MODELING GENOTYPE BY ENVIRONMENT INTERACTION OF EUCALYPTUS USING ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION APPROACH

BY

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I56/65322/2010

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THIS DISSERTATION IS SUBMITTED IN PARTIAL FULFILLMENT FOR THE DEGREE OF MASTER OF SCIENCE IN

BIOMETRY

(APPLIED STATISTICS)

NOVEMBER 2012.

DECLARATION

I, the undersigned, hereby declare that the work contained in this project is my own original work and has not previously been submitted at any University for a degree.

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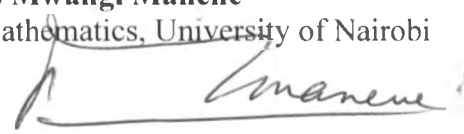

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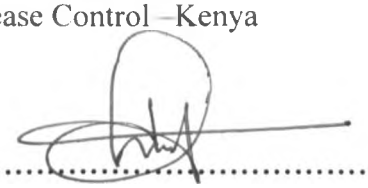

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ACKNOWLEDGMENT

I would like to thank my supervisors Professor Moses M. Manene, Dr. Vincent O. Oeba and Dr. Antony Gichangi for their guidance and advice towards the success of this project. I take this early opportunity to most sincerely express my gratitude forthe unwavering support, kindness, and patience that I have experienced during this entire project. My special appreciation goes to Dr. Vincent O. Oeba whose critical eye and enlightened mentoring were instrumental in realization of this thesis. For his inspiration, endurance, guidance in problem formulation and provision of data from Kenya Forestry Research Institute (KEFRI) was critical to enable me accomplish this task. I am indebted to KEFRI management for providing me serene environment and materials to build up this project. Special thanks to the university of Nairobi administration and school of mathematics lecturers for walking us through the course work and project supervision with so much flair that we were left asking for more. I also appreciate and acknowledge support from Henry Jackson Foundation Medical Research International for partially funding my tuition and with whose support, this work was made possible.

I am especially grateful and respectful to my wife Jackline Kemuma, twin sons Mark and Maxwel & Twin daughters Mitchel and Stacy for being supportive, kind and a blessing to me. To my parents, beloved Dad, John Karuntimi M'kiambati and mum Magadlene Kathambi, words cannot adequately express my gratitude for all their continued support, love and guidance that they showered on their beloved son. The strong foundation they laid for me has culminated to this higher academic achievement which remains in my memory forever. I acknowledge immense support received from my dear siblings Catherine Karwitha, Andrew Mutuma, Bridget Makena, Boniface Mwongera and Julius Kinoti and my dear in-laws during my period of study. Finally many people contributed in a big way especially my classmates to the realization of this thesis project. Lack of mention of their names and many more others does not in any way mean their deserved contribution is not appreciated but to you all I say thank you and God bless.

DEDICATION

I dedicate this Project to my Twin daughters Stacy and Mitchel and Twin sons Mark and Maxwell.

Abstract

Selection of eucalyptus genotypes with wide adaptability across diverse environments is important for adoption recommendation. When selecting superior genotypes one is usually confronted with the problem of genotype by environment interaction. An extension of analysis of variance (ANOVA) for studying genotype by environment interaction (GEI) is Additive Main Effects and Multiplicative Interaction (AMMI) Model, which is a hybrid analysis that incorporates both additive and multiplicative components of a two way data structure. This study applied AMMI to evaluate genotype by environment interaction of eucalyptus species in Kenya grown at different locations, determined genotypes stability and pattern of response across environmental sites. The model is applied to data on eucalyptus research undertaken by Kenya Forestry Research Institute (KEFRI) for the tree improvement programme from 1998 and assessed till 2006 with an aim of determining stable and adaptable genotypes across the diverse environmental sites. The trials were set in a randomized complete block design replicated two to four times. The combined analysis of variance indicates that environments (E), genotypes (G) and genotype by environment interaction (GEI) effects were significant, suggesting differential responses of the genotypes and the need for stability analysis. Analysis of variance for AMMI model revealed that two interaction principal components (IPCAs) were significant by using Gollob's F- test and accounted for over 90% of GE interaction. Therefore, successful genotypes need to be adapted to a broad range of environmental conditions in Kenya in order to ensure their yield stability and economic profitability. Of the Eucalyptus hybrid clones experimented across sites GC 14 ,GC 581, and GC 642 were found to be most stable genotypes for the highlands while GC 540 ,GC 514, and GC 14 were found to be most stable genotypes for the lowland environments implying they can be planted in a wide range of environments similar to the one tried. This resolves the complication of tree breeding program, where breeders are particularly interested in searching for fewer widely adapted genotypes. The interaction was best predicted by the first two principal components of genotypes and environments. Consequently, bi-plots generated using genotypic and environmental scores of the first twoAMMI components can help breeders have an overall picture of the behavior of the genotypes, the environments and GEIs. The AMMI and ASV were found useful in describing GEI of various eucalyptus clones.

Key words: Eucalyptus clones, genotype by environment interaction (GEI) and Additive Main effect Multiplicative Interaction (AMMI)

Abbreviations and Acronyms

AMMI	Additive Main effects and Multiplicative Interaction
ANOVA	Analysis of variance
ASV	AMMI Stability Value
BLUP	Best Linear Unbiased Predictors
CV	Coefficient of Variation
DBH	Diameter at Breast Height
DF	Degrees of Freedom
GE	Genotype by Environment
GEI	Genotype by Environnent Interaction
IPCA	Interaction Principal Component Analyses
JLR J	Joint Linear Regression
KEFRI	Kenya Forestry Research Institute
LR	Linear Regression
LSD	Least Significant Difference
MET	Multi-environment Trials
CM	Centimeter
M	Metre
ML	Maximum Likelihood
MS	Mean Square
PCA	Principal Component Analysis
REML	Restricted Maximum Likelihood
SAS	Statistical Analysis System
SS	Sum of Squares
ES	*Eucalyptus saligna*
EG	*Eucalyptus grandis*
ET	*Eucalytptustereticornis*
EU	*Eucalyptus urophylla*
EC	*Eucalyptus camaldulensis*

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CHAPTER ONE: INTRODUCTION

1.0 Introduction

Statistical models have wide applications in various fields of biological and social sciences. They help scientists to describe the phenomena under which variables are applied with specific assumptions. In particular, parametric statistical procedures have been developed over the years to meet the needs of different research problems of different disciplines. In the discipline of tree/crop breeding, scientists (crop breeders) have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions. Genotype x environment (G x E) interaction is one of the main complications in the selection of genotypes for broad adaptation in most breeding programmes. The phenotype of an organism is determined by the combined effect of the environment and the genotype which interact with one another. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant GXE system could have a large impact on plant breeding (Magariand Kang, 1993; Basfordand, 1998).

When environmental differences are large it may be expected that the interaction of genotype by environment will also be higher. As a result, one genotype may have the highest yield in some environments while a second one may excel in others. Hence, it is important to know the magnitude of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Fehr, 1991; Gauch and Zobel, 1997).To reduce the effect of G x E interaction, crop improvement

programmes usually run performance trials across a wide range of environments to ensure that the selected genotypes have a high and stable performance across several environments.

Under any crop improvement programme a sample of promising genotypes are performance tested at a number of sites to identify genotypes which possess the dual qualities of high yield, sustainability and low sensitivity to adverse changes in diverse environmental conditions. Various studies have shown that quite often that varieties perform differently in different environments. The interplay of genetic and non-genetic effects causing differential relative performances of genotypes in different environments is called Genotype by Environment Interaction(GEI). GEI causes difficulty in identifying superior genotypes and many ways of reducing and analyzing this interaction have been explored.

The adaptability of a variety over diverse environments is usually tested by its degree of interaction with different growing environments. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environments. Failure of genotypes to respond consistently to variable environmental conditions is attributed to Genotype by Environment Interaction (GEI). Understanding the implication of GEI structure is an important consideration in tree breeding programs. Traditional statistical analyses of yield trials do not provide good insight into the particular pattern and structure of GEI. The additive main effects and multiplicative interaction model (AMMI) incorporates both the additive and multiplicative components of a two-way data structure to effectively account for the underlying interaction patterns.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G x E interaction. In the initial analysis of variance, the total variation is partitioned into three sources, namely; genotypes, environment

and GEI. AMMI has proven useful for understanding complex genotype by environment interactions with the results graphed in a useful bi-plot that shows both main and interaction effects for both genotypes and environments. Purchase (1997) revealed that, in most yield trials, the proportion of sum of squares due to differences among sites ranged from 80 to 90% and the variation due to genotype by environment interactions is often larger than that of the genotypes. The AMMI model can produce bi-plot graphs, which display the variability of genotypes and genotype by environment interactions unlike the other traditional methods like ANOVA and regression.

The usual analysis of variance (ANOVA), having a merely additive model, identifies the GEI as a source but does not analyze it, principal components analysis (PCA) on the other hand is a multiplicative model and hence contains no sources for additive genotype or environment main effects and linear regression (LR) analysis is able to effectively analyze interaction terms only where the pattern fits a specific regression model. The consequence of fitting inappropriate statistical models to yield trial data is that the interaction may be declared not significant, although a more appropriate analysis would find agronomically important and statistically significant patterns in the interaction. Therefore, agronomists and plant breeders may fail to perceive important interaction effects. AMMI model has helped achieve accurate yield estimates, reliable selections across environmental sites, insightful models and efficient designs.

AMMI is an ordinary model of choice when the main effects and interaction are both significant, which happens to be the most common case. AMMI often offers a tremendously cost effective option for increasing accuracy because its yield estimates are routinely as accurate as means based on two to four as many replications (Gauch and Zobel, 1988; Crossa et al., 1990) AMMI helps agronomists and breeders in several ways namely; to understand or model complex

data sets especially the interactions, to estimate yields more accurately even with less data and to make better selections and to design more efficient yield trial experiments.

The current study attempts to estimate genotype by environment interaction of eucalyptus hybrid clones in Kenya. The study is motivated by the desire to identify the stable genotypes and characterize the GEI in the eucalyptus local and hybrid clones tested in diverse environments at the ongoing KEFRI trials. The growth performance of eucalyptus tree species vary considerably across environments and to enhance the yield/productivity of the eucalyptus, in 1998, Kenya Forestry Research Institute systematically started establishing trials of eucalyptus hybrid clones across various agro-ecological zones in Kenya with a goal to transfer clonal tree propagation technologies from Mondi forests, South Africa to Kenya as a means of hastening large-scale improvement of plantations.

From these studies one of the main objectives is to identify the best performing genotypes for recommendation for adaptation and hence there is a need to understand the performance and adaptability of eucalyptus hybrid clones across different agro-ecological zones to be able to accomplish this mission. A significant GEI seriously limits efforts in finding superior genotypes in tree breeding trials. Traditional statistical methods do not provide good insight into the particular pattern and structure of GE interaction. ANOVA fails to detect a significant interaction component, PCA fails to identify and separate the significant genotype and environment main effects, and LR accounts for only a small portion of the interaction sum of squares. On the other hand, AMMI model analysis reveals a highly significant interaction component that has clear agronomic meaning.

Several methods have been developed to analyse GEI and evaluate genotype stability over a range of environments. AMMI which combines analysis of variance and principal

component analysis is the most widely used in analyzing GEI. AMMI uses ANOVA followed by principal component analysis (PCA) applied to sum of squares allocated to GEI by ANOVA.

