YIELD STABILITY AND MEGA ENVIRONMENT ANALYSIS BASED ON THE PERFORMANCE OF QUALITY PROTEIN MAIZE IN SUB-SAHARAN AFRICA

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By

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DECLARATION

I, the undersigned, hereby declare that this thesis, prepared for the degree of Philosophiae Doctor in Agriculture which was submitted by me to the University of the Free State, is my original work and has not been submitted previously to any other University/Faculty. All sources of materials and financial assistances used for the study have been duly acknowledged. I further cede copyright of the thesis in favour of the University of the Free State.

AbduRahman Beshir Issa 30/06/2013

DEDICATION

This piece of work is dedicated to my late father Beshir Issa and my late mother Rukiya Abdo, both would have loved to see this work. May their soul rest in eternal peace!

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LIST OF ABBREVIATIONS AND SYMBOLS

AD	Anthesis date
AEA	Average environment axis
AEC	Average environment coordinate
AMMI	Additive main effects and multiplicative interactive model
ANOVA	Analysis of variance
ASI	Anthesis-silking interval
ASV	AMMI stability value
ATA	Average tester axis
ATC	Average tester coordinate
AWAOP	Awassa optimum environment
BAKOP	Bako optimum environment
BAKLN	Bako low-N stress environment
bi	Regression coefficient
Ca	Calcium
Cap	Capita
CHIDT	Chiredzi drought stress environment
CHSDT	Chisumbanje drought stress environment
CIMMYT	International Maize and Wheat Improvement Centre
CML	CIMMYT maize line
CV`	Coefficient of variation
Cu	Copper
DA	Days to anthesis
DF	Degrees of freedom
DRC	Democratic Republic of Congo
ECA	Eastern and Central Africa
EMBOP	Embu optimum environment
Env	Environment
ESA	Eastern and Southern Africa
FAO	Food and Agricultural Organization
Fig	Figure
fl2	Floury-2 allele

g	Grams
G x E	Genotype by environment interaction
GGE	Genotype and genotype by environment interaction
GLM	General linear model
GW	Grain weight
ha	Hectare
HRELN	Harare low-N stress environment
HREOP	Harare optimum environment
ID	Identification
IFPRI	International Food Policy Research Institute
IITA	International Institute of Tropical Agriculture
IPCA	Interaction principal component axis
JLR	Joint linear regression
KAKOP	Kakamega optimum environment
KARI	Kenyan Agricultural Research Institute
KBODT	Kiboko drought stress environment
K	Potassium
Kg	Kilogram
log	Logarithm
Low-N	Low nitrogen
LSD	Least significant difference
M	Million
Max	Maximum
METs	Multi environment trials
Mg	Magnesium
Min	Minimum
Mn	Manganese
MLKOP	Melkassa optimum environment
MS	Mean square
MSEs	Managed stress environments
N	Nitrogen
NARS	National Agricultural Research Systems
NCSS	Number cruncher statistical software

o2	Opaque-2 allele
OPV	Open pollinated variety
P	Phosphorous
PC	Principal component
PCA	Principal component analysis
Pi	Lin and Binns cultivar superiority measure
PROC	Procedure
QI	Protein Quality index
QPM	Quality protein maize
RATOP	Ratray Arnold optimum environment
Rep	Replication
S^2di	Deviation mean square
SADC	Southern Africa Development Community
SARI	Selian Agricultural Research Institute
SAS	Statistical Analysis Software
SDS-PAGE	Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis
SREG	Sites Regression
SS	Sum of square
SSA	Sub-Saharan Africa
SVD	Singular value decomposition
SVP	Singular value partitioning
t	Ton
t ha $^{-1}$	Ton per hectare
TRP	Tryptophan
UN	United Nation
UNDP	United Nation Development Program
UPGMA	Unweighted Pair Group Method with Arithmetic Mean
US	United States
USA	United States of America
USD	United States Dollar
Wi	Ecovalence of Wricke
YS_i	Yield stability statistic
Zn	Zinc

σ^2_i	Shukla's stability variance
%	percent
®	Registered
^{0}C	Degree Celsius
2D	Two dimensional

CHAPTER 1
General introduction

Maize (*Zea mays* L.), also known as corn, is one of the world's leading cereal crops along with rice (*Oryza sativa* L.) and wheat (*Triticum aestivum* L.). Data from the United Nations (UN) Food and Agriculture Organization (FAO) showed that in 2010 world maize production was over 840 million metric ton, with the United States and China as the leading producers. The world maize area during 2010 was 161 million hectares of which Africa's share was about 31 million ha, comprising 19.3% of the world's maize area. However, the production share of Africa was 64 million metric ton or about 7% of the world production (FAOSTAT, 2010). The low average yield per unit area is the main reason why Africa's share of global maize production is so small (Heisey and Edmeades, 1999; Pingali and Pandey, 2001). According to the study by the International Maize and Wheat Improvement Centre (CIMMYT), the demand for maize in developing countries will exceed that of wheat and rice by the year 2020. Furthermore, between the periods 1995 and 2020 global and sub-Saharan Africa (SSA) maize consumption is projected to increase by 50% and 93% respectively (CIMMYT, 2001), indicating the importance of the crop both in Africa and the world.

Maize's attractiveness as a staple crop is largely due to its diverse role as a food source for both humans and animals. Kernels can be consumed off the cob, parched, boiled, fried, roasted, ground and fermented for use in bread, porridges, gruels, cakes and alcoholic beverages. Further processing leads to its use as food thickeners, sweeteners, oils and non-consumables (Inglett, 1970; Gardner and Inglett, 1971; Alexander, 1987). Maize, a dietary staple for more than 200 million people, is providing an estimated 15% of the world's protein and 20% of the world's calories (Brown et al., 1988; NRC, 1988). This number can be expected to grow as the world's population approaches 8 billion in 2025 (Lutz et al., 2001; USDA, 2009; Emily and Sherry, 2010), indicating maize's status as an important crop in global nutrition.

Maize is also the most important cereal food crop in SSA, particularly in eastern and southern Africa (ESA) where it accounts for 53% of the total cereal area (FAOSTAT, 2010) and 30-70% of total caloric consumption (Langyintuo et al., 2010). Consumption of maize is high throughout most of the region, reflecting its role as the primary food staple (Hassan et al., 2001; Diallo et al., 2004; Bänziger and Diallo, 2004; Smalberger and du Toit, 2004). The

annual per capita consumption of maize is high in southern African countries compared to the rest of the continent. It ranges from 138 kg in Swaziland to 195 kg in South Africa (CIMMYT, 1999). In eastern Africa, per capita annual consumption ranges from 40 kg in Burundi to 105 kg in Kenya (Hassan et al., 2001). Maize in Africa is grown by small and medium-scale farmers who cultivate 10 ha or less (DeVries and Toenniessen, 2001) under extremely low-input systems where average maize yields are 1.3 ton per ha (Bänziger and Diallo, 2004). In SSA countries there is a wide gap between maize consumption and production. The mismatch of demand and supply is mitigated by importation of about three million ton of maize annually (Pingali and Pandey, 2001; FAOSTAT, 2008). Use of improved varieties and good management practices can increase maize yields and reduce imports in these countries (Heisey and Edmeades, 1999; Reeves et al., 1999; Pingali and Pandey, 2001).

Unlike in the developed world where maize is produced mainly for animal feed, human consumption of maize in SSA is estimated to be around 70% (Aquino et al., 2001). Research indicates that 20% of global food calories and 15% of all food-crop protein is provided by maize (Brown et al., 1988; NRC, 1988). However, the protein quality of normal maize and most cereals is poor as it lacks the essential amino acids, lysine and tryptophan (Bhatia and Rabson, 1987). The deficiency of the essential amino acids in normal maize causes serious protein malnutrition and associated problems for people with high protein requirements, e.g., young children, pregnant or lactating women, and the ill in communities where maize is a dietary staple and often a major source of protein (Pixley and Bjarnason, 2002). In SSA where maize farming system is dominant, the malnutrition rate particularly for pre-school children is reported to be high. Hyman et al. (2008) reported that the prevalence of stunting is over 40% in areas where maize is a dominant diet. In addition, the proportion of poor people (who live on USD 2 per day or less) in the maize farming communities of SSA is about 65% (Wood et al., 2010) which implies that protein sources like meat, milk and eggs are unaffordable.

The study to improve the nutritional quality of normal maize begun almost a century ago (Osborne and Mendel, 1914). The protein of a matured maize kernel is principally stored in the endosperm and the germ. However, the protein in the germ is superior in both quality and quantity as compared to the endosperm protein which is not only low in quantity but also it is of poor quality. The relative amounts of protein contributed by the endosperm and germ vary

and are dependent on the type of maize, genotype, texture and size. In most field maize, the endosperm accounts for 80 to 85%, while the embryo accounts for about 8 to 10% of the total kernel dry weight (Zuber and Darrah, 1987). The endosperm contains a high proportion of prolamine fraction (zein in maize) which is low in lysine, containing only 0.1g $100g^{-1}$ of protein and the other amino acids. Tryptophan is also low in zein. The high proportion of the zein fraction is the principal cause of poor protein quality in maize. Hence, reducing the zein fraction will result in a proportional increase of other non-zein fractions which are higher in lysine and tryptophan (Vasal, 2001).

The discovery of mutant alleles in maize in the mid 1960's by researchers of the Purdue University was the major breakthrough in enhancing the nutritional quality of maize. The biochemical effects of these mutant alleles, the first discovered was *opaque-2* (*o2*) (Mertz et al., 1964) followed by *floury-2* (*fl2*) (Nelson et al., 1965), were found to cause changes in the amino acid profile and composition of maize endosperm protein and resulted in twofold increase in the levels of lysine and tryptophan compared to normal maize. The biological value of normal maize is about 40% that of milk (Bressani, 1991). However, the increase in lysine content in the endosperm protein had doubled the biological value of the *o2* maize protein and this increase in protein quality was due to increase in the ratio of non-zein to zein proteins (Gibbon and Larkins, 2005). The reduction of the zein fraction in *o2* maize further reduced the leucine content of the endosperm which was found to be beneficial as it caused the leucine-isoleucine ratio to be more balanced and helped in liberating more tryptophan for niacin biosynthesis (Bjarnason and Vasal, 1992).

Although the discovery of mutant alleles in maize improved the nutritional quality of maize and excited many researchers, the undesirable agronomic characters associated with the *o2* maize hindered progress. The pleiotropic effects of the *o2* gene manifested in the form of soft endosperm, low kernel weight, increased susceptibility to insect-pests and fungal diseases, inferior food processing and most importantly reduction in grain yield, discouraged its acceptance (Bjarnason and Vasal, 1992). However, scientists at CIMMYT used various breeding techniques to convert several maize populations to *o2* and subsequently to modify the undesirable traits associated with the mutation (NRC, 1988; Bjarnason and Vasal, 1992; Villegas et al., 1992). The continued work at CIMMYT in the 1970's and 80's resulted in the identification of maize cultivars with superior protein quality, similar to *o2* maize, but resembling normal-endosperm maize both phenotypically and agronomically. Hence,

CIMMYT scientists named this maize Quality Protein Maize (QPM) (CIMMYT, 1972; Vasal et al., 1980).

In most cases farmers in SSA, grow maize under conditions that differ in input application and crop husbandry from researcher managed plots. Several biotic and abiotic factors limit maize production and productivity across countries in SSA (Badu-Apraku et al., 2003). Biotic factors limiting maize production in the region include insect pests, diseases, and parasitic weeds. The major abiotic factors limiting maize production in ESA are low soil fertility and drought, and these are among the most important challenges of maize production, food security and economic growth in ESA (CIMMYT, 2003; Bänziger and Diallo, 2004). Bänziger and Lafitte (1997) reported low level of nitrogen (N) in soils as a major yield limiting factor often found in farmers' fields in the tropics where fertilizer is not commonly used and organic matter is rapidly mineralised. The majority of farmers in the tropics produce maize under rain-fed conditions and are vulnerable to drought. Although drought at any stage of crop growth and development affects production, the greatest impact occurs around flowering (Edmeades et al., 1992). The incidence of moisture stress in maize farming is predicted to increase partly due to climate change and displacement of maize to marginal environments by high value crops (Bänziger et al., 2000). The adoption of cultivars that utilise N more efficiently as well as tolerate the recurrent droughts facing the region will mitigate the challenges of abiotic stresses in maize (Diallo et al., 2003).

Plant 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 complicates the testing and selection of genotypes for broad adaptation in breeding programmes. The phenotype of an organism is determined by the combined effect of the environment and the genotype which interact with one another. Several 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 G x E system could have a large impact on plant breeding (Magari and Kang, 1993; Basford and Cooper, 1998). G x E interaction occurs most often when genotypes are evaluated across environments (Becker and Leon, 1988; Magari, 1989; Kang, 1990) and complicates the selection of superior genotypes across environments due to changes in ranks. Magari and Kang (1993) found that the contribution of different environmental factors to the yield stability of maize in multi-location trials, had a significant impact on the heterogeneity

of the results. The effects of G x E are more apparent in multi environment trials (METs) that have three main objectives: a) to precisely estimate and forecast yield levels based on experimental data; b) to determine yield stability and adaptation of genotypes across environments; and c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990).

The current focus of QPM research in SSA is on the development and deployment of high yielding hybrids and open pollinated varieties (OPVs) for communities with a high malnutrition rate and where maize is a dietary staple. However, the diverse environmental conditions in SSA make the development of widely adapted, high yielding and stable QPM cultivars a challenging activity. Stability in common usage denotes consistency in performance that would mean minimum variation among environments for a particular genotype (Chahal and Gosal, 2002). The presence of high G x E interaction necessitates the systematic grouping of the maize growing environments of SSA into useful mega-environments. The grouping of mega- environments will facilitate germplasm exchange and help to predict cultivar performance in similar mega-environments.

The evaluation of QPM cultivars under diverse environments (drought, low N stress and optimum) for grain yield and other agronomic traits will improve the adaptation of QPM varieties in SSA. Unlike normal maize where such studies are many, the information on the grain yield performance of QPM cultivars of both hybrids and OPVs under stress and non stress conditions in SSA is limited. Since the target environments of breeding programmes in SSA include low input and marginal farming environments, QPM germplasm developed for these environments should have a better or comparable yield than normal maize for wider adoption by farmers. Therefore, identification of competitive QPM cultivars will enhance the adoption of QPM in SSA and contribute reduction of malnutrition. The maize growing environments of SSA are very diverse and the classification of these environments into similar mega-environments will facilitate germplasm exchange among environments and predict performance of cultivars for wider environments, which is an effective approach to reduce cost of METs. However, studies on the grouping of mega-environments based on grain yield performance of QPM in SSA are limited thus hindering wide adoption of QPM.

In this study, the grain yield performance and stability of newly developed early maturing QPM hybrids were investigated based on parametric and non-parametric stability measures.

The QPM hybrids were also evaluated for their adaptation pattern and G x E interaction based on multivariate analysis. In addition, mega-environments were identified for future germplasm testing. Furthermore, early maturing QPM OPVs were evaluated in eastern and central Africa (ECA) for grain yield performance and days to anthesis which helped to identify widely adapted QPM cultivars for the region. This study also addressed the level of grain yield reduction of QPM OPVs due to seed recycling. Specific objectives of this study were to:

(i) evaluate the grain yield performance and stability of newly developed early maturing QPM hybrids under stress and non stress environments of ESA based on various stability measures,
(ii) analyse mega-environments of SSA based on the primary and secondary traits of QPM,
(iii) assess the adaptation pattern of QPM in SSA based on multivariate analysis techniques,
(iv) identify and recommend best performing and widely adapted early maturing QPM OPVs for large scale production in the region,
(v) enhance the role of QPM in combating protein energy malnutrition and attendant diseases in SSA.

1.1 References

Alexander, R.J. 1987. Corn dry milling: processes, products, and applications. In: S.A. Watson, S.A and P.E. Ramstad (Eds.). Corn: chemistry and technology. American Association of Cereal Chemists, St. Paul, Minnesota. pp. 351–376.

Aquino, P., F. Carrion, R. Calvo, and D. Flores. 2001. Selected maize statistics. In: P.L. Pingali (Ed.). CIMMYT 1999-2000 World Maize Facts and Trends. Meeting world maize needs: Technological opportunities and priorities for the public sector. CIMMYT, Mexico, D.F.

Badu-Apraku, B., F.J. Abamu, A. Menkir, M.A.B. Fakorede, K.Obeng-Antwi, and C. The. 2003. Genotype by environment interactions in the regional early maize variety trials in west and central Africa. *Maydica* 48:93-104.

Bänziger, M., and H.R. Lafitte. 1997. Efficiency of secondary traits for improving maize for low-nitrogen target environments. *Crop Science* 37:1110-1117.

Bänziger, M., and A.O. Diallo. 2004. Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference.5-11 February 2002. CIMMYT/KARI Nairobi, Kenya. pp.189-194.

Bänziger, M., G.O. Edmeades, D. Beck, and M. Bellon. 2000. Breeding for Drought and N Stress Tolerance in Maize: From Theory to Practice. CIMMYT, Mexico, D.F.

Basford, K.E., and M. Cooper. 1998. Genotype-by-environment interactions and some considerations of their implications for wheat breeding in Australia. *Australian Journal of Agricultural Research* 49:153-174.

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

Bhatia, C.R., and R. Rabson. 1987. Relationship of grain yield and nutritional quality. In: R.A. Olson and K.J. Frey (Eds.). Nutritional Quality of Cereal Grains: Genetic and Agronomic Improvement. Agronomy Monograph No. 28. ASA, CSSA, and SSSA, Madison, Wisconsin, USA. pp. 11-43.

Bjarnason, M., and S.K. Vasal. 1992. Breeding of quality protein maize (QPM). *Plant Breeding Review* 9:181-216.

Bressani, R. 1991. Protein quality of high lysine maize for humans. *Cereal Foods World* 36:806-811.

Brown, W.L., R. Bressani, D.V. Glover, A.R. Hallauer, V.A. Johnson, and C.O. Qualset. 1988. Quality-protein maize: report of an ad hoc panel of the advisory committee on technology innovation, Board on Science and Technology for International Development, National Research Council, in cooperation with the Board on Agriculture, National Research Council. National Academy Press, Washington, D.C.

Chahal, G.S., and S.S. Gosal. 2002. Principles and procedures of plant breeding: Biotechnological and Conventional approaches. Narosa Publishing House, New Delhi, India.

CIMMYT. 1972. CIMMYT annual report 1970 -1971 Mexico, D. F.

CIMMYT. 1999. 1997/98 CIMMYT World Maize Facts and Trends. Maize Production in Drought Stressed Environments: Technical Options and Research Resource Allocation. CIMMYT, Mexico D.F.

CIMMYT. 2001. 2000/2001 World maize facts and trends. Mexico D.F.

CIMMYT. 2003. Innovation for Development: Annual Report 2002-2003. CIMMYT, Mexico D.F.

Crossa, J. 1990. Statistical analyses of multilocation trials. *Advances in Agronomy* 44:55-85.

DeVries, J., and G. Toenniessen. 2001. Securing the Harvest: Biotechnology, Breeding and Seed Systems for African Crops. CABI Publishing, Wallingford, UK.

Diallo, A.O., W. Muasya, and H. de Groote. 2003. Combining ability of early maize inbred lines and yield responses of their single cross hybrids tested under drought, low N and optimum conditions In: Book of Abstracts: Arnel R. Hallauer International Symposium on Plant Breeding. 17-22 August 2003, CIMMYT, Mexico D.F. pp. 36-37.

Diallo, A.O., J. Kikafunda, L. Welde, O. Odongo, Z.O. Mduruma, W.S. Chivatsi, D.K.Friesen, S. Mugo, and M. Bänziger. 2004. Drought and low nitrogen tolerant hybrids for the moist mid altitude ecology of eastern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 206-212.

Edmeades, G.O., J. Bolaños, and H.R. Lafitte. 1992. Progress in breeding for drought tolerance in maize. In: D. Wilkinson (Eds.). Proceedings of the 47th Annual Corn and Sorghum Industrial Research Conference. ASTA, Washington, D.C., USA. pp. 93-111.

Emily, T.N., and A.T. Sherry. 2010. Maize: A Paramount Staple Crop in the Context of Global Nutrition. *Comprehensive Reviews in Food Science and Food Safety* 9:417-436.

FAOSTAT. 2008. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org (accessed November, 2012).

FAOSTAT. 2010. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org (accessed November, 2012).

Gardner, H.W., and G.E. Inglett. 1971. Food products from corn germ: enzyme activity and oil stability. *Journal of Food Science* 36:645-648.

Gibbon, B.C., and B.A. Larkins. 2005. Molecular genetic approaches to developing quality protein maize. *Trends in Genetics* 21:227-233.

Hassan, R.M., M. Mekuria, and W. Mwangi. 2001. Maize breeding research in eastern and southern Africa: Current status and impacts of past investments made by public and private sectors 1966-1997. CIMMYT, Mexico D.F.

Heisey, P.W., and G.O. Edmeades. 1999. Maize production in drought stressed environments:Technical options and research resource allocation. CIMMYT 1997/98 World Maize Facts and Trends. CIMMYT, Mexico, D. F.

Hyman, G., S. Fujisaka, P. Jones, S. Wood, C. de Vincente, and J. Dixon. 2008. Strategic approaches to targeting technology generation: Assessing the coincidence of poverty and drought-prone crop production. *Agricultural Systems* 98:50–61.

Inglett, G.E. 1970. Food uses of corn around the world. In: G.E. Inglett (Ed). Corn: culture, processing, products. Avi Publishing, Westport Conn. pp. 138–150.

Kang, M.S. 1990. Genotype-by-environment interaction and plant breeding. Louisiana State University, Baton Rouge, LA, USA.

Langyintuo, A.S., W. Mwangi, A.O. Diallo, J. MacRobert, J. Dixon, and M. Bänziger. 2010. Challenges of the maize seed industry in eastern and southern Africa: A compelling case for private-public intervention to promote growth. *Food Policy* 35:323-331.

Lutz, W., W. Sanderson, and S. Scherbov. 2001. The end of world population growth. *Nature* 412:543-545.

Magari, R. 1989. Stability of some Albanian maize local varieties and hybrids (in Albania). *Bull. Agric. Sci.* 4:123-129.

Magari, R., and M.S. Kang. 1993. Genotype selection via a new yield-stability statistics in maize yield trials. *Euphytica* 70:105-111.

Mertz, E.T., L.S. Bates, and O.E. Nelson. 1964. Mutant gene that changes protein composition and increase lysine content of maize endosperm. *Science* 145:279-280.

Nelson, O.E., E.T. Mertz, and L.S. Bates. 1965. Second mutant gene affecting the amino acid pattern of maize endosperm proteins. *Science* 150:149-170.

NRC. 1988. Quality Protein Maize. National Research Council. National Academic Press, Washington, DC.

Osborne, T.B., and L.B. Mendel. 1914. Nutritive properties of maize kernel. *Journal of Biological Chemistry* 18:1-16.

Pingali, P.L., and S. Pandey. 2001. Meeting world maize needs: Technological opportunities and priorities for public sector. CIMMYT 1999/2000 World Maize Facts and Trends, CIMMYT, Mexico, D. F.

Pixley, K.V., and M.S. Bjarnason. 2002. Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42:1882-1890.

Reeves, T., P. Pinstrup-Andersen, and R. Pandia-Lorch. 1999. Food security and the role of agricultural research. In: J.G. Coors and S. Pandey (Eds.). The Genetics and Exploitation of Heterosis in Crops. ASA, CSSA, and SSSA, Madison, Wisconsin. pp.1-5.

Smalberger, S., and A.S. du Toit. 2004. Identification of maize cultivars tolerant to low soil fertility in south Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 202-205.

USDA. 2009. National nutrient database for standard reference. [Online]. Available by United States Department of Agriculture http://www.nal.usda.gov/fnic/foodcomp/search/. (accessed November, 2012).

Vasal, S.K. 2001. High quality protein corn. In: A. R. Hallauer (Ed.). Speciality Corns. 2nd ed. CRC Press, Washington, D.C., USA. pp. 85–129.

Vasal, S.K., E. Villegas, M. Bjarnason, B. Gelaw, and P. Goertz. 1980. Genetic modifiers and breeding strategies in developing hard endosperm opaque-2 materials. In: W.G. Pollmer and R.H. Phipps (Eds.). Improvement of quality traits of maize for grain and silage use. Nijhoff, The Hague, Netherlands. pp. 37–71.

Villegas, E., S.K. Vasal, and M. Bjarnason. 1992. Quality protein maize – What is it and how was it developed. In: E. T Mertz (Ed.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minnesota, USA. pp. 27-48.

Wood, S., G. Hyman, U. Deichmann, E. Barona, R. Tenorio, Z. Guo, S. Castano, O. Rivera, E. Diaz, and J. Marin. 2010. Sub-national poverty maps for the developing world using international poverty lines: Preliminary data release. [Online] http://povertymap.info.

Zuber, M.S., and L.L. Darrah. 1987. Breeding, genetics and seed corn production. In: A.W., Stanley, and E.R. Paul, (Eds.).Corn Chemistry and Technology. American Association of Cereal Chemists, St. Paul, Minnesota, USA.

CHAPTER 2

Literature review

2.1 Maize production and uses

Globally, maize (*Zea mays* L.) is among the leading cereals in production along with rice and wheat. World's maize production exceeds 840 million metric ton from an area of 161 million ha with the United States and China being the top producers. Based on the data from the UN-FAO, Africa's share for world's maize area was about 31 million ha during 2010 (FAOSTAT, 2010). The low contribution of Africa to world's maize production is mainly due to the low average yield per unit area (Heisey and Edmeades, 1999; Pingali and Pandey, 2001). Based on a study by CIMMYT, maize's worldwide demand is forecasted to increase by 50% and in SSA it will increase by 93% by the year 2020 from its base year 1995. The forecasted increase for SSA is mainly for human consumption (CIMMYT, 2001).

The diverse uses of maize in food and feed as well as its industrial products allow the crop to be utilised extensively for both human and animal consumption (Inglett, 1970; Whistler, 1970; Gardner and Inglett, 1971; Alexander, 1987). Maize, providing an estimated 15% of the world's protein and 20% of the world's calories (Brown et al., 1988; NRC, 1988), is a dietary staple for more than 200 million people. This number can be expected to grow as the world's population approaches 8 billion in 2025 (Lutz et al., 2001; USDA, 2009; Emily and Sherry, 2010), indicating maize's status as an important crop in the context of global nutrition.

Based on the FAO data, maize accounts for 53% of the total cereal area in ESA (FAOSTAT, 2010) and 30-70% of total caloric consumption (Langyintuo et al., 2010). Maize is the primary food staple in most parts of SSA with the highest annual per capita consumption in southern Africa followed by eastern Africa (Hassan et al., 2001; Diallo et al., 2004; Bänziger and Diallo, 2004; Smalberger and du Toit, 2004). The annual per capita consumption of maize in southern Africa ranges from 138 kg in Swaziland to 195 kg in South Africa (CIMMYT, 1999), while in eastern Africa it ranges from 40 kg in Burundi to 105 kg in Kenya (Hassan et al., 2001). Maize in Africa is grown by small- and medium-scale farmers who cultivate 10 ha or less (DeVries and Toenniessen, 2001) under extremely low-input

systems with average maize yields at 1.3 t ha^{-1} (Bänziger and Diallo, 2004). SSA countries do not produce enough maize to meet their needs and must therefore import approximately three million tons of maize annually (Pingali and Pandey, 2001; FAOSTAT, 2008). South Africa leads the continent's maize production followed by Nigeria (Table 2.1). The productivity of maize in Africa is less than the global average which is currently 5.2 t ha^{-1}. The exception is Egypt where the farming system is supported by irrigation (FAOSTAT, 2010). Use of improved cultivars and management practices should help increase maize productivity and reduce imports in Africa (Heisey and Edmeades, 1999; Reeves et al., 1999; Pingali and Pandey, 2001).

Table 2.1: The top 10 producers of maize in Africa (FAOSTAT, 2010)

Rank	Country	Production (t)	Area (ha)	Yield (t ha^{-1})
1	South Africa	12815000	2 742,000	4.67
2	Nigeria	7305530	3 335,860	2.19
3	Egypt	7041100	968,519	7.27
4	Tanzania	4475420	3 100 000	1.44
5	Ethiopia	4400000	1 772 250	2.48
6	Malawi	3800000	1 655 000	2.30
7	Kenya	3222000	2 008 350	1.60
8	Zambia	2795480	1 080 560	2.59
9	Mozambique	1878000	1 573 000	1.19
10	Ghana	1871700	991 669	1.89

Although maize is estimated to be a source of about 20% of world food calories and 15% of crop protein (Brown et al., 1988; NRC, 1988), the protein quality of normal maize is poor due to the deficiency of the essential amino acids, mainly lysine and tryptophan (Bhatia and Rabson, 1987). The high consumption of maize in SSA as food, which is estimated to be around 70% of the total maize production (Aquino et al., 2001), is causing severe protein energy malnutrition in some parts of SSA. The rate of stunting is reported to be over 40% in areas where maize is the only source of protein (Hyman et al., 2008). In addition, 65% of the population in the maize farming system of SSA is reported to live on USD 2 or less per day (Wood et al., 2010) implying the difficulty of affording animal sources of protein.

Normal maize protein in comparison to milk has a biological value of 40% (Bressani, 1991) and therefore needs to be consumed with complementary protein sources such as legumes or animal products. The need to improve the nutritional value of maize has been recognized for a long time (Osborne and Mendel, 1914) and decades long research have resulted in the development of nutritionally enhanced maize germplasm.

2.2 Development of high quality protein maize

Cereals are the source of more than half of the dietary protein of human beings. However, the protein of most cereals is of poor quality as the most abundant storage protein of cereals, prolamin, is deficient in several amino acids essential for monogastric animals, lysine being the most limiting (Bhan et al., 2003). Most cereal grains contain 1.5–2% lysine of the required 5% for optimal human nutrition (Young et al., 1998). Most of the protein in a mature maize kernel is stored in the endosperm and the germ. The endosperm protein is of low quality whereas the germ protein is of better quality. However, the endosperm accounts for about 80% of the total kernel protein (Zuber and Helm, 1972). Thus, any major improvements in the quality of kernel protein should target the endosperm.

Several mutants have been identified over the past 50 years that can favourably modify characteristics of the maize endosperm protein by elevating levels of two deficient amino acids, namely lysine and tryptophan. The value, use and inheritance of characteristics of such genes, however, vary tremendously (Vasal, 2001). The first high lysine mutant discovered was opaque-2 (*o2*) (Mertz et al., 1964), and shortly after, the biochemical effects of floury-2 (*fl2*) were discovered (Nelson et al., 1965). The discovery of the biochemical effects of these mutant alleles *o2* and floury-2 (*fl2*) by the Purdue University researchers opened an exciting opportunity for improving the quality of maize endosperm protein. These mutants were found to cause changes in the amino acid profile and composition of maize endosperm protein and resulted in twofold increase in the levels of lysine and tryptophan compared to normal maize. The lysine in maize is the most and tryptophan the second most limiting amino acids. In addition, the mutants also cause some amino acids such as histidine, argentine, aspartic acid and glycine to increase and other amino acids like glutamic acid, alanine, and leucine to decrease compared to those of normal maize. A most notable decrease occurs in leucine. This is desirable because it makes the leucine-isoleucine ratio more favourable, which in turn

helps to liberate more tryptophan for niacin biosynthesis (Vasal et al., 1984a; Mertz, 1992; Villegas et al., 1992; Vasal, 2001).

During the initial stages, breeders were using both *o2* and *fl2* genes either separately or in combination. However, in the later stage the use of *fl2* discontinued due to its undesirable effects (Bjarnason and Vasal, 1992; Vasal, 2000). The *o2* mutants are the most widely used in most breeding programmes (NRC, 1988; Glover, 1992; Villegas et al., 1992). Maize, which is homogenous for the recessive *o2* allele (with two copies of the mutation) has significantly higher lysine (+69%) in grain endosperm compared to normal maize (Mertz et al., 1964). It was further determined that *o2* mutants also showed an increase in tryptophan content and that the increased concentration of these two essential amino acids (normally deficient in the maize endosperm) effectively doubled the biological value of maize protein (Bressani, 1992).

After the discovery of the nutritional advantages of the *o2* gene, many breeding programmes around the world tried to convert normal endosperm populations and inbred lines to *o2* through a direct backcross approach (Gevers, 1995; Prasanna et al., 2001). However, the early excitement over the direct use of the *o2* mutation in the breeding programmes soon subsided due to the negative secondary (pleiotropic) effects of this mutation (Bjarnason and Vasal, 1992; Prasanna et al., 2001). The pleiotropic effects of the mutants resulted in reduced grain yield (as compared to normal maize), low kernel density, soft and chalky kernel phenotype, greater vulnerability to ear rot, greater moisture content during dry-down of kernels following physiological maturity, lower rate of germination and greater kernel breakage (Lambert et al., 1969; Sreeramulu and Baumann, 1970; Wessel-Beaver and Lambert., 1982; Vasal et al., 1984a; Bjarnason and Vasal, 1992; Villegas et al., 1992; Glover, 1992; Moro et al., 1995; Lin et al., 1997; Vasal, 2001; Prasanna et al., 2001). The soft and chalky endosperm texture was not acceptable to many in the developing world who were used to harder kernel types (Krivanek et al., 2007). The negative agronomic characters severely limited practical use of the mutants in the field.

In order to overcome the negative effects of *o2* mutants, breeders shifted their breeding goals towards incorporating the gene into normal hard endosperm maize types and looking for modified kernels. CIMMYT took the initiative in this breeding effort by converting a range of sub-tropical and tropical lowland adapted, normal endosperm populations to *o2* versions through a backcross-cum-recurrent selection procedure, with a focus on selecting for the hard

endosperm phenotype, maintaining protein quality and increasing yield and resistance to ear rot (NRC, 1988; Villegas et al., 1992; Bjarnason and Vasal, 1992; Vasal, 2001; Prasanna et al., 2001). Scientists are not sure of the number of genes involved in modifying the *o2* endosperm to translucent and similar to that of normal maize. However, what is known so far is the complex inheritance of the genes (Bjarnason and Vasal, 1992; Lopes and Larkins, 1996).

The continued breeding efforts at CIMMYT eventually resulted in the development of maize genotypes with high lysine and tryptophan content relative to normal maize but without the negative pleiotropic effects of the *o2* mutants. Scientists at CIMMYT termed this maize Quality Protein Maize (QPM) (Vasal et al., 1984b; Bjarnason and Vasal, 1992). The term QPM now refers to maize homozygous for the *o2* allele, with increased lysine and tryptophan content but without the negative secondary effects of soft endosperm (Vasal, 2001). QPM looks, tastes and performs like normal maize and it can only be differentiated by laboratory tests (Villegas et al., 1992). QPM germplasm was developed through conventional breeding techniques and is not the result of genetic engineering (Pixley and Bjarnason, 1993).

In addition to CIMMYT, the University of Kwazulu-Natal (previously University of Natal), South Africa and the Crow's Hybrid Seed Company at Milford, Illinois, USA, were the pioneers that continued the research vigorously and persistently to improve the protein quality of normal maize (Vasal, 2000; Prasanna et al., 2001). The South African breeding programme has developed soft and hard endosperm, white and yellow kernel, high-lysine maize inbred lines, hybrids and OPVs with good agronomic characteristics (Gevers and Lake, 1992; Hohls et al., 1996; Bhatnagar et al., 2004). Crow's Hybrid Seed Company developed an *o2* hybrid with good yield characteristics and a thick protective husk for animal feed (Mertz, 1995). In the USA, Texas A&M has also maintained a breeding programme to develop QPM germplasm adapted to the southern part of the USA (Betran et al., 2003a; 2003b; 2003c). As a result of these efforts, today QPM cultivars (hybrids and OPVs) suitable for temperate, tropical highlands and for subtropical and tropical lowland growing conditions are available.

Development of QPM hybrids has been given emphasis within CIMMYT since the mid 80's because of the growing interest in hybrids among national programmes, especially in developing countries (Bjarnason and Vasal, 1992; Vasal et al., 1993b; Vasal, 2001). Various

benefits were advocated for QPM hybrids over OPVs including i) better yield due to heterosis; ii) facilitating maintenance of the seed purity of inbred progenitors with respect to agronomic traits, the genetic modifiers and the protein quality; iii) less laboratory work needed to check the protein quality as long as the lines are fixed and not adulterated; iv) uniformity in field performance and; v) good business for seed companies (Gevers and Lake, 1992; Pixley and Bjarnason, 1993; Vasal et al., 1993a; 1993b; CIMMYT, 2000; Vasal, 2001). QPM germplasm development efforts have been strengthened at CIMMYT and national breeding programmes and QPM inbreds and hybrids have been evaluated for combining ability and yield stability (Vasal, 2001; Prasanna et al., 2001; Bhatnagar et al., 2004; Hadji, 2004; Xingming et al., 2004; Gissa, 2008).

2.3 Biosynthesis and genetic basis of storage proteins in maize

The maize genome is richly endowed with a whole array of endosperm mutants that can modify protein, starch and oil characteristics of the mature corn kernel, particularly the endosperm (Vasal, 2001). The variants already known to affect endosperm characteristics are numerous. The mutants worth mentioning are opaque-7 (*o7*) (McWhirter, 1971; Misra et al., 1975), opaque-6 (*o6*), floury-3 (fl_3) (Ma and Nelson, 1975), mucronate (Mc) (Salamini et al., 1983) and defective endosperm (De-B30) (Salamini et al., 1979). However, of particular interest in this section is the *o2* mutant that affects protein quality.

Cereal proteins are classified into the following four groups based on their solubility (Singh, 2005): (1) albumins (water soluble); (2) globulins (salt soluble); (3) prolamines (relatively highly alcohol soluble); (4) glutelins (dilute alkalin soluble). Cereals can be divided into three groups on the basis of their prolamine content. Rice and oats have the lowest prolamine content (5 - 15%) and an excellent balance of amino acids in their proteins. Barley and wheat form the second group with 30 – 40% prolamines, while maize and sorghum have the highest prolamine content (50 - 60%) (Singh, 2005). In normal maize endosperm, the proportions of various protein fractions on average are albumins 3%, globulins 3%, prolamines (zein) 60% and glutelin 34% (Schnieder, 1955). Prolamines are poor in basic amino acids, including lysine (Singh, 2005) and therefore, they have very poor nutritional value (Glover, 1992; Villegas et al., 1992). In each genus, the major seed storage protein is named on the basis of the genus name; thus, the major seed storage proteins in maize are called the zeins for the genus *Zea* and belong to the prolamine class of proteins (Darrigues et al., 2006).

The proportion of the zein fraction in maize endosperm determines the amino acid composition of the kernels (Larkins et al., 1993; Singh, 2005). Osborne and Clapp (1908) were the first to describe the amino acid profile of the zein proteins and reported the lack of the two essential amino acids, lysine and tryptophan. Zeins contain 0.1 g 100 g^{-1} lysine while glutelins are considerably richer in lysine with 2 g 100 g^{-1} or more (Misra et al., 1975; Lin et al., 1997). Darrigues (2006) showed that in the amino acid balance of maize, lysine and tryptophan are the most deficient; histidine and leucine are surplus amino acids compared to the egg protein which is a nearly balanced source of protein.

The introduction of high QPM mutants altered the relative amounts of four major protein fractions present in maize (Mertz et al., 1964; Lopes et al., 1995; Darrigues et al., 2006). Kernels carrying the homozygous *o2* mutant have elevated levels of lysine and tryptophan by suppressing or reducing the synthesis of the lysine-deficient zein fraction (Mertz et al., 1964; Habben et al., 1993). Since fractions other than zein are higher in lysine and tryptophan, zein reduction causes proportional elevation of other fractions which are rich in lysine, hence, the overall amino acid profile shows an increase in lysine. It may, however, be remembered that no new proteins are formed and that the composition of various protein fractions remains unaffected. An increase in protein quality requires reduction of the zein fraction (Mertz et al., 1964; Habben et al., 1993; Vasal, 2001).

Sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) reveals that zein of normal maize contains six separable components, Z_1, Z_2, Z_3, Z_4, Z_5 and Z_6. Z_1 and Z_2 are the two predominant types with molecular weights of 21 800 and 19 000 daltons and are rich in glutamic acid, leucine, and proline, but low in lysine. Of the four minor bands, Z_3, Z_4, Z_5 and Z_6, the latter two exist in only trace amounts. The non-allelic high quality mutants suppress one or more of these polypeptide bands. The *opaque-2* particularly suppresses synthesis of Z_1 whereas the floury-2 suppresses the major polypeptide components, Z_1 and Z_2. The opaque-7 strongly suppresses the synthesis of Z_3 and Z_4 while strongly reducing Z_2. The defective endosperm De-B30 affects only Z_1 subunits (Salamini et al., 1979).

The specific chromosome and position on the chromosome is known for some of the mutants. The *o2* mutant is located on chromosome 7 (position 16), *fl2* on chromosome 4 (position 63), *opaque -7* on chromosome 10 (position 87), *floury-3* on chromosome 8 (long arm) and De-B30 on chromosome 7 (short arm). The mutants *o2, o6, o7* and 0_{11} are completely recessive

and manifest their biochemical effects on zein synthesis only when present in homozygous recessive condition. The two floury mutants, *fl2* and *fl3*, are semi-dominant and exhibit variable expression for kernel opacity and protein quality, depending on the presence of one or more recessives in the triploid endosperm. The mutant De-B30 behaves like a dominant allele in respect of dosage effects on kernel opacity and zein content (Soave et al., 1981). The Mc allele is dominant in reducing zein content and is specific to the zein subunits (Soave et al., 1982). Except for opaque-6, considered as a structural gene, the others are regulatory genes. All these mutants have several common features, including low prolamine protein fraction, soft chalky endosperm, and a deficiency in the amount of dry matter produced.

2.4 QPM breeding approaches and germplasm

The discovery of the biochemical effects of the high QPM mutants spurred enthusiasm and led to a worldwide effort of converting elite inbreds and open pollinated cultivars to *opaque-2* and *floury-2*. Efforts were initially concentrated at Purdue University, but as donor stocks carrying these genes were made available, concerted conversion programmes were undertaken by most maize breeders in many countries (Prasanna et al., 2001). The breeding of QPM involves the manipulation of three distinct genetic systems (Krivanek et al., 2007). The recessive mutant allele of the *o2* gene is an important component of the QPM breeding (Villegas et al., 1992; Vasal, 2001).

The second genetic system in QPM breeding is the involvement of modifier genes which alter the soft/opaque mutant endosperm to a hard/vitreous endosperm without compromising the protein quality (Hohls et al., 1996; Vasal, 2002). Paez and co-workers (1969) were the first to report on endosperm modification in *o2* kernels (50% translucent and 50% opaque). Subsequently, modified *o2* kernels with varying proportions of translucent and opaque fractions have been observed and studied by a number of scientists (Annapurna and Reddy, 1971; Bjarnason et al., 1976; Lodha et al., 1976). These endosperm modifiers along with the *o2* mutant allele can be utilised as a fast and inexpensive method of selection of QPM germplasm (Hohls et al., 1996), using light that is projected through the vitreous grains but blocked by the opaque ones (Vasal et al., 1980; Vasal, 2001; Krivanek et al., 2007). Kernel modification is rated on a 1-5 scale where 1 indicates a completely hard/vitreous grain and 5 a soft/opaque endosperm (Vasal et al., 1980; Lopes et al., 1995; Hohls et al., 1996; Vasal et

al., 1997a). Grains with a score of 2 - 5 can be considered as homozygous for the *o2* allele, while grains with a score 2 - 3 are adequately modified and are the ones selected as QPM (Krivanek et al., 2007). Hohls et al. (1996) reported that screening of QPM kernels based on visual scores makes the hard task of measuring kernel density and kernel hardness unnecessary.

The third genetic system distinct to a QPM breeding programme involves a unique set of amino acid modifier genes which changes the relative levels of lysine and tryptophan in the grain endosperm (Mertz et al., 1964; Villegas et al., 1992; Krivanek et al., 2007). A study on the level of lysine and tryptophan in whole maize grain flour indicated that lysine levels average about 2% in normal maize while about 4% in QPM, similarly tryptophan averages 0.4% in normal maize and 0.8% in QPM, which shows a doubling of the essential amino acids in QPM (Moro et al., 1996). However, lysine ranges across genetic backgrounds from 1.6 - 2.6% in normal maize and 2.7 - 4.5% in their *o2* converted counterparts, while tryptophan ranges from 0.2 - 0.5% in normal maize and 0.5 - 1.1% in QPM counterparts (Villegas et al., 1992; Moro et al., 1996; Vasal, 2001; CIMMYT, 2002). Biochemical studies showed a high correlation between lysine and tryptophan levels (Hernandez and Bates, 1969). Hence, an assay for either amino acid can be adopted for analysing protein quality, although in practice tryptophan is most often chosen due to relatively cheaper laboratory costs (Krivanek et al., 2007). Multigenes have been identified as controlling the amino acid content (Wang et al., 2001; Wu et al., 2002). As a result, the simple genetic nature of *o2* maize has been transferred into a classic polygenic trait in reference to QPM and must be manipulated as such in breeding programmes. Krivanek et al. (2007) also recommended the need to continuously monitor lysine and tryptophan levels so as not to lose the additional gain in protein quality, although the *o2o2* genotype is maintained.

CIMMYT has the largest collection of modified *opaque-2* germplasm (Tables 2.2 and 2.3). The materials developed at CIMMYT include several QPM populations and pools. These breeding populations possess different ecological adaptation, maturity, grain colour, and texture traits. Crow's Hybrid Seed Company in the USA has perhaps the most extensive programme to develop QPM germplasm. They have used CIMMYT QPM populations and Russian lines in developing this type of germplasm. Purdue University, Texas A&M, and the University of Illinois have also used CIMMYT QPM germplasm in developing source breeding populations and lines adapted to US conditions. Good modified *opaque-2*

germplasm has also been developed in South Africa, in addition to two good source populations POWS1 (Modified White Opaque) and DOYS (Yellow modified opaque) developed for the purpose of producing modified *opaque-2* hybrids (Vasal, 2001). The availability and the continued development of QPM germplasm in the different parts of the world show the prospect of QPM to be widely cultivated.

Table 2.2 QPM populations and their characteristics (Vasal, 2001)

Population Number	Name	Adaptation	Maturity	Seed Colour	Seed texture
61	Early Yellow Flint QPM	Tropical	Early	Yellow	Flint
62	White Flint QPM	Tropical	Late	White	Flint-Semi flint
63	Blanco Dentado-1 QPM	Tropical	Late	White	Dent
64	Blanco Dentado-2 QPM	Tropical	Late	White	Dent
65	Yellow Flint QPM	Tropical	Late	White	Flint
66	Yellow Dent QPM	Tropical	Late	Yellow	Dent
67	Templado Blanco Cristalino QPM	Subtropical	Intermediate	White	Flint
68	Templado Blanco Dentado QPM	Subtropical	Intermediate	White	Dent
69	Templado Amarillo QPM	Subtropical	Intermediate	Yellow	Flint
70	Templado Amarillo Dent QPM	Subtropical	Intermediate	Yellow	Dent

Table 2.3 QPM gene pools and their characteristics (Vasal, 2001)

QPM pool number	Adaptation	Maturity	Seed Colour	Seed Texture
Pool 15 QPM	Tropical	Early	White	Flint-Dent
Pool 17 QPM	Tropical	Early	Yellow	Flint
Pool 18 QPM	Tropical	Early	Yellow	Dent
Pool 23 QPM	Tropical	Late	White	Flint
Pool 24 QPM	Tropical	Late	White	Dent
Pool 25 QPM	Tropical	Late	Yellow	Flint
Pool 26 QPM	Tropical	Late	Yellow	Dent
Pool 27 QPM	Subtropical	Early	White	Flint-Dent
Pool 29 QPM	Subtropical	Early	Yellow	Flint-Dent
Pool 31 QPM	Subtropical	Intermediate	White	Flint
Pool 32 QPM	Subtropical	Intermediate	White	Dent
Pool 33 QPM	Subtropical	Intermediate	Yellow	Flint
Pool 34 QPM	Subtropical	Intermediate	Yellow	Dent

Currently, there are QPM research activities in SSA led by CIMMYT and the International Institute of Tropical Agriculture (IITA) in collaboration with National Agricultural Research Systems (NARS). In the region, activities are highly integrated and coordinated enabling joint development, exchange and broad testing of promising genotypes for all agro-ecological niches (CIMMYT, 2005). The long-term goals of all breeding programmes are focused on broadening the genetic base of adapted QPM germplasm to suite their particular biotic and abiotic constraints (Krivanek et al., 2007). So far, a large number of elite QPM inbred lines adapted to the SSA region have been developed and the suitability of these inbreds in hybrid combination and in OPVs needs to be extensively evaluated.

2.5 Nutritional and economic benefits

Quality protein maize offers significant benefits in the nutrition of monogastric animals including humans; because the essential amino acids (lysine and tryptophan) cannot be synthesized through metabolism of these groups of animals. The nutritional and biological superiority of QPM to normal maize has been amply demonstrated in rats (Bressani et al.,

1969; Gupta et al., 1970), pigs (Lopez-Pereira, 1992; Osei et al., 1994a), infants and small children (Bressani, 1995), adults (Clark et al., 1977; Bressani, 1991; 1992), broiler chickens (Osei et al., 1994b; 1994c) and dairy cattle (Glover, 1992).

QPM has superior biological value (the amount of N that is retained in the body) due to the 60 to 100% increase in concentrations of lysine and tryptophan, increased digestibility and increased N uptake which causes QPM to have a biological value of 80% compared to about 40% of normal maize (Bressani, 1992). Bressani (1995) reported that protein quality of *o2* maize is 43% higher than that of normal maize and 95% of the value of casein. QPM is 50% more effective than normal maize at fostering growth and in recovering malnourished children (Graham et al., 1980; NRC, 1988). Protein quality of *o2* maize is 90% of the value of milk (Bressani, 1992; 1995).

Osei et al. (1994a) reported that pigs fed on QPM grew 2.3 times faster than pigs of the same age fed on the same quantity of normal maize. A QPM based diet is regarded as sufficient in fulfilling the energy and protein requirements of infants and children (Graham et al., 1980; Graham et al., 1990). The health of children suffering from Kwashiorkor (a severe protein deficiency disease) was restored on a diet containing only *o2* maize as a protein source (Clark et al., 1977). Recovering malnourished children fed on QPM further showed similar growth as those fed modified cow milk formula (Graham et al., 1990). QPM has been seen both as a preventer of deficiency diseases such as kwashiorkor and as a remedy for serious cases of malnutrition (Bressani, 1992). QPM has a potential impact on disadvantaged populations whose maize consumption is high and access to complementary sources of protein are limited (Rahmanfer and Hamaker, 1999). Recent studies in China and Pakistan demonstrated that lysine fortification of cereal-based diets (wheat) improved growth in children and various health indicators for children and adults, confirming that lysine enrichment of cereal-based diets remains beneficial to improve problems associated with malnutrition (Hussain et al., 2004; Pellet and Gosh, 2004; Zhao et al., 2004).

Gupta et al. (1970) found modified *o2* maize to be nutritionally superior to normal maize in rat (*Rattus norvegicus*) feeding experiments. According to Glover (1992), US farmers who fed *o2* maize silage to dairy cattle benefited from increased milk production of their dairy cows. QPM silage may hold distinct nutritional and economic advantages in the feeding of dairy animals (Gevers, 1995). Substituting normal maize with high-lysine maize on an equal

weight basis for piglets and cows can reduce the use of artificial lysine in animal feeds to maintain a proper amino acid balance (Asche et al., 1985; Burgoon et al., 1992; Knabe et al., 1992). In the USA feed industry, doubling lysine content in maize alone can add an estimated annual gross value of $360 million per year and can reach $480 million per year if protein is also increased (Johnson et al., 2001). These findings indicate that QPM has an added advantage of being superior in protein quality and higher in food and feed efficiency.

2.6 Effects of low N and drought stress on maize production

The rapid growth of the human population coupled with increasing scarcity of water and fertile land resources are major constraints to food production in semi arid tropics (Beck et al., 1997). Poor soil fertility, particularly low N deficiency and recurrent droughts are widespread in SSA. Consequently, crop yields are low which affect food security (Kamara et al., 2004).

Edmeades et al. (2006) estimated a 50% potential yield loss due to abiotic constraints. Their study also suggested that good agronomic practices and stress tolerant cultivars may reduce this yield gap by 20-30% and the remaining balance will depend on additional inputs such as water and N. Improved maize varieties that tolerate drought, heat and low soil fertility will help maize farmers in stress-prone areas to obtain better harvests under stress conditions (Zaidi et al., 2003; CIMMYT, 2007). The effects of low N and drought on maize production make stress tolerant cultivars more desirable (Betran et al., 2003d). Zaidi et al. (2003) also suggested that utilisation of drought-tolerant and N-efficient cultivars in maize production of the tropics could lead to better stability of grain yield across the environments. Breeding maize for tolerance to drought and low N conditions has been ongoing at CIMMYT since the 1980's, and germplasm with tolerance to both stresses has been developed (Edmeades et al., 1992; Bolaños et al., 1993; Bolaños and Edmeades, 1993a; Lafitte and Edmeades, 1994a; 1994b; 1994c; Bänziger and Lafitte, 1997; Bänziger et al., 1999a; Bänziger and Diallo, 2004; Bänziger et al., 2006).

Several researchers have reported genetic variability in maize grain yield under drought and low N conditions (Bolaños and Edmeades, 1993b; Lafitte and Edmeades, 1994c; Vasal et al., 1997b; Link et al., 1999; Betran et al., 1999; Bänziger et al., 2000; Dencic et al., 2000; Diallo et al., 2004). Modern maize hybrids have increased stress tolerance rather than a higher yield

potential (Duvick and Cassman, 1999). Increased yield and yield stability of some recent tropical and temperate maize genotypes have been attributed to increased abiotic stress tolerance (Byrne et al., 1995; Tollenaar and Wu, 1999). Betran et al. (2003e) observed hybrids performing well across stress levels and suggested the possibility of combining stress tolerance and yield potential in tropical maize hybrids. One approach to reducing the impact of N deficiency and water stress on maize production may be to select cultivars that are superior in their capacity to take up N and water from the soil and utilise them efficiently (Kamara et al., 2004). Tolerance of maize to stress from low N and drought is partly related to the development of the root system, which in turn influences water and nutrient uptake by crop plants (Moll et al., 1982; Kamara et al., 2004). In general, however, the amount of grain yield recorded from maize genotypes fall with the severity of low N and moisture stress (Betran et al., 2003e). As recommended by Edmeades et al. (2006), it is more efficient to select for improved yield under stress when stressed yields are less than 50 to 60% of the potential.

Bänziger et al. (1997) have identified secondary traits which can be used for selecting maize under drought and low N. Improvement in drought tolerance of maize for better anthesis-silking interval (ASI) was found to be associated with improved N use efficiency (Bänziger et al., 1999c; Muza et al., 2004). The highest grain yielding genotypes under low N and drought tend to show lower ASI, delayed senescence, and a higher number of ears per plant (Jacobs and Pearson, 1991; Bolaños and Edmeades, 1993b; Moll et al., 1994; Bänziger et al., 1997; Bänziger et al., 1999b; Diallo et al., 2004). An increase in ASI in maize indicates that pollen shed is essentially over by the time silks emerge (Bänziger and Lafitte, 1997; Edmeades et al., 2006). Edmeades et al. (1993) found that delayed silking is related to less assimilate being partitioned to growing ears around anthesis, which results in lower ear growth rates, increased ear abortion, and more barren plants.

CIMMYT (2003a) reported the negative effects of drought and low N stress on endosperm modification of QPM germplasm. Severe drought stress can significantly increase the frequency of soft or poorly modified grains relative to the same genotypes under optimal moisture growing conditions (Ngaboyisonga et al., 2006). Protein concentration and trypthophan are lower under low N compared to optimum N conditions (CIMMYT, 2003b). However, the tryptophan level of QPM under both low N and optimum conditions is higher than the tryptophan level of normal maize under optimum conditions (CIMMYT, 2003b;

Mosisa, 2005). Similary, Pixley and Bjarnason (2002) reported that protein quality is very stable, whereas protein content and endosperm modification of QPM varieties are less stable across environments. Feil et al. (2005) evaluated the effect of pre-anthesis drought and different rates of N fertilization on mineral composition of grains of tropical maize varieties. The results showed that N, P, K, Mg, Ca, Mn, Zn, and Cu are fairly stable across the levels of N and pre-anthesis water supply.

2.6.1 Low nitrogen stress

Studies have identified low N as the second most important constraint of maize production in the tropics after drought (Lafitte, 2000). Maize is a very responsive crop to high or low N levels. Low N in maize hinders photosynthesis by reducing leaf area development and accelerating leaf senescence. At the beginning of the season the N supply usually exceeds the demand by the crop; however, as the season progresses and the crop grows, N is utilised, leading to N depletion in the soil. Consequently N becomes scarce and the crop starts to show the signs of N stress (Bänziger and Lafitte, 1997).

N is the most essential nutrient required in large amounts by maize, thus efficient N uptake and use by maize is of fundamental importance to maize production systems in Africa (Muza et al., 2004). Ma and Dwyer (1998) identified N fertiliser as the most energy-consuming component of maize grain production. N is the most limiting nutrient as it is the most mobile in the soil (Laegreid et al., 1999). As the economic and environmental costs of N use increase, there is a need to develop and select varieties with good N use efficiency (Ma and Dwyer, 1998). In low-input agriculture, N efficient varieties (varieties with better grain yield under low N conditions) are recommended as one of the key elements for sustainable agriculture (Sattelmacher et al., 1994).

Most of commercial maize hybrids and varieties are not N-use efficient as they were developed under optimum conditions and therefore do not perform well under small holder conditions which lacks inputs (Muza et al., 2004). Inorganic fertiliser use in SSA is constrained by high cost, inaccessibility and lack of credit faced by small holders farmers even in high yield potential areas (Kamara et al., 2004; Diallo et al., 2004; Bänziger and Diallo, 2004; Bänziger et al., 2006). In addition, poor weed management which normally

increases the N stress level are among the challenges that result in low N being a common feature of maize-growing environments in the tropics (Bänziger and Lafitte, 1997).

The time and rate of N application has a direct effect on the growth and development of a maize plant (McCullough et al., 1994). The beginning of grain filling is a key phase of N supply (Christensen et al., 1981) and as a result of grain filling, transport of carbohydrates to the roots is reduced and N uptake decreases (Monneveux et al., 2005). N affects photosynthetic rate, leaf area, size of the sink and yield (Dass et al., 1997). In low N conditions leaves become the main source of mobilised N to the ear (Below, 1997), this will result in reduction of chlorophyll concentration that causes yellowing of leaves, which are clear signs of N deficiency (Dwyer et al., 1995). The stay green character (physiological maturity/drying of ears while leaves are still green) can reflect N balance in cereals during grain filling (Borrell et al., 2001); however greenness can also be cosmetic rather than functional (Thomas and Howarth, 2000). Lack of N enhances kernel abortion (Pearson and Jacob, 1987) and reduces final grain number and weight (Lemcoff and Loomis, 1986; Uhart and Andrade, 1995) and grain yield (Monneveux et al., 2005). Reduction of grain weight under low N conditions is more attributable to reduction in grain filling period than in growth rate (Monneveux et al., 2005).

Cultivars yield differently in different N environments due to genetic differences (Smalberger and du Toit, 2004). Relative grain yield reduction due to N stress also depends on the type of progeny and N stress intensity (Bänziger and Lafitte, 1997). Smalberger and du Toit (2004) recorded a grain yield ranging from 0.65 - 3.85 t ha^{-1} under low N and 4.17 - 6.93 t ha^{-1} under optimum N for South African cultivars. They observed that the cultivar that yielded the best (6.93 t ha^{-1}) under optimum N also yielded as low as 0.98 t ha^{-1} under low N. Betran et al. (2003e) compared maize hybrid yield under low and high N environments and found that grain yield for hybrids in the low N environment was 33% of grain yield in the high N environment. This indicates the need for developing cultivars that will yield well under both optimum and low N conditions.

Diallo et al. (2004) evaluated 63 single cross hybrids along with seven local checks under low N and optimal conditions and reported grain yields ranging from 1.2 - 3.5 t ha^{-1} under low N and 3.1 - 7.4 t ha^{-1} under optimal conditions. Bänziger et al. (1997) observed a relative grain yield reduction of 37 to 78% in different experiments conducted under low N in tropical

maize. In other experiments, Bänziger and Lafitte (1997), and Bänziger et al. (1999b) reported relative grain yield reductions ranging from 37 to 89% and 20 to 50%, respectively. Monneveux et al. (2005) found an average yield reduction of 67.4% for maize hybrids under low N compared to optimum conditions. Experiments under low N, yielding on average 25 – 35% (1.5 – 3.5 t ha^{-1}) of the yields expected under favourable conditions (6 – 9 t ha^{-1}) is regarded as optimal for expressing N stress tolerance in tropical maize (Bänziger et al., 1997).

2.6.2 Drought stress

The major causes of drought stress in the tropical environments includes poor rainfall distribution, poor water holding capacity of soil, shallow effective root depths, high surface runoff and evapotranspiration (Lal et al., 1982). Drought stress can affect the performance of maize plants from crop establishment up to grain filling. Although the ultimate grain yield could be affected by drought stress at almost all growth stages, flowering period is the most sensitive (Bänziger et al., 2000). Therefore, selection under managed drought stress at flowering is suggested as an effective means of increasing tolerance to a number of stresses occurring during flowering (Chapman et al., 1997). Drought stress delays silking relative to anthesis period which, in turn, prolongs the anthesis-silking interval (ASI). Unlike silks where their elongation is based on water status and which are very sensitive to drought, anthers are little affected by drought stress (Westgate and Boyer, 1986; Bolaños and Edmeades, 1993a). The most drought sensitive period during flowering is -2 to 22 days after silking, with the peak at seven days. Maize plants will be severely affected and complete yield loss can be expected, if drought stress occurs just before tassel emergence to the onset of grain filling (Grant et al., 1989).

Drought stress caused by uneven distribution and rate of rainfall is one of the most important constraints to maize production in Africa. It has been reported that 50% of the losses in maize grain yield in the developing world are caused by pre-anthesis drought stress (Edmeades et al., 1994). The reduction in grain yield due to drought stress during the vegetative, silking and ear stages are 25%, 50%, and 21%, respectively (Denmead and Shaw, 1960). A dry spell of a day or two at pollination has the potential of reducing grain yield by up to 22% (Fischer et al., 1983).

Elite tropical maize germplasm contains considerable genetic variability for drought tolerance. Manda and Mwambula (1999) screened 96 maize genotypes for drought tolerance and observed significant genotypic differences for grain yield, with a range of 0.5 - 5.7 t ha^{-1}. By managing drought stress levels, it is possible to observe genetic variation in grain yield and drought adaptive secondary traits which can be exploited (Manda and Mwambula, 1999). Commercial hybrids developed using multi-location testing that supposedly included results from random drought stress sites, showed inferior performance to those selected under managed drought stress (Bänziger et al., 1999c). Commercial hybrids yielded 23% higher than drought tolerant test-crosses under optimal conditions but 27% less under severe drought stress. Diallo et al. (2004) reported that an average grain yield of the hybrids under drought was 45% of the average grain yield under optimal conditions.

2.6.3 Managed stress environments

Maize production in the tropics is highly affected by drought and N stress conditions (Simmonds, 1991; Bänziger et al., 1997; Bänziger and Cooper, 2001). However, most of the maize breeding activities are conducted under optimum growing conditions and do not take into account the conditions of the smallholder farmers (Bolaños et al., 1993; Bänziger and Diallo, 2004; Muza et al., 2004). Therefore, for maximum breeding progress, testing should be done in the environments that represent the target production environments (Allen et al., 1978). Thus, the unpredictable nature of climate-related stresses and the limited number of testing sites have necessitated the development and use of managed stress sites (Edmeades et al., 2006).

Managed stress environments (MSEs) are selection environments targeted to simulate abiotic stress conditions (Bänziger and Cooper, 2001). Edmeades et al. (2006) described MSEs as specialised testing sites that allow strict control of the nature, timing and intensity of stresses applied to the target crop. The use of MSEs permits controlled and quantifiable consideration of the factors that affect breeding progress (Rosielle and Hamblin, 1981; Bänziger and Cooper, 2001). Managed drought stress trials are usually conducted in rain-free natural environments equipped with irrigation facilities while managed N stress trials are conducted under spatially uniform N depleted fields (Edmeades et al., 2006).

CIMMYT and national programmes in SSA have prioritised the major stresses found in farmers' fields (drought, low soil fertility, insect pests, acid soils) and have established stress screening sites at several breeding stations (Bänziger and Cooper, 2001; Bänziger et al., 2006). Furthermore, to develop low N and drought tolerant genotypes for the region, selection is done using three types of environments: (i) recommended agronomic management/high rainfall conditions, (ii) low N stress, and (iii) managed drought (Bänziger et al., 2006).

Statistical analysis of grain yield from stress environments often shows non-significant differences or higher coefficients of variation than experiments conducted under optimum conditions (Bänziger and Cooper, 2001). This suggests that the error variance of grain yield does not decrease as much as the genetic variance when moving from high to low yielding environments (Bänziger et al., 1997). To improve genetic gains from selection, careful management of MSEs is very important to reduce environmental variance and increase heritability for stress tolerance plant attributes (Bänziger et al., 2006).

2.7 G x E interaction, grain yield stability, AMMI and GGE biplots

2.7.1 G x E interaction

The performance of a cultivar depends on the genetic structure and the environment where it grows (Cooper and Byth, 1996). Environmental factors have a larger effect on quantitative traits than on qualitative traits, therefore performance tests of potential cultivars are conducted in multiple years and locations (Bernardo, 2002). In addition to genotype and environment main effects, performance of cultivars is determined by the G x E interactions, which is the differential response of cultivars to environmental changes (Hallauer et al., 1988; Crossa et al., 1990; Vargas et al., 1999). G x E interaction can occur due to various biotic and abiotic stresses. Different factors such as temperature, season rainfall, season length, within-season drought, sub-soil pH and socio-economic factors that result in sub-optimal input application are among the major causes of G x E interaction in the African maize growing environment (Bänziger et al., 2006). Conducting multi-environment trials (METs) is an efficient approach to select stable varieties across the different environments. It is also

important to note that G x E interactions are complex and when poorly understood, they represent a significant impediment to genetic improvement (Basford and Cooper, 1998).

The relative magnitude of G x E provides information regarding the likely area of adaptation of a given genotype. It is also useful in determining efficient methods of using time and resources in a breeding programme (Ceccarelli, 1989; Kang, 1998). Development of genotypes resistant/tolerant to various stresses to which they would likely be exposed might minimise G x E interaction (Kang, 1998). Mid-season drought tolerant genotypes that perform well under variable moisture regimes (Chapman et al., 1997; Bogale et al., 2008) and N levels (Bänziger et al., 1999b) are expected to give a better yield with increased stability across variable growing conditions compared to conventionally developed genotypes.

Large G x E interaction is expected when genotypes are grown under a wide range of environments and outside their normal zone of adaptation (Beck et al., 1991). Selection of multi-environment sites to sample stresses adequately, where G x E and genotype-by-year interaction are major sources of variation, is a crucial step in a successful breeding programme (Edmeades et al., 2006). The extent of performance testing depends on the magnitude of G x E, which occurs when genotypes differ in their relative performance across environments (Bernardo, 2002). Yield trials frequently have both significant main effects and significant G x E interaction (Zobel et al., 1988). The existence of G x E interaction necessitates breeders to evaluate genotypes in more than one environment to obtain repeatable rankings of genotypes (Hallauer et al., 1988). G x E interaction becomes of practical significance only when crossover interactions occur (Baker, 1988; Crossa and Cornelius, 1997). Crossover interactions occur in evaluation trials when ranks of cultivars change across environments (Russel et al., 2003). Trials conducted under stress environments usually produce rankings that differ significantly from one trial to another due to the presence of G x E interaction and this makes it difficult to choose the best performing genotype (Bänziger et al., 2000).

Under varying environments, genotypes that provide high average yields with minimum G x E interaction have been gaining importance over increased yields (Ceccarelli, 1989; Gauch and Zobel, 1997; Kang, 1998). The analysis of G x E interaction is closely linked with the quantitative estimation of phenotypic stability of genotypes over environments (Kang, 1996). When significant G x E interactions are present, the effects of genotypes and environments

are statistically non-additive, which means that the differences between genotypes depend on the environment. Existing G x E interactions may, but will not necessarily lead to different rank orders of genotypes in different environments.

Various methods have been used to investigate and better understand the causes and effects of G x E interactions (Van Eeuwijk et al., 1996). These methods can be divided into two broad categories. The first category involves factorial regression analysis of the G x E matrix (i.e. the yield matrix after the environment and genotype main effects are removed) against environmental factors, genotypic traits, or combinations thereof (Baril et al., 1995). The second category involves the correlation or regression analysis, which relates the genotypic and environmental scores, derived from principal component analysis (PCA) of the G x E interaction matrix to genotypic and environmental covariates.

2.7.2 Stability analysis

The presence of G x E interaction in METs leads to the need for the analysis of genotype stability. Stability has been described in many different ways over the years and there have also been different concepts of stability (Lin et al., 1986). Researchers use the terms adaptation, phenotypic stability and yield stability in different ways (Becker and Leon, 1988). Stability indicates consistency in performance that would mean minimum variation among environments for a particular genotype (Chahal and Gosal, 2002). The stability with which a plant breeder is concerned implies stability in those aspects of phenotype which are important economically, such as grain yield and quality. Such stability may depend on holding some aspects of morphology and physiology in a steady state but allowing traits to vary. In this way, the desirable varieties will show low G x E interaction for agriculturally important characters, especially grain yield, but not necessarily for other characteristics. Two basic concepts of phenotypic stability are distinguished: i) the biological concept, and ii) the dynamic concept. The biological concept of stability refers to the consistency of performance of a genotype over a wide range of environments. This idea of stability is in agreement with the concept of homeostasis widely used in genetics. According to Becker and Léon (1988) static stability genotypes possess unchanged performance regardless of variation of the environments, thus implying that its variance among environments is zero. This type is seldom a desired feature of crop cultivars, since no response to improved growing conditions would be expected.

On the other hand, dynamic stability, also termed as the agronomical concept of stability, implies that a stable genotype should always give high yield expected at the level of productivity of the respective environments, i.e., a variety with G x E interaction as small as possible (Becker, 1981; Dabholkar, 1999). With quantitative traits, the majority of genotypes often react similarly to favourable or unfavourable environmental conditions. Becker and Léon (1988) stated that all stability procedures based on quantifying G x E interaction effects belong to the dynamic stability concept. This includes the procedures for partitioning the G x E interactions of Wricke's (1962) ecovalence and Shukla's (1972) stability of variance procedures which use the regression approach such as those proposed by Finlay and Wilkinson (1963), Eberhart and Russel (1966) and Perkins and Jinks (1968), as well as non-parametric stability statistics.

