
	TG12	0,0000			

APPENDIX 8 : Table 3. Analysis of covariance: Test for homogeneity of regressions, for mean *Endothia* infestation, over all sites, age 5 years

GLM:

SOURCE	DF	SS	MS	F value	Pr > F
Controls (mean)	1	192,610	192,6099	2166,27	0,0001
Clones	32	1,322	0,04266	0,48	0,9920
Controls (mean) x clones	31	3,919	0,12641	1,42	0,0740
Error	272	24,184	0,08891		
Total	335				

SS Type III Sum of squares

R-square	C.V.	Root MSE	Mean
0,9249	33,047	0,2982	0,9023

TEST:

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Intercept		0,0394	0,08246	0,48	0,6332
Control (mean)		1,0679	0,06435	16,60	0,0001
Clones:	38046	-0,0162	0,11662	-0,14	0,8899
	38047	0,0110	0,11662	-0,09	0,9251
	KFT23/33	-0,0471	0,15812	-0,30	0,7657
	KFT81/13/2	0,0601	0,15891	0,38	0,7057
	SGR009	-0,0544	0,15589	-0,35	0,7274
	SGR013	-0,2141	0,18883	-1,13	0,2579
	SGR041	0,0474	0,18521	0,26	0,7981
	SGR042	-0,0897	0,17379	-0,52	0,6061
	SGR046	-0,1027	0,17619	-0,58	0,5605
	SGR047	0,1560	0,26467	0,59	0,5561
	SGR048	-0,0554	0,17134	-0,32	0,7466
	SGR051	-0,0884	0,18744	-0,47	0,6376
	SGR052	0,0709	0,17236	0,41	0,6811
	SGR053	-0,0482	0,17588	-0,27	0,7841
	SGR054	-0,0783	0,16651	-0,47	0,6384
	SGR071	-0,0674	0,11662	-0,58	0,5635
	SGR072	-0,0850	0,11662	-0,73	0,4668
	SGR112	-0,1122	0,16939	-0,66	0,5082
	SGR183	0,0006	0,18261	0,00	0,9974
	SGR192	-0,0136	0,16967	-0,08	0,9363
	SGR202	-0,1702	0,17248	-0,99	0,3246
	SGR428	0,0771	0,18657	0,41	0,6798
	SGR438	-0,0594	0,15801	-0,38	0,7075
	SGR451	-0,1403	0,15951	-0,88	0,3800
	SGR467	0,1876	0,14247	1,32	0,1890
	SGR470	-0,0803	0,19476	-0,41	0,6803
	SGR472	0,2336	0,15779	1,48	0,1399
	SGR481	0,1905	0,28071	0,68	0,4979
	SGR482	-0,0117	0,15777	-0,07	0,9409
	SGR494	-0,0459	0,14864	-0,31	0,7578
	SGR515	-0,0705	0,17373	-0,41	0,6853
	TG12	0,0000			

(Table 3 continued overleaf)

Table 3 (continued)

Parameter		Estimate	Std. Err (of estimate)	T for H_0 : (Parameter = 0)	Pr > T
Control x clones:	38046	-0,0973	0,09100	-1,07	0,2861
	38047	-0,1147	0,09100	-1,26	0,2088
	KFT23/33	0,0194	0,11027	0,18	0,8608
	KFT81/13/2	-0,2668	0,15994	-1,67	0,0964
	SGR009	-0,3431	0,13618	-2,52	0,0123
	SGR013	-0,2360	0,12885	-1,83	0,0681
	SGR041	-0,3208	0,13076	-2,45	0,0148
	SGR042	0,1609	0,16317	0,99	0,3249
	SGR046	-0,1026	0,14828	-0,69	0,4897
	SGR047	-0,0042	0,15963	-0,03	0,9789
	SGR048	-0,1587	0,13967	-1,14	0,2569
	SGR051	0,2457	0,15430	1,59	0,1125
	SGR052	-0,2061	0,13633	-1,51	0,1318
	SGR053	-0,0337	0,15328	-0,22	0,8262
	SGR054	-0,3253	0,11820	-2,75	0,0063
	SGR071	-0,0047	0,09100	-0,05	0,9590
	SGR072	-0,1149	0,09100	-1,26	0,2077
	SGR112	-0,0681	0,12453	-0,55	0,5848
	SGR183	0,0693	0,13606	0,51	0,6108
	SGR192	-0,0764	0,12512	-0,61	0,5419
	SGR202	-0,0095	0,13134	-0,07	0,9422
	SGR428	0,1040	0,13309	0,78	0,4354
	SGR438	-0,1649	0,15372	-1,07	0,2844
	SGR451	-0,2740	0,16855	-1,63	0,1052
	SGR467	-0,1202	0,16254	-0,74	0,4604
	SGR470	-0,0984	0,15309	-0,64	0,5207
	SGR472	0,0676	0,11001	0,61	0,5394
	SGR481	-0,1301	0,16422	-0,79	0,4291
	SGR482	-0,0178	0,12719	-0,14	0,8886
	SGR494	-0,1269	0,13302	-0,95	0,3410
	SGR515	-0,1775	0,13727	-1,29	0,1969
	TG12	0,0000			