In Kenya, Eucalyptus species were introduced as early as 1902 by the colonial government to provide energy for the locomotives. Since then about 100 species have been planted in the country. Most of these were subjected to extensive research and currently less than 20 species have been recommended for wide scale planting. The area under eucalyptus species in the country is estimated to be about 100,000 ha of plantations, 15,000 ha in gazetted forests, about 35,000 ha planted by private companies and 50,000 ha by farmers.

The main reason for the introduction of eucalypts was its fast growth, ability to re-sprout and the straight nature of its stems. The wide range of products such as firewood, charcoal, building materials, fencing posts, transmission poles, pulpwood, timber and plywood obtained from Eucalyptus have made the genus very versatile. As a result of these attributes, the government promoted the planting of eucalyptus spp. With the increasing demand for wood, the government has further promoted and supported extensive growing of eucalyptus spp which culminated in the introduction of high-yielding, shorter-rotation varieties through biotechnology between 1997 and 2006. The recent past has therefore experienced unprecedented growth in eucalyptus supported farm forests in various configurations throughout the country.

1.1 Problem Statement

Genotype x environment (G x E) interaction is one of the main complications in the selection of genotypes for broad adaptation in most breeding programmes. When environmental differences are large it may be expected that the interaction of genotype by environment will also be higher. As a result, one genotype may have the highest yield in some environments while a second one may excel in others. Hence, it is important to know the magnitude of the interactions

in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation. A significant GEI seriously limits efforts in finding superior genotypes in tree breeding trials. Traditional statistical methods do not provide good insight into the particular pattern and structure of GE interaction. ANOVA fails to detect a significant interaction component, PCA fails to identify and separate the significant genotype and environment main effects, and LR accounts for only a small portion of the interaction sum of squares. On the other hand, AMMI model analysis reveals a highly significant interaction component that has clear agronomic meaning. Therefore, this study attempted to reveal the genotype by interaction of eucalyptus hybrid clones which were introduced in Kenya from Mondi Forest of South Africa by Tree Biotechnology Project at Karura. The trials have been conducted by Kenya Forestry Research Institute since 1997. This poses a need for information about the performance, adaptability and stability of these eucalyptus hybrid clones to farmers and other interested stakeholders across the country. For instance, it's known that performance of species on a particular site depends on the interaction of that species with the climatic, edaphic and other physical and biotic factors (Hills et al., 1984). Such interactions complicate testing and selection in Tree breeding programs and result in reduced overall genetic gain. Often, tree breeders search for genotypes that show stability, vigor and high yield over years and across locations. In general, a genotype is considered stable when its performance across environments does not deviate from the average performance of a group of standards genotype (Paulo de-souuza Gonclaves et al., 2003). In this particular case, the trials were established both at highland and lowland areas in Kenya. The data was subjected to AMMI model to determine GEI, growth performance and stability of eucalyptus hybrid clones. This is because; knowledge of GEI is

advantageous to have a species that gives consistently high yield in a broad range of environments and to increase efficiency of breeding program and selection of best genotypes

1.2 Research Objectives

The overall objective of this study was to apply AMMI model in analyzing genotype by environment interaction of eucalyptus hybrid clones in Kenya and to identify the best performing and stable genotypes.

1.2.1 Specific Research Objectives

i. Evaluate the genotype by environment interaction of eucalyptus hybrid clones using AMMI model.

ii. To evaluate the performance and adaptability of eucalyptus clones under various environments and to identify the best performing ones.

iii. To determine stability of eucalyptus clones and pattern of their response across environmental sites.

CHAPTER TWO: LITERATURE REVIEW

2.0 Literature review

The environment of a genome includes the molecular biology in the cell, other cells, other individuals, populations, species, as well as the abiotic environment. In agricultural experimentation, a large number of genotypes are normally tested over a wide range of environments (locations, years, growing seasons, etc.) and the underlying statistical and genetic theories used to model this system may be rather complicated. The occurrence of the GEI effect further complicates the selection of superior genotypes for a target population of environments. In the absence of GEI, the superior genotype in one environment may be regarded as the superior genotype in all, whereas the presence of the GEI confirms particular genotypes being superior in particular environments. Genotype by environment interaction is a common phenomenon in agricultural research. Differences between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments (Bondari, 1999)

The physical or visible characteristics resulting from the interaction between the genetic makeup and the environment are referred to as phenotype. Phenotypes can be observed, measured, classified, or counted. The association between the environment and the phenotypic expression of a genotype constitute the Genotype by environment interaction (GEI). The GEI determines if a genotype is widely adapted for an entire range of environmental conditions or separate genotypes must be selected for different sub-environments. When GEI occurs, factors present in the environment (temperature, rainfall, etc.) as well as the genetic constitution of an

individual (genotype), influence the phenotypic expression of a trait. Statistically, GEI occur if the performance of genotypes varies significantly across environments (Bondari, 1999)

Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant Genotype by Environment (GxE) system could have a large impact on plant breeding (Magari and Kang, 1993; Basford and Cooper, 1998). GEI occurs universally when genotypes are evaluated in several different environments (Becker and Léon, 1988; Magari, 1989; Kang, 1990). Magari and Kang (1993) found that the contribution of different environmental factors, to the yield stability of maize in yield trials, had a significant impact on the heterogeneity of the results.

The effect of GE becomes more apparent by conducting multi-location and multi-years trials, to accurately estimate and predict yield based on limited experimental data, to determine yield stability and the pattern of response of genotypes across environments and to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990).Kaya et al.(2002)used AMMI to determine the yield performances of 20 bread wheat genotypes across six environments in Central Anatolia, Turkey, in the 2000-2001 growing season. Additive main effects and multiplicative interactions analysis (AMMI) indicated that the yield performances of genotypes were under the major environmental effects of genotype by environmental interactions. The first two principal component axes (PCA 1 and 2) were significant ($p < 0.01$) and cumulatively contributed to 78.64% of the total genotype by environment interaction. A bi-plot generated using genotypic and environmental scores of the first two AMMI components also showed that genotypes with larger PCA 1 and lower PCA 2

scores gave high yields (stable genotypes), and genotypes with lower PCA 1 and larger PCA 2 scores had low yields (unstable genotypes), as in the sites tested.

A typical regional yield trial design is a genotype by environment two way factorial usually with replication. Genotype by environment interaction in plants is the differential response of genotypes to changing environmental conditions. Such interactions complicate testing and selection in tree breeding programs and result in reduced overall genetic gain. Tree breeders often search for genotypes that show stability, vigor and high yield over the years and locations. In general, a genotype is considered stable when its performance across environments does not deviate from the average performance of a group of standards genotype (Paulo de-souuza-Gonclaves et al., 2003). According to Williams and Matheson (1994), selecting suitable species based on the results of the series of field trials, knowledge about the stability of species over sites can be very important.

Gene expression is subject to modification by the environment and therefore, genotypic expression of the phenotype is environmentally dependent (Kang, 1998). The development of new cultivars involves breeding of cultivars with desired characteristics such as high economic yield, tolerance or resistance to biotic and abiotic stresses, traits that add value to the product, and the stability of these traits in target environments. Inconsistent genotypic responses to environmental factors such as temperature, soil moisture, soil type, or fertility level from location to location and year to year are a function of GEI. GEI have been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988).

Knowledge of GEI is advantageous to have a species that gives consistently high yield in a broad range of environments and to increase efficiency of breeding program and selection of best genotypes. A number of parametric statistical procedures have been developed over the

years to analyze GEI and especially yield stability over environments. The effects of genotype and environments are statistically non-additive, which means that differences between genotypes depend on the environment. For data sets with more than two genotypes and more than two environments, the GEI are commonly calculated by analysis of variance (ANOVA), leading to an estimated variance component for GEI. Performance tests over a series of environments give information on GEI at population level, but from a practical point view, it is important to measure the stability of the performance of individual genotypes (Eberhart and Russell, 1966).

Regarding agricultural problems from GEI, there exist two basic options, one aimed at the genotypes and the other at the environments (Ceccarelli, 1989; Simmonds, 1991; Zavala-Garcia *et al.*, 1992). One option is to seek a high yielding, widely adapted genotype that wins throughout the growing region of interest. The other option, particularly relevant when the first fails, is to sub divide the growing region into several relatively homogeneous macro-environments (with little interaction within each macro-environment).

Several methods have been proposed to analyse GEI and phenotypic stability (lin et al., 1986; Becker and Leon 1988; Piepho, 1998; Truberg and Huhn, 2000). These methods can be divided into two major groups, namely; univariate and multivariate stability statistics (Lin et al., 1986). Joint regression is the most popular among the univariate methods because of the simplicity in calculation and application (Becker and Leon, 1988) whereas Additive Main effect Multiplicative Interaction (AMMI) is gaining a popularity and is currently the main alternative multivariate approach to joint analysis in many breeding programmes (Annicchiarico, 1997).

Joint regression provides a conceptual model for genotypic stability (Becker and Leon, 1988; Ramagosa and Fox, 1993). The regression of the height or diameter at breast height (dbh) of an individual genotype on environment mean height or dbh is determined. Finlay and

Wilkinson (1963) defined a genotype with regression coefficient equal to zero ($\beta i=0$) as stable, while Eberhart and Russell (1966) defined genotype with $\beta_i=1$ to be stable. According to the joint regression model a stable genotype is one with high mean yield, $\beta_i = 1$ and $\Sigma s^2d_i = 0$ (Eberhart and Russsell, 1966). The genotype by environment interaction from the analysis of variance is partitioned into heterogeneity of regression coefficient (β_i) and the sum of deviation (Σs^2d_i) from regressions. If the regression means square is significant and the mean square for the deviation is not significant, then joint regression analysis model has been successful in explaining the interaction (Williams and Matheson, 1994).

Additive Main Effects and Multiplicative Interaction (AMMI) model combines the conventional analyses of variance (ANOVA) for additive main effects with the principal components analysis (PCA) for the non-additive residuals. It is one of the most common methods in a GEI study for analyzing the data in a two-way table of means. The salient feature of ANOVA is that it computes a genotype deviation (difference from the grand mean) and an environment deviation whose sum (plus the grand mean) estimates the yield for that genotype in that environment. Hence ANOVA is an additive model. An ANOVA model leaves a non-additive residual namely the genotype environment interaction.

Fisher and Mackenzie (1923) were the first to apply both ANOVA and PCA, separately to a single data set; namely a yield trial having 12 Potato varieties grown with six fertilizers (environments) with three replications. They found for this particular yield that PCA's multiplicative model fit data somewhat better than ANOVA additive model. Williams (1952) and Pike and Silverberg (1952) invented the AMMI model. The genotype and environment main effects are usually retained in an AMMI model. If the main effects are retained in the model, the result is AMMI zero (AMMI0) which is identically ANOVA. Furthermore if both main effects

and all IPCA axes are retained in the model the result is AMMI full (AMMIF) which is identical to the treatment means model. ANOVA, principal component analysis (PCA) and treatment means are rather naturally spoken as sub-cases of AMMI. AMMIN where N is an arbitrary value containing the number of Interaction Principal Component Axes (IPCA) has been chosen to minimize the Root Mean Square Prediction Difference (RMSPD) so as to increase the predictive accuracy of yield estimates.

ANOVA fails to detect a significant interaction component, PCA fails to identify and separate the significant genotype and environment main effects, and LR accounts for only a small portion of the interaction sum of squares. On the other hand, AMMI analysis reveals a highly significant interaction component that has clear agronomic meaning. Since ANOVA, PCA, and LR are sub-cases of the more complete AMMI model, AMMI offers a more appropriate first statistical analysis of yield trials that may have a GEI. AMMI analysis can then be used to diagnose whether or not a specific sub-case provides a more appropriate analysis. AMMI has no specific experimental design requirements, except for a two-way data structure.