The statistics, which can be used to identify stable genotypes, are classified into parametric and non-parametric approaches. Parametric (empirical and statistical) approach is more common and involves relating observed genotypic responses, in terms of yield, to a sample of environmental conditions. It is useful when the data are continuous. The non-parametric (analytical clustering) approach defines environments and phenotypes in terms of biotic and abiotic factors and is useful when the data are discontinuous. Non-parametric data analysis has the potential to reduce complex data into intuitive measures of stability. However, the use of some elements of both approaches is common in most breeding programmes (Becker and Leon, 1988; Ramagosa and Fox, 1993).

Lin et al. (1986) described eight parametric stability statistics: (1) the variance of a genotype across environments (S_i^2); (2) coefficient of variability (CV_i); (3) Plaisted and Peterson's mean variance component of pairwise G x E interaction ($\bar{\theta}_i$); (4) Plaisted's variance component for G x E interaction ($\theta_{(i)}$); (5) Wricke's ecovalence (W_i) ; (6) Shukla's stability variance (σ^2_i); (7) Finlay and Wilkinson's regression coefficient (b_i); (8) Eberhart and Russell's deviation parameters (S^2_{di}) (Plaisted and Peterson, 1959; Plaisted, 1960; Wricke, 1962; Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Shukla, 1972; Lin et al., 1986).

According to Becker and Léon (1988) the parametric approach described above gives only the individual aspects of the stability but cannot provide an overall picture of the response.

The basic reason for this apparent difficulty is that a genotype's response to environment is multivariate yet the multivariate approach tries to transform it into an univariate problem, via a stability index. To avoid this problem, a different line of thought has emerged, namely to cluster genotypes according to their response structure (i.e. non-parametric method). Although the parametric approach to stability is relatively simple, it does not provide information for the resolution of any conflicting type I and type II inferences. Under these circumstances, quantitative mathematical characterisation should be considered as well as qualitative descriptions of genotype, as like or unlike genotypes; i.e. to adopt a non-parametric clustering procedure (Lin et al., 1986).

2.7.2.1 Description of parametric approaches for stability analysis

A general summary of the response patterns of genotypes to different environments is given by the stability analysis. The main type of stability analysis, namely joint linear regression (JLR), was first proposed by Yates and Cochran (1938) and then widely used and described by many authors (Yates and Cochran, 1938; Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968; Shukla, 1972; Becker and Leon, 1988; Baker, 1988; Crossa, 1990). Linear regression models combine additive and multiplicative components and thus analyse main effects and their interaction (Zobel et al., 1988). Joint regression analysis provides a method of testing a genotype for characteristic linear response to changes in environments. This process is done by regression of the genotypic means on an environmental index.

2.7.2.1.1 Regression coefficient (b_i) and deviation mean square (S^2_{di})

According to Ramagosa and Fox (1993) simple linear regression provides a conceptual model for genotypic stability and is the most widely used statistical technique in plant breeding. This model is also called the Finlay and Wilkinson (1963) approach. The regression of each genotype's mean yield against the mean yields of an environment is determined and the stability range is determined by the main effects multiplied by the regression coefficients of genotypes.

The G x E interaction is divided into two segments i) a component due to linear regression (b_i) of the i^{th} genotype on the environment mean and ii) a deviation (d_{ij}) :

$$GE_{ij} = b_i E_j + d_{ij}$$

therefore, $Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij}$

The marginal means of the environments is used as independent variables in the regression analysis and the interaction is restricted to multiplicative form. The G x E from analysis of variance (ANOVA) is partitioned into heterogeneity of regression and deviations from regressions (Becker and Leon, 1988). Different authors used different b_i values to define genotype stability. Finlay and Wilkinson (1963) defined a genotype with $b_i = 0$ as stable (static concept) and Eberhart and Russel (1966) defined a genotype with $b_i = 1$ as stable (dynamic concept). Becker and Léon (1988) suggested that ecovalence rather be used, since it combines b_i and S^2_{di} as a stability parameter. Many scientists consider b_i as a response parameter and S^2_{di} as a stability parameter, since additional information on the average response of a genotype to favourable environments is given by b_i, this is schematically presented in Figure 2.1.

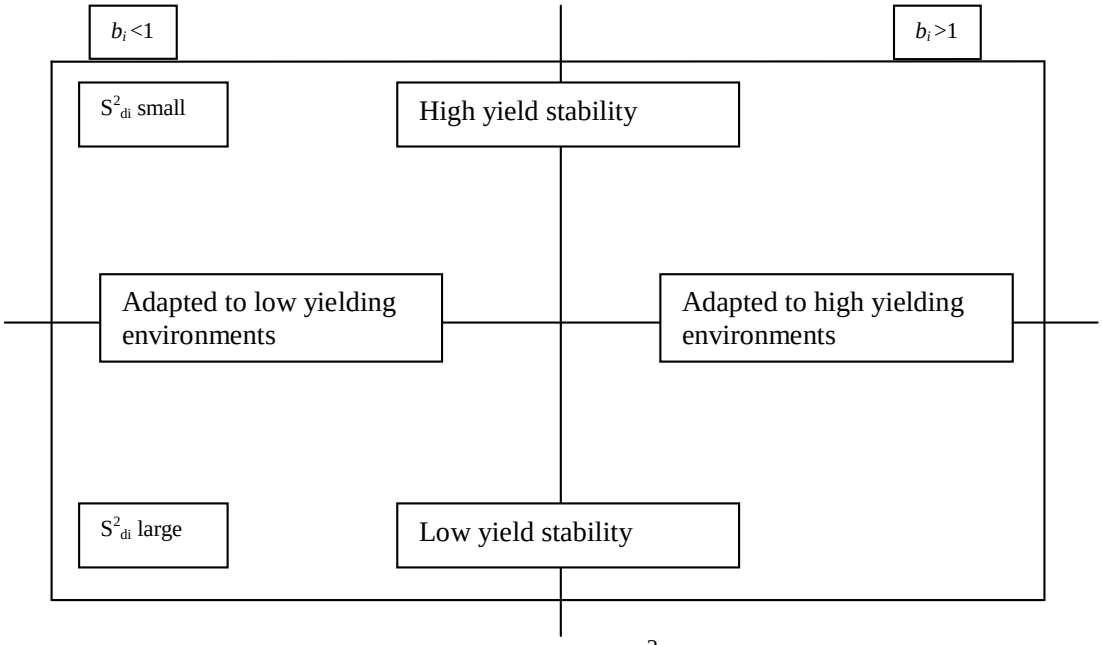

Figure 2.1. Interpretation of the parameters b_i and S^2_{di} of the regression approach (Becker and Léon, 1988).

Finlay and Wilkinson (1963) determined the regression coefficient by regressing the mean of all genotypes on the environmental mean and plotting the obtained genotype regression coefficients against the genotype mean yields. The pattern of genotype stability when genotype regression coefficient is plotted against genotype mean yield, is illustrated in Figure

2.2. According to Finlay and Wilkinson (1963), a genotype with a b_i value less than 1.0 has above average stability and is especially adaptable to low-performing environments and if it is greater than 1.0 the genotype has below average stability and is especially adaptable to high performing environments. Whereas, a genotype with b_i value equals to 1.0 is adapted to the widest range of environments or an indication of its average stability. When this value is associated with high mean yield it indicates a genotype's good general adaptability; and when it is associated with low mean yield it shows the genotype's poor adaptability to all environments (Fig. 2.2). Hence, in most cases the deviation from regression (S^2_{di}) is taken as a parameter for stability rather than b_i which is more about responsiveness of genotypes (Eberhart and Russell, 1966; Becker and Léon, 1988).

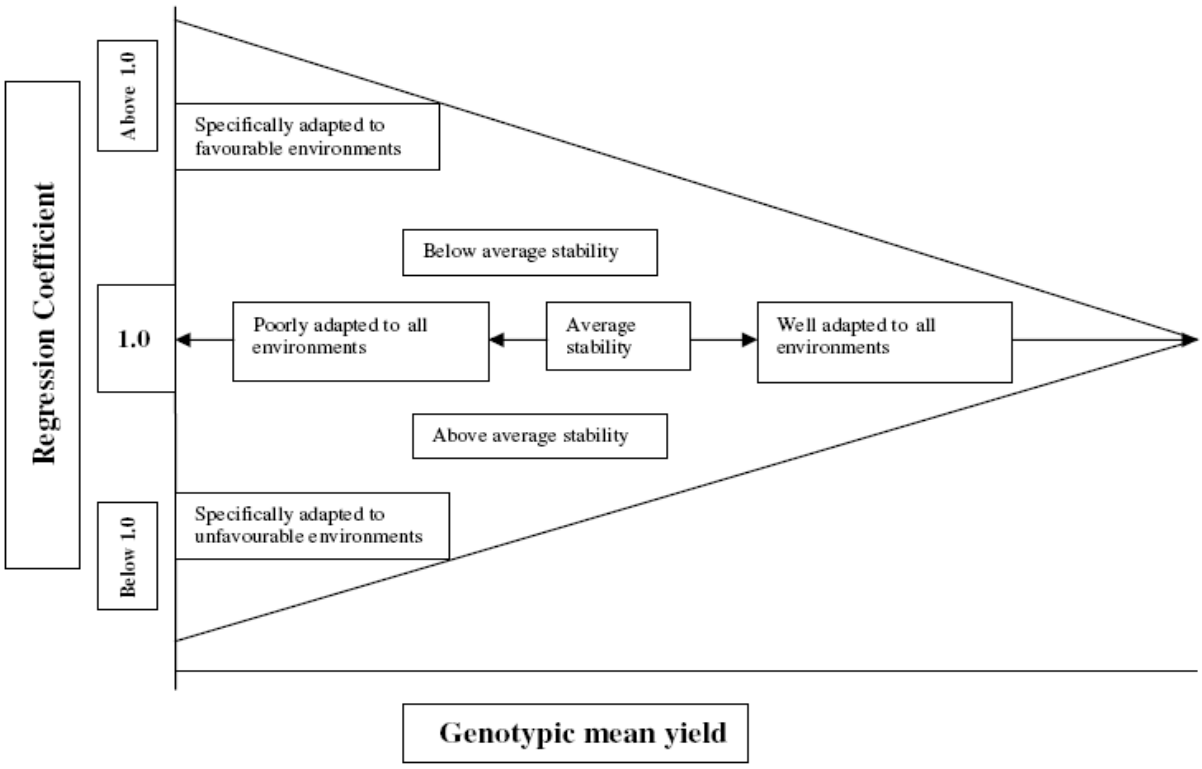

Figure 2.2 A generalised interpretation of the genotypic pattern obtained from genotypic regression coefficients plotted against genotypic mean, adapted from Finlay and Wilkinson (1963).

The deviation sums of squares are the sums of variance due to deviation from regression divided by (S-2) and subtracting pooled error mean square, where S stands for the number of locations for each variety (Eberhart and Russel, 1966). Therefore, varieties which have a less predictable response for a given set of environments, have a probability of a F value close to zero and will deviate significantly from linearity.

$$S^2 d_i = \frac{1}{S-2}\left[E_j(X_{ij} - \overline{X}_i - \overline{X}_j + \overline{X}...)^2 - (b_i - 1)^2 E_j(\overline{X}_j - \overline{X}...)^2\right]$$

Although many authors and breeders used the regression approach, simultaneous studies emphasised the limitations, biologically and statistically (Freeman and Perkins, 1971; Westcott, 1986). There are statistical limitations: firstly the genotype's mean and marginal means of the environments are not independent from one another. This problem may be overcome if a large number of genotypes are used (Freeman and Perkins, 1971). Secondly, errors associated with the slopes of the genotypes are not statistically independent (Crossa, 1990) and thirdly, this method assumes a linear relationship between interaction and environmental means, which is not always the case and results may be misleading (Westcott, 1986).

Biologically the limitation seems to be in the case where only a few low or high yielding sites are included in the analysis and the genotype's position in the range is mostly determined by its performance in a few extreme environments (Westcott, 1986; Crossa, 1990).

2.7.2.1.2 Ecovalence (W_i)

Wricke (1962) proposed using the contribution of each genotype to the G x E interaction sum of squares as a stability measure and defined this concept of statistics as ecovalence (W_i). Ecovalence is simple to calculate and it is expressed as:

$$W_i = r\sum_j(\overline{Y}_{ij.} - \overline{Y}_{i..} - \overline{Y}_{.j.} + \overline{Y}...)^2$$

where, Y_{ij} is the mean performance of genotype *i* in the j^{th} environment and $Y_{i.}$ and $Y_{.j.}$ are the genotype and environment mean deviations respectively, and $\overline{Y}...$ is the overall mean. For this reason, genotypes with a low W_i value have smaller deviations from the overall mean across environments and are thus more stable (Wricke, 1962). According to Becker and Léon (1988) ecovalence measures the contribution of a genotype to the G x E interaction; a genotype with zero ecovalence is regarded as stable. According to the meaning of the ecovalence, this stable genotype possesses a high ecovalence (low values of W_i = high ecovalence).

Becker and Léon (1988) illustrated (Fig. 2.3) ecovalence by using a numerical example of plot yields of genotypes *i* in various environments against the respective mean of environments.

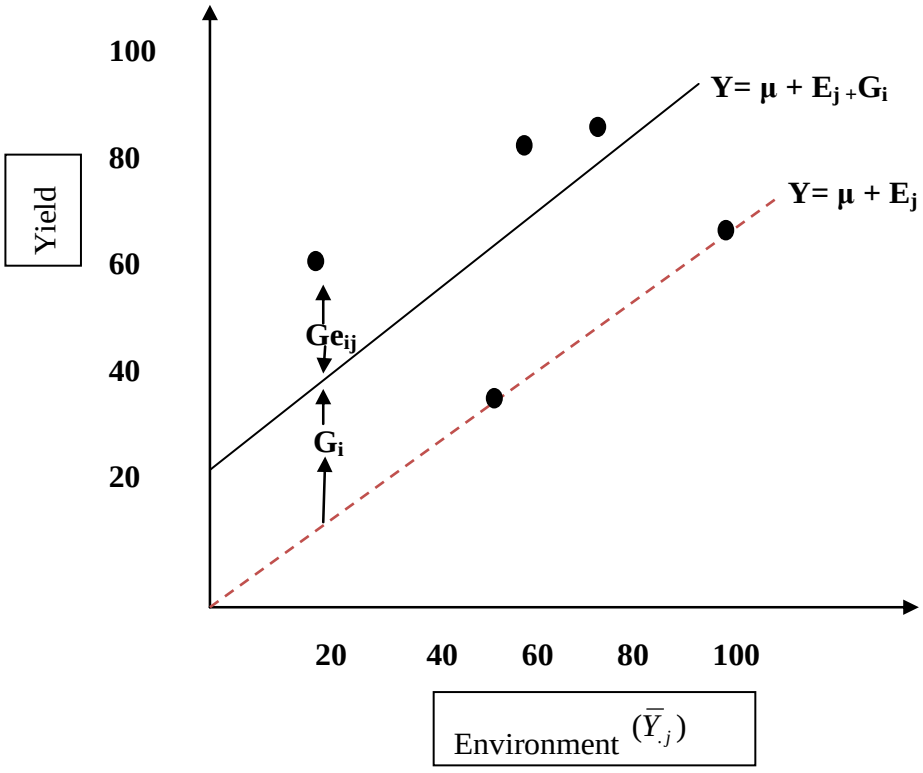

Figure 2.3. Graphical representation of G x E interactions: the stability statistics ecovalence (W_i) is the sum of squares of deviations from the upper straight line (Becker and Léon,1988).

The lower straight line estimates the average yield of all genotypes simply using information about the general mean (μ**)** and the environmental effects (E_j), while the upper line takes into account the genotype effect (G_i) and therefore estimates the yield of genotypes *i*. Deviations of yield from the upper straight line are the G x E interaction effects of genotype i and are summed and squared across environments and constitutes ecovalence.

2.7.2.1.3 Shukla's stability variance parameter (σ^2)

According to Shukla (1972), stability variance of genotype *i* is its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual (GE_{ij+} e_{ij})

matrix in a two way classification. Shukla (1972) termed this stability statistic as "stability variance" (σ^2) and is calculated as follows:

$$\sigma_i^2 = \frac{1}{(G-1)(G-2)(E-1)}\left[G(G-1)\sum_j (Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}..)^2 - \sum_i \sum_j (Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}..)^2 \right]$$

where Y_{ij} is the mean yield of the ith genotype in the jth environment, $\bar{Y}_{.j}$ is the mean of all genotypes in jth environments and $\bar{Y}..$ is the mean of all genotypes in all environments. For a genotype to be classified as stable, its stability variance (σ^2) should be equal to the environmental variance σ_e^2 which means that $\sigma_i^2 = 0$. Larger value of (σ_i^2) will thus indicate greater instability of genotype *i.* As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variance are not uncommon in variance component analysis. Negative estimates of (σ_i^2) may be equated to zero as usual (Shukla, 1972). Homogeneity of variance estimates can be tested using Shukla's (1972) approximate test (Lin et al., 1986). The stability variance is a linear combination of the ecovalence, and therefore both W_i and (σ_i^2) are equivalent for ranking purposes (Wricke and Weber, 1980).

2.7.2.1.4 Cultivar performance measure

Lin and Binns (1988) defined the superiority measure (Pi) of the i^{th} genotype as the mean square of distance between the i^{th} genotype and the genotype with the maximum response as:

$$P_i = \frac{\left[n(Y_{i.} - M..)^2 + (Y_{ij} - Y_i + M_{j.} + M..)^2 \right]}{2n}$$

where Y_{ij} is the average response of the i^{th} genotype in the j^{th} environment, Y_i. is the mean deviation of genotype *i,* M_j is the genotype with maximum response among all the genotypes in the j^{th} locations, and n is the number of locations. The smaller the value of P_i, the less its distance to the genotype with maximum yield and a better the genotype (Lin and Binns, 1988). A pairwise G x E interaction mean square between the maximum and each genotype is also calculated and it is similar to the method used by Plaisted and Peterson (1959), except that a) the stability statistics are based on both the average genotypic effects and G x E

interaction effects and b) each genotype is compared only with the one maximum response at each environment (Crossa, 1990).

2.7.2.2 Cross over interactions and non-parametric techniques for stability analysis

Lin and his colleagues (1986) explained this approach as the grouping of genotypes according to their similarity of response to a range of environments. These interactions may (not necessarily), result in different rank orders of genotypes in different environments. Crossover or qualitative interactions are more important in agricultural production than non-crossover or quantitative interactions (Baker, 1988; Crossa, 1990).

If a breeder is only interested in the existence of rank order differences over different environments, the non-parametric statistics for G x E interactions based on ranks provide a useful alternative to parametric statistics approaches currently used, which are based on absolute data. In these cases, the relative characteristics and comparisons of the genotypes are more important than absolute characterisation and comparisons. Other advantages are that the non-parametric measures are expected to be less sensitive to errors of measurement than parametric estimates and the addition or deletion of one or a few observations is not likely to cause great variation in the estimate as would be expected for parametric stability statistics (Nassar and Huehn, 1987). Huehn (1990) also indicated as advantages of non-parametric over the parametric statistics, the reduction or avoidance of the bias caused by outliers, and the fact that assumptions are not needed on the distribution of the phenotypic values and for many applications (e.g. selection in plant breeding and testing programme) the rank orders of the genotypes are the most essential information. It was therefore concluded that this method appeared to be the most relevant measure. However, the use of any of the stability parameters (parametric or non-parametric), understanding of the relationship and differences underlying the different stability parameters, the consistent relationships among the parameters and their repeatability are important for the efficient use of the methods in practical situations (Huehn, 1990).

According to Ramagosa and Fox (1993), analysis of ranks (stratified ranking) evaluates the proportion of sites where any genotype ranks in the top, middle or bottom third of the entries. A genotype found in the top third of the entries across sites may be considered as relatively well adapted. A genotype *'i'* is stable over environments if its ranks are the same over

environments. These measures of stability define it in the sense of homeostasis or ability of genotype to stabilise itself in different environments (Huehn, 1990). The similarity of two rankings in any two environments can be estimated by Spearman's rank correlation coefficient. Any two environments in which ranking of tested genotypes remains the same can be used for selection purposes, even if their overall yield levels are substantially different.

2.7.3 Additive main effects and multiplicative interactive method (AMMI)

Zobel et al. (1988) explained the limitations of the classical stability models. Accordingly, ANOVA falls short to detect a significant interaction component. Under PCA the significant genotype and environment main effects are not identified and linear regression models account for only a small portion of the interaction sum of squares. However, AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two-way data structure.

The AMMI method is used for three main purposes. The first is model diagnoses. AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool for diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the G x E interaction and it summarises patterns and relationships of genotypes and environments (Zobel et al., 1988; Crossa et al., 1990). The third use is for improving the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel et al., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes.

The AMMI model combines the ANOVA for the genotype and environment main effects with PCA of the G x E interaction. It has proven useful for understanding complex G x E interactions. The results can be graphed in a useful biplot that shows both main and interaction effects for genotypes and environments. AMMI combines ANOVA into a single model with additive and multiplicative parameters. The model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

where Y_{ij} is the yield of the i^{th} genotype in the j^{th} environment; μ is the grand mean; G_i and E_i are the genotype and environment deviations from the grand mean, respectively; λ_k is the eigenvalue of the PCA axis k; α_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k; n is the number of principal components retained in the model and e_{ij} is the error term.

In the ANOVA, the total variation is partitioned into three sources, namely genotypes, environment and G x E interactions. In this regard, a review of 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 G x E interactions is often larger than that of the genotypes. Hence, AMMI model can produce biplot graphs, which display the variability of genotypes and G x E interactions.

Regarding agricultural problems due to G x E interactions, 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). The first option is to select a high yielding, widely adapted genotype that is outstanding throughout the growing region of interest. The second option which is 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) and then breed and recommend varieties for each.

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 the performance of cultivars in similar sites and future years (Gauch, 1988).

The PCA of AMMI partitions G x E interactions into several orthogonal axes, the interaction principal component analyses (IPCA). Gauch and Zobel (1996) showed that AMMI 1 with IPCA 1 and AMMI 2 with IPCA 1 and IPCA 2 are usually selected and the graphical representation of axes, either as IPCA 1 or IPCA 2 against main effects or IPCA 1 against

IPCA 2 is generally informative. When AMMI 3 and higher models are presented for agricultural data, the third and higher IPCA axes are dominated by noise and have no predictive value (Van Eeuwijk, 1995).

Since AMMI has the biplot 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 1 value 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 score of the same sign. AMMI provides a better biological explanation of G x E 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 ANOVA and PCA in the AMMI model, along with prediction assessment, is a valuable approach for understanding G x E interaction and obtaining better yield estimates. The interaction is explained in the form of a biplot display where PCA scores are plotted against each other and it provides visual inspection and interpretation of the G x E interaction components. Integrating biplot display and genotypic stability statistics allows genotypes to be grouped based on similarity of performance across diverse environments (Tsige, 2002).

Like every other model, AMMI has its weaknesses. The nature of the residuals after fitting the additive main effects inevitably produces the appearance of multiplicative effects. Consequently the sum of square for fitting the multiplicative term, which may be read directly from the latent root proportions of explained variation, will tend to be much larger than the expected value. Therefore, it is not possible to recommend a single model to be used at all times, because these models, depending on the type of data and research purposes, can be complimentary rather than being competitive to each other. However, various studies indicate that, depending on the quality of the data, the different methods applied to an experiment will lead to similar conclusions (Baril et al., 1995).

Maideni et al. (2004) characterised maize testing environments in the Southern African Development Community (SADC) region and identified six groups based on consistent G x E

interactions across years and trials. They reported that drought and low N managed environments were each located in different categories. Long term climatic conditions and crop management affect site similarity but not national boundaries, demonstrating a scientific rationale for regional development and deployment of maize varieties. Mosisa and Habtamu (2008) studied the G x E interaction and stability of 20 genotypes at nine locations in Ethiopia for two years and identified cultivars with stable and specific adaptation. Bogale et al (2008) analysed G x E interaction of 28 drought tolerant maize hybrids along with two standard checks across 12 drought stressed and non-stressed environments. Based on specific adaptation, they successfully categorised the hybrids into four groups using the AMMI model.

Vasal et al. (1993a) evaluated diallel crosses of 10 QPM populations across locations and reported highly significant G x E interaction for grain yield, time to silk, plant height, and endosperm hardness. Pixley and Bjarnason (2002) evaluated stability of grain yield, endosperm modification and protein quality of hybrid and open pollinated QPM cultivars and reported high stability of open pollinated cultivars followed by double crosses, three-way- and single cross progeny, successively. They observed the reverse trend for endosperm modification score and suggested that more homogenous cultivars have greater stability for this trait. Glover et al. (2005) evaluated diallel crosses among Chinese and US germplasm and observed significant G x E interaction effects for grain yield, stalk lodging, ear height and days to silking.

2.7.4 GGE biplot and mega-environment analysis

Phenotypic expression of an organism is a function of its genotype (G), the surrounding environment (E) and the interaction between the two (G x E). The presence of significant G x E interactions challenges the process of selecting genotypes with higher performance. As a result, METs are broadly used to assess the suitability of genotypes for target environments (DeLacy et al., 1996). Numerous methods have been developed to reveal patterns of G x E interaction as discussed in the previous sections. Genotype plus Genotype x Environment (GGE) biplot analysis was developed to allow the use of some of the functions of these methods jointly. In total phenotypic variation, environment explains most of the variation and genotype and the interaction GE are usually small (Yan, 2002). However, only the G and G x

E interaction are relevant to cultivar evaluation, particularly when G x E interaction is identified as repeatable (Hammer and Cooper, 1996).

The term "GGE biplot" was first used by Yan and co-workers (Yan et al., 2000). It refers to a biplot as developed by Gabriel (1971) that displays the G plus GE of genotype-by-environment data. The key property of a GGE biplot is that it is based on environment-centred data, with the environment (tester) main effects (E) removed, and the genotype main effect (G) and the genotype by environment interaction (GE) retained and combined. Therefore, a biplot based on environment-centred data contains only G+GE, shortened as GGE (Yan et al., 2000; Yan, 2001).

GGE biplot is a data visualisation tool, which graphically shows a G x E interaction in a two way table (Yan et al., 2000). The analysis of GGE biplots is useful for: 1) mega-environment identification (e.g. “which-won-where” pattern), that facilitates the identification of specific genotypes for their mega-environment 2) evaluation of genotype performance and 3) environmental evaluation (the power to discriminate among genotypes in target environments) (Yan and Kang, 2003; Yan and Tinker, 2006). The construction of a GGE-biplot is based on the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environment-centred yield data, i.e. the yield variation due to GGE, to singular value decomposition. It is used to identify some of the least discriminating locations and representative test locations (Yan et al., 2007).

The difference between this method and AMMI analysis is that GGE biplot analysis is based on environment-centred PCA, whereas AMMI analysis is referred to as double centred PCA. The GGE model allows more functions and visualisation than AMMI and removes the impact of the environment main effect (E), allowing the breeder to focus on G and G x E, as only G and G x E interaction are very relevant to cultivar evaluation (Ding et al., 2007). The two sources of variation in the sites regression model (SREG) analysis of GGE are G and G x E. Samonte et al. (2005) considered the AMMI model best for: 1) estimating the magnitude and significance of the effects of G x E interaction and its principal components relative to G and E; 2) estimating the stability and adaptability of specific genotypes by plotting yield versus environment; 3) identifying mega-environments (environments with overlapping highest

yielding genotypes); and 4) identifying appropriate check genotypes for all locations as well as for specific locations. On the other hand the GGE biplot SREG analysis is best for:
1) illustrating the relative yield performance of genotypes at specific environments; 2) comparing performance of a genotype at different environments; 3) identifying the highest yielding genotypes at the different mega-environments; and 4) identifying ideal genotypes and test locations (Samonte et al., 2005).

The presence of biophysical and socioeconomic factors has an influence on the priority objectives of agricultural research. Agricultural production environments vary in terms of climate, soil, input use and consumer and producer preferences, among others. Hence, effective agricultural intervention programmes – like input supply, agronomic practices– should consider the importance of these factors. Development and deployment of cultivars for different mega-environments is the ultimate purpose of G x E interaction analysis (Yan et al., 2007). A mega-environment is defined as a group of locations that consistently share the same best cultivar(s) (Yan and Rajcan, 2002). This definition involves several essential elements:

1) mega-environments are defined by different winning cultivars, noting that different genotypes can be equally adapted to the same mega-environment and that a mega-environment may need different types of genotypes to stabilise the overall production;
2) mega-environment is a concept of geographical locations; and
3) cultivar x location interaction pattern should be repeatable across years.

All three aspects are essential for the classification of environments into different mega-environments. According to CIMMYT, a mega-environment is "a broad, not necessarily contiguous area, occurring in more than one country and frequently transcontinental, characterised by similar biotic and abiotic stresses, cropping systems, consumer preferences and for convenience, by volume of production" (Hartkamp et al., 2000).

The idea of mega-environments was originally proposed to help crop breeders utilise the presence of significant G x E interaction in the recommendation of varieties to specific environments. In the late 1980s and early 1990s, mega-environment analysis was an important condition in strategic planning, resource allocation and conduct of collaborative

research world-wide (CIMMYT, 1989). Since then, the concept has also been applied to the design and testing of new crop management practices (Sayre and Ramos, 1997) and other products of research. Mega-environment analysis also facilitates germplasm exchange among breeders, depending on the similarity of the target environments (Setimela et al., 2005; 2007).

Hartkamp et al. (2000) summarised the advantages of characterising global maize growing mega-environments as 1) priority setting and resource allocation by research managers; 2) directing efforts of scientists to relevant products; i.e., those most urgently needed for the most important mega-environments; 3) testing of the right type of germplasm in the appropriate environments which also helps to reduce the number of testing sites; 4) enhancing germplasm exchange among national research programmes and other partners based on their needs for target environments. Fig. 2.4 shows the classification of maize growing mega-environments of SSA based on the agro-climatic conditions of the countries. The dark and light green areas in each country are considered to be high potential environments for maize production.

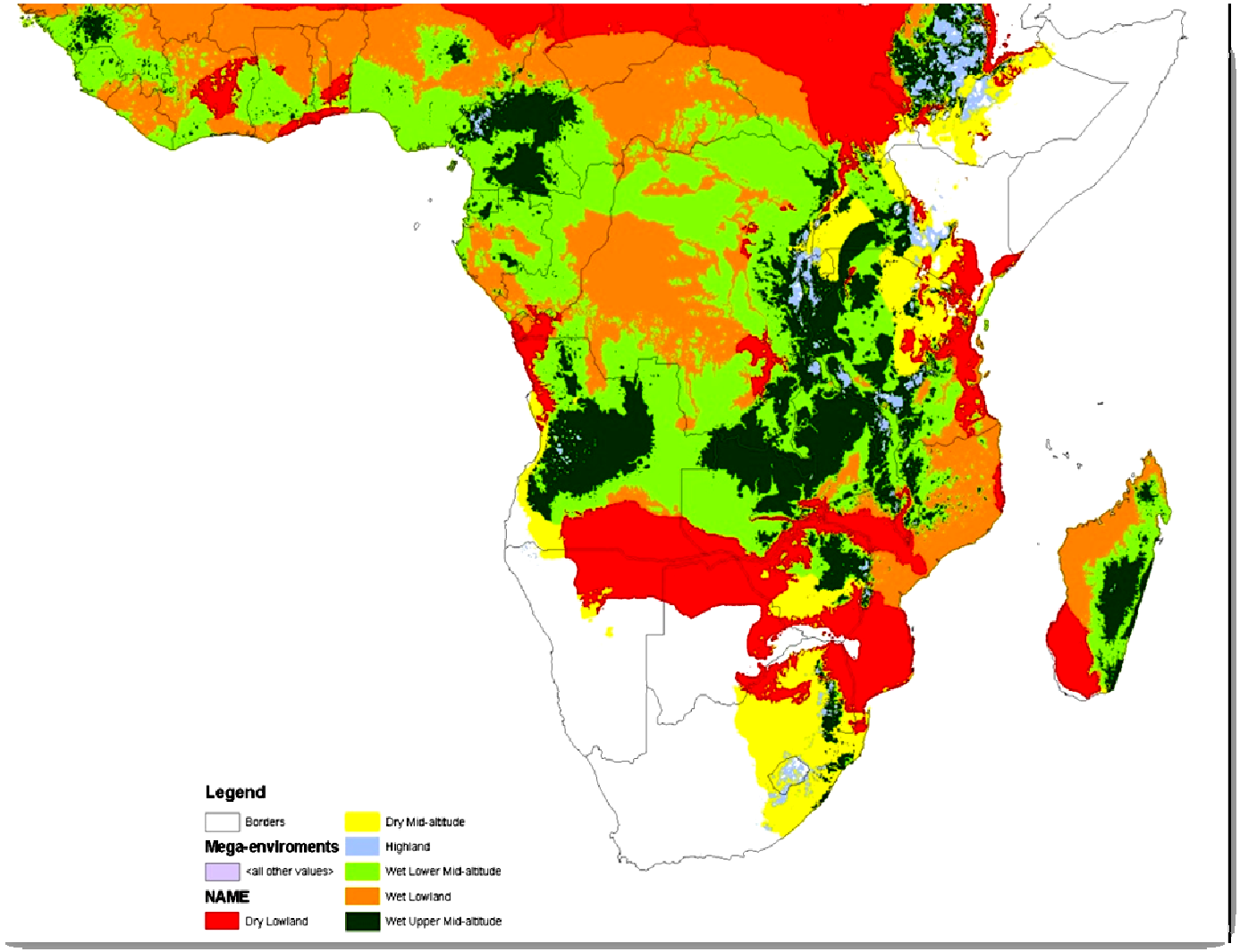

Figure 2.4 Maize mega-environments map of SSA (Setimela et al., 2005)

2.8 References

Alexander, R.J. 1987. Corn dry milling: processes, products, and applications. In: S.A. Watson, and P.E. Ramstad (Eds.). Corn: chemistry and technology. American Association of Cereal Chemists, St. Paul, Minnesota. pp. 351–376.

Allen, F.L., R.E. Comstock, and D.C. Rasmusson. 1978. Optimal environments for yield testing. *Crop Science* 18:747-751.

Annapurna, S., and G.M. Reddy. 1971. Modified opaque maize for possible applied use. *Current Science* 40:581-582.

Annicchiarico, P. 1997. Joint regression versus AMMI analysis of genotype-environment interactions for cereals in Italy. *Euphytica* 94:53-62.

Aquino, P., F. Carrion, R. Calvo, and D. Flores. 2001. Selected maize statistics. In: P.L. Pingali (Ed.) CIMMYT 1999-2000 World Maize Facts and Trends. Meeting world maize needs: Technological opportunities and priorities for the public sector. CIMMYT, Mexico, D.F.

Asche, G.L., A.J. Lewis, E.R.P. Jr, and J.D. Crenshaw. 1985. The nutritional value of normal and high lysine corns for weanling and growing-finishing swine when fed at four lysine levels. *Journal of Animal Science* 60:1412-1428.

Baker, R.J. 1988. Test for crossover genotype-environmental interactions. *Canadian Journal of Plant Sciences* 68:405-410.

Bänziger, M., and H.R. Lafitte. 1997. Efficiency of secondary traits for improving maize for low-nitrogen target environments. *Crop Science* 37:1110-1117.

Bänziger, M., and M. Cooper. 2001. Breeding for low input conditions and consequences for participatory plant breeding: Examples from tropical maize and wheat. *Euphytica* 122:503-519.

Bänziger, M., and A.O. Diallo. 2004. Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference.5-11 February 2002. CIMMYT/KARI Nairobi, Kenya. pp.189-194.

Bänziger, M., F.J. Betrán, and H.R. Lafitte. 1997. Efficiency of high nitrogen selection environments for improving maize for low nitrogen target environments. *Crop Science* 37:1103-1109.

Bänziger, M., S. Mugo, and G.O. Edmeades. 1999a. Breeding for drought tolerance in tropical maize - conventional approaches and challenges to molecular approaches. In: J.-M. Ribaut and D. Poland (Eds.). Molecular Approaches for the Genetic Improvement of Cereals for Stable Production in Water-Limited Environments. A Strategic Planning Wokshop.21-25 June 1999., CIMMYT, El Batan, Mexico. pp 69-72.

Bänziger, M., G.O. Edmeades, and H.R. Lafitte. 1999b. Selection for drought tolerance increases maize yields across a range of nitrogen levels. *Crop Science* 39:1035-1040.

Bänziger, M., N. Damu, M. Chisenga, and F. Mugabe. 1999c. Evaluating the drought tolerance of some popular maize hybrids grown in sub-Saharan Africa.In CIMMYT and EARO(Eds.).Maize Production Technologies for the Future: Challenges and Opportunities. Proceedings of the 6th Eastern and Southern African Regional Maize Conference. 21-25 September 1998. CIMMYT and EARO. CIMMYT and EARO, Addis Ababa, Ethiopia. pp. 61-63.

Bänziger, M., G.O. Edmeades, D. Beck, and M. Bellon. 2000. Breeding for Drought and N Stress Tolerance in Maize: From Theory to Practice. CIMMYT, Mexico, D.F., Mexico.

Bänziger, M., P.S. Setimela, D. Hodson, and B. Vivek. 2006. Breeding for improved abiotic stress tolerance in maize adapted to southern Africa. *Agricultural Water Management* 80:212-224.

Baril, C.P., J.B. Denis, R. Wustman, and F.A. Van Eeuwijk. 1995. Analyzing genotype-byenvironment interaction in Dutch potato variety trials using factorial regression. *Euphytica* 82:149-155.

Basford, K.E., and M. Cooper. 1998. Genotype-by-environment interactions and some considerations of their implications for wheat breeding in Australia. *Australian Journal of Agricultural Research* 49:153-174.

Beck, D.L., S.K. Vasal, and J. Crossa. 1991. Heterosis and combining ability among subtropical and temperate intermediate maturity maize germplasm. *Crop Science* 31:68-73.

Beck, D.L., F.J. Betran, M. Bänziger, and M. Willcox. 1997. From landrace to hybrid:Strategies for the use of source populations and lines in the development of drought tolerant cultivars. In: G.O. Edmeades, M. Bänziger, H.R. Mickelson and C.B. Pena-Valdiva (Eds.). Developing Drought and Low N-Tolerant Maize. Proceedings of a Symposium. 25-29 March 1996.CIMMYT, Mexico, D.F, Mexico. pp. 369-382.

Becker, H.C. 1981. Correlations among some statistical measures of phenotypic stability. *Euphytica* 30:835-840.

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

Below, F.E. 1997. Growth and productivity of maize under nitrogen stress. In: G.O. Edmeades, M. Bänziger, H.R. Mickelson and C.B. Pena-Valdiva (Eds.). Developing Drought and Low N-Tolerant Maize. Proceedings of a Symposium. 25-29 March 1996, CIMMYT, Mexico, D.F, Mexico. pp. 235-240.

Bernardo, R. 2002. Breeding for quantitative traits in plants. Stemma Press, Woodbury, Minnesota, USA.

Betran, F.J., A.J. Bockholt, F. Fojit, and G. Odvoy. 2003a. Registration of Tx807 maize line. *Crop Science* 43:1892-1893.

Betran, F.J., A.J. Bockholt, F. Fojit, and L. Rooney. 2003b. Registration of Tx811 maize line. *Crop Science* 43:1893-1894.

Betran, F.J., A.J. Bockholt, F. Fojit, and R. Waniska. 2003c. Registration of Tx802 maize line. *Crop Science* 43:1891-1892.

Betran, F.J., J.M. Ribaut, D.L. Beck, and D.G.d. Leon. 2003d. Genetic diversity,specific combining ability, and heterosis in tropical maize under stress and non stress environments. *Crop Science* 43:797-806.

Betran, F.J., J.M. Ribaut, D.L. Beck, and D.G.d. Leon. 2003e. Genetic analysis of inbred and hybrid grain yield under stress and non stress environments. *Crop Science* 43:807-817.

Betran, F.J., D. Beck, G.O. Edmeades, J.M. Ribaut, M.Bänziger, and C. Sanchez. 1999. Genetic analysis of abiotic stress tolerance in tropical maize hybrids. In: CIMMYT and EARO (Eds.). Maize Production Technology for the Future: Challenges and Opportunities.Proceedings of the 6th Eastern and Southern African Regional Maize Conference. 21-25 September, CIMMYT and EARO, Addis Ababa, Ethiopia. pp.69-71.

Bhan, M.K., N. Bhandari, and R. Bahl. 2003. Management of the severely malnourished child: perspective from developing countries. *Br. Med. J.* 326:146–151.

Bhatia, C.R., and R. Rabson. 1987. Relationship of grain yield and nutritional quality. In: R.A. Olson and K.J. Frey (Eds.). Nutritional Quality of Cereal Grains: Genetic and Agronomic Improvement. Agronomy Monograph No. 28. ASA, CSSA, and SSSA, Madison, Wisconsin, USA. pp. 11-43.

Bhatnagar, S., F.J. Betran, and L.W. Rooney. 2004. Combining ability of quality protein maize inbreds. *Crop Science* 44:1997-2005.

Bjarnason, M., and S.K. Vasal. 1992. Breeding of quality protein maize (QPM). *Plant Breeding Review* 9:181-216.

Bjarnason, M., W.G. Pollmer, and D. Klein. 1976. Inheritance of modified endosperm structure and lysine content in opaque-2 maize: I. Modified endosperm structure. *Cereal Research Communications* 4:401-410.

Bogale, G., J.B.J. van Rensburg, and C.S. van Deventer. 2008. AMMI analysis of genotype x environment interaction for grain yield in drought-tolerant maize (*Zea mays* L.). *East African Journal of Sciences* 2:1-6.

Bolaños, J., and G.O. Edmeades. 1993a. Eight cycles of selection for drought tolerance in low land maize. II. Response in reproductive behaviour. *Field Crops Research* 31:253-268.

Bolaños, J., and G.O. Edmeades. 1993b. Eight cycles of selection for drought tolerance in lowland tropical maize. I. Responses in grain yield, biomass and radiation utilization. *Field Crops Research* 31:233-252.

Bolaños, J., G.O. Edmeades, and L. Martinez. 1993. Eight cycles of selection for drought tolerance in lowland tropical maize. III. Responses in drought-adaptive physiological and morphological traits. *Field Crops Research* 31:269-286.

Borrell, A.K., G.L. Hammer, and E.V. Oosterom. 2001. Stay green: a consequence of the balance between supply and demand for nitrogen during grain filling. *Annals of Applied Biology* 138:91-95.

Bressani, R. 1991. Protein quality of high lysine maize for humans. *Cereal Foods World* 36:806-811.

Bressani, R. 1992. Nutritional value of high-lysine maize in humans. In: E.T. Mertz (Ed.). Quality Protein Maize. American Association of Cereal Chemists, St. Paul, Minessota, USA. pp. 205-224.

Bressani, R. 1995. Opaque-2 in human nutrition and utilization. In: B.A. Larkins and E.T.Mertz (Eds.). Quality Protein Maize: 1964-1994. Proceedings of International Symposium on Quality Protein Maize. 1-3 December 1994, EMBRAPA/CNPMS, Sete Lagoas, Brazil. pp. 41-63.

Bressani, R., L.G. Elias, and R.A. Gomez-Brenes. 1969. Protein quality of opaque-2 maize.Evaluation in rats. *Journal of Nutrition* 97:173-180.

Brown, W.L., R. Bressani, D.V. Glover, A.R. Hallauer, V.A. Johnson, and C.O. Qualset. 1988. Quality-protein maize: report of an ad hoc panel of the advisory committee on technology innovation, Board on Science and Technology for International Development, National Research Council, in cooperation with the Board on Agriculture, National Research Council. National Academy Press, Washington, D.C.

Burgoon, K.G., J.A. Hansen, D.A. Knabe, and A.J. Bockholt. 1992. Nutritional value of quality protein maize for starter and finisher swine. *Journal of Animal Science* 70:811-817.

Byrne, P.F., J. Bolaños, G.O. Edmeades, and D.L. Eaton. 1995. Gains from selection under drought versus multilocation testing in related tropical maize populations. *Crop Science* 35:63-69.

Ceccarelli, S. 1989. Wide adaptation: How wide? *Euphytica* 40:197-205.

Chahal, G.S., and S.S. Gosal. 2002. Principles and procedures of plant breeding: Biotechnological and Conventional approaches. Narosa Publishing House, New Delhi, India.

Chapman, S.C., J. Crossa, and G.O. Edmeades. 1997. Genotype by environment effects and selection for drought tolerance in tropical maize. I. Two mode pattern analysis of yield. *Euphytica* 95:1-9.

Christensen, L.E., F.E. Below, and R.H. Hageman. 1981. The effect of ear removal on senescence and metabolism of maize. *Plant Physiology* 68:1180-1185.

CIMMYT. 1989. Toward the 21st Century: CIMMYT's Strategy. CIMMYT, Mexico D.F.

CIMMYT. 1999. 1997/98 CIMMYT World Maize Facts and Trends. Maize Production in Drought Stressed Environments: Technical Options and Research Resource Allocation. CIMMYT, Mexico D.F., Mexico.

CIMMYT. 2000. CIMMYT in 1999-2000: Science and Sustenance. CIMMYT, Mexico D.F., Mexico.

CIMMYT. 2001. 2000/2001 World maize facts and trends. Mexico D.F.

CIMMYT. 2002. The development and promotion of quality protein maize in sub-Saharan Africa. Progress Report Submitted to the Nippon Foundation. CIMMYT, Harare, Zimbabwe.

CIMMYT. 2003a. The development and promotion of quality protein maize in sub-Saharan Africa. Progress Report Submitted to Nippon Foundation. CIMMYT, Mexico, D.F.,Mexico.

CIMMYT. 2003b. The development and promotion of quality protein maize in sub-Saharan Africa. Progress Report Submitted to Nippon Foundation. CIMMYT, Mexico, D.F.

CIMMYT. 2005. The development and promotion of quality protein maize in sub-Saharan Africa. Progress Report Submitted to the Nippon Foundation. CIMMYT, Mexico, D.F.

CIMMYT. 2007. Seeding Innovation.Nourishing Hope: CIMMYT Annual Report 2006-2007. CIMMYT, Mexico, D.F.

Clark, H.E., D.V. Glover, J.L. Betz, and L.B. Bailey. 1977. Nitrogen retention of young men who consumed isonitrogenous diets containing normal, opaque-2, or sugary-2 opaque-2 corn. *Journal of Nutrition* 107:404-414.

Cooper, M., and D.E. Byth. 1996. Understanding plant adaptation to achieve systematic applied crop improvement: A fundamental challenge. In: M. Cooper and G.L. Hammer (Eds.). Plant Adaptation and Crop Improvement. CAB International and IRRI, UK. pp. 5-23.

Crossa, J. 1990. Statistical analyses of multilocation trials. *Advances in Agronomy* 44:55-85.

Crossa, J., and P.L. Cornelius. 1997. Sites regression and shifted multiplicative model clustering of cultivar trial sites under heterogeneity of error variances. *Crop Science* 37:406-415.

Crossa, J., H.G. Gauch, and R.W. Zobel. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials *Crop Science* 30:493-500.

Dabholkar, A.R. 1999. Elements of biometrical genetics. Concept Publishing Company, New Delhi, India.

Darrigues, A., K.R. Lamkey, and M.P. Scott. 2006. Breeding for grain amino acid composition in maize. In: K.R. Lamkey and M. Lee (Eds.). Plant breeding: The Arnel R. Halluar international symposium. Blackwell Publishing Iowa, USA. pp. 335-344.

Dass, S., Y.P. Dang, A.K. Dhawan, N.N. Singh, and S. Kumar. 1997. Morhophysiological basis for breeding drought and low-N tolerant maize genotypes in India. In: G.O.Edmeades, M. Bänziger, H.R. Mickelson and C.B. Pena-Valdiva (Eds.). Developing Drought and Low N-Tolerant Maize. Proceedings of a Symposium. 25-29 March 1996, CIMMYT, Mexico, D.F. pp. 106-111.

DeLacy, I.H., M. Cooper, and K.E. Basford. 1996. Relationships among analytical methods used to study genotype-by-environment interactions and evaluation of their impact on response to selection. In: M.S. Kang and Jr. H.G. Gauch (Eds.). Genotype-by-Environment Interaction. CRC press: Boca Raton, New York. pp. 51-84.

Dencic, S., R. Kastori, B. Kobiljski, and B. Duggan. 2000. Evaluation of grain yield and its components in wheat cultivars and landraces under near optimal and drought conditions. *Euphytica* 113:43–52.

Denmead, O.T., and R.H. Shaw. 1960. The effects of soil moisture stress at different stages of growth on the development and yield of corn. *Agronomy Journal* 52:272-274.

DeVries, J., and G. Toenniessen. 2001. Securing the Harvest: Biotechnology, Breeding and Seed Systems for African Crops. CABI Publishing, Wallingford, UK.

Diallo, A.O., J. Kikafunda, L. Welde, O. Odongo, Z.O. Mduruma, W.S. Chivatsi, D.K.Friesen, S. Mugo, and M. Bänziger. 2004. Drought and low nitrogen tolerant hybrids for the moist mid altitude ecology of eastern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 206-212.

Ding, M., B. Tier, and W. Yan. 2007. Application of GGE biplot analysis to evaluate genotype(G), environment(E) and GxE interaction on *P. radiata*: case study. Australasia Forest Genetics Conference, 11-14 April 2007, The Old Woolstore, Hobart, Tasmania, Australia.

Duvick, D.N., and K.G. Cassman. 1999. Post-green revolution trends in yield potential of temperate maize in the North-Central United States. *Crop Science* 39:1622-1630.

Dwyer, L.M., A.M. Anderson, B.L. Ma, D.W. Stewart, M. Tollenaar, and E. Gregorich. 1995. Quantifying the non-linearity and chlorophyll meter response to corn leaf nitrogen concentration. *Canadian Journal of Plant Science* 75:179-182.

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

Edmeades, G.O., J. Bolaños, and H.R. Lafitte. 1992. Progress in breeding for drought tolerance in maize. In: D. Wilkinson (Eds.). Proceedings of the 47th Annual Corn and Sorghum Industrial Research Conference. ASTA, Washington, D.C., USA. pp. 93-111.

Edmeades, G.O., J. Bolaños, M. Hernandez, and S. Bello. 1993. Causes for silk delay in a lowland tropical maize population. *Crop Science* 33:1029-1035.

Edmeades, G.O., M. Bänziger, H. Campos, and J. Schussler. 2006. Improving tolerance to abiotic stresses in staple crops: A random or planned process. In: K.R. Lamkey and M. Lee (Eds.). Plant Breeding: The Arnel R. Hallauer International Symposium. Blackwell Publishing, Iowa, USA. pp. 293-309.

Edmeades, G.O., H.R. Lafitte, J. Bolaños, S. Chapman, M. Bänziger, and J.A. Deutsch. 1994. Developing maize that tolerates drought or low nitrogen conditions. In: G. O. Edmeades and J. A. Deutsch (Eds.). Stress Tolerance Breeding: Maize that Resists Insects, Drought, Low Nitrogen, and Acid Soils. CIMMYT, Mexico, D.F. pp. 21-68.

Emily, T.N., and A.T. Sherry. 2010. Maize: A Paramount Staple Crop in the Context of Global Nutrition. *Comprehensive Reviews in Food Science and Food Safety* 9:417-436.

FAOSTAT. 2008. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

FAOSTAT. 2010. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

Feil, B., S.B. Moser, S. Jampatong, and P. Stamp. 2005. Mineral composition of the grains of tropical maize variteis as affected by pre-anthesis drought and rate of nitrogen fertilization. *Crop Science* 45:516-523.

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

Fischer, K.S., E.C. Jonson, and G.O. Edmeades. 1983. Breeding and Selection for Drought Resistance in Tropical Maize. CIMMYT, Mexico D.F.

Freeman, G.H. 1990. Modern statistical methods for analysing genotype x environment interactions. In: Kang, M.S. (Ed.). Genotype-by-environment interaction and plant breeding. Louisiana State University Agricultural Center, Baton Rouge, La. pp. 118-125.

Freeman, G.H., and J.M. Perkins. 1971. Environmental and genotype-environmental components variability. VIII. Relations between genotypes grown in different environments and measures of these environments. *Heredity* 27:15-23.

Gardner, H.W., and G.E. Inglett. 1971. Food products from corn germ: enzyme activity and oil stability. *Journal of Food Science* 36:645-648.

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

Gauch, H.G., and R.W. Zobel. 1996. AMMI analyses of yield trials. In: M.S. Kang and H.G. Gauch (Eds.). Genotype by Environment Interaction. CRC, Boca Raton, Florida, USA. pp. 85-122.

Gauch, H.G., and R.W. Zobel. 1997. Identifying mega-environments and targeting genotypes. *Crop Science* 37:311-326.

Gevers, H.O. 1995. QPM breeding in Africa. In: B.A. Larkins and E.T. Martz (Eds.). Quality Protein Maize: 1964-1994. Proceedings of the International Symposium on Quality Protein Maize. 1-3 December 1994, EMBRAPA/CNPMS, Sete Lagoas, Brazil. pp. 217-229.

Gevers, H.O., and J.K. Lake. 1992. Development of modified opaque-2 maize in South Africa. In: E. T Mertz (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minnesota, USA. pp. 49-78.

Gissa, D.W. 2008. Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. PhD Thesis, Department of Plant Sciences (Plant Breeding), University of the Free State, Bloemfontein, South Africa.

Glover, M.A., D.B. Willmot, L.L. Darrah, B.E. Hibbard, and X. Zhu. 2005. Diallel analyses of agronomic traits using Chinese and U.S. maize germplasm. *Crop Science* 45:1096-1102.

Glover, D.V. 1992. Corn protein - Genetics, breeding, and value in foods and feeds. In: E.T Mertz (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St.Poul, Minnesota, USA. pp. 9-26.

Graham, G.G., J. Lembcke, and E. Morales. 1990. Quality protein maize as the sole source of dietary protein and fat for rapidly growing young children. *Pediatrics* 85:85-91.

Graham, G.G., D.V. Glover, G.L.d. Romana, E. Morales, and W.C. MacLean. 1980. Nutritional value of normal, opaque-2 and sugary-2 opaque-2 maize hybrids for infants and children. I. Digestibility and utilization. *Journal of Nutrition* 110:1061-1069.

Grant, R.F., B.S. Jackson, J.R. Kiniry, and A. G.F. 1989. Water deficit timing effects on yield components in maize. *Agronomy Journal* 81:61-65.

Gupta, S.C., U.L. Asnani, and B.P. Khare. 1970. Effect of the opaque-2 gene in maize (*Zea mays* L.) on the extent of infestation by Sitophilus oryzae L. *Journal of Stored Products Research* 6:191-194.

Habben, J.E., A.W. Kirlies, and B.A. Larkins. 1993. The origin of the lysine containing proteins in opaque-2 maize endosperm. *Plant Molecular Biology* 23:825-838.

Hadji, T.H. 2004. Combining ability analysis for yield and yield-related traits in quality protein maize (QPM) inbred lines. M.Sc. Thesis., School of graduate studies, Alemaya University, Ethiopia.

Hallauer, A.R., W.A. Russell, and K.R. Lamkey. 1988. Corn breeding. In: G.F. Sprague and J.W. Dudley (Eds.). Corn and corn improvement. 3rd ed. Agronomy Monograph No.18. ASA, CSSA, and SSSA, Madison, Wisconsin. pp. 463-564.

Hammer, G.L., and M. Cooper. 1996. Plant Adaptation and Crop Improvement. CAB International, Wallingford.

Hartkamp, A.D., J.W. White, A.R. Aguila, M. Bänziger, G. Srinivasan, G. Granados, and J. Crossa. 2000. Maize Production Environments Revisited: A GIS-based Approach. CIMMYT, Mexico, D.F.

Hassan, R.M., M. Mekuria, and W. Mwangi. 2001. Maize breeding research in eastern and southern Africa: Current status and impacts of past investments made by public and private sectors 1966-1997. CIMMYT, Mexico, D.F.

Heisey, P.W., and G.O. Edmeades. 1999. Maize production in drought stressed environments:Technical options and research resource allocation. CIMMYT 1997/98 World Maize Facts and Trends. CIMMYT, Mexico, D. F.

Hernandez, H.H., and L.S. Bates. 1969. A modified method for rapid tryptophan analysis in maize. CIMMYT Research Bulletin no. 13.

Hohls, T., P.E. Shanahan, G.P. Clarke, and H.O. Gevers. 1996. Genetic control of kernel modification found in South African quality protein maize inbred lines. *Euphytica* 87:103-109.

Huehn, M. 1990. Non-parametric estimation of and testing of genotype-environment interactions by ranks. In: M.S. Kang (Ed.). Genotype-by-environment interactions and plant breeding. Louisiana State University Agricultural Center. pp. 63-69.

Hussain, T., S. Abbas, M.A. Khan, and N.S. Scrimshaw. 2004. Lysine fortification of wheat flour improves selected indices of the nutritional status of predominately cereal eating families in Pakistan. *Food and Nutr. Bull.* 25:114-122.

Hyman, G., S. Fujisaka, P. Jones, S. Wood, C. de Vincente, and J. Dixon. 2008. Strategic approaches to targeting technology generation: Assessing the coincidence of poverty and drought-prone crop production. *Agricultural Systems* 98:50–61.

Inglett, G.E. 1970. Food uses of corn around the world. In: G.E. Inglett (Ed.). Corn: culture, processing, products. Avi Publishing, Westport Conn. pp. 138–150.

Jacobs, B.C., and C.J. Pearson. 1991. Potential yield of maize, determined by rates of growth and development of ears. *Field Crops Research* 27:281-298.

Johnson, L.A., C.L. Hardy, C.P. Baumel, T.H. Yu, and J.L. Sell. 2001. Identifying valuable corn quality traits for livestock feed. *Cereal Foods World* 46:472-481.

Kamara, A.Y., J.G. Kling, S.O. Ajala, and A. Menkir. 2004. Vertical root-pulling resistance in maize is related to nitrogen uptake and yield. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 228-232.

Kang, M.S. 1996. Using genotype-by-environment interaction for crop cultivar development. *Advances in Agronomy* 62:199-252.

Kang, M.S. 1998. Using genotype by environment interaction for crop cultivar development. *Advances in Agronomy* 62:199-246.

Knabe, D.A., J.S. Sullivan, K.G. Burgoon, and A.J. Bockholt. 1992. QPM as a swine feed. In: E. T Mertz (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St. Paul, Minnesota, USA. pp. 225-238.

Krivanek, A.F., H.D. Groote, N.S. Gunaratna, A.O. Diallo, and D.K. Friesen. 2007. Breeding and disseminating quality protein maize (QPM) for Africa. *African Journal of Biotechnology* 6:312-324.

Laegreid, M., O.C. Bockman, and O. Kaarstad. 1999. Agriculture, Fertilizers and the Environment. CBI Publishing, U.K.

Lafitte, H.R. 2000. Abiotic stresses affecting maize. In: R.L. Paliwal (Ed.). Tropical maize improvement and production. FAO plant production and protection series No. 28, Rome, Italy. pp. 93-103.

Lafitte, H.R., and G.O. Edmeades. 1994a. Improvement for tolerance to low soil nitrogen in tropical maize. I. Selection criteria. *Field Crops Research* 39:1-14.

Lafitte, H.R., and G.O. Edmeades. 1994b. Improvement for tolerance to low soil nitrogen in tropical maize. III. Variation in yield across environments. *Field Crops Research* 39:27-38.

Lafitte, H.R., and G.O. Edmeades. 1994c. Improvement for tolerance to low soil nitrogen in tropical maize. II. Grain yield, biomass production, and N accumulation. . *Field Crops Research* 39:15-25.

Lal, R., A.S.R. Juo, and B.T. Kang. 1982. Chemical appraoches towards increasing water availability to crops including minimum tillage systems.In: L.W. Shemilt (Ed.). Chemistry and World Food Supplies: the new frontiers CHEMRAWN II, Manila, Philippines. pp.55-77.

Lambert, R.J., D.E. Alexander, and J.W. Dudley. 1969. Relative performance of normal and modified protein (opaque-2) maize hybrids. *Crop Science* 9:242-243.

Langyintuo, A.S., W. Mwangi, A.O. Diallo, J. MacRobert, J. Dixon, and M. Bänziger. 2010. Challenges of the maize seed industry in eastern and southern Africa: A compelling case for private-public intervention to promote growth. *Food Policy* 35:323-331.

Larkins, B.A., C.R. Lending, and J.C. Wallace. 1993. Modification of maize-seed-protein quality. *American Journal of Clinical Nutrition* 58:264-269.

Lemcoff, J.H., and R.S. Loomis. 1986. Nitrogen influences on yield determination in maize. *Crop Science* 26:1017-1022.

Lin, C.S., and M.R. Binns. 1988. A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Sciences* 68:193-198.

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

Lin, K.R., A.J. Bockholt, C.W. Magill, and J.D. Smith. 1997. Changes in soluble endosperm proteins associated with selection of quality protein maize lines. *Maydica* 42:355-362.

Link, W., A.A. Abdelmula, E.v. Kittlitz, S. Bruns, H. Riemer, and D. Stelling. 1999. Genotypic variation for drought tolerance in Vicia faba. *Plant Breeding* 118:477-483.

Lodha, M.L., H.O. Gupta, P.C. Ram, and J. Singh. 1976. Some biochemical characteristics of modified phenotype strains of opaque-2. *Current Science* 45:285-286.

Lopes, M.A., and B.A. Larkins. 1996. Molecular biology and traditional breeding applied to the improvement of maize nutritional quality. In: B.W.S. Sobral (Ed.). The Impact of Plant Molecular Genetics. Birkhauser, Boston, USA. pp. 273-296.

Lopes, M.A., K. Takasaki, D.E. Bostwich, T. Helentjaris, and B.A. Larkins. 1995. Identification of two opaque-2 modifier loci in quality protein maize. *Molecular Genetics and Genomics* 247:603-613.

Lopez-Pereira, M.A. 1992. The economics of quality protein maize as an animal feed. Case studies of Brazil and El Salvador. CIMMYT Economics working paper 92-06. CIMMYT, Mexico, D.F.

Lutz, W., W. Sanderson, and S. Scherbov. 2001. The end of world population growth. *Nature* 412:543-545.

Ma, B.L., and L.M. Dwyer. 1998. Nitrogen uptake and use of two contrasting maize hybrids differing in leaf senescence. *Plant and Soil* 199:283-291.

Ma, Y., and O.E. Nelson. 1975. Amino acid composition and storage proteins in two new high-lysine mutants in maize. *Cereal Chemistry* 52:412.

Maideni, F., M. Bänziger, P. Setimela, and J. Betran. 2004. Characterization of maize testing environments in the southen Africa Development Community (SADC) region. In: D. Polland, M. Sawkins, J. M. Ribaut and D. Hoisington (Eds.). Resilient crops for water limited Environments: Proceedings of a workshop Held at Cuernavaca, Mexico. 24-28 May 2004. CIMMYT, Mexico D.F., Mexico. pp. 110-11.

Manda, T.H.E., and C. Mwambula. 1999. Screening and selection of tropical maize genotypes for drought tolerance using primary and secondary traits. In: CIMMYT and EARO (Eds.). Maize Production Technology for the Future: Challenges and Opportunities. Proceedings of the 6th Eastern and Southern African Regional Maize Conference.21-25 September, CIMMYT and EARO, Addis Ababa, Ethiopia. pp. 32-34.

McCullough, D.E., P. Girardin, M. Mihajlovic, A. Aguilera, and M. Tollenaar. 1994. Influence of N supply on development and dry matter accumulation of an old and new maize hybrid. *Canadian Journal of Plant Science* 74:471-477.

McWhirter, K.S. 1971. A floury endosperm, high lysine locus in chromosome 10. *Maize Gent. Coop. News Lett* 45:184.

Mertz, E.T. 1992. Discovery of high-lysine, high tryptophan cereals. In: E. T. Mertz (Eds.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minesota, USA. pp. 1-8.

Mertz, E.T. 1995. Thirty years of opaque-2 maize. In: B.A. Larkins and E.T. Mertz (Eds.). Quality protein maize: 1964-1994. Proceedings of the International Symposium on Quality Protein Maize.1-3 December 1994, EMBRAPA/CNPMS, Sete Lagos, Brazil. pp.1-9.

Mertz, E.T., L.S. Bates, and O.E. Nelson. 1964. Mutant gene that changes protein composition and increase lysine content of maize endosperm. *Science* 145:279-280.

Misra, P.S., R. Jambunathan, E.T. Mertz, D.V. Glover, H.M. Barbosa, and K.S.M. Whirter. 1975. Endosperm protein synthesis in maize mutants with increased lysine content. *Science* 176:1426-1427.

Moll, R.H., E.J. Kamprath, and W.A. Jackson. 1982. Analysis and interpretation of factors which contribute to efficiency of N utilization. *Agronomy Journal* 74:502-564.

Moll, R.H., W.A. Jackson, and R.L. Mickelsen. 1994. Recurrent selection for maize grain yield: Dry matter and nitrogen accumulation and partitioning changes. *Crop Science* 34:874-881.

Monneveux, P., P.H. Zaidi, and C. Sanchez. 2005. Population density and low nitrogen affects yield-associated traits in tropical maize. *Crop Science* 45:535-545.

Moro, G.A., M.A. Lopes, J.E. Habben, B.R. Hamaker, and B.A. Larkins. 1995. Phenotypic effects of opaque-2 modifier genes in normal maize endosperm. *Cereal Chemistry* 72:94-99.

Moro, G.L., J.E. Habben, B.R. Hamaker, and B.A. Larkins. 1996. Characterization of the variability in lysine content for normal and opaque-2 maize endosperm. *Crop Science* 36:1651-1659.

Mosisa, W. 2005. Genetic and Crop-Physiological Basis of Nitrogen Efficiency in Tropical Maize: Field Studies, PhD Dissertation, University of Hannover, Hannover, Germany.

Mosisa, W., and Z. Habtamu. 2008. Genotype x Environment interaction and yield stability of maize. *East African Journal of Sciences* 2:7-12.

Muza, L., S.R. Waddington, and M. Bänziger. 2004. Preliminary results on the response of 'nitrogen use efficient' OPV and hybrid maize to N fertilizer on smallholder fields in Zimbabwe. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 245-250.

Nassar, R., and M. Huehn. 1987. Studies in estimation of phenotypic stability: Test of significance for non-parametric measures of phenotypic stability. *Biometrics* 43:45-53.

Nelson, O.E., E.T. Mertz, and L.S. Bates. 1965. Second mutant gene affecting the amino acid pattern of maize endosperm proteins. *Science* 150:149-170.

Ngaboyisonga, C., K. Njoroge, D. Kirubi, and S.M.Githiri. 2006. Effects of low nitrogen and drought on grain yield and endosperm hardness of quality protein maize single cross hybrids. In: International plant breeding symposium, Mexico D.F.

NRC. 1988. Quality Protein Maize. National Research Council. National Academic Press, Washington, DC.

Osborne, T.B., and S.H. Clapp. 1908. Hydrolysis of the proteins of maize, Zea mays. *American Journal of Physiology* 20:477-493.

Osborne, T.B., and L.B. Mendel. 1914. Nutritive properties of maize kernel. *Journal of Biological Chemistry* 18:1-16.

Osei, S.A., D.B. Okai, K. Ahenkora, B.D. Dzah, W. Haag, S. Twumasi-Afriyie, and A.K. Tua. 1994a. Quality protein maize as main source of energy and amino acids in the diets of starter pigs.Proceedings of Ghanaian Animal Science Symposium 22: 31-36. .

Osei, S.A., C.C. Atuahene, A. Donkoh, K. Kwarteng, K. Ahenkora, B.D. Azah, W. Haag, and S. Twumasi-Afriyie. 1994b. Further studies on the use of quality protein maize as a feed ingrident for broiler chickens. Proceedings of Ghanaian Animal Science Symposium 22: 51-55.

Osei, S.A., A. Donkoh, C.C. Atuahene, D.B. Okai, A.K. Tua, W. Haag, B.D. Dzah, K.Ahenkora, and S. Twumasi-Afriyie. 1994c. Quality protein maize as a broiler feed ingredient. Proceedings of Ghanaian Animal Science Symposium 22: 45-49.

Paez, A.V., J.L. Helm, and M.S. Zuber. 1969. Lysine content of opaque-2 maize kernels having different phenotypes. *Crop Science* 9:251-252.

Pearson, C.J., and B.C. Jacob. 1987. Yield components and nitrogen partitioning of maize in response to nitrogen before and after anthesis. *Australian Journal of Agricultural Research* 38:1001-1009.

Pellet, P.L., and S. Gosh. 2004. Lysine fortification: Past, present, and future. *Food and Nutr. Bull* 25:107-113.

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

Pingali, P.L., and S. Pandey. 2001. Meeting world maize needs: Technological opportunities and priorities for public sector. CIMMYT 1999/2000 World Maize Facts and Trends, CIMMYT, Mexico, D. F., Mexico.

Pixley, K.V., and M.S. Bjarnason. 1993. Combining ability for yield and protein quality among modified endosperm opaque-2 tropical maize inbreds. *Crop Science* 33:1229-1234.

Pixley, K.V., and M.S. Bjarnason. 2002. Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42:1882-1890.

Plaisted, R.L. 1960. A shorter method for evaluating the ability of selections to yield consistently over locations. *American Potato Journal* 37:166-172.

Plaisted, R.L., and L.C. Peterson. 1959. A technique for evaluating the ability of selections to yield consistently in different locations or seasons. *American Potato Journal* 36:381-385.

Prasanna, B.M., S.K. Vasal, B. Kassahun, and N.N. Singh. 2001. Quality Protein Maize. *Current Science* 81:1308-1319.

Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Rahmanfer, A., and B.R. Hamaker. 1999. Potential nutritional contribution of quality protein maize: A close-up on children in poor communities. *Ecology of food and nutrition* 38:165-182.

Ramagosa, I., and P.N. Fox. 1993. Genotype x Environment interaction and adaptation. In: M.D. Hayward, N.O. Bosemark and I. Ramagosa (Eds.). Plant breeding: Principles and prospects. Chapman and Hall, London. pp. 373-390.

Reeves, T., P. Pinstrup-Andersen, and R. Pandia-Lorch. 1999. Food security and the role of agricultural research. In: J.G. Coors and S. Pandey (Eds.). The Genetics and Exploitation of Heterosis in Crops. ASA, CSSA, and SSSA, Madison,, Wisconsin. pp.1-5.

Rosielle, A.A., and J. Hamblin. 1981. Theoretical aspects of selection for yield in stress and non-tress environments. *Crop Science* 21:943-946.

Russel, W.K., K.M. Eskridge, D.A. Travnicek, and F.R. Guillen-Portal. 2003. Clustering environments to minimize changes in rank of cultivars. *Current Science* 43:858-864.