APPENDIX 9

FACTOR ANALYSIS

(PRINCIPLE COMPONENT ANALYSIS)

APPENDIX 9 : Table 1. Factor analysis of common controls, including mean volume production, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Volume	-0,13656	0,76677	0,22863	-0,26708	0,04411
LAT	0,53840	-0,19397	0,01901	0,73431	-0,13722
LON	0,79420	-0,17103	0,15870	0,48204	-0,04538
ALT	-0,94517	0,05240	-0,15768	-0,23057	-0,00235
MAP	-0,05906	0,85239	0,24150	-0,10821	0,21732
DRY	0,77232	0,35479	0,10471	0,42368	0,06403
MAT	0,95313	-0,08819	0,15480	0,12164	0,02601
MAX	0,88279	-0,31725	0,14388	-0,16117	-0,07289
MIN	0,86509	0,11834	0,13265	0,42274	0,11738
ERD	0,47863	0,48370	-0,02451	0,25237	-0,47541
SLP	-0,63487	0,29272	0,17537	0,27000	0,41790
ASP	0,01717	0,61505	0,25309	0,30768	0,44001
pH(H_2O)	0,24865	-0,53232	0,65836	-0,28711	0,23205
pH(KCl)	0,09747	-0,23906	0,87860	-0,17240	0,05706
Sand	0,82834	0,30503	-0,29885	-0,22185	0,14667
Silt	-0,75762	0,05401	0,53874	0,20117	-0,24547
Clay	-0,51151	-0,70839	-0,22992	0,13971	0,08328
Org.Mat	-0,85818	0,08807	0,36899	0,19928	-0,18266
C	-0,85580	0,10090	0,38099	0,19483	-0,17859
EA	-0,71784	-0,14515	-0,41128	0,43788	0,23027
Al	-0,69696	-0,21853	-0,46489	0,41227	0,20312
N	-0,74789	0,17329	0,50177	0,26624	-0,16101
P	0,46047	0,23100	0,02332	-0,07821	0,02465
S-value	0,15653	-0,72453	0,54607	0,06488	0,24147

Eigenvalue	10,31	3,92	3,22	2,30	1,08

APPENDIX 9 : Table 2. Factor analysis of common controls, including mean stem form, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Stem form	-0,37370	-0,15909	-0,44715	-0,70376	0,06036
LAT	0,56227	0,17291	0,030200	0,67130	-0,11706
LON	0,81014	0,22205	0,27692	0,37496	-0,03122
ALT	-0,95173	-0,11716	-0,18136	-0,11324	-0,01384
MAP	-0,05487	-0,65942	0,42248	-0,38328	0,22030
DRY	0,78873	-0,27170	0,38073	0,23130	0,08021
MAT	0,95577	0,15194	0,11067	0,02758	0,03331
MAX	0,87433	0,35807	-0,11429	-0,16451	-0,07474
MIN	0,87963	-0,05121	0,32090	0,26112	0,13307
ERD	0,49161	-0,45608	0,27967	0,13039	-0,46791
SLP	-0,62002	-0,19420	0,39644	0,12451	0,41910
ASP	0,03058	-0,48293	0,57300	-0,01720	0,46393
pH(H_2O)	0,24420	0,76956	0,19584	-0,40908	0,21699
pH(KCl)	0,09943	0,57736	0,54201	-0,48447	0,05505
Sand	0,82027	-0,39530	-0,25896	-0,14526	0,14031
Silt	-074464	0,16368	0,57488	-0,05538	-0,23500
Clay	-0,51528	0,55310	-0,36796	0,38366	0,07994
Org.Mat	-0,84763	0,06986	0,43891	0,00914	-0,17241
C	-0,84510	0,06203	0,45254	-0,00290	-0,16828
EA	-0,70932	-0,04083	-0,16082	0,60459	0,23874
Al	-0,69035	0,00320	-0,24176	0,62068	0,21027
N	-0,73360	0,04774	0,60189	-0,01370	-0,14622
P	0,45890	-0,21148	0,06080	-0,15192	0,03227
S-value	0,15517	0,89023	0,18057	-0,05200	0,24607