AMMI is a significant resource statistical resource for understanding GE interaction as first emphasized by Kempton (1984). Furthermore special graphs (called bi-plots) can communicate the AMMI model very effectively showing both the main and interaction effects for both genotype and environment. AMMI has proved to provide a more adequate biological explanation of GEI than the regression model and it has been found useful when applied to across years analyses with a higher element of unpredictability (Crossa*et al.*, 1990; Yau, 1995; Gauch and Zobel, 1996; Annicchiarico, 1997).The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates. The interaction is

explained in the form of a bi-plot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI components. Integrating bi-plot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments (Tsige, 2002).

The advantages of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). Within limits, any model may be expected to fit the data from which it was derived. However, the AMMI model has a good chance of being able to predict for new sites and New Year's, thus contributing a real advance (Gauch, 1988).

CHAPTER THREE: METHODOLOGY

3.0 Materials and Methods

3.1 Study design and experimental sites

The improved eucalyptus hybrid clones and seedlings of local landraces known to perform well in selected sites were used to establish experimental trials on 15 sites in different years (Table 3.1 and Table 3.2). The experimental design at each test location was randomized complete block design with two to four replications. However not all hybrid clones and available Landraces were established in all the sites.

Table 3.1 Study sites and experimental details

Item	Highland Site(s)				Lowland Site(s)		
	Karura	**Machakos**	**Hombe**	**Timboroa**	**Gede**	**Sokoke**	**Msambweni**
Year of planting	Apr-98	May-99	May-99	Jul-99	June2002	2-Jul	2-Jun
Planting material	3local landraces and 8 GCs	4local landraces and 6 GCs	4local landraces and 6 GCs	4local landraces and 5 GCs	3local landraces and 9 GCs and 3 GUs	3local landraces and 9 GCs and 3 GUs	3local landraces and 9 GCs and 3 GUs
Escapement (M)	2.5x2.5	2.5x2.5	2.5x2.5	2.5x2.5	2.5x2.5	2.5x2 5	2.5x2.5
Planting density (trees)per plot	5x5	5x5	5x5	5x5	4x4	4x4	4x4
Number of trees assessed	6	6	6	6	16	16	16
Number of replicates	3	3	3	3	3	2	4
Total area (ha)	0.33	0.3	0.3	0.27	0.25	0.17	0.34
Altitude (M)	1600	2066	2300	3000	13	25	10
Latitude	1 15'S	1 27'S	0 23'S	0 05'N	3 12'S	6 14'N	05N
Longitude	36 50'E	37 16'E	37 4'E	35 32'E	40 02'E	10 59'E	59E
Mean annual rainfall (MM)	900	1400	1300	1200	940	700	1175

Table 3.2Summary of the planting material experimental establishment and ages assessed.

Site	Plant species or hybrid clone	Ages assessed in months
Karura	ES, EG, ET, GC10, GC12, GC14, GC15, GC17 GC522, GC581 and GC642	27, 34, 66, 71 and 100
Machakos	ES, EG, ET, EC, GC10, GC14, GC15, GC522, GC581 and GC642	12, 26, 46, 59 and 90
Hombe	ES, EG, ET, EC, GC10, GC14, GC15, GC522, GC581 and GC642	24, 28 and 60
Timboroa	ES, EG, ET, EC, GC3, GC14, GC15, GC581 and GC642	6, 12, 24, 36, 49 and 60
Gede	EU, ET, EC, GC14, GC167, GC514, GC540, GC581, GC584, GC784, GC785, GC796, GU7, GU8 and GU21.	6, 12, 24, 36, 49 and 60
Sokoke	EU, ET, EC, GC14, GC167, GC514, GC540, GC581, GC584, GC784, GC785, GC 796, GU7, GU8 and GU21.	6, 12, 24, 41 and 55
Msambweni	EU, ET, EC, GC14, GC167, GC514, GC540, GC581, GC584, GC784, GC785, GC 796, GU7, GU8 and GU21.	7, 12, 24, 38 and 45

The tree height was measured in cm within the first six months and there after assessment was done yearly in metres. Diameter at breast height (dbh) in cm was taken after two years. Both of these measurements were used for assessing growth and stability of eucalyptus hybrid clones across study sites.

3.2Additive Main Effects and Multiplicative Interaction Model

AMMI model combines ANOVA and PCA into a single analysis with both additive and multiplicative parameters and takes the general form of.

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_{k=1}^{n} \lambda_k \gamma_{gk} \delta_{ek} + \rho_{ge} + \varepsilon_{ger} \quad (3.1)$$

Where

Y_{ger} is the yield observation of the r^{th} replica of the g^{th}genotype in the e^{th}environment;

μ is the overall mean effect;

α_g and β_e are the genotype and environment effect, respectively;

λ_k is the eigenvalue of the PCA axis k;

γ_{gk} and δ_{ek} are the g^{th} genotype and e^{th} environment principal component scores for axis k;

n is the number of principal components retained in the model and

ε_{ger} is the error term.

The first three terms in the model (equation 3.1) $\mu + \alpha_g + \beta_e$ are the additive part of the AMMI model that uses ordinary ANOVA. ANOVA additive model partitions a yield observation Y_{ger} into an additive model with three parameters namely the grand mean, genotype and environment deviation, the non-additive residual or interaction and error term. The analysis of variance table for the ANOVA model is of the form given in Table 3.3.

Table 3.3 Analysis of Variance for the ANOVA Additive model

Source	df	SS
Total	GER-1	$\sum_g \sum_e \sum_r (Y_{ger} - \bar{Y})^2$
Treatments	GE-1	$R\sum_g \sum_e (\bar{Y}_{ge} - \bar{Y})^2$
Genotypes	G-1	$ER\sum_g (\bar{Y}_g - \bar{Y})^2$
Environments	E-1	$GR\sum_g (\bar{Y}_e - \bar{Y})^2$
Interactions	(G-1)(E-1)	$R\sum_g \sum_e (\bar{Y}_{ge} - \bar{Y}_g - \bar{Y}_e + \bar{Y})^2$
Error	GE(R-1)	$\sum_g \sum_e \sum_r (Y_{ger} - \bar{Y}_{ge})^2$

ANOVA additive model leaves the interaction as the non-additive residual which typically contains 10% to 50% of the treatment SS and often several times as large as the genotype SS. Usually the interaction is significant at 0.05 and higher level and even if it's not significant partitioning it by means of linear regression, AMMI or other models can often reveal significant sources within the interaction. Although the interaction component carries most of the degree of freedom (G-1)(E-1) and usually much of the SS, the ANOVA additive model merely comments that the interaction is or is not significant. A serious deficiency with ANOVA Additive Model is in partitioning the interaction, into significant sources with relatively few d.f and a non-significant residual with most of the d.f. indicating a need to apply the tree yield data to AMMI statistical model. The AMMI model incorporates both the additive and multiplicative components of a two way data structure and uses analysis of variance and PCA applied to sum of squares applied to GEI.

To estimate the unknown parameters in the model, one usually first uses row/column means for the main effects and then performs a singular value decomposition of the residual matrix for the interaction parameters. This classical approach corresponds essentially to a least squares fit of the full model. Non-additive effects are frequently observed in two-way tables, and, as Daniel (1976) points out, the non-additivity is often associated with just a few rows or columns of the table. As observed by Snee (1982), the interpretation of non-additivity is less of a problem if replicate observations are present for each of the cells of the table. However, when there is only one observation per cell, it is not possible to distinguish between row- or column-related non-homogeneous variance and interaction from the observed data alone. In this situation, the use of a model that will detect a variety of different types of non-additivity in two-way tables can be very helpful.

The grand mean μ is estimated by $\bar{Y}$, which is the average yield over all genotypes across the sites and replications. The genotype deviation α_g is estimated from the grand mean by $\bar{Y}_g - \bar{Y}$ which is the grand mean subtracted from the average yield of genotypes, the environmental deviation β_e is estimated by subtracting the grand mean from the environment average yields i.e. $\bar{Y}_e - \bar{Y}$.

ANOVA leaves a non-additive residual, the interaction denoted by δ_{ge} i.e. $Y_{ger} = \mu + \alpha_g + \beta_e + \delta_{ge} + \varepsilon_{ger}$, second the multiplicative part of the AMMI model uses PCA to decompose the interaction into PCA axes 1 to N and a residual remains if not all axes are used. AMMI data are assumed to come in the form of a two-way table. The classical model for such a table is the ANOVA model $Y_{ger} = \mu + \alpha_g + \beta_e + \delta_{ge}$ where Y_{ger} is the r-th observation in the g-th row and the e-th column of the table, μ is the overall mean effect, α_g represents the g-th row effect, and β_e the e-th column effect.

The terms δ_{ge} can either be seen as residuals or as interaction terms between rows and columns. The above model is called the additive model. However, it is quite possible that the interaction terms δ_{ge} still contain some structure, and therefore one can model them by a set of multiplicative components plus residual error: $\delta_{ge} = \sum_{i=1}^{n} \lambda_k \gamma_{gk} \delta_{ek} + \rho_{ge} + \varepsilon_{ger}$

Combining the two expressions above yields an additive main effect and multiplicative interaction (AMMI) model for the two-way table as given in equation (3.1)

The multiplicative parameters are λ_k the singular value for PCA axes k, γ_{gk} the genotype eigen vector for axis k and δ_{ek} the environment eigen vector. The genotypic and environment eigen vectors γ_g and δ_e are unit less whereas the singular value λ has the units of yield. Least squares parameter estimates are obtained by iterative calculations. For AMMI these calculations are applied to the interaction values δ_{ge} rather than the original data minus the grand mean

$\bar{Y}_{ge} - \bar{Y}$, as in PCA. As with PCA, a convenient scaling for the multiplicative parameter is $\lambda^{0.5}\gamma_g$ and$\lambda^{0.5}\delta_e$ because their product gives the interactions expected value directly, without needing further multiplication by the singular value.

However, to reinforce the distinction between PCA and AMMI these AMMI multiplicative parameters $\lambda^{0.5}\gamma_g$and $\lambda^{0.5}\delta_e$ are termed "interaction PCA scores" or "IPCA scores" (rather than merely PCA scores). Again these scores have the units of square root of yield.

The first approach in running AMMI analysis is to produce bi-plots. In this feature, genotypes and environments are plotted on the same diagram, facilitating inference about specific interactions of individual genotypes and environments by using the sign and magnitude of PCA 1 values. Any genotype with a PCA 1value close to zero shows general adaptation to the tested environment. A large genotypic PCA 1 scores reflects more specific adaptation to environments with PCA 1 scores of the same sign.

The AMMI solution is unique up to the simultaneous reflections (polarity reversals) of the genotype and eigen vectors for any given axis. The IPCA axes are ordered by their singular values the largest first, the order within tied singular values being arbitrary. There are at most min (G-1, E-1) axes but usually only the first one or a few IPCA axes are of interest. IPCA axes n is assigned G+E-2-2n d.f. If the experiment is replicated there is an error termε_{ger}. The member of the AMMI family with one IPCA axes (while relegating all higher axes to the residual) is denoted AMMI1, while AMMI2 retains two IPCA axes and so on. In general AMMIN denotes the AMMI model with IPCA axes 1 to N. AMMI0 has no IPCA axes and is identically ANOVA. The full model with min (G-1, E-1) IPCA axes is denoted by AMMIF and equals the treatment means model. The equation for the expected values $\bar{Y}_{ge}$ of the AMMI model

deletes the residuals and the errors from the general equation 3.1 and stipulates a specific AMMI model rather than the entire AMMI family.