Salamini, F., N. Di Fonzo, E. Gentinetta, and C. Soave. 1979. A dominant mutation interfering with protein accumulation in maize seeds, in seed protein improvements in cereals and grain legumes. IAEA, Vienna.

Salamini, F., N. Di Fonzo, E. Fornasari, E. Gentinetta, R. Reggiani, and C. Soave. 1983. Mucronate, Mc, a dominant gene of maize which interacts with opaque-2 to suppress zein synthesis. *Theoretical and Applied Genetics* 65:123.

Samonte, S.O.P.B., L.T. Wilson, A.M. McClung, and J.C. Medley. 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. *Crop Science* 45:2414-2424.

Sattelmacher, B., W.J. Horst, and H.C. Becker. 1994. Factors that contribute to genetic variation for nutrient efficiency of crop plants. *Journal of Plant Nutrition and Soil Science* 157:215-224.

Sayre, K.D., and O.H.M. Ramos. 1997. Applications of raised-bed planting systems to wheat. Wheat special report no. 31. CIMMYT, Mexico D.F.

Schnieder, B.H. 1955. The nutritive value of corn. In: G.F. Sprague (Eds.). Corn and corn improvement. American Society of Agronomy, Madison, Wiscosin, USA. pp. 637-678.

Setimela, P.S., B. Vivek, M. Bänziger, J. Crossa, and F. Maideni. 2007. Evaluation of early to medium maturing open pollinated maize varieties in SADC region using GGE biplot based on the SREG model. *Field Crops Research* 103:161–169.

Setimela P.S., Z. Chitalu, J. Jonazi, A. Mambo, D. Hodson, and M. Bänziger. 2005. Environmental classification of maize testing sites in the SADC region and its implication for collaborative maize breeding strategies in the subcontinent. *Euphytica* 145:123-132.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity* 29:237-245.

Simmonds, N.W. 1991. Selection for local adaptation in a plant breeding programme. *Theoretical and Applied Genetics* 82:363-367.

Singh, B.D. 2005. Plant breeding: Principles and methods. 7th ed. Kalyani Publishers, New Delhi, India.

Smalberger, S., and A.S. du Toit. 2004. Identification of maize cultivars tolerant to low soil fertility in south Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 202-205.

Soave, C., R. Reggiani, N. Di Fonzo, and F. Salamini. 1981. Clustering of genes for 20 kd zein subunits in the short arm of chromosome 7. *Genetics* 97:363.

Soave, C., R. Reggiani, N. Di Fonzo, and F. Salamini. 1982. Genes for zein subunits on maize chromosome 4. *Biochem. Genet.* 20:1027.

Sreeramulu, C., and L.F. Baumann. 1970. Yield components and protein quality of opaque-2 and normal diallels of maize. *Crop Science* 10:262-265.

Thomas, H., and C.J. Howarth. 2000. Five ways to stay green. *Journal of Experimental Botany* 51:329-337.

Tollenaar, M., and J. Wu. 1999. Yield improvement in temperate maize is attributable to greater stress tolerance. *Crop Science* 39:1597-1604.

Tsige, G.K. 2002. Genetic diversity analysis and genotype x environment interaction in Ethiopian Mustard. Ph.D. Thesis. Department of Plant Sciences / Plant Breeding , Faculty of Natural and Agricultural Sciences, University of the Free State Bloemfontein, South Africa.

Uhart, S.A., and F.H. Andrade. 1995. Nitrogen deficiency in maize: I. Effects on crop growth, development, dry matter partitioning, and kernel set. *Crop Science* 35:1376-1383.

USDA. 2009. National nutrient database for standard reference. [Online]. Available by United States Department of Agriculture http://www.nal.usda.gov/fnic/foodcomp/search/.

Van Eeuwijk, F.A. 1995. Multiplicative interaction in generalised linear models. *Biometrics* 51:1017-1032.

Van Eeuwijk, F.A., J.B. Denis, and M.S. Kang. 1996. Incorporating additional information on genotypes and environments in models for two-way genotype by environment tables. In: M.S. Kang, and Jr. H.G. Gauch, (Eds.). Genotype-by-Environment interaction. CRC press, Boca Raton, FL. pp. 15-49.

Vargas, M., J. Crossa, F.A.v. Eeuwijk, M.E. Ramirez, and K.Sayre. 1999. Using AMMI, factorial regression, partial least squares regression models for interpreting genotype x environment interaction. *Crop Science* 39:955-967.

Vasal, S.K. 2000. The quality protein maize story. *Food and Nutrition Bulletin* 21:445-450.

Vasal, S.K. 2001. High quality protein corn. In: A. R. Hallauer (Ed.). Speciality Corns. 2nd ed. CRC Press, Washington, D.C., USA. pp. 85–129.

Vasal, S.K. 2002. Quality protein Maize: Overcoming the hurdles. In: P.K. Kataki and S.C. Babu (Eds.). Food Systems for Improved Human Nutrition: Linking Agriculture, Nutrition, and Productivity. Food Products Press, an Imprint of the Haworth Press, Inc. pp. 193–227.

Vasal, S.K., E. Villegas, and C.Y. Tang. 1984a. Recent advances in the development of quality protein maize germplasm at Centro Internacional De Mejoramento De Maiz Y Trigo (CIMMYT). In: Cereal Grain Protein Improvement (Eds.). International Atomic Energy Agency, Vienna. pp. 167-189.

Vasal, S.K., E. Villegas, C.Y. Tang, J. Werder, and M. Read. 1984b. Combined use of two genetic systems in the development and improvement of quality protein maize. *Kulturpflanze* 32:171-185.

Vasal, S.K., B.S. Dhillon, and S. Pandey. 1997a. Recurrent selection methods based on evaluation-cum-recombination block. *Plant Breeding Reviews* 14:139-163.

Vasal, S.K., H. Cordova, D.L. Beck, and G.O. Edmeades. 1997b. Choices among breeding procedures and strategies for developing stress tolerant maize germplasm. In: G.O.Edmeades, M. Bänziger, H.R. Michelson and C.B. Pena-Valdiva (Eds.). Developing Drought and Low N-Tolerant Maize. Proceedings of a Symposium. 25-29 March 1996, Mexico, D.F., Mexico. pp. 336-347.

Vasal, S.K., E. Villegas, M. Bjarnason, B. Gelaw, and P. Goertz. 1980. Genetic modifiers and breeding strategies in developing hard endosperm opaque-2 materials. In: W.G. Pollmer and R.H. Phipps (Eds.). Improvement of quality traits of maize for grain and silage use. Nijhoff, The Hague, Netherlands. pp. 37–71.

Vasal, S.K., G. Srinivasan, S. Pandey, F. Gonzalez, D.L. Beck, and J. Crossa. 1993a. Heterosis and combining ability of CIMMYT's quality protein maize germplasm: II. Subtropical. *Crop Science* 33:51-57.

Vasal, S.K., G. Srinivasan, S. Pandey, F. Gonzalez, J. Crossa, and D.L. Beck. 1993b. Heterosis and combining ability of CIMMYT's quality protein maize germplasm: I. Lowland tropical. *Crop Science* 33:46-51.

Villegas, E., S.K. Vasal, and M. Bjarnason. 1992. Quality protein maize – What is it and how was it developed. In: E. T Mertz (Ed.). Quality Protein Maize. American Association of Cereal Chemists, St. Poul, Minnesota, USA. pp. 27-48.

Wang, X.L., Y.M. Woo, C.S. Kim, and B.A. Larkins. 2001. Quantitative trait locus mapping of loci influencing elongation factor 1 alpha content in maize endosperm. *Plant Physiology* 125:1272-1282.

Wessel-Beaver, L., and R.J. Lambert. 1982. Genetic control of modified endosperm texture in opaque-2 maize. *Crop Science* 22:1095-1098.

Westcott, B. 1986. Some methods of analyzing genotype–environment interaction. *Heredity* 56:243-253.

Westgate, M.E., and J.S. Boyer. 1986. Reproduction at low silk and pollen water potentials in maize. *Crop Science* 26:951-956.

Whistler, R.L. 1970. Industrial uses of corn starches. In: G.E. Inglett (Ed.). Corn: culture, processing, products. Avi Publishing, Westport Conn. p171–194.

Wood, S., G. Hyman, U. Deichmann, E. Barona, R. Tenorio, Z. Guo, S. Castano, O. Rivera, E. Diaz, and J. Marin. 2010. Sub-national poverty maps for the developing world using international poverty lines: Preliminary data release. [Online] http://povertymap.info.

Wricke, G. 1962. Über eine Method zur Erfassung der Ökologischen Streuberite in Feldversuchen. *Z. Pflanzenzüchtg.* 47:92-96.

Wricke, G., and W.E. Weber. 1980. Erweiterte analyse von wechselwirkungen in versuchsserien.In: Biometrie-heute und morgen. W. Köpcke and K. Überla. (Eds.). Springer-Verlag, Berlin.

Wu, R.L., X.Y. Lou, C.X. Ma, X.L. Wang, B.A. Larkins, and G. Casella. 2002. An improved genetic model generates high resolution mapping of QTL for protein quality in maize endosperm. *Proceedings of the National Academy of Sciences of the United States of America* 99:11281-11286.

Xingming, F., T. Jing, H. Bihua, and L. Feng. 2004. Analysis of combining ability and heterotic groups of yellow grain quality protein maize inbreds. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium: Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 143–148.

Yan, W. 2001. GGEbiplot – a Windows application for graphical analysis of multi-environment trial data and other types of two way data. *Agronomy Journal* 93:1111-1118.

Yan, W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agronomy Journal* 94:990-996.

Yan, W., and I. Rajcan. 2002. Biplot evaluation of test sites and trait relations of soybean in Ontario. *Crop Science* 42:11-20.

Yan, W., and M.S. Kang. 2003. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL.

Yan, W., and N.A. Tinker. 2006. Biplot analysis of multi-environment trial data: Principles and application. *Canadian Journal of Plant Science* 86:623-645.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot *Crop Science* 40: 597-605.

Yan, W., M.S. Kang, B.L. Ma, S. Wood, and P.L. Cornelius. 2007. GGE Biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science* 47: 443-655.

Yates, F., and W.G. Cochran. 1938. The analysis of group experiments. *Journal of Agricultural Science* 28:566-580.

Yau, S.K. 1995. Regression and AMMI analyses of genotype x environment interactions: an empirical comparison. *Agronomy Journal* 87:121-126.

Young, V.R., N.S. Scrimshaw, and P.L. Pellet. 1998. Significance of dietary protein source in human nutrition: animal and/or plant proteins? In: J.C. Waterlow, D.G. Armstrong, , L. Fowden, and R. Riley (Eds.). Feeding a world population of more than eight billion people. Oxford University Press in associate with Rank Prize Funds, New York. pp. 205–221.

Zaidi, P.H., G. Srinivasan, and C. Sanchez. 2003. Gains from stress-adaptive changes with selection for mid-season drought tolerance in tropical maize In: Book of Abstracts. Arnel R. Hallauer International Symposium on Plant Breeding. 17-22 August 2003, CIMMYT, Mexico, D.F., Mexico. pp. 80-81.

Zavala-Garcia, F., P.J. Bramel-Cox, J.D. Eastin, M.D. Witt, and D.J. Andrews. 1992. Increasing the efficiency of crop selection for unpredictable environments. *Crop Science* 32:51-57.

Zhao, W., F. Zhai, D.Zhang, Y.An, Y.Liu, Y. He, K. Ge, and N.S. Scrimshaw. 2004. Lysine-fortified wheat flour improves the nutritional and immunological status of wheat-eating families in northern China. *Food and Nutr. Bull* 25:123-129.

Zobel, R.W., M.J. Wright, and H.G.G. Jr. 1988. Statistical analysis of yield trial. *Agronomy Journal* 80:388-393.

Zuber, M.S., and J.L. Helm. 1972. Approaches to improving protein quality in maize without the use of specific mutants. In: L.F. Bauman, P.L. Crane, D.V. Glover, E.T. Mertz, and D.W. Thomas (Eds.). High-quality protein maize. Dowden, Hutchinson & Ross, Inc., Stroudsburg, PA, USA. pp.241-252.

CHAPTER 3

Parametric and non-parametric approaches for the assessment of G x E interaction and grain yield stability of QPM single cross hybrids under stress and non-stress environments

3. 1 Abstract

Quality protein maize (QPM) is nutritionally enhanced maize which helps to curb protein malnutrition and infant mortality in communities where maize is a dietary staple. Improved QPM genotypes have to perform better or comparable in yield and be relatively stable across environments to be adopted by farmers. The objective of this study was to evaluate the extent of G x E interaction and grain yield stability of the QPM single cross hybrids across stress and non-stress environments and to compare the level of association among the different stability parameters in identifying stable genotypes. Ninety six QPM hybrids, including a normal endosperm maize check, were evaluated in 8 x 12 alpha-lattice design with two replicates in 15 stress and non-stress environments of eastern and southern Africa (ESA) during the 2010 and 2011 growing seasons. Nine parametric and non-parametric stability models were used to analyse stability. The ANOVA for the single and combined environments showed a highly significant ($P < 0.001$) variation among the genotypes. From the combined ANOVA, environments contributed the highest percentage of the total sum of squares mainly due to the inclusion of extreme (stress) environments in the analysis. The mean grain yield under optimum conditions was 5.24 t ha^{-1} and genotypes under low nitrogen (N) stress yielded an average of 35% and under drought 38% of grain yields obtained under optimum conditions. Mean yield and Linn and Binn's cultivar superiority measures were found to be highly significantly correlated. However the two methods were non-significantly and poorly correlated with all the other parameters. Spearman's rank correlation matrix revealed highly significant correlation among Eberhart and Russell's deviation from regression, Wricke's ecovalence, Shukla's stability variance with no covariates, Shukla's stability variance with covariates, Nassar and Hühn's absolute rank difference and variance of ranks and Purchase's AMMI stability value (ASV). Results of the individual location analysis showed that entry 52 gave the highest yield (9.12 t ha^{-1}) in 2010 and entry 40 the highest (8.84 t ha^{-1}) in 2011 under optimum environments in Zimbabwe and Kenya respectively. Entry 40 ranked first based on across environment means (4.57 t ha^{-1}) and entry 80 (3.39 t ha^{-1}) was identified as a relatively stable hybrid by the majority of the parameters. This study further established the importance of multivariate analysis techniques in a situation where diverse environments are included in the analysis of G x E interaction and grain yield stability.

Key words: QPM, G x E interaction, grain yield stability and stability parameters

3.2 Introduction

Africa contributes about 20% of the 161 million ha of the maize area and about 8% of maize production of the world. Maize in SSA is a dietary staple for millions of small holder farmers and accounts for about 53% of the total land allocated to all cereals (FAOSTAT, 2010). By the year 2020 the demand for maize consumption in SSA is expected to increase by 93% from its level in 1995 while in the world it is projected to increase by 50% (CIMMYT, 2001). Although maize is one of the widely cultivated crops in Africa, its share of the global maize production is very low, mainly due to low average yield per unit area (Heisey and Edmeades, 1999; Pingali and Pandey, 2001).

Developing high yielding varieties adapted to more diverse environments is a major objective of breeders. However, environmental conditions affect the yield performance of a genotype. Hence, genotype performance is a function of the genotype and the nature of the production environments (Cooper and Byth, 1996). In addition, performance of a genotype is also determined by the G x E interactions, which is a differential response of genotypes to changes in environment (Hallauer et al., 1988; Crossa et al., 1990; Vargas et al., 1999). The maize growing environment of Africa is characterised by high G x E interaction caused by differing temperatures, seasonal rainfalls, soil types, within-season drought and socio-economic factors that result in sub-optimal input application (Bänziger et al., 2006).

The presence of G x E interaction and its magnitude in METs provides valuable information regarding the adaptation area of a given genotype and helps to determine effective time and resource management in a breeding programme (Ceccarelli, 1989; Kang, 1998). Various studies indicated that high G x E interaction is expected when genotypes are grown under diverse environments and when evaluated outside their normal zone of adaptation (Beck et al., 1991). Selection of varieties in diverse environments generally targets genotypes that provide relatively high yields with minimum expression of G x E interaction (Ceccarelli, 1989; Gauch and Zobel, 1997; Kang, 1998). In other words, breeders are interested in cultivars with high average yield and which give positive response to improved environments (Hallauer et al., 1988).

Various parametric and non-parametric methods have been developed to evaluate the effect of G x E interaction and to select stable genotypes from METs. Yates and Cochran (1938)

were the first to develop the linear regression model based on the G x E interaction expressed as the linear regression coefficient of the genotype on the site mean. This was later used by Finlay and Wilkinson (1963) and modified by Eberhart and Russell (1966), who incorporated the deviation from regression as a stability parameter.

According to the joint regression model, a stable variety is the one with a high mean yield, regression coefficient of one (b_i=1) and deviation from regression of zero (S^2_{di}=0) (Eberhart and Russel, 1966). In most cases, S^2_{di} is considered as a stability parameter rather than b_i (Eberhart and Russel, 1966; Becker and Leon, 1988). Wricke (1962) developed a stability concept based on the contribution of each genotype to the G x E interaction which is termed as ecovalence (W_i). Genotypes with low W_i are considered to be more stable as their deviation from the overall mean is small. A genotype with zero ecovalence is regarded as the most stable. In another study Shukla (1972) defined the stability variance of genotype *i* as its variance across environments after the main effects of environmental means have been removed. According to Shukla (1972) a genotype is considered stable if its stability variance (σ^2) is equal to the environmental variance σ_e^2 which means that $\sigma_i^2 = 0$. A relatively large value of σ_i^2 will thus indicate greater instability of genotype.

The AMMI model, which combines the standard ANOVA with PCA (Zobel et al., 1988), was used to investigate the agronomic nature of G x E interaction. In order to rank genotypes in terms of stability, Purchase (1997) proposed the AMMI stability value (ASV) as follows:

$$\text{ASV}=\sqrt{\left[\frac{IPCA1\,Sum\,of\,Squares}{IPCA2\,Sum\,of\,Squares}(IPCA1\,score)\right]^2+[IPCA2\,score]^2}$$

AMMI stability value is the distance from zero in a two dimensional scattergram of IPCA1 (Interaction Principal Component 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 to total G x E sum of squares. According to Purchase (1997) genotypes with lower values of ASV are considered to be more stable.

Besides the numerous parametric methods available, non-parametric methods also provide useful information for comparing rank order differences across different environments. Several advantages of non-parametric approaches were indicated by Nassar and Huehn (1987) who listed, among others, the model as less sensitive to errors such as measurements because the method only uses ranks rather than absolute values as in the case of parametric methods. Analysis of ranks (stratified ranking) evaluates the proportion of sites where any genotype ranks in the top, middle or bottom third of the entries (Ramagosa and Fox, 1993). A genotype found in the top third of the entries across sites can be considered relatively well adapted. A genotype *'i'* is stable over environments if it ranks the same over environments.

However, Huehn (1990) suggested that for an efficient use of stability estimation techniques in practical applications, knowledge of the following aspects is essential: relations between different statistical measures of phenotypic stability (parametric and non-parametric); consistency of relationships among stability parameters; and repeatability of stability parameters.

Several researchers have reported significant G x E interaction and stability of QPM genotypes (Vasal et al., 1993a; 1993b; Pixley and Bjarnason, 1993; 2002; Glover et al., 2005; Gissa, 2008). However, no information is available on the G x E interaction and grain yield stability patterns of the hybrids included in this study. Hence, the objectives of this study were to evaluate the extent of G x E interaction and grain yield stability of the QPM single cross hybrids across stress and non-stress environments and to compare the level of association among the different stability parameters in identifying stable genotypes.

3.3 Materials and methods

Germplasm

Fourteen advanced CIMMYT QPM inbred lines with tropical adaptation, early to medium maturity and white grain colour, were crossed using the diallel mating design at the Kenyan agricultural research institute (KARI) and CIMMYT maize drought stress screening site in Kiboko - Kenya. The nursery was planted in July 2009. Ninety one cross combinations were made and the seeds of the reciprocal crosses were bulked. Four QPM and normal endosperm maize hybrids were included as checks making the total number of entries 96. The QPM parents were derived from a drought tolerant QPM source population using the pedigree

breeding method. The parental lines showed good combining ability and agronomic performance under drought environments of ESA. Generally, the plant materials were adapted to tropical environments and had a high level of tryptophan in the endosperm. The characteristics and pedigrees of the parents are presented in Table 3.1.

Description of the trial sites and field management

The 96 QPM hybrids and checks were evaluated in a total of 15 environments during the 2010 and 2011 cropping seasons. In Ethiopia the trials were conducted at Bako, Melkassa and Awassa. At Bako the QPM hybrids were tested under low N stress coded as BAKLN and under optimum management coded as BAKOP. At Melkassa and Awassa the trials were evaluated under optimum management and are coded as MLKOP and AWAOP, respectively. In Kenya, the trials were conducted in two optimum management fields at Embu (EMBOP) and Kakamega (KAKOP) and in a managed drought stress field at Kiboko (KBODT). In Zimbabwe the trials were conducted at research stations of Harare-CIMMYT and Ratray-Arnold, and at Chiredzi and Chisumbanje experimental sites. The trials at Harare were conducted under low-N stress in 2010 (HRELN1) and 2011 (HRELN2). Two trials were also conducted (HREOP1 and HREOP2) under optimum conditions in 2010 and 2011, respectively. Another trial was also conducted at the Rattray-Arnold research station (RATOP) under optimum conditions. At Chiredzi and Chisumbanje all the trials were evaluated under managed drought stress environments and coded as CHIDT1 and CHIDT2 (Chiredzi trials during 2010 and 2011 respectively) and CHSDT (Chisumbanje).

The optimum trials at Awassa, Bako and Kakamega as well as the low N trials at Harare had single row plots while the other trials had two row plots per entry. All the managed drought trials were grown in the dry season, allowing the control of drought stress intensity by withdrawing or delaying irrigation for varying lengths of time during the flowering and grain filling stages of the maize plants (Edmeades et al., 1999). At Chiredzi and Chisumbanje, drought stress was achieved by applying a total of 220 mm irrigation water during the first 50 days from planting. This regime caused severe drought stress at flowering and grain filling. The trials at Kiboko were irrigated from planting until two weeks before anthesis after which watering was withheld until 15 days after anthesis when additional irrigation was applied to prevent zero-yield (Bänziger et al., 2000). All essential measures were taken to make

irrigation water and stress level uniform and blocks were protected from irrigation water from neighbouring blocks, leaking pipes or wind drift.

The low N stress was achieved by continuously cropping maize for a minimum of five years without applying N. Optimum N conditions were maintained by applying the recommended N rate for the respective locations, followed by crop rotation and residue incorporation. All agronomic practices followed the recommendations for the trial sites. Details on the description of the experimental environments is presented in Table 3.2 and illustrated in Figure 3.1.

Table 3.1 List of the parental QPM inbred lines and their major characteristics

Parent	Pedigree	Origin and characteristics
1	CML205/CML144//CML159//POOL15QPMSR-B-68-B-B-B-B-B	KB09A-0A69-1, good combiner, DT-tolerant
2	CML212/CML144//CML159//POOL15QPMSR-B-41-B-B-B-B-B	KB09A-0A69-2, good combiner, DT-tolerant
3	CML312/CML144//CML159//POOL15QPMSR-B-59-B-8-B-B-B	KB09A-0A69-4, good combiner, DT-tolerant
4	CML445/CML144//CML159//POOL15QPMSR-B-1-B-B-B-B-B	KB09A-0A69-6, good combiner, DT-tolerant
5	CML445/CML144//CML159//POOL15QPMSR-B-30-B-B-B-B-B	KB09A-0A69-7, good combiner, DT-tolerant
6	CML445/CML144//CML159//POOL15QPMSR-B-5-B-B-B-B-B	KB09A-0A69-8, good combiner, DT-tolerant
7	ECA-EE-DLN-PL1 - 1/PL15QPMC7SRC1F2//POOL15QPMSR-B-18-B-B-B-B-B	KB09A-0A69-9, good combiner, DT-tolerant
8	ECA-MOROSR(BC1)F2-4-ECAVEE4/PL15QPMC7SRC1F2//POOL15QPMSR-B-115-B-3-B-B-B	KB09A-0A69-10, good combiner, DT-tolerant
9	ECA-MOROSR(BC1)F2-7-ECAVEE7/PL15QPMC7SRC1F2//POOL15QPMSR-B-35-B-B-B-B-B	KB09A-0A69-11, good combiner, DT-tolerant
10	ECA-MOROSR(BC1)F2-5-ECAVEE5/PL15QPMC7SRC1F2//POOL15QPMSR-B-58-B-B-B-B-B	KB09A-0A69-12, early maturing, MSV- resistant
11	LLSYNTH1/PL15QPMC7SRC1F2//POOL15QPMSR-B-17-B-B-B-B-B	KB09A-0A69-14, medium maturing, MSV- resistant
12	Pool15QPMFS756-B-4-B-#-B-B-B-B-B-B	KB09A-0A69-15, drought tolerant, good combiner
13	Pool15QPMFS440-B-4-B-#-B-B-B-B-B-B	KB09A-0A69-16, drought tolerant
14	Pool15QPMFS309-B-1-B-B-B-B-B-B-B	KB09A-0A69-17 , drought tolerant

Table 3.2 Description of the environments used for the evaluation of the QPM hybrids

Location	Country	Year	Latitude	Longitude	Altitude	Rain fall (mm)	Type of Environment	Code	Plot size (m x m)	Density (plants ha^{-1})
Awassa	Ethiopia	2011	7^0 08'N	$38^0$48'E	1700	1100	Optimum	AWAOP	5.0 x 0.75	53,333
Bako	Ethiopia	2010	$9^0$06'N	$37^0$09'E	1650	1245	Optimum	BAKOP	4.8 x 0.75	44,444
Bako	Ethiopia	2010	$9^0$06'N	$37^0$09'E	1650	1245	Low-N	BAKLN	4.8 x 1.50	44,444
Melkassa	Ethiopia	2011	8^0 24'N	$39^0$21'E	1550	680	Optimum	MLKOP	4.0 x 1.50	53,333
Embu	Kenya	2011	0^0 30'S	$37^0$27'E	1502	1200	Optimum	EMBOP	5.0 x 1.50	53,333
Kakamega	Kenya	2011	0^0 17'N	$34^0$45'E	1585	1850	Optimum	KAKOP	5.0 x 0.75	53,333
Kiboko	Kenya	2011	2^0 10'N	$37^0$40'E	975	680	Drought	KBODT	4.0 x 1.50	53,333
Harare	Zimbabwe	2010	17^0 49'S	31^0 1'E	1489	890	Optimum	HREOP1	4.0 x 1.50	53,333
Harare	Zimbabwe	2010	17^0 49'S	31^0 1'E	1489	890	Low-N	HRELN1	4.0 x 0.75	53,333
Harare	Zimbabwe	2011	17^0 49'S	31^0 1'E	1489	890	Optimum	HREOP2	4.0 x 1.50	53,333
Harare	Zimbabwe	2011	17^0 49'S	31^0 1'E	1489	890	Low-N	HRELN2	4.0 x 1.50	53,333
RARS	Zimbabwe	2010	17^0 16'S	31^0 03'E	1341	865	Optimum	RATOP	4.0 x 1.50	53,333
Chiredzi	Zimbabwe	2010	21^0 02'S	31^0 58'E	433	450	Drought	CHIDT1	4.0 x 1.50	53,333
Chiredzi	Zimbabwe	2011	21^0 02'S	31^0 58'E	433	450	Drought	CHIDT2	4.0 x 1.50	53,333
Chisumbaje	Zimbabwe	2011	20^0 48'S	32^0 14'E	415	420	Drought	CHSDT	4.0 x 1.50	53,333

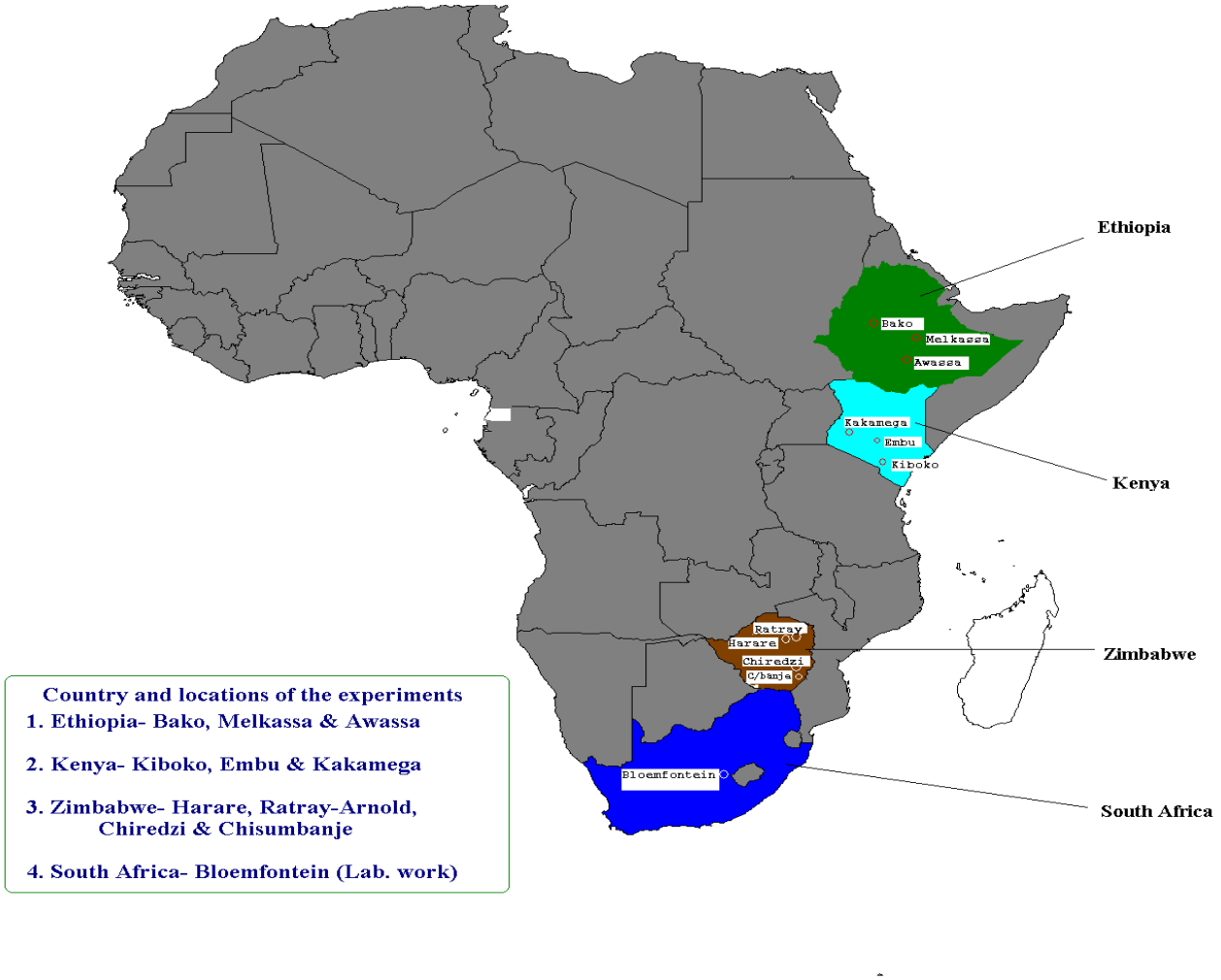

Figure 3.1 Experimental sites of the study in ESA

Experimental design and statistical analysis

The 96 hybrids (91 F1s and five checks) were planted in a 8 x 12 alpha-lattice design (Patterson and Williams, 1976) with two replicates at each test site. Analysis of variance for grain yield of each environment was conducted with the PROC MIXED procedure in SAS (2003). The effects of the genotypes, locations and years as well as their first and second order interactions were determined from the ANOVA. Genotypes were assumed to be fixed, while year and location effects, replications and blocks within replications were considered as random. The following analyses were performed to test the significance level of grain yield of the genotypes, locations and their interactions:

- Separate trial analysis for each location and year was done for the 15 separate trials planted across the different maize growing environments for the years 2010-2011.
- Separate analysis for the different environments viz. drought stress, low N stress and optimum management.
- The combined analyses of the trials (across years and locations) were done in order to determine differences between genotypes across environments and also to examine differences among the different environments.

Where G x E interaction means squares were significant, the QPM hybrids were evaluated for their grain yield stability across the different environments. The stability analyses were conducted using Agrobase Generation II SQL (Agronomix, 2011). The following models were used to analyse stability:

- Lin and Binns cultivar superiority measure (P_i), (Lin and Binns, 1988)
- Joint linear regression model (b_i and S^2_{di}) (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966)
- Wricke's ecovalence (W_i), (Wricke, 1962)
- Shukla's stability variance (σ^2) (Shukla, 1972)
- Nassar and Huehn's non-parametric measure (Nassar and Huehn, 1987)
- The AMMI stability value (ASV) (Purchase, 1997)

Spearman's coefficient of rank correlation (r_s) was employed (Steel and Torrie, 1980) to compare the stability procedures. The correlation assumption is that n genotypes are arranged in the same chronological order to two stability parameters, X_i indicates the ranking order (or

ranking number) of the i^{th} genotype for the first parameter, Y_i , indicates the ranking number of the i^{th} genotype of the second parameter, then $d_i = X_i - Y_i$ (i= 1,2,...n) and Spearman's rank correlation coefficient (r_s) described as:

$$r_s = \frac{6\sum d_i^2}{n(n^2-1)}$$

The correlation of the parameters and the significance levels were determined by using NCSS software (Hintze, 2001).

3.4 Results and discussion

3.4.1 Individual environment analysis

Trial season 2010

The analysis of variance of the trials conducted under stress and non-stress (optimum) environments in Ethiopia and Zimbabwe showed highly significant ($P \leq 0.01$) mean squares for entries across the environments. The percentage contribution of the entries sum of squares to the total variation was above 50% in most of the environments. However, the contribution of the entries to the total variation was 18.21% at HREOP1 and 48.49% at CHIDT1 which was an indication of the effect of environmental factors on the trials. BAKOP was among the sites where entries contributed the highest percentage (72%) to the total variation (Table 3.3).

In Table 3.4 results of grain yield performance of the top 25 of the 96 QPM hybrids is presented, including a non-QPM check (entry 96) tested across different environments during 2010. The complete results are presented in Appendix 1. Under optimum environments, entries 96, 52 and 46 were the highest yielders at BKOPT, HREOP and RATOP, yielding 9.28 t ha^{-1}, 9.12 t ha^{-1} and 6.10 t ha^{-1} respectively. Entries 15, 23 and 40 out yielded the rest in the stress environments by yielding 4. 93 t ha^{-1}, 4.77 t ha^{-1} and 2.32 t ha^{-1} at BKOLN, CHIDT1 and HRELN1 respectively. At HRELN1, entries 16 and 96 were among the top yielders performing similarly with entry 40. During this season, the highest yields were recorded at BKOPT under the non-stress environments and at BKOLN under the stress environments. However, the general mean performance for the 96 entries was better at HREOP1 (6.45 t ha^{-1}) for the non-stress and at BKOLN (3.18 t ha^{-1}) for the stress environments (Table 3.4).

Trial season 2011

Results of trials conducted in 2011 in nine environments (four stress and five optimum) in Ethiopia, Kenya and Zimbabwe showed that the variation among the entries was highly significant ($P \leq 0.01$) across the environments except for CHIDT2 that was significant (Table 3.5). The percentage contribution of the entries to the total sums of squares was highest at HREOP2 and KAKOP followed by MLKOP and KBODT. However, the percentage sum of squares for the entries was lowest at CHSDT which could be an indication of the influence of environmental factors that contributed to the variability apart from the entries. The block effects were high at CHSDT and AWAOP and low or insignificant at HREOP2. Generally the coefficients of variation (CV) for the stress environments were relatively high compared to the optimum environments. The trial at AWAOP had a higher CV compared to the other optimum environments probably due to the erratic nature of rainfall during the season (Table 3.5).

Entry 37 was the highest yielding QPM hybrid under the optimum environments at HREOP2 and AWAOP and was ranked second at EMBOP, yielding 8.68 t ha^{-1}, 7.62 t ha^{-1} and 8.32 t ha^{-1} respectively (Table 3.6). The highest QPM yield in the optimum environments was recorded at EMBOP for entry 40 with an average yield of 8.84 t ha^{-1}. Entries 41 and 42 were also the best performing QPM hybrids at MLKOP and KAKOP with an average grain yield of 7.06 t ha^{-1} and 6.64 t ha^{-1} respectively. Under the stress environments neither of the hybrids showed repeatable performance across the environments except entry 22 which was the highest yielding at KBODT and number three at HRELN2 yielding 4.66 t ha^{-1} and 1.82 t ha^{-1} respectively. Entries 31, 51 and 94 were the highest yielders at CHSDT, HRELN2 and CHIDT2 with an average grain yield of 2.44 t ha^{-1}, 2.16 t ha^{-1} and 2.02 t ha^{-1} respectively. The performance of the entries was high at HREOP2 (6.12 t ha-^{1}) and low at AWAOP (4.30 t ha^{-1}) under the optimum environments. However, the general performance of the 96 entries in the stress environments was high at KBODT (4.42 t ha^{-1}) and it was low at HRELN2 (0.97 t ha^{-1}). Generally the performance of the entries under the optimum environments was better than the previous season. However, the entries performed poorer under the stress environments when compared to the previous year. The results of the grain yield performance of the top 25 entries across the different environments during 2011 are presented in Table 3.6 while the complete results are presented in Appendix 2.

Table 3.3 Mean squares from analysis of variance and percentage contribution of variance components for grain yield of 96 QPM hybrids plus the normal check tested across the different growing environments of ESA, in 2010

Environments	Sources of variation															
	Entry			Block			Replications			Error			Total			
	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	%SS	LSD	CV%
HREOP1	95	2.31**	18.21	23	2.18**	0.32	1	0.87**	79.76	72	0.06	1.71	191	100	0.56	9
HRELN1	95	0.47**	60.52	23	0.76**	23.51	1	0.09	0.12	72	0.16	15.85	191	100	0.81	29.85
RATOP	95	1.04**	61.31	23	0.91	13.03	1	1.58	0.98	72	0.55	24.68	191	100	1.47	16.64
CHIDT1	95	0.71**	48.49	23	1.71**	28.30	1	22.67**	16.31	72	0.13	6.90	191	100	0.73	12.79
BAKLN	95	1.01**	62.30	23	2.12**	31.74	1	1.99**	1.30	72	0.10	4.66	191	100	0.63	9.93
BAKOP	95	2.12**	72.03	23	1.72**	14.16	1	7.25**	2.60	72	0.43	11.21	191	100	1.31	12.03

***P ≤ 0.01**

Table 3.4 Grain yield performance (t ha^{-1}) of the top 25 QPM hybrids tested across six environments in ESA, during 2010

	Environments											
	HREOP1		RATOP		BKOPT		HRELN1		BKOLN		CHIDT1	
Rank	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
1	52	9.12	46	6.10	96	9.28	40	2.32	15	4.93	23	4.77
2	4	8.87	96	5.75	40	8.03	16	2.32	22	4.74	73	4.50
3	43	8.71	82	5.68	45	7.83	96	2.32	29	4.70	29	4.04
4	37	8.59	92	5.60	59	7.45	87	2.28	64	4.65	16	3.90
5	6	8.28	47	5.56	15	7.28	55	2.26	48	4.51	22	3.90
6	45	8.21	76	5.54	55	7.13	26	2.24	37	4.38	27	3.80
7	46	8.19	52	5.47	49	7.00	79	2.20	55	4.35	58	3.73
8	10	8.10	10	5.47	4	6.92	85	2.12	75	4.29	60	3.71
9	87	7.89	33	5.46	48	6.85	67	2.12	4	4.20	61	3.69
10	40	7.88	60	5.42	60	6.67	93	2.10	35	4.17	40	3.67
11	12	7.84	15	5.36	37	6.37	73	2.09	92	4.14	8	3.66
12	8	7.83	64	5.35	70	6.37	88	1.95	56	4.14	67	3.65
13	54	7.80	12	5.31	12	6.28	17	1.93	45	4.03	12	3.65
14	53	7.79	84	5.28	17	6.27	86	1.91	49	3.99	92	3.61
15	48	7.63	37	5.18	16	6.27	12	1.91	96	3.98	33	3.60
16	7	7.55	43	5.08	69	6.25	39	1.91	54	3.93	11	3.58
17	82	7.52	91	5.08	63	6.23	54	1.90	91	3.93	86	3.53
18	1	7.50	7	5.04	54	6.20	18	1.84	51	3.86	19	3.53
19	42	7.46	4	5.02	52	6.19	51	1.84	73	3.83	94	3.49
20	55	7.35	49	5.01	38	6.18	47	1.82	69	3.82	59	3.48
21	51	7.27	13	5.01	91	6.18	61	1.69	40	3.80	14	3.48
22	49	7.24	57	5.01	67	6.16	22	1.68	47	3.70	79	3.45
23	73	7.20	54	5.01	29	6.15	46	1.66	12	3.62	13	3.41
24	39	7.17	5	4.98	51	6.12	52	1.66	60	3.62	10	3.38
25	16	7.16	2	4.97	5	6.10	23	1.65	14	3.61	88	3.38
Mean	**6.45**		**4.46**		**5.48**		**1.36**		**3.18**		**2.94**	
Max	**9.12**		**6.10**		**9.28**		**2.32**		**4.93**		**4.77**	
Min	**4.63**		**2.66**		**2.96**		**0.49**		**1.80**		**1.71**	
LSD $_{0.05}$	**0.56**		**1.47**		**1.31**		**0.81**		**0.63**		**0.73**	
CV %	**4.29**		**16.64**		**12.03**		**29.85**		**9.93**		**12.79**	

Table 3.5 Mean squares of the analysis of variance and percentage contribution of variance components for grain yield (t ha^{-1}) of 96 QPM hybrids including the normal endosperm check tested across the different growing environments of ESA, during 2011

	Sources of variation															
	Entry			Block			Replications			Error			Total			
Environments	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	%SS	LSD	CV%
HREOP2	95	2.72**	85.69	23	0.40	2.95	1	0.41	0.14	72	0.46	11.22	191	100	1.36	11.12
HRELN2	95	0.32**	57.32	23	0.50**	21.97	1	0.03	0.06	72	0.15	20.65	191	100	0.77	40.07
CHIDT2	95	0.36*	48.56	23	0.42*	12.89	1	9.97**	14.00	72	0.24	24.55	191	100	0.65	37.22
CHSDT	95	0.32**	43.15	23	0.83**	26.82	1	9.46**	13.28	72	0.16	16.75	191	100	0.81	31.52
KBODT	95	1.26**	67.35	23	0.94*	12.15	1	0.15	0.08	72	0.50	20.42	191	100	1.41	29.05
KAKOP	95	1.76**	82.18	23	0.88**	9.88	1	1.79**	0.88	72	0.20	7.06	191	100	0.89	10.11
EMBOP	95	1.48**	60.34	23	1.82	17.87	1	18.49**	7.91	72	0.45	13.88	191	100	1.34	11.19
AWAOP	95	3.34 **	54.86	23	6.36**	25.30	1	13.57**	2.35	72	1.40	17.49	191	100	2.36	27.57
MLKOP	95	2.25**	67.55	23	2.59**	18.05	1	1.13	0.35	72	0.61	14.05	191	100	1.56	16.54

***P ≤ 0.05, ** P ≤ 0.01**

Table 3.6 Grain yield performance (t ha^{-1}) of the top 25 QPM hybrids selected across nine environments in ESA, 2011

	Environments																	
	HRELN2		HREOP2		CHIDT2		CHSDT		EMBOP		KAKOP		KBODT		MLKOP		AWAOP	
Rank	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
1	51	2.16	37	8.68	94	2.02	31	2.44	40	8.84	42	6.64	22	4.66	41	7.06	37	7.62
2	54	1.90	43	8.24	52	1.98	84	2.13	37	8.32	95	6.26	10	4.33	92	6.82	55	7.62
3	22	1.82	12	8.06	68	1.91	33	2.04	41	7.98	96	6.10	25	4.31	60	6.76	54	6.73
4	53	1.69	3	8.05	18	1.91	4	2.00	54	7.65	45	5.97	73	4.22	63	6.64	46	6.60
5	55	1.69	10	7.85	33	1.90	66	1.98	96	7.40	9	5.95	63	4.16	58	6.55	15	6.48
6	67	1.68	52	7.79	64	1.87	7	1.90	48	7.40	10	5.91	78	4.07	38	6.48	61	6.35
7	89	1.57	40	7.73	73	1.87	24	1.88	51	7.33	51	5.86	43	3.92	8	6.41	3	6.35
8	84	1.55	92	7.73	92	1.86	46	1.87	45	7.31	15	5.82	88	3.77	57	6.36	91	6.35
9	82	1.55	82	7.71	60	1.84	56	1.84	4	7.05	4	5.80	60	3.62	76	6.25	95	6.35
10	68	1.54	54	7.69	56	1.84	73	1.81	27	6.96	38	5.78	82	3.55	49	6.18	96	6.22
11	25	1.52	6	7.67	23	1.82	65	1.77	13	6.88	3	5.57	86	3.53	56	6.14	40	6.10
12	46	1.46	84	7.40	90	1.80	14	1.75	18	6.87	21	5.54	8	3.46	94	6.13	26	5.97
13	75	1.43	4	7.33	70	1.80	38	1.73	50	6.83	32	5.48	52	3.36	64	6.13	53	5.97
14	49	1.41	8	7.31	40	1.80	89	1.71	29	6.68	1	5.47	87	3.30	55	6.00	52	5.59
15	48	1.40	45	7.29	57	1.77	26	1.69	5	6.67	24	5.45	62	3.26	50	5.96	38	5.46
16	44	1.40	62	7.28	7	1.76	63	1.69	82	6.64	39	5.45	15	3.26	15	5.91	60	5.46
17	83	1.38	2	7.22	65	1.76	34	1.66	25	6.64	50	5.37	30	3.15	44	5.80	79	5.46
18	24	1.38	39	7.22	67	1.74	28	1.64	91	6.60	40	5.33	20	3.02	10	5.72	2	5.33
19	52	1.33	1	7.11	44	1.71	90	1.62	76	6.59	55	5.30	21	2.93	21	5.70	25	5.21
20	16	1.30	7	7.09	71	1.71	43	1.61	42	6.57	46	5.30	96	2.93	62	5.59	84	5.08
21	93	1.27	66	7.08	48	1.70	69	1.60	9	6.55	48	5.27	67	2.91	47	5.56	33	5.08
22	10	1.25	51	7.07	74	1.70	76	1.58	38	6.55	37	5.25	42	2.90	12	5.56	50	5.08
23	90	1.25	41	7.00	22	1.70	11	1.57	1	6.49	54	5.22	38	2.90	72	5.53	87	5.08
24	88	1.22	22	6.99	61	1.69	55	1.56	31	6.46	47	5.18	51	2.88	40	5.51	76	5.08
25	66	1.21	32	6.98	41	1.69	44	1.56	63	6.46	56	5.17	28	2.87	5	5.45	63	5.08
Mean	**0.97**		**6.12**		**1.31**		**1.29**		**5.99**		**4.42**		**2.44**		**4.72**		**4.30**	
Max	**2.16**		**8.68**		**2.02**		**2.44**		**8.84**		**6.64**		**4.66**		**7.06**		**7.62**	
Min	**0.13**		**3.47**		**0.16**		**0.32**		**3.66**		**2.12**		**0.82**		**2.00**		**1.27**	
$LSD_{0.05}$	**0.77**		**1.36**		**0.65**		**0.81**		**1.34**		**0.89**		**1.41**		**1.56**		**2.36**	
CV %	**40.07**		**11.12**		**37.22**		**31.52**		**11.19**		**10.11**		**29.05**		**16.54**		**27.57**	

3.4.2 Combined analysis of variance

Results of the combined ANOVA for grain yield in 2010 showed that entries, environments and the entry x environment interactions were highly significant (Table 3.7). The percentage sum of squares for the environments was the largest source of variation followed by entry by environment interaction. Similar results were observed for the year 2011 with the variation in grain yield among entries and environments being highly significant. The percentage sum of squares for the interaction between entry and environments was the second largest contributor to variation. The combined ANOVA for grain yield across years and environments showed the existence of high variation among entries and test environments. Entry by year interaction was the second largest contributor to the variation indicating that variation across years was highly significant (Table 3.7 and Table 3.8).

In Table 3.9 is presented the grain yield of the top 25 entries evaluated across 15 environments in 2010 and 2011. Entry 40 was the highest yielder in 2010 with an average grain yield of 5.09 t ha^{-1} followed by entry 4 (4.84 t ha^{-1}) and entry 15 (4.82 t ha^{-1}). However the rank order for 2011 was different from that of 2010 as entry 40 ranked fourth with an average grain yield of 4.22 t ha^{-1}. Entries 10, 37 and 55 were the top three entries yielding 4.30 t ha^{-1}, 4.25 t ha^{-1} and 4.23 t ha^{-1} respectively. Results of the ANOVA combined across years showed the QPM entries 40 (4.57 t ha^{-1}), 37 and 55 (4.42 t ha^{-1}) and 10 (4.38 t ha^{-1}) as the top yielding entries. The normal endosperm maize commercial check hybrid (entry 96) ranked fifth with an average grain yield of 4.34 t ha^{-1}. The complete results are presented in Appendix 3. Grain yield during the first season was higher than that of the second season. Table 3.9 showed lack of consistency in performance among the different entries indicating the presence of significant genotype by environment interaction. This necessitated the selection of entries based on their yield stability which will is addressed in the next section.

The combined ANOVA was also done for stress and non-stress environments which included eight optimum, four drought stress and three low N stress environments. Entries 55, 73 and 37 were the top yielding QPM hybrids under low N, drought and optimum environments respectively, with an average yield of 2.77 t ha^{-1}, 3.10 t ha^{-1} and 6.82 t ha^{-1} respectively (Table 3.10). The low N environment yielded on average 35% of the yield recorded under optimum environments. This result corroborated the findings of other researchers (Bänziger

et al., 1997). Similarly, drought stress environments yielded about 38% of what was obtained under optimum environments.

Table 3.7 Combined analyses of variance for grain yield of 96 QPM single cross hybrids tested across the different growing environments of ESA, in 2010 and 2011

Years	Sources	DF	MS	%SS
2010	Entry	95	2.48**	5.39
	Environments (Env)	5	658.07**	75.24
	Replication	1	6.13**	0.14
	Block	23	1.40**	0.74
	Rep(Env)	5	5.66**	0.65
	Block (Rep x Env)	109	1.37**	3.42
	Entry x Env	475	1.04**	11.25
	Error	438	0.32	3.17
	R-square (%)	97		
	Mean yield (t ha^{-1})	3.98		
	LSD	0.45		
	CV %	14.15		
2011	Entry	95	2.87**	3.25
	Environments (Env)	8	797.75**	76.07
	Replication	1	0.42	0.01
	Block	23	2.43**	0.66
	Rep(Env)	8	6.82**	0.65
	Block (Rep x Env)	175	1.82**	3.81
	Entry x Env	760	1.37**	12.41
	Error	657	0.40	3.14
	R-square (%)	97		
	Mean yield (t ha^{-1})	3.51		
	LSD	0.41		
	CV %	18.04		

**$p \leq 0.01$

Table 3.8 Mean squares of the combined analyses of variance and percentage of the variance components for grain yield of 96 QPM single cross hybrids tested across growing environments of ESA, 2010-2011

Years	Sources		DF	MS	%SS
2010-2011	Entry		95	4.49**	3.30
	Environments (Env)		14	701.71**	76.07
	Year		1	151.55**	1.17
	Replication		1	1.13**	0.01
	Block		23	2.41**	0.43
	Rep (Env)		14	6.31**	1.30
	Block (Rep x Env)		307	1.63**	3.88
	Entry x Env		1330	1.21**	0.63
	Entry x year		95	0.86**	12.51
	Error		999	0.37	1.30
	R-square(%)	99			
	Mean yield (t ha^{-1})	3.70			
	LSD	0.21			
	CV %	11.11			

**p≤0.01

Table 3.9 Grain yield performance (t ha^{-1}) of the selected top 25 QPM hybrids tested across 15 environments in ESA, 2010-2011

	Trial years					
	2010		2011		2010-2011	
Rank	Entry	Yield	Entry	Yield	Entry	Yield
1	40	5.09	10	4.30	40	4.57
2	4	4.84	37	4.25	37	4.42
3	15	4.82	55	4.23	55	4.42
4	96	4.78	40	4.22	10	4.38
5	12	4.77	41	4.19	15	4.37
6	48	4.76	63	4.18	52	4.34
7	52	4.72	43	4.17	96	4.34
8	55	4.69	60	4.12	60	4.27
9	45	4.69	52	4.09	54	4.27
10	37	4.66	54	4.08	48	4.26
11	49	4.56	15	4.07	45	4.23
12	54	4.54	96	4.04	43	4.18
13	92	4.52	84	3.98	63	4.13
14	73	4.51	62	3.98	41	4.13
15	16	4.50	50	3.97	12	4.12
16	10	4.50	38	3.95	51	4.09
17	60	4.49	45	3.93	4	4.09
18	51	4.46	48	3.92	22	4.08
19	67	4.46	42	3.90	92	4.06
20	22	4.43	3	3.89	46	4.06
21	29	4.41	46	3.88	49	4.03
22	87	4.38	22	3.86	50	4.02
23	64	4.38	51	3.84	73	3.99
24	46	4.32	24	3.80	84	3.99
25	8	4.25	91	3.77	87	3.94
Mean		**3.98**		**3.51**		**3.70**
Max		**5.09**		**4.30**		**4.57**
Min		**2.84**		**2.62**		**2.71**
$LSD_{0.05}$		**0.45**		**0.41**		**0.21**
CV %		**14.15**		**18.04**		**11.11**

Table 3.10 Grain yield performance (t ha^{-1}) of the selected top 25 QPM hybrids tested under different growing environments and the percentage yield levels of stress environment compared to the optimum, 2010-2011

Rank	Environments						% yield levels compared to optimum environment	
	Low N Stress		Drought Stress		optimum		Low N Stress	Drought stress
	Entry	Yield	Entry	Yield	Entry	Yield		
1	55	2.77	73	3.10	37	6.82	40.55	45.41
2	22	2.75	23	2.73	40	6.78	40.53	40.21
3	51	2.62	22	2.67	96	6.38	41.08	41.87
4	54	2.58	63	2.63	55	6.36	40.49	41.32
5	48	2.45	60	2.60	54	6.34	38.70	40.95
6	67	2.45	78	2.58	45	6.32	38.84	40.87
7	15	2.44	10	2.56	10	6.23	39.25	41.02
8	40	2.39	33	2.52	52	6.21	38.41	40.63
9	96	2.38	25	2.46	41	6.14	38.79	39.96
10	37	2.35	67	2.45	15	6.11	38.51	40.17
11	16	2.35	43	2.44	3	6.10	38.44	39.91
12	29	2.33	52	2.43	46	6.06	38.41	40.03
13	64	2.29	8	2.41	4	6.04	37.91	39.82
14	49	2.27	88	2.39	60	6.04	37.63	39.60
15	73	2.26	82	2.35	43	6.01	37.62	39.05
16	92	2.22	15	2.33	48	5.96	37.29	39.14
17	12	2.20	86	2.32	12	5.90	37.23	39.34
18	75	2.16	56	2.31	42	5.88	36.77	39.33
19	53	2.13	94	2.30	50	5.86	36.29	39.25
20	66	2.10	58	2.25	49	5.86	35.92	38.48
21	4	2.10	76	2.22	38	5.82	36.09	38.04
22	85	2.10	79	2.22	84	5.77	36.36	38.41
23	56	2.09	48	2.21	63	5.72	36.46	38.68
24	23	2.08	70	2.21	92	5.70	36.51	38.79
25	88	2.08	87	2.20	51	5.69	36.51	38.61
Mean	**1.83**		**2.00**		**5.24**		**34.92**	**38.15**
LSD $_{0.05}$	**0.43**		**0.59**		**0.36**			
CV %	**20.81**		**30.40**		**10.00**			

3. 4. 3 Assessments of grain yield stability based on parametric and non-parametric stability measurements

Lin and Binns cultivar superiority measure (P_i)

According to Lin and Binns (1988), cultivar superiority measure (P_i) is calculated by the square of differences between a genotype's and the maximum genotype mean at location, summed and divided by twice the number of locations. Entries with the lowest (P_i) values are considered as the most stable (Table 3.11).

Table 3.11 Lin and Binns' cultivar superiority measure and mean grain yield (t ha^{-1}) of 96 QPM hybrids tested across 15 environments in ESA, 2010-2011

Entry	Pi	Pi rank	Mean yield	Mean yield rank	Entry	Pi	Pi rank	Mean Yield	Mean yield rank
40	0.964	1	4.57	1	85	2.758	49	3.66	53
45	1.405	2	4.23	11	8	2.767	50	3.79	38
10	1.408	3	4.38	4	32	2.768	51	3.52	66
15	1.412	4	4.37	5	7	2.774	52	3.77	40
52	1.422	5	4.34	7	21	2.780	53	3.69	48
55	1.433	6	4.42	2	16	2.787	54	3.67	52
54	1.470	7	4.27	9	53	2.799	55	3.70	45
37	1.475	8	4.42	3	30	2.890	56	3.59	58
60	1.491	9	4.27	8	33	2.914	57	3.70	46
96	1.502	10	4.34	6	25	2.951	58	3.65	55
48	1.550	11	4.26	10	64	2.980	59	3.80	36
63	1.774	12	4.13	13	58	2.986	60	3.58	60
43	1.821	13	4.18	12	77	3.008	61	3.53	64
41	1.854	14	4.13	14	72	3.070	62	3.52	65
49	1.925	15	4.03	21	35	3.080	63	3.50	68
12	1.945	16	4.12	15	59	3.082	64	3.44	73
50	1.949	17	4.02	22	19	3.122	65	3.46	80
4	2.002	18	4.09	17	56	3.189	66	3.68	50
51	2.004	19	4.09	16	9	3.310	67	3.49	69
46	2.047	20	4.06	20	94	3.315	68	3.55	62
84	2.083	21	3.99	23	66	3.401	69	3.54	63
24	2.084	22	3.90	29	80	3.404	70	3.39	74
38	2.108	23	3.89	30	88	3.476	71	3.56	61
3	2.109	24	3.84	34	57	3.507	72	3.51	67
62	2.126	25	3.91	27	18	3.517	73	3.46	71
87	2.130	26	3.94	25	20	3.565	74	3.37	76
91	2.133	27	3.90	28	89	3.666	75	3.29	79
42	2.165	28	3.87	32	61	3.672	76	3.39	75
1	2.229	29	3.78	39	81	3.685	77	3.26	81
76	2.232	30	3.93	26	78	3.868	78	3.44	72
22	2.259	31	4.08	18	11	4.027	79	3.18	86
5	2.283	32	3.76	44	93	4.038	80	3.28	80
92	2.296	33	4.06	19	65	4.185	81	3.24	83
73	2.328	34	3.99	24	79	4.223	82	3.26	82
44	2.369	35	3.80	37	68	4.258	83	3.22	85
6	2.405	36	3.82	35	86	4.279	84	3.30	78
29	2.472	37	3.76	42	83	4.312	85	3.13	89
75	2.582	38	3.68	49	28	4.351	86	3.10	91
82	2.593	39	3.85	33	31	4.385	87	3.14	88
39	2.597	40	3.69	47	23	4.405	88	3.31	77
67	2.607	41	3.87	31	17	4.475	89	3.16	87
2	2.621	42	3.66	54	71	4.541	90	3.03	95
47	2.627	43	3.76	41	74	4.556	91	3.04	94
13	2.641	44	3.76	43	95	4.585	92	3.22	84
26	2.692	45	3.64	56	34	4.672	93	3.05	93
69	2.712	46	3.61	57	14	4.762	94	3.10	92
70	2.723	47	3.67	51	90	4.966	95	3.12	90
27	2.725	48	3.59	59	36	5.780	96	2.71	96

The results of the cultivar superiority measure indicated that the most stable entries were entry 40 followed by entry 45 and entry 10. The ranks of the P_i are similar to the ranks based on the mean performance. This shows that P_i is more an indication of performance of an entry than stability. Similarly, the most unstable entries identified by this measure were entries 36, 90 and 14.

Joint linear regression model

The joint regression model was developed based on the idea of G x E interaction expressed as the linear regression coefficient of a genotype over the site mean (Yates and Cochran, 1938). The model was further improved by Finlay and Wilkinson (1963) and modified by Eberhart and Russel (1966). According to this model a stable genotype should have high mean yield, regression coefficient of one (b_i=1) and deviation from regression of zero (S^2_{di}=0). Generally the b_i value is more an indication of the adaptation environment of a genotype. According to Finlay and Wilkinson (1963), a genotype with a b_i value less than 1.0 has above average stability and is adaptable particularly to low-performing environments and if it is greater than 1.0 the genotype has below average stability and is adapted to high performing environments. A genotype with a b_i value of 1.0 is adapted to the widest range of environments or an indication of its average stability. Hence, in most cases the deviation from regression (S^2_{di}) is taken as a parameter for stability rather than b_i which is more about responsiveness of genotypes (Eberhart and Russell, 1966; Becker and Léon, 1988).

The ANOVA for the regression model is presented in Table 3.12. The sum of squares due to environments and G x E interaction are partitioned into environments (linear), G x E (linear) and the pooled deviations from the regression model. Based on this model, the genotypes showed significant variation for the stability parameter; similarly G x E interaction was highly significant. In addition, the value for the G x E (linear) sum of squares was not a large portion of the G x E interaction compared with the environment E (linear) sum of squares and the residual indicating that the environment was the main source of variation (Table 3.12).

Table 3.12 Analysis of variance for stability analysis according to the joint regression model (Eberhart and Russell, 1966)

Sources	DF	SS	MS	F-value	Pr>F
Total	2879	5925			
Genotypes	95	213.92	2.52	4.44	0.0000
Env. + in Gen. x Env.	1344	5711.08	4.25		
Env. In linear	1	4915.63			
Gen. x Env.(linear)	95	163.07	1.72	3.39	0.0000
Pooled deviation	1248	632.38	0.51		
Residual	1440	469.30	0.33		
Grand Mean= 3.70			R-Squared= 0.89		

Table 3.13 shows that mean grain yield ranged from 2.71 – 4.57 t ha^{-1}, b_i ranged from 0.581 – 1.505, absolute values of S^2_{di} ranged from -0.215 to 1.680. A stable variety is defined as the one with highest mean performance, $b_i = 1.0$ and $S^2_{di} = 0$ (Eberhart and Russel, 1966). When $b_i > 1$ the hybrid is adapted to high yielding environments and when $b_i < 1$ it is an indication of hybrid's adaptation to low yielding environments. The three top yielding QPM hybrids, entries 40, 37 and 55 were among the stable varieties identified by this parameter because of their high mean grain yield (4.57, 4.42, 4.42 t ha^{-1} respectively), b_i value of 1.423, 1.505 and 1.138 respectively and deviation (S^2_{di}) values of 0.283, 0.702 and 0.563, respectively. The b_i values for the three top hybrids which are significantly ($P \leq 0.01$ for entries 37 and 55 and $P \leq 0.05$ for entry 40) different from unity, indicate the predictability of good performance of the QPM hybrids in the high potential areas. In addition entries 30, 81 and 89 were the top three QPM hybrids selected by this parameter as stable based on their deviation from regression values of 0.002, 0.005 and 0.005 respectively. The b_i values for these hybrids are shown as not significantly different from unity which is an indication of a wider range of adaptation for the hybrids. However, all three hybrids ranked low based on their mean grain yields. This can be attributed to the inclusion of both high yielding and low yielding environments in the analysis. The limitation of this parameter is worth mentioning here as it assumes a linear relationship between interaction and environmental means, which is not always the case and inclusion of extreme environments like low N, drought and optimum will also bias the regression slopes which make selection of stable varieties difficult (Westcott, 1986; Lin et al., 1986; Crossa, 1990; Flores, 1993).

Table 3.13 Mean grain yield (t ha^{-1}) and stability parameters of 96 QPM hybrids tested across the different environments in ESA, 2010-2011

Ent.	Pr. > F	b_i	S^2_{di}	Rank	Mean	Rank	Ent.	Pr. > F	b_i	S^2_{di}	Rank	Mean	Rank
1	0.570	1.195	-0.038	15	3.78	39	49	0.236	1.183	0.082	29	4.03	21
2	0.326	1.152	0.043	19	3.66	53	50	0.916	1.114	-0.157	51	4.02	22
3	0.020	1.329	0.316	75	3.84	34	51	0.039	1.101	0.259	66	4.09	16
4	0.010	1.322	0.371	81	4.09	16	52	0.099	1.228	0.174	54	4.34	6
5	0.983	1.180	-0.211	58	3.76	41	53	0.005	0.926	0.431	85	3.70	46
6	0.138	1.151	0.140	43	3.82	35	54	0.025	1.292	0.296	73	4.27	8
7	0.167	1.078	0.120	39	3.77	40	55	0.001	1.138	0.563	89	4.42	2
8	0.000	1.158	0.764	94	3.79	38	56	0.017	0.812	0.329	77	3.68	49
9	0.017	1.113	0.329	78	3.49	69	57	0.000	1.095	0.676	92	3.51	67
10	0.246	1.174	0.077	28	4.38	4	58	0.040	1.031	0.256	65	3.58	60
11	0.419	0.808	0.010	5	3.18	86	59	0.006	1.067	0.416	83	3.44	72
12	0.125	1.178	0.150	50	4.12	15	60	0.516	1.091	-0.022	6	4.27	8
13	0.384	0.996	0.022	6	3.76	41	61	0.001	0.795	0.535	87	3.39	74
14	0.001	0.803	0.517	86	3.10	91	62	0.332	1.096	0.041	17	3.91	27
15	0.021	1.060	0.313	74	4.37	5	63	0.329	1.007	0.042	18	4.13	13
16	0.067	0.924	0.210	57	3.67	51	64	0.028	0.976	0.288	70	3.80	36
17	0.035	0.676	0.267	67	3.16	87	65	0.538	0.741	-0.028	11	3.24	83
18	0.001	0.854	0.596	91	3.46	70	66	0.089	0.896	0.183	55	3.54	63
19	0.720	0.901	-0.083	30	3.46	70	67	0.671	0.853	-0.068	25	3.87	31
20	0.060	0.902	0.221	60	3.37	76	68	0.750	0.682	-0.093	32	3.22	84
21	0.135	1.044	0.142	45	3.69	48	69	0.348	1.032	0.035	14	3.61	57
22	0.010	0.906	0.373	82	4.08	18	70	0.382	0.933	0.022	6	3.67	51
23	0.027	0.581	0.291	71	3.31	77	71	0.203	0.853	0.099	34	3.03	95
24	0.965	0.998	-0.191	56	3.90	28	72	0.826	1.038	-0.119	37	3.52	65
25	0.013	0.815	0.352	80	3.65	55	73	0.146	0.859	0.134	41	3.99	23
26	0.142	0.957	0.137	42	3.64	56	74	0.824	0.835	-0.118	36	3.04	94
27	0.262	1.050	0.070	26	3.59	58	75	0.885	1.037	-0.143	45	3.68	50
28	0.367	0.856	0.028	11	3.10	91	76	0.551	0.980	-0.032	13	3.93	26
29	0.169	0.997	0.119	37	3.76	41	77	0.831	1.060	-0.121	40	3.53	64
30	0.442	1.039	0.002	1	3.59	58	78	0.019	0.775	0.318	76	3.44	72
31	0.026	0.770	0.295	72	3.14	88	79	0.044	0.644	0.248	64	3.26	81
32	0.470	1.171	-0.007	4	3.52	65	80	0.986	0.914	-0.215	59	3.39	74
33	0.127	0.907	0.149	48	3.70	45	81	0.434	0.928	0.005	2	3.26	81
34	0.569	0.801	-0.038	15	3.05	93	82	0.001	1.091	0.560	88	3.85	33
35	0.110	0.991	0.163	52	3.50	68	83	0.676	0.768	-0.070	27	3.13	89
36	0.370	0.710	0.027	10	2.71	96	84	0.622	1.091	-0.053	21	3.99	23
37	0.000	1.505	0.702	93	4.42	2	85	0.899	0.925	-0.149	48	3.66	53
38	0.029	1.165	0.284	69	3.89	30	86	0.211	0.705	0.095	33	3.30	78
39	0.268	1.119	0.067	24	3.69	47	87	0.378	1.029	0.024	9	3.94	25
40	0.029	1.423	0.283	68	4.57	1	88	0.271	0.801	0.066	23	3.56	61
41	0.129	1.241	0.147	47	4.13	13	89	0.434	0.854	0.005	2	3.29	79
42	0.052	1.215	0.233	62	3.87	31	90	0.102	0.673	0.170	53	3.12	90
43	0.014	1.210	0.345	79	4.18	12	91	0.046	1.045	0.245	63	3.90	28
44	0.878	1.028	-0.140	43	3.80	36	92	0.005	1.085	0.425	84	4.06	19
45	0.184	1.363	0.110	35	4.23	11	93	0.601	0.798	-0.047	20	3.28	80
46	0.001	1.138	0.592	90	4.06	19	94	0.059	0.823	0.222	61	3.55	62
47	0.279	1.013	0.063	22	3.76	41	95	0.000	0.970	1.680	96	3.22	84
48	0.734	1.170	-0.088	31	4.26	10	96	0.000	1.198	1.222	95	4.34	6

Wricke's ecovalence analysis (W_i)

Wricke's (1962) ecovalance stability concept is based on the contribution of each genotype to the G x E interaction sum of squares. Entries with a minimum W_i value have smaller deviations from the overall mean across environments and are considered to be stable. According to this parameter a genotype with zero ecovalence is regarded as stable. Wricke's ecovalence was calculated for each of the 96 maize genotypes evaluated across the stress and non-stress environments of ESA during the years 2010 and 2011 (Table 3.14). Based on this model the most stable entries were 24, 80 and 75. However these entries ranked 28th, 74th and 50th based on their mean grain yields (Table 3.13). The high yielding entries were considered as least stable by this parameter because of their high ecovalence value which is an indication of their large deviation from the mean yield across environments. Similar to the Eberhart and Russel (1966) stability parameter, this method is also unable to pick the high yielding entries as stable ones. This is mainly because of the inclusion of data from diverse or extreme environments.