Eigenvalue	10,37	3,54	3,12	2,79	1,08

APPENDIX 9 : Table 3. Factor analysis of common controls, including mean *Endothia* infestation, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Endothia	-0,48367	-0,28405	-0,17003	-0,70558	0,16457
LAT	0,70714	0,29339	0,07316	0,54837	-0,14542
LON	0,84174	0,30941	0,11396	0,30906	-0,03295
ALT	-0,95551	-0,18232	-0,12473	-0,08198	-0,02732
MAP	-0,12867	-0,57346	0,64038	-0,03587	0,23244
DRY	0,80655	-0,15326	0,35665	0,33348	0,07503
MAT	0,94829	0,19643	0,07318	0,00632	0,05207
MAX	0,84919	0,35845	-0,13879	-0,22909	-0,06729
MIN	0,89615	0,04612	0,23983	0,26634	0,14565
ERD	0,50305	-0,37332	0,33900	0,15001	-0,41564
SLP	-0,57703	-0,11504	0,36953	0,21670	0,48867
ASP	0,06312	-0,33548	0,62843	0,20237	0,45023
pH(H_2O)	0,07934	0,84530	0,12908	-0,30022	0,29273
pH(KCl)	-0,00990	0,68535	0,52710	-0,31729	0,12850
Sand	0,80231	-0,45679	-0,11648	-0,23111	0,16957
Silt	-0,72434	0,29445	0,53940	0,10863	-0,24221
Clay	-0,48985	0,45941	-0,59346	0,29417	0,03285
Org.Mat	-0,82627	0,19142	0,44029	0,06085	-0,18114
C	-0,82384	0,18600	0,45938	0,05176	-0,17318
EA	-0,64772	-0,06471	-0,39696	0,56131	0,23850
Al	-0,62192	-0,03453	-0,50078	0,53508	0,19752
N	-0,69921	0,19845	0,59426	0,14947	-0,15952
P	0,41709	-0,19197	0,14719	-0,06706	0,05786
S-value	0,10103	0,91361	-0,01510	-0,03765	0,25040

Eigenvalue	10,23	3,79	3,47	2,23	1,18

APPENDIX 9 : Table 4. Factor analysis of the test clones, including mean volume production, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Volume	-0,10724	0,73469	0,26798	-0,25631	0,06261
LAT	0,52971	-0,18060	0,01675	0,73297	-0,14971
LON	0,79521	-0,16161	0,16239	0,48895	0,02439
ALT	-0,94421	0,05884	-0,15704	-0,24103	-0,00371
MAP	-0,06572	0,83341	0,23234	-0,10369	0,22350
DRY	0,76860	0,35239	0,09933	0,43094	0,06004
MAT	0,95350	-0,09427	0,15646	0,13327	0,03727
MAX	0,88695	-0,32212	0,15056	-0,14682	-0,05715
MIN	0,86262	0,11599	0,12957	0,43083	0,12271
ERD	0,47243	0,50002	-0,02021	0,23999	-0,46709
SLP	-0,64545	0,29429	0,16650	0,25931	0,42077
ASP	0,00038	0,63370	0,25084	0,28973	0,44923
pH(H_2O)	0,23805	-0,54127	0,66096	-0,28045	0,22156
pH(KCl)	0,07853	-0,23352	0,88800	-0,17922	0,03804
Sand	0,82742	0,29438	-0,30305	-0,22528	0,14436
Silt	-0,75687	0,06888	0,54297	0,20180	-0,23763
Clay	-0,50542	-0,70820	-0,23017	0,14429	0,07680
Org.Mat	-0,85644	0,08195	0,36323	0,21170	-0,18321
C	-0,85485	0,09436	0,37374	0,20527	-0,18268
EA	-0,71588	-0,14800	-0,42188	0,43686	0,21521
Al	-0,69267	-0,22126	-0,47507	0,41420	0,19303
N	-0,74756	0,16405	0,49184	0,27890	-0,16478
P	0,44769	0,21878	0,00950	-0,08973	-0,07087
S-value	0,15633	-0,73178	0,54396	0,08439	0,24850