For AMMIN $\bar{Y}_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en}$ With n = 1,2,……,N (3.2)

For AMMI an alternative form of the general equation 3.1 involves several changes. For the additive part of the AMMI model, genotype means τ_g and environment means $\pi_e$may be used instead of deviations since means are more easily understood but the grand mean μ is subtracted instead of added. For the multiplicative part the subscript n for axis number may be deleted and the scaling of IPCA scores used. The result is

$Y_{ger} = \tau_g + \pi_e - \mu + \lambda^{0.5} \gamma_g \lambda^{0.5} \delta_e + \rho_{ge} + \varepsilon_{ger}$(3.3)

Where,μ is the grand mean, τ_g is the genotype means, $\pi_e$is the environment means and $\lambda^{0.5} \gamma_g \lambda^{0.5} \delta_e$ is the multiplicative part.

3.3. Assumptions of AMMI Model

For AMMI model and related models to be applicable to a data set the following requirements must be met.

i. Data should be structured as two way factorial with at least three rows and three columns, replicated or not. The data must be organized in a two way table or matrix such as genotypes by environment factorial design. The reason for this restriction is that although the ANOVA part of AMMI is flexible, the PCA part demands a two way data structure. The data may be replicated or not when AMMI is used for estimation, selection, modeling and some other purposes. If F-tests are desired, the error mean square is needed and this requires replication.

ii. Data should contain one kind, quantitative rather than categorical. The data for AMMI must be of one kind such as yields. Various matrix rows (or columns) are not allowed to contain different data and units, such as concentrations and temperatures, since such a mixture would cause model parameters for columns to have no meaningful units. Also enormous differences in numerical ranges within rows as are typically encountered with such data, would cause rows with very small sum of squares to be practically ignored in the AMMI analysis. Also the data must be quantitative and not mere presence or absence data, and not categorical data such as colours and nationalities. A rough scale such as zero to five for increasing levels of insect damage is fine when increasing values signify increasing levels of a single thing, in contrast to different values coding for different entities such as nationalities, which do not have a single or simple logical relationship.

iii. The data should be fitted by AMMI model reasonably well, as ordinarily happens when main effects and interaction are both Significant. For AMMI to be truly useful and not merely mathematically applicable the model has to fit the data set. Like every statistical analysis AMMI has a particular model and only if this model happens to fit a given data set reasonably well will the results be truly useful. Whether this condition is met in a particular instance usually cannot be determined by mere inspection of data but rather AMMI must be applied to the data and the output scanned. AMMI is the model of choice when the data exhibit significant main effects and significant interaction. However even when AMMI is not appropriate and a different model fits the data better, an initial analysis by AMMI is ordinarily the easiest means of diagnosing this better model (Bradu and Gabriel 1978).

3.4 Linear and joint modified regression Models

Historically the first statistical method for partitioning and analyzing the interaction was simple linear regression. Plant breeders noticed that often a large portion of the variation in yield could be accounted for by linear regressions of yield (for each individual genotype) over environment means (over genotypes). Applying Hilder-brand and Russell method, the yield for each variety can be related to the environment by a simple linear regression

$$Y_{ij} = a + bX_i$$

Where Y_{ij}= the yield of the i^{th} variety at the j^{th} environment, X_i = mean of variety yields per environment.

By fitting the regression equation independently and then plotting the yield response to environment for each variety on the same graph, it is possible to visually compare varieties.
A variety with unit regression coefficient (b=1) is said to be stable. In this case we are interested in testing the hypothesis

$$H_o: b = 1$$

$$Vs$$

$$H_1: b \neq 1$$

At α% level of significance and n d.f the tabular value is compared to the absolute value of the calculated t value t = (b-1)/S_b

Using the fitted regression equations the yield response to environment for each variety is plotted on the same graph and a visual comparison of variety response to environment is assessed. The regression model partitions the interaction into regression and residuals (that is deviation from the regressions). The regression effect equals the genotype slope $\xi_g$times the environment deviationβ_e. So the Finlay –Wilkinson regression model equation is

$$Y_{ger} = \mu + \alpha_g + \beta_e + \xi_g\beta_e + \rho_{ge} + \varepsilon_{ger} \quad (3.4)$$

The least square fit is obtained by estimating the additive effects α_g and β_e in the usual way first, and then estimating the genotype slopes ξ_g. The slope is estimated by $\sum xy/\sum x^2$ and the correlation by

$\sum xy/\sqrt{(\sum x^2)(\sum y^2)}$.

Accordingly for genotype g, linear regression of the interaction Θ_{ge} on the environment deviations β_e gives the slope ξ_g estimate $\sum_e(\Theta_{ge}\beta_e)/\sum_e \beta_e{}^2$ and the correlation estimates $\sum_e(\Theta_{ge}\beta_e)/\sqrt{\sum_e \Theta_{ge}{}^2 \sum_e \beta_e{}^2}$.

When attention focuses on the environments rather than the genotypes the converse analyses regresses each environment yield on the genotype means (Fox and Rathgen, 1981). Again viewing these regressions as an analysis of the interaction a more appropriate scaling is to regress each environments interaction Θ_{ge} on the genotype deviations α_g giving the slope $\Phi_e \frac{\sum_g(\Theta_{ge}\alpha_g)}{\sum_g \alpha_g{}^2}$

The environment regression model with the interaction as the environment slope Φ_e times the genotype deviation α_g is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Phi_e\,\alpha_g + \rho_{ge} + \varepsilon_{ger} \quad (3.5)$$

In addition to the genotype regression and environment regressions, there exist a third kind of regression, the joint regression, which involves both the genotype and environment deviations (Tukey, 1949 and Wright, 1971). Joint regression models the interaction as the joint regression coefficient k times the genotype deviation α_g times the environment deviation β_e resulting in the model

$$Y_{ger} = \mu + \alpha_g + \beta_e + k\,\alpha_g\beta_e + \rho_{ge} + \varepsilon_{ger} \quad (3.6.)$$

The joint constant k is estimated by $\sum_g \xi_g \alpha_g / \sum_g \alpha_g^2$. The joint regression has 1 d.f and a SS $Rk^2(\sum_g \alpha_g^2)\sum_e \beta_e^2$. To analyse the interaction more aggressively both the regular genotype regressions and the converse environment regressions may be applied to the interaction, but in this case it is also necessary to include the joint regression. The most complete model for the linear regression approach is

$$Y_{ger} = \mu + \alpha_g + \beta_e + \xi_g\beta_e + \Phi_e \alpha_g + k \alpha_g\beta_e + \rho_{ge} + \varepsilon_{ger} \qquad (3.7.)$$

With both sets of regressions present the genotype regressions are assigned G-2 d.f, the environment regressions E-2 df, and the joint regression 1 d.f, while the residual have the remaining (G-2)(E-2) d.f of the (G-1)(E-1) df in the interaction. The genotype slopes have a SS $R(\sum_g \xi_g^2)(\sum_e \beta_e^2)$ minus the joint regression SS, and the environment slopes $R(\sum_g \Phi_e^2)(\sum_g \alpha_g^2)$ minus the joint regression SS.

The modified joint regression model is of the form (Eberhart and Rusell, 1966):

$Y_{ij} = \mu + g_i + \beta_i S_j + \varepsilon_{ij}$ *(3.8)*

where, Y_{ij} is the i^{th} observation on the g^{th} genotype in j^{th} site (environment) with i=1....7 and

j = 1,2,3 and 4,

g_i are the genotype means,

S_j are site (environment) effects,

β_i are linear regression coefficient of the j^{th} genotype at the environment index which measures the response of this genotype to varying locations with mean (β_i) = 1 , and ε_{ij} = experiment error (random effect associated with plot ij)

The regression coefficient, which is the variation of each genotype under different sites on the environment, means is calculated. This is estimated as:

$\beta_i = \Sigma Y_{ij} S_j / \Sigma S^2_j$ *(3.9)*

Where, $\Sigma Y_{ij}S_j$ is the sum of products and ΣS^2_j is the sum of squares.

3.5 Stability and combined analysis

The conclusions drawn from an experiment in a single locality will have little value for the whole area covered in the experiment, because performance of varieties will vary depending on the underlying differences prevalent in different localities within a target area. An important objective of on farm trial is to examine which treatment is adapted to which kind of environment. The analysis of variance over different sites or seasons shows whether treatment effects change under different environmental conditions. A tree breeder needs to know the area of adaptation of the new varieties developed. To achieve this objective, the varieties are tested in field experiments repeated in several locations. The conclusion drawn from an experiment in a single locality will have little value for the whole area, because performance of varieties will vary depending on the type of soil, amount of rainfall and rainfall pattern, diseases and pests prevalent in different locations within the target area. When varieties respond in different ways to changes in environment we conclude that there is a variety by location interaction.

The initial steps in the analysis of data from a series of similar experiments are to analyze and interpret the data separately for each individual experiment. Before proceeding with the combined analysis we examine first whether the difference among the treatments are of the same order in all the experiments. The next step is to test equality of the experimental error variances using Bartlett's test. When the error variance is homogenous we can then carry out combined analysis of variances. A general format for combined analysis over sites for an experiment carried out at L locations (sites) with t test treatments replicated r times at each location is as shown in Table 3.4 below

Table 3.4: General format for combined analysis of variance over sites

Source of Variation	Df	SS	MS
Locations	L-1	SS_L	MS_L
Reps within Locations	L(t-1)	SS_R	MS_R
Treatments	t-1	SS_t	MS_t
Interaction	(L-1)(t-1)	SS_I	MS_I
Pooled Error	L(r-1)(t-1)	SS_E	MS_E

3.5.1.The AMMI Stability Value

The AMMI Stability value (ASV) was calculated using the following as suggested by Purchase (1997);

$$ASV = \sqrt{\left\{\left\{\frac{SS\ IPCA1}{SS\ IPCA2}\ X\ IPCA\ 1\ Score\right\}^2 + (IPCA2\ score)^2\right\}} \qquad (3.10)$$

where, *ASV* = AMMI's stability value

SS = Sum of squares

IPCA1 = Interaction of principal component and analysis one

and

IPCA2 = Interaction of Principal component analysis two.

This was done because the computed two IPCA had different values and meanings hence ASV becomes the better option of obtaining estimated values between two IPCAs scores. According to Purchase (1997) ASV was reported to produce a balanced measurement between

the two IPCA scores. The ASV is the distance from zero in a two dimensional scatter gram of IPCA1 (Interaction Principal Component Analysis axis 1) score against IPCA2 scores. Since the IPCA1 score contributes more G x E sum of squares, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total G x E sum of squares.

3.6 Cluster Analysis

Cluster analysis or clustering is the task of assigning a set of objects into groups (called clusters) so that the objects in the same cluster are more similar (in some sense or another) to each other than to those in other clusters. Cluster analysis is a numerical classification technique that defines groups or clusters of individuals. Two types of classification can be distinguished. The first is non-hierarchical classification, which assigns each item into a class. The second type is hierarchical classification, which groups individuals into clusters and arranges these into a hierarchy for the purpose of studying relationships in the data (Crossa, 1990).