Table 3.14 Ecovalance values and their ranks for 96 maize genotypes tested in 15 environments of ESA, 2010-2011

Entry	Ecovalence	Rank	Entry	Ecovalence	Rank
24	1.758	1	6	7.221	49
80	1.818	2	16	7.260	50
75	2.449	3	65	7.303	51
44	2.460	4	91	7.523	52
85	2.587	5	20	7.603	53
72	2.767	6	58	7.619	54
50	2.850	7	12	7.812	55
77	2.852	8	64	8.011	56
5	3.149	9	51	8.116	57
19	3.651	10	68	8.194	58
76	3.840	11	15	8.497	59
84	3.969	12	94	8.724	60
74	4.097	13	36	8.900	61
30	4.341	14	41	9.120	62
60	4.383	15	52	9.152	63
67	4.462	16	9	9.168	64
13	4.522	17	38	9.328	65
81	4.568	18	22	9.546	66
48	4.572	19	42	9.637	67
87	4.593	20	59	9.876	68
69	4.742	21	86	9.915	69
70	4.757	22	53	10.126	70
63	4.785	23	92	10.140	71
47	5.058	24	56	10.328	72
62	5.236	25	25	10.562	73
27	5.273	26	31	10.779	74
89	5.386	27	78	10.978	75
32	5.644	28	43	10.979	76
28	5.668	29	90	11.921	77
1	5.687	30	82	11.944	78
93	5.709	31	45	12.406	79
34	5.774	32	54	12.454	80
29	5.789	33	55	12.522	81
39	5.838	34	46	12.906	82
2	5.987	35	14	12.945	83
83	6.087	36	18	13.072	84
7	6.112	37	17	13.087	85
26	6.118	38	61	13.349	86
21	6.187	39	57	13.481	87
11	6.259	40	3	13.882	88
35	6.362	41	79	13.965	89
33	6.613	42	4	14.387	90
71	6.627	43	8	15.446	91
10	6.793	44	23	17.003	92
73	7.004	45	40	17.080	93
49	7.012	46	96	22.127	94
88	7.133	47	95	26.121	95
66	7.177	48	37	26.436	96

Shukla's stability variance (σ^2)

Shukla's (1972) stability variance is basically a modification of Wricke's ecovalence in order to give an unbiased estimate of the G x E variance for every genotype. A genotype is described as stable if its stability variance (σ^2) is equal to the environmental variance (σ_e^2) which means that $\sigma_i^2 = 0$. A relatively large value of σ_i^2 will thus indicate greater instability of genotype *i.* Shukla (1972) also proposed criteria for testing the significance of the stability variance of each genotype and extended the model to allow the removal of the linear effects due to covariates.

Similar to Wricke's (1962) ecovalence the parameter of Shukla (1972) also identified similar entries as most stable regardless of their yield level. Entries 24, 80 and 75 were considered s stable, while the highest yielding entries were categorised as the least stable (Table 3.15). From the results of this analysis it can be seen that the stability estimates by Wricke (1962) and Shukla (1972) are almost identical. However, Shukla's (1972) model differs in the ranking of the genotypes from Wricke (1962) when covariates (locations means) were considered (Table 3.16). The rank order of the entries slightly differs when the parameter considered the covariates. Accordingly the most stable entries were 80, 5 and 24. In addition, the highest yielding entry (40) was ranked 68th but was ranked 93rd by the parameter when covariates were not considered. Similar rank changes can be seen when the Shukla (1972) parameter considered the covariates (Table 3.16).

Table 3.15 Shukla's stability variance and ranks for 96 maize genotypes tested in 15 environments of ESA, 2010-2011

Entry	σ_i^2	Rank	Entry	σ_i^2	Rank
24	0.244	1	6	1.041	49
80	0.253	2	16	1.047	50
75	0.345	3	65	1.053	51
44	0.346	4	91	1.085	52
85	0.365	5	20	1.097	53
72	0.391	6	58	1.099	54
50	0.403	7	12	1.127	55
77	0.403	8	64	1.156	56
5	0.447	9	51	1.171	57
19	0.520	10	68	1.183	58
76	0.548	11	15	1.227	59
84	0.566	12	94	1.260	60
74	0.585	13	36	1.286	61
30	0.621	14	41	1.318	62
60	0.627	15	52	1.323	63
67	0.638	16	9	1.325	64
13	0.647	17	38	1.348	65
48	0.654	18	22	1.380	66
81	0.654	19	42	1.393	67
87	0.657	20	59	1.428	68
69	0.679	21	86	1.434	69
70	0.681	22	53	1.465	70
63	0.685	23	92	1.467	71
47	0.725	24	56	1.494	72
62	0.751	25	25	1.528	73
27	0.757	26	31	1.560	74
89	0.773	27	43	1.589	75
32	0.811	28	78	1.589	76
28	0.814	29	90	1.726	77
1	0.817	30	82	1.730	78
93	0.820	31	45	1.797	79
34	0.830	32	54	1.804	80
29	0.832	33	55	1.814	81
39	0.839	34	46	1.870	82
2	0.861	35	14	1.876	83
83	0.875	36	18	1.894	84
7	0.879	37	17	1.897	85
26	0.880	38	61	1.935	86
21	0.890	39	57	1.954	87
11	0.900	40	3	2.013	88
35	0.915	41	79	2.025	89
33	0.952	42	4	2.086	90
71	0.954	43	8	2.241	91
10	0.978	44	23	2.468	92
73	1.009	45	40	2.479	93
49	1.010	46	96	3.216	94
88	1.028	47	95	3.798	95
66	1.034	48	37	3.844	96

Table 3.16 Shukla's stability variance with locations means as covariate and ranks for 96 maize genotypes tested in 15 environments of ESA, 2010-2011

Entry	S_i^2	Rank	Entry	S_i^2	Rank
80	0.216	1	26	0.935	49
5	0.224	2	6	0.940	50
24	0.265	3	21	0.946	51
50	0.333	4	41	0.954	52
85	0.351	5	33	0.958	53
75	0.363	6	12	0.961	54
44	0.369	7	35	0.988	55
77	0.408	8	90	1.003	56
72	0.412	9	52	1.010	57
74	0.413	10	66	1.029	58
68	0.465	11	16	1.083	59
48	0.475	12	20	1.106	60
19	0.485	13	94	1.108	61
83	0.512	14	42	1.131	62
67	0.515	15	91	1.154	63
84	0.546	16	79	1.161	64
93	0.558	17	58	1.179	65
1	0.577	18	51	1.183	66
34	0.578	19	17	1.201	67
76	0.589	20	40	1.234	68
65	0.597	21	38	1.236	69
60	0.611	22	64	1.243	70
32	0.641	23	23	1.249	71
30	0.659	24	31	1.258	72
89	0.664	25	54	1.260	73
81	0.665	26	15	1.295	74
11	0.674	27	3	1.299	75
13	0.700	28	78	1.305	76
70	0.700	29	9	1.327	77
87	0.704	30	56	1.327	78
36	0.710	31	43	1.359	79
28	0.712	32	25	1.374	80
69	0.726	33	4	1.414	81
62	0.738	34	22	1.417	82
63	0.741	35	59	1.505	83
2	0.743	36	92	1.524	84
47	0.783	37	53	1.536	85
88	0.790	38	14	1.711	86
39	0.793	39	61	1.747	87
27	0.797	40	82	1.799	88
10	0.813	41	55	1.804	89
49	0.822	42	46	1.865	90
86	0.849	43	18	1.871	91
71	0.857	44	57	2.035	92
45	0.880	45	37	2.088	93
29	0.899	46	8	2.215	94
7	0.900	47	96	3.150	95
73	0.929	48	95	4.086	96

Non-parametric measures of stability

The stability parameters described in the previous section are based on the absolute yield data of the entries across the different environments indicating that the methods are parametric. However, stability can also be measured by non-parametric approaches which are based on rank differences rather than absolute values. In this approach a genotype can be considered stable if its ranking is relatively constant across the different environments. The apparent advantages of this method are that there is no need to make assumptions about the distribution of the phenotypic data and the application and the interpretation of ranks are easy and not sensitive to errors of measurement as compared to the parametric methods. Furthermore, addition or deletion of one or a few observations will not create a big variation as opposed to parametric stability measures (Nassar and Hühn, 1987). They expressed two rank stability measures as S1 and S2. According to their procedure, S1 measures the mean absolute rank difference of a genotype over environments and it estimates all possible pair wise rank differences across locations for each genotype. S2 gives the variance among the ranks over environments. Accordingly, S1 = 0 indicates a genotype's maximum stability and for variance of ranks (S2) smaller estimates indicate relative stability and zero variance is an indication of maximum stability of a genotype. Approximate tests of significance Z1 and Z2 were developed based on the chi-squared distribution for these two non-parametric measures (Nassar and Hühn, 1987). For S1, genotypes may be tested as significantly less stable or more stable than the average stability/instability. For several reasons, S1 against the S2 parameter is preferred, because S1 is easily computed and allows a clear and relevant interpretation (mean absolute rank difference between the environments). Furthermore, an efficient test of significance is available (Huehn, 1990).

Based on this procedure the most stable hybrid was entry 80 and hybrids with high mean yield were found to be less stable by this stability parameter. Entry 80 was also among the most stable hybrids selected by the methods of Wricke and Shukla, which is an indication of a positive correlation. The two overall chi-square calculated stabilities (Z1=163.90 and Z2=159.52) were greater than the tabulated chi-square values ($\chi^2_{0.01,}96 = 131.14$) which is an indication of the existence of significant differences in stability among the hybrids. The ranks for the selected top 25 QPM hybrids from the parameters are presented in Table 3.17.

Table 3.17 Mean absolute rank difference (S1) and variance of ranks (S2) for grain yield of the selected top 25 QPM hybrids tested across 15 environments of ESA, 2010-2011

No	Entry	S(1)	Rank	Z(1)	Entry	S(2)	Rank	Z(2)
1	80	17.505	1	11.968**	80	213.022	1	8.309**
2	48	18.419	2	10.505**	48	233.529	2	7.706**
3	74	19.429	3	9.001**	74	299.182	3	5.929**
4	50	21.352	4	6.456**	44	328.516	4	5.210**
5	36	21.695	5	6.047**	50	335.582	5	5.044**
6	44	22.019	6	5.673**	24	336.622	6	5.020**
7	63	22.343	7	5.311**	63	340.596	7	4.928**
8	24	22.381	8	5.269**	72	361.316	8	4.461**
9	34	22.457	9	5.186**	34	367.182	9	4.334**
10	71	23.010	10	4.603**	77	379.982	10	4.061**
11	75	23.200	11	4.410**	75	383.716	11	3.983**
12	72	23.238	12	4.371**	71	386.516	12	3.926**
13	77	23.676	13	3.945**	85	388.640	13	3.882**
14	85	23.848	14	3.784**	10	395.929	14	3.734**
15	10	24.019	15	3.627**	76	405.529	15	3.544**
16	76	24.324	16	3.355**	36	414.249	16	3.375**
17	60	24.876	17	2.889**	15	427.227	17	3.132**
18	52	24.971	18	2.812**	60	436.907	18	2.957**
19	15	25.124	19	2.692**	5	438.773	19	2.924**
20	6	25.162	20	2.662**	6	446.382	20	2.790**
21	28	25.238	21	2.603**	52	451.893	21	2.695**
22	5	25.390	22	2.487**	70	463.396	22	2.502**
23	70	26.152	23	1.946**	87	467.840	23	2.430**
24	19	26.381	24	1.797**	19	475.796	24	2.303**
25	87	26.495	25	1.725**	81	480.222	25	2.234**

Overall Chi-square for stability 163.90, 96 df. Individual Z (1) distributed as single df Chi-squares. Overall Chi-square for stability = 159.52, 96 df. Individual Z (2) distributed as single df Chi-squares

The AMMI Stability Value (ASV)

The ASV as described by Purchase (1997) was calculated for each hybrid. According to this method, entries with lower ASV values were considered more stable than entries with higher ASV. Table 3.18 shows the ASV for the 96 entries compared with mean grain yield.

Table 3.18 AMMI Stability Value, mean grain yield and ranks for 96 maize genotypes tested in 15 environments of ESA, 2010-2011

Entry	ASV	**Rank**	**Mean yield (t ha^{-1})**	**Rank**	**Entry**	ASV	**Rank**	**Mean yield (t ha^{-1})**	**Rank**
47	0.054	1	3.760	44	39	0.539	49	3.690	48
60	0.070	2	4.270	11	11	0.552	50	3.180	86
35	0.109	3	3.500	68	83	0.555	51	3.130	89
87	0.125	4	3.940	25	32	0.557	52	3.520	65
75	0.148	5	3.680	50	2	0.562	53	3.660	53
63	0.151	6	4.130	14	28	0.564	54	3.100	92
13	0.151	7	3.760	42	73	0.569	55	3.990	23
44	0.153	8	3.800	36	53	0.574	56	3.700	46
24	0.161	9	3.900	28	1	0.585	57	3.780	39
66	0.189	10	3.540	63	94	0.588	58	3.550	62
89	0.198	11	3.290	79	41	0.589	59	4.130	13
85	0.199	12	3.660	54	6	0.597	60	3.820	35
27	0.207	13	3.590	58	25	0.599	61	3.650	55
76	0.214	14	3.930	26	12	0.613	62	4.120	15
77	0.222	15	3.530	64	52	0.623	63	4.340	6
69	0.222	16	3.610	57	26	0.626	64	3.640	56
81	0.245	17	3.260	82	92	0.627	65	4.060	20
72	0.258	18	3.520	66	64	0.638	66	3.800	37
80	0.264	19	3.390	75	14	0.659	67	3.100	91
16	0.282	20	3.670	51	18	0.670	68	3.460	70
29	0.282	21	3.760	43	31	0.692	69	3.140	88
62	0.291	22	3.910	27	56	0.722	70	3.680	49
20	0.306	23	3.370	76	43	0.724	71	4.180	12
33	0.324	24	3.700	45	42	0.735	72	3.870	31
58	0.351	25	3.580	60	68	0.751	73	3.220	84
7	0.357	26	3.770	40	65	0.764	74	3.240	83
70	0.362	27	3.670	52	88	0.768	75	3.560	61
59	0.377	28	3.440	72	82	0.789	76	3.850	33
19	0.391	29	3.460	71	36	0.833	77	2.710	96
48	0.391	30	4.260	10	46	0.844	78	4.060	19
84	0.396	31	3.990	24	78	0.876	79	3.440	73
93	0.402	32	3.280	80	61	0.902	80	3.390	74
30	0.427	33	3.590	59	96	0.907	81	4.340	7
22	0.443	34	4.080	18	57	0.915	82	3.510	65
49	0.450	35	4.030	21	86	0.943	83	3.300	78
5	0.450	36	3.760	41	4	0.946	84	4.090	16
50	0.458	37	4.020	22	79	0.950	85	3.260	81
34	0.473	38	3.050	93	45	0.983	86	4.230	11
74	0.479	39	3.040	94	8	1.017	87	3.790	38
10	0.487	40	4.380	4	17	1.022	88	3.160	87
38	0.495	41	3.890	30	55	1.079	89	4.420	3
21	0.501	42	3.690	47	95	1.116	90	3.220	85
9	0.512	43	3.490	69	40	1.125	91	4.570	1
71	0.515	44	3.030	95	90	1.133	92	3.120	90
51	0.521	45	4.090	17	54	1.177	93	4.270	8
67	0.521	46	3.870	32	3	1.206	94	3.840	34
15	0.531	47	4.370	5	23	1.374	95	3.310	77
91	0.533	48	3.900	29	37	1.789	96	4.420	2

According to the ASV parameter the most stable hybrids were entries 47, 60 and 35. However, these hybrids were not the top hybrids for their mean grain yield. One of the top

entries for grain yield (entry 37) was identified as the least stable hybrid by this parameter. This method shows similarity with Wricke's (1962) ecovalence and Shukla's (1972) stability variance in identifying the least stable hybrids across the different environments.

3.4.4 Comparison of the different stability measures

The ranking of the 96 maize genotypes based on the different parametric and non-parametric stability measures is presented in Table 3.19. According to Lin and Binns' (1988), cultivar superiority measure and mean grain yield value, the most stable entry was 40 and the least stable was entry 36. Since both parameters focus on the average yield across the different environments, their ranking order is highly correlated. However, these entries were not identified by the other parameters as stable. Entry 80 was among the most stable entries identified by Wricke's (1962) ecovalence, Shukla's (1972) stability variance and by both non-parametric measures. Similarly entries 37, 96, and 95 were the least stable entries identified by all the stability parameters except by Lin and Binns's (1988) cultivar superiority measure and mean yield. The AMMI stability value identified entries 47, 60 and 35 as the most stable entries (Table 3.19).

The different stability parameters showed variability in ranking of the most stable entries. Apart from the inconsistency in performance of the QPM hybrids across the diverse environments, the nature of the parameters in defining stability also contributed to the disparity in order of ranking the stable entries. Hence, to further understand the relationship between the different parameters, a correlation analysis was performed.

Table 3.20 shows the pair wise comparison of the nine stability parameters based on Spearman's coefficient of rank correlation (Steel and Torie, 1980). The correlation between mean yield and P_i were found to be very high ($P \leq 0.001$) in the ranking of the entries (r = 0.97**). However, both were generally quite poorly correlated with the rest of the parameters. Mean yield was found to be negatively correlated with all the other stability parameters used in this study. This indicates that selecting a variety from METs based on average yield will not guarantee its stability. The parameter P_i was non-significantly and negatively correlated with S^2_{di} and Shukla's S_i^2 and non-significantly and positively correlated with the other parameters.

Highly significant correlation (P ≤0.001) was observed between Eberhart and Russell's (1966) deviation from regression, Wricke's (1962) ecovalence, Shukla's (1972) stability variance, Shukla's (1972) stability variance with covariates, Nassar and Huehn's (1987) absolute rank difference and variance of ranks S(1) and S(2) and ASV. This indicates that the ranking order of the entries by these parameters is significantly correlated. However, parameters with very high correlation values (r) ranked the entries very similarly. Wricke's procedure of stability statistic showed the highest significant positive correlation (P < 0.01) with Shukla (no covariates, r=1.00**), Shukla (with covariates, r=0.90**) and ASV (r=0.83**). The perfect correlation between Wricke's and Shukla's methods indicates that the two procedures are equivalent for ranking purposes. This result is further supported by the fact that Shukla's stability variance is a linear combination of the ecovalence and therefore, both W_i and σ_i^2 are equivalent for ranking (Wricke and Weber, 1980). The perfect correlation among Wricke and Shukla (with no covariate) is also consistent with other reports (Purchase, 1997; Tsige, 2002; Alberts, 2004; Issa, 2009). However, the inclusion of covariates in the analysis of Shukla did not show a perfect correlation with that of Wricke, although there exists a highly significant correlation (r=0.90**) (Table 3.20).

The rank order of the entries by the non-parametric measures S(1) and S(2) showed highly significant (P ≤ 0.001) positive correlation with most of the parametric measures except for P_i and mean yield, which showed non-significant positive correlation with P_i and negative correlation with mean yield (Table 3.20). The very high correlation (r=0.98**) between S(1) and S(2) indicates that the stability estimates by the two methods are nearly identical. The significant correlation of the non-parametric measures with the parametric estimates suggests their importance as an alternative option for identifying stable genotypes from METs (Yue et al., 1997), although they do not supply information about genotype adaptation.

Table 3.19 The ranking order of the 96 QPM hybrids according to the different stability parameters (shaded cells shows the rank of the most stable entries)

No	Entry	yield	Pi	S^2_{di}	W_i	σ^2_i	S^2_i	S(1)	S(2)	ASV
1	40	1	1	68	93	93	68	36	83	91
2	45	11	2	35	79	79	45	80	76	86
3	10	4	3	28	44	44	41	15	14	40
4	15	5	4	74	59	59	74	19	17	47
5	52	7	5	54	63	63	57	18	21	63
6	55	2	6	89	81	81	89	41	52	89
7	54	9	7	73	80	80	73	89	94	93
8	37	3	8	93	96	96	93	95	96	96
9	60	8	9	6	15	15	22	17	18	2
10	96	6	10	95	94	94	95	92	93	81
11	48	10	11	31	19	18	12	2	2	30
12	63	13	12	18	23	23	35	7	7	6
13	43	12	13	79	76	75	79	37	31	71
14	41	14	14	47	62	62	52	43	43	59
15	49	21	15	29	46	46	42	57	50	35
16	12	15	16	50	55	55	54	56	58	62
17	50	22	17	51	7	7	4	4	5	37
18	4	17	18	81	90	90	81	93	92	84
19	51	16	19	66	57	57	66	49	54	45
20	46	20	20	90	82	82	90	87	87	78
21	84	23	21	21	12	12	16	29	28	31
22	24	29	22	56	1	1	3	8	6	9
23	38	30	23	69	65	65	69	94	91	41
24	3	34	24	75	88	88	75	91	89	94
25	62	27	25	17	25	25	34	32	29	22
26	87	25	26	9	20	20	30	25	23	4
27	91	28	27	63	52	52	63	34	30	48
28	42	32	28	62	67	67	62	82	85	72
29	1	39	29	15	30	30	18	40	41	57
30	76	26	30	13	11	11	20	16	15	14
31	22	18	31	82	66	66	82	83	82	34
32	5	44	32	58	9	9	2	22	19	36
33	92	19	33	84	71	71	84	64	65	65
34	73	24	34	41	45	45	48	51	46	55
35	44	37	35	43	4	4	7	6	4	8
36	6	35	36	43	49	49	50	20	20	60
37	29	42	37	37	33	33	46	68	67	21
38	75	49	38	45	3	3	6	11	11	5
39	82	33	39	88	78	78	88	79	81	76
40	39	47	40	24	34	34	39	54	53	49
41	67	31	41	25	16	16	15	33	35	46
42	2	54	42	19	35	35	36	55	49	53
43	47	41	43	22	24	24	37	53	48	1
44	13	43	44	6	17	17	28	46	44	7
45	26	56	45	42	38	38	49	39	39	64
46	69	57	46	14	21	21	33	42	38	16

Table 3.19 continued…. (shaded cells show the rank of most stable entries)

No	Entry	yield	Pi	S^2_{di}	W_i	σ_i^2	S_i^2	S(1)	S(2)	ASV
47	70	51	47	6	22	22	29	23	22	27
48	27	59	48	26	26	26	40	35	37	13
49	85	53	49	48	5	5	5	14	13	12
50	8	38	50	94	91	91	94	90	88	87
51	32	66	51	4	28	28	23	50	51	52
52	7	40	52	39	37	37	47	63	57	26
53	21	48	53	45	39	39	51	38	33	42
54	16	52	54	57	50	50	59	70	69	20
55	53	45	55	85	70	70	85	67	63	56
56	30	58	56	1	14	14	24	47	42	33
57	33	46	57	48	42	42	53	84	80	24
58	25	55	58	80	73	73	80	81	73	61
59	64	36	59	70	56	56	70	62	60	66
60	58	60	60	65	54	54	65	60	61	25
61	77	64	61	76	8	8	8	13	10	15
62	72	65	62	37	6	6	9	12	8	18
63	35	68	63	52	41	41	55	45	40	3
64	59	73	64	83	68	68	83	44	55	28
65	19	80	65	30	10	10	13	24	24	29
66	56	50	66	77	72	72	78	69	68	70
67	9	69	67	78	64	64	77	66	64	43
68	94	62	68	61	60	60	61	75	72	58
69	66	63	69	55	48	48	58	61	56	10
70	80	74	70	59	2	2	1	1	1	19
71	88	61	71	23	47	47	38	52	45	75
72	57	67	72	92	87	87	92	74	71	82
73	18	71	73	91	84	84	91	76	74	68
74	20	76	74	60	53	53	60	27	26	23
75	89	79	75	2	27	27	25	58	59	11
76	61	75	76	87	86	86	87	85	86	80
77	81	81	77	2	18	19	26	26	25	17
78	78	72	78	76	75	76	76	48	47	79
79	11	86	79	5	40	40	27	28	32	50
80	93	80	80	20	31	31	17	30	36	32
81	65	83	81	11	51	51	21	59	66	74
82	79	82	82	64	89	89	64	86	84	85
83	68	85	83	32	58	58	11	77	79	73
84	86	78	84	33	69	69	43	72	77	83
85	83	89	85	27	36	36	14	31	34	51
86	28	91	86	11	29	29	32	21	27	54
87	31	88	87	72	74	74	72	73	75	69
88	23	77	88	71	92	92	71	96	95	95
89	17	87	89	67	85	85	67	71	70	88
90	71	95	90	34	43	43	44	10	12	44
91	74	94	91	36	13	13	10	3	3	39
92	95	84	92	96	95	95	96	88	90	90
93	34	93	93	15	32	32	19	9	9	38
94	14	92	94	86	83	83	86	78	78	67
95	90	90	95	53	77	77	56	65	62	92
96	36	96	96	10	61	61	31	5	16	77

Table 3. 20 Spearman rank correlation between parametric and non-parametric stability measures for 96 maize genotypes evaluated across ESA (2010-2011).

	Mean yield	P_i	S^2_{di}	W_i	σ_i^2	S_i^2	S(1)	S(2)	ASV
Mean yield									
P_i	0.968**								
S^2_{di}	-0.171	-0.079							
W_i	-0.065	0.039	0.714**						
σ_i^2	-0.063	0.041	0.713**	1.000**					
S_i^2	-0.177	-0.058	0.787**	0.899**	0.899**				
S(1)	-0.019	0.073	0.541**	0.766**	0.766**	0.728**			
S(2)	-0.031	0.057	0.551**	0.811**	0.812**	0.741**	0.976**		
ASV	-0.003	0.071	0.512**	0.831**	0.831**	0.607**	0.586**	0.642**	

** $P \leq 0.01$

Note: $P_{i=}$ Linn and Binns's (1988) cultivar superiority performance; S^2_{di}= Eberhart and Russell's (1966) deviation from regression parameter; W_i = Wricke's(1962) ecovalence; σ_i^2 = Shukla's (1972) stability variance with no covariates; S_i^2 Shukla's (1972) stability variance with covariates; S(1) and S(2) Nassar and Hühn's (1987) absolute rank difference and variance of ranks respectively; ASV = AMMI stability value.

3.5 Conclusions

From the individual environment analysis the variation among the 96 entries was highly significant, which is an indication of the existence of variability within the genotypes and the potential for further selection. In most of the individual environments the contribution of entries to the total variation was high, except at a few locations where the variation caused by replication and block was important. Under the optimum environments, entries contributed more to the variation (except HREOP1) compared to replication and blocks. Under the stress environments replications and blocks contributed significantly to variation (Tables 3.3 and 3.5).

The grain yield performance of the QPM hybrids was better than the normal commercial check hybrid across all the environments except under the optimum environment at Bako in 2010 (BKOPT) where the normal maize (entry 96) ranked first with a yield of 9.28 t ha^{-1}. The QPM entries 52 and 46 were also the top yielding QPM hybrids in 2010 with a yield of 9.12 t ha^{-1} and 6.10 t ha^{-1} at HREOP1 and RATOP, respectively. In 2010 the entries showed better performance at BKOPT under the non-stress environments and at BKOLN under the stress environments. Results of the combined ANOVA showed that the variation among entries, environments and their interactions were highly significant. Environmental sum of squares were high in both years, mainly because of the inclusion of extreme (stress) environments in the analysis. The minimum and maximum yield of the entries from the combined analysis in 2010 ranged from 2.84 to 5.09 t ha^{-1} and in 2011 from 2.62 to 4.30 t ha^{-1}, respectively. As expected, the entries performed better under the optimum compared to the stress environments. The trials under N-stress environments yielded about 35% and drought stress 38% of the yield obtained under the optimum environments (Tables 3.7 - 3.10).

Nine different stability measurements were compared in order to identify stable genotypes across environments. Most of the parameters ranked the entries differently mainly due to the inclusion of extreme (stress) environments in the analysis. However, there was a highly significant association among the major stability parameters based on the results of the Spearman rank correlation analysis. Significant and positive correlations were observed among Eberhart and Russel (1966) deviation from regression parameter, Wricke's (1962) ecovalence (W_i), Shukla's (1972) stability variance with no covariates (σ_i^2), Shukla's (1972) stability variance with covariates (S_i^2), Nassar and Huehn's (1987) absolute rank

difference and variance of ranks (S(1) and S(2)) and Purchase's (1997) ASV. There was a perfect correlation between Wricke's (1962) ecovalence and Shukla's (1972) stability variance with no covariates (σ_i^2) which indicates the similarity of the parameters in ranking the stable genotypes. Entry 80 was the most stable hybrid and was identified by Nassar and Hühn's (1987) absolute rank difference and variance of ranks [(S (1) and S(2)], as well as the parameters of Wricke's (1962) ecovalence (W_i) and Shukla's (1972) stability variance with no covariates (σ_i^2). Based on mean grain yield and Linn and Binns's (1988) cultivar superiority measures the most stable entry was 40. However, superior entries in grain yield were found to be the least stable hybrids. This is mainly because of the sensitivity of single cross QPM hybrids to diverse environments which was also reported by Pixley and Bjarnason (2002) and the inclusion of diverse environments in the analysis.

Finally, the use of the different univariate stability models to identify stable genotypes from diverse environments was inadequate for a reliable prediction on the potential of entries as the models gave inconsistent ranking. Furthermore, to choose the best informative stability parameter that meets the interest of breeders (repeatable high yield) from the linear regression models will be complex if extreme environments are considered in the analysis. The findings of Crossa (1990) also suggested that when linearity of response fails in the classical linear regression models, multivariate analysis methods are useful to better exploit the information contained in the data. In a situation where diverse environments are included, multivariate analysis such as AMMI and cluster analysis will be more appropriate to identify stable entries and their specific adaptation environment which is the subject of the next chapter.

3.6 References

Agronomix software, Inc. 2011. Agrobase Generation II SQL. Agronomix software, Inc., 171 Waterloo St. Winnipeg, Manitoba, R3N054, Canada.

Alberts, M.J.A. 2004. A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials. MSc. Thesis, University of the Free State, Bloemfontein, South Africa.

Bänziger, M., F.J. Betrán, and H.R. Lafitte. 1997. Efficiency of high nitrogen selection environments for improving maize for low nitrogen target environments. *Crop Science* 37:1103-1109.

Bänziger, M., G.O. Edmeades, D. Beck, and M. Bellon. 2000. Breeding for Drought and N Stress Tolerance in Maize: From Theory to Practice. CIMMYT, Mexico, D.F.

Bänziger, M., P.S. Setimela, D. Hodson, and B. Vivek. 2006. Breeding for improved abiotic stress tolerance in maize adapted to southern Africa. *Agricultural Water Management* 80:212-224.

Beck, D.L., S.K. Vasal, and J. Crossa. 1991. Heterosis and combining ability among subtropical and temperate intermediate maturity maize germplasm. *Crop Science* 31:68-73.

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

Ceccarelli, S. 1989. Wide adaptation: How wide? *Euphytica* 40:197-205.

CIMMYT. 2001. 2000/2001 World maize facts and trends. Mexico D.F.

Cooper, M., and D.E. Byth. 1996. Understanding plant adaptation to achieve systematic applied crop improvement: A fundamental challenge. In: M. Cooper and G.L. Hammer (Eds.). Plant Adaptation and Crop Improvement. CAB International and IRRI, UK. pp. 5-23.

Crossa, J. 1990. Statistical analyses of multilocation trials. *Advances in Agronomy* 44:55-85.

Crossa, J., H.G. Gauch, and R.W. Zobel. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials *Crop Science* 30:493-500.

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

Edmeades, G.O., J. Bolaños, S.C. Chapman, M. Bänziger, and H.R. Lafitte. 1999. Selection improves drought tolerance to mid/late season drought in tropical maize populations. I. Gains in biomass, grain yield, and harvest index. *Crop Science* 39:1306- 1315.

FAOSTAT. 2010. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

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

Flores, F. 1993. Interaccio´n Genotipo–Ambiente en *Vicia faba* L. Doctoral dissertation, University of Cordoba,Spain.

Gauch, H.G., and R.W. Zobel. 1997. Identifying mega-environments and targeting genotypes. *Crop Science* 37:311-326.

Gissa, D.W. 2008. Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. PhD Thesis, Department of Plant Sciences (Plant Breeding), University of the Free State, Bloemfontein, South Africa.

Glover, M.A., D.B. Willmot, L.L. Darrah, B.E. Hibbard, and X. Zhu. 2005. Diallel analyses of agronomic traits using Chinese and U.S. maize germplasm. *Crop Science* 45:1096-1102.

Hallauer, A.R., W.A. Russell, and K.R. Lamkey. 1988. Corn breeding. In: G.F. Sprague and J.W. Dudley (Eds.). Corn and corn improvement. 3rd ed. Agronomy Monograph No.18. ASA, CSSA, and SSSA, Madison, Wisconsin. pp. 463-564.

Heisey, P.W., and G.O. Edmeades. 1999. Maize production in drought stressed environments:Technical options and research resource allocation. CIMMYT 1997/98 World Maize Facts and Trends. CIMMYT, Mexico, D. F.

Hintze, J. 2001. NCSS and PASS, Number Cruncher Statistical Systems. Kasville, Utah.

Huehn, M. 1990. Non-parametric estimation of and testing of genotype-environment interactions by ranks. In: Kang, M.S. (Ed.). Genotype-by-environment interactions and plant breeding. Louisiana State University Agricultural Center. pp. 63-66.

Issa, A.B. 2009. Genotype by environment interaction and yield stability of maize hybrids evaluated in Ethiopia. MSc. Thesis, Department of Plant Sciences/Plant Breeding, University of the Free State, Bloemfontein, South Africa.

Kang, M.S. 1998. Using genotype by environment interaction for crop cultivar development. *Advances in Agronomy* 62:199-246.

Lin, C.S., and M.R. Binns. 1988. A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Sciences* 68:193-198.

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

Nassar, R., and M. Huehn. 1987. Studies in estimation of phenotypic stability: Test of significance for non-parametric measures of phenotypic stability. *Biometrics* 43:45-53.

Patterson, H.D., and E.R. Williams. 1976. A new class of resolvable incomplete block designs. *Biometrika* 63: 83-89.

Pingali, P.L., and S. Pandey. 2001. Meeting world maize needs: Technological opportunities and priorities for public sector. CIMMYT 1999/2000 World Maize Facts and Trends, CIMMYT, Mexico, D. F.

Pixley, K.V., and M.S. Bjarnason. 1993. Combining ability for yield and protein quality among modified endosperm opaque-2 tropical maize inbreds. *Crop Science* 33:1229-1234.

Pixley, K.V., and M.S. Bjarnason. 2002. Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42:1882-1890.

Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Ramagosa, I., and P.N. Fox. 1993. Genotype x Environment interaction and adaptation. In: M.D. Hayward, N.O. Bosemark and I. Ramagosa (Eds.). Plant breeding: Principles and prospects. Chapman and Hall, London. pp. 373-390.

SAS Institute, Inc. 2003. SAS proprietary Software. SAS Institute, Inc, CARY, NC, Canada.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity* 29:237-245.

Steel, R.G., and J.H. Torrie. 1980. Principles and procedures of statistics. McGraw-Hill, New York.

Tsige, G.K. 2002. Genetic diversity analysis and genotype x environment interaction in Ethiopian Mustard. Ph.D. Thesis. Department of Plant Sciences / Plant Breeding , Faculty of Natural and Agricultural Sciences, University of the Free State Bloemfontein, South Africa.

Vargas, M., J. Crossa, F.A.v. Eeuwijk, M.E. Ramirez, and K.Sayre. 1999. Using AMMI, factorial regression, partial least squares regression models for interpreting genotype x environment interaction. *Crop Science* 39:955-967.

Vasal, S.K., G. Srinivasan, S. Pandey, F. Gonzalez, D.L. Beck, and J. Crossa. 1993a. Heterosis and combining ability of CIMMYT's quality protein maize germplasm: II. Subtropical. *Crop Science* 33:51-57.

Vasal, S.K., G. Srinivasan, S. Pandey, F. Gonzalez, J. Crossa, and D.L. Beck. 1993b. Heterosis and combining ability of CIMMYT's quality protein maize germplasm: I. Lowland tropical. *Crop Science* 33:46-51.

Westcott, B. 1986. Some methods of analyzing genotype–environment interaction. *Heredity* 56:243-253.

Wricke, G. 1962. Über eine Method zur Erfassung der Ökologischen Streuberite in Feldversuchen. *Z. Pflanzenzüchtg* 47:92-96.

Wricke, G., and W.E. Weber. 1980. Erweiterte analyse von wechselwirkungen in versuchsserien. In: W. Köpcke and K. Überlan (Eds.). Biometrie-heute und morgen. Springer-Verlag, Berlin.

Yates, F., and W.G. Cochran. 1938. The analysis of group experiments. *Journal of Agricultural Science* 28:566-580.

Yue, G.L., K.L. Roozeboom, W.T. Schapaugh Jr., and G.H. Liang. 1997. Evaluation of soybean cultivars using parametric and nonparametric stability estimates. *Plant Breeding* 116:271-275.

Zobel, R.W., M.J. Wright, and H.G.G. Jr. 1988. Statistical analysis of yield trial. *Agronomy Journal* 80:388-393.

CHAPTER 4

Evaluation of grain yield stability and adaptation pattern of QPM hybrids under stress and optimal growing conditions in ESA based on the models of AMMI and GGE

4. 1 Abstract

The application of multivariate analysis techniques is important when a non-linear genotypic response across environments is expected. A total of 96 maize hybrids (95 QPM and one normal hybrid) were evaluated for grain yield stability and adaptation under 15 stress and optimal growing conditions in Ethiopia, Kenya and Zimbabwe during 2010 and 2011. The ANOVA of the AMMI model showed highly significant variances for environments, genotypes and G x E interaction. The F-test was highly significant (P < 0.001) for all five IPCA axes which explained 100% of the variation due to G x E interaction. The first two IPCA axes (AMMI2) explained about 60% of the variation. Among the entries, the QPM hybrid entry 40 was identified as the best genotype across environments. Another high yielding QPM entry 37 was among the most responsive entries specifically adapted to the optimum environment of Awassa, Ethiopia (AWAOP). The first two principal components of the GGE analysis were able to capture about 50% of the total variability due to the G x E interaction. Among the environments HREOP2, the optimum environment at Harare-Zimbabwe, was found to be the most discriminating and representative environment while entry 40 was identified as the best performing and stable entry due to its proximity to the ideal genotype in the GGE biplot. GGE biplot grouped the environments into four major mega-environments each having more than one site except Chisumbanje (CHSDT) which was categorised as a separate mega-environment. The comparison of the two models based on this study showed that AMMI2 (60%) was better than GGE2 (50%) which was better than the AMMI1 (35.73%) model in explaining the variability due to G x E interaction. However, the various and useful biplot display options by GGE makes it preferable for easy visualisation of the complex multi-environment data. This study also emphasized the importance of additional statistical tests including ANOVA for a critical evaluation and selection of genotypes from the G x E data.

Key words: AMMI, GGE, multivariate analysis, biplots, QPM

4.2 Introduction

The development of high yielding and stable genotypes and identification of suitable growing environments are the primary goals of a successful breeding programme. To ensure continuous cultivation of a genotype, it should have good performance and wide adaptation. Hence, evaluation of genotypes across environments and thorough analysis of G x E interactions help to identify those with stable performance as well as to delineate environments based on genotypic response. Various univariate and multivariate methods have been developed to analyse G x E interaction and to identify stable genotypes from METs. In a situation where the G x E interaction is highly significant due to the inclusion of diverse environments the use of multivariate techniques and data visualisation methods are more appropriate than the conventional linear regression models.

Zobel et al. (1988) pointed out the limitations of the classical linear stability models. Accordingly, ANOVA falls short in detecting significant interaction components. Significant genotype and environment main effects are not required using PCA and linear regression models since they account for only a small portion of the interaction sum of squares. However, the AMMI model effectively reveals interaction components that have a clear agronomic meaning. The AMMI model is easy to use as it has no specific design requirements, except for a two-way data structure.

The AMMI model combines the ANOVA for the genotype and environment main effects with principal components analysis of the G x E interaction. It has proved useful for understanding of complex G x E interactions. The results can be graphed in a useful biplot that shows both main and interaction effects for genotypes and environments. Gauch and Zobel (1996) showed that AMMI1 with IPCA1 and AMMI2 with IPCA1 and IPCA2 are usually selected and the graphical representation of axes, either as IPCA1 or IPCA2 against main effects or IPCA1 against IPCA2 is generally informative. When AMMI3 and higher models are presented for agricultural data, the third and higher IPCA axes are dominated by noise and have no predictive value (Van Eeuwijk, 1995).

Since AMMI has the biplot 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 PCA1 values. Any genotype with a PCA1

value close to zero shows general adaptation to the tested environments. A large genotypic PCA1 score reflects more specific adaptation to environments with PCA1 scores of the same sign. AMMI provides a more adequate biological explanation of G x E than the regression models and it has been found useful when applied to across year analyses with a higher element of unpredictability (Crossa et al., 1990; Yau, 1995; Gauch and Zobel, 1996; Annicchiarico, 1997).

The GGE biplot method was developed by using some of the functions of the classical joint regression, the AMMI and the genetic correlation models (Ding et al., 2007). In total phenotypic variation, environment (E) explains most of the variation and genotype (G) and the G x E interaction are usually small (Yan, 2002). However, only the G and G x E interaction are relevant to cultivar evaluation, particularly when G x E interaction is identified as repeatable (Hammer and Cooper, 1996). The term "GGE biplot" was first coined by Yan et al. (2000) and refers to a biplot as developed by Gabriel (1971) that displays the G and GE of a genotype-by-environment data. The key property of a GGE biplot is that it is based on environment-centred data, whereby the environment (tester) main effects (E) are removed, and the genotype main effect (G) and the genotype by GE are retained and combined. Therefore, a biplot based on environment-centred data contains only G+GE effects, abridged as GGE (Yan, 2001; Yan et al., 2000). The GGE biplot helps to visualise, among others, the relationship among the genotypes, which genotype-won-where, the discriminating power and representativeness of the test-environments and the different groups of mega-environments.

Several workers have reported the usefulness of the GGE model for different purposes including, but not limited to, mega-environment analysis (Yan and Rajcan, 2002; Casanoves et al., 2005; Samonte et al., 2005; Yan and Tinker, 2005; Dardanellia et al., 2006), genotype evaluation (Bhan et al., 2005; Voltas et al., 2005; Kang et al., 2006; Setimela et al., 2007; Fatma et al., 2011), test-environment evaluation (Yan and Rajcan, 2002; Xing-Ming et al., 2007; Weikai and James, 2010), and heterotic pattern analysis (Narro et al., 2003; Andio et al., 2004; Bertoia et al., 2006).

There are similarities and differences between AMMI and GGE models. The AMMI analysis partitions the overall variation into genotype main effects (G), environment main effects (E) and G x E interaction. The GGE biplot gives similar results as the AMMI except that the environment main effects (E) are excluded; instead GGE biplot focuses on capturing more G

and GE effects. The exclusion of the environment main effects by the GGE biplot is based on the insignificance of environment *per se* for cultivar selection and test-environment evaluation. The inclusion of environment main effects in the AMMI model is supported by interdisciplinary teams in agricultural research such as soil scientists and others. The merits and demerits of the two models have been extensively reviewed. Various authors gave different reasons for the preference of one model over the other (Yan et al., 2000; Yan and Kang, 2003; Gauch, 2006; Yan et al., 2007; Gauch et al., 2008). However, the two models are currently the best choices for the analysis of yield data from METs and the preference of either of the models will depend mainly on the type of research and the information required. Hence, the objectives of this research were to analyse the grain yield stability and adaptation pattern of the QPM hybrids included in this study, based on AMMI and GGE models and to highlight the benefits and limitations of the two models based on the results of this study.

4.3 Materials and methods

Germplasm

The details of the germplasm used in the study are presented under Section 3.3. However, for the construction of biplots by AMMI and GGE the top 25 hybrids were selected to avoid genotypes congestion in the biplots. The list of the top 25 hybrids and their IPCA scores from the AMMI analysis is presented in Table 4.1.

Table 4.1 IPCA1, IPCA2 scores and mean grain yield (t ha^{-1}) of the top 25 genotypes evaluated across 15 environments in ESA, during 2010 and 2011

No	Entry No	IPCA 1 scores	IPCA 2 scores	Mean yield
1	40	-0.7909	-0.0601	4.57
2	37	-1.2431	-0.2929	4.42
3	96	-0.5362	-0.4931	4.42
4	10	-0.2457	0.3394	4.38
5	55	-0.6067	-0.6496	4.37
6	15	-0.1949	-0.4530	4.34
7	52	-0.4251	0.1522	4.34
8	54	-0.7981	-0.3167	4.27
9	45	-0.6884	0.0997	4.27
10	48	-0.2025	0.2649	4.26
11	43	-0.3159	0.5679	4.23
12	60	-0.0477	-0.0164	4.18
13	12	-0.2824	0.4630	4.13
14	4	-0.5531	0.5276	4.13
15	51	-0.1183	0.4930	4.12
16	63	0.1059	0.0089	4.09
17	41	-0.3457	0.3252	4.09
18	46	-0.5606	-0.2797	4.08
19	92	0.0178	0.6269	4.06
20	22	0.2971	0.1356	4.06
21	49	-0.2889	0.1854	4.03
22	73	0.3996	0.0463	4.02
23	84	-0.2749	0.0641	3.99
24	24	-0.1080	-0.0479	3.99
25	50	-0.3141	-0.1043	3.94

Description of the environments and field management

The field management and description of trial sites are presented in detail under Section 3.3. The list of the test environments and their corresponding IPCA values based on the AMMI analysis are presented in Table 4.2. While the description of the environmental codes used in the different biplots is presented in Table 4.3.

Table 4.2 IPCA1, IPCA2 scores and mean grain yield (t ha^{-1}) of the 15 test environments in ESA used for the evaluation of the QPM hybrids

No	Environments	IPCA 1 scores	IPCA 2 scores	Mean yield
1	AWAOP	-1.3377	-2.6841	4.30
2	BAKOP	-0.7082	-0.1821	5.49
3	BAKLN	0.3547	-0.1735	3.18
4	MLKOP	0.0052	1.0463	4.72
5	EMBOP	-0.7928	0.0147	6.00
6	KAKOP	-0.9101	0.0274	4.42
7	KBODT	1.3819	0.4837	2.44
8	HREOP1	-1.1348	0.9521	6.44
9	HRELN1	0.6469	-0.4101	1.36
10	HREOP2	-1.4403	1.4441	6.12
11	HRELN2	0.6046	-0.2767	0.97
12	RATOP	-0.2217	0.2836	4.46
13	CHIDT1	1.4148	-0.2245	2.94
14	CHIDT2	1.1933	-0.1510	1.31
15	CHSDT	0.9442	-0.1502	1.29

Table 4.3 Description of environmental codes used in the AMMI and GGE biplots

No	Environmental codes	Country	Location	Trial Season	Environment type
1	AWAOP	Ethiopia	Awassa	2011	Optimum
2	BAKOP	Ethiopia	Bako	2010	Optimum
3	BAKLN	Ethiopia	Bako	2010	Low-N
4	MLKOP	Ethiopia	Melkassa	2011	Optimum
5	EMBOP	Kenya	Embu	2011	Optimum
6	KAKOP	Kenya	Kakamega	2011	Optimum
7	KBODT	Kenya	Kiboko	2011	Managed drought
8	HREOP1	Zimbabwe	Harare	2010	Optimum
9	HRELN1	Zimbabwe	Harare	2010	Low-N
10	HREOP2	Zimbabwe	Harare	2011	Optimum
11	HRELN2	Zimbabwe	Harare	2011	Low-N
12	RATOP	Zimbabwe	Rattray Arnold	2010	Optimum
13	CHIDT1	Zimbabwe	Chiredzi	2010	Managed drought
14	CHIDT2	Zimbabwe	Chiredzi	2011	Managed drought
15	CHSDT	Zimbabwe	Chisumbanje	2011	Managed drought

Experimental design and statistical analysis

The description of experimental designs is presented under Section 3.3. The AMMI analysis including the combined ANOVA was conducted using Agrobase Generation II® SQL (Agronomix, 2011), statistical software. The biplots of the AMMI1 model based on IPCA 1 scores versus genotype means and IPCA 1 scores versus environmental means for the 96 hybrids were constructed using GenStat® 15th edition (GenStat, 2012) as this programme gives a better visual for the graphs. The biplots for the best 25 hybrids and the 15 test environments as well as the combination of the two were constructed based on the first two principal components of the AMMI model using Biplot v1.1 (http://www.stat.vt.edu/facstaff/epsmith.html), a Windows application that functions with MS Excel to illustrate the relationships among genotypes, environments and between genotypes

and environments. Environments and genotypes are shown as vectors and points on the AMMI biplot. Genotypes and environments that are close together tend to be similar. The angle between two vectors indicates the degree of association or correlation either among the genotypes or the environments. An angle of less than 90^0 or larger than 270^0 between a genotypic vector and an environmental vector indicates that the genotype has a positive response to that environment. If the angle is between 90^0 and 270^0 it indicates a negative response of a genotype to that environment. Similarly the cosine of the angle between two environments or genotypes gives an indication of the phenotypic correlation between the two genotypes (or environments). Hence, an angle of 0^0 indicates a correlation of r = 1 (100% positively correlated), an angle of 90^0 (-90^0) shows a correlation of r = 0 meaning that the testers are independent and an angle of 180^0 means a correlation of r = -1 (100% negatively correlated) (Gower and Hand, 1996; Yang et al., 2009).

The GGE biplot was constructed for the 96 genotypes as well as for the top 25 hybrids. The GGE biplot model based on the two principal components (PC1 and PC2) helps to explain the variation due to G+GE unlike the total variation which is caused by environment, genotype and G x E interaction (Yan, 2001). The GGE biplot further shows the performance of the genotypes across environments, relationship among the genotypes and environments, and the grouping of mega-environments. A genotype(s) plotted closer to an environment(s) indicates that it is adapted to that environment(s). Environments that are closely plotted in the biplot indicate their similarity as test environments. A solid line with an arrow passing through the biplot origin helps either to see the performance of different genotypes at a specific environment (in this case it is called the *tester axis*) or to identify the relative adaptation of a given genotype in different environments which is referred to as the *entry axis*. The biplot also has another solid line that passes through the centre of the biplot and perpendicular to either of the axis named the *perpendicular line*. The *perpendicular line* differentiates above or below average performance of either the genotype(s) or the environment(s). Another feature of the GGE biplot is the identification of which genotype wins where or which is best for what. It is illustrated by a convex-hull (polygon) and each vertex or corner of the polygon connects the genotypes that are furthest from the origin of the biplot and keeps the remaining genotypes within the polygon. The perpendicular lines from the centre of the biplot intersect the sides of the convex-hull creating several sectors which cause the environments to fall into one of these sectors. Hence, a corner or vertex genotype is the best or winner genotype in one or more of the environments included in that sector.

Similarly, vertex genotypes with no environment in the sector indicates the genotype's poor performance at all environments or not the best at any of the environments (Yan, 2001). The oval or the concentric circles allow the comparison of genotype(s) or environment(s). Mega-environments are shown as independent or intersecting circles (spheres) in the biplot. Environments that fall in the same sphere are considered to be similar mega-environments and the total number of spheres in the biplot shows the number of mega-environments.

Finally, cluster analysis of genotypes and environments based on AMMI adjusted means was also performed using the NCSS 2004 Software (Hintze, 2001). For the purpose of classification, cluster analysis with the unweighted pair group method with arithmetic average (UPGMA) clustering method was employed and Euclidean distance matrix was computed.

4.4 Results and discussion

4.4.1 AMMI analysis

The combined ANOVA for the 96 hybrids evaluated across 15 environments based on the AMMI model is presented in Table 4.4. The ANOVA indicated highly significant differences ($P \leq 0.001$) for environments, genotypes and G x E interaction. The IPCA axes are ordered according to decreasing contribution to variation. The F-test was highly significant ($P \leq 0.001$) for all the IPCA axes. The environments explained 76.88% of the total yield variation followed by the G x E interaction (12.44%). Genotypes contributed only 3.35% which indicates that in the METs genotypes contribute the least to the total variation. Environment was the major factor that influences yield performance of maize in most parts of ESA. The first five IPCA axes were highly significant and explained 100% of the G x E interaction. The first IPCA captured 35.73% of the total interaction sum of squares in 8.12% of the G x E interaction degrees of freedom. The second IPCA also explained 25.22% of the interaction sum of squares in 7.6% of the interaction degrees of freedom (Table 4.4).

Table 4.4 Analysis of variance (ANOVA) based on the AMMI model for grain yield (t ha^{-1}) for 96 maize hybrids evaluated across 15 environments in ESA (2010-2011)

Sources	Df	SS	MS	Total variation explained (%)	G x E explained (%)	Cumulative (%)
Total	2879	12788.60				
Environments	14	9831.25	702.23**	76.88		
Reps within Env.	15	31.73	2.11			
Genotype	95	427.84	4.50**	3.35		
Genotype x Env.	1330	1590.91	1.11**	12.44		
IPCA1	108	408.74	3.78**		35.73	35.73
IPCA2	106	288.48	2.72**		25.22	60.95
IPCA3	104	192.48	1.85**		16.83	77.77
IPCA4	102	138.94	1.36**		12.15	89.92
IPCA5	100	115.36	1.15**		10.08	100
IPCA residual	810	446.90	0.55			
Residual	1425	906.87	0.64			

Grand mean = 3.69 R-squared=0.93 CV = 21.58%

** P < 0.001; IPCA= Interaction principal component axis

The AMMI1 model biplot based on IPCA1 and the genotype means for the 96 hybrids was constructed to show the performance and association of the genotypes (Fig. 4.1) and the 15 environments was shown based on IPCA1 values of the environments plotted against the environmental means (Fig. 4.2). Another biplot was constructed based on IPCA1 values of the genotypes and environments plotted against the mean values of the genotypes and the environments to show the G x E interaction biplot (Fig. 4.3). From Fig. 4.1 it can be seen that entry 40 (G40) was the highest yielding followed by entry 55 (G55) and entry 37 (G37). The lowest yielding among the 96 genotypes was entry 36 (G36) located at the top left corner of the biplot. Entry 60 (G60) was the most stable as it is the closest to the IPCA1 axis (the green dotted line as the x-axis) and can be considered as adaptable to all the environments. On the other hand entry 37(G37) was the least stable as it is far from the IPCA1 axis, however, due to its high mean grain yield it can be considered as a responsive entry for a specific environment. Among the 15 environments HREOP1 was the most responsive for the evaluation of the genotypes, RATOP was a relatively stable environment unlike AWAOP. The AMMI1 model grouped all the optimum environments together. In contrast, the stress environments which produced below average grain yield were grouped in the left upper

quadrant of the biplot (Fig. 4.2). From the G x E interaction biplot (Fig. 4.3) it can be seen that entry 37(G37) was responsive to environment AWAOP and entry 40 and 54 to KAKOP. Because of the congestion of the genotypes, a separate biplot was constructed for the top performing 25 hybrids using the AMMI2 model based on IPCA1 and IPCA2 values. The first two principal components explained more than 60% of the G x E interaction thus making the AMMI2 model a better fit than AMMI1. To use AMMI3, another model family of AMMI, which is a component of IPCA2 and IPCA3, could be more accurate than AMM1 and AMMI2, however, Gauch et al. (2008) recommended AMMI2 for its practicality, less noise and more informativeness than the other AMMI model families.

The IPCA scores of a genotype in the AMMI analysis indicate 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 approach zero, the more stable the genotypes over all environments. Fig. 4.4 shows the biplot constructed based on the first two IPCA scores of the top performing 25 genotypes. According to the model, entry 60 was the most stable genotype as it is the closest to the origin of the biplot. Hence, entry 60 can be considered as a widely adapted genotype although it was ranked 12^{th} based on grain yield. On the other hand entry 37 was identified as less stable as it is located far from the origin of the biplot. However, this also shows the genotype's adaptation to a specific environment. Genotypes that are grouped in the same quadrant of the biplot are closely associated while those grouped in the opposite directions of the quadrant have no association.

The different environments were also plotted based on the first two IPCA values to show the relationship among the environments (Fig. 4.5). AWAOP was the most discriminating environment for the genotypes as indicated by its longest distance from the origin of the biplot. However, AWAOP may not be a representative environment due to its high IPCA scores. The AMMI2 biplot also grouped the environments according to their responsiveness. Stress environments were grouped together at the top left corner of the biplot and the optimum environments at the bottom right of the biplot. Environments plotted next to each other show the closer association or similarity of the environments for the evaluation of the genotypes. Hence, evaluation of genotypes in the closely associated environments is expected to produce fairly similar results. If environments show a repeatable association, then these environments can be delineated under a similar mega-environment. Grouping locations under

similar mega-environments will help to develop and recommend similar genotypes or agronomic practices to several locations under the same mega-environment. The small vector angle among the managed drought environments shows the closer association among them. However, there is a closer similarity between CHIDT1 and CHIDT2 than CHSDT, the other managed drought environment in the same country, Zimbabwe. Similarly the N-stress environments showed closer similarity between HRELN1 and HRELN2 than BAKLN. The close association between the optimum environments, EMBOP and KAKOP is an indication of the similarity of the environments used for the evaluation of the genotypes. RATOP and BAKOP may be classified as relatively stable optimum environments and BAKLN in the low-N environments based on their proximity to the origin of the biplot. The biplot also divided the environments based on the mean performance and accordingly the eight optimum environments clustered in the similar direction and have above average performance and the seven stress environments grouped together and show below average performance (Fig. 4.5).

Figure 4.6 shows the association of the 25 genotypes in the different environments. Entries 54, 46, 96, and 55 clustered close to BAKOP indicating their better performance in this optimum environment. Entries 73, 22 and 63 were more adapted to the stress environments with entry 73 closer to the managed drought environment of KBODT. Entries 92, 40 and 37 were specifically adapted to MLKOP, EMBOP and AWAOP respectively based on their proximity to these environments. Most of the genotypes clustered around the relatively stable optimum environment of RATOP and indicating their superior performance in this environment. Generally, the graphs from AMMI2 biplots helped to visualise the relationship among the genotypes and environments. However, a detailed and convenient display is addressed by the use of GGE biplot in Section 4.4.2.

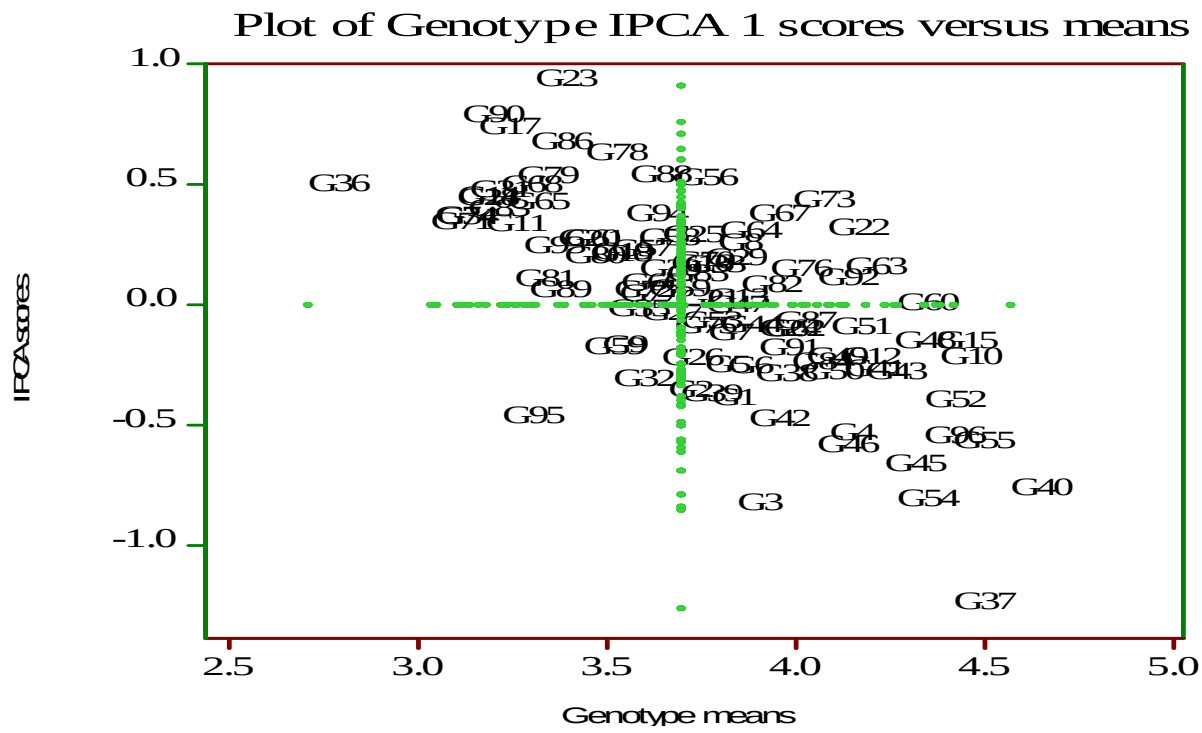

Figure 4.1 AMMI1 biplot of grain yield of 96 maize genotypes based on IPCA1 and genotype means.

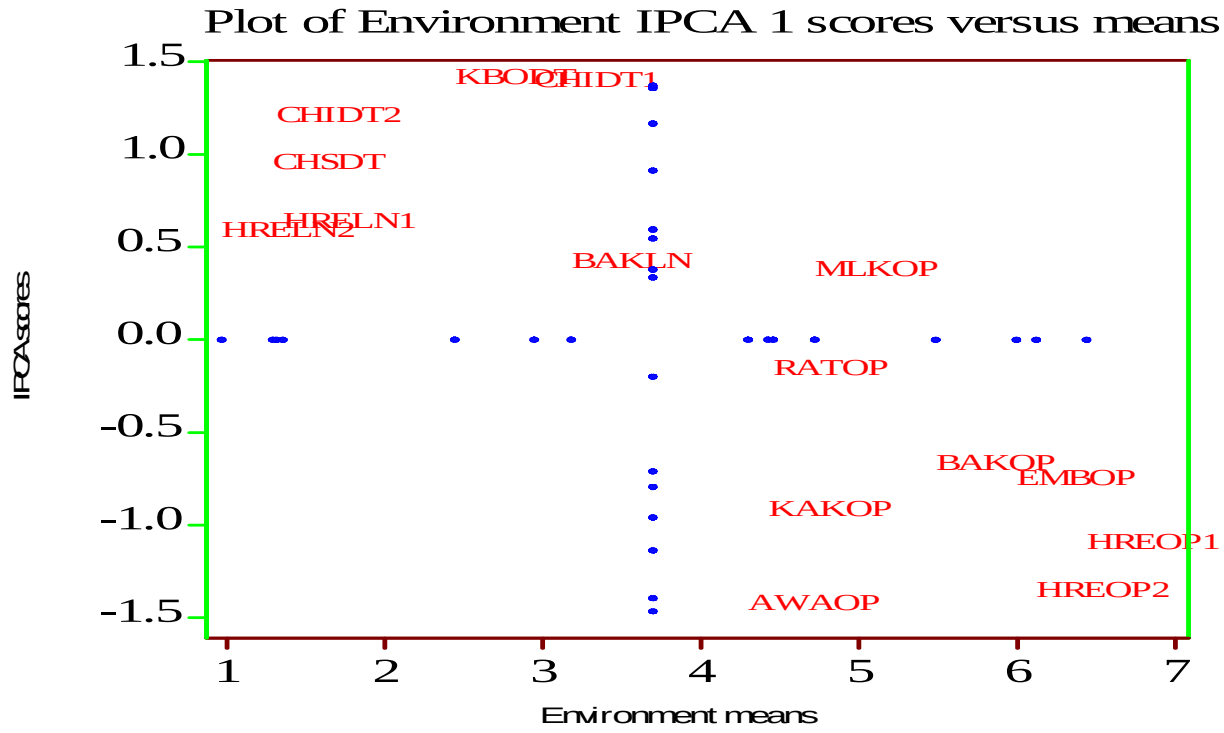

Figure 4.2 AMMI 1 biplot of the 15 environments based on IPCA1 values of the environments plotted against environmental means.

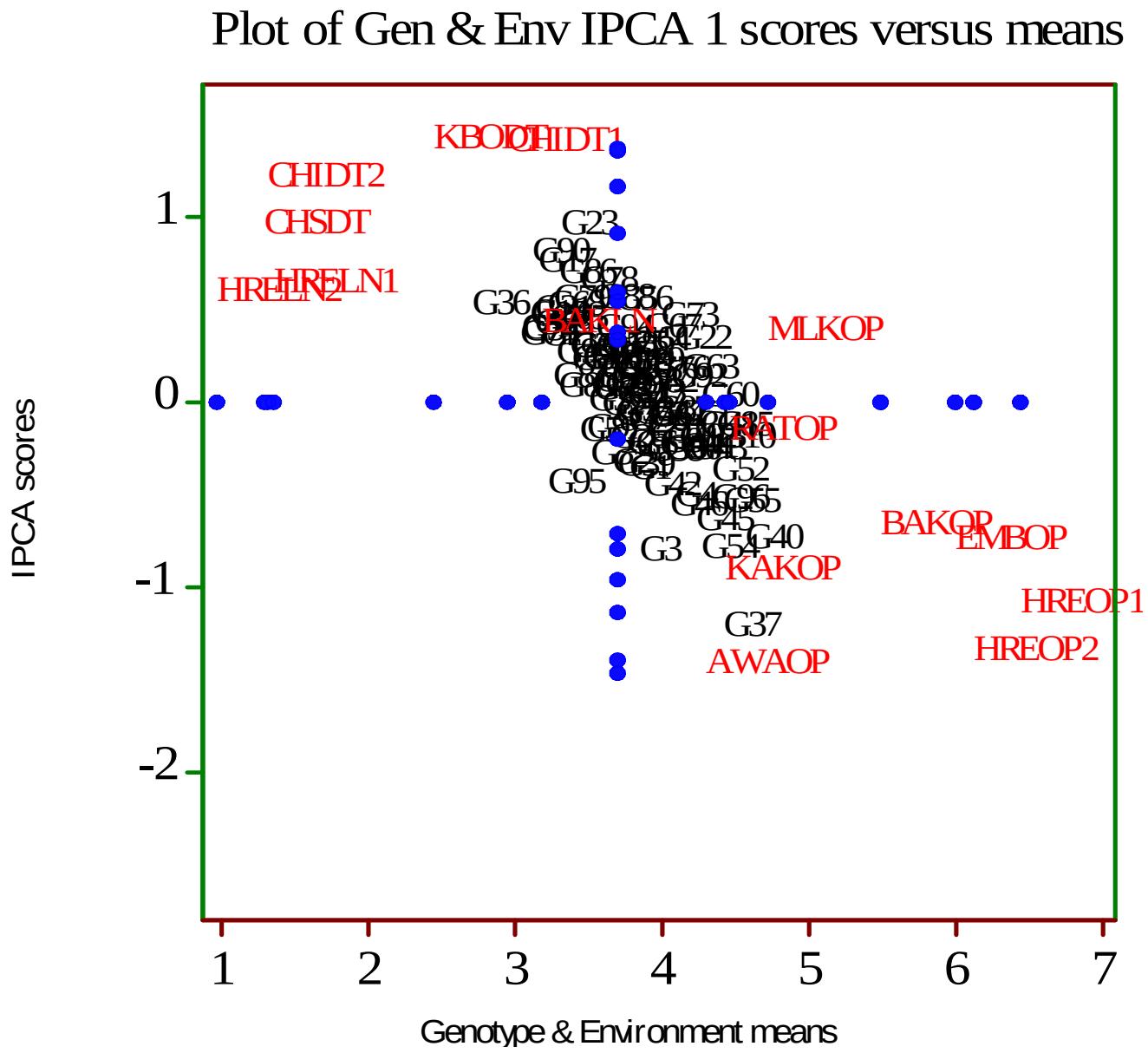

Figure 4.3 AMMI 1 biplot of the G x E interaction of 96 maize genotypes tested across 15 environments of ESA based on IPCA1 scores of the genotypes and the environments.

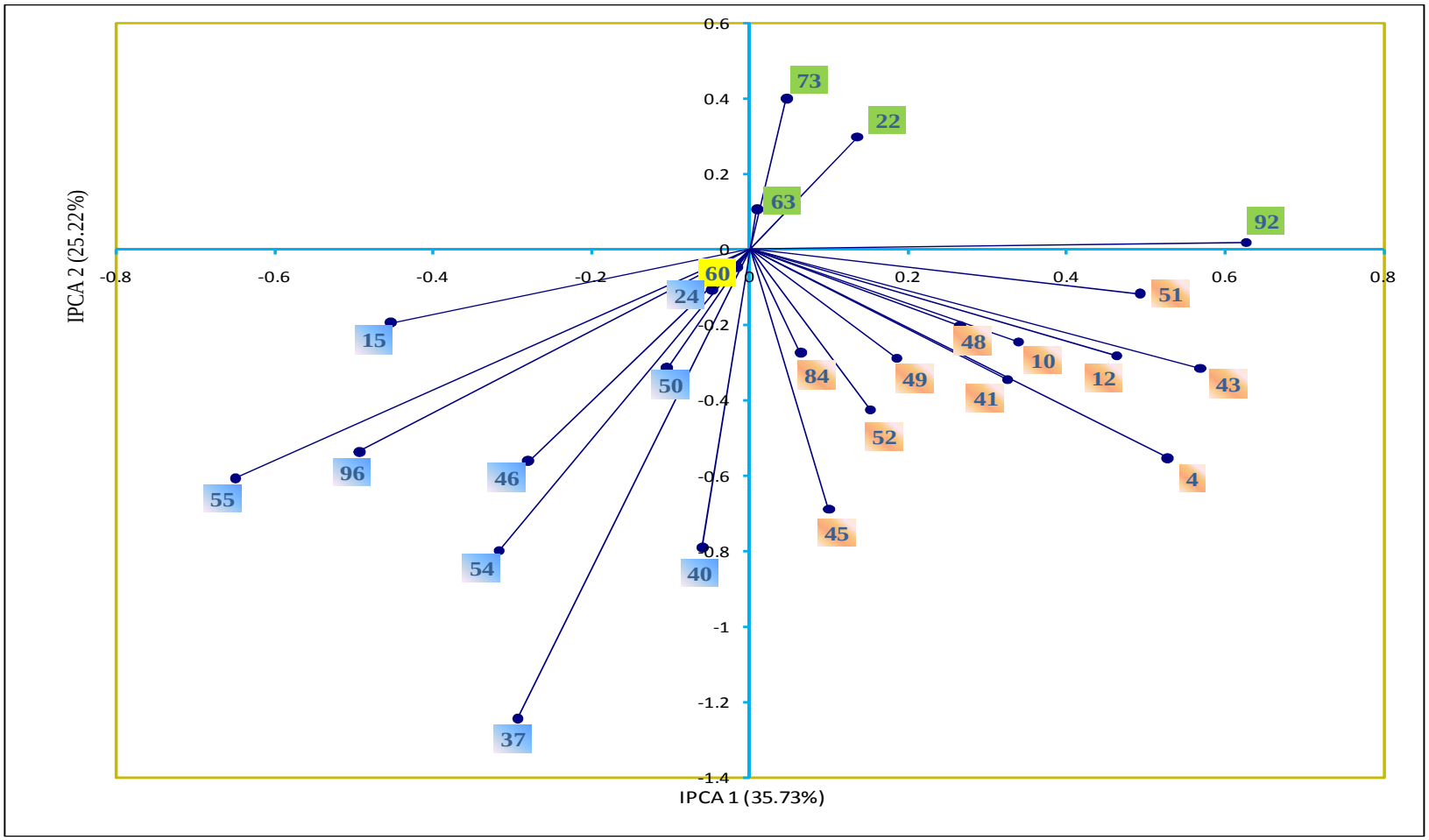

Figure 4.4 AMMI 2 biplot of grain yield of 25 selected QPM hybrids (including a normal check) evaluated under stress and non-stress growing environments of ESA. Entries with closer association are grouped under the same quadrant and indicated with similar colours. Entry 60 was the most stable hybrid and is highlighted in yellow. Entries in the opposite quadrant have no association among them.