Eigenvalue	10,29	3,76	3,47	2,23	1,19

APPENDIX 9 : Table 5. Factor analysis of the test clones, including mean stem form, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Stem form	-0,29356	-0,14071	-0,31129	-0,75719	0,08481
LAT	0,54736	0,16425	0,22035	0,69828	-0,12334
LON	0,80744	0,21383	0,24749	0,41102	-0,00805
ALT	-0,94920	-0,11815	-0,18069	-0,14589	-0,01987
MAP	-0,06272	-0,64724	0,47199	-0,32739	0,22676
DRY	0,78104	-0,27360	0,36544	0,28146	0,08147
MAT	0,95581	0,15260	0,12372	0,05540	0,04668
MAX	0,88129	0,35904	-0,07609	-0,15558	-0,06028
MIN	0,87360	-0,05305	0,30211	0,30505	0,14309
ERD	0,48146	-0,45983	0,26747	0,14251	-0,46008
SLP	-0,63594	-0,19228	0,35735	0,14545	0,42210
ASP	0,00956	-0,48023	0,56628	0,02905	0,47631
pH(H_2O)	0,23386	0,78424	0,22672	-0,37607	0,20267
pH(KCl)	0,07793	0,59700	0,57448	-0,43363	0,03723
Sand	0,82105	-0,39469	-0,23650	-0,17705	0,13853
Silt	-0,74731	0,16532	0,57666	0,00747	-0,22669
Clay	-0,50734	0,54690	-0,41858	0,34955	0,07159
Org.Mat	-0,84884	0,07048	0,43693	0,06344	-0,16714
C	-0,84739	0,06342	0,44805	0,05050	-0,16604
EA	-0,70968	-0,05240	-0,24056	0,57399	0,23029
Al	-0,68752	-0,01002	-0,31987	0,58595	0,20578
N	-0,73727	0,05089	0,59968	0,06191	-0,14290
P	0,44511	-0,20600	0,06049	-0,15802	-0,04535
S-value	0,15540	0,89257	0,18568	-0,00687	0,25461
Eigenvalue	10,47	3,52	3,16	2,78	1,08

APPENDIX 9 : Table 6. Factor analysis of the test clones, including mean *Endothia* infestation, age 5 years

Variable	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5
Endothia	0,46136	-0,30126	-0,15510	-0,69823	0,16726
LAT	-0,70034	0,29917	0,06006	0,54654	-0,16421
LON	-0,84305	0,31232	0,11503	0,31065	-0,01435
ALT	0,95436	-0,18826	-0,12528	-0,08627	-0,03060
MAP	0,13981	-0,55249	0,65518	-0,02881	0,24630
DRY	-0,80084	-0,14189	0,36405	0,33920	0,07258
MAT	-0,94874	0,19943	0,07692	0,01156	0,06535
MAX	-0,85525	0,35267	-0,13507	-0,22564	-0,04860
MIN	-0,89315	0,05556	0,24304	0,27360	0,15144
ERD	-0,49546	-0,36362	0,35445	0,14761	-0,41633
SLP	0,58956	-0,09994	0,35699	0,22297	0,48580
ASP	-0,04510	-0,31511	0,63297	0,20913	0,45898
pH(H_2O)	-0,06878	0,85405	0,09318	-0,30109	0,27870
pH(KCl)	0,03014	0,70877	0,49556	-0,32725	0,10926
Sand	-0,80086	-0,46220	-0,10079	-0,22679	0,16987
Silt	0,72471	0,31119	0,53237	0,10550	-0,23385
Clay	0,48119	0,44166	-0,61503	0,28898	0,02064
Org.Mat	0,82566	0,20585	0,43720	0,06440	-0,17513
C	0,82419	0,20098	0,45319	0,05470	-0,17132
EA	0,64488	-0,07687	-0,40648	0,55997	0,22044
Al	0,61568	-0,05089	-0,50882	0,53525	0,18593
N	0,70096	0,21783	0,58621	0,15428	-0,15700
P	-0,40162	-0,18959	0,13749	-0,07465	-0,02393
S-value	-0,10321	0,91332	-0,04276	-0,03166	0,25769
Eigenvalue	10,36	3,96	3,18	2,28	1,08

APPENDIX 10

MULTIPLE REGRESSION ANALYSIS

APPENDIX 10 : Table 1. Stepwise regression analysis of common controls, for mean volume production, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	1	0,1958	0,1958	160,79	0,0001
Error	93	0,1132	0,0012		
Total	94	0,3090			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	-0,1603	0,02113	0,07012	57,57	0,0001
MAP	0,0002	0,00002	0,19583	160,79	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	MAP	0,6336	0,6336	117,5331	160,79	0,0001