In the process of 'clustering', all genotypes are assessed for similarity of response and grouped together on the basis of proximity to each other such that clubbing any other genotype in a group, leads to relatively higher sum of squares within the groups. So starting from individual values of genotypes or environments, the subgroups are made which further are continued to be successively grouped until all variation is covered in one large group. The whole structure from the individual values to final groups is represented like branches of a tree in a dendrogram that depicts composition of groups and degree of dissimilarity among groups both for genotypes as well as environments. The genotypes or environments in each group or cluster are expected to

have a similar contribution towards G x E interaction as compared to the constituents of the other group at each level of clustering (Ramagosa and Fox, 1993).

All the analyses were performed using Genstat V13 and data management techniques were done using Ms-Excel 2010.

CHAPTER FOUR: RESULTS AND DISCUSSION

4.1 Introduction

This chapter presents the results and discussions based on the three research objectives of this study. It is divided into three major sections, namely; genotype by environment interaction of eucalyptus clones using AMMI model; AMMI analysis on performance and adaptability of eucalyptus genotypes under various environments; and AMMI analysis on stability. Each of these sections is subdivided into various subsections detailing the findings of different parameters assessed in each research objectives.

4.2 Genotype by Environment Interaction Characterization

4.2.1. Genotype by environment interaction of eucalyptus hybrid clones at highland sites

According to combined analysis of variance for tree yield, GE interaction was significant ($p<0.01$) at 24 months and indicated the high influence of environments in genotypes changes. The environment (E) and genotype (G) effects were also significant for DBH at 24, 36 and 60 months. The results showed that IPCA1 and IPCA2 accounted over 90% of variation for GEI across environmental sites. Both of these IPCAs were significantly different ($p<0.05$) at age of 24 months whereas IPCA1 was the only significant at 36 months. At age of 60 months, both IPCAs were not significant ($p>0.05$, Table 4.1). This implied the interaction effect of the genotype varied with age of growth of the species. Moreover there was rank difference in genotypes response at different environments prompting a need for extension to stability analysis. The partitioning of variance components indicated that environments was apportioned to 30.6%, 30.4% and 26.2%of the total variation, 8.5%,7.3% and 4.6% due to replications within

environments, 25%,14% and 39.7% due to genotypes, 22.8%,18.9% and 8.01% due to GEI and 6%,9.6,4.5%due to residual for DBH at 24, 36 and 60 months, respectively. The higher proportion of variance due to environment over genotypes indicates that location effects on tree DBH at 24 months and 36 months for the three local landraces and four hybrid clones tested at the four highland locations was large and vice versa for DBH at 60 months.

Results from AMMI analysis (Table 4.1) further showed that the first principal component axis (IPCA 1) of the interaction captured 55%, 60%, 65% of the interaction sum squares in 8 degrees of freedom for DBH at 24, 36 and 60 months respectively. Similarly, the second principal component axis (IPCA 2) explained a further 39%, 31% and 31% of the GEI sum of squares for DBH at 24,36 and 60 months respectively. The mean squares for IPCA 1 and IPCA 2 were significant at $p = 0.01$ for DBH at 24 months and IPCA1 significant for DBH at 36 months. Moreover the IPCA 1 and IPCA2 cumulatively contributed 94%, 91% and 96% of the total GEI for DBH at 24, 36 and 60 months, respectively.

Further comparison of the IPCA mean sum of squares with the residual sum of squares revealed that mean squares (MS) of the first IPCA axis for tree DBH at 24 months was 4.5 times that of the residual MS and the second IPCA axis was 4.4 times that of the residual MS and the combined MS for the two IPCA axis are 8.9 times that of the residual MS. At 36 months IPCA axis was 3.1 times that of the residual MS and the second IPCA axis was 2.1 times that of the residual MS with combined MS for the two IPCA axes being 5.3 times that of the residual MS. Finally for DBH at 36 months the first IPCA axis was 7.2 times that of the residual MS and the second IPCA axis was MS 4.6 times that of the residual MS with combined MS for the two IPCA axes being 11.8 times that of the residual MS. AMMI with only two-interaction principal component axis was the best predictive model with further interaction principal component axis

mostly capturing noise and therefore, did not help to predict validation of observations. Thus the interaction of the 7 genotypes in the four environments was best predicted by the first two interaction principal component of genotypes and environments.

Table 4.1: Analysis of variance across ages for highland trials

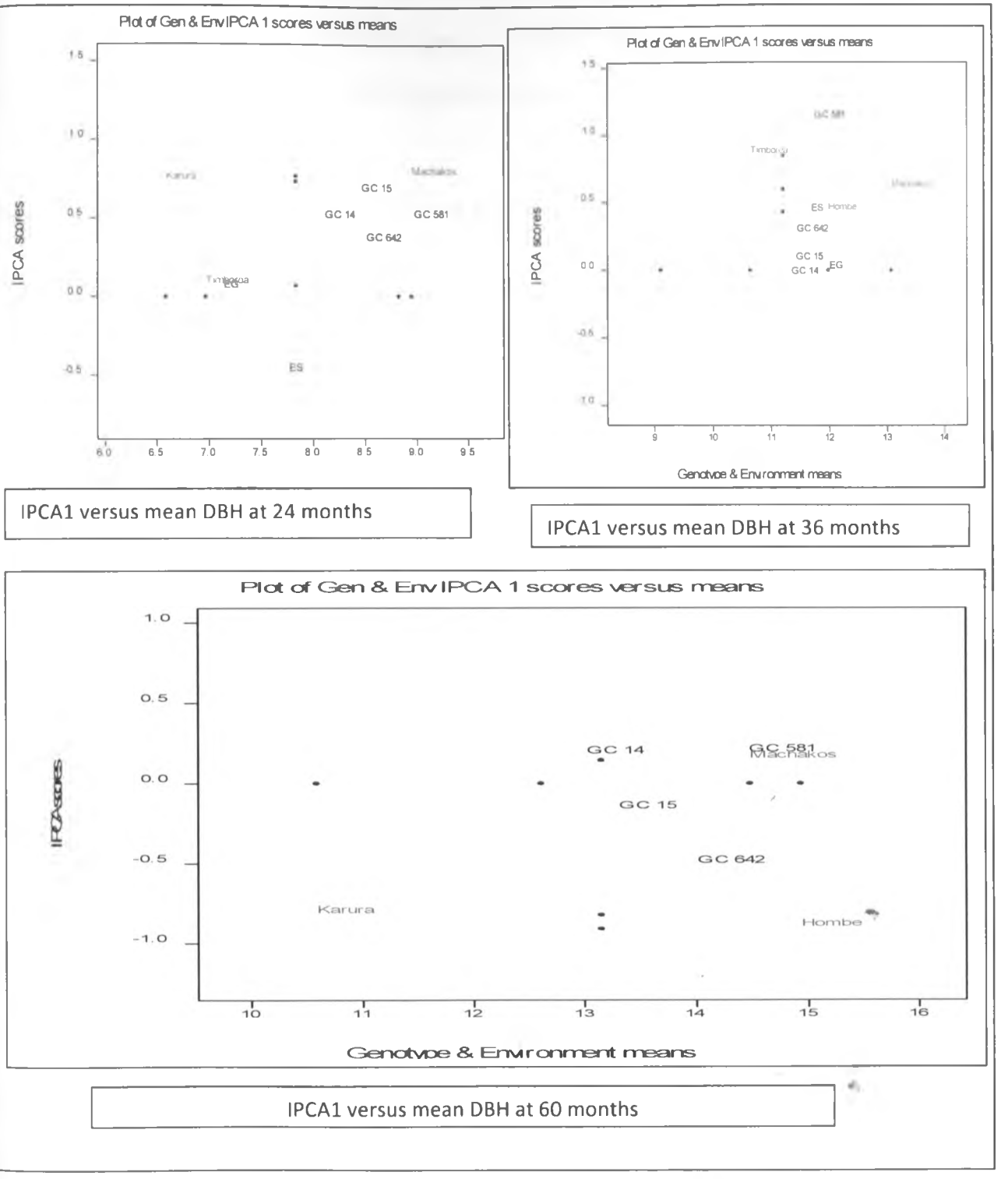
Source	df	DBH AT 24 MONTH(S)			DBH AT 36 MONTH(S)			DBH AT 60 MONTH(S)		
		%SS	MS	F prob	%SS	MS	F_prob	%SS	MS	F_prob
Total	83		3.8	*		7.3	*		11.4	*
Treatments	27	79	9.1	0.00	63	14.3	0.00002	74	25.9	0.00
Genotypes	6	25	13.2	0.000	14	14.2	0.0035	40	62.7	0.00
Environments	3	31	31.7	0.00004	31	61.6	0.00001	27	82.7	0.00
Block	8	8	3.1	0.00112	7	5.6	0.18394	5	5.4	0.27981
Interactions	18	23	3.9	0.00001	19	6.4	0.06865	8	4.2	0.48192
IPCA1	8	55	4.9	0.00003	60	8.6	0.03424	65	6.1	0.20376
IPCA2	6	39	4.7	0.00018	31	5.9	0.17528	31	3.9	0.48485
Residuals	4	6	1.1	0.28802	10	2.8	0.57036	5	0.9	0.93642
Error	48	13	0.8	*	30	3.7	*	22	4.2	*

NB: the block source of variation refers to blocks within environments

There was further evidence of varied location response of eucalyptus hybrid clones and local land races at different sites on the bi-plot graph. For instance GCs 14, 15, 642 and 581 clustered on the first quadrant of the bi-plot with low IPCA1 score indicating close performance at age 24 months at Machakos site (Figure 4.1). Comparatively, local landrace *Eucalyptus saligna* was in third quadrant of the bi-plot implying distinct traits with other hybrid clones on the tested sites. At age of 36 months, ES, EG, GCs 642, 14 and 15 had low IPCA1 within the first quadrant and clustered within Hombe whereas GC 581 had high IPCA1 and was

discriminatory against Timboroa and Machakos. This pointed out varied interaction effect of eucalyptus hybrid clones and local land races among sites across time, hence posing challenges of stability of traits of improved materials. Overall among these genotypes GC581 showed little GxE interaction because of the relatively small distance from the coordinates to the abscissa and was stable at 24, 36 and60 months.