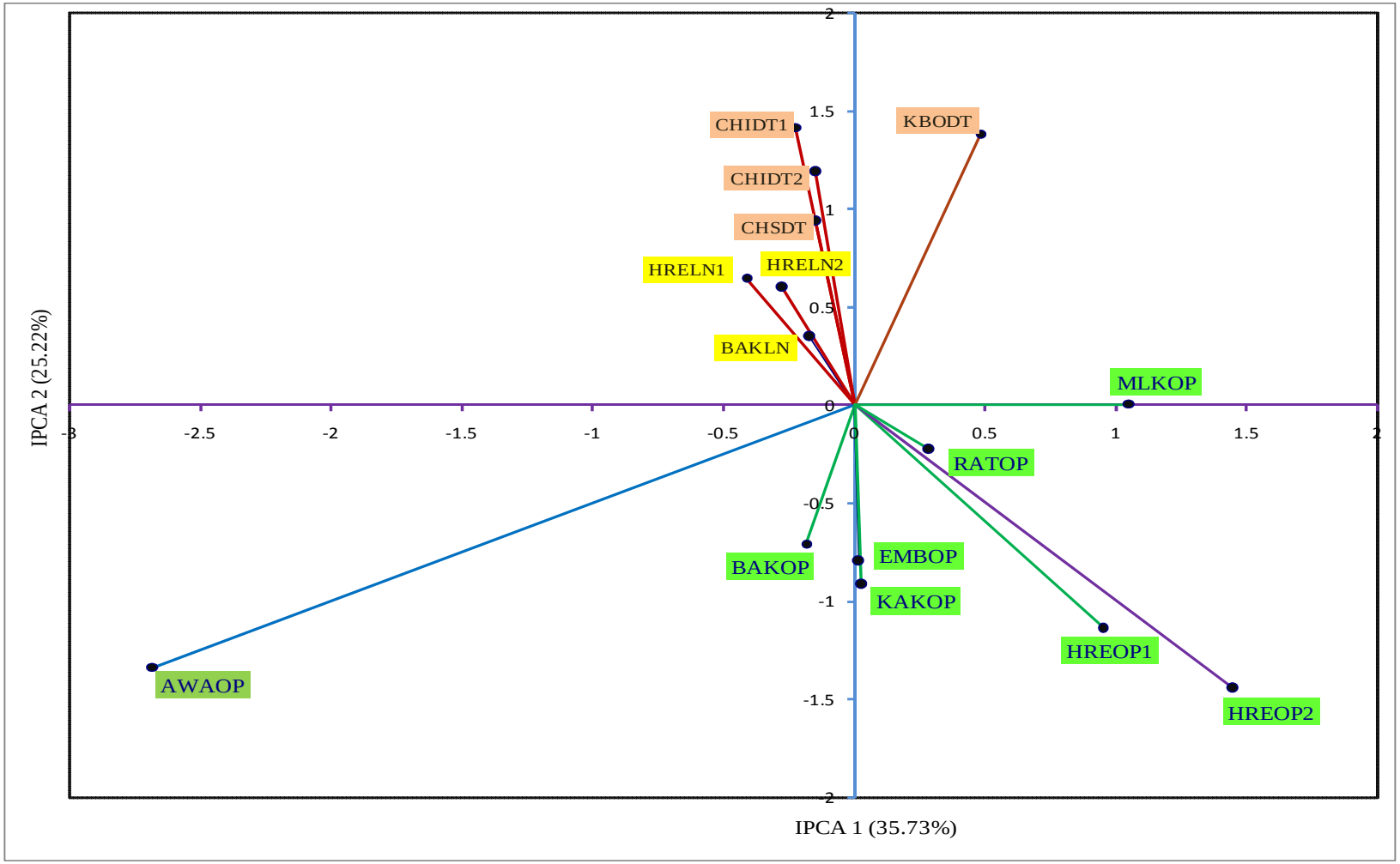

Figure 4.5 AMMI 2 biplot showing the association of the 15 stress and non-stress growing environments in ESA. Optimum environments are shaded in green, low-N stress in yellow and drought stress in orange. AWAOP was the most discriminating environment followed by HEROP2.

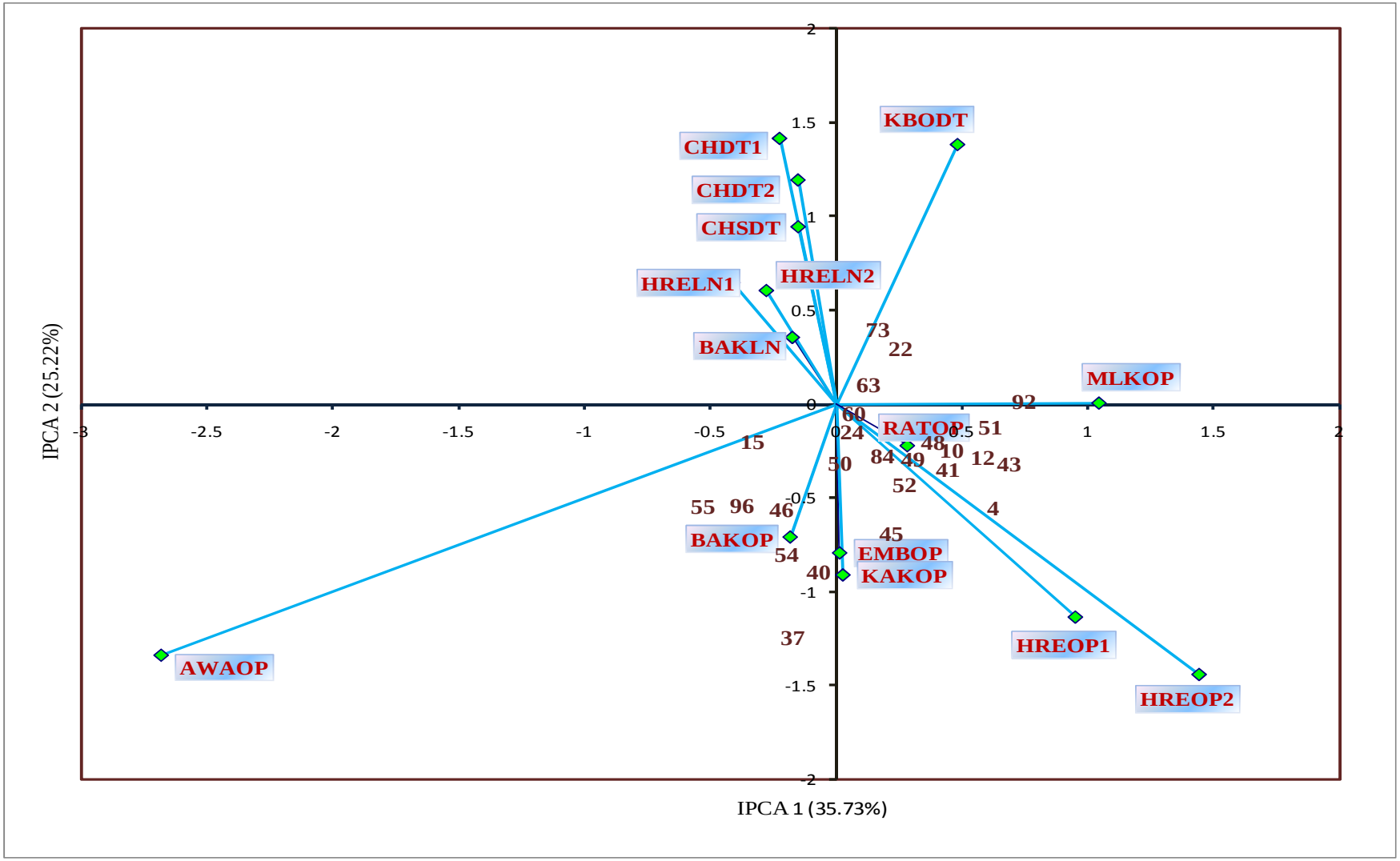

Figure 4.6 AMMI 2 biplot showing the association between the top 25 QPM hybrids (numbers) (including a normal check) and the 15 stress and non-stress growing environments (texts) in ESA.

4.4.2 GGE biplot analysis

Performance of genotypes and environments

The GGE biplots based on the performance of 96 maize genotypes evaluated under 15 stress and non-stress environments were constructed based on the values of the first two principal components (PC1 and PC2) which explained almost 50% of the grain yield variation due to genotype and G x E interaction (Fig. 4.7). From Fig. 4.7 it can be seen that the QPM entries 37 and 40 were the highest yielding entries among the 96 genotypes. Among the environments HREOP2, HREOP1 and AWAOP were the most responsive.

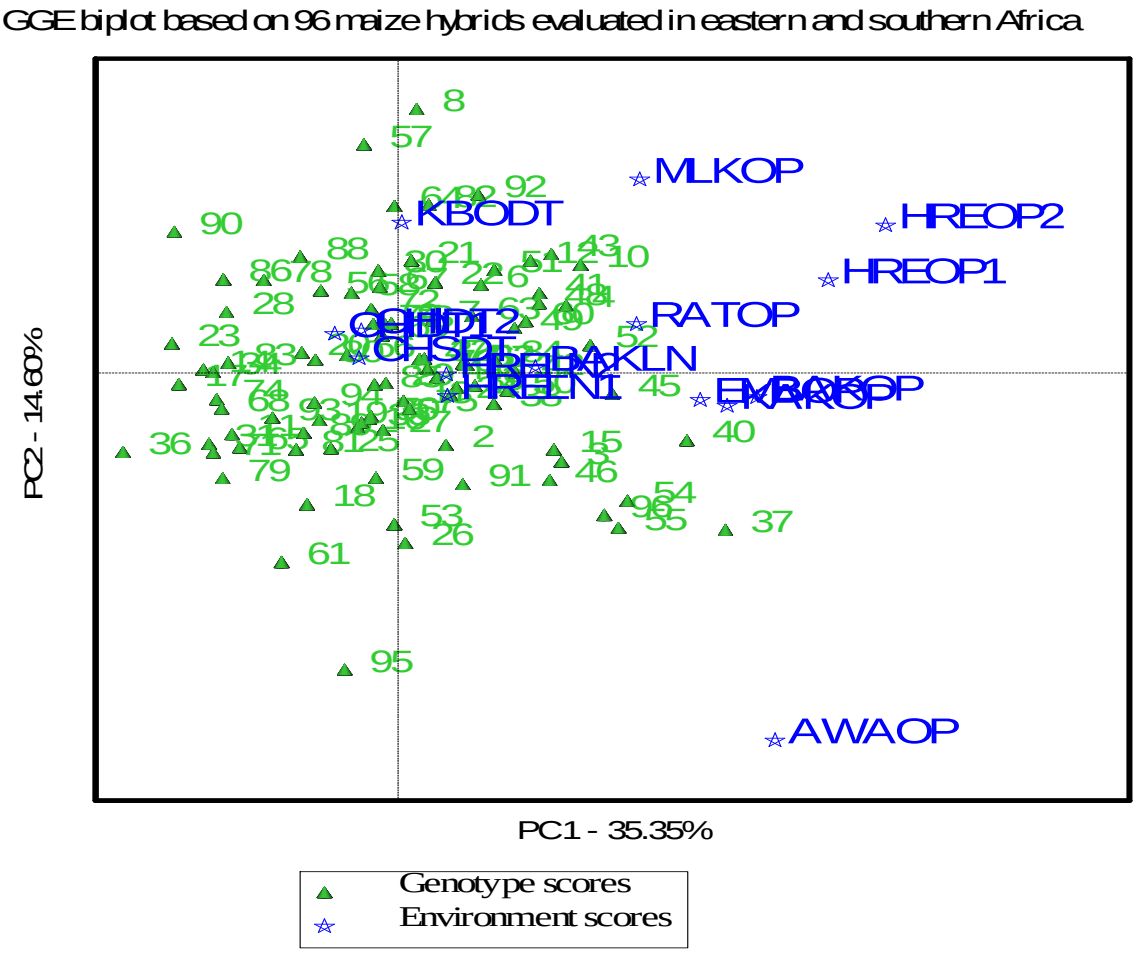

Figure 4.7 GGE biplot based on 96 QPM hybrids (including a normal check) evaluated under 15 stress and non-stress environments of ESA.

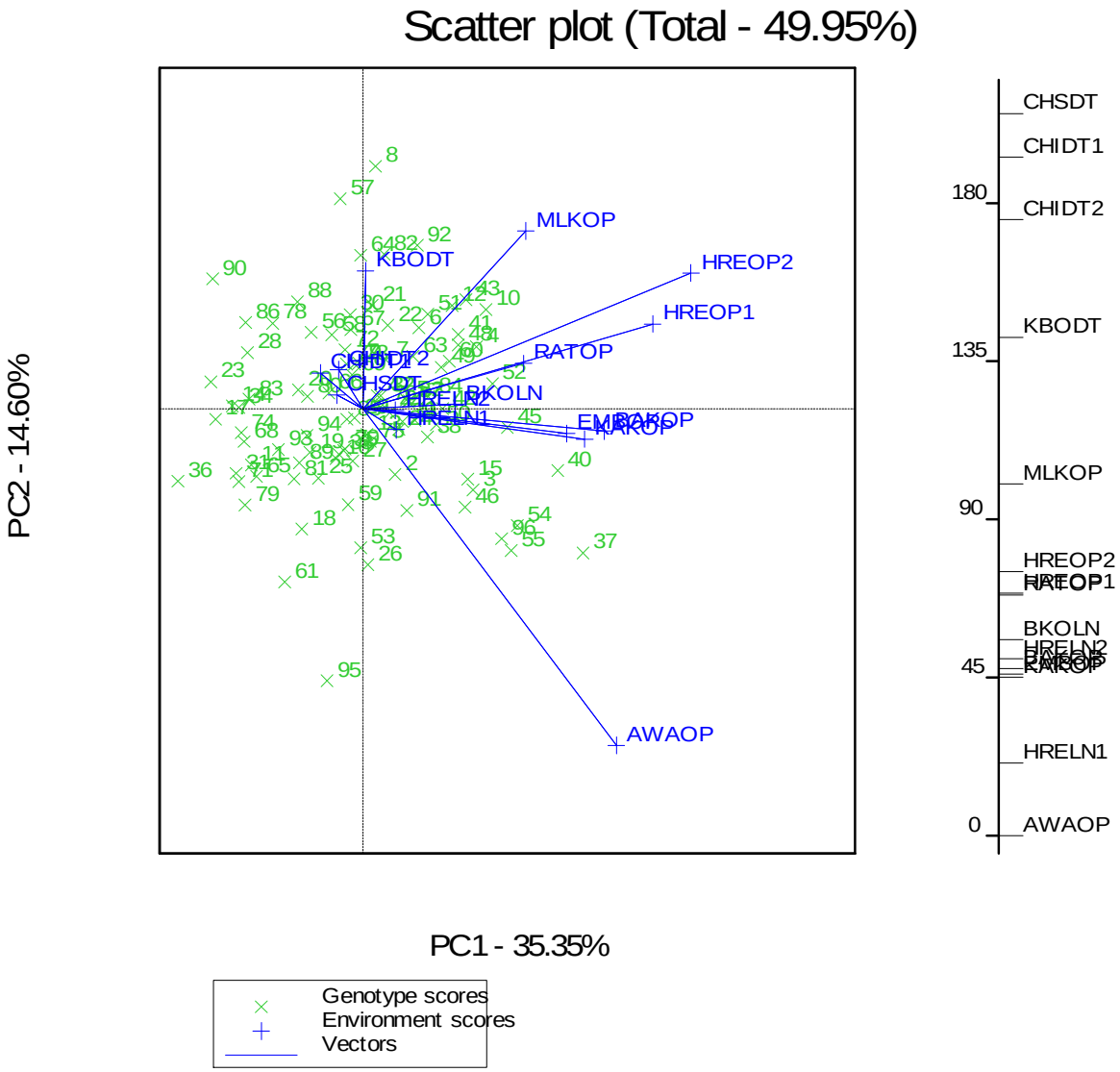

Figure 4.8 GGE biplot based on 96 QPM hybrids (including a normal check) evaluated under 15 stress and non-stress environments of ESA. The vectors and the rug plot display the association/relation among the different environments.

Figure 4.8 shows the association or relationship between the different environments. AWAOP was the most discriminating environment due to its longest distance from the origin of the biplot. Environments with small vector angles tend to have closer similarity and those with wide vector angles show minimum association. Similarly the rug plot also displays the proximity among the different environments based on the angle variation of the vectors. All the managed drought environments were displayed close to each other as their deviation from each other was small. However, the wider angle between AWAOP and CHSDT and other

managed drought environments indicated the absence of association among the environments.

Which-won-where

An important feature of a GGE biplot is its ability to display top performing cultivars in a specific environment as well as the low yielding cultivars across environments. Figure 4.9 illustrates the association of the 96 entries within the 15 test environments. There are seven sectors in the biplot created by the perpendicular line that starts from the origin of the biplot and runs perpendicular to the side of the polygon. Out of the seven sectors four have environments included within them and three sectors have no environments within them. Hence entry(ies) that fall in sectors where environment(s) are included indicate the association of the entry(ies) with that specific environment(s). The hybrids at the different vertices of the polygon are expected to be responsive as they are the furthest from the origin. However, the responsive vertex hybrids can be either the best performing or the poorest at one or additional environments (Yan and Rajcan, 2002). Entries 37, 40, 52 and those included in the sector were the most suitable entries at AWAOP, EMBOP, KAKOP, BAKOP, HREOP1, RATOP, HRELN1, HRELN2 and BAKLN. Entries 8, 92, 57 and others fell in the sector that contained the managed drought environments, MLKOP, KBODT and CHIDT1. Entries 90, 86, 28 and a few more were found to be outstanding in performance at CHSDT and CHIDT2. All entries included under the sectors where entries 95 and 36 were located showed poor performance in all the environments. Similarly no entry performed well at HREOP2. However, the small angle between the sectors of HREOP1 and HREOP2 indicates the close similarity of the two environments. Hence, entries selected for HREOP1 were expected to show similar performance at HREOP2. To avoid congestion of genotypes a separate biplot was constructed for the 25 top performing entries based on their average grain yield (Fig. 4.10). As a result the biplot was divided into eight sectors and seven of the sectors included one or more of the test environments. Entries 37, 40, 54, 45, 46 were found to be associated with the environments, EMBOP, KAKOP and RATOP. Among the genotypes entry 37 was the winner in these environments based on the average grain yield. Entries 96, 15, 55, 49 and 50 showed close association with the environments BAKOP, AWAOP, BAKLN and HRELN1 while entries 15 and 96 were the best performing in these environments. Entries 63 and 60 were the best performing at MLKOP and CHIDT2.The position of entry 60 on the sector line indicates its good adaptation to other environments as

well. Although the environment KBODT has no vertex entry in its exact sector, the proximity of entry 22 to this sector indicates the suitability of the entry both at KBODT and CHIDT2. Entries 73 and 92 were grouped with the environment of CHIDT2 while entries 43, 51, 12, 10 and 84 were found to be associated with the environments of CHSDT and HRELN2 (Fig.4.10).

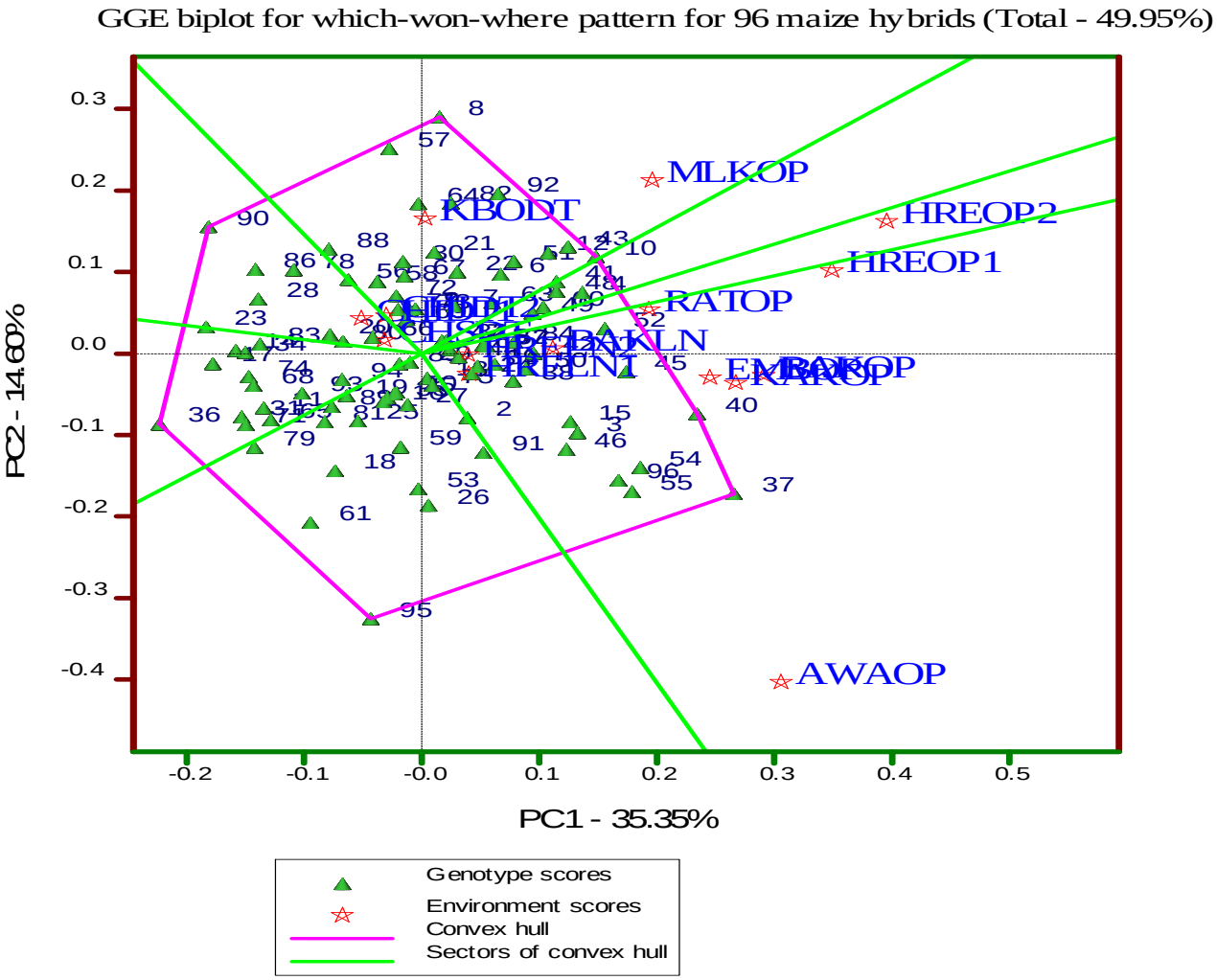

Figure 4.9 Which-won-where patter of the GGE biplot based on 96 QPM hybrids (including a normal check) evaluated in 15 stress and non-stress environments of ESA.

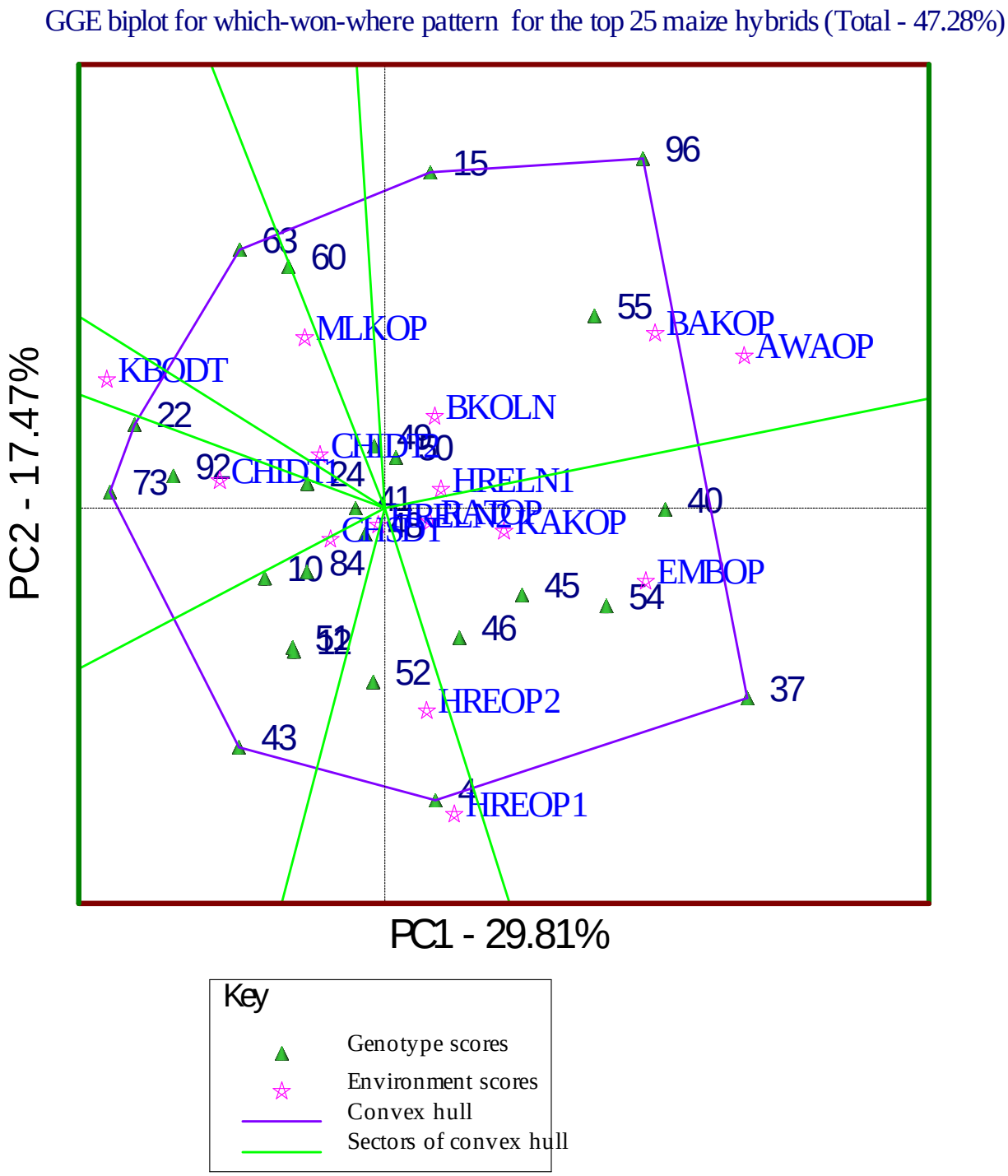

Figure 4.10 Which-won-where pattern of the GGE biplot based on selected 25 QPM hybrids (including a normal check) evaluated in 15 stress and non-stress maize growing environments of ESA.

Discriminating ability and representativeness of the environments

In a biplot analysis the vector length of an environment indicates its discriminating power; the longer the vector from the plot origin to the marker of an environment, the more discriminating the environment. The absolute length of the projection from the marker of an environment onto the *tester axis* or the average tester y-axis (ATC y-axis) indicates its representativeness; the longer the projection, the less representative the environment. Similarly genotypes projected further from the ATC y-axis are considered to be less stable. The centre of the concentric circle in a biplot is where an ideal genotype should be. An ideal genotype is considered to be one with the highest yield across test environments and one which is absolutely stable in performance. The ideal genotype projection on the ATC x-axis is designed to be equal to the longest vector of all the genotypes and its projection on the ATC y-axis should be zero, indicating its stability. Hence, the smaller the distance of a genotype to this ideal/virtual genotype the more ideal the genotype (Yan and Kang, 2003). This also applies for the ideal environment. Further details on this topic can be read from the GGE website, www.ggebiplot.com.

The GGE biplot in Fig. 4.11 was constructed based on environment-centred singular value partitioning (SVP) which helps to visualise the ideal environment/tester. A genotype-centred singular value partitioning also gives a biplot that can identify the ideal genotype/entry. However, the conclusion from both types of biplots remains the same; the only difference is the slight shape variation among the biplots. To avoid redundancy, only the environment-focused GGE biplot (Fig. 4.11) was used for the interpretation in this study. According to Fig. 4.11, HREOP2 was the most representative environment as it had relatively small projection from the ATC y-axis and was also highly discriminating because of its large projection on the ATC x-axis. AWAOP was also a discriminating environment because of its large projection from the origin; however, it is not a representative environment because of its large distance from the ATC y-axis. The managed drought environments of Chiredzi (CHIDT1, CHIDT2) and Chisumbanje (CHSDT) in Zimbabwe were the least representative environments as they were far from the average environment coordinate (AEC). The optimum environments of Embu (EMBOP), Kakamega (KAKOP) both from Kenya and Bako (BAKOP) from Ethiopia were positioned similarly following the ideal environment from Zimbabwe (HREOP). This indicates the close similarity of the environments for the evaluation of genotypes in the three countries. The genotype closest to the ideal was entry 40

followed by entry 37, however, entry 40 showed a better stability than entry 37 because of its relative position on the ATC y-axis. Entry 36 was the poorest performing genotype due to its furthest position on the ATC-axis. Entries 95, 61, 90 and 57 were the least stable in addition to their below average performances (Fig.4.11).

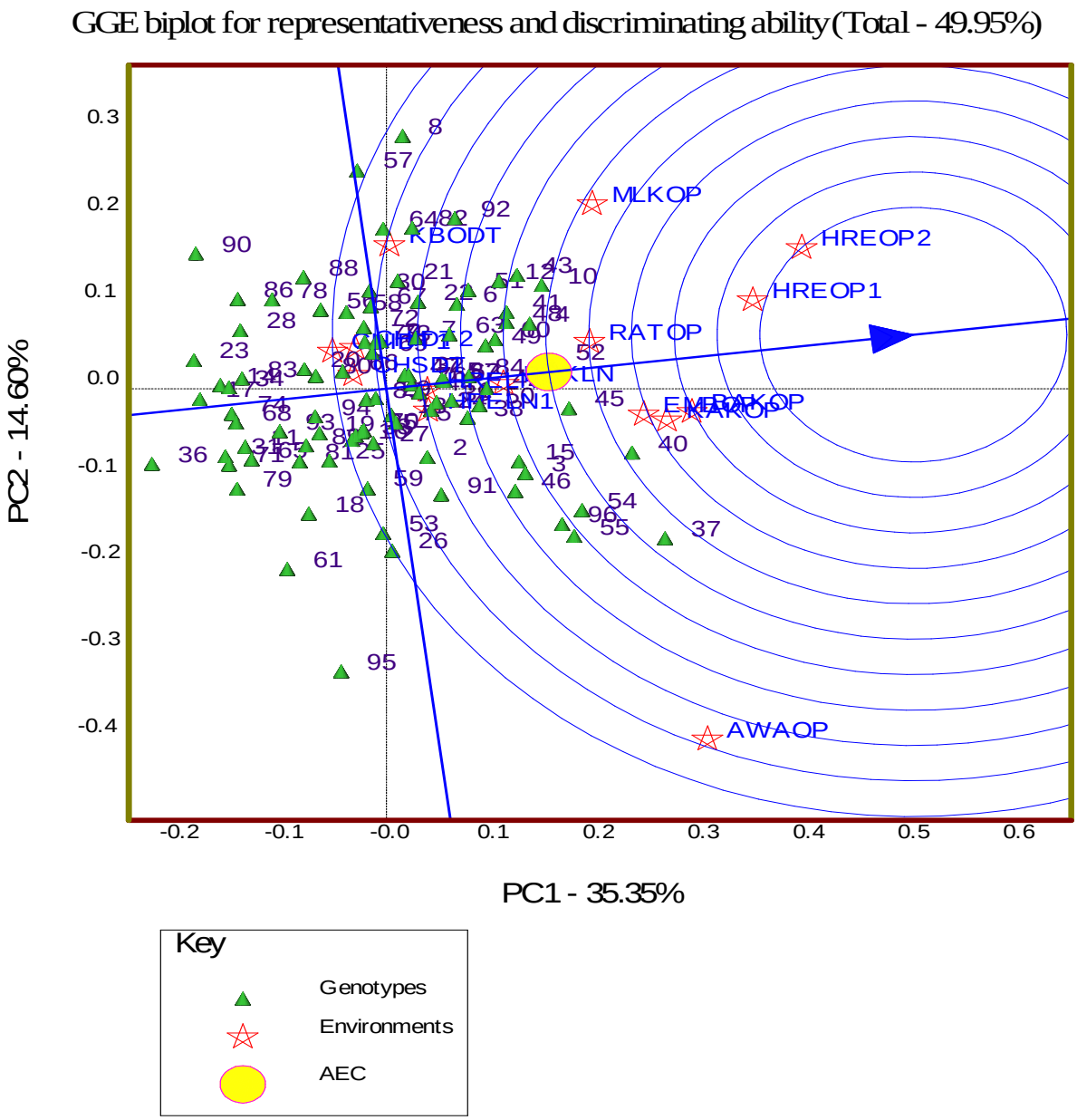

Figure 4.11 GGE biplot showing representativeness and discriminating power based on the grain yield of 96 maize genotypes evaluated in 15 stress and non-stress environments of ESA.

Grouping of mega-environments

The main purpose of GxE interaction analysis is to identify target environments for the deployment of suitable genotypes. Environments that consistently share the same best cultivar are considered to be mega-environments. Hence, this mega-environment concept, which is about geographical location, necessitates the continued winning of similar genotype(s) which are equally adapted to other similar mega-environments, in addition the genotype by location interaction should be repeatable across years in order to assign a permanent grouping of mega-environments (Yan and Rajcan, 2002; Yan et al., 2007).

Figure 4.12 illustrates the biplot for the classification of the different mega-environments. It is constructed based on the mean grain yield of the 96 maize genotypes. The data was partitioned based on environment-centred values (eigenvectors) and it was normalised to get meaningful mega-environments. As a result, the 15 environments were classified into four broader groups with almost all the optimum environments grouped in the same mega-environment. The environments of AWAOP, EMBOP, KAKOP, HREOP1, HREOP2, BAKOP and RATOP (yellow oval) were placed in the same mega-environment which indicates that those genotypes which performed well in one of these locations can be tested in the others and similar performance can be expected. The managed drought sites of CHIDT1, CHIDT2 and KBODT which are clustered closely can form another mega-environment together with MLKOP and BAKLN (BKOLN) (white oval) which share similarity with the other managed drought locations as indicated by the intersection of the spheres. MLKOP, which was a managed optimum site, was closer to the drought sites than the other optimum sites. The low-N stress environments of HRELN1 and HRELN2 were grouped together, and may be considered as another mega-environment for evaluation of genotypes for low-N stress. The fourth category of the mega-environment was Chisumbanje (CHSDT) (brown circle) located in Zimbabwe. Though this site was considered to be similar to the other managed drought sites, this study confirmed the site as another mega-environment. Hence, genotypes that performed well at CHSDT are not expected to show similar performance in the other managed drought sites and vice versa.

These mega-environment groupings appear consistent with the current germplasm characterisation system at CIMMYT by which MLKOP, KBODT, CHIDT are among the sites identified for the development of drought tolerant maize genotypes for the mid altitude

dry areas of Ethiopia, Kenya and Zimbabwe, respectively. Similarly, the optimum sites in Ethiopia (BAKOP, AWAOP), Kenya (EMBOP, KAKOP) and Zimbabwe (HREOP1, HREOP2 and RATOP) are among the sites identified for the evaluation and characterisations of CIMMYT's maize germplasm for the mid-altitude moist ecologies of ESA (Magorokosho et al., 2009; 2010; Makumbi, 2011; Setimela et al., 2012) which are also grouped together in this study. The grouping of CHSDT indicates the site's dissimilarity with the other sites that are grouped under the mid altitude dry ecologies. Hence, there is a need or revision of the mega-environments by CIMMYT in order to place CHSDT in a different/unique mega-environment.

In Fig. 4.12 the green lines connecting the genotype scores shows the distance of the genotypes onto the ATC-x axis. The longer the projection from the ATC-x axis, the lower the stability of the genotype. The presence of high projection of the genotypes also indicates the presence of enormous G x E interaction. The genotype scores also help to construct the convex-hull (polygon) to see the which-won-where pattern of the GGE biplot.

Cluster analysis

Finally, cluster analysis was used to classify the environments or genotypes into homogeneous groups based on the performance of the best 25 genotypes. The analysis operates on a matrix of dissimilarity (or similarity) indices for all possible pairs of genotypes or pairs of environments, depending on what is being clustered. The dendrograms (Fig. 4.13 and 4.14) were constructed with the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering technique. The dendrogram for the genotypes was constructed for the top 25 entries based on the AMMI adjusted mean yields. The environmental means from AMMI were also used for the construction of dendrograms for the 15 stress and non-stress environments.

Clustering of genotypes at a cut-off value of 1.0 produced six clusters (Fig 4.13). Cluster one is separated from the others by the highest yielding entry 40. Cluster two consisted of five entries (54, 15, 55, 96 and 37) which are among the top yielders and were grouped similarly by the AMMI2 biplot (Fig. 4.4.). The third cluster contained five entries (48, 60, 45, 52 and 10) while the fourth group had six entries (41, 92, 51, 4, 12 and 43) which are projected in a similar direction in the AMMI 2 biplot (Fig.4.6.). The fifth group consisted of two entries (46

and 63) which are in opposite position in the AMMI2 biplot showing the difference between the AMMI2 biplot and the cluster analysis. The last group consisted of entries 50, 24, 84, 73, 49 and 22 which are grouped closely to the origin of the AMMI2 biplot (Fig. 4.6). Entries 50 and 24 were similar in grain yield performance based on the AMMI adjusted mean yield (Fig. 4.13).

Cluster analysis of environments at cut-off point 1.0 produced two broad clusters which are clearly separated based on the nature of the environments (Fig.4.14). The eight optimum environments were grouped into one cluster while the stress environments constituted the second cluster. However, the cluster analysis at the cut-off point of 0.5 grouped the environments into four. The first group comprised BAKOP, EMBOP, HREOP1 and HREOP2 which are among the mid altitude moist agro ecologies in Ethiopia, Kenya and Zimbabwe. The environments under the first cluster were the top yielding according to the AMMI adjusted environmental mean yield (Table 4.2). The second cluster consisted of KAKOP, AWAOP, MLKOP and RATOP which were among the optimum environments and yielded less than the first cluster. The third cluster grouped CHIDT1, KBODT and BAKLN as the stress environments which were categorized under mid altitude dry agro ecologies in Zimbabwe, Kenya and Ethiopia respectively. The fourth cluster consisted of CHIDT2, CHSDT, HRELN1 and HRELN2 which had environmental mean yield that was lower than that of the third cluster (Fig.4.14).

The clustering technique helps to visualize on the relationship either between the genotypes or the environments based on their performance. However, the method does not facilitate better understanding of the genotype's performance across environments, or help in identifying stable and high ranking genotypes. The method is also less useful for visualising the genotype interaction with the environments as compared to AMMI and GGE biplot.

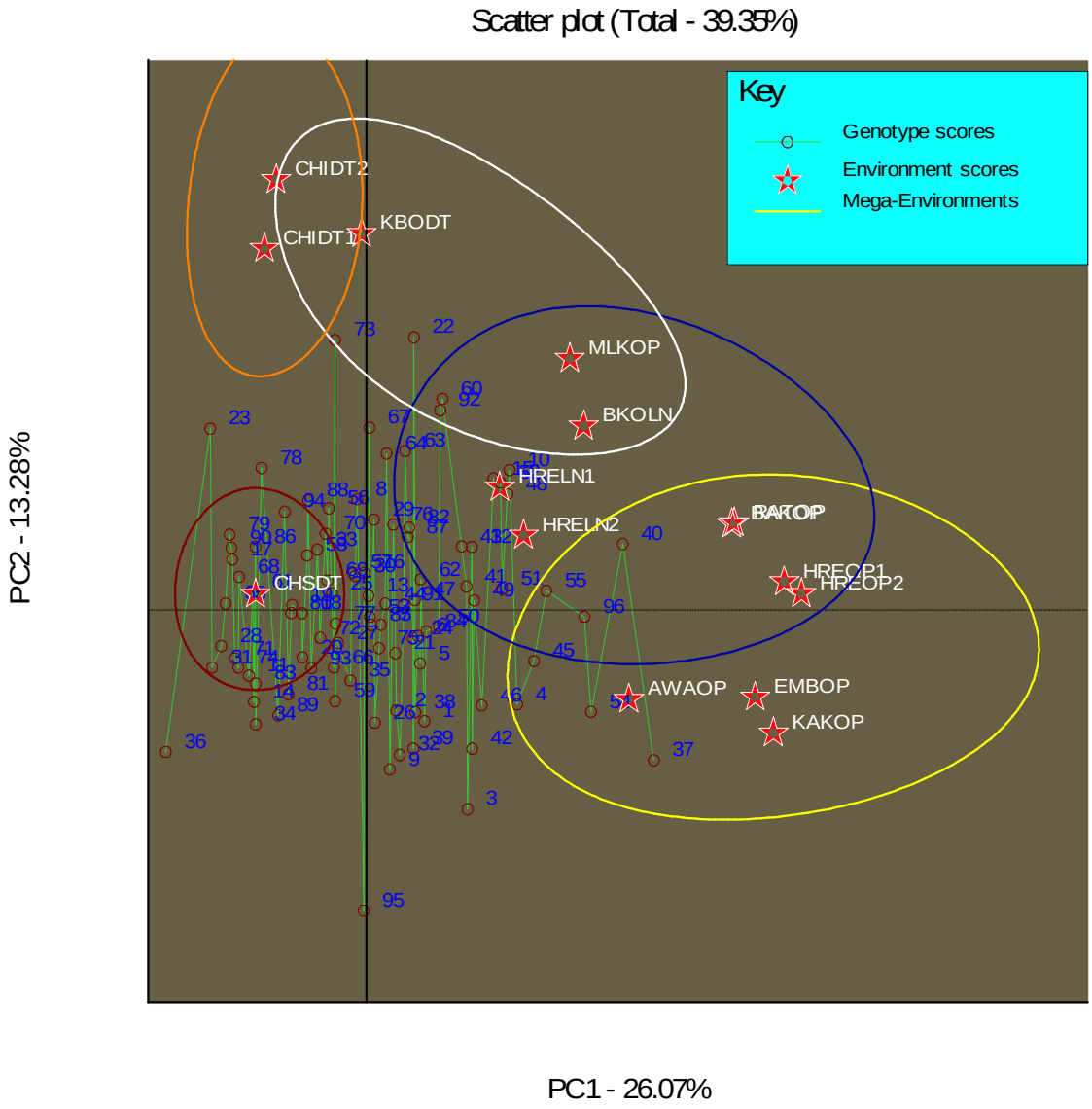

Figure 4.12 GGE biplot showing the different mega-environments (the different circles) based on the grain yield performance of 96 maize genotypes evaluated in 15 stress and non-stress environments of ESA.

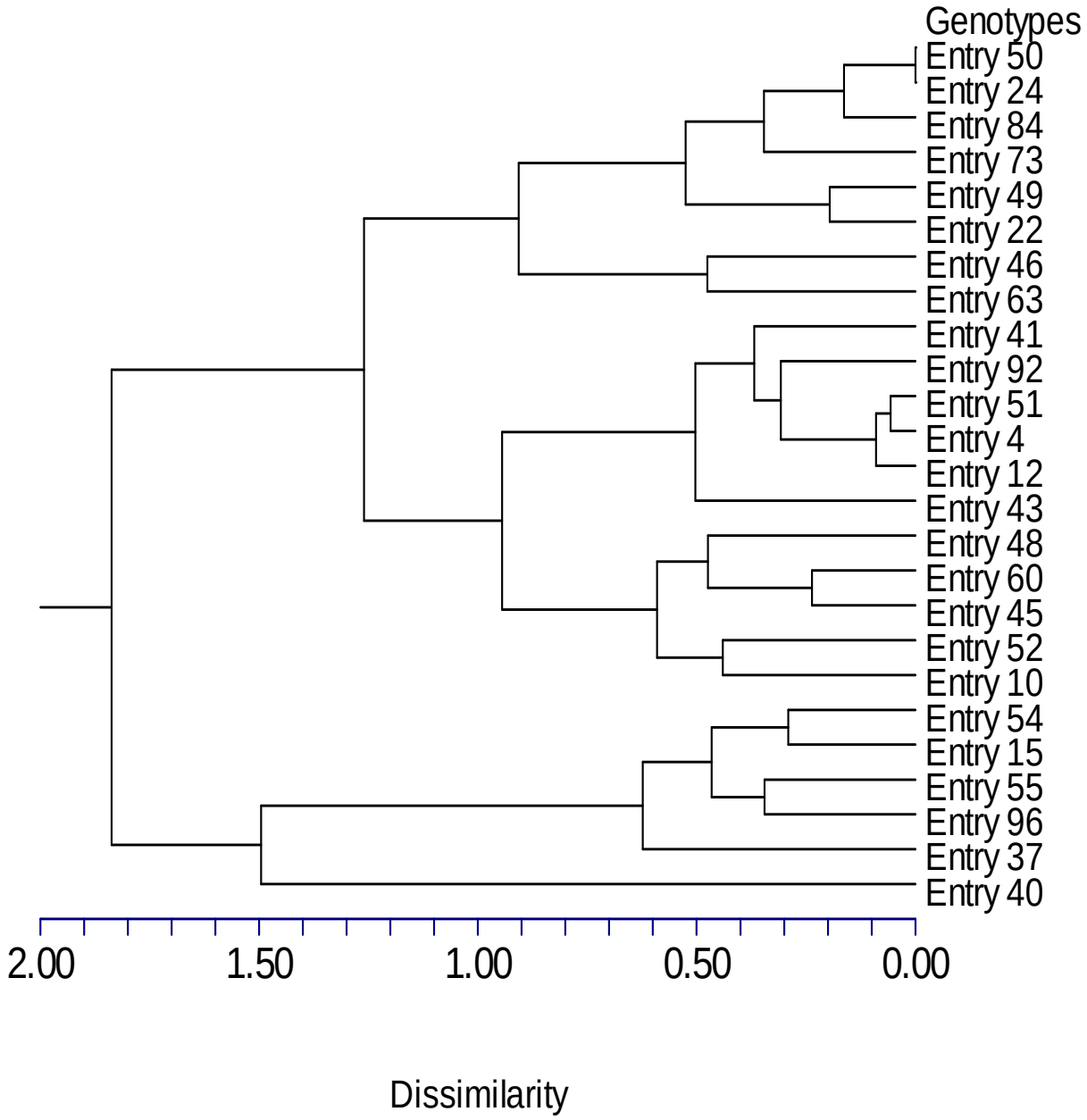

Figure 4.13 Dendrogram showing the clustering of 25 top performing maize genotypes based on AMMI2 adjusted mean grain yield evaluated in 15 stress and non-stress environments of ESA.

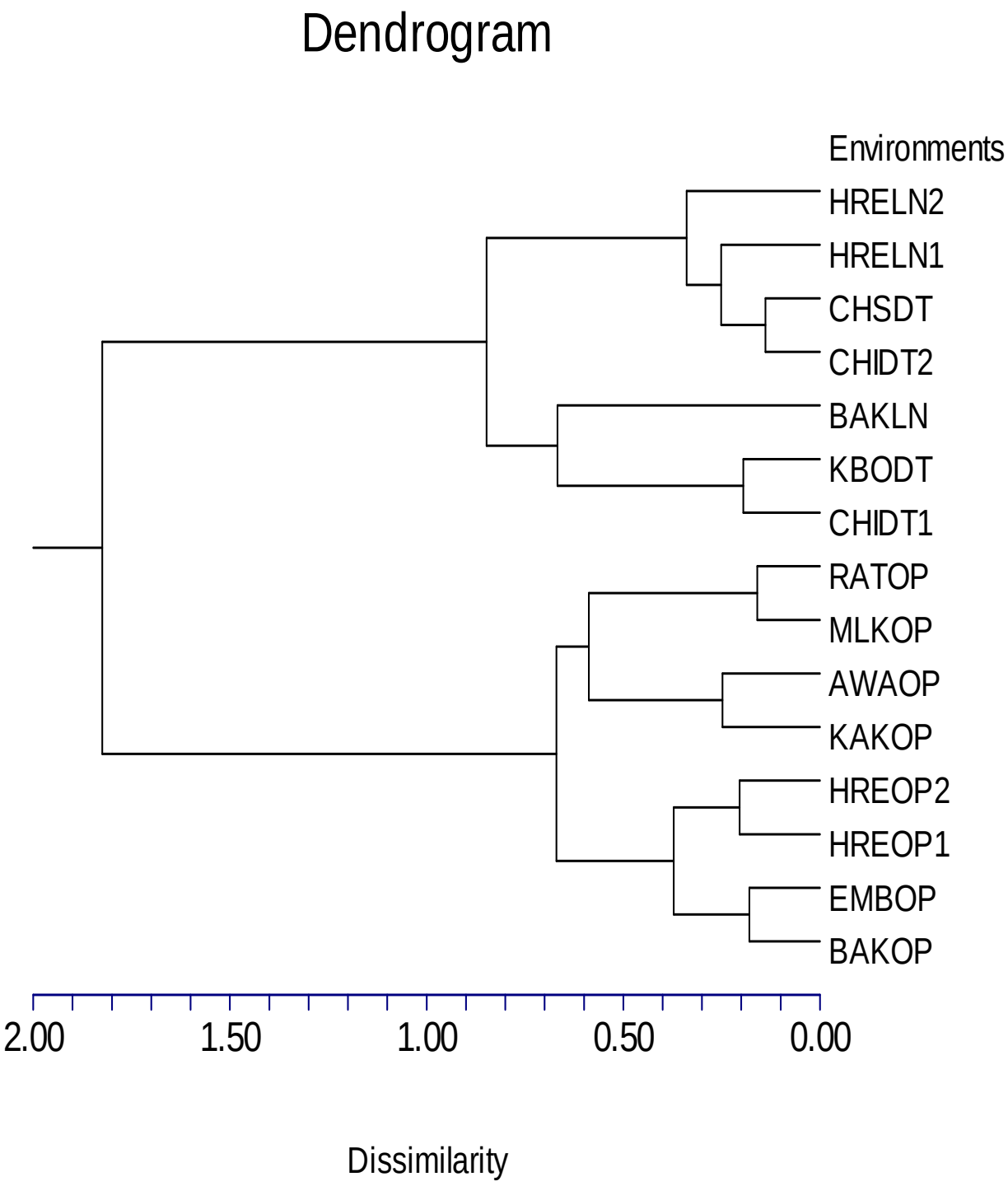

Figure 4.14 Dendrogram showing the clustering of 15 stress and non-stress environments in ESA based on AMMI2 adjusted environmental means.

4.4.3 Comparison of AMMI with GGE Biplot

Among the different statistical procedures, AMMI and GGE are the two foremost techniques available at present for analysis of data from METs. The main focus of this section is to highlight the main differences as well as the advantages and disadvantages of the two models based on the data used in this study. The arguments from the critics and/or supporters of the models were discussed to substantiate or negate some of the findings of this chapter. However, detailed explanations and in depth analysis of the models is considered beyond the scope of this section.

The main difference between AMMI and GGE is based on the procedures of PCA of the original data. The GGE biplot model, also referred to as environment centred PCA, applies singular value decomposition (SVD), a lengthy mathematical procedure, to the original data and subtracts the environment means which also removes the grand mean from the analysis (equation 1). The AMMI model uses the same procedure but subtracts both the genotype and environment means from the PCA and adds back the grand mean (equation 2) (Gauch, 2006). The mathematical equations of the models are presented below to support the above explanation. Hence, GGE biplot focuses on genotype main effect and genotype by environment interaction effect (G+GE) while AMMI focuses on genotype and environment main effects and the G x E interaction effects (G + E+ GE). The main reason for excluding environment effect from the GGE biplot model is based on the fact that contribution of environment *per se* is not an important component in evaluating the performance of genotypes (Yan et al., 2007). In addition, in multi-environment yield trials, environment is often the main contributor for the variation, hence removing this effect will give enough room to analyse the genotype and G x E interaction main effects, which is the main interest of a crop breeder in evaluating the potential of his/her germplasm. However, the inclusion of environmental effect in the AMMI analysis received support because of the interdisciplinary approach of the crop improvement research which can include soil scientists and others who are interested on the effect of environment (Gauch et al., 2008). Based on this assumption the ANOVA part of AMMI separates genotype and environment main effects and the G x E interaction effects whereas in the case of GGE it is only G and G x E interaction effects. The differences on the model equations for GGE and AMMI are presented below for comparison purposes.

The model equation for GGE is:

$$Y_{ger} - \beta_e = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad \text{.....1}$$

where, Y_{ger} is the yield for genotype *g* in environment *e* for replicate *r*, β_e is the mean for environment *e*, λ_n is the singular value for principal component *n*, γ_{gn} is the eigenvector score for genotype *g* and environment *n*, δ_{en} is the eigenvector score for environment e and component n, ρ_{ge} is the residual for genotype g and environment e, and ε_{ger} is the error for genotype *g* and environment *e* and replicate *r*.

The model equation for AMMI can be written as:

$$Y_{ger} - \alpha_g - \beta_e + \mu = \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \quad \text{.....2}$$

where α_g is the mean of the genotype *g* and μ is the grand mean. The other variables are similar to those of GGE.

There are various opinions on whether the AMMI is superior to GGE biplot or vice versa in the analysis of METs (Yan, 2001; 2002; Gauch, 2006; Yan et al., 2007; Gauch et al., 2008). GGE's prime advantage seems to be the visualisation options of the biplot by which the which-won-where pattern and discriminating power and representativeness of test environments can be clearly sketched by GGE which is not the case with AMMI though it is not entirely impossible (Yan et al., 2007). Proponents of AMMI claim that the capturing ability of AMMI2 of the variability caused by G and GE is better than GGE2 and they outlined the general trend as AMMI1< GGE2 < AMMI2 (Gauch et al., 2008). The assertion by the AMMI group was also supported by the present study. In this study where there was high G x E interaction due to the inclusion of extreme environments, AMMI1 captures 35.73% , AMMI2 captures 61% of the total variability due to G x E interaction whereas GGE2 captures about 50% (Fig. 4.6 and Fig. 4.7). The delineation of meaningful mega-environments and its visualisation on the biplot is more convenient and easier on GGE than the AMMI biplot. The GGE biplot gives an option on data scaling, transformation and

singular value partitioning (SVP) options (Fig. 4.11) to visualise and interpret the biplot which is not the case with AMMI, at least by the currently available statistical software.

Apart from the argument within AMMI and GGE, critics have also shared their concern on the limitations of the biplot techniques in general. According to Yang et al. (2009) the use of biplot beyond its simple visualisation tool needs further caution. To understand whether the which-won-where pattern is always realistic or not, whether the biplots are capable to indicate the nature and causes of the G x E interactions amongst others needs further scrutiny and should stand the test of various statistical procedures. They also suggested the application of the bootstrap statistical method to the multi-environment data by which the data needs to be resampled with a certain confidence limit for genotype and environment scores in biplots to reach critical decision on genotype selection or recommendation (Yang et al., 2009). However, the idea of bootstrapping procedure was rejected by Yan et al. (2010) who claim resampling of multi-environment data will destroy the very essence of G x E interaction pattern, an important aspect of biplot analysis. Meanwhile, the idea of Yang et al. (2009) to test biplots with additional statistics looks sound and is supported by this study. In the GGE biplot analysis, the which-won-where pattern (Fig. 4.9) listed entries 90, 86, 28, 23 and 83 as the best for the environment of CHSDT, whereas these entries were not among the top yielders according to the ANOVA results presented in Table 3.6 and Appendix 2.

In conclusion, the critical evaluation of biplot techniques in general and AMMI and GGE in particular in recent years will open windows of opportunity for further improvement of the dark-side of the models. However, the general consensus among scientists is that for the foreseeable future, AMMI and GGE biplot will be the only available good options to extract valuable information from complex multi-environment data. The application of either of the models should take into account the purpose of the research and the inclusion of other statistical test for critical genotype selection. Further research on biplots will not only harmonize some of the existing disagreements but also enhance the usefulness of the techniques in a wider perspective.

4.5 Conclusions

The yield stability and adaptation pattern of 96 maize genotypes evaluated in 15 stress and non-stress environments of ESA was assessed based on the two most important multivariate analyses procedures, AMMI and GGE. The ANOVA of the AMMI model showed highly significant differences ($P < 0.001$) for environments, genotypes and G x E interaction. The F-test was highly significant ($P < 0.001$) for all the five IPCA axes that explained 100% of the variation due to G x E interaction. The environment main effect explained 76.88% of the total yield variation followed by the G x E interaction (12.44%). The genotypes explained only 3.35% of the variation which is a common occurrence, particularly when trials are conducted in very diverse environments.

The AMMI analysis identified entry 40 (G40) as the top yielder among the 96 genotypes evaluated across all the environments and entry 36 (G36) was the lowest yielder. The most stable entry identified by this model was entry 60 (G60) while entry 37 was categorized among the least stable entries due to its furthest position on the IPCA1 axis. However due to its high mean grain yield it can be considered as responsive entry for a specific environment. Among the 15 environments HREOP1 was the most responsive environment for the evaluation of the genotypes while RATOP was a relatively stable environment unlike AWAOP which was identified as the least stable environment.

The AMMI2 biplot identified entry 37(G37) as the most responsive to the optimum environment of Awassa, Ethiopia (AWAOP) and entry 40 and 54 to the optimum environment of Kakamega, Kenya (KAKOP). Among the environments, AWAOP was found to be the most discriminating due to its long distance from the origin of the AMMI2 biplot. AMMI2 biplot grouped environments based on the mean performance; as a result all the optimum environments were grouped similarly in the bottom right quadrant of the biplot and all the stress environments in top left quadrant. The AMMI2 biplot for the top 25 genotypes showed that entries 54, 46, 96, and 55 were closer to BAKOP indicating their better performance in this optimum environment of Ethiopia. Entries 73, 22 and 63 were more adapted to the stress environments and more specifically entry 73 was closer to the managed drought environment of Kiboko-Kenya (KBODT). Entries 92, 40 and 37 were adapted to MLKOP, EMBOP and AWAOP.

The two principal components of the GGE biplot captured about 50% of the total G x E variation. Entries 37 and 40 were ranked the top performing genotypes by the GGE analysis and among the environments HREOP2, HREOP1 and AWAOP were the most responsive environments during the evaluation of the 96 hybrids across all the environments. In the which-won-where analysis, the GGE biplot was divided into seven sectors and the environments distributed in the four sectors. Entries included under the sector where one or more environments grouped were considered to be the best entries for that particular environment(s). Entries grouped in a sector with no environment(s) were considered to be poorly performing entries or that the entries did not win at any of the environment(s). Entries 37, 40, 52 and others in the same sector were the most suitable entries in the environments of AWAOP, EMBOP, KAKOP, BAKOP, HREOP1, RATOP, HRELN1,HRELN2 and BAKLN (Fig. 4.9).

To identify ideal genotypes and ideal test environments, a GGE biplot was constructed to analyse the discriminating ability and representativeness of the environments. Among the environments HREOP2 was the most representative environment as it had relatively small projection from the ATC y-axis; it was also highly discriminating because of its large projection onto the ATC x-axis. AWAOP was also a discriminating environment because of its large projection from the origin. However, it is not a representative environment because of its large distance from the ATC y-axis (Fig. 4.11). The closest entry to the ideal genotype was entry 40 followed by entry 37. However, entry 40 showed a better stability than entry 37 because of its relative position on the ATC y-axis. Entry 36 was the poorest performing genotype due to its furthest position on the ATC x-axis.

In the delineation of mega-environments, the GGE analysis created four broader groups from the 15 environments. The environments of AWAOP, EMBOP, KAKOP, HREOP1, HREOP2, BAKOP and RATOP were classified under the same mega-environment which indicates those genotype performed well in one of these locations can be deployed to the others with an expected similar performance. Most of the drought stress environments viz. CHIDT1, CHIDT2, KBODT MLKOP and BAKLN (BKOLN) were grouped in to the same mega-environment. Furthermore, the optimum environment of MLKOP and the low-N stress site of BAKLN (BKOLN) also fell in this group. The low-N stress environments of HRELN1 and HRELN2 were grouped together to form another mega-environment for the screening of genotypes for low-N stress. The fourth mega-environment identified was Chisumbanje

(CHSDT) a drought stress screening site located in Zimbabwe. This site was isolated from the other drought stress sites because of the below average performance of the genotypes. Hence, CHSDT needs to be considered as a separate mega-environment for screening drought tolerant genotypes (Fig. 4.12).

Cluster analysis of genotypes at a cut-off value of 1.0 produced six clusters while the environments were grouped into two broad clusters. However, the cluster analysis at the cut-off point of 0.5 classified the environments into four groups. The first group comprised BAKOP, EMBOP, HREOP1 and HREOP2 which are among the mid altitude moist agro ecologies in Ethiopia, Kenya and Zimbabwe. The second cluster consisted of KAKOP, AWAOP, MLKOP and RATOP, the third cluster contained CHIDT1, KBODT and BAKLN which were among the stress environments in the mid altitude dry agro ecologies in Zimbabwe, Kenya and Ethiopia respectively. The fourth cluster which consisted of CHIDT2, CHSDT, HRELN1 and HRELN2 were among the drought and low-N stress environments.

The comparison of AMMI and GGE biplot revealed the merits and drawbacks of the two models. AMMI2 was found to capture more of the variability due to G x E interaction than GGE2. The GGE2 biplot offers an easy visualization and understanding of the complex multi-environment data than the different model family of AMMI. Critics of biplot techniques in general argue about the over use and abuse of the method and recommended the application of other statistical procedures in order to make critical decisions on genotype evaluation or selection. However, the application of AMMI and GGE biplot will remain important for the foreseeable future and further research is expected not only to harmonize the existing differences but also to enhance the better use of biplot techniques in general.

4.6 References

Agronomix software, Inc. 2011. Agrobase Generation II SQL. Agronomix software, Inc., 171 Waterloo St. Winnipeg, Manitoba, R3N054, Canada.

Andio, F.L., V. Cravero, P. Asprelli, T. Firpo, S.M. García, and E. Cointry. 2004. Heterotic patterns in hybrids involving cultivar-groups of summer squash. *Euphytica* 135:355–360.

Annicchiarico, P. 1997. Joint regression versus AMMI analysis of genotype-environment interactions for cereals in Italy. *Euphytica* 94:53-62.

Bertoia, L., C. López, and R. Burak. 2006. Biplot analysis of forage combining ability in maize landraces. *Crop Science* 46:1346–1353.

Bhan, M.K., S. Pal, B.L. Rao, A.K. Dhar, and M.S. Kang. 2005. GGE biplot analysis of oil yield in lemongrass. *Journal of New Seeds* 7:127-139.

Casanoves, F., J. Baldessari, and M. Balzarini. 2005. Evaluation of multi environment trials of peanut cultivars. *Crop Science* 45:18-26.

Crossa, J., H.G. Gauch, and R.W. Zobel. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials *Crop Science* 30:493-500.

Dardanellia, J.L., M. Balzarinic, M.J. Martíneza, M. Cunibertib, S. Resnikd, S.F. Ramundaa, R. Herrerob, and H. Baigorrib. 2006. Soybean maturity groups, environments, and their interaction defi ne mega-environments for seed composition in Argentina. *Crop Science* 46:1939-1947.

Ding, M., B. Tier, and W. Yan. 2007. Application of GGE biplot analysis to evaluate genotype(G), environment(E) and GxE interaction on *P. radiata*:case study. Australasia Forest Genetics Conference, 11-14 April 2007, The Old Woolstore, Hobart, Tasmania, Australia.

Fatma, A.T., E. Ilker., and M. Tosun. 2011. Evaluation of genotype x environment interactions in maize hybrids using GGE biplot analysis. *Crop Breeding and Applied Biotechnology. Brazilian Society of Plant Breeding* 11: 1-9.

Gabriel, K.R. 1971. The biplot graphic display of matrices with application to principal component analysis. *Biometrika* 58:453-467.

Gauch, H.G. 2006. Statistical analysis of yield trials by AMMI and GGE. *Crop Science* 46:1488-1500.

Gauch, H.G., and R.W. Zobel. 1996. AMMI analyses of yield trials. In: M.S. Kang and H.G. Gauch (Eds.). Genotype by Environment Interaction. CRC. Boca Raton, Florida, USA. pp. 85-122.

Gauch, H.G., H.P. Piepho, and P. Annicchiarico. 2008. Statistical analysis of yield trials by AMMI and GGE: Further considerations. *Crop Science* 48:866-889.

GenStat. 2012. GenStat Fifteenth Edition, Statistical Software. Release 15.1.0.8035. GenStat, VSN International Ltd. Hertfordshire, HP1, 1ES,UK.

Gower, J.C., and D.J. Hand. 1996. Biplots. Chapman and Hall, London.

Hammer, G.L., and M. Cooper. 1996. Plant Adaptation and Crop Improvement. CAB International, Wallingford.

Hintze, J. 2001. NCSS and PASS, Number Cruncher Statistical Systems. Kasville, Utah. http://www. ggebiplot.com. Accessed Aug. 2012.

Kang, M.S., V.D. Aggarwal, and R.M. Chirwa. 2006. Adaptability and stability of bean cultivars as determined via yield-stability statistic and GGE biplot analysis. *Journal of Crop Improvement* 15:97-120.

Magorokosho, C., B. Vivek, and J. MacRobert. 2009. Characterization of maize germplasm grown in eastern and southern Africa: Results of the 2008 regional trials coordinated by CIMMYT. CIMMYT, Harare, Zimbabwe.

Magorokosho, C., B. Vivek, J. MacRobert, and A. Tarekegne. 2010. Characterization of maize germplasm grown in eastern and southern Africa: Results of the 2009 regional trials coordinated by CIMMYT. CIMMYT, Harare, Zimbabwe.

Makumbi, D. 2011. Results of the 2010 regional trials coordinated by CIMMYT-Kenya. CIMMYT, Nairobi, Kenya.

Narro, L., S. Pandey, J. Crossa, C.D. León, and F. Salazar. 2003. Using line × tester interaction for the formation of yellow maize synthetics tolerant to acid soils. *Crop Science* 43:1718-1728.

Samonte, S.O.P.B., L.T. Wilson, A.M. McClung, and J.C. Medley. 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. *Crop Science* 45:2414-2424.

Setimela, P., J. MacRobert, G.N. Atlin, C. Magorokosho, A. Tarekegne, and D. Makumbi. 2012. Evaluation of regional On-farm variety trials in Eastern and Southern Africa 2011 CIMMYT, Harare, Zimbabwe.

Setimela, P.S., B. Viveka, M. Bänziger, J. Crossa, and F. Maideni. 2007. Evaluation of early to medium maturing open pollinated maize varieties in SADC region using GGE biplot based on the SREG model. *Field Crops Research* 103:161–169.

Van Eeuwijk, F.A. 1995. Multiplicative interaction in generalised linear models. *Biometrics* 51:1017-1032.

Voltas, J., H. López-Córcoles, and G. Borrás. 2005. Use of biplot analysis and factorial regression for the investigation of superior genotypes in multi-environment trials. *European Journal of Agronomy* 22:309-324.

Weikai, Y., and H.B. James. 2010. A heritability-adjusted GGE biplot for test environment evaluation. *Euphytica* 171:355–369.

Xing-Ming, F., S.K. Manjit, C. Hongmei, Z. Yudong, T. Jing, and X. Chuxia. 2007. Yield Stability of Maize Hybrids Evaluated in Multi-Environment Trials in Yunnan, China. *Agronomy Journal* 99:220–228.

Yan, W. 2001. GGEbiplot – a Windows application for graphical analysis of multi-environment trial data and other types of two way data. *Agronomy Journal* 93:1111-1118.

Yan, W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agronomy Journal* 94:990-996.

Yan, W., and I. Rajcan. 2002. Biplot evaluation of test sites and trait relations of soybean in Ontario. *Crop Science* 42:11-20.

Yan, W., and M.S. Kang. 2003. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL.

Yan, W., and N.A. Tinker. 2005. An integrated biplot analysis system for displaying, interpreting, and exploring genotype-by-environment interactions. *Crop Science* 45:1004-1016.

Yan, W., K.D. Glover, and S.K. Manjit. 2010. Comment on "Biplot Analysis of Genotype x Environment Interaction: Proceed with Caution," by R.C.Yang, J.Crossa, P.L. Cornelius, and J.Burgueno in *Crop Science* 2009 49:1564-1576. *Crop Science* 50:1121-1123.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Science* 40:597-605.

Yan, W., M.S. Kang, B.L. Ma, S. Wood, and P.L. Cornelius. 2007. GGE Biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science* 47:443-655.

Yang, R.-C., J. Crossa, P.L. Cornelius, and J. Burgueno. 2009. Biplot analysis of genotype x environment interaction: proceed with caution. *Crop Science* 49:1564-1576.

Yau, S.K. 1995. Regression and AMMI analyses of genotype x environment interactions: an empirical comparison. *Agronomy Journal* 87:121-126.

Zobel, R.W., M.J. Wright, and H.G.G. Jr. 1988. Statistical analysis of yield trial. *Agronomy Journal* 80:388-393.