($\alpha = 0,001$)

APPENDIX 10 : Table 2. Stepwise regression analysis of common controls, for mean stem form, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	5	93,908	18,782	144,38	0,0001
Error	89	11,577	0,1301		
Total	94	105,485			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	53,0218	4,9769	14,7645	113,50	0,0001
Controls	0,6894	0,1857	1,7922	13,78	0,0004
LAT	-0,0039	0,0004	10,8340	83,28	0,0001
LON	-0,0148	0,0021	6,2646	48,16	0,0001
MAT	0,3161	0,0589	3,7496	28,82	0,0001
SLP	-0,0593	0,0131	2,6505	20,38	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,7420	0,7420	206,9717	267,45	0,0001
2	SLP	0,0699	0,8119	128,2450	34,19	0,0001
3	LON	0,0258	0,8377	100,4229	14,47	0,0003
4	MAT	0,0355	0,8733	61,3717	25,24	0,0001
5	Controls	0,0170	0,8902	43,7509	13,77	0,0004

($\alpha = 0,001$)

APPENDIX 10 : Table 3. Stepwise regression analysis of common controls, for mean *Endothia* infestation over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	2	62,507	31,2538	203,85	0,0001
Error	87	13,339	0,1533		
Total	89	75,846			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	16,9417	0,84723	61,3052	399,86	0,0001
MAP	-0,0058	0,00029	58,7189	382,99	0,0001
Org.Mat	-0,1830	0,03831	3,5005	22,83	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,7780	0,7780	301,7272	308,37	0,0001
2	Org.Mat	0,0462	0,8241	223,1268	22,83	0,0001

($\alpha = 0,001$)

APPENDIX 10 : Table 4. Stepwise regression analysis of *E. grandis* test clones, for mean volume production, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	2	0,2992	0,1496	146,16	0,0001
Error	155	0,1587	0,0010		
Total	157	0,4579			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	-0,2099	0,19954	0,11332	110,70	0,0001
Clone	0,8278	0,15134	0,03063	29,92	0,0001
MAP	0,0002	0,00001	0,25158	245,78	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	MAP	0,5866	0,5866	176,4913	221,36	0,0001
2	Clone	0,0669	0,6535	125,0136	29,92	0,0001

($\alpha = 0,001$)

APPENDIX 10 : Table 5. Stepwise regression analysis of *E. grandis* test clones, for mean stem form, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	5	179,531	35,906	98,83	0,0001
Error	152	55,222	0,363		
Total	157	234,752			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	56,0187	6,8254	24,4721	67,36	0,0001
Clone	0,5788	0,1087	10,2983	28,35	0,0001
LAT	-0,0034	0,0005	12,6947	34,94	0,0001
LON	-0,0161	0,0029	10,6343	29,27	0,0001
MAT	0,3194	0,0822	5,4803	15,08	0,0002
SLP	-0,0568	0,0174	3,8592	10,62	0,0014

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,6092	0,6092	183,4825	243,22	0,0001
2	Clone	0,0558	0,6651	137,2569	25,84	0,0001
3	SLP	0,0482	0,7132	97,6556	25,87	0,0003
4	LON	0,0282	0,7414	75,3236	16,67	0,0001
5	MAT	0,0233	0,7648	57,1613	15,08	0,0002

(α = 0,001)

APPENDIX 10 : Table 6. Stepwise regression analysis of *E. grandis* test clones, for mean *Endothia* infestation over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	2	103,050	51,5249	247,18	0,0001
Error	146	30,433	0,2084		
Total	148	133,483			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	16,7120	0,75174	103,019	494,22	0,0001
LAT	-0,0058	0,00027	97,994	470,11	0,0001
Org.Mat	-0,1819	0,03502	5,621	26,97	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,7299	0,7299	212,6510	397,22	0,0001
2	Org.Mat	0,0421	0,7720	158,8892	26,97	0,0001

(α = 0,001)

APPENDIX 10 : Table 7. Stepwise regression analysis of *E. grandis* test clones, for mean volume production, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	6	0,33402	0,05567	67,87	0,0001
Error	151	0,12385	0,00082		
Total	157	0,45787			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	-1,1341	0,3872	0,00703	8,58	0,0039
Clone	0,7108	0,1373	0,02199	26,81	0,0001
LON	0,0003	0,0001	0,00536	6,54	0,0115
MAP	0,0002	0,0000	0,11064	134,89	0,0001
MIN	-0,0126	0,0029	0,01552	18,93	0,0001
ERD	0,0003	0,0001	0,00586	7,15	0,0083
Clay (A hor)	-0,0009	0,0003	0,00973	11,86	0,0007