Figure 4.1 Genotype and Environment IPCA 1 Score vs DBH means (cm) highlands biplots



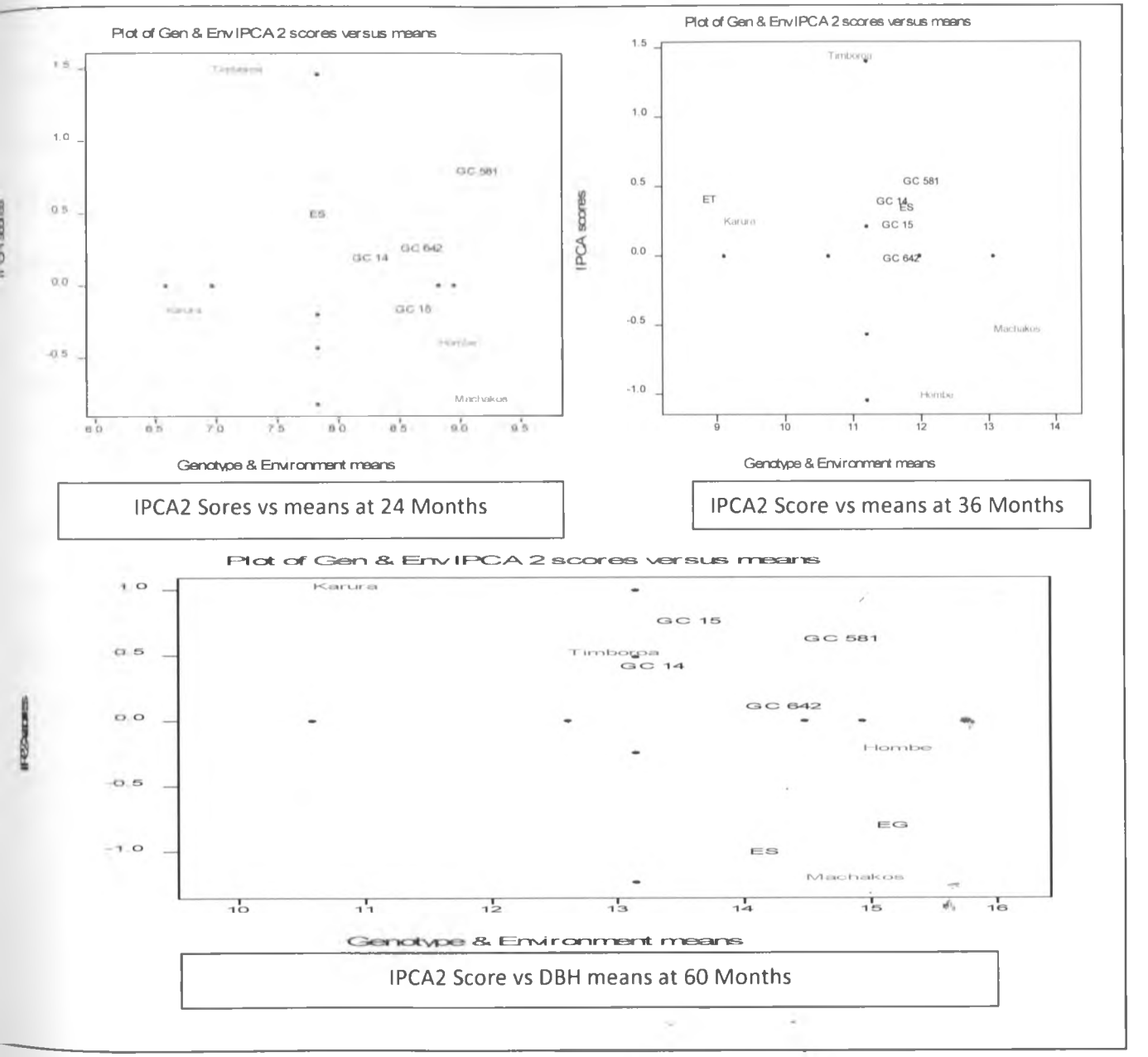
IPCA1 versus mean DBH at 24 months

IPCA1 versus mean DBH at 36 months

IPCA1 versus mean DBH at 60 months

Consequently, the variations on genotype by environment interaction on IPCA2 scores and mean DBH continued to demonstrate large interaction among eucalyptus clones and sites. Further taking IPCA 2 into consideration (Figure 4.2) most of GC's had shown relatively little GxE interaction in terms of both axis and therefore the most stable and high yielding for DBH at 24,36 and 60 months.

Figure 4.2 Genotype and Environment IPCA 2 Score vs highlands DBH means (cm) biplot



4.2.2 Genotype by environment interaction of eucalyptus hybrid clones at Lowland sites

The AMMI analysis of variance of DBH (cm) of the 14 genotypes tested in the three environments showed that 71.1% and 68.2% of the total sum of squares was attributable to environmental effects whereas 15.2% and 26.4% to genotypic effects for the tree DBH at 24 and 36 months respectively. Further, we see that 9.4 % and 12.9% of total sum of squares was attributed to GEI effects for tree DBH at 24 and 36 months respectively (Table 4.2). A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in tree DBH. Results from AMMI analysis also showed that the first principal component axis (PCA 1) of the interaction captured 78.4% and 70.4% of the interaction sum of squares in 53.8% of the interaction degrees of freedom for DBH at 24 and 36 months respectively. Similarly, the second principal component axis (PCA 2) explained a further 21.6% and 29.6% of the GEI sum of squares in 46.2% of interaction degrees of freedom for DBH at 24 and 60 months respectively.

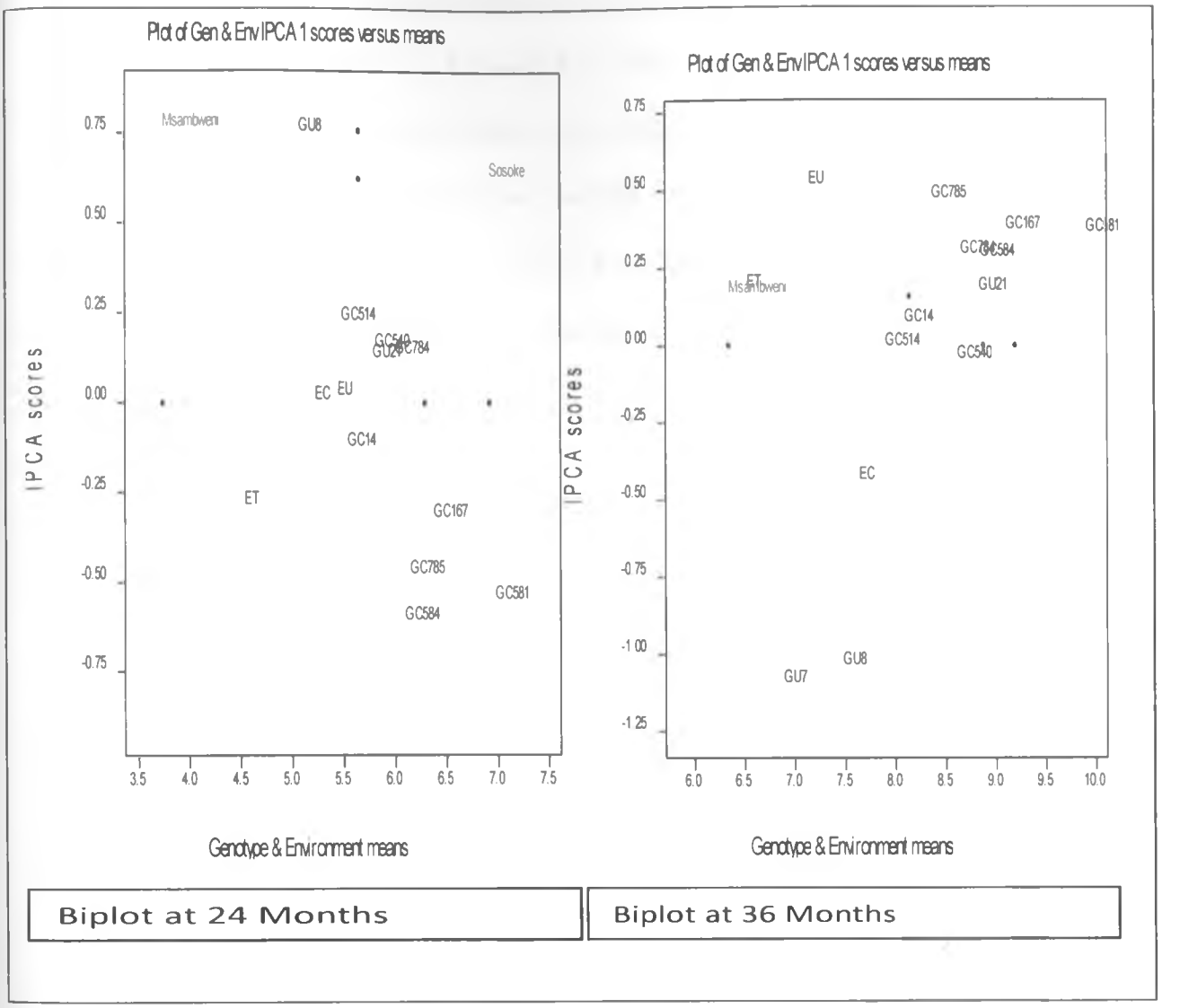
The mean squares for the PCA 1 were significant at $p = 0.01$. Both PCA cumulatively contributed to 100% of the total GEI for height at 24 and 36 months and hence the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (Zobel et al., 1988). This model (AMMI 1 and AMMI 2) had 26 degrees of freedom. Thus, the interaction of the 14 genotypes with three environments was best predicted by the first two principal components of genotypes and environments.

Table 4.2 ANOVA table for AMMI model at ages 24 and 36 Months for Lowlands

Source of variation	df	DBH at 24 Months				DBH at 36 Months				
		SS	%SS	MS	F_prob	SS	%SS	MS	F	F_prob
Total	83	223.7		2.7	*	260.4		3.1	*	*;
Treatments	41	214.1	95	5.2	0	239.2	92	5.8	12	0
Genotypes	13	34	15	2.6	0	68.9	26	5.3	11	0
Environments	2	159	71	79.5	0	136.6	5	68.3	88.5	0
Block	3	1.7	1	0.6	0.05644	2.3	1	0.8	1.6	0.20603
Interactions	26	21	9	0.8	0.00005	33.8	13	1.3	2.7	0.00256
IPCA	14	16.5	78	1.2	0.00001	23.8	70	1.7	3.5	0.00096
IPCA	12	4.6	21	0.4	0.07096	10	30	0.8	1.7	0.09903
Residuals	0	0		*	*	0		*	*	*
Error	39	7.9	4	0.2	*	18.9	7	0.5	*	*

The Genotype by Environment Interaction of eucalyptus clones at lowland across ages revealed further that, genotypes GC581 and GC 167 had highest means at 24 and 36 months respectively (largest PCA 1 scores), and were stable over the sites, due to the fact that they did give small absolute PCA 2 scores. The average yield of genotypes ET, GGC 167,GC 785,GC 584,GC 581 at 24 months and EC, ET, GU7 at 36 Months were below average (PCA 1 scores < 0) and further ET at 24 months and ET,EU, EC at 36 months were highly unstable (large absolute PCA 2 score). Figure (4.3 and 4.4)

Figure 4.3 Biplot of Genotype and Environment IPCA1 scores vs DBH means (cm) at lowlands