CHAPTER 5

Evaluation of early maturing open pollinated QPM varieties for grain yield and days to anthesis under the diverse mega-environments of ECA

5. 1 Abstract

According to the global hunger index, countries in ECA are currently categorised as having either "serious" or "alarming" levels of hunger because of low agricultural productivity and prevalence of abject poverty, among others. The development and deployment of high performing early maturing OPVs of quality protein maize (QPM) will benefit resource poor and marginal communities to attain food and nutritional security at household and country levels. A total of 38 (37 QPM and a normal check) early maturing OPVs were evaluated in two sets in a total of 37 environments for grain yield and 35 environments for days to anthesis in the diverse environments of ECA during 2006-2008. Mean squares for entries and the test environments as well as the interaction between entries and environments were highly significant ($P \leq 0.01$) both for grain yield and days to anthesis for the two sets of trials. From the first set of trials, entry 19 showed a 40%, and from the second set entry 31 showed a 44% grain yield advantage over the normal check variety (Katumani). The average days to anthesis of the candidates from both sets were 65 and for the check was 58 days. The AMMI model identified entry 7 as the most stable variety and Kiboko (Kenya) (KIB3) as the most responsive environment, and entry 20(Katumani) as the least stable and low yielding, and Kakamega (Kenya) and Gandajika (DR Congo) as the least responsive environments for grain yield. Similarly entries 12, 15 and 18 were the most stable entries and Melkassa (Ethiopia) and Kiboko (Kib2) were the most stable environments for days to anthesis for the first set of trials. The GGE biplot grouped the test environments into five mega-environments based on grain yield and four mega-environments based on days to anthesis of the second set of trials. Out of the five groups, the environment Weruweru (Tanzania) was identified as a separate mega-environment and Mosso (Burundi) and Elgon Downs (Kenya) were grouped under similar mega-environments. Based on days to anthesis, the environment Mparambo (Burundi) and Rahd and Wad Madani (Sudan) were distinguished as different mega-environments. The GGE biplot also identified entry 31 and Embu (Kenya) as an ideal genotype and environment, respectively. Recycling of QPM OPVs after the third generation showed a 39% and the normal maize (Katumani) a 32% yield loss which indicated the threshold year for the maintenance of OPVs. This study will contribute significantly to the release of widely adapted QPM varieties in the region, facilitate germplasm exchange among environments and will enhance the livelihood of maize based communities in the region and beyond.

Key words: QPM; Mega-environments; AMMI; GGE; tropical open pollinated maize; grain yield; days to anthesis.

5.2 Introduction

According to the global hunger index for the year 2012, most of the countries in SSA are categorised under “serious” and some countries as “alarming” for levels of hunger, South Africa being the only exception where it is categorised under ”moderate” (von Grebmer et al., 2012). Although the level of hunger and malnutrition in SSA is in a declining trend from its level in 1990, the situation in some countries worsened and millions of people in the region are still in a state of malnutrition. Twenty three percent of sub-Saharan children are under weight and countries like Burkina Faso, Chad, Democratic Republic of Congo, Mali, Sierra Leone, and Somalia have the highest under age five child mortality rate in the world (IFPRI, 2012). According to the IFPRI (2012) report, in two ECA countries (Burundi and Eritrea) more than 50% of the population is undernourished. Although various factors contributed to the severe food security situation in SSA, the base of the problem relates to low agricultural productivity.

Maize is the most important cereal food crop in SSA, particularly in ESA where it accounts for 53% of the total cereal area (FAOSTAT, 2010) and 30-70% of total caloric consumption (Langyintuo et al., 2010). Maize covers about 25 million ha in SSA (Smale et al., 2011) and is produced largely in smallholder systems, primarily for food (Hassan et al., 2001; Diallo et al., 2004; Bänziger and Diallo, 2004; Smalberger and du Toit, 2004; Smale et al., 2011)

Maize is cultivated on about 10 million ha in eastern (7.79 M ha) and central (2.31 M ha) Africa and it is increasing by 2% annually (based on 1961-2008 estimates). Based on the 2005-2008 estimates, the average maize yield for eastern Africa is about 1.5 t ha^{-1} and for central Africa about 1.10 t ha^{-1} (Smale et al., 2011). The average per capita consumption of maize in ECA is lower than in southern Africa. In eastern Africa, per capita annual consumption ranges from 40 kg in Burundi to 105 kg in Kenya (Hassan et al., 2001). Based on the 2003-2005 estimates of the World Bank, however, the average per capita consumption of maize for eastern Africa is 27 $kg^{-1}cap^{-1}year^{-1}$ and for central Africa it is 25 $kg^{-1}cap^{-1}year^{-1}$ which is less than in southern Africa (82 $kg^{-1}cap^{-1}year^{-1}$). However, the annual maize production growth for ECA is about 3% compared to 1.3% for southern Africa (Smale et al., 2011).

Although maize is a dominant food crop in ECA, its nutritional quality is poor due to the low levels of lysine and tryptophan content in normal maize, which dominates the region and

Africa at large. QPM has superior protein quality because it has twice the level of these essential amino acids compared to normal maize and has proved to mitigate protein energy malnutrition and hunger in communities where maize is a dietary staple. Many researchers indicated the competitiveness of QPM for grain yield with the best normal maize counterparts (Bjarnason and Vasal, 1992; Pixley and Bjarnason, 1993; Cordova and Pandey, 1999; Vergara et al., 2000). This confirms the advantages of QPM both in nutrition and grain yield, particularly in SSA where animal sources of protein are not affordable for many people.

The majority of the maize area in SSA is planted with either local varieties, improved OPVs or recycled hybrids, although hybrid maize production started almost five decades ago (Hassan et al., 2001). Among the reasons for the slow pace of hybrid adoption in SSA are the requirements of technical knowledge and capital for the production of hybrid seeds (Pixley and Bänziger, 2001). Furthermore, the seed industry in SSA is not well developed, as a result the bulk of maize seed planted in the region comes from the informal seed sector (MacRobert, 2009). The hybrid seed market targets only better off farmers who can afford the seed. However, many people in ECA live below the poverty line and are categorised under "low human development index" with a high percentage of severe poverty (UNDP, 2011) and cannot afford the high price of hybrid seeds and associated inputs. Hence, under resource-poor farmer conditions, in areas where the seed system is underdeveloped, with the current high input costs together with the low purchasing power of farmers, particularly in rural areas, improved OPVs are the only viable option. The main reason for OPVs remaining a viable option for marginal farmers is the ease of OPV seed production which results in low unit price of seed and the recycling of OPV seeds for more than one season. Therefore, development and deployment of improved and superior QPM OPVs in ECA will be an effective strategy to alleviate both food and nutritional insecurity which will, in turn, help to attain economic growth. Grain yield advantage and its stability across the diverse environments of ECA are the key solutions to fast-track the adoption of QPM cultivars in ECA as well as SSA.

Besides improving the primary trait (yield) of QPMs, it is also important to develop climate resilient cultivars that can adapt to the heterogeneous maize growing conditions of ECA and SSA. Secondary traits like days to anthesis, days to silking, anthesis-silking interval among others, greatly affect the ultimate yield of a cultivar. Similar to yield, secondary traits in maize are also affected by growing environments. Among the secondary traits, male

flowering is more important than silking, as the latter is more influenced by abiotic stress and tasseling is more stable in adverse environmental conditions (Koester et al., 1993).

Temperature and photoperiod are the two most important factors that influence the time of flowering (an important secondary trait) in tropical maize cultivars. Temperature is a major determinant of the rate of plant development and with the global climate change; warmer temperatures that shorten development stages of determinate crops will most probably reduce the yield of a given variety (Craufurd and Wheeler, 2009). Earlier studies on wheat show that a 1°C rise in mean seasonal temperature caused yield reduction of up to 10% and accelerated days to anthesis and grain maturity (Mitchell et al., 1993; Wheeler et al., 1996). Photoperiod (the relative length of the light and dark periods) is an equally important environmental factor that induces flower formation and together with temperature they determine the timing of flowering within a season (Roberts and Summerfield, 1987; Wallace and Yan, 1998; Kikuchi and Handa, 2009; Xu et al., 2012).

In general, the ideal estimation of the time between planting and days to anthesis (when 50% of the plants start shedding of pollen) in maize is important to adjust planting dates, to exchange germplasm among environments, to adapt to both abiotic (for example temperature and water) and biotic (pest and disease) stress. Other uses of days to anthesis include mega-environment analysis and advancing genetic gains through conventional and molecular breeding, including introgression with exotic gene pools.

Among the different multivariate analysis, the AMMI and the GGE biplot are the current best options to identify and group stable genotypes and environments. The models also help to visualise large G x E data sets from METs in an informative biplot. The AMMI model combines the ANOVA for the genotype and environment main effects with PCA of the G x E interaction. It has proven useful for understanding of complex G x E interaction. Gauch and Zobel (1996) showed that AMMI 1 with IPCA 1 and AMMI 2 with IPCA 1 and IPCA 2 are usually selected and the graphical representation of axes, either as IPCA 1 or IPCA 2 against main effects or IPCA 1 against IPCA 2 is generally informative. GGE biplot helps to visualise, among others, the relationship among the genotypes, which genotype-won-where, the discriminating power and representativeness of the test-environments and the different groups of mega-environments (Yan et al., 2000; Yan, 2001).

A study by Erenstein et al. (2011) indicated that improved OPVs are the major cultivars in the maize growing areas of Ethiopia and Uganda. The study also showed that farmers in eastern Africa recycle local varieties for an average of 8.4 years in Tanzania and 4.6 years in Ethiopia. The recycling rate of improved OPVs in Ethiopia and Tanzania was 2.3 and 3.5 years respectively. Among the reasons for the non-continuous use of improved varieties include; lack of knowledge, shortage of money and absence of suitable varieties (Erenstein et al., 2011). Compared to hybrids, the yield loss due to recycling is much less with OPVs due to their broad genetic base. Pixley and Bänziger (2001) reported a yield loss of 32% for elite conventional hybrids and 16% for top cross hybrids by recycling seeds from the first generation of plants and only 5% for OPVs by recycling seeds from the second generation of plants. This indicates the advantage of OPVs over hybrids for small-holder marginal farmers. However, a continued use of recycled OPVs will result in significant yield loss, hence, it is important to determine when to obtain fresh OPV seed, particularly for QPMs where such information is seriously lacking. Therefore, the objectives of this study were to:

1. evaluate early maturing tropical open pollinated QPM varieties for grain yield and days to anthesis in ECA
2. analyse the association of the candidate QPM OPVs and to identify responsive genotypes and environments based on grain yield and days to anthesis using the AMMI model
3. sub-divide the maize growing environments of ECA into different mega-environments based on the genotype response to grain yield and days to anthesis using GGE biplot
4. determine the threshold year for replacing QPM OPVs with fresh seed

The output of this study will contribute to enhanced food and nutritional security, and foster sustainable and equitable economic growth in the region and beyond.

5.3 Materials and methods

Germplasm

Nineteen early maturing QPM OPV's were included in the first set of trials (set A) which was conducted during 2006 and 2007. The 19 QPM varieties were compared with a normal endosperm OPV - Katumani which is an extra early maturing white, semi-dent variety, developed at Katumani, Kenya and widely grown in drought prone areas of eastern Africa (Mugo et al., 1998) and an additional local check which made the total number of entries in the trials 21. The QPM cultivars were developed for their earliness in maturity, high tryptophan level and protein quality. The materials were selected for adaptation to the low and mid altitude agro ecologies of the diverse tropical environments.

The second set of trials (set B) which were conducted from 2007-2008 consisted of 37 early maturing QPM varieties, one non QPM commercial variety (Katumani) and a local check that made the total number of entries 39. Of the 37 QPM cultivars, 19 were included in the first set of trials and the other 18 had basically the same genetic background as the first 19 cultivars except that their advancement to OPV was achieved through successive bulking of selected ears. Seed production for the trials was done by plant-to-plant (full-sib) manual pollination ensuring the seed stock was protected from external pollen sources or adulteration from other varieties.

The development of the QPM varieties was through backcross breeding by which selected F_2 parents were recurrently backcrossed to the QPM donor so as to increase the allele frequency of the modifier genes (Vivek et al., 2008). Samples of each entry were sent to CIMMYT Maize Nutrition Quality and Plant Tissue Analysis Laboratory for the determination of tryptophan (TRP) and total N content following the procedures described by Villegas (1975). Percentage of protein concentration of the samples was determined by the formula of Nkonge and Balance (1982):

$$\% \text{ Protein} = \% \text{ N} \times 6.25$$

where N is the value of nitrogen and 6.25 is a conversion factor for maize. The protein quality index (QI) was calculated as follows:

$$\text{Quality Index (QI)} = \frac{\%\, tryptophan}{\%\ protein} x100$$

Seed production for the trials was done at Kiboko, Kenya, one of the drought tolerant maize screening stations of CIMMYT. In Table 5.1 the pedigrees of the germplasm are presented with their entry code, tryptophan (TRP) and N levels of the materials included in the 2006-2007 trials. Table 5.2 shows the pedigrees of the 39 QPM-OPVs and the checks included in the 2007-2008 trials. Each year the seed was produced by manual self pollination at Kiboko nursery as indicated by the codes of the stock identification (ID). The stock ID explains the place, year, season and blocks of the seed production and it served as a reference for tracing the seed in the store. Table 5.3 shows the description of the test environments and Fig.5.1 shows the geographical location of the countries included in this study.

Table 5.1 Pedigree and description of 21 early maturing open pollinated maize varieties evaluated in ECA during 2006-2007

No.	Pedigree	Stock ID	Code	TRP (%)	N (%)	Protein (%)	Quality index
1	EEQPMOPV-1-EA-#	KB05B-0B17-1	V1	0.075	1.23	7.72	0.97
2	EEQPM-HT -#	KB05B-0B17-2	V2	0.071	1.39	8.66	0.82
3	EEQPM-6-EA -#	KB05B-0B17-3	V3	0.068	1.33	8.34	0.81
4	EEQPM-9-EA-#	KB05B-0B17-4	V4	0.069	1.43	8.91	0.77
5	EEQPM-8-EA-#	KB05B-0B17-5	V5	0.069	1.26	7.85	0.88
6	EEQPM-13-EA-#	KB05B-0B17-6	V6	0.072	1.42	8.90	0.80
7	EEQPM-16-EA-#	KB05B-0B17-7	V7	0.075	1.45	9.05	0.83
8	EEQPM-18-EA-#	KB05B-0B17-8	V8	0.075	1.35	8.41	0.89
9	EEQPM-29-EA-#	KB05B-0B17-9	V9	0.078	1.48	9.25	0.84
10	EEQPM-34-EA-#	KB05B-0B17-10	V10	0.076	1.49	9.34	0.82
11	EEQPM-36-EA-#	KB05B-0B17-11	V11	0.078	1.41	8.83	0.88
12	EEQPM-38-EA -#	KB05B-0B17-12	V12	0.064	1.42	8.87	0.72
13	EEQPM-45-EA -#	KB05B-0B17-13	V13	0.068	1.44	9.01	0.75
14	EEQPM-49-EA-#	KB05B-0B17-14	V14	0.065	1.29	8.04	0.81
15	EEQPM-21-EA-#	KB05B-0B17-15	V15	0.071	1.34	8.37	0.85
16	EEQPM-33-EA-#	KB05B-0B17-16	V16	0.071	1.30	8.12	0.87
17	EEQPM-42-EA-#	KB05B-0B17-17	V17	0.077	1.39	8.68	0.88
18	EEQPMS2-#-GEASP - 1-#	KB05B-0B17-18	V18	0.073	1.33	8.30	0.88
19	POOL15QPM-SR-#-#	KB05A-0A36-13	V19	0.084	1.68	10.51	0.80
20	Katumani (Normal Maize)	COMMERCIAL	V20	0.045	1.37	8.57	0.53
21	Local check (Normal Maize)	LOCAL CHECK	V21	-	-	-	-

Table 5.2 List and pedigree of 39 early maturing open pollinated maize varieties evaluated in ECA during 2007-2008

No.	2007		2008		
	Stock ID	**Pedigree**	**Stock ID**	**Pedigree**	**Code**
1	KB06B-0B13-1	EEQPMOPV-1-EA-B-B-#-#	KB07A-0A15-1	EEQPMOPV-1-EA-B-B-#-#-#	OPV1
2	KB06B-0B13-2	EEQPMOPV--HT-B-B-#-#	KB07A-0A15-2	EEQPMOPV--HT-B-B-#-#-#	OPV2
3	KB06B-0B13-3	EEQPMOPV--6-EA-B-B-#-#	KB07A-0A15-3	EEQPMOPV--6-EA-B-B-#-#-#	OPV3
4	KB06B-0B13-4	EEQPMOPV--9-EA-B-B-#-#	KB07A-0A15-4	EEQPMOPV--9-EA-B-B-#-#-#	OPV4
5	KB06B-0B13-5	EEQPMOPV-8-EA-B-B-#-#	KB07A-0A15-5	EEQPMOPV-8-EA-B-B-#-#-#	OPV5
6	KB06B-0B13-6	EEQPMOPV--13EA-B-B-#-#	KB07A-0A15-6	EEQPMOPV--13EA-B-B-#-#-#	OPV6
7	KB06B-0B13-7	EEQPMOPV--16-EA-B-B-#-#	KB07A-0A15-7	EEQPMOPV--16-EA-B-B-#-#-#	OPV7
8	KB06B-0B13-8	EEQPMOPV--18-EA-B-B-#-#	KB07A-0A15-8	EEQPMOPV--18-EA-B-B-#-#-#	OPV8
9	KB06B-0B13-9	EEQPMOPV--29-EA-B-B-#-#	KB07A-0A15-9	EEQPMOPV--29-EA-B-B-#-#-#	OPV9
10	KB06B-0B13-10	EEQPMOPV--34-EA-B-B-#-#	KB07A-0A15-10	EEQPMOPV--34-EA-B-B-#-#-#	OPV10
11	KB06B-0B13-11	EEQPMOPV--36-EA-B-B-#-#	KB07A-0A15-11	EEQPMOPV--36-EA-B-B-#-#-#	OPV11
12	KB06B-0B13-12	EEQPMOPV--38-EA-B-B-#-#	KB07A-0A15-12	EEQPMOPV--38-EA-B-B-#-#-#	OPV12
13	KB06B-0B13-13	EEQPMOPV--45-EA-B-B-#-#	KB07A-0A15-13	EEQPMOPV--45-EA-B-B-#-#-#	OPV13
14	KB06B-0B13-14	EEQPMOPV--49-EA-B-B-#-#	KB07A-0A15-14	EEQPMOPV--49-EA-B-B-#-#-#	OPV14
15	KB06B-0B13-15	EEQPMOPV--21-EA-B-B-#-#	KB07A-0A15-15	EEQPMOPV--21-EA-B-B-#-#-#	OPV15
16	KB06B-0B13-16	EEQPMOPV--33-EA-B-B-#-#	KB07A-0A15-16	EEQPMOPV--33-EA-B-B-#-#-#	OPV16
17	KB06B-0B13-17	EEQPMOPV--42-EA-B-B-#-#	KB07A-0A15-17	EEQPMOPV--42-EA-B-B-#-#-#	OPV17
18	KB06B-0B13-18	EEQPMOPV--#-GEASP-1-B-B-#-#	KB07A-0A15-18	EEQPMOPV--#-GEASP-1-B-B-#-#-#	OPV18
19	KB06B-0B13-19	EEQPMOPV-1-EA-#-#	KB07A-0A15-19	EEQPMOPV-1-EA-#-#-#	OPV19
20	KB06B-0B13-20	EEQPM-HT -#-#	KB07A-0A15-20	EEQPM-HT -#-#-#	OPV20
21	KB06B-0B13-21	EEQPM-6-EA -#-#	KB07A-0A15-21	EEQPM-6-EA -#-#-#	OPV21
22	KB06B-0B13-22	EEQPM-9-EA-#-#	KB07A-0A15-22	EEQPM-9-EA-#-#-#	OPV22
23	KB06B-0B13-23	EEQPM-8-EA-#-#	KB07A-0A15-23	EEQPM-8-EA-#-#-#	OPV23
24	KB06B-0B13-24	EEQPM-13-EA-#-#	KB07A-0A15-24	EEQPM-13-EA-#-#-#	OPV24
25	KB06B-0B13-25	EEQPM-16-EA-#-#	KB07A-0A15-25	EEQPM-16-EA-#-#-#	OPV25
26	KB06B-0B13-26	EEQPM-18-EA-#-#	KB07A-0A15-26	EEQPM-18-EA-#-#-#	OPV26
27	KB06B-0B13-27	EEQPM-29-EA-#-#	KB07A-0A15-27	EEQPM-29-EA-#-#-#	OPV27
28	KB06B-0B13-28	EEQPM-34-EA-#-#	KB07A-0A15-28	EEQPM-34-EA-#-#-#	OPV28
29	KB06B-0B13-29	EEQPM-36-EA-#-#	KB07A-0A15-29	EEQPM-36-EA-#-#-#	OPV29
30	KB06B-0B13-30	EEQPM-38-EA -#-#	KB07A-0A15-30	EEQPM-38-EA -#-#-#	OPV30
31	KB06B-0B13-31	EEQPM-45-EA -#-#	KB07A-0A15-31	EEQPM-45-EA -#-#-#	OPV31
32	KB06B-0B13-32	EEQPM-49-EA-#-#	KB07A-0A15-32	EEQPM-49-EA-#-#-#	OPV32
33	KB06B-0B13-33	EEQPM-21-EA-#-#	KB07A-0A15-33	EEQPM-21-EA-#-#-#	OPV33
34	KB06B-0B13-34	EEQPM-33-EA-#-#	KB07A-0A15-34	EEQPM-33-EA-#-#-#	OPV34
35	KB06B-0B13-35	EEQPM-42-EA-#-#	KB07A-0A15-35	EEQPM-42-EA-#-#-#	OPV35
36	KB06B-0B13-36	EEQPMS2-#-GEASP - 1-#-#	KB07A-0A15-36	EEQPMS2-#-GEASP - 1-#-#-#	OPV36
37	KB06B-0B30-1	POOL15QC7-SRC1-F2-#-#-#	KB07A-0A15-37	POOL15QC7-SRC1-F2-#-#-#-#	OPV37
38	COMMERCIAL	KATUMANI	COMMERCIAL	KATUMANI	OPV38
39	LOCAL CHECK	LOCAL CHECK	LOCAL CHECK	LOCAL CHECK	OPV39

Table 5.3 Description of the test environments in ECA

Country	Location	Latitude	Longitude	Altitude (m)	Plot area (m^2)	Code
D.R. Congo	Gandajika	$6^0$45' S	$23^0$57' E	780	8.25	GAN
Ethiopia	Melkassa	$8^0$24' N	$39^0$17' E	1552	7.875	MEL
Kenya	Bungoma	$0^0$32' N	$34^0$33' E	1388	7.3125	BUN
Kenya	Embu	$0^0$30' S	$37^0$27' E	1502	7.875	EMB
Kenya	Kiboko	$2^0$12' S	$37^0$43' E	925	6.30	KIB
Kenya	Kakamega	$0^0$16' N	$34^0$45' E	1585	7.50	KAK
Rwanda	Rubona	$2^0$29' S	$29^0$39' E	1650	7.875	RUB
Rwanda	Nyagatare	$1^0$17' S	$30^0$18' E	1415	7.875	NYA
Uganda	Namulonge	$0^0$31' N	$32^0$37' E	1133	7.95	NAM
Kenya	E.Downs	$1^0$03' N	$34^0$51' E	1900	7.875	EDO
Kenya	Siaya	$0^0$02' N	$34^0$18' E	1330	7.875	SIA
Kenya	Alupe	$0^0$29' N	$34^0$07' E	1170	2.875	ALU
Kenya	Thika	$1^0$03' S	$36^0$58' E	1564	7.875	THI
Kenya	Kimaeti	$0^0$36' N	$34^0$25' E	1300	7.875	KIM
Kenya	Kitale	$1^0$03' N	$34^0$56' E	1850	9.00	KIT
Burundi	Mosso	NA	NA	NA	8.25	MOS
Burundi	Mparambo	NA	NA	AN	8.25	MPA
Sudan	Wad Madani	14^0 23' N	$33^0$29' E	411	8.40	WAD
Sudan	Rahad	13^0 56' N	$34^0$03' E	422	8.40	RAH
Tanzania	SARI	$3^0$22' S	$36^0$37'E	1387	7.875	SAR
Tanzania	Arusha	$3^0$18'S	$36^0$38'E	1525	7.875	ARU
Tanzania	Selian	$3^0$22' S	$36^0$36'E	1300	7.875	SEL
Tanzania	Mbulumbulu	$4^0$24' S	36^0 10'E	1210	7.875	MBU
Tanzania	Weruweru	$3^0$19' S	$37^0$15'E	929	7.875	WER

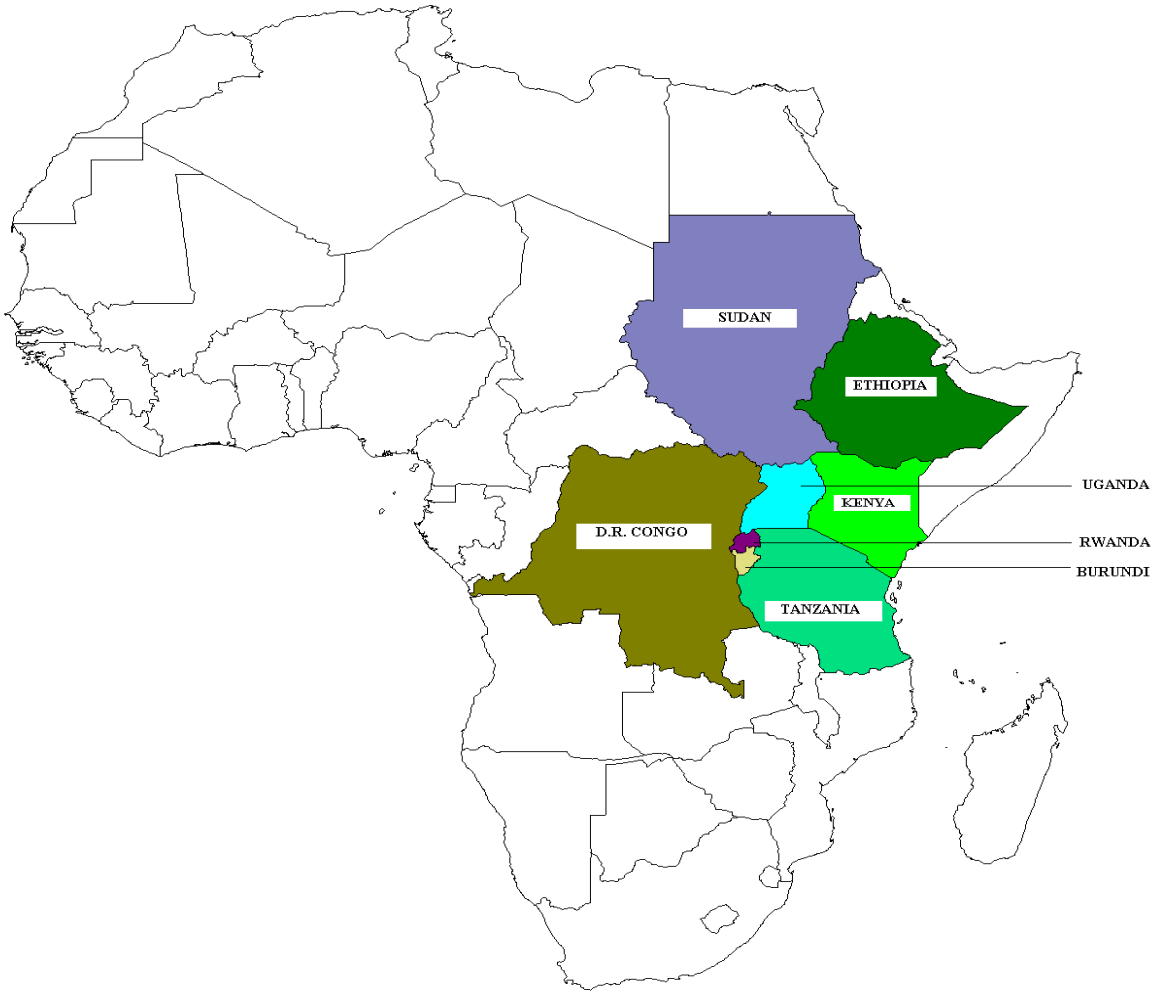

Figure 5.1 ECA countries included in the evaluation of early maturing QPM varieties during 2006-2008.

Experimental design and statistical analysis

All the trials were planted in an α (0,1) lattice experimental design (Patterson and Williams, 1976) with three replications and two row plots at all locations in 2006 and 2007. In the other set of trials (set B) that was conducted during 2007 and 2008, the number of replications and rows were two across all the locations. ANOVA for grain yield for each environment was conducted with the PROC MIXED procedure in SAS (2003). Local checks were included in the analysis of individual locations, but were excluded in the analysis of combined environments as local checks differed from location to location and country to country. The effects of the genotypes, locations and years as well as their interactions were determined from the PROC GLM procedure in SAS (2003). Genotypes were assumed to be fixed, while year and location effects, replications and blocks within replications were considered as random. Statistical analyses were performed to test the significance level of grain yield and days to anthesis of the genotypes for each location and year as well as the combined analysis of variance across locations and years.

Biplot analysis was performed to visualise the relationships among the genotypes and environments using GenStat® 15thedition (GenStat, 2012). AMMI and GGE biplot analyses were done to identify stable genotypes and to classify the different locations into different mega-environments based on the grain yield performance and days to anthesis of the QPM OPVs. Detailed procedures and interpretation of AMMI and GGE biplots are presented under the materials and methods section of Chapter 4.

5.4 Results and discussion

5.4.1 Evaluation of genotypes for grain yield and days to anthesis

Trial set A (2006-2007)

The results of the ANOVA for individual locations for grain yield and days to anthesis for the year 2006 are presented in Table 5.4 and Table 5.5 respectively. Entries showed significant and highly significant ($P \leq 0.05$ and $P \leq 0.01$) mean squares for grain yield and days to anthesis across all environments. The percentage sum of squares for grain yield (Table 5.4) and days to anthesis (Table 5.5) show that entries were the major contributors to the total variation in all the environments. Kakamega and Kiboko1 were the locations where entry

contribution to variation was most high (72.38% and 70.47% respectively) for grain yield (Table 5.4) while entries at Kiboko1 and Melkassa contributed 87.97% and 80.11 % variation for days to anthesis respectively (Table 5.5). Environmental (blocks, reps and errors) contributions were high at Rubona and Namulonge for grain yield and at Selian for days to anthesis (Table 5.4 and Table 5.5).

During 2007, the entries showed significant and highly significant ($P \leq 0.05$ and $P \leq 0.01$) variation for grain yield (Table 5.6) and days to anthesis (Table 5.7) at all locations except at Wad Madani where days to anthesis within the entries was not significant. In spite of this, the number of days for male flowering at Wad Madani was quite low compared to other locations (see later Table 5.11). However, the data from Wad Madani was not included in the across locations analysis.

Table 5.8 and 5.9 present results of grain yield performance while Tables 5.10 and 5.11 present days to anthesis for the 21 varieties tested across ECA. The shaded cells in the tables show the grain yield of top performing varieties and the variety with the least days to anthesis among the 21 hybrids across locations. The local check variety (V21) out yielded the candidates at five locations in 2006 and two locations in 2007.The candidate varieties were the best at six locations in 2006 and four locations in 2007 (Tables 5.8 and 5.9). However, the candidate varieties were superior in grain yield in almost all the locations compared to the commercial check variety, Katumani (V20) in grain yield. The inclusion of local checks which varied from location to location was used to monitor the advantage of the candidate varieties at the specific area and were excluded from the across environment analysis. The commercial check variety V20 (Katumani) was the earliest maturing at all the locations during 2006 and 2007 except at Kiboko1 (2006) and Arusha (2007) where the local check (V21) was the earliest (Tables 5.10 and 5.11).

Table 5.4 Mean squares from analysis of variance and percentage of variance components for **grain yield** of 21 OPVs tested across 11 environments of ECA, in 2006

		Sources of variations													
		Entry			Block			Replications			Error			Total		
Country	Location	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
D.R. Congo	Gandajika	20	0.75**	58.86	18	0.49**	31.49	2	0.72**	5.18	22	0.12	9.47	62	0.58	16.96
Ethiopia	Melkassa	20	1.83**	69.16	18	0.33	11.28	2	1.60*	6.06	22	0.32	13.50	62	0.96	9.15
Kenya	Bungoma	20	0.49**	50.10	18	0.28	25.74	2	0.62	6.31	22	0.16	17.85	62	0.68	11.15
Kenya	Embu	20	1.08**	66.81	18	0.29	16.41	2	0.08	0.51	22	0.24	16.27	62	0.83	11.51
Kenya	Kiboko1	20	3.50**	70.47	18	0.80**	14.59	2	4.84**	9.75	22	0.23	5.19	62	0.82	8.47
Kenya	Kiboko2	20	0.52*	52.92	18	0.24	21.62	2	0.25	2.62	22	0.20	22.84	62	0.76	7.88
Kenya	Kakamega	20	0.36**	72.38	18	0.06	10.02	2	0.07	1.35	22	0.07	16.25	62	0.46	37.47
Rwanda	Rubona	20	1.17*	42.46	18	0.74	24.14	2	3.97**	14.37	22	0.48	19.03	62	1.17	17.01
Rwanda	Nyagatare	20	0.94*	52.14	18	0.51	25.51	2	0.24	1.31	22	0.35	21.04	62	0.99	11.62
Tanzania	Arusha	20	0.79**	66.95	18	0.26	19.67	2	0.12	1.00	22	0.13	12.37	62	0.62	13.42
Uganda	Namulonge	20	1.19**	44.61	18	0.47	15.68	2	7.25**	27.08	22	0.31	12.63	62	0.94	12.50

*P ≤ 0.05, ** P ≤ 0.01, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.5 Mean squares from analysis of variance and percentage of variance components for **days to anthesis** of 21 OPVs tested across 11 environments of ECA, in 2006

Country	Location	Sources of variations														
		Entry			Block			Replications			Error			Total		
		DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
D.R.Congo	Gandajika	20	9.82**	74.47	18	1.24*	8.49	2	16.00**	12.13	22	0.59	4.91	62	1.30	1.40
Ethiopia	Melkassa	20	16.25**	80.11	18	2.61*	11.56	2	4.33*	2.14	22	1.14	6.18	62	1.81	1.64
Kenya	Bungoma	20	23.94**	74.41	18	4.86	13.60	2	10.11*	3.14	22	2.59	8.44	62	2.72	2.53
Kenya	Embu	20	16.31**	64.02	18	5.12*	18.10	2	18.78**	7.37	22	2.43	10.51	62	2.64	2.49
Kenya	Kakamega	20	33.55**	73.07	18	5.21	10.21	2	4.63	1.01	22	6.56	15.71	62	4.34	3.78
Kenya	Kiboko1	20	12.92**	87.97	18	0.83	5.11	2	1.44	0.98	22	0.79	5.94	62	1.51	1.43
Kenya	Kiboko2	20	21.69**	60.94	18	9.26	23.43	2	4.11	1.15	22	4.68	14..47	62	3.66	3.60
Rwanda	Nyagatare	20	19.52**	67.19	18	4.80	14.89	2	24.21**	8.33	22	2.53	9.59	62	2.70	2.28
Tanzania	Arusha	20	49.72**	73.02	18	14.09**	18.62	2	7.19	1.05	22	4.52	7.29	62	3.60	2.60
Tanzania	Selian	20	24.57**	49.27	18	17.89*	32.28	2	5.54	1.11	22	7.86	17.33	62	4.75	3.31
Uganda	Namulonge	20	17.35*	52.39	18	7.16	19.45	2	2.59	0.78	22	8.24	27.37	62	4.86	5.20

*P ≤ 0.05, ** P ≤ 0.01, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.6 Mean squares from analysis of variance and percentage of variance components for **grain yield** of 21 OPVs tested across six environments of eastern Africa, in 2007

		Sources of variation													
		Entry			Block			Replications			Error			Total	
Country	Location	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Kenya	E.Downs	20	0.43**	41.38	18	0.19	17.23	2	2.64**	25.59	22	0.15	17.35	62	0.65	16.83
Kenya	Embu	20	5.26**	63.03	18	1.39	14.95	2	13.26**	15.75	22	0.48	6.27	62	1.17	8.35
Kenya	Kiboko	20	2.85**	69.26	18	0.65*	14.16	2	3.92**	9.53	22	0.26	7.05	62	0.87	5.91
Kenya	Siaya	20	0.98**	61.04	18	0.48**	27.05	2	0.42	2.60	22	0.14	9.31	62	0.67	15.88
Sudan	W.Madani	20	0.41*	40.58	18	0.35*	31.14	2	1.11**	11.07	22	0.16	17.21	62	0.67	13.89
Tanzania	Arusha	20	1.13**	41.43	18	0.97**	32.16	2	3.48**	12.79	22	0.34	13.61	62	0.98	17.91

*$P \leq 0.05$, ** $P \leq 0.01$, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.7 Mean squares from analysis of variance and percentage of variance components for **days to anthesis** of 21 OPVs tested across five environments of eastern Africa, in 2007

Country	Location	Sources of variation													
		Entry			Block			Replications			Error			Total	
		DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Kenya	E. Downs	20	49.81**	75.76	18	6.06	8.30	2	68.83**	10.47	22	3.27	5.47	62	3.06	2.23
Kenya	Embu	20	20.48**	83.89	18	1.89	6.96	2	12.25**	5.02	22	0.92	4.13	62	1.62	1.45
Kenya	Kiboko	20	10.25**	58.62	18	4.50**	23.25	2	21.25**	12.16	22	0.96	6.07	62	1.66	1.77
Sudan	W. Madani	20	2.31^{ns}	38.66	18	1.12	16.91	2	6.78*	11.34	22	1.80	30.08	62	2.27	2.70
Tanzania	Arusha	20	18.25**	88.66	18	1.26	5.53	2	1.33	0.65	22	0.96	5.16	62	1.66	1.42

*P ≤ 0.05, ** P ≤ 0.01, ns= non-significant, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.8 **Grain yield** performance (t ha^{-1}) of 21 OPVs tested across 11 environments of eastern Africa, in 2006

	Environments											
Variety	Gan	Mel	Bun	Emb	Kib1	Kib2	Kak	Rub	Nya	Aru	Nam	Mean
V1	1.41	5.85	3.66	4.48	5.31	5.20	0.97	3.73	4.77	2.40	4.57	3.85
V2	1.87	5.87	3.17	4.49	6.44	6.40	0.46	3.01	4.44	2.94	4.43	3.96
V3	2.45	6.73	3.53	4.01	5.39	5.55	0.55	3.87	4.64	2.19	4.48	3.94
V4	1.64	5.95	3.75	4.02	6.79	5.64	0.67	3.75	5.71	2.43	4.19	4.05
V5	1.85	5.69	3.69	3.62	5.34	6.23	0.69	3.72	4.91	2.61	4.33	3.88
V6	2.02	6.55	3.68	3.61	5.99	6.49	0.74	4.27	5.01	2.99	5.14	4.23
V7	2.84	6.18	3.20	4.72	5.88	5.56	0.66	3.65	5.36	3.63	4.46	4.19
V8	1.63	5.83	4.19	4.85	5.30	5.88	0.49	4.08	4.71	2.71	4.55	4.02
V9	1.82	6.00	2.82	4.60	5.56	5.98	0.33	4.20	5.14	3.07	4.85	4.03
V10	2.11	6.96	3.57	4.09	6.74	5.13	0.71	4.41	5.61	2.35	4.82	4.23
V11	1.67	5.95	3.39	4.36	6.85	5.95	0.98	4.56	4.91	2.55	4.00	4.11
V12	2.14	5.46	3.15	4.08	7.06	6.04	0.76	3.61	5.64	2.50	4.58	4.09
V13	2.15	6.80	3.87	4.54	5.79	6.23	0.59	5.38	5.28	2.66	4.55	4.35
V14	2.72	6.49	3.30	4.06	5.54	5.83	0.63	3.99	4.65	2.38	4.64	4.02
V15	2.57	6.67	4.43	4.21	5.77	5.50	1.00	4.76	5.07	3.02	4.57	4.32
V16	2.21	6.42	3.48	4.22	5.50	5.53	0.84	3.98	4.48	2.71	5.21	4.05
V17	2.30	5.85	3.43	3.79	5.83	5.56	0.55	4.35	5.03	3.04	4.60	4.03
V18	1.97	6.23	4.01	4.98	5.59	5.41	0.61	3.85	5.51	2.62	4.11	4.08
V19	2.80	6.58	3.80	5.25	7.14	5.54	0.76	3.79	5.28	3.13	4.54	4.42
V20	0.72	4.24	3.04	2.47	3.42	4.87	0.28	2.91	3.73	1.39	1.99	2.64
V21	1.91	8.44	4.14	4.85	2.66	5.73	2.00	5.39	6.37	3.85	4.61	4.54
Mean	**2.04**	**6.22**	**3.58**	**4.25**	**5.71**	**5.73**	**0.73**	**4.06**	**5.06**	**2.72**	**4.44**	**4.05**
Max	**2.84**	**8.44**	**4.43**	**5.25**	**7.14**	**6.49**	**2.00**	**5.39**	**6.37**	**3.85**	**5.21**	**4.84**
Min	**0.72**	**4.24**	**2.82**	**2.47**	**2.66**	**4.87**	**0.28**	**2.91**	**3.73**	**1.39**	**1.99**	**2.93**
$LSD_{0.05}$	**0.58**	**0.96**	**0.68**	**0.83**	**0.82**	**0.76**	**0.46**	**1.17**	**0.99**	**0.62**	**0.94**	**0.80**
CV %	**16.96**	**9.15**	**11.15**	**11.51**	**8.47**	**7.88**	**37.47**	**17.01**	**11.62**	**13.42**	**12.49**	**14.28**
R^2	**0.91**	**0.86**	**0.82**	**0.84**	**0.95**	**0.77**	**0.84**	**0.81**	**0.79**	**0.88**	**0.87**	**0.85**

Table 5.9 **Grain yield** performance (t ha^{-1}) of 21 OPVs tested across six environments of eastern Africa, in 2007

	Environments						
Variety	Edo	Emb	Kib	Wad	Sia	Aru	Mean
V1	2.24	8.11	7.53	2.59	2.27	2.37	4.19
V2	2.44	8.77	8.94	3.16	3.12	3.70	5.02
V3	2.19	7.23	9.17	2.32	2.15	3.38	4.41
V4	2.78	7.90	8.24	2.69	2.57	2.48	4.44
V5	2.32	8.30	8.24	3.11	1.90	3.09	4.49
V6	2.36	8.45	7.71	2.84	2.38	2.98	4.45
V7	2.02	8.05	8.04	3.17	1.80	3.47	4.42
V8	2.68	8.95	9.28	3.68	2.86	4.27	5.29
V9	2.62	9.13	9.23	2.74	1.86	4.24	4.97
V10	1.76	6.83	9.05	3.08	1.88	2.49	4.18
V11	2.26	8.33	9.30	3.28	3.73	3.09	5.00
V12	2.15	6.93	9.37	2.88	1.77	2.57	4.28
V13	3.16	8.63	7.90	2.85	2.22	3.13	4.65
V14	1.92	8.51	9.04	2.90	2.45	3.66	4.75
V15	2.75	8.65	9.07	2.42	3.46	3.63	5.00
V16	1.76	7.56	9.56	2.30	2.15	3.33	4.44
V17	1.93	7.82	9.16	2.96	2.74	3.09	4.62
V18	2.18	7.63	8.97	2.16	2.23	3.10	4.38
V19	2.16	8.87	9.94	3.20	2.23	3.30	4.95
V20	1.74	6.06	5.53	2.65	1.37	2.27	3.27
V21	2.57	12.93	9.37	2.87	2.64	4.41	5.80
Mean	**2.29**	**8.27**	**8.70**	**2.85**	**2.37**	**3.24**	**4.62**
Max	**3.16**	**12.93**	**9.94**	**3.68**	**3.73**	**4.41**	**6.31**
Min	**1.74**	**6.06**	**5.53**	**2.16**	**1.37**	**2.27**	**3.19**
$LSD_{0.05}$	**0.65**	**1.17**	**0.87**	**0.67**	**0.67**	**0.98**	**0.84**
CV %	**16.83**	**8.35**	**5.91**	**13.89**	**15.88**	**17.91**	**13.13**
R^2	**0.84**	**0.94**	**0.93**	**0.83**	**0.91**	**0.86**	**0.89**

Table 5.10 Mean **days to anthesis** of 21 OPVs tested across 11 maize growing environments of ECA, in 2006

	Environments											
Variety	Gan	Mel	Bun	Emb	Kib1	Kib2	Kak	Nya	Aru	Sel	Nam	Mean
V1	54.00	63.33	60.00	59.00	62.00	59.67	65.00	68.67	79.33	82.67	51.33	64.09
V2	57.00	65.33	66.67	62.67	62.33	60.00	69.00	68.33	80.33	85.67	55.33	66.61
V3	56.00	66.00	64.67	64.67	63.00	55.33	67.67	72.33	84.33	86.67	57.67	67.12
V4	55.00	66.00	65.00	63.67	62.67	59.67	69.33	69.67	81.33	85.33	56.33	66.73
V5	54.67	64.67	62.67	60.00	61.67	61.33	66.00	70.00	85.00	85.33	52.67	65.82
V6	52.67	64.67	61.67	62.67	62.00	62.33	63.33	68.67	76.67	86.33	52.00	64.82
V7	53.67	66.00	64.33	64.00	62.00	58.67	67.00	70.00	83.67	84.67	58.00	66.55
V8	56.33	65.33	63.67	63.33	62.67	59.33	69.67	70.00	80.00	86.00	55.33	66.52
V9	57.00	66.33	65.67	63.33	62.33	60.67	69.00	68.67	84.00	87.33	56.00	67.30
V10	56.33	64.67	63.00	62.33	62.67	62.33	67.33	71.33	83.67	86.67	55.00	66.85
V11	56.00	67.00	67.33	63.33	62.67	60.00	66.33	70.67	80.33	86.33	56.67	66.97
V12	55.00	64.67	64.67	61.67	62.00	60.00	67.67	68.00	82.00	85.67	53.00	65.85
V13	55.67	64.00	60.67	63.33	62.33	60.00	68.67	70.00	84.33	84.67	56.67	66.39
V14	53.67	64.67	66.00	63.67	63.00	61.00	68.33	69.67	81.33	86.33	57.67	66.85
V15	55.00	66.33	64.67	62.00	62.33	60.00	70.00	69.67	84.00	79.00	54.00	66.09
V16	53.33	64.00	63.67	62.33	62.67	63.00	67.00	69.33	81.33	84.00	53.33	65.82
V17	56.00	65.33	65.00	63.33	62.67	61.67	69.33	70.67	79.33	86.33	56.67	66.94
V18	54.67	65.33	65.00	62.33	62.67	59.67	69.33	69.67	85.00	85.33	53.00	66.55
V19	57.67	68.00	66.00	64.67	64.33	65.00	69.67	73.67	85.67	81.67	59.67	68.73
V20	50.33	57.33	56.33	54.33	62.00	51.67	57.33	60.33	68.33	75.33	51.33	58.61
V21	58.00	70.00	58.00	64.67	53.33	60.00	75.33	72.33	88.00	84.33	57.67	67.42
Mean	**55.14**	**65.19**	**63.56**	**62.44**	**62.06**	**60.06**	**67.73**	**69.60**	**81.81**	**84.56**	**55.21**	**66.12**
Max	**58.00**	**70.00**	**67.33**	**64.67**	**64.33**	**65.00**	**75.33**	**73.67**	**88.00**	**87.33**	**59.67**	**70.30**
Min	**50.33**	**57.33**	**56.33**	**54.33**	**53.33**	**51.67**	**57.33**	**60.33**	**68.33**	**75.33**	**51.33**	**57.82**
$LSD_{0.05}$	**1.13**	**1.81**	**2.72**	**2.64**	**1.51**	**3.66**	**4.34**	**2.70**	**3.60**	**4.75**	**4.86**	**3.07**
CV %	**1.40**	**1.64**	**2.53**	**2.49**	**1.43**	**3.60**	**3.78**	**2.28**	**2.60**	**3.31**	**5.20**	**2.75**
R^2	**0.95**	**0.94**	**0.91**	**0.89**	**0.94**	**0.86**	**0.84**	**0.90**	**0.93**	**0.83**	**0.73**	**0.88**

Table 5.11 Mean **days to anthesis** of 21 OPVs tested across five environments of eastern Africa, in 2007

	Environments					
Variety	E.Downs	Embu	Kiboko	Wad Madani	Arusha	Mean
V1	79.33	64.00	53.67	48.33	72.33	63.53
V2	84.33	65.33	55.00	50.33	72.00	65.40
V3	82.33	68.33	56.33	48.00	71.67	65.33
V4	82.33	66.67	55.67	49.33	70.67	64.93
V5	82.67	63.67	54.67	50.33	70.67	64.40
V6	77.33	63.33	54.00	49.00	70.67	62.87
V7	84.67	66.67	57.00	50.00	70.33	65.73
V8	84.00	66.33	55.33	49.33	70.33	65.07
V9	83.67	67.67	57.33	48.33	70.00	65.40
V10	85.00	67.00	56.67	50.33	70.00	65.80
V11	81.67	66.67	56.33	50.33	69.67	64.93
V12	77.00	66.00	53.67	49.00	69.67	63.07
V13	80.67	65.33	54.67	50.00	69.67	64.07
V14	81.67	65.33	53.67	50.33	69.33	64.07
V15	83.33	66.00	54.67	50.67	68.33	64.60
V16	82.00	65.33	55.00	50.33	68.00	64.13
V17	80.67	66.67	55.67	49.33	67.67	64.00
V18	83.33	67.33	56.00	49.00	67.67	64.67
V19	86.33	69.33	60.67	50.67	66.67	66.73
V20	68.33	57.00	51.33	48.00	66.67	58.27
V21	75.00	69.67	54.33	49.67	61.00	61.93
Mean	**81.22**	**65.89**	**55.32**	**49.56**	**69.19**	**64.23**
Max	**86.33**	**69.67**	**60.67**	**50.67**	**72.33**	**67.94**
Min	**68.33**	**57.00**	**51.33**	**48.00**	**61.00**	**57.13**
LSD $_{0.05}$	**3.06**	**1.62**	**1.66**	**2.27**	**1.66**	**2.05**
CV %	**2.23**	**1.45**	**1.77**	**2.70**	**1.42**	**1.91**
R^2	**0.95**	**0.96**	**0.94**	**0.67**	**0.95**	**0.89**

Trial set B (2007-2008)

The results of the ANOVA for individual locations for grain yield and days to anthesis for 2007 are presented in Tables 5.12 and 5.13. Entries showed significant mean squares for grain yield (Table 5.12) and days to anthesis (Table 5.13) across environments. Furthermore entries accounted for the major proportion of the total variation in sum of squares of the environments. At Thika and Embu entries contributed 78.77% and 76.44% of the total sum of squares for grain yield, respectively (Table 5.12) while at Embu and E.Downs entries contributed 91.40% and 85.41% respectively to the variation in days to anthesis (Table 5.13).

In 2008, the entries showed significant variation in grain yield (Table 5.14) and days to anthesis (Table 5.15) at all locations except at Kimaeti, Rahad and Wad Madani where days to anthesis among the entries were not significant. Although entries at these three locations did not differ in days to anthesis results have been presented here for comparison reasons with those of other locations. Entries contributed highly to the variation at Kitale and Elgon Downs for grain yield and days to anthesis respectively (87.44% for grain yield and 91.97% for days to anthesis) (Table 5.14 and Table 5.15). Table 5.16 and Table 5.17 present results of grain yield performance and Table 5.18 and Table 5.19 present days to anthesis for the 39 varieties tested in 2007 and 2008 across ECA. Shaded cells in the tables show the top varieties for grain yield and the variety with earliest days to anthesis among the 39 varieties across the different locations. Candidate varieties out yielded the local check variety (OPV39) in nine out of the ten locations during 2007 (Table 5.16) while during 2008 the candidates were better than the local check variety (OPV39) only at four out of the ten locations for grain yield. This might be an indication of the start of the declining of yield levels of the QPM OPVs at the fourth generation (2006, 2007(two seasons) and 2008). The commercial check variety (OPV38) was the earliest variety almost at all locations during 2007 (Table 5.18) except at Kakamega (Kak) and Mbulumbulu (Mbu) where the candidate QPM variety (OPV19) was the earliest with similar days to anthesis (61 days) at both locations. In 2008 the candidate variety OPV19 was early only at Rahad (Rah) and in the other locations the commercial variety (OPV38) followed by the local check (OPV39, at Mpa and Kim) were the earliest in maturity (Table 5.19).

Table 5.12 Mean squares from analysis of variance and percentage of variance components for **grain yield** of 39 OPVs tested across ten environments of eastern Africa, in 2007

		Sources of variations													
		Entry			Block			Replications			Error			Total	
Country	Location	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Kenya	Alupe	38	10.48**	54.36	24	12.00**	39.28	1	2.97	0.40	14	3.12	5.96	77	3.79	26.71
Kenya	Bungoma	38	0.45*	60.60	24	0.31	27.54	1	0.58	2.09	14	0.19	9.77	77	0.94	15.31
Kenya	E.Downs 1	38	0.47*	55.92	24	0.45*	34.12	1	0.65	2.04	14	0.18	7.91	77	0.91	18.24
Kenya	E.Downs 2	38	0.40**	65.57	24	0.26*	26.42	1	0.47*	2.02	14	0.10	5.98	77	0.68	13.41
Kenya	Embu	38	2.74**	76.44	24	0.94	16.57	1	3.60*	2.64	14	0.42	4.35	77	1.39	7.42
Kenya	Kakamega	38	0.61**	63.92	24	0.42	27.95	1	0.02	0.06	14	0.19	8.06	77	0.87	18.83
Kenya	Thika	38	1.58**	78.77	24	0.45	14.31	1	0.56	0.73	14	0.34	6.18	77	1.25	12.66
Tanzania	Arusha	38	0.71**	58.63	24	0.61*	31.95	1	1.73**	3.75	14	0.19	5.67	77	0.93	11.80
Tanzania	Mbulumbulu	38	2.52**	57.09	24	2.58**	36.88	1	0.18	0.11	14	0.71	5.91	77	1.80	20.10
Tanzania	Selian	38	0.87*	69.88	24	0.43	21.56	1	0.16	0.34	14	0.28	8.22	77	1.13	9.42

*$P \leq 0.05$, ** $P \leq 0.01$, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.13 Mean squares from analysis of variance and percentage of variance components for **days to anthesis** of 39 OPVs tested across nine environments of eastern Africa, in 2007

		Sources of variations													
		Entry			Block			Replications			Error			Total	
Country	Location	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Kenya	Alupe	38	13.49**	77.36	24	5.24	18.97	1	0.21	0.03	14	1.72	3.63	77	2.81	2.14
Kenya	Bungoma	38	7.52**	80.90	24	1.47	10.00	1	19.50**	5.52	14	0.90	3.58	77	2.04	1.47
Kenya	E.Downs	38	22.10**	85.41	24	4.40	10.75	1	0.32	0.03	14	2.67	3.81	77	3.51	2.06
Kenya	Embu	38	12.73**	91.40	24	1.48	6.72	1	0.63	0.12	14	0.66	1.75	77	1.75	1.30
Kenya	Kakamega	38	1.57*	65.27	24	0.91	24.02	1	1.45	1.59	14	0.55	9.12	77	1.50	1.18
Kenya	Thika	38	15.34**	79.15	24	3.90	12.70	1	13.96	1.90	14	3.28	6.25	77	3.89	2.24
Tanzania	Arusha	38	15.51**	74.81	24	5.53	16.85	1	19.50*	2.47	14	3.30	5.87	77	3.90	2.43
Tanzania	Mbulumbulu	38	14.70**	73.21	24	6.44*	20.23	1	17.55*	2.30	14	2.32	4.26	77	3.27	2.37
Tanzania	Selian	38	15.29*	73.32	24	5.04	15.26	1	15.70	1.98	14	5.34	9.44	77	4.96	3.79

*$P \leq 0.05$, ** $P \leq 0.01$, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.14 Mean squares from analysis of variance and percentage of variance components for **grain yield** of 39 OPVs tested across ten environments of ECA, in 2008

		Sources of variations														
		Entry			Block			Replications			Error			Total		
Country	Location	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Burundi	Mosso	38	1.07**	71.29	24	0.48	20.15	1	1.91**	3.35	14	0.86	5.21	77	0.99	12.53
Burundi	Mparambo	38	0.92**	79.27	24	0.21	11.53	1	0.24	0.55	14	0.27	8.65	77	1.12	14.92
Ethiopia	Melkassa	38	2.13**	27.41	24	3.19**	25.85	1	135.74**	45.87	14	0.18	0.86	77	0.92	11.13
Kenya	Kimaeti	38	0.36*	51.31	24	0.19	17.40	1	6.37**	24.06	14	0.14	7.22	77	0.79	16.32
Kenya	Kitale	38	1.45**	87.44	24	0.19	9.21	1	0.01	0.02	14	0.12	3.33	77	0.74	18.18
Sudan	Rahad	38	0.64*	45.23	24	1.08**	48.52	1	0.59	1.10	14	0.19	5.15	77	0.95	18.63
Sudan	W. Madani	38	0.52**	65.55	24	0.31*	24.46	1	1.42**	4.67	14	0.12	5.32	77	0.73	15.97
Tanzania	SARI	38	0.60*	40.98	24	0.68*	29.58	1	13.55**	24.38	14	0.20	5.05	77	0.96	16.40
Tanzania	Weruweru	38	0.69**	46.17	24	1.12**	46.99	1	1.52**	2.67	14	0.17	4.17	77	0.88	11.92

*P ≤ 0.05, ** P ≤ 0.01, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.15 Mean squares from analysis of variance and percentage of variance components for **days to anthesis** of 39 OPVs tested across 11 environments of ECA, in 2008

Country	Location	Sources of variations													
		Entry			Block			Replications			Error			Total		
		DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	MS	%SS	DF	LSD	CV%
Burundi	Mosso	38	21.55**	91.05	24	2.50*	6.68	1	6.78*	0.75	14	0.97	1.52	77	2.12	1.67
Burundi	Mparambo	38	6.72**	82.67	24	1.27	9.85	1	12.32**	4.00	14	0.77	3.49	77	1.88	1.73
Ethiopia	Melkassa	38	7.10**	46.37	24	5.93*	24.47	1	144.05**	24.76	14	1.83	4.39	77	2.90	1.97
Kenya	E. Downs	38	14.31**	91.97	24	21.10	3.57	1	1.04	0.18	14	1.81	4.29	77	2.89	1.87
Kenya	Kakamega	38	16.38**	90.54	24	2.22*	7.76	1	2.51	0.37	14	0.65	1.33	77	1.73	1.15
Kenya	Kimaeti	38	4.06	43.53	24	3.87	26.16	1	64.63**	18.20	14	3.07	12.11	77	3.76	2.85
Kenya	Kitale	38	14.17**	86.09	24	2.63	10.07	1	0.46	0.07	14	1.68	3.76	77	2.78	1.85
Sudan	Rahad	38	4.24	50.26	24	3.93	29.44	1	21.55*	6.72	14	3.11	13.57	77	3.78	3.07
Sudan	W. Madani	38	5.89	54.08	24	4.24	24.59	1	46.15**	11.15	14	3.00	10.17	77	3.72	3.16
Tanzania	SARI	38	16.57**	78.64	24	5.00*	14.97	1	22.62**	2.82	14	2.04	3.57	77	3.06	2.11

*P ≤ 0.05, ** P ≤ 0.01, DF= Degrees of freedom, MS=mean square, %SS=percent sum of squares, LSD=Least Significant Difference, CV= Coefficient of Variation

Table 5.16 **Grain yield** performance (t ha^{-1}) of 39 OPVs tested across ten environments of ECA, in 2007

	Environments										
Variety	Alu	Bun	Edo1	Edo2	Emb	Kak	Thi	Aru	Mbu	Sel	Mean
OPV1	4.97	3.32	2.11	1.97	7.99	2.51	5.93	4.22	2.72	4.96	4.07
OPV2	6.91	2.56	3.30	2.89	9.42	2.04	5.39	4.40	5.50	5.40	4.78
OPV3	8.44	2.59	1.85	2.24	8.48	2.00	4.07	3.58	4.07	6.02	4.33
OPV4	8.84	3.24	2.25	2.64	8.81	3.29	4.36	3.41	4.40	4.74	4.60
OPV5	9.17	3.36	2.20	2.09	6.88	1.81	4.23	3.31	2.59	5.50	4.11
OPV6	3.24	2.73	1.92	1.78	8.57	2.66	3.57	3.76	3.29	5.08	3.66
OPV7	6.32	2.80	2.75	2.51	9.89	2.28	6.01	3.75	4.25	6.11	4.67
OPV8	8.55	2.97	3.67	3.41	9.52	2.34	3.62	3.45	5.03	4.98	4.75
OPV9	3.54	2.08	2.25	1.32	8.01	1.84	4.00	3.95	3.00	4.79	3.48
OPV10	4.59	2.29	1.69	1.97	8.99	2.47	4.96	4.64	4.95	5.04	4.16
OPV11	7.05	2.24	2.84	2.54	9.88	2.30	5.98	3.52	4.58	5.57	4.65
OPV12	7.32	3.23	1.89	2.28	8.75	2.70	5.73	2.89	4.12	5.40	4.43
OPV13	7.21	3.22	2.34	2.43	9.32	2.42	5.23	3.83	3.25	6.03	4.53
OPV14	5.39	2.31	2.22	2.23	9.57	2.37	4.89	3.85	5.73	6.03	4.46
OPV15	3.87	2.99	3.07	2.73	9.80	2.64	4.39	4.52	3.26	6.71	4.40
OPV16	3.76	2.49	2.05	2.99	8.29	2.03	5.15	3.98	4.66	6.21	4.16
OPV17	7.42	3.11	1.93	2.42	7.89	2.68	5.23	4.30	4.25	5.97	4.52
OPV18	5.28	2.39	2.19	1.87	8.83	2.13	4.51	4.09	3.73	6.10	4.11
OPV19	7.22	3.07	1.94	2.34	8.50	2.03	4.57	3.86	4.56	6.26	4.43
OPV20	2.49	2.81	2.08	2.64	8.32	2.46	5.46	4.23	3.30	5.82	3.96
OPV21	3.71	3.45	2.09	1.75	8.82	2.23	3.62	3.21	4.43	5.95	3.93
OPV22	6.45	3.04	1.76	2.54	9.28	3.30	4.63	3.73	2.52	5.12	4.24
OPV23	7.43	3.28	2.46	2.90	7.81	3.19	3.55	3.66	3.70	6.40	4.44
OPV24	5.82	2.39	1.83	2.08	9.11	2.27	4.34	4.04	3.73	5.73	4.13
OPV25	3.96	2.35	3.30	2.21	9.09	3.06	3.81	2.94	3.41	5.77	3.99
OPV26	11.98	3.73	2.83	2.99	9.36	2.31	3.99	3.89	5.65	5.58	5.23
OPV27	9.22	3.08	2.75	2.17	8.93	2.18	4.07	4.05	2.28	5.78	4.45
OPV28	7.29	2.76	1.98	2.03	8.34	2.73	4.91	3.80	7.07	5.21	4.61
OPV29	6.08	3.73	2.73	2.28	8.37	2.16	5.58	3.13	6.03	5.75	4.58
OPV30	9.64	3.03	1.82	2.63	8.71	2.13	5.05	3.88	5.11	6.07	4.81
OPV31	11.11	3.66	1.78	3.05	9.10	2.83	5.26	3.81	5.48	5.37	5.14
OPV32	5.88	2.25	2.17	2.17	7.96	1.97	3.76	3.15	4.70	5.97	4.00
OPV33	4.24	3.50	2.37	2.30	9.38	2.78	4.21	2.83	4.94	5.67	4.22
OPV34	6.98	2.93	1.97	2.54	8.56	2.94	3.81	4.04	4.86	5.76	4.44
OPV35	6.53	1.99	2.22	1.74	9.02	2.04	3.49	3.47	4.35	5.83	4.07
OPV36	5.87	2.59	2.59	2.14	8.66	2.37	3.95	3.70	3.98	6.26	4.21
OPV37	9.61	2.65	2.41	2.48	9.01	2.35	6.19	2.87	4.88	6.35	4.88
OPV38	4.55	2.43	2.01	1.52	4.28	1.82	2.10	1.28	1.75	4.39	2.61
OPV39	10.11	3.05	2.96	2.88	12.88	NA	5.38	3.82	3.38	3.09	5.28
Mean	**6.62**	**2.86**	**2.32**	**2.35**	**8.78**	**2.35**	**4.59**	**3.66**	**4.19**	**5.61**	**4.33**
Max	**11.98**	**3.73**	**3.67**	**3.41**	**12.88**	**3.30**	**6.19**	**4.64**	**7.07**	**6.71**	**6.36**
Min	**2.49**	**1.99**	**1.69**	**1.32**	**4.28**	**1.81**	**2.10**	**1.28**	**1.75**	**3.09**	**2.18**
$LSD_{0.05}$	**3.79**	**0.94**	**0.91**	**0.68**	**1.39**	**0.87**	**1.25**	**0.93**	**1.80**	**1.13**	**1.37**
CV %	**26.71**	**15.31**	**18.24**	**13.41**	**7.42**	**18.83**	**12.66**	**11.80**	**20.10**	**9.42**	**15.39**
R^2	**0.94**	**0.90**	**0.92**	**0.94**	**0.97**	**0.92**	**0.94**	**0.94**	**0.94**	**0.92**	**0.93**

Table 5.17 **Grain yield** performance (t ha^{-1}) of 39 OPVs tested across ten environments of ECA, in 2008

	Environments										
Variety	Mos	Mpa	Mel	Kak	Kim	Kit	Rah	Wad	SARI	Wer	Mean
OPV1	3.45	3.67	3.42	1.03	2.31	2.39	2.55	2.43	2.20	3.14	2.55
OPV2	3.71	3.74	3.19	0.83	2.75	2.32	3.31	2.40	3.04	3.84	2.99
OPV3	3.34	3.57	4.27	0.68	2.46	1.41	2.55	1.45	2.15	2.09	2.43
OPV4	3.45	3.20	2.67	0.83	1.87	1.73	2.60	3.46	3.14	3.33	2.74
OPV5	3.29	2.77	2.33	1.14	2.78	2.44	2.88	1.86	3.50	3.23	2.71
OPV6	3.62	3.83	3.46	1.08	2.13	1.94	2.38	2.50	3.15	2.93	2.70
OPV7	3.13	2.95	3.96	0.83	1.73	2.24	2.10	2.21	2.56	3.51	2.51
OPV8	4.21	3.81	4.13	1.18	1.94	1.97	2.33	1.97	2.64	3.55	2.66
OPV9	2.13	3.29	3.92	0.32	2.09	1.19	2.81	2.09	2.19	3.55	2.23
OPV10	2.94	3.09	2.87	0.99	2.07	1.38	1.60	2.68	3.36	3.11	2.40
OPV11	4.12	4.48	2.94	1.22	2.38	1.68	2.98	2.08	3.21	4.10	2.93
OPV12	2.68	3.05	4.44	0.49	2.15	0.89	1.49	2.41	2.50	4.37	2.42
OPV13	4.00	4.55	2.98	1.52	3.37	2.42	1.81	1.96	2.04	4.12	2.92
OPV14	3.55	4.09	4.28	1.03	2.20	2.19	2.90	1.98	2.94	3.25	2.89
OPV15	4.11	3.68	4.17	1.00	1.98	1.35	2.38	2.28	2.35	3.50	2.77
OPV16	3.34	2.87	3.41	0.90	1.67	2.42	1.54	2.22	2.86	3.69	2.50
OPV17	4.54	3.65	4.27	0.91	2.07	1.74	2.86	1.84	2.35	2.65	2.67
OPV18	4.12	3.76	3.87	1.01	1.75	1.24	2.18	2.44	2.35	3.93	2.73
OPV19	3.71	4.12	3.48	1.00	3.31	2.21	2.17	2.31	3.11	3.54	3.01
OPV20	2.42	3.47	2.74	0.82	2.23	1.45	2.73	2.43	3.04	4.00	2.57
OPV21	3.44	3.62	3.87	0.40	2.36	1.40	1.62	2.71	2.45	4.27	2.57
OPV22	3.39	2.93	3.42	1.31	2.73	2.33	1.86	1.93	3.04	2.74	2.73
OPV23	3.52	2.98	3.47	1.33	1.89	2.93	2.83	1.71	3.77	2.82	2.62
OPV24	3.59	2.89	3.12	0.76	1.67	1.93	2.10	2.47	2.70	4.19	2.78
OPV25	4.43	4.28	2.86	0.92	2.17	2.57	2.94	2.35	3.43	4.14	3.11
OPV26	3.41	2.33	3.68	1.09	1.99	2.28	2.88	1.86	2.76	3.34	2.69
OPV27	3.28	3.07	4.63	0.77	1.96	1.67	2.10	1.48	2.65	4.08	2.64
OPV28	3.48	3.36	4.14	0.62	1.86	1.54	3.40	1.86	3.83	3.60	2.78
OPV29	3.01	3.79	3.18	1.51	2.84	1.39	2.21	1.77	2.26	4.18	2.60
OPV30	3.53	3.16	2.98	0.99	2.14	1.30	2.19	2.32	2.65	2.54	2.35
OPV31	4.45	3.55	3.29	0.92	2.58	1.59	2.64	2.22	2.23	3.99	2.86
OPV32	3.33	3.03	3.41	0.64	2.22	1.50	3.24	2.05	2.79	4.03	2.95
OPV33	4.23	4.10	4.56	1.44	2.37	1.39	2.05	1.84	2.56	2.80	2.69
OPV34	3.53	3.47	3.63	0.55	2.07	2.18	2.38	1.67	2.39	3.04	2.62
OPV35	3.47	2.67	3.96	0.83	2.24	1.15	2.30	2.18	2.91	3.25	2.54
OPV36	3.12	3.17	2.89	0.71	2.39	1.30	2.95	2.20	1.83	3.73	2.37
OPV37	3.21	3.87	3.72	0.63	2.33	1.93	1.52	1.93	1.57	3.59	2.54
OPV38	2.52	2.20	1.18	1.07	2.44	1.44	0.90	0.74	2.10	3.02	1.84
OPV39	6.65	6.23	5.27	2.93	2.84	5.48	2.64	2.98	3.90	2.15	4.16
Mean	**3.58**	**3.50**	**3.54**	**0.98**	**2.26**	**1.89**	**2.38**	**2.14**	**2.73**	**3.46**	**2.69**
Max	**6.65**	**6.23**	**5.27**	**2.93**	**3.41**	**5.48**	**3.40**	**3.46**	**3.90**	**4.37**	**4.65**
Min	**2.13**	**2.20**	**1.75**	**0.32**	**1.56**	**0.89**	**0.90**	**0.74**	**1.57**	**2.09**	**1.43**
LSD $_{0.05}$	**0.99**	**1.12**	**1.02**	**0.63**	**0.79**	**0.74**	**0.95**	**0.73**	**0.90**	**0.88**	**0.87**
CV %	**12.53**	**14.90**	**11.13**	**29.95**	**16.32**	**18.18**	**18.63**	**15.97**	**16.00**	**11.92**	**16.55**
R^2	**0.95**	**0.91**	**0.99**	**0.93**	**0.93**	**0.97**	**0.95**	**0.95**	**0.95**	**0.96**	**0.95**

Table 5.18 Mean **days to anthesis** of 39 OPVs tested across nine environments of ECA, in 2007