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	MAP	0,5866	0,5866	176,4913	221,36	0,0001
2	Clone	0,0669	0,6535	125,0136	29,92	0,0001
3	MIN	0,0153	0,6688	114,7734	7,12	0,0084
4	Clay (A hor)	0,0373	0,7061	86,9679	19,41	0,0001
5	ERD	0,0117	0,7178	79,6098	6,30	0,0131
6	LON	0,0117	0,7295	72,2448	6,55	0,0115

($\alpha = 0,05$)

APPENDIX 10 : Table 8. Stepwise regression analysis of *E. grandis* test clones, for mean stem form, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	5	179,531	35,906	98,83	0,0001
Error	152	55,222	0,363		
Total	157	234,752			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	56,0187	6,8254	24,4721	67,36	0,0001
Clone	0,5788	0,1087	10,2983	28,35	0,0001
LAT	-0,0034	0,0005	12,6947	34,94	0,0001
LON	-0,0161	0,0029	10,6343	29,27	0,0001
MAT	0,3194	0,0822	5,4803	15,08	0,0002
SLP	-0,0568	0,0174	3,8592	10,62	0,0014

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,6092	0,6092	183,4825	243,22	0,0001
2	Clone	0,0558	0,6651	137,2569	25,84	0,0001
3	SLP	0,0482	0,7132	97,6556	25,87	0,0003
4	LON	0,0282	0,7414	75,3236	16,67	0,0001
5	MAT	0,0233	0,7648	57,1613	15,08	0,0002

($\alpha = 0,05$)

APPENDIX 10 : Table 9. Stepwise regression analysis of *E. grandis* test clones, for mean *Endothia* infestation, over all sites, age 5 years

Regression analysis:

SOURCE	DF	SS	MS	F value	Pr > F
Regression	12	119,545	9,9621	97,21	0,0001
Error	136	13,938	0,1025		
Total	148	133,481			

SOURCE	Parameter estimate	SE	SS	F value	Pr > F
Intercept	67,7164	6,2911	11,8738	115,86	0,0001
Clone	0,2253	0,0669	1,1641	11,36	0,0010
LAT	-0,0066	0,0009	4,7038	45,90	0,0001
LON	-0,0146	0,0019	6,0634	59,16	0,0001
ALT	-0,0028	0,0004	5,2647	51,37	0,0002
MAP	-0,0023	0,0007	0,9869	9,36	0,0023
DRY	0,0023	0,0050	0,0212	0,21	0,6503
ERD	0,0170	0,0020	7,7545	75,67	0,0001
Ph(H_2O) (A hor)	5,8408	0,6762	7,6464	74,61	0,0001
pH(KCl) (A hor)	-7,7103	0,9898	6,2182	60,68	0,0002
Org.Mat (A hor)	-7,0157	1,2211	3,3829	33,01	0,0014
C (A hor)	12,6743	2,2106	3,3688	32,87	0,0001
P (A hor)	0,0981	0,0160	3,8349	37,42	0,0001

SS Type II Sum of squares

Stepwise summary:

Step	Variable	Partial R^2	Model R^2	C(p)	F value	Pr > F
1	LAT	0,7299	0,7299	215,4235	397,23	0,0001
2	Org.Mat	0,0435	0,7734	159,3634	28,04	0,0001
3	pH(KCl) (A hor)	0,0252	0,7986	127,7276	18,15	0,0001
4	Clone	0,0135	0,8122	111,6595	10,38	0,0016
5	ERD	0,0051	0,8172	106,8752	3,98	0,0480
6	LON	0,0057	0,8229	101,3314	4,53	0,0350
7	pH(H_2O) (A hor)	0,0109	0,8338	88,7318	9,28	0,0028
8	ALT	0,0208	0,8546	62,9656	20,04	0,0001
9	P (A hor)	0,0080	0,8626	54,3151	8,08	0,0052
10	DRY	0,0077	0,8703	46,0318	8,20	0,0048
11	C (A hor)	0,0179	0,8882	24,1951	21,89	0,0001
12	MAP	0,0074	0,8956	16,3295	9,63	0,0023

($\alpha = 0,05$)