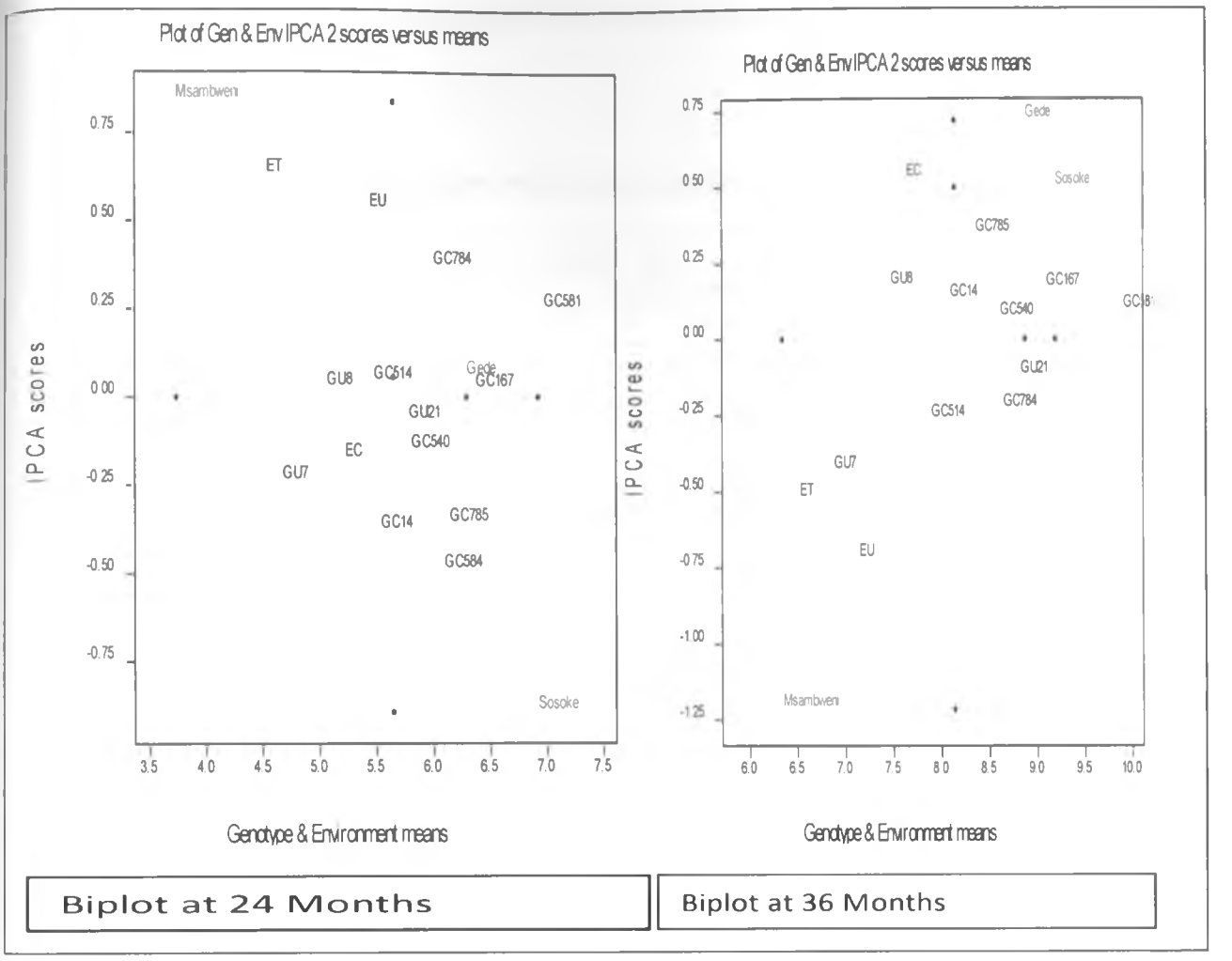
Biplot at 24 Months

Biplot at 36 Months

By plotting both the hybrids and the environments on the same graph, the associations between the hybrids and the environments can be seen clearly. The IPCA scores of a genotype in the AMMI analysis are an indication of the stability of a genotype over environments. The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype to over all environments sampled.

From the bi-plot, environments are distributed from lower yielding environments in quadrants I (top left) and IV (bottom left) to the high yielding environments in quadrants II (top right) and III (bottom right) (Fig.4.3 and 4.4). The high yielding environments classified according to the AMMI model are Gede and Sokoke. The lower yielding environment is Msambweni. Genotypes grouped under low yielding environments are shown at the lower left quadrant of the bi-plot. Generally GU7 and GU 8 are the most unstable genotype identified by the AMMI model (Fig. 4.3).Moreover genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. Genotypes GC514, GU8 GU 21 and GU 167 tend to be similar while ET, GC584, GC785, EC and EU seems to be quite different for both DBH at 36 and 60 months.

Figure 4.4Biplot of Genotype and Environment IPCA2 scores vs DBH (CM)means at lowlands



4.3 Analysis on performance of eucalyptus hybrid clones and local landraces

4.3.1 AMMI analysis on performance of eucalyptus hybrid clones and local landraces at highland environments sites

The Growth assessment of highland eucalyptus clones at different ages across environments revealed varied performance of genotypes across environments. The mean-DBH at 24, 36 and 60 months averaged over genotypes and environments is presented in Table 4.3. The hybrid clones (GCs 14, 15, 581 and 642) performed better in most sites than local landraces (EG,

ES and ET) for DBH at 24 months whereas EG had the highest mean for DBH at 36 and 60 months. We also see varied performance of the genotypes across sites in the different assessment periods.

Table 4.3 Mean DBH growth of genotype means across environments at ages 24, 36 and 60 Months for highland trials

	Genotype means across ages		
Genotype	24 months	36 months	60 months
EG	7.1	12.0	15.0
ES	7.8	11.7	14.0
ET	5.9	8.8	8.2
GC 14	8.1	11.3	13.0
GC 15	8.5	11.4	13.3
GC 581	9.0	11.7	14.5
GC 642	8.5	11.4	14.0

Further assessment of the genotype ranking across environments showed that the eucalyptus clones, GC 15 and EG performed best in Machakos, GC581, ET and EG performed best in Karura,GC581 performed best in Timboroa, ES and EG performed best in Hombe for the DBH at 24, 36 and 60 months respectively (Table 4.4).

Table 4.4: Ranks of the best four genotypes per site on the basis of DBH at ages24, 36 and 60 months across the four environments for highland trials

Environment	DBH at 24 Months				DBH at 36 Months				DBH at 60 Months			
	1	2	3	4	1	2	3	4	1	2	3	4
Machakos	GC 14	GC 15	EG	GC 642	EG	GC 15	GC 642	GC 14	EG	GC 15	GC 14	GC 642
Karura	GC 14	GC 15	GC 642	EG	ET	GC 14	GC 15	EG	GC 14	GC 581	GC 15	GC 642
Timboroa	GC 581	GC 642	GC 14	ES	GC 581	ES	GC 642	GC 15	GC 581	GC 642	GC 15	GC 14
Hombe	ES	GC 642	GC 14	GC 581	GC 642	GC 15	GC 14	GC 581	EG	GC 581	GC 15	ES

The genotype performance across environments and ages shows that GC 581 and GC 642 performed well in most sites at 24, 36 and 60 months. (Table 4.5).

Table 4.5.Highlands Growth performance (DBH) of genotypes among environments across ages

	24 Months				36 Months				60 Months			
Environment	Hombe	Karura	Machakos	Timboroa	Hombe	Karura	Machakos	Timboroa	Hombe	Karura	Machakos	Timboroa
Genotype	AMMI Estimates											
EG	8.7	6.2	9.5	4.1	14.5	9.6	14.8	9.1	18.3	12.8	17.2	11.9
ES	9.3	6.1	8.1	7.5	12.3	8.9	13.6	11.9	15	9.5	16.8	14.9
ET	9.2	3.5	5.8	5	8.4	10.2	9.4	7.2	9.5	5.3	9.5	8.6
GC 14	8.3	7.2	9.5	7.5	11.7	9.4	13.0	11.2	14.6	10.7	13.9	12.9
GC 15	8.5	7.7	10.3	7.3	12	9.3	13.2	11.2	15.1	11.6	13.7	12.8
GC 581	8.9	7.9	9.8	9.3	12.5	7.7	14.0	12.8	15.9	12.3	15.1	14.5
GC 642	8.9	7.5	9.7	8	12.4	8.8	13.5	11	16.2	11.9	15.2	12.7

We also found that the environment mean of pooled DBH for all the genotypes ranged from a low of 6.6 cm at Karura to a high of 8.9 cm at Machakos for DBH at 24 months of age. Similar trend was observed at 36 months where average of 9.1cm was recorded at Karura and a high of 13.1 cm at Machakos and finally at age of 60 months the least average DBH growth was 10.6 cm at Karura and a high of 14.9 cm at Hombe, respectively (Table 4.6).

Table 4.6 Environment means yield of DBH at ages 24, 36 and 60 months for highlands

	Environment means across ages		
Environment	24 months	36 months	60 months
Hombe	8.8	12.0	14.9
Karura	6.6	9.1	10.6
Machakos	8.9	13.1	14.5
Timboroa	7.0	10.6	12.6

The results also showed that eucalyptus local land races and hybrid clones performed better at Machakos and Hombe as compared to Karura and Timboroa environments. Consequently the variation in environmental and genotype means could be attributed to the wide range of environmental conditions primarily resulting from varying amounts of temperature, and rainfall. We also see variation in performance of genotypes from location to location with GC 581 recording the highest for DBH at 24 Months and 36 Months and EG recording the highest at 60 Months.

On assessing the environment variance we see the biggest variance recorded in Timboroa and Machakos for the DBH at 24, 36 and 60 Months respectively (Table 4.7).

Table 4.7 Environment means and variances of genotypes for DBH at ages 24, 36 and 60 months for highlands

Environment	24 months		36 months		60 months	
	Mean	Variance	Mean	Variance	Mean	Variance
Hombe	8.8	1.6	12.0	5.8	14.9	9.1
Karura	6.6	3.0	9.1	2.5	10.6	7.6
Machakos	8.9	2.7	13.1	8.4	14.5	12.4
Timboroa	7.0	3.5	10.6	4.5	12.6	5.9
Margin	7.8	3.8	11.2	7.3	13.15	11.4

4.3.2. AMMI analysis on performance of eucalyptus hybrid clones and local landraces at lowland environments sites

The Genotype and Environment Mean and Scores for DBH at 24 and 36 Months showed varied performance of genotypes across the environments and ages. The mean DBH at 24 and 36 months averaged over genotypes and environments is presented in Table 4.7 and Table 4.8. The genotype means of DBH at the lowland environments ranged from a low of 4. 6 to a high of 7.0 at 24 months, a low of 6.5 and a high of 9.9 at 36 months (Table 4.8).

Table 4.8 Genotype means (DBH) and scores at ages 24 and 36 months for low lands

Genotype	NG	24 Months			36 Months		
		Gm	IPCAg[1]	IPCAg[2]	Gm	IPCAg[1]	IPCAg[2]
EC	1	5.2	0.00091	-0.17624	7.6	-0.44428	0.52484
ET	2	4.5	-0.29216	0.62825	6.5	0.17604	-0.5222
EU	3	5.4	0.0139	0.53161	7.1	0.50767	-0.721
GC14	4	5.5	-0.12859	-0.37883	8.1	0.06449	0.12842
GC167	5	6.4	-0.32873	0.02055	9.1	0.36289	0.16545
GC514	6	5.5	0.22002	0.04202	7.9	-0.01205	-0.26439
GC540	7	5.8	0.14619	-0.15153	8.6	-0.05292	0.06723
GC581	8	7.0	-0.55865	0.24975	9.9	0.35439	0.09251
GC584	9	6.1	-0.61544	-0.49125	8.9	0.27539	0.79952
GC784	10	6.0	0.12766	0.36804	8.7	0.28379	-0.23079
GC785	11	6.1	-0.48608	-0.36003	8.4	0.46275	0.34313
GU21	12	5.8	0.11716	-0.06819	8.8	0.16631	-0.12208
GU7	13	4.7	1.03724	-0.23964	6.9	-1.10171	-0.43228
GU8	14	5.1	0.74656	0.02548	7.5	-1.04277	0.17166

It was further revealed that Sokoke had the highest environmental mean followed by Gede and Msambweni for DBH at 24 months while Sokoke scored the best followed by Gede and finally Msambweni for DBH at 36 months.(Table 4.9).