Variety	Environments									Mean
	Alu	Bun	Edo 1	Emb	Kak	Thi	Aru	Mbu	Sel	
OPV1	58.50	61.50	74.00	60.50	62.00	75.50	71.50	63.50	57.50	64.94
OPV2	61.00	64.50	80.00	63.50	62.50	82.00	79.00	63.50	60.00	68.44
OPV3	60.50	65.50	81.00	64.00	64.00	84.50	76.50	67.00	64.50	69.72
OPV4	60.50	67.00	81.50	63.00	64.00	83.00	75.00	61.50	64.50	68.89
OPV5	59.50	61.50	78.00	62.00	63.00	79.50	74.00	62.50	59.50	66.61
OPV6	59.50	64.00	75.50	57.50	61.00	76.00	72.00	62.00	57.00	64.94
OPV7	60.50	64.00	78.50	62.00	63.00	79.50	74.50	63.00	58.50	67.06
OPV8	61.50	67.50	79.00	63.50	64.00	84.00	77.50	67.00	65.00	69.89
OPV9	64.50	66.00	80.50	66.00	63.50	84.00	79.00	68.00	66.50	70.89
OPV10	63.50	65.50	82.50	63.50	62.00	81.50	78.00	65.00	63.50	69.44
OPV11	62.00	68.00	84.00	63.50	64.00	82.50	78.00	66.00	60.50	69.83
OPV12	61.00	65.00	81.50	63.50	64.00	83.50	77.00	65.00	61.50	69.11
OPV13	60.00	65.00	82.50	63.50	63.50	82.50	78.00	64.50	59.50	68.78
OPV14	63.50	65.50	80.00	63.00	62.00	81.00	74.00	63.50	60.00	68.06
OPV15	65.00	65.50	81.00	63.50	64.00	81.50	74.50	66.50	59.50	69.00
OPV16	63.50	65.50	79.50	63.50	64.00	83.50	74.50	63.00	61.50	68.72
OPV17	61.50	65.00	81.00	63.50	64.00	84.00	74.50	65.00	63.00	69.06
OPV18	63.00	66.00	81.00	64.00	63.50	83.00	80.00	65.50	64.50	70.06
OPV19	59.00	62.50	76.50	59.00	61.00	77.50	72.00	61.00	57.50	65.11
OPV20	64.50	64.50	81.00	61.50	62.50	80.50	74.50	65.00	61.50	68.39
OPV21	64.50	63.00	83.00	62.00	64.00	83.50	76.50	63.00	61.50	69.00
OPV22	61.00	65.00	82.00	62.00	63.00	82.00	74.50	66.50	64.50	68.94
OPV23	59.00	63.00	78.00	62.00	63.00	79.50	72.50	62.50	58.50	66.44
OPV24	58.00	62.50	79.00	60.00	63.00	77.50	71.00	61.50	60.00	65.83
OPV25	63.00	64.00	80.00	62.00	63.00	82.00	73.50	63.50	60.00	67.89
OPV26	58.50	64.00	80.00	63.00	62.50	81.50	74.00	62.00	64.00	67.72
OPV27	61.00	65.50	80.50	65.50	63.50	82.50	77.50	67.50	62.50	69.56
OPV28	61.50	65.00	82.00	63.50	64.00	82.00	79.00	61.50	60.00	68.72
OPV29	61.00	65.50	79.00	63.50	64.00	81.50	74.00	63.50	61.50	68.17
OPV30	57.50	62.50	77.50	61.50	61.67	79.50	73.50	62.00	57.00	65.85
OPV31	58.50	64.00	81.00	61.00	64.00	77.50	72.50	62.00	59.50	66.67
OPV32	61.00	65.50	78.00	62.00	63.00	77.00	72.00	63.00	58.50	66.67
OPV33	61.00	64.50	80.50	62.50	63.00	81.00	75.00	64.00	60.50	68.00
OPV34	60.00	63.00	80.00	63.00	62.50	82.50	74.00	63.50	59.00	67.50
OPV35	60.50	64.50	78.50	60.50	63.50	81.00	72.50	62.00	59.00	66.89
OPV36	60.50	64.00	79.00	62.50	63.00	80.50	74.00	64.00	61.50	67.67
OPV37	63.00	67.00	83.00	65.00	64.00	85.50	79.00	66.50	66.50	71.06
OPV38	55.00	57.00	64.50	52.00	62.00	74.00	66.50	62.00	54.50	60.83
OPV39	70.00	65.50	74.50	68.00	63.50	76.00	75.00	76.00	62.50	70.11
Mean	**61.21**	**64.47**	**79.45**	**62.45**	**63.12**	**80.91**	**74.88**	**64.22**	**60.94**	**67.96**
Max	**70.00**	**68.00**	**84.00**	**68.00**	**64.00**	**85.50**	**80.00**	**76.00**	**66.50**	**73.56**
Min	**55.00**	**57.00**	**64.00**	**52.00**	**61.00**	**74.00**	**66.50**	**61.00**	**54.50**	**60.56**
LSD $_{0.05}$	**2.81**	**2.04**	**3.51**	**1.75**	**1.50**	**3.89**	**3.90**	**3.27**	**4.96**	**3.07**
CV %	**2.14**	**1.47**	**2.06**	**1.30**	**1.18**	**2.24**	**2.43**	**2.37**	**3.79**	**2.11**
R^2	**0.96**	**0.96**	**0.96**	**0.98**	**0.91**	**0.94**	**0.94**	**0.96**	**0.91**	**0.95**

Table 5.19 Mean **days to anthesis** of 39 OPVs tested across 11 environments of ECA, in 2008

	Environments											
Variety	Mos	Mpa	Mel	Edo	Kak	Kim	Kit	Rah	Wad	Sar	Wer	Mean
OPV1	56.50	59.50	67.50	68.00	68.50	61.00	69.00	55.00	51.50	65.00	55.50	61.55
OPV2	58.50	54.00	67.00	71.50	69.00	61.50	69.00	57.50	54.50	65.00	58.00	62.32
OPV3	62.00	51.50	71.50	73.00	69.00	60.50	69.50	58.50	59.00	68.50	60.00	63.91
OPV4	59.50	51.50	69.50	74.50	73.00	64.00	71.00	58.00	54.50	67.50	60.00	63.91
OPV5	59.00	51.50	68.00	71.50	70.00	61.50	69.50	58.50	55.50	66.50	57.50	62.64
OPV6	53.00	51.50	67.00	70.50	69.00	58.50	70.00	58.50	55.50	66.00	56.50	61.45
OPV7	59.50	51.50	68.00	73.00	70.50	62.50	70.00	58.00	57.00	67.00	56.00	63.00
OPV8	60.00	51.50	70.00	75.00	73.00	61.50	71.00	58.50	58.50	70.00	58.50	64.32
OPV9	62.50	51.00	73.50	76.00	73.00	64.00	72.50	59.50	54.50	70.50	61.00	65.27
OPV10	58.00	51.00	65.00	72.00	70.00	60.50	71.00	56.50	54.50	65.00	60.00	62.14
OPV11	62.50	51.00	72.50	74.00	69.00	62.50	73.00	57.50	57.00	69.50	58.50	64.27
OPV12	62.50	51.00	69.50	75.00	74.50	62.00	73.00	58.50	53.50	69.50	59.00	64.36
OPV13	59.50	50.50	70.00	74.00	69.00	61.50	70.50	56.50	54.50	68.50	58.50	63.00
OPV14	58.00	50.50	69.00	73.00	71.00	61.00	70.50	59.00	55.00	70.50	59.00	63.32
OPV15	58.00	50.50	69.50	74.50	71.00	61.00	71.50	58.50	55.00	67.00	61.00	63.41
OPV16	58.50	50.50	67.50	73.50	71.00	63.00	70.00	55.50	53.00	67.50	58.00	62.55
OPV17	61.50	50.50	71.50	73.50	72.00	62.50	70.00	59.00	54.50	68.00	58.50	63.77
OPV18	62.00	50.50	69.00	72.50	72.00	61.00	70.50	58.00	56.00	69.00	58.50	63.55
OPV19	57.00	50.50	66.50	70.50	69.00	60.00	68.50	54.50	53.00	66.00	55.00	60.95
OPV20	60.00	50.50	69.00	71.50	69.00	63.00	69.50	59.50	55.50	67.00	55.00	62.68
OPV21	60.50	50.50	71.50	74.00	71.00	62.50	69.50	58.50	55.00	70.00	57.50	63.68
OPV22	58.50	50.00	68.50	73.00	72.00	62.00	70.00	57.50	54.50	68.00	61.00	63.18
OPV23	58.00	50.00	68.00	70.50	69.00	62.50	69.50	54.50	52.50	64.50	56.50	61.41
OPV24	57.00	50.00	67.50	69.00	66.50	60.00	69.00	59.50	54.50	65.00	55.00	61.18
OPV25	58.00	50.00	68.50	72.50	71.00	61.00	70.00	56.00	55.50	66.00	56.00	62.23
OPV26	61.50	50.00	68.50	73.00	73.00	61.50	69.50	58.00	56.00	69.50	61.00	63.77
OPV27	62.00	50.00	69.50	75.00	72.00	61.50	73.00	58.00	55.50	70.00	60.00	64.23
OPV28	57.00	50.00	68.00	73.50	72.00	61.50	70.00	56.00	55.50	64.50	58.50	62.41
OPV29	61.00	50.00	70.00	74.00	71.00	63.00	69.50	56.50	56.50	69.50	59.00	63.64
OPV30	57.50	50.00	68.00	69.00	69.00	61.50	69.00	56.50	55.50	67.00	57.50	61.86
OPV31	57.00	50.00	69.50	70.50	72.00	62.50	69.00	57.00	55.50	68.50	56.00	62.50
OPV32	58.00	50.00	68.00	72.50	72.00	61.50	69.00	56.00	53.50	64.50	59.00	62.18
OPV33	58.50	50.00	69.50	71.50	69.00	61.00	70.00	57.00	54.00	68.50	61.00	62.73
OPV34	57.50	49.50	66.00	71.50	70.00	61.00	69.00	57.50	57.00	68.00	58.00	62.27
OPV35	57.50	49.50	67.00	72.00	69.00	61.50	69.00	57.50	55.00	67.00	58.00	62.09
OPV36	60.00	49.00	69.50	71.50	71.00	59.50	70.00	57.00	56.50	69.00	57.00	62.73
OPV37	62.00	49.00	69.00	75.00	72.00	63.00	73.00	60.00	56.00	71.00	61.00	64.64
OPV38	49.00	49.00	64.00	61.50	57.50	58.00	59.50	55.00	51.00	58.50	50.00	55.73
OPV39	71.00	46.50	68.50	67.00	76.50	57.50	80.00	55.50	51.50	77.50	67.00	65.32
Mean	**59.22**	**50.60**	**68.72**	**72.14**	**70.46**	**61.42**	**70.18**	**57.40**	**54.95**	**67.69**	**58.28**	**62.82**
Max	**71.00**	**59.50**	**73.50**	**76.00**	**74.50**	**64.00**	**80.00**	**60.00**	**59.00**	**77.50**	**67.00**	**69.27**
Min	**49.00**	**46.50**	**64.00**	**61.50**	**57.50**	**57.50**	**59.00**	**54.50**	**51.00**	**58.50**	**50.00**	**55.36**
LSD $_{0.05}$	**2.12**	**1.88**	**2.90**	**2.89**	**1.73**	**3.76**	**2.78**	**3.78**	**3.72**	**3.06**	**2.42**	**2.82**
CV %	**1.67**	**1.73**	**1.97**	**1.87**	**1.15**	**2.85**	**1.85**	**3.07**	**3.16**	**2.11**	**1.94**	**2.12**
R^2	**0.98**	**0.97**	**0.96**	**0.96**	**0.99**	**0.88**	**0.96**	**0.86**	**0.89**	**0.96**	**0.98**	**0.94**

Combined analysis for trial set A (2006-2007)

The results of the combined ANOVA for the individual years 2006 and 2007 show that entries and the test environments as well as the interaction between the two were highly significant ($P \leq 0.01$) for both grain yield and days to anthesis. The contribution of the environment to variation in both characteristics was high during the two years (Tables 5.20 and 5.21).

The combined ANOVA across years and locations for entries and the test environments were highly significant ($P \leq 0.01$) for both grain yield (Table 5.22) and days to anthesis (Table 5.23). However, the effect of years on days to anthesis was not significant while the effect on grain yield was highly significant ($P \leq 0.01$). The entry x year and entry x environment interactions were significant for grain yield but entry x year interaction was not significant for days to anthesis (Table 5.23).

In Tables 5. 24 and 5. 25 are presented the yield performance and rankings of 20 varieties as well as the days to anthesis across locations during 2006-2007. Candidate variety (V19) was the number one variety in terms of grain yield (4.61 t ha^{-1}) followed by V15 (4.56 t ha^{-1}) and V8 (4.47 t ha^{-1}). The candidate varieties were superior in grain yield than the commercial check variety Katumani (V20) in all the environments which yielded 2.75 t ha^{-1} which is 40.34% less than that of the candidate V19 (Table 5. 24).

The commercial variety Katumani (V20) was the earliest variety among the entries, with 57 days to anthesis. The candidate variety V19 was the latest flowering with 68 days to anthesis. The result of this study confirmed the earliness of the commercial variety, Katumani (V20) for its male flowering as well as maturity as compared to all the candidate varieties and the local checks in the 20 environments of ECA during 2006-2007.

Table 5.20 Combined analyses of variance for **grain yield** of 20 OPVs tested across the different environments of ECA, in 2006 and 2007

Years	Sources	DF	MS	%SS
2006	Entry	19	4.26**	3.86
	Environments (Env)	10	174.40**	83.24
	Replication	2	0.41	0.04
	Block	18	0.51**	0.44
	Rep(Env)	20	1.76**	1.68
	Block (Rep x Env)	180	0.60**	5.12
	Entry x Env	190	0.36**	3.24
	Error	220	0.23	2.38
	R-square (%)	98		
	Mean yield (t ha^{-1})	4.03		
	LSD	0.23		
	CV %	11.83		
2007	Entry	19	4.29**	2.76
	Environments (Env)	5	520.49**	88.27
	Replication	2	4.50**	0.31
	Block	18	0.92**	0.56
	Rep(Env)	10	4.66**	1.58
	Block (Rep x Env)	90	1.01**	3.06
	Entry x Env	95	0.70**	2.25
	Error	657	0.30	1.22
	R-square (%)	99		
	Mean yield (t ha^{-1})	4.54		
	LSD	0.36		
	CV %	12.05		

** $P \leq 0.01$

Table 5.21 Combined analyses of variance for **days to anthesis** of 20 OPVs tested across the different maize growing environments of ECA, in 2006 and 2007

Years	Sources		DF	MS	%SS
2006	Entry		19	109.06**	0.79
	Environments (Env)		10	25660.66**	97.93
	Replication		2	0.61	0.01
	Block		18	7.36**	0.05
	Rep(Env)		20	10.06**	0.08
	Block (Rep x Env)		180	6.82**	0.47
	Entry x Env		190	6.19**	0.45
	Error		220	2.73	0.23
	R-square (%)	100			
	Mean AD (Days)	58.37			
	LSD	0.80			
	CV %	2.83			
2007	Entry		19	75.08**	6.13
	Environments (Env)		3	6973.97**	89.86
	Replication		2	2.11	0.02
	Block		18	4.55**	0.35
	Rep (Env)		6	35.49**	0.91
	Block (Rep x Env)		54	4.80**	1.11
	Entry x Env		57	4.00**	0.98
	Error		80	1.86	0.64
	R-square (%)	99			
	Mean AD (Days)	67.91			
	LSD	1.11			
	CV %	2.00			

** $P \leq 0.01$

Table 5.22 Combined analyses of variance for **grain yield** of 20 OPVs tested across 17 environments of ECA, during 2006-2007

Years	Sources	DF	MS	%SS
2006-2007	Entry	19	7.33**	2.73
	Environments (Env)	16	271.65**	85.14
	Year	1	61.81**	1.21
	Replication	2	1.91**	0.08
	Block	18	0.66**	0.23
	Rep (Env)	32	2.75**	1.72
	Block (Rep x Env)	288	0.77**	4.35
	Entry x Env	304	1.21**	2.63
	Entry x year	19	0.62**	0.23
	Error	320	0.27	1.68
	R-square(%)	98		
	Mean yield (t ha^{-1})	4.21		
	LSD	0.20		
	CV %	11.94		

** $P \leq 0.01$

Table 5.23 Combined analyses of variance for **days to anthesis** of 20 OPVs tested across 15 environments of ECA, during 2006-2007

Years	Sources	DF	MS	%SS
2006-2007	Entry	19	181.17**	4.49
	Environments (Env)	14	4917.03**	89.71
	Year	1	0.20	0.00
	Replication	2	0.39	0.00
	Block	18	6.87**	0.16
	Rep (Env)	28	15.50**	0.57
	Block (Rep x Env)	252	6.37**	2.10
	Entry x Env	266	5.40**	1.87
	Entry x year	19	3.04	0.07
	Error	280	2.81	1.03
	R-square(%)	99		
	Mean AD (Days)	64.22		
	LSD	0.67		
	CV %	2.52		

** $P \leq 0.01$

Table 5.24 **Grain yield** performance (t ha^{-1}) and the rankings of 20 OPVs tested across the different environments of ECA during 2006-2007

	Trial years					
	2006		2007		2006-2007	
Rank	Entry	Yield	Entry	Yield	Entry	Yield
1	19	4.42	8	5.29	19	4.61
2	13	4.35	11	5.00	15	4.56
3	15	4.32	15	5.00	8	4.47
4	6	4.23	9	4.97	13	4.45
5	10	4.23	2	4.96	11	4.42
6	7	4.19	19	4.95	9	4.37
7	11	4.11	14	4.75	2	4.31
8	12	4.09	13	4.65	6	4.31
9	18	4.08	17	4.62	14	4.28
10	16	4.05	5	4.49	7	4.28
11	4	4.05	6	4.45	17	4.24
12	9	4.03	16	4.44	10	4.21
13	17	4.03	4	4.44	16	4.19
14	8	4.02	7	4.42	4	4.19
15	14	4.02	3	4.41	18	4.19
16	2	3.96	18	4.38	12	4.16
17	3	3.94	12	4.28	3	4.11
18	5	3.88	1	4.19	5	4.10
19	1	3.85	10	4.18	1	3.97
20	20	2.64	20	2.94	20	2.75
Mean		**4.02**		**4.54**		**4.21**
Max		**4.42**		**5.29**		**4.61**
Min		**2.64**		**2.94**		**2.75**
LSD $_{0.05}$		**0.23**		**0.36**		**0.20**
CV %		**11.83**		**12.05**		**11.94**

Table 5.25 **Mean days to anthesis** and the rankings of 20 OPVs tested across the different environments of ECA during 2006 and 2007

	Trial years					
	2006		2007		2006-2007	
Rank	Entry	AD	Entry	AD	Entry	AD
1	19	61.30	19	72.08	19	67.56
2	9	59.36	10	70.17	9	65.49
3	3	59.24	9	70.25	10	65.31
4	11	59.12	18	69.25	3	65.16
5	17	59.09	7	69.00	7	64.89
6	14	59.00	3	69.42	11	64.87
7	4	58.97	8	69.00	4	64.84
8	10	58.97	15	68.42	18	64.84
9	15	58.91	4	68.67	17	64.84
10	7	58.85	17	68.33	15	64.82
11	2	58.82	11	68.08	8	64.73
12	18	58.79	2	67.92	2	64.60
13	8	58.70	16	67.92	14	64.44
14	13	58.70	5	67.75	13	64.33
15	16	58.18	13	67.33	16	64.13
16	12	58.06	14	66.83	5	64.00
17	5	58.06	12	66.58	12	63.60
18	6	56.97	1	66.08	6	62.58
19	1	56.58	6	65.75	1	62.33
20	20	51.76	20	59.42	20	57.00
Mean		**58.37**		**67.91**		**64.22**
Max		**61.30**		**72.08**		**67.56**
Min		**51.76**		**59.42**		**57.00**
LSD $_{0.05}$		**0.80**		**1.11**		**0.67**
CV %		**2.83**		**2.00**		**2.50**

Combined analysis for trial set B (2007-2008)

The results of the combined ANOVA across years and locations showed that entries and the test environments as well as their interactions were highly significant ($P \leq 0.01$) both for grain yield and days to anthesis. The contribution of the environment to the total sum of squares was high for both grain yield and days to anthesis (Tables 5.26 and 5.27).

The combined ANOVA across years and localities showed that entries and the test environments were highly significant ($P \leq 0.01$) for both grain yield (Table 5.28) and days to anthesis (Table 5.29). The entry x year and entry x environment interactions were significant for both grain yield and days to anthesis. The percentage contribution of the sum of squares of total variation for grain yield during 2007-2008 was high for environment (71.28%) followed by block (rep x env) interaction (12.96%) (Table 5.28). The environment contribution to variation in days to anthesis was highest with 85.05% followed by entries with 5.32% (Table 5.29). The significant value of year and its interaction with environments was an indication of the year to year fluctuation of the weather and the variable response of the entries for the year and its interaction effect.

Table 5. 30 and Table 5. 31 list the performance and ranking of 38 varieties for their grain yield and days to anthesis tested across locations during 2007-2008. Candidate variety (OPV31) was the number one variety for its grain yield of 4.00 t ha^{-1} followed by OPV26 (3.96 t ha^{-1}) and OPV2 (3.89 t ha^{-1}). All the candidate varieties were better than the commercial check variety Katumani (OPV38) for grain yield which yielded 2.23 t ha^{-1}, a 44.25% lower yield than OPV31 (Table 5.30).

The commercial variety Katumani (OPV38) was the earliest variety among all the entries for its days to anthesis with 58.47 days. The candidate varieties OPV1 and OPV 6 ranked second and third with male flowering periods of 63.74 and 63.85 respectively, a five days gap in maturity with Katumani. The candidate varieties OPV 37 and OPV 9 were late in male flowering with 69.06 and 69.29 days to anthesis (Table 5.31).

Table 5.26 Combined analyses of variance for **grain yield** of 38 OPVs tested across the different environments of ECA, during 2007 and 2008

Years	Sources		DF	MS	%SS
2007	Entry		37	4.30**	3.78
	Environments (Env)		9	337.52**	72.15
	Replication		1	5.20**	0.12
	Block		24	3.33**	1.90
	Rep(Env)		9	1.21*	0.26
	Block (Rep x Env)		216	2.42**	12.42
	Entry x Env		333	0.99**	7.74
	Error		131	0.52	1.63
	R-square (%)	98			
	Mean yield (t ha^{-1})	4.32			
	LSD	0.54			
	CV %	16.77			
2008	Entry		37	1.15**	3.60
	Environments (Env)		9	65.35**	49.52
	Replication		1	14.58**	1.23
	Block		24	1.34**	2.70
	Rep(Env)		9	16.22**	12.92
	Block (Rep x Env)		216	1.13**	20.50
	Entry x Env		333	0.29**	8.24
	Error		130	0.18	1.93
	R-square (%)	99			
	Mean yield (t ha^{-1})	2.65			
	LSD	0.26			
	CV %	15.85			

*$P \leq 0.05$, ** $P \leq 0.01$

Table 5.27 Combined analyses of variance for **days to anthesis** of 38 OPVs tested across the different environments of ECA, during 2007 and 2008

Years	Sources		DF	MS	%SS
*P ≤ 0.05, ** P ≤ 0.01	Entry		37	69.22**	5.58
	Environments (Env)		8	5105.80**	89.06
	Replication		1	1.41	0.003
	Block		24	3.63*	0.19
	Rep(Env)		8	11.20**	0.20
2007	Block (Rep x Env)		192	5.93**	2.48
	Entry x Env		296	3.05**	1.97
	Error		118	2.00	0.52
	R-square (%)	99			
	Mean AD (days)	67.89			
	LSD	1.12			
	CV %	2.08			
	Entry		37	60.27**	6.16
	Environments (Env)		7	4587.36**	88.85
	Replication		1	53.88**	0.15
	Block		24	4.91**	0.33
	Rep(Env)		7	30.22**	0.58
2008	Block (Rep x Env)		168	4.04**	1.87
	Entry x Env		259	2.50**	1.79
	Error		104	1.30	0.37
	R-square (%)	99			
	Mean AD (days)	64.50			
	LSD	0.80			
	CV %	1.76			

*P ≤ 0.05, ** P ≤ 0.01

Table 5.28 Combined analyses of variance for **grain yield** of 38 OPVs tested across 20 environments of ECA, during 2007 and 2008

Years	Sources	DF	MS	%SS
2007-2008	Entry	37	3.79**	2.17
	Environments (Env)	19	242.38**	71.28
	Year	1	84.65**	1.31
	Replication	1	1.16	0.02
	Block	24	2.98**	1.11
	Rep (Env)	19	9.21**	2.71
	Block (Rep x Env)	456	1.84**	12.96
	Entry x Env	703	0.60**	6.56
	Entry x year	37	0.85**	0.49
	Error	223	0.41	1.41
	R-square(%)	98		
	Mean yield (t ha^{-1})	3.48		
	LSD	0.40		
	CV %	17.00		

** $P \leq 0.01$

Table 5.29 Combined analyses of variance for **days to anthesis** of 38 OPVs tested across 17 environments of ECA, during 2007 and 2008

Years	Sources	DF	MS	%SS
2007-2008	Entry	37	123.39**	5.32
	Environments (Env)	16	4558.85**	85.05
	Year	1	3715.93**	4.33
	Replication	1	17.29**	0.02
	Block	24	3.70**	0.10
	Rep (Env)	16	21.19**	0.40
	Block (Rep x Env)	384	5.25**	2.35
	Entry x Env	592	2.62**	1.82
	Entry x year	37	4.09**	0.18
	Error	184	2.02	0.43
	R-square(%)	99		
	Mean AD (days)	66.30		
	LSD	1.02		
	CV %	1.95		

** $P \leq 0.01$

Table 5.30 **Grain yield** performance and the rankings of 38 OPVs tested across the environments of ECA during 2007 and 2008

	Trial seasons					
	2007		***2008***		***2007-2008***	
Rank	Entry	GW	Entry	GW	Entry	GW
1	26	5.23	25	3.10	31	4.00
2	31	5.14	19	3.01	26	3.96
3	37	4.88	2	2.99	2	3.89
4	2	4.78	32	2.95	11	3.79
5	8	4.75	11	2.93	19	3.72
6	30	4.68	13	2.91	13	3.72
7	7	4.67	14	2.88	37	3.71
8	11	4.65	31	2.85	8	3.71
9	28	4.61	28	2.77	28	3.70
10	4	4.60	24	2.77	14	3.67
11	29	4.58	15	2.77	4	3.67
12	13	4.53	4	2.73	17	3.60
13	17	4.52	22	2.72	29	3.59
14	14	4.46	18	2.72	7	3.59
15	27	4.45	5	2.70	15	3.58
16	34	4.44	6	2.69	25	3.55
17	23	4.44	26	2.69	30	3.54
18	19	4.43	33	2.68	27	3.54
19	12	4.43	17	2.67	34	3.53
20	15	4.40	8	2.66	23	3.53
21	3	4.33	27	2.63	22	3.48
22	22	4.24	23	2.61	32	3.47
23	33	4.22	34	2.61	24	3.45
24	36	4.21	29	2.59	33	3.45
25	16	4.16	21	2.57	12	3.42
26	10	4.16	20	2.57	18	3.42
27	24	4.13	1	2.55	5	3.41
28	5	4.11	37	2.54	3	3.38
29	18	4.11	35	2.53	16	3.33
30	1	4.07	7	2.51	1	3.31
31	35	4.07	16	2.50	35	3.30
32	32	4.00	3	2.42	36	3.29
33	25	3.99	12	2.41	10	3.28
34	20	3.96	10	2.39	20	3.27
35	21	3.93	36	2.36	21	3.25
36	6	3.66	30	2.35	6	3.18
37	9	3.48	9	2.23	9	2.86
38	38	2.61	38	1.83	38	2.23
Mean		**4.32**		**2.65**		**3.48**
Max		**5.23**		**3.10**		**4.00**
Min		**2.61**		**1.83**		**2.23**
LSD $_{0.05}$		**0.54**		**0.26**		**0.39**
CV %		**16.77**		**15.85**		**17.00**
R^2		**0.98**		**0.98**		**0.98**

Table 5.31 **Mean days to anthesis** and the rankings of 38 OPVs tested across the different environments of ECA, 2007 and 2008

	Trial seasons					
	2007		***2008***		***2007-2008***	
Rank	Entry	AD	Entry	AD	Entry	AD
1	38	60.83	38	55.81	38	58.47
2	6	64.94	24	62.38	1	63.74
3	1	64.94	1	62.38	6	63.85
4	19	65.11	6	62.63	19	63.97
5	30	65.63	19	62.69	24	64.21
6	24	65.83	30	63.31	30	64.57
7	23	66.44	23	63.31	23	64.97
8	5	66.61	2	63.56	5	65.38
9	31	66.67	34	63.75	35	65.41
10	32	66.67	35	63.75	32	65.47
11	35	66.89	20	63.88	31	65.53
12	7	67.06	10	64.00	7	65.74
13	34	67.50	25	64.00	34	65.74
14	36	67.67	5	64.00	25	66.06
15	26	67.72	32	64.13	2	66.15
16	25	67.89	28	64.19	20	66.26
17	33	68.00	7	64.25	36	66.29
18	14	68.06	31	64.25	33	66.50
19	29	68.17	16	64.50	28	66.59
20	20	68.39	36	64.75	16	66.74
21	2	68.44	33	64.81	26	66.82
22	16	68.72	13	65.06	10	66.88
23	28	68.72	22	65.13	14	66.91
24	13	68.78	15	65.38	29	66.91
25	4	68.89	3	65.38	13	67.03
26	22	68.94	18	65.50	22	67.15
27	21	69.00	29	65.50	15	67.29
28	15	69.00	21	65.56	21	67.38
29	17	69.06	14	65.63	4	67.44
30	12	69.11	17	65.75	17	67.50
31	10	69.44	26	65.81	3	67.68
32	27	69.56	4	65.81	18	67.91
33	3	69.72	8	66.06	12	68.03
34	11	69.83	11	66.31	8	68.09
35	8	69.89	27	66.63	11	68.18
36	18	70.06	12	66.81	27	68.18
37	9	70.89	37	66.81	37	69.06
38	37	71.06	9	67.50	9	69.29
Mean		**67.89**		**64.50**		**66.30**
Max		**71.06**		**67.50**		**69.29**
Min		**60.83**		**55.81**		**58.47**
LSD $_{0.05}$		**1.12**		**0.80**		**1.02**
CV %		**2.08**		**1.76**		**1.95**
R^2		**0.99**		**0.99**		**0.99**

5.4.2 Evaluation of grain yield stability and days to anthesis based on the AMMI model

The AMMI model was used to examine grain yield stability and days to anthesis of 20 QPM OPVs included in trial set A (excluding local checks) conducted during 2006 and 2007 in 17 environments for grain yield and 15 environments for days to anthesis in ECA countries. The combined ANOVA from the AMMI model for grain yield and days to anthesis showed that mean squares for grain yield were highly significant ($P \leq 0.001$) for environments, genotypes and G x E interactions (Tables 5.32 and 5.33). The F-test was highly significant ($P \leq 0.001$) for all the IPCA axes. The environments explained 86.35% of the total grain yield variation followed by the G x E interaction (4.36%). The contribution of genotype to the total variation was low (2.72%). The first five IPCAs were highly significant and explained 78.03% of the G x E interaction. The first IPCA captured 27.35% of the total interaction sum of squares in 11.20% of the G x E interaction degrees of freedom. The second IPCA also explained 19.28% of the interaction sum of squares in 10.53% of the interaction degrees of freedom (Table 5.32).

Table 5.32 Analysis of variance based on the AMMI model for grain yield (t ha^{-1}) of 20 OPVs (19 QPM and a normal check) evaluated across 17 environments in ECA during 2006 and 2007

Sources	DF	SS	MS	Total variation explained (%)	G x E explained (%)	Cumulative (%)
Total	1019	5105	5.01			
Treatments	339	4770	14.07			
Environments	16	4408	275.52**	86.35		
Genotypes	19	139	7.33**	2.72		
Blocks in Env.	34	92	2.71			
Genotype x Env.	304	223	0.73**	4.36		
IPCA1	34	61	1.8**		27.35	27.35
IPCA2	32	43	1.36**		19.28	46.64
IPCA3	30	26	0.87**		11.67	58.30
IPCA4	28	24	0.84**		10.76	69.06
IPCA5	26	20	0.76**		8.97	78.03
IPCA residual	154	49	0.32			
Residual	646	243	0.38			

** $P < 0.01$; IPCA= Interaction principal component axis

The ANOVA for the days to anthesis showed highly significant mean squares ($P \leq 0.001$) for environments, genotypes and G x E interactions. The F-test was highly significant ($P \leq 0.001$) for the first four IPCA. The environments were the major source of variation for days to anthesis among the 20 genotypes and explained 89.71% of the total variation followed by the genotypes (4.48%) and the interaction between the two (2.57%). The first four IPCA were significant and explained 76.23% of the G x E interaction. The first IPCA captured 40.04% of the total interaction sum of squares in 12.03% of the G x E interaction degrees of freedom. The second IPCA also explained 17.13% of the interaction sum of squares in 11.28% of the interaction degrees of freedom (Table 5.33).

Table 5.33 Analysis of variance based on the AMMI model for days to anthesis of 20 OPVs (19 QPM and a normal check) evaluated across 17 environments in ECA during 2006 and 2007

Sources	DF	SS	MS	Total variation explained (%)	G x E explained (%)	Cumulative (%)
Total	899	76730	85.4			
Treatments	299	74253	248.3			
Environments	14	68838	4917**	89.71		
Genotypes	19	3442	181.2**	4.48		
Blocks in Env.	30	440	14.7			
Genotype x Env.	266	1973	7.4**	2.57		
IPCA1	32	790	24.7**		40.04	40.04
IPCA2	30	338	11.3**		17.13	57.17
IPCA3	28	219	7.8**		11.67	68.27
IPCA4	26	157	6.1*		7.95	76.23
IPCA5	24	119	4.9		6.03	82.26
IPCA residual	126	349	2.8			
Residual	570	2037	3.6			

** $P < 0.01$; * $P < 0.05$; IPCA= Interaction principal component axis

The AMMI biplot based on the values of IPCA2 scores for the genotypes and the value of the genotype means for the grain yield of 20 open pollinated QPM varieties was constructed to show the performance and association of the genotypes (Fig. 5.2). From the biplot it can be seen that the open pollinated QPM genotype 19(G19) was the highest yielder followed by the QPM genotypes G15 and G8. The non QPM commercial check G20 (Katumani) ranked last indicating the potential of the candidate QPM varieties for possible commercial release based on their grain yield advantage over the check.

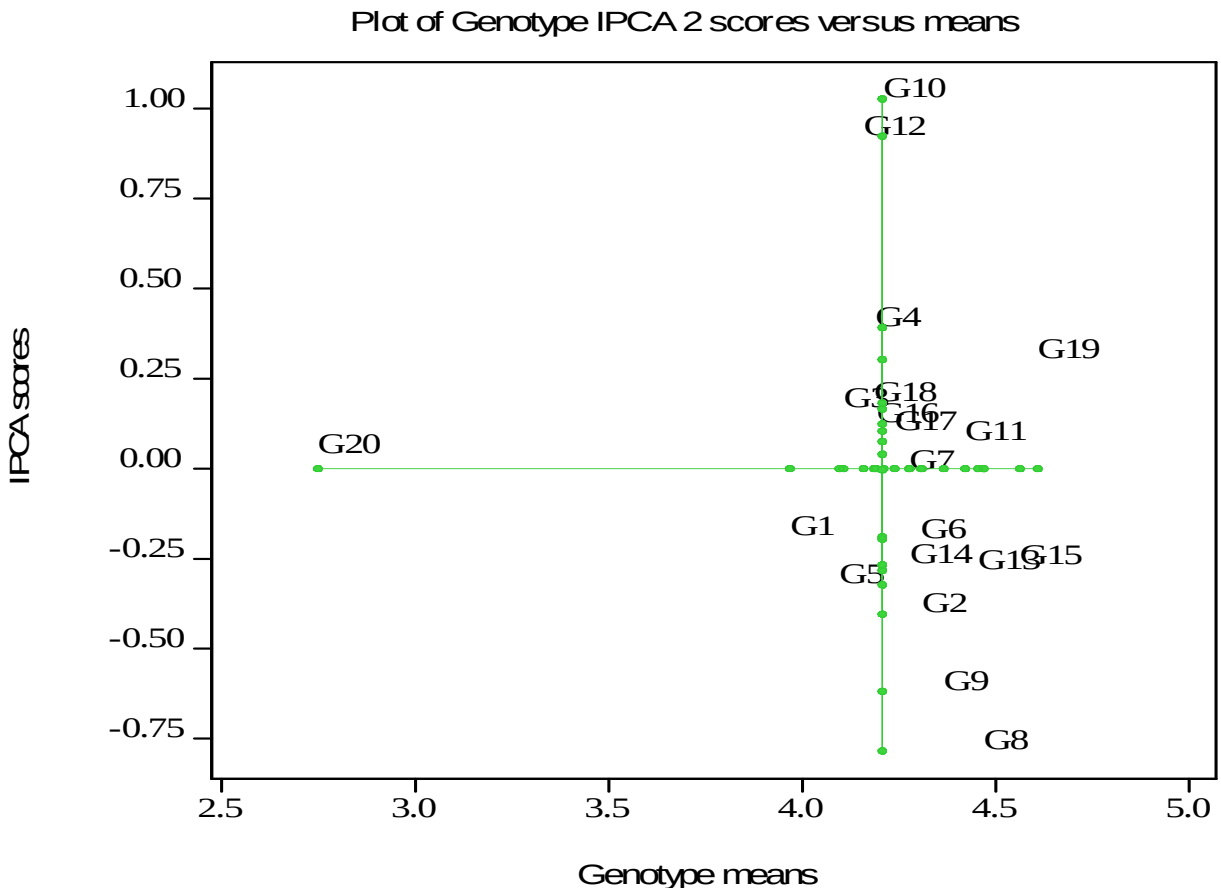

Figure 5.2 AMMI biplot based on environmental means versus IPCA2 scores for grain yield of 20 open pollinated (19 QPM and a normal check) varieties evaluated in 17 environments of ECA.

Furthermore, Fig. 5.2 shows that most of the genotypes were clustered around the centre of the biplot an indication of superior grain yield stability of OPVs compared to hybrids. This finding is in agreement with the results of Pixley and Bjarnason (2002) who reported open pollinated cultivars to be the most stable followed by double-cross, three-way and finally single cross hybrids following the evaluation of the different QPM cultivars at 13 locations in four continents.

AMMI Stability Value (ASV) (Purchase, 1997) was calculated to identify the most stable entries across environments. Detailed description of ASV is presented in Chapter 3. The most stable genotypes across the environments were G7 followed by G17. Although the two

entries ranked 10th and 11th in terms of mean grain yield, the entries showed above average grain yield performance (Table 5.34).

Table 5.34 AMMI Stability Value (ASV), mean grain yield and ranks of 20 OPVs tested in 17 environments of ECA

Entry	ASV	**Rank**	**Mean yield (t ha^{-1})**	**Rank**
G7	0.035	1	4.275	10
G17	0.171	2	4.238	11
G18	0.197	3	4.185	15
G3	0.199	4	4.106	17
G11	0.205	5	4.421	5
G15	0.269	6	4.562	2
G6	0.382	7	4.307	8
G1	0.410	8	3.967	19
G5	0.430	9	4.095	18
G4	0.437	10	4.188	14
G14	0.479	11	4.277	9
G16	0.510	12	4.191	13
G13	0.558	13	4.454	4
G2	0.712	14	4.309	7
G8	0.799	15	4.469	3
G9	0.944	16	4.365	6
G12	0.954	17	4.158	16
G10	1.028	18	4.210	12
G19	1.057	19	4.608	1
G20	2.463	20	2.748	20
Grand Mean	0.612		4.206	

Figure 5.3 shows the two dimensional graph based on the data of ASV (Y-axis) and mean grain yield (X-axis) of the 20 OPVs. The X-axis and Y-axis data were transformed into their log (base 10) and antilog (base 10) values, respectively for better visualisation using GenStat® 15th edition (GenStat, 2012) statistical software. Genotype seven (G7) had the smallest ASV value an indication of better stability, followed by G17. Entry 19 (G19) had the highest mean grain yield but was less stable across environments due to its high ASV. However, G19 was a responsive entry an indication of adaptation to high yielding environments. The least stable and lowest yielding entry was G20 (Katumani) due to its high ASV and low mean grain yield. The graph also shows that most of the QPM OPVs were closely plotted and their ASV was below 1.00 indicating closer similarity among the entries in their grain yield stability.

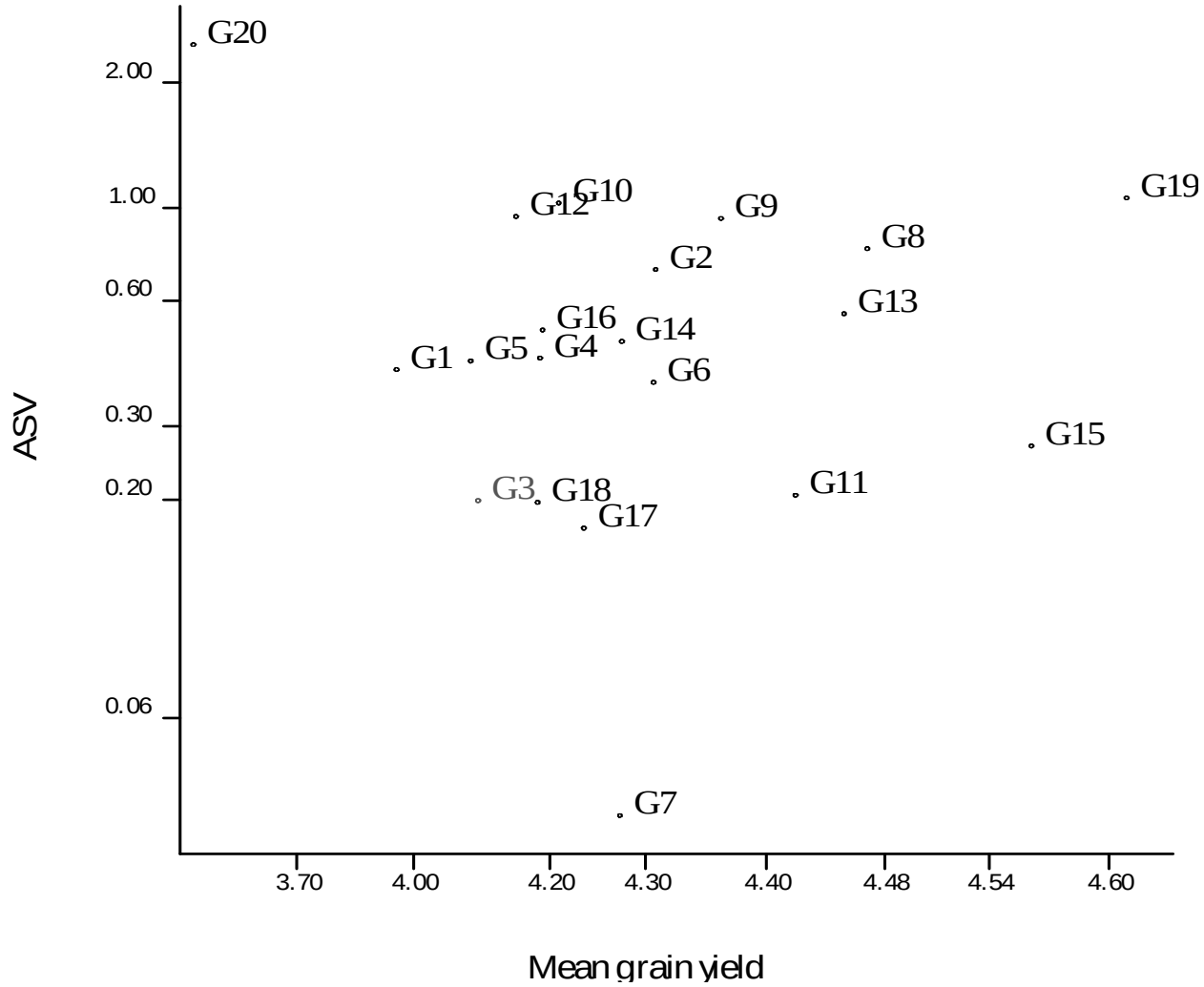

Figure 5.3 Two dimensional (2D) graph for AMMI stability value and mean grain yield of 20 OPVs (19 QPM and a normal check) evaluated in 17 environments of ECA. Data transformed based on antilog (base 10) and log (base 10) values of X-axis and Y-axis respectively for better visualisation.

The AMMI biplot was constructed based on IPCA2 values of the environments plotted against the environmental means of grain yield (Fig. 5.4). Description of the test environments, the environmental mean grain yield and the environment codes are presented in Table 5.35.

Table 5.35 Description of the test environments and their environment code for grain yield AMMI biplot

No	Country	Site name	Trial year/ Season	Environment code	Mean grain yield (t ha^{-1})
1	Tanzania	Arusha	2006	ARU1	2.67
2	Tanzania	Arusha	2007	ARU2	3.18
3	Kenya	Bungoma	2006	BUN	3.56
4	Kenya	Elgon Downs	2007	EDO	2.24
5	Kenya	Embu	2006	EMB1	4.22
6	Kenya	Embu	2007	EMB2	7.95
7	DR Congo	Gandijika	2006	GAN	2.05
8	Kenya	Kakamega	2006	KAK	0.66
9	Kenya	Kiboko	2006 (Nov./1st season planting)	KIB1	5.73
10	Kenya	Kiboko	2006 (June/2nd season planting)	KIB2	5.86
11	Kenya	Kiboko	2007 (Oct./1st season planting)	KIB3	8.66
12	Ethiopia	Melkassa	2006	MEL	6.11
13	Uganda	Namlonge	2006	NAM	4.43
14	Rwanda	Nyagatare	2006	NYA	4.99
15	Rwanda	Rubona	2006	RUB	4.00
16	Kenya	Siaya	2007	SIA	2.36
17	Sudan	Wad Madani	2007	WAD	2.85

The AMMI biplot for the test environments (Fig. 5.4) identified KIB3 as the highest yielding environment followed by EMB2 and MEL. The high yielding environments were not the most stable as they were further from the centre of the biplot. However, these environments were highly responsive as genotypes displayed good performance. The least stable and lowest yielding environment was Kakamega - Kenya (KAK) an indication of the unsuitability of this test environment for these early maturing QPM OPVs. EMB2 and KIB2 were also identified as responsive for specific genotypes as they are far from the origin of the biplot. It can be concluded that the second season planting at Kiboko was less stable than the first season (KIB1) which is relatively closer to the origin of the biplot. Similarly RUB, EMB1 and NAM

were close to the centre of the biplot indicating the relative stability of the environments as well as the similarity of the environments for testing of genotypes (Fig. 5.4).

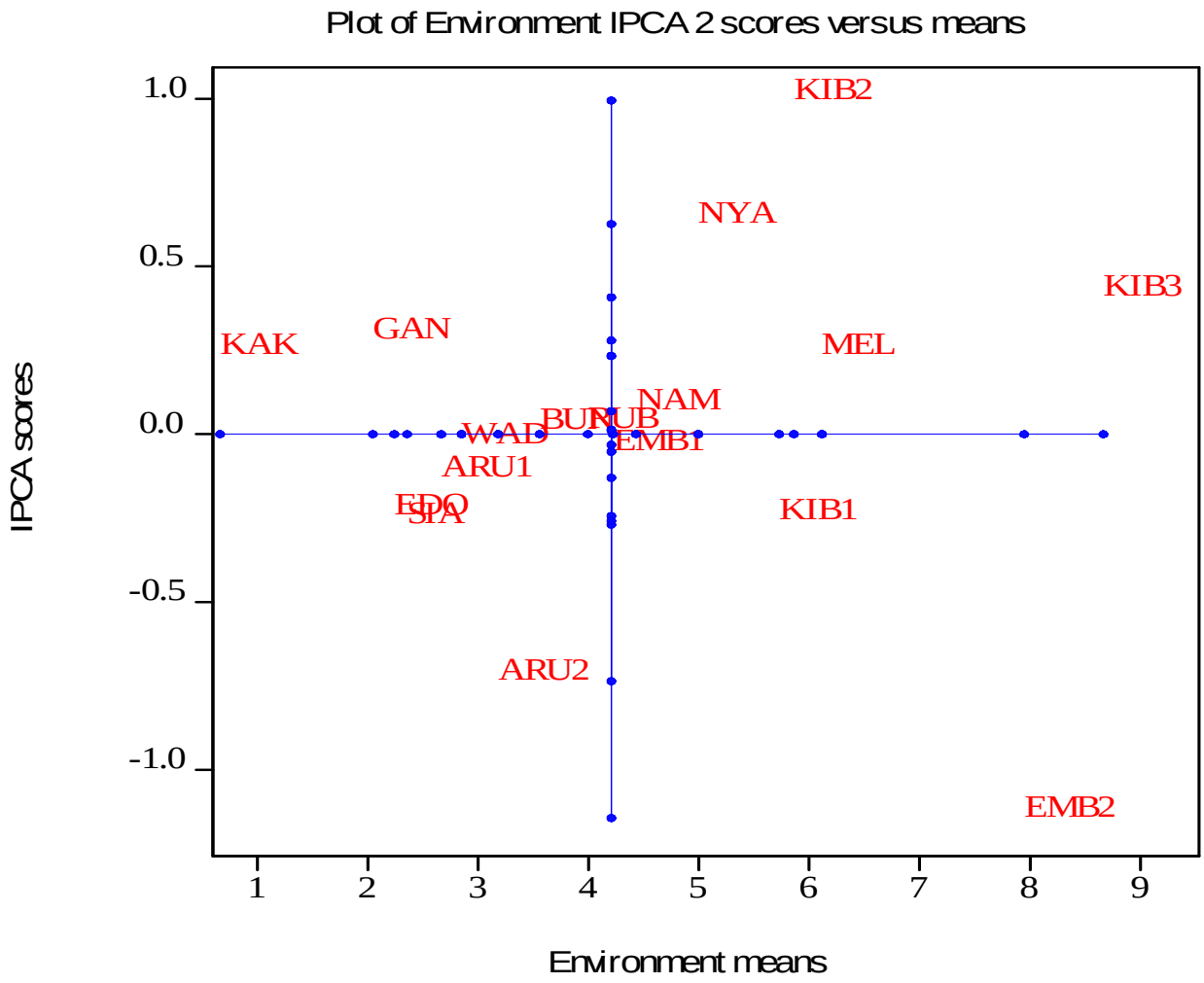

Figure 5.4 AMMI biplot based on genotype means versus IPCA 2 scores for grain yield of 20 open pollinated (19 QPM and a normal check) varieties evaluated in 17 environments of ECA.

To demonstrate the association and relationship among genotypes and the test environments another AMMI biplot was constructed based on IPCA1 and IPCA2 scores (Fig. 5.5). Based on this, Emb2 and Kib3 were the most discriminating environments followed by Kib2 as shown by the longest arm directed to the positive IPCA scores from the centre of the biplot. G19 was close to the highest yielding environment of Kib3 indicating its responsiveness to that environment while G9 was found to be more responsive to the Emb2 environment. The

environments Kib1 and Kib2 were in the opposite direction of the biplot indicating the existence of within season variation at Kiboko. However, the short arm of Kib1 from the centre of the biplot could mean that there was little variation. The commercial normal endosperm open pollinated check variety (G20) was low yielding and not closely associated with any of the test environments in this study. Hence, the candidate varieties proved to be a better option for maize farmers in ECA than the widely grown normal endosperm OPV (Katumani) for both grain yield and nutritional advantage. Based on their small vector angle and their similar direction on the biplot, Aru1 (2006) and Aru2 (2007) may be considered as similar environments for testing the genotypes. Two genotypes, G15 and G8, showed a close association with Aru1 and Aru2, respectively. Most of the high yielding genotypes were clustered in the bottom right quadrant of the biplot and G7 was identified as stable due to its closeness to the centre of the biplot as well as its lowest ASV (Fig. 5.5).

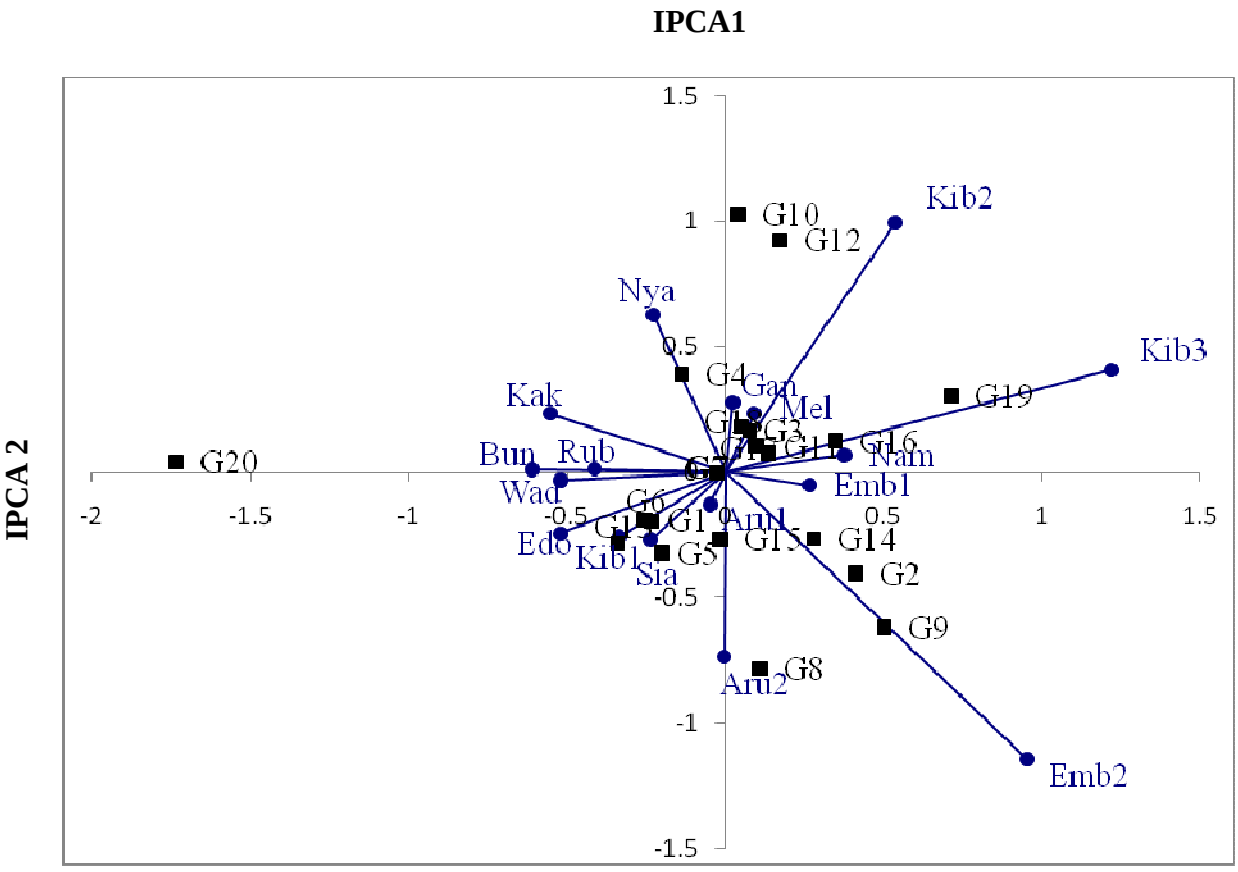

Figure 5.5 AMMI biplot based on IPCA1 versus IPCA 2 score for grain yield of 20 open pollinated varieties evaluated in 17 environments of ECA.

Among the secondary traits, days to anthesis is more important than silking as the latter is more influenced by abiotic stress and tasseling is more stable in adverse environmental conditions (Koester et al., 1993). Hence, prediction of the time of flowering will facilitate the exchange of germplasm among national research systems and recommendation of varieties to similar mega-environments. The ANOVA for days to anthesis for the 20 OPVs evaluated in 15 environments of ECA indicated that days to anthesis were highly and significantly influenced by environments (Table 5.23).

Figure 5.6 and Fig. 5.7 show the association among the genotypes based on their days to anthesis and the relationship among environments based on mean performance respectively. Most of the genotypes clustered around the genotype mean axis, which indicates the stable performance of the genotypes for days to anthesis and the similarity of the genotypes in maturity across the environments (Fig. 5.6). The highest number of days to anthesis was recorded for genotype G19 (67.56) and the lowest for G20 (Katumani) with 57.00 days while the average days to anthesis for the 20 genotypes was 64.22 indicating the earliness of the materials. Although the use of the term “earliness” may vary from place to place, CIMMYT classified germplasm that flowers between 55 and 60 days as early maturing and those flowering up to 70 days as intermediate. This classification is adopted for the regional trials in SSA (Vivek and Pswarayi, 2008; Magorokosho et al., 2009; 2010; Makumbi, 2011). Out of the 20 genotypes six flowered below the average 64.22 days viz. G1, G6, G5, G16, G12 and G20. The days to anthesis for 12 entries were in the range of 64 days. In addition, G12, G15 and G18 were more stable in their days to anthesis than the other genotypes while G3 was the least stable. Early entries showed below average grain yield performance. The average maximum difference in days to anthesis was ten and this was between G19 and G20; however the yield advantage of G19 was about 40% over G20. Similarly, the flowering gap between G20 and the mean days to anthesis was just a week; however, there was a 35% grain yield gap between G20 and the mean yield of the 20 genotypes. Hence, this study further corroborated the effect of variation in maturity on the ultimate grain yield of early maturing tropical maize genotypes.

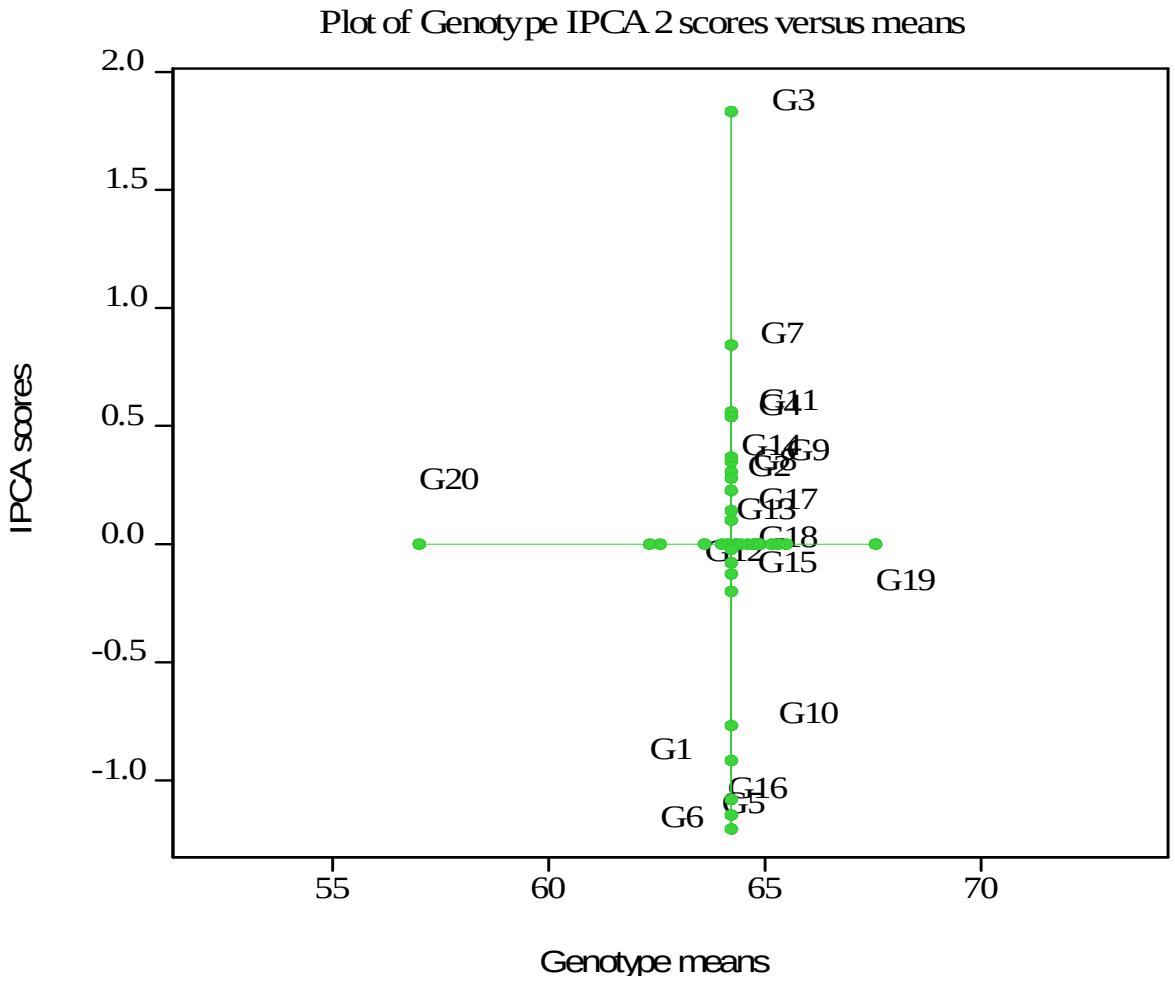

Figure 5.6 AMMI biplot based on the genotypes means and IPCA2 scores for days to anthesis of 20 open pollinated (19 QPM and a normal check) varieties evaluated in 15 environments of ECA.

Unlike the genotypes, the test environments showed greater variability in response to days to anthesis (Fig. 5.7). In the biplot the environment Selian was excluded as the data on days to anthesis was far above average and not repeatable. Wad Madani (Wad) was considered to visualise its interaction with other environments of ECA and to identify genotypes adapted to this tropical lowland environment. Aru1 (Arusha, Tanzania-2006) and Edo (Elgon Downs, Kenya) were the two most extreme environments and recorded the highest days to anthesis record of more than 80 days. The lowest days to anthesis of about 50 days was recorded at Wad (Wad Madani, Sudan). The lowest elevation (411m above sea level) and the annual average minimum and maximum temperatures (20-37^{0}C) at Wad Madani were the most important environmental factors that may have contributed to the earliness in days to anthesis. Mel (Melkassa, Ethiopia) and Kib2 (Kiboko, Kenya-2nd season planting) were close

in the biplot and were among the stable environments based on days to anthesis of the genotypes and their proximity to the centre of the biplot. The closeness of the two environments is an indication of their similarity suggesting that the two environments may be used for testing germplasm and that the results from one of the environments can help to predict performance in the other. If these two environments correlate consistently over years, one of them may considered as redundant and be dropped to minimise evaluation cost. Similarly environments Bun (Bungoma, Kenya), Emb1 (Embu, Kenya) showed close relationship on the biplot indicating their similarity in the days to flowering the genotypes. The year-to-year fluctuations in weather patterns were reflected at Aru1 (Arusha, 2006) and Aru2 (Arusha, 2007) where the days to anthesis was inconsistent for the two years. However, the two environments were in similar direction of the biplot indicating the presence of association. In general, Fig. 5.7 explains how environments affect the flowering time of maize as well as the heterogeneity of tropical environments. Table 5.36 describes the test environments, the IPCA scores and the mean performance of the genotypes based on days to anthesis.

Table 5.36 Description of the test environments and graph ID based on mean days to anthesis (DA) of the AMMI model

Country	**Environment**	**Graph ID**	**Mean DA**	**IPCA1**	**IPCA2**
Tanzania	Arusha-2006	Aru1	81.50	2.18395	-0.03742
Tanzania	Arusha-2007	Aru2	69.07	0.48265	-0.27681
Kenya	Bungoma	Bun	63.83	-0.17399	0.73279
Kenya	Elgon Downs	Edo	81.52	1.82904	-0.2899
Kenya	Embu-2006	Emb1	62.33	-0.14189	0.64506
Kenya	Embu-2007	Emb2	65.70	0.41106	0.5703
DRC	Gandajika	Gan	55.00	-0.60014	0.11468
Kenya	Kakamega	Kak	67.35	0.74577	0.4120
Kenya	Kiboko-2006 (1st planting)	Kib1	60.07	-0.19724	-2.44158
Kenya	Kiboko-2006 (2nd planting)	Kib2	62.50	-1.71893	-0.24848
Kenya	Kiboko-2007 (1st planting)	Kib3	55.37	-0.61833	0.06334
Ethiopia	Melkassa	Mel	64.95	-0.07777	0.11678
Uganda	Namlonge	Nam	55.08	-0.96299	1.53383
Rwanda	Nyagatare	Nya	69.47	0.35872	-0.13381

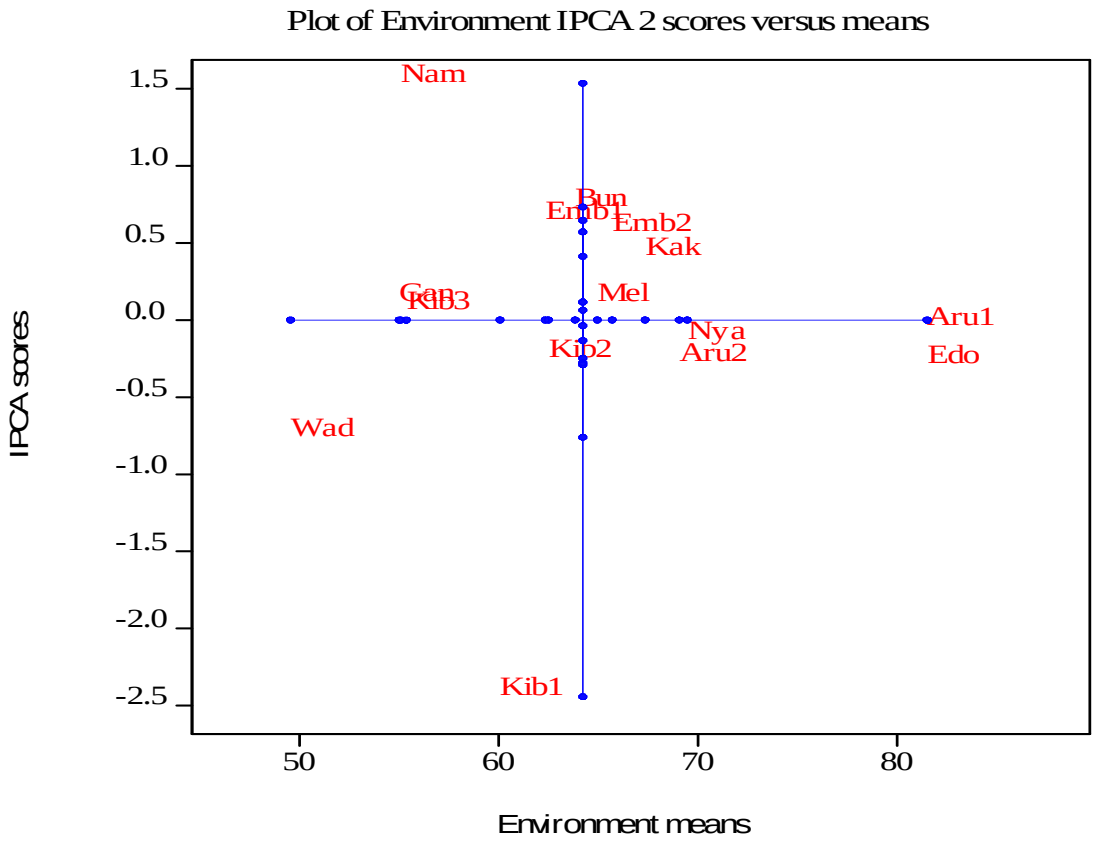

Figure 5.7 AMMI biplot based on the environment means and IPCA2 scores of days to anthesis of 20 open pollinated (19 QPM and a normal check) varieties evaluated in 15 environments of ECA.

In Figure 5.8 is presented the AMMI biplot based on the values of IPCA1 and IPCA2 of the genotypes and the environments. The majority of the genotypes were close to each other and clustered towards the centre of the biplot. This indicates the close similarity among the genotypes for days to anthesis and the minimum deviation from the mean value. Figure 5.9 shows the association of grain yield with mean days to anthesis of the environments based on IPCA1 scores. G20 (Katumani) was more adapted to the environments Kib2, Wad, Gan, Kib3 and Nam. The high yielding G19 was close to Kak where the mean days to anthesis at Kak were similar with that of G19. Most of the genotypes were clustered around Mel (Melkassa, Ethiopia) where its mean days to anthesis were about 65. This shows that for good grain yield performance of the genotypes, an ideal environment would be where male flowering is expected to be around 65 days. No genotypes were near to Aru1 and Edo indicating the unsuitability of these environments for grain production (Fig. 5.9).

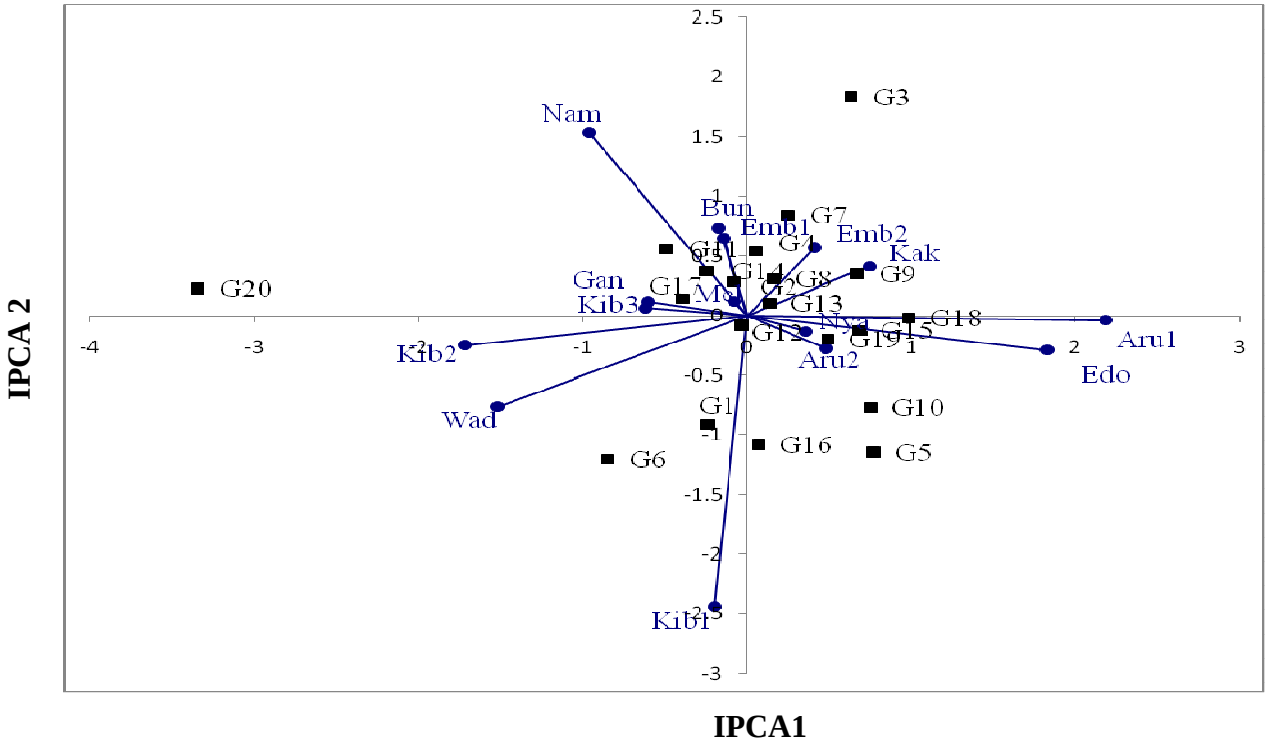

Figure 5.8 AMMI biplot based on IPCA1 and IPCA2 scores of genotypes and environments for days to anthesis of 20 open pollinated varieties evaluated in 15 environments of ECA.

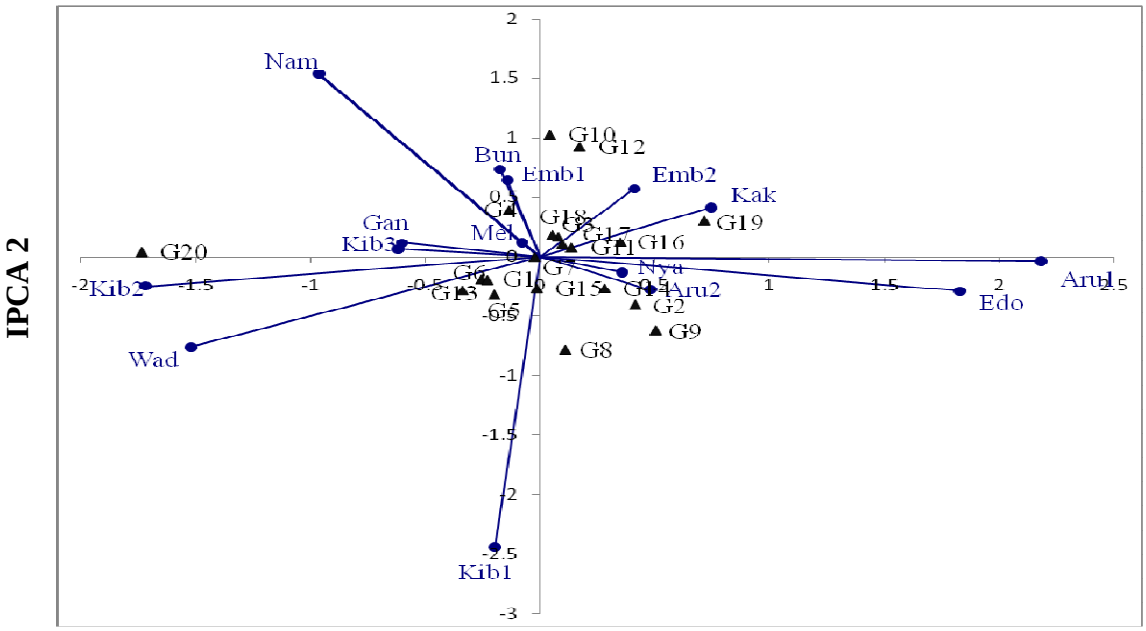

Figure 5.9 AMMI biplot based on IPCA1 scores of grain yield of genotypes and environments mean days to anthesis.

5.4.3 Evaluation of grain yield stability and days to anthesis based on the GGE biplot

This section presents the results of the GGE biplot analysis of 38 OPVs evaluated in ECA countries for grain yield and days to anthesis during 2007 and 2008. The list of the entries is presented in Table 5.2. The ANOVAs were reported in Section 5.4.1. In the GGE biplots genotypes are indicated by numbers and the environments by text codes. All the data used in the GGE biplots were standardised to facilitate visualisation of the genotypes and environments. Table 5.37 presents the list of environments and the environment codes.

Table 5.37 List of the test environments and graph code used in the GGE biplots based on the grain yield performance and days to anthesis of 38 OPVs (37 QPM and a normal check) evaluated in ECA countries during 2007-2008

No.	Country	Environment	Code
1	Burundi	Mosso	Mo/Mos
2	Burundi	Mparambo	Mp/Mpa
3	Ethiopia	Melkassa	Me/Mel
4	Kenya	Alupe	Al/Alu
5	Kenya	Bungoma	Bu/Bun
6	Kenya	Elgon Downs	Ed/Edo
7	Kenya	Embu	Em/Emb
8	Kenya	Kakamega	Ka/Kak
9	Kenya	Kimaeti	Ki/Kim
10	Kenya	Kitale	Kt/Kit
11	Kenya	Thika	Th/Thi
12	Sudan	Rahad	Ra/Rah
13	Sudan	Wad Madani	Wa/Wad
14	Tanzania	Arusha	Ar/Aru
15	Tanzania	Mbulumbulu	Mb/Mbu
16	Tanzania	SARI	Sa/Sar
17	Tanzania	Selian	Se/Sel
18	Tanzania	Weruweru	We/Wer

Yield stability and ranking of genotypes and environments

The yield-stability statistic (YS_i) (Kang, 1993) and the GGE distance (i.e. the distance from the markers of individual genotypes to the ideal genotype) (Yan, 2001; Yan and Kang, 2003; Yan and Tinker, 2006) help to select for high yield and stability. Stability is measured from Kang's yield stability statistic (YS_i) which involves cultivar rankings based on Shukla's stability value (σ_i^2) (Shukla, 1972). The GGE biplot jointly uses some of the functions of linear joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968), the AMMI model (Gauch and Zobel, 1996) and type B genetic correlation (Yamada, 1962). The various interpretations of GGE biplot analysis is presented in Chapter 4.

Figures 5.10 and 5.11 show the rankings of the genotypes and environments based on grain yield and days to anthesis, respectively. The high yielding and most stable genotype based on proximity to the Average Environment Coordinate (AEC) was genotype 31 followed by 2 and 11. The least stable and low yielding entries were 38 followed by 9 and 5 which are very far from the AEC. This shows the presence of maximum G x E interaction (Fig. 5.10). From Fig. 5.10 the ranking of the environments can be visualised. The highest yielding environment was Embu (Em) followed by Elgon Downs (Ed) and Mosso (Mo) while the lowest yielding environments were Kimaeti (Km) and Weruweru (We). The most unstable environment was Kakamega (Ka) while the most stable environment was Rahad (Ra).

Based on the days to anthesis the late flowering genotypes were ranked first and close to the AEC while the early flowering genotypes were far from the AEC (Fig. 5.11). Entries 37 and 9 were the late flowering genotypes while entries 38 and 1 were the early flowering entries. Unlike yield performance of the unstable genotypes, the days to anthesis was closer to the Average Tester Axis (ATA) (Yan, 2001) an indication of relative stability. Genotypes that were less stable for days to anthesis were 38, 1 and 2 which are far from the ATA. The environment Elgon Downs (Edo) was ranked first as the genotypes took many days to reach anthesis followed by Arusha (Aru), Thika (Thi) and Mosso (Mos). The lowest ranking environment was Mparambo (Mpa) indicating that genotypes flowered early at this environment. The environments Wad, Rah, Kim and Mpa were below the AEC meaning that flowering was below average, an indication of early flowering. In contrast, flowering was average at Kak, Mbu and Mel (Fig. 5.11).

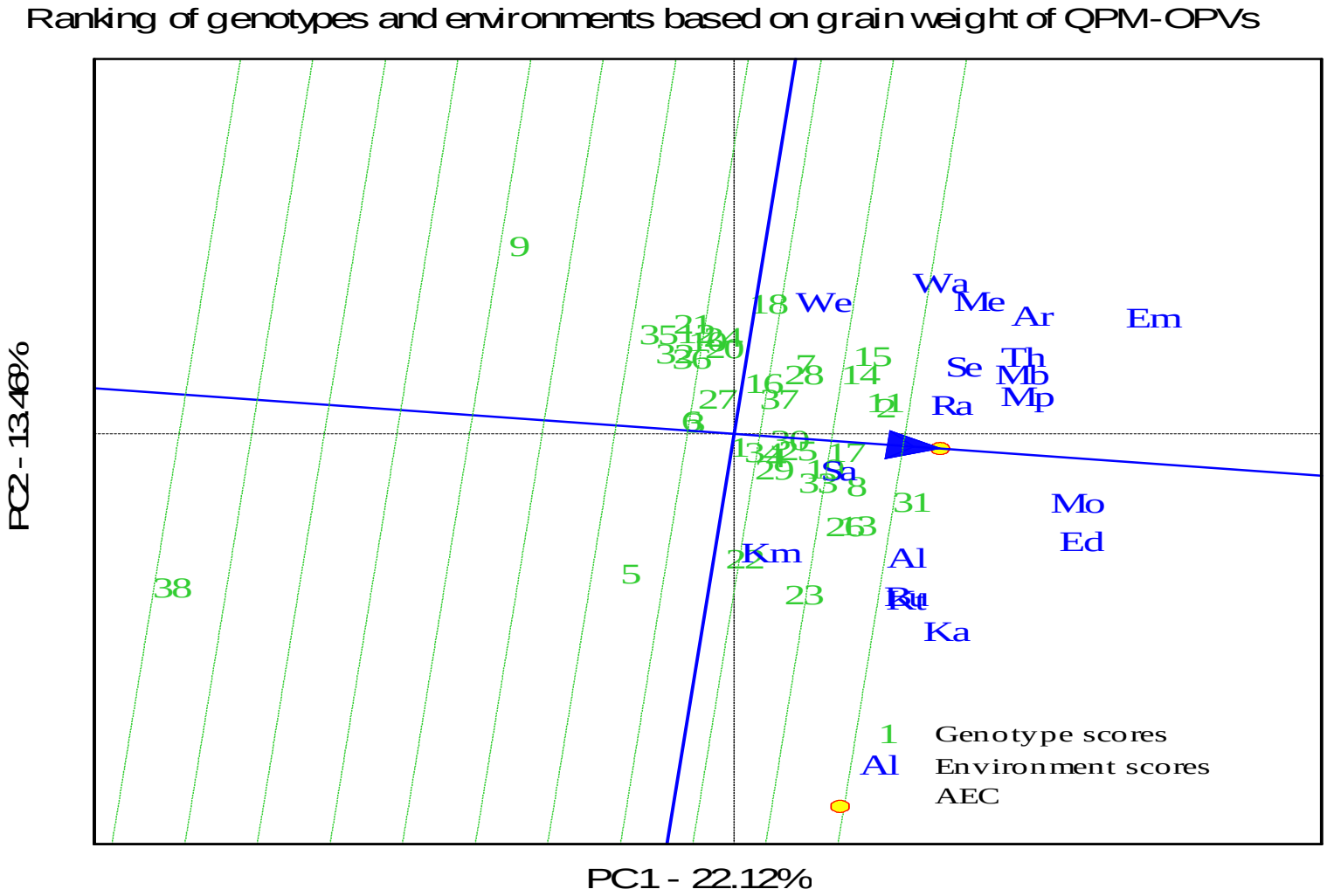

Figure 5.10 GGE biplot ranking of 38 OPVs (37 QPM and a normal check) based on grain yield evaluated at 18 environments of ECA during 2007-2008. Numbers indicate genotypes, texts show environments and yellow circle shows the AEC. Graph key also in the biplot.

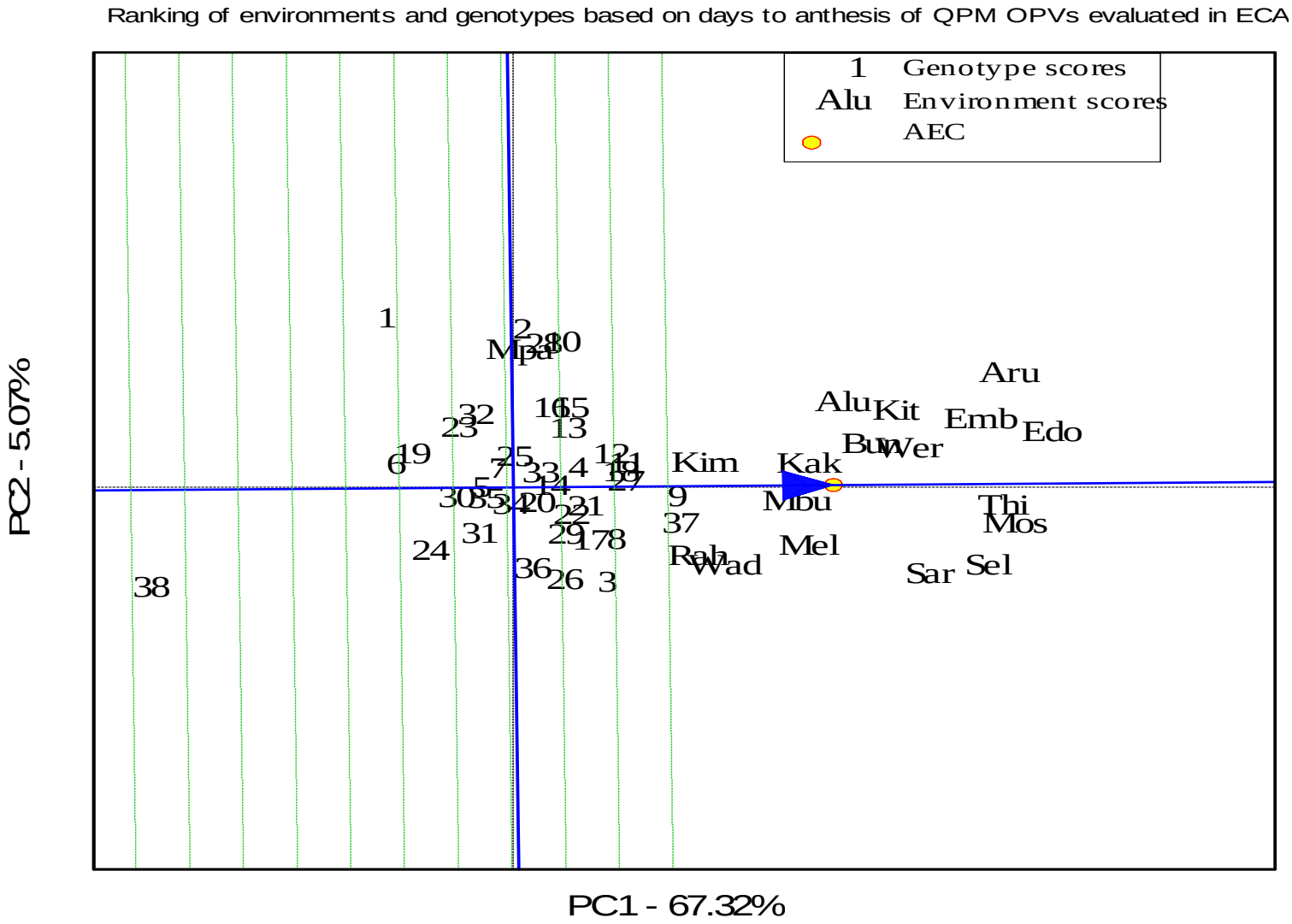

Figure 5.11 GGE biplot ranking of 38 OPVs (37 QPM and a normal check) based on days to anthesis evaluated at 18 environments of ECA during 2007 - 2008.

Association between test environments

Fig. 5.12 shows the relationship among the test environments. The vectors connect the biplot origin with the markers of the test environments. The angle between the two vectors indicates the correlation between two environments. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them (Kroonenberg, 1995; Yan, 2002). Acute angles indicate a positive correlation, obtuse angles a negative correlation and right angles no correlation (Yan and Kang, 2003). A short vector may indicate that the test environment is not related to other environments. Test environments that are consistently non-discriminating (non-informative) provide little information on the genotypes and, therefore should not be used as test environments (Yan and Tinker, 2006).

Based on the vector angle between the two environments, there was a close association between Mosso-Burundi (Mo) and Elgon Downs-Kenya (Ed) based on the grain yield performance of the 38 genotypes. Similarly Kitale (Kt) and Bungoma (Bu) both in Kenya; Mparambo (Mp) and Mbulumbulu-Tanzania were closely associated. Embu (Em) was the most discriminating environment for having a long vector followed by Elgon Downs and Kakamega. The distance between two environments measures their dissimilarity in discriminating ability of the genotypes (Yan and Tinker, 2006). As a result Embu discriminated the genotypes based on yield performance; on the contrary Kakamega was considered discriminating due to the below average grain yield performance of the genotypes in this environment. SARI (Sa) was the least discriminating environment due to its short vector which is also a less informative environment regarding the grain yield performance of the QPM OPVs. There was a negative correlation, an indication of strong crossover G x E interaction, between the environments of Weruweru (We) and Kimaeti (Km) and the relatively short vector also indicates the non-informativeness of the environments. The rug plot also portrays the association of the different environments based on the angle of the vectors (Fig. 5.12).

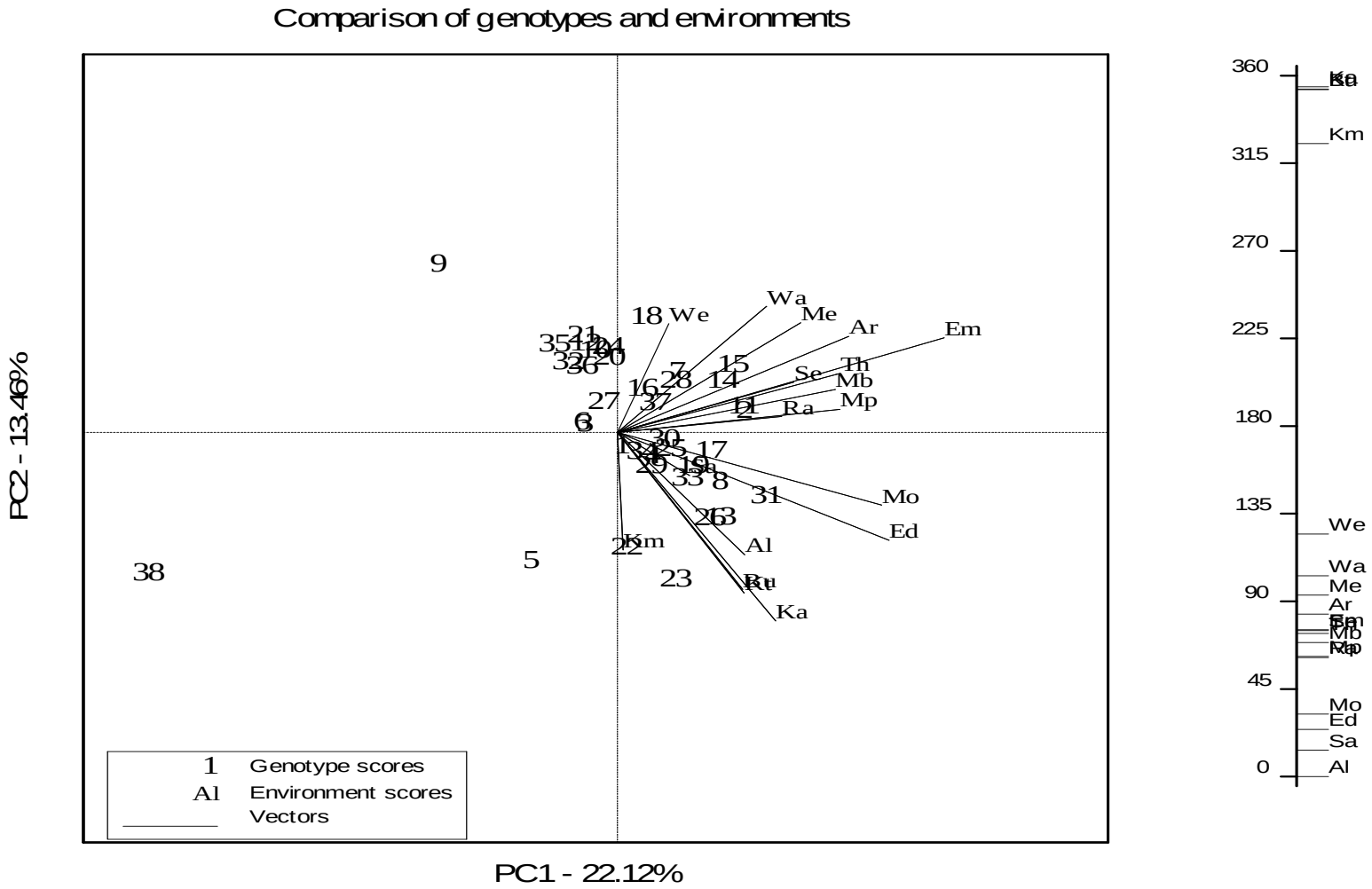

Figure 5.12 Association of the 18 test environments (texts) of ECA based on the grain yield of 38 OPVs (37 QPM and a normal check) evaluated during 2007-2008. The vectors and the rug plot display the association/relation of the different environments.

Which-won-where or which was the best for what?

An important feature of a GGE biplot is its ability to graphically display the presence of crossover G x E interaction, mega-environment differentiation and indication on the specific adaptation of genotypes. In a which-won-where pattern, a polygon is first drawn on genotypes that are furthest from the biplot origin so that all the other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin (Yan and Tinker, 2006). More details on this pattern are presented in Chapter 4.

In Figures 5.13 and 5.14 are presented the which-won-where pattern based on the grain yield performance and days to anthesis of the 38 OPVs, respectively. In Figure 5.13, five sectors of the polygon contained all 18 environments suitable for the different vertex genotypes based on the grain yield performance. Genotype 23 was the best genotype for the environments of Kimaeti (Km), Alupe (Al), Bungoma (Bu), Kitale (Kt) and Kakamega (Ka), all in Kenya. Genotype 31 was best for Mosso (Mo)-Burundi, Elgon Downs (Ed)- Kenya and SARI(Sa)-Tanzania. Genotype 2 was the best entry for Rahad (Ra)-Sudan, Mparambo (Mp)-Burundi and Mbulumbulu (Mb)-Tanzania followed by entry 11 within the same environment. However, genotype 15 excelled in many of the environments viz. Wad Madani (Wa), Melkassa (Mel), Arusha (Ar), Embu (Em), Selian (Se) and Thika (Th). Genotype 18 was closer to Weruweru (We) than genotype 9. The commercial OPV check (Katumani) was not the best in any of the environments (Figure 5.13).

Figure 5.14 shows the which-won-where pattern based on days to anthesis. Since the genotypes were in the early maturity group, the best genotypes were identified based on the highest days to anthesis (late flowering) in the assigned environments. Hence, entry 3 was the latest flowering at Wad Madani (Wad), entry 37 was late at Rahad (Ra), Mbulumbulu (Mb), Selian (Se) and SARI (Sa). Entry 1 was late in days to anthesis at Mparambao (Mp) while entry 9 was late maturing in the rest of the environments. However, Katumani (38) was not late maturing in any of the environments indicating that the variety was the best in terms of early maturity in the range of environments of ECA. The relatively late flowering entries were not high yielding, rather they were winners for being late in flowering than for grain yield (Fig. 5.14).

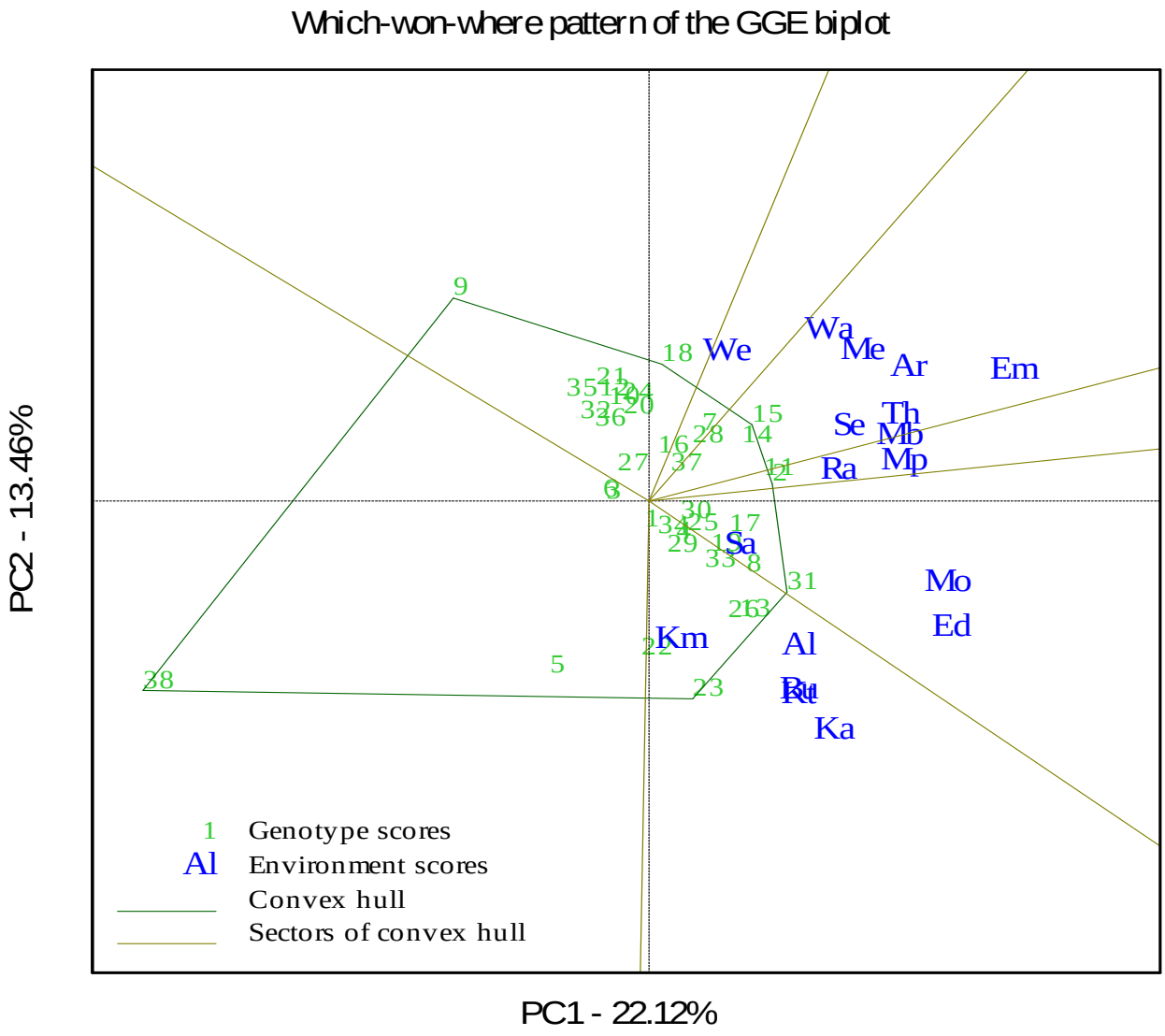

Figure 5.13 Which-won-where pattern of the GGE biplot based on the grain yield performance of 38 OPVs evaluated in 18 environments of ECA during 2007-2008.

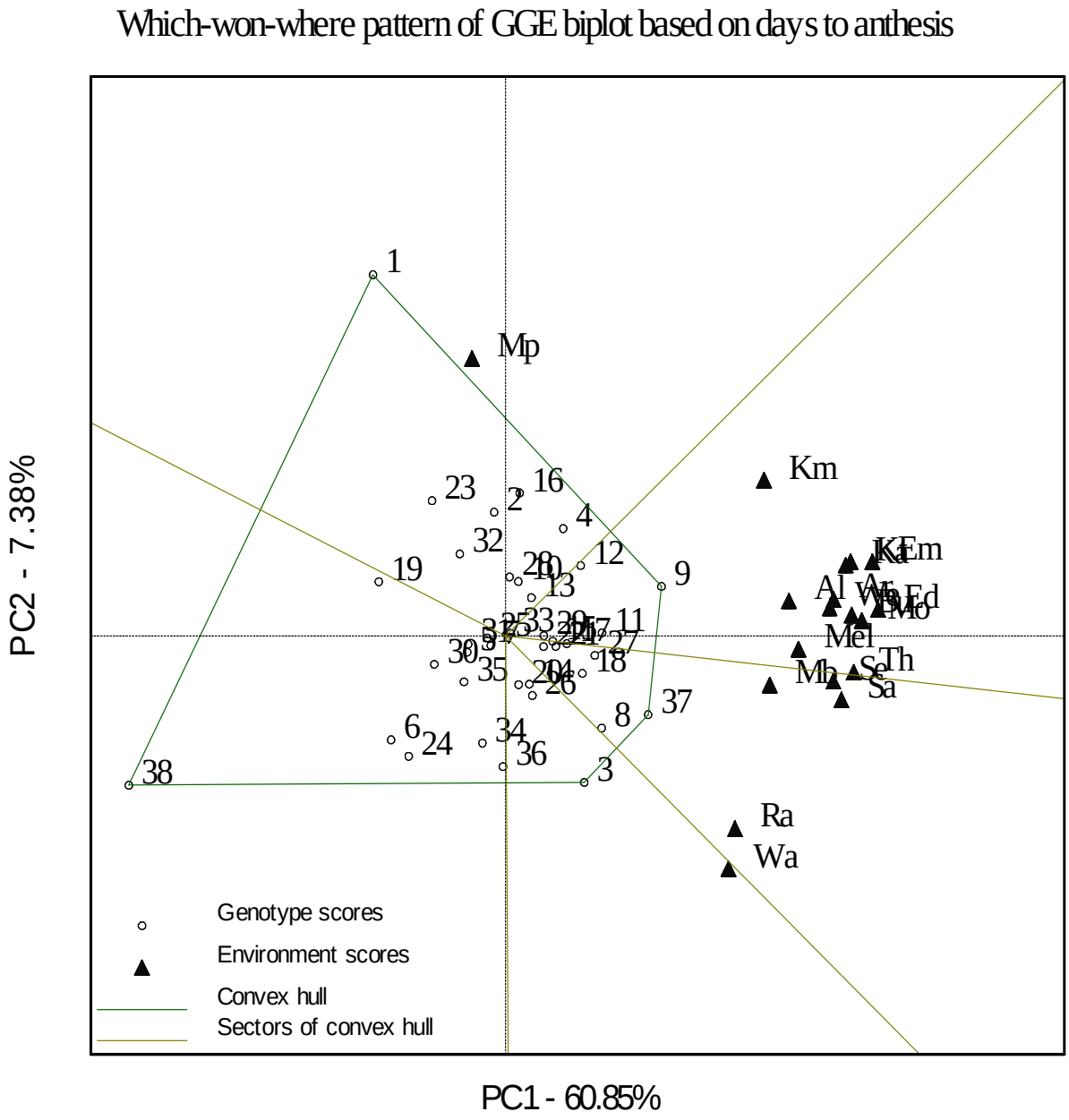

Figure 5.14 Which-won-where pattern of the GGE biplot based on days to anthesis of 38 OPVs (37 QPM and a normal check) evaluated in 18 environments of ECA during 2007-2008.

Mega-environment analysis based on grain yield and days to anthesis

The environments were examined in order to delineate them into mega-environments. However, multi-year data will be required to confirm that groupings are repeatable across years. Figures 5.15 and 5.16 show the mega-environments identified based on grain yield performance and days to anthesis, respectively. The 18 test environments of ECA were grouped into five interlinked mega-environments based on the grain yield performance of the 38 OPVs (Fig. 5.15). The environments Sa, Km, Al, Kt, Bu and Ka were grouped into a similar mega-environment. The second mega-environment comprised Kenya (Embu-Em), Tanzania (Arusha-Ar), Ethiopia (Melkassa-Me) and Sudan (Wad Madani-Wa). Embu, Arusha and Melkassa are geographically similar as they are located within the 1500m elevation zone. However, the inclusion of Wad Madani, which is at 411m elevation, in this group needs to be confirmed. The main reason for the inclusion of Wad Madani in the second mega-environment seems to be the poor performance of the OPVs during the 2008 season resulting in the deviation of the environments from the overall mean minimum. The small deviation from the overall mean indicates similar performance of genotypes in the environments during the season. The third mega-environment consisted of Selian (Se), Thika (Th), Mparambo (Mp), Mbulubulu (Mb) and Rahad (Ra). The fourth and fifth mega-environments contained of fewer environments with Mosso (Mo) and Elgon Downs (Ed) constituting the fourth mega-environment while Weruweru (We) was the only in the fifth mega-environment (Fig.5.15).

Figure 5.16 presents the grouping of the 18 environments based on the response to days to anthesis of the 38 genotypes. The environments were grouped into four categories. Mparambo (Mp) in Burundi and Rahad (Ra) and Wad Madani (Wa) in Sudan constituted the first two mega-environments. The third group was made up of environments in Kenya viz. Kimaeti (Km), Kakamega (Ka), Kitale (Kt) and Embu (Em). The fourth group comprised the remaining 11environments (Al, Ar, We, Bu, Mo, Ed, Mel, Th, Mb, Se, Sa). From the grouping of the mega-environments it may be concluded that the environments, Mp, Ra and Wa are best for evaluating genotypes with days to anthesis ranging between 50 and 58 days. Therefore, these environments are ideal for testing early to extra early maize germplasm. The remaining environments would be suitable for testing germplasm with days to anthesis of between 60 and 67 days. However, the environments, Arusha (Ar), Elgon Downs (Ed) and Thika (Th) need to be evaluated further as the days to anthesis was above the over all mean of

66 days. The average days to anthesis at Thika was 81 days, Elgon Downs 79 and 72 days (for 2007 and 2008) and Arusha, 75 days. These environments would be more appropriate for the evaluation of genotypes with more than 70 days to anthesis (Fig. 5.16).

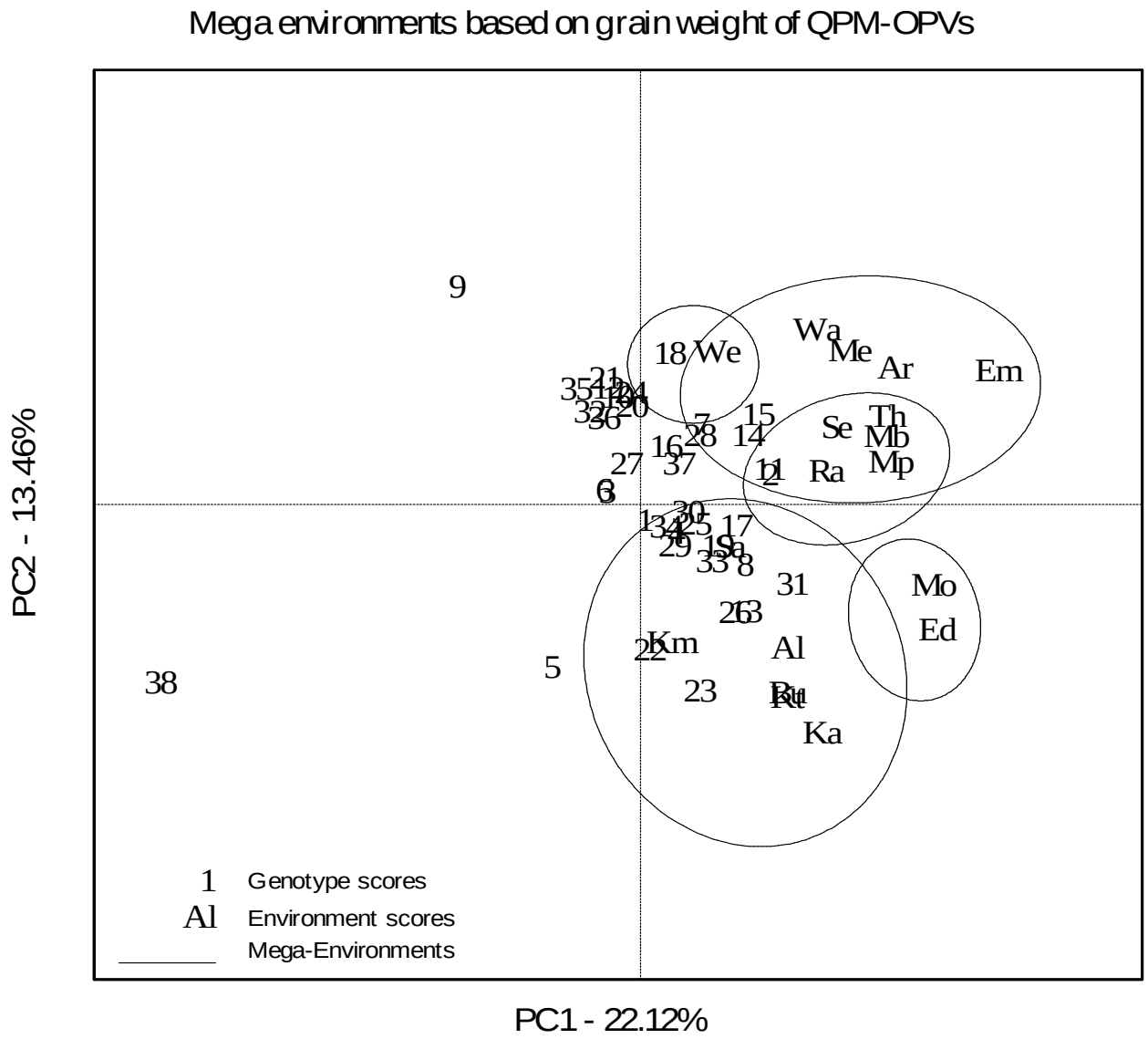

Figure 5.15 Grouping of mega-environments based on the grain yield performance of 38 OPVs evaluated in 18 environments of ECA during 2007-2008.

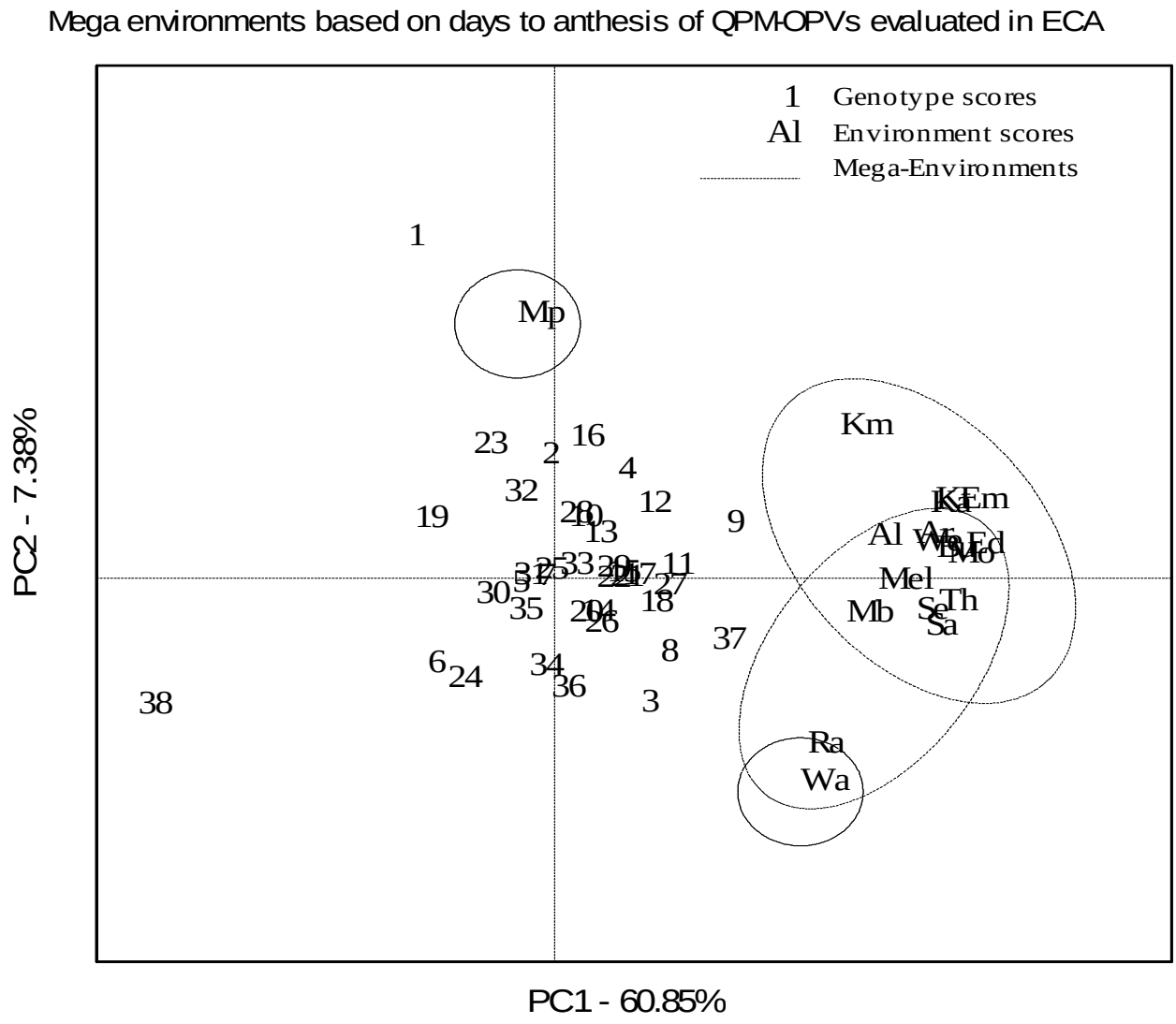

Figure 5.16 Grouping of mega-environments based on days to anthesis of 38 OPVs evaluated in 18 environments of ECA during 2007-2008.

Discriminating ability and representativeness of test environments

Figure 5.17 and 5.18 show the discriminating power and representativeness of the test environments based on grain yield and days to anthesis, respectively. The concentric circles on the biplot of the environment vectors, which are proportional to the standard deviation within the respective environments, are the measures of the discriminating ability of the test environments (Yan and Tinker, 2006). The small circle on the average environment axis (AEA) is defined by the average principal component 1(PC1) and principal component 2 (PC2) scores across all test environments or it has the average coordinates of all the environments. The average tester sign helps, among others, to visualise the mean performance of the entries across testers and to identify the ideal tester (Yan, 2001; Yan and

Tinker, 2006). Accordingly, the most discriminating environments based on grain yield performance were Embu (Emb), Mosso (Mos) and Elgon Downs (Edo) because of their large projection. The least discriminating environments were Weruweru (Wer) and Kimaeti (Kim). The representative environment is the one close to the average environment axis. Hence, Rah (Rahad) and Sar (SARI) were more representative environments. Kim, Wer, Wad and Kak were less representative. Test environments that are both discriminating and representative are desirable for selecting widely adapted genotypes (Yan and Tinker, 2006). Hence, Rah and Sar were not discriminating, as a result they were not good environments to select generally adapted environments. Discriminating but non-representative environments (e.g Emb, Mos and Edo) are useful for recommending specifically adapted genotypes provided the target environments can be divided into mega-environments (Fig 5.17). Non-discriminating test environments are less useful because they provide little information on the genotypes.

The ideal test environment is the one most representative and most discriminating and it is the centre of the concentric circles. The ideal environment is a point on the AEA in the positive direction (most representative) with a distance to the biplot origin equal to the longest vector of all environments (most informative) (Yan and Tinker, 2006). Mosso (Mos) was the closest to the centre of the concentric circle and it was the best environment, whereas Wer and Kim were the poorest environments for selecting cultivars for wider adaptation (Fig. 5.17). Yan and Tinker, 2006 recommended that experiments should be repeated in order to confirm a specific test location as an “ideal” environment.

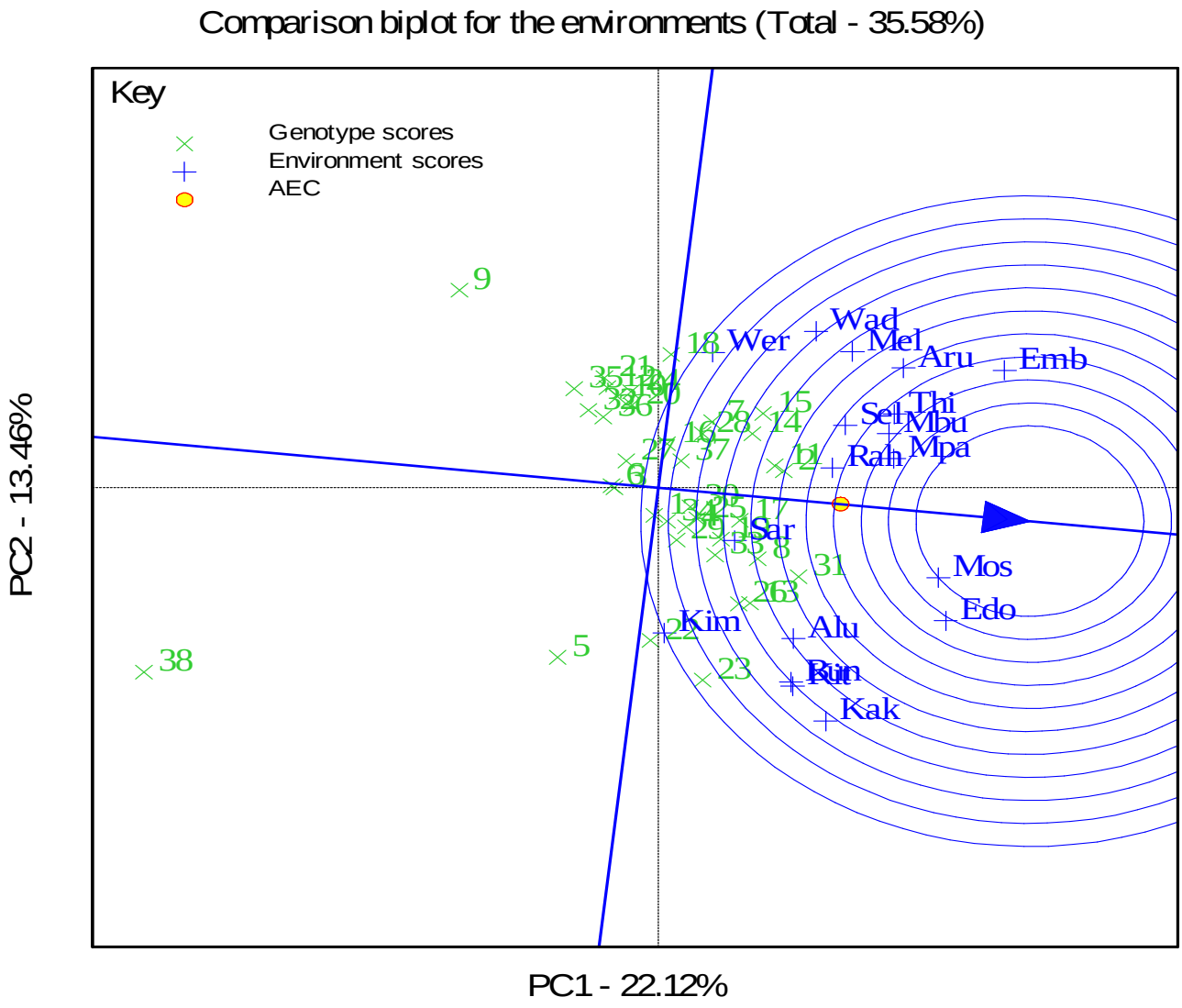

Figure 5.17 Discriminativeness vs. representativeness of test environments based on the grain yield performance of 38 OPVs (37 QPM and a normal check) evaluated in 18 environments of ECA during 2007-2008.

Similarly, the test environments were evaluated for their discriminating ability and representativeness based on the days to anthesis of the 38 genotypes (Fig. 5.18). Unlike the grain yield, the environments showed closer performance for days to anthesis. This is an indication of the relatively stable performance of the genotypes based on their days to anthesis across the diverse environments. Accordingly, the environments, Mp, Wa, Ra and Km were the most discriminating. However, Mel and Mo were right in the centre of the concentric circle, much closer on to the AEA than the other genotypes; hence, they are more representative (Fig. 5.18).

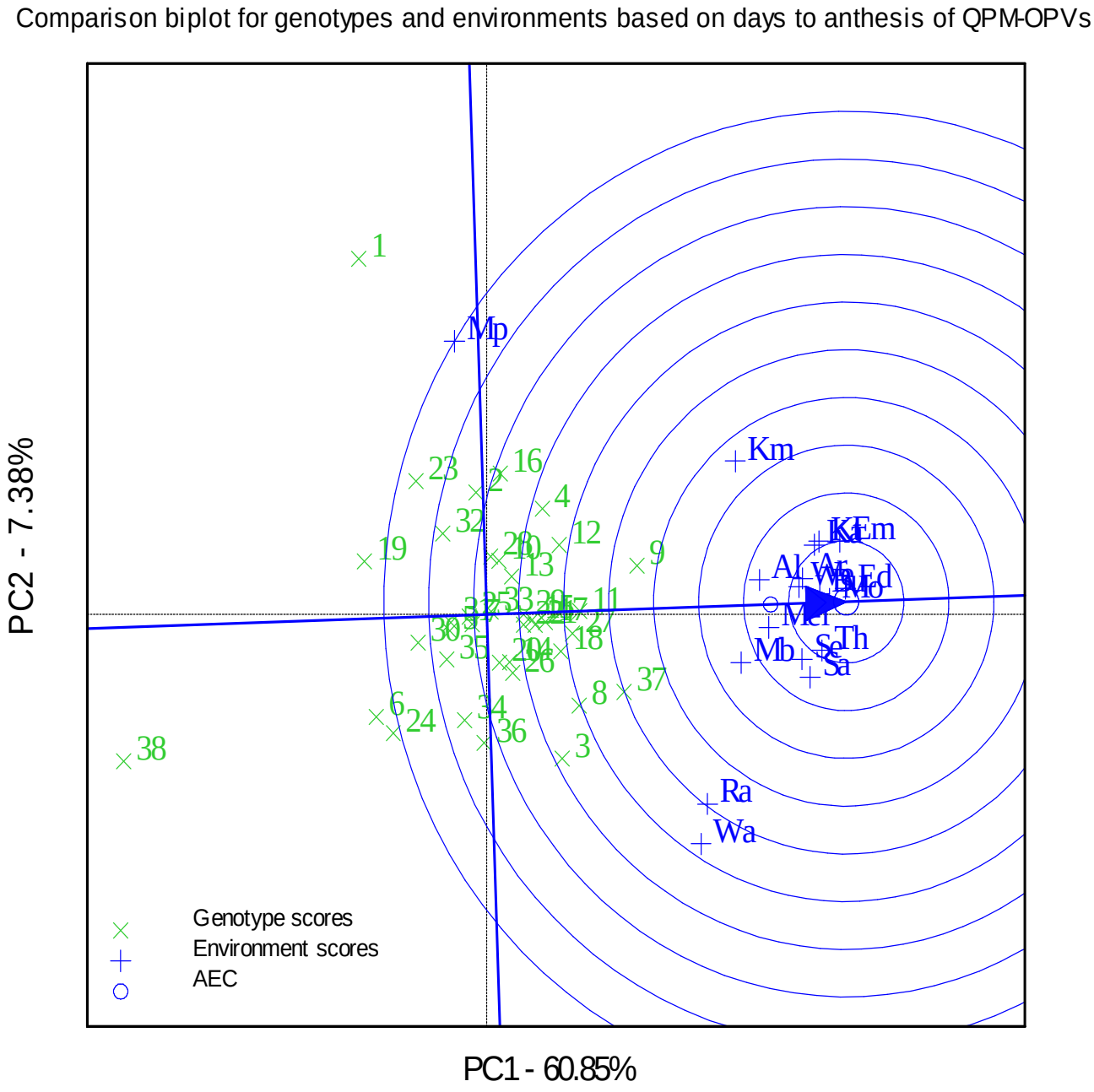

Figure 5.18 Discriminitiveness vs. representativeness of test environments based on the days to anthesis of 38 OPVs (37 QPM and a normal check) evaluated in 18 environments of ECA during 2007-2008.

From Fig.5.18 it can be further concluded that the environments, Mp, Ra and Wa, may be used for the evaluation of genotypes with earliness in their days to anthesis. The other environments may be used for testing genotypes with average days to anthesis between 60-67 days. However, additional seasons might be required to establish these recommendations.

Comparison of genotypes relative to the ideal genotype based on grain yield

An ideal genotype is one with high mean performance and high stability across environments. It is at the centre of the concentric circles and a point on the AEA ("absolute stability") in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of the AEA ("highest mean performance"). Genotypes located close to the 'ideal genotype' are more desirable than others (Yan and Tinker, 2006).

Figure 5.19 shows the ranking of the genotypes relative to the ideal genotype. Entry 31 was the closest to the ideal genotype hence it was the most preferred genotype followed by entries 2 and 11. Entries 17 and 8 were also close to the ideal genotype. Entries 6, 3, 30 and 17 were considered as stable due their minimum projection onto the AEA. Entry 38 (Katumani) was identified as poor performing and highly unstable followed by entry 9 and entry 5 (Fig. 5.19).

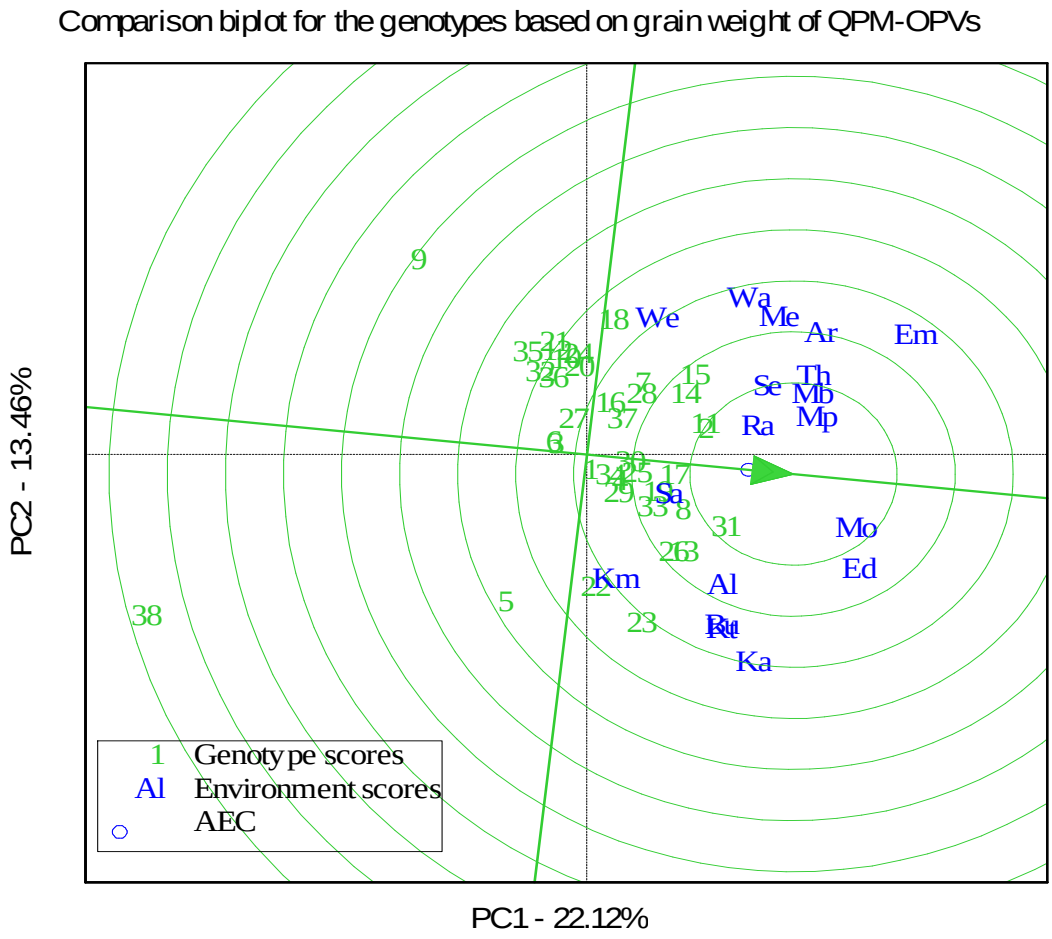

Figure 5.19 Ranking of genotypes relative to the ideal genotype based on the grain yield of 38 OPVs (37 QPM and a normal check) evaluated in 18 environments of ECA during 2007-2008.

Comparison between two genotypes

The GGE biplot also provides an option for visually comparing any two genotypes. This can be done by connecting two genotypes with a straight line, followed by drawing of a perpendicular line that passes through the biplot origin. According to Yan and Tinker (2006) this perpendicular line is the "equality line" of the two genotypes. That is, the two genotypes to be compared should be equal in all environments that are located on this line. A genotype has superior value in environments that are located on its side of the equality line.

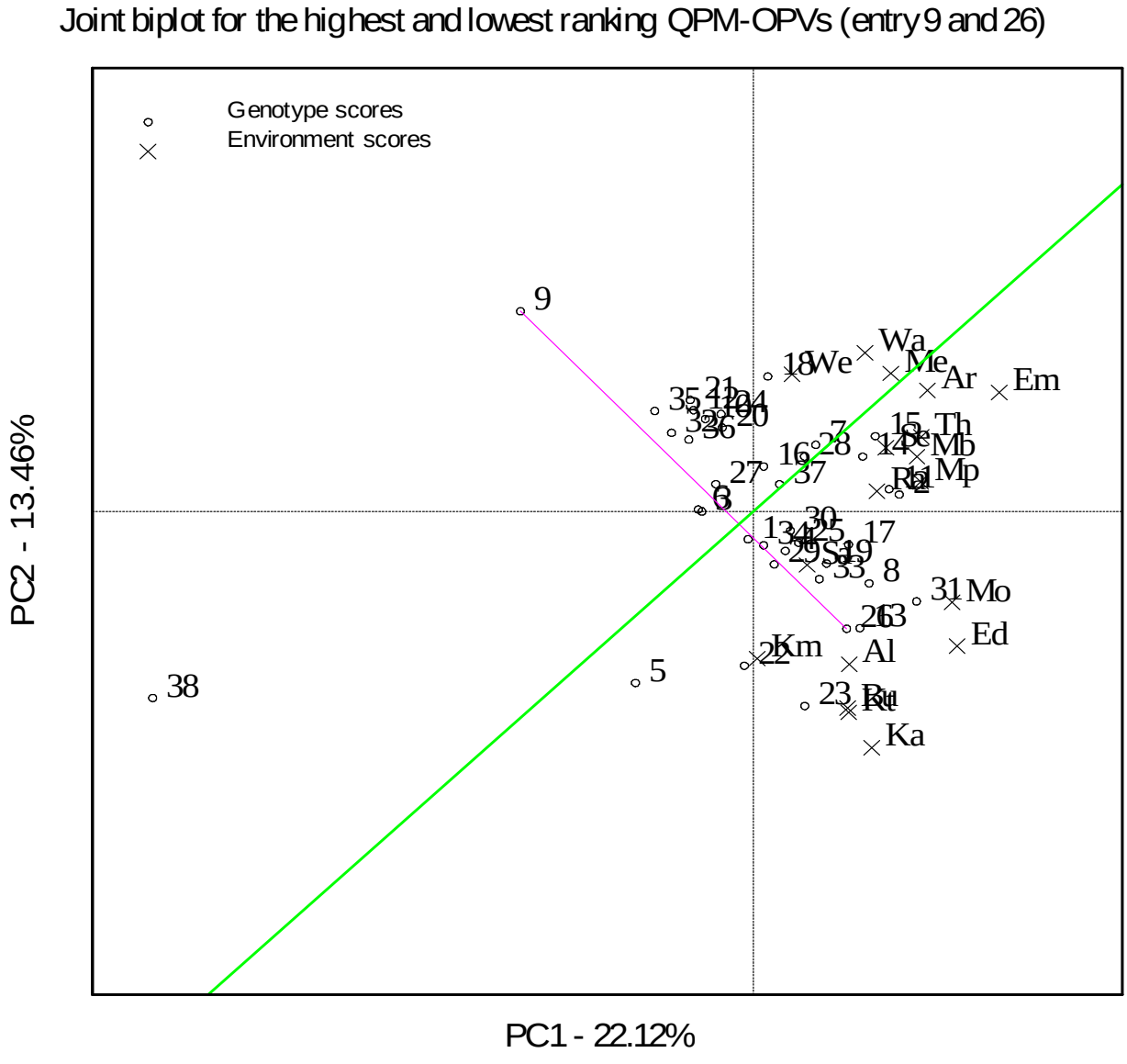

Figure 5.20 Comparison between two genotypes (entry 9 and 26) based on grain yield performance in individual environments.

A comparison between a high ranking and low ranking open pollinated QPM variety entry 9 and entry 26 was made, based on their grain yield performance to visualise the entries' favourable environments (Fig.5.20). Entry 9 had better yield at We, Wa and Me. However, entry 26 was higher yielding in the other environments indicating the presence of crossover G x E interaction. In addition the difference between the two genotypes was relatively high at Ka and We but very small at Ar which is very close to the equality line (Fig.5.20). The differences between two genotypes vary with the environment, and it is proportional to the distance of the environment to the equality line (Yan and Tinker, 2006).

Genotypes and environments centred comparison

Comparison of specific genotypes or environments will help to understand in detail the performance of the genotypes or environments. Genotype-centred data will help to visualise the response of specific genotypes across the test environments. In genotype-centred data analysis the singular value is entirely partitioned into the genotypes eigenvectors, i.e., alpha=1, beta=0. This singular value partitioning is mainly required for comparisons between genotypes. In the environment-centred data analysis, the singular value is entirely partitioned into environment eigenvectors, i.e., alpha = 0, beta = 1 and this facilitates comparisons of test environments (Yan and Tinker, 2006; www.ggebiplot.com).

Figure 5.21 presents the comparison of two environments (Melkassa and Embu) based on grain yield performance. Melkassa represents an average yielding environment (3.54 t ha^{-1}) while Embu represents a high yielding environment (8.78 t ha^{-1}). When comparing two genotypes or environments, the biplot will change to a mono-plot as it will have only entries or environments. The diagonal line is the equality line and genotypes or environments on this line are expected to have similar performance in the two environments (genotype-centred) or on the two genotypes (environment-centred). Entries above the equality line are better for the environment Embu and others below the equality line are better for Melkassa. Thus, entries 8, 2, 31 and those above the equality line were better for Embu while entries 11, 13, 25, 9 and others below the equality line are superior in Melkassa. The performance of entries 35 and 36 were similar at Melkassa and Embu. The check variety, Katumani was better at Embu than Melkassa in terms of grain yield (Fig.5.21). It is important to evaluate the genotypes over years to determine their repeatability in performance in the specific environments.

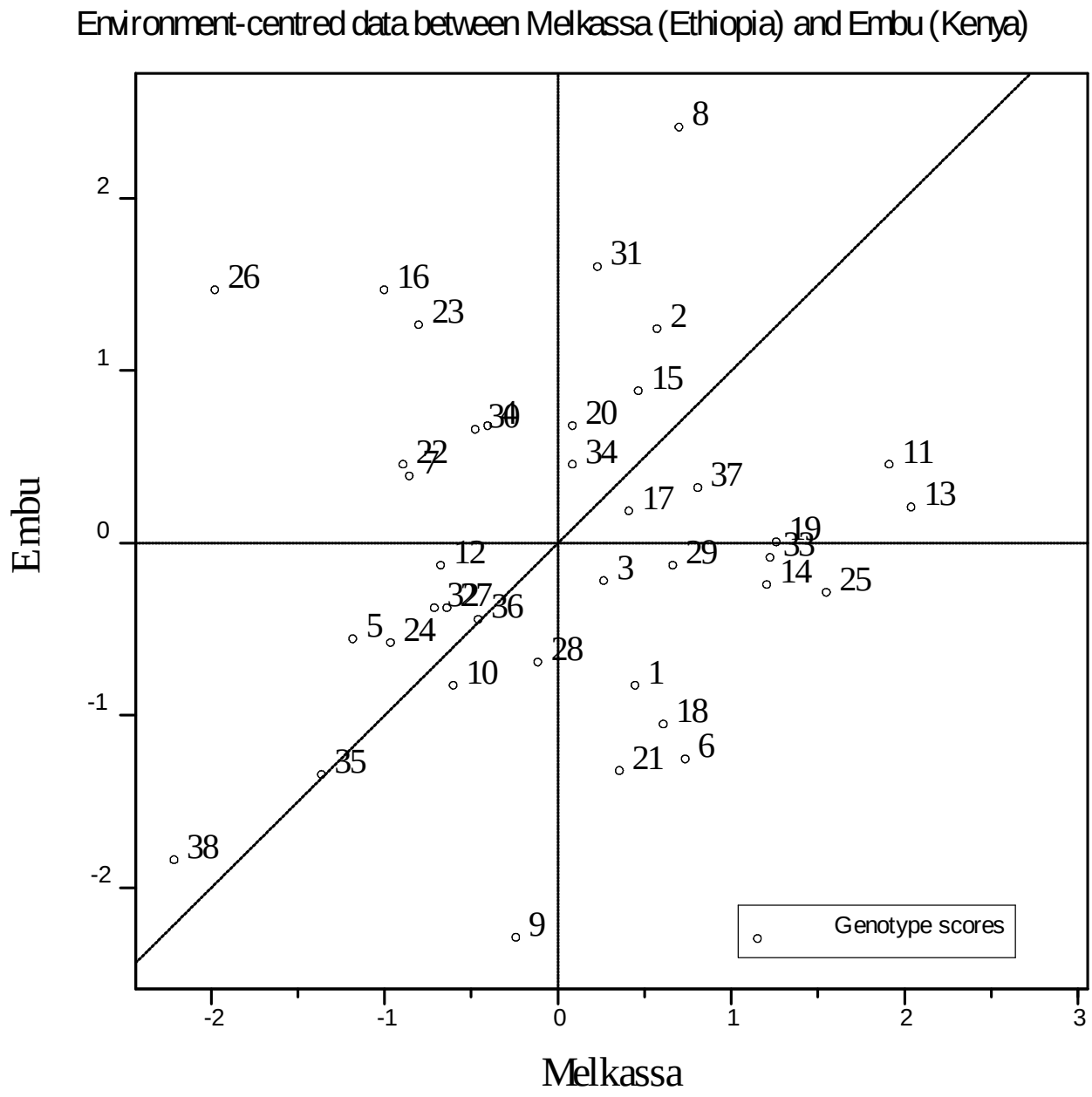

Figure 5.21 Comparison of genotypes based on the performance at Melkassa and Embu for grain yield based on environment-centred data.

Figure 5.22 shows the comparison of Katumani (entry 38) and the candidate variety (entry, 37) based on days to anthesis. Katumani was the earliest normal endosperm OPV in terms of days to anthesis; however, the QPM entry 37 was late flowering based on the average records of the 38 genotypes included in the study. Katumani was quite early and no QPM OPV was earlier than it in any of the environments. The environment Mparambo in Burundi, which is on the equality line, was the only environment where entry 37 was similar to Katumani in days to anthesis. Hence, it may be concluded that Katumani was the earliest open pollinated

variety evaluated in the 18 environments of ECA during 2007 and 2008. On the other hand entry 37 was a high ranking genotype for its lateness in days to anthesis in almost all the environments. It was the latest maturing at Ra, Se, Th, Sa and Kt (Fig. 5.22).

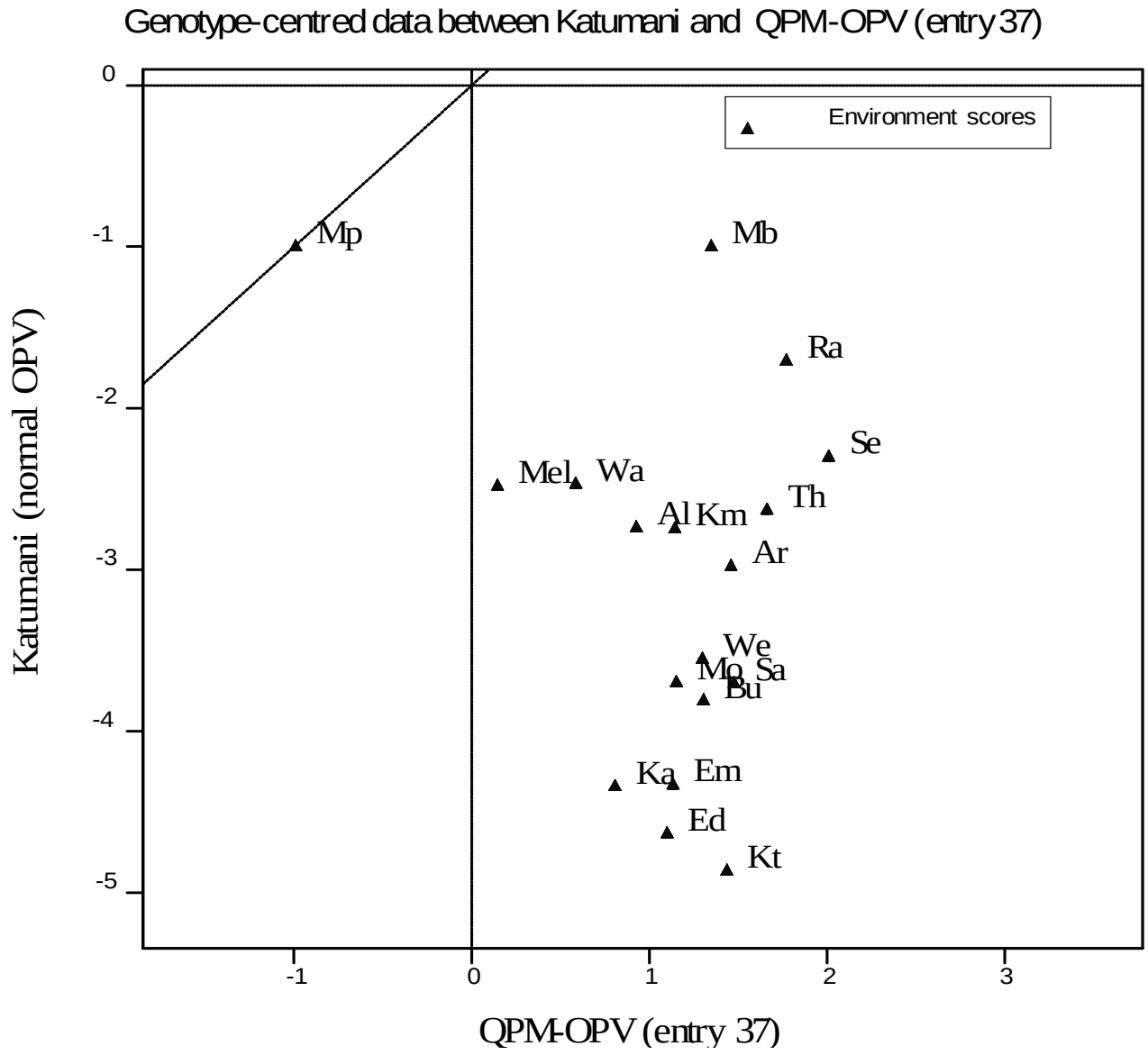

Figure 5.22 Comparison of environments based on the days to anthesis of entry 37 (QPM-OPV) and Katumani using the genotype-centred data.

5.4.4 The effect of recycling of QPM OPVs on grain yield

One of the advantages of OPVs over hybrids is the recycling