Table 4.9 Environment means and scores at ages 24 and 36 months at lowlands

Environment	NE	24 Months			36 Months		
		Em	IPCAe[1]	IPCAe[2]	Em	IPCAe[1]	IPCAe[2]
Gede	1	6.3	-1.38111	0.05646	8.9	1.22725	0.71731
Msambweni	2	3.7	0.758	0.83888	6.3	0.15793	-1.21437
Sosoke	3	6.9	0.62311	-0.89534	9.2	-1.38518	0.49707

The result also showed variation in performance of genotypes from location to location with GC 581 recording the highest DBH at both 24 and 36 months. The biggest variance was recorded in Gede for the tree DBH at 24 and 36 months, respectively (Table 4.10).

Table 4.10 Environment means and variances at ages 24 and 36 Months at lowlands

Site	No observed	Mean 24 Months	Variance	Mean 36 Months	Variance
Gede	28	6.3	1.5	8.9	2.4
Msambweni	28	3.7	0.4	6.4	1.0
Sosoke	28	6.9	0.5	9.2	1.2
Margin	84	5.7	2.7	8.1	3.1

The first four genotypes selected in each environment show a variation in selections in each environment across the two assessment ages. However, GC 581 emerges as the best genotype for both ages24 and 36 months in all the environments (Table 4.11)

Table 4.11AMMI first four selections per environment at ages 24 and 36 months at lowlands.

Environment/Genotype Ranks	DBH at 24 Months				DBH at 36 Months			
	1	2	3	4	1	2	3	4
Msambweni	GC581	GC784	GC167	EU	GC581	GU21	GC784	GC167
Sosoke	GC581	GC785	GC584	GC167	GC581	GU8	GC584	GC540
Gede	GC581	GC584	GC167	GC785	GC581	GC584	GC167	GC785

The AMMI estimates per environment revealed that GC 581 was the best genotype in all the three environments for DBH at both 24 and 36 months respectively. The AMMI estimate of each genotype in each of the three environments is as shown in (Table 4.12).

Table 4.12AMMI-estimates per environment at ages 24 and 36 months at lowlands

DBH	24 Months			36 Months		
Environment Genotype	Gede	Msambweni	Sokoke	Gede	Msambweni	Sosoke
	AMMI Estimate					
EC	5.9	3.2	6.7	8.2	5.2	9.6
ET	5.6	2.9	5.1	7.1	5.4	7.1
EU	6.1	4.0	6.2	8.0	6.3	7.1
GC14	6.3	3.2	7.1	9.0	6.1	9.1
GC167	7.5	4.2	7.4	10.4	7.2	9.7
GC514	5.8	3.8	6.8	8.4	6.4	8.8
GC540	6.2	3.9	7.3	9.4	6.7	9.8
GC581	8.4	4.9	7.7	11.1	8.1	10.5
GC584	7.6	3.3	7.4	10.5	6.1	9.9
GC784	6.5	4.5	7.0	9.6	7.2	9.2
GC785	7.4	3.6	7.4	9.9	6.2	8.9
GU21	6.3	3.9	7.2	9.7	7.2	9.6
GU7	3.9	3.4	6.8	6.0	5.4	9.3
GU8	4.7	3.7	6.9	7.1	5.3	10.1

4.4 AMMI analysis on adaptability and stability

4.4. 1 AMMI analysis on adaptability and stability eucalyptus hybrid clones and local landraces at highland

The AMMI stability scores/values (ASV) of genotypes across the three environments comparatively for DBH at 24, 36 and 60 months respectively shows that GC642 was ranked best for DBH at 24months, GC15 at 36 months and GC14 emerged as most stable genotype for DBH at 60 months(Table 4.13)

According to the ASV ranking the most stable clones were GC 642, GC 14 and ES for DBH at 24 months while the most stable clones were GC 15, GC 14 whereas GC 642 for DBH

at 36 months and finally the most stable hybrids were GC 14, GC 581 and GC642 for DBH at 60 months. The most unstable hybrids according to the ASV were EG and ET at 24 months, ET and EG at 36 months and ES and EG for DBH at 60 months showing that the local landraces were generally unstable in highlands.

Table 4.13 Genotypes AMMI Stability Value (ASV) for highlands at ages 24, 36 and 60 Months at lowlands

Genotype	NG	24 Months		36 Months		60 Months	
		ASV	RANK	ASV	RANK	ASV	RANK
EG	1	1.4667	6	1.6660	6	2.1201	7
ES	2	0.8218	3	0.6624	4	1.9592	6
ET	3	2.1213	7	2.5548	7	0.7517	4
GC 14	4	0.6917	2	0.3596	2	0.4471	1
GC 15	5	0.9348	4	0.2029	1	0.7611	5
GC 581	6	1.0194	5	1.6234	5	0.6401	2
GC 642	7	0.5223	1	0.3801	3	0.7149	3

4.4.2 AMMI analysis on adaptability and stability eucalyptus hybrid clones and local landraces at highland and lowland sites

We found out that genotype EC was ranked first at 24 months and GC 540 was ranked as best stable genotype for DBH at 36 months (Table 4.14). The assessment of ASV ranking showed that the most stable clones were EC, GU 21 and EU for DBH at 24 months while the most stable clones were GC 540, GC 514 and GC 14 in a decreasing order, respectively for DHB at 36 months. The most unstable hybrids according to the ASV were GU 7 and GU 8 for DBH at both 24 and 36 months respectively.

Table 4.14AMMI-Stability Value for Lowlands at ages 24 and 36 Months at lowlands

Genotype	NG	24 Months		36 Months	
		ASV	RANK	ASV	RANK
EC	1	0.1763	1	1.6926	10
ET	2	1.2306	9	0.8242	5
EU	3	0.5340	3	1.9751	12
GC14	4	0.6004	6	0.2666	3
GC167	5	1.1908	8	1.3248	9
GC514	6	0.7980	7	0.2680	2
GC540	7	0.5508	4	0.2031	1
GC581	8	2.0388	11	1.2869	8
GC584	9	2.2826	12	1.2783	7
GC784	10	0.5910	5	1.0535	6
GC785	11	1.7970	10	1.7108	11
GU21	12	0.4298	2	0.6146	4
GU7	13	3.7645	14	4.0137	14
GU8	14	2.7041	13	3.7808	13

4.5 Discussion

Genotype by environment interaction (GxE) is widely reported in a number of agricultural trials (Ofversten et al., 2002; Wagoire et al., 1999; Adugna and Labuchagne (2002); Goncalves et al., 2003; Laghari et al., 2003 and Montagnon et al., 2000). In this study, similar principles of GEI for forestry trials were followed as reported by Varelides et al., (2001). Ideally, when many genotypes (hybrid clones) or breeding lines are tested in a sufficiently large environmental range as in the case in this study, GE interaction are of common occurrence. The high significant differences of GE in this study indicate the fluctuations of genotypes to different environments. Therefore, successful genotypes need to be adapted to a broad range of environmental conditions in Kenya in order to ensure their yield stability and economic profitability. Of the eucalyptus hybrid clones experimented across sites GC 14 ,GC 581, and GC

642 were found to be most stable genotypes for the highlands while GC 540 ,GC 514, and GC 14 were found to be most stable genotypes for the lowland environments implying they can be planted in a wide range of environments similar to the one tried. This resolves the complication of tree breeding program, where breeders are particularly interested in searching for fewer widely adapted genotypes.

However, this inhibits the positive assessment of GE interactions where a plant breeder can breed genotypes for specific environment, rather than modifying the environment to fit the new genotypes. Therefore, the best five performing genotypes of eucalypts should be grown on the specified sites and breeding of similar ones need to be encouraged. This argument is in line with Ceccarelli (1989) and Hildebrand (1990) where they stated that in case of unfavourable environment; breeders may look at GE interactions in a different way as sites tend to differ on mean annual rainfall, temperature, soils and altitude among other related environmental factors.

Breeding for a specific adaptation not only offers a solution on how to improve eucalyptus productivity in marginal environments, but also how they can be sustained. This implies a re-evaluation of the role of genetic resources such as landraces which can play an important role because they possess adaptive features to these environments. For example, *E. grandis* which is commonly grown in Kenyan highlands has doubled its productivity from $20m^3ha^{-1}yr^{-1}$ to $70m^3ha^{-1}yr^{-1}$ through breeding programme (Oballa and Giathi, 1996). Overall, the problem of transfer and adoption of new genotypes can be possibly solved by extreme use of a positive attitude towards GEI's. This can be achieved through farmers' participation in the selection of genotypes under their own conditions. This idea is not new as it was introduced by Rhoades and Booth (1982) and later modified by Chambers and Ghildyal (1985) from "the

farmer-back-to farmer model'' into "farmer first-and –last- model'' and more recently it has been discussed by Sperling *et al.* (1993).

The process has been very effective for those farming systems which are sufficiently similar or not too dissimilar from those experimental stations. Thus any formal plant breeding program could combine the concept of a positive use of GEI's with utilization of farmers' knowledge by evaluating a wide range of germplasm under farmers' field conditions and in conjunction with farmers. This can be easily achieved under the current strategy where Tree Biotechnology Programme (TBP) is distributing seedlings across the country to individual farmers, corporate bodies and organized groups. There is therefore a need of follow-up for growth assessment and other relevant measurements that can adequately explain GE interactions.

CHAPTERFIVE: CONCLUSIONS AND RECOMMENDATIONS

The stable genotypes GC 14, GC 581 and GC 642 for high lands and GC 540, GC 514 and GC 14 for lowland environments across range of study sites need further investigations on similar sites and breeding for specific adaptation of clones on the trial regions covered in this study. However, there is a need to propose suitable response parameters in assessing GE to effectively characterize their stability across the sites. The use of height and diameter sometimes provides different results. There is therefore need to use a combination of the two parameters to derive volume for assessing GE interactions. Equally, there is need to carry out further studies on performance and adaptability of eucalyptus clones to strengthen the use of broad mix of methods to characterise GE interactions and be able to recommend clones with maximum yield production.

It can be concluded that genotype by environment interaction was significant establishment with GC14 and GC 540 being the most stable across the highland and lowland environments, respectively. This can be assessed over time to see whether the stability remains the same throughout to enable tree breeders for rightful recommendation to the users. Other GCs that were equally stable included GC581, and GC 642, GC514, GC14 and GU21.The eucalyptus clones, GC 15 and EG performed best in Machakos, GC581, ET and EG performed best in Karura, GC581 performed best in Timboroa, ES and EG performed best in Hombe for the DBH at 24, 36 and 60 months respectively for the highland.The growth performance of genotypes among highland environments across ages shows that GC 581 and GC 642 performed well in most sites at 24, 36 and 60 months respectively.The species GC581 performed best in all sites for DBH at both 24 and 36 months for the lowland environments. These genotypes might be recommended for planting on sites with almost similar environmental characteristics.

The AMMI and ASV were found useful in describing genotype by environment interaction of various hybrid clones; for better description and prediction, the environmental variables have to be adequately measured and analysed along with the data from the genotypes. The selection process of good performing and stable genotypes is mainly complicated by the phenomenon of genotype by environment GEI; a differential genotypic expression across environments or generally the inconsistency of relative performance of genotypes over environments. The large occurrence of GEI's causes the relative rankings of genotypes to change from location to location and/or from year to year. Hence, it is imperative to have a proper understanding of the effects of G x E interactions on variety evaluation, which will help to apply appropriate analytical methods and wise utilisation of resources.

The interaction was best predicted by the first two principal components of genotypes and environments. Consequently, bi-plots generated using genotypic and environmental scores of the first two AMMI components can help breeders have an overall picture of the behavior of the genotypes, the environments and GEIs. The AMMI model proves to be an effective and efficient tool to characterize the GEI and analyze the genotype performance over various environments with efficient utilization of resources during experimentation.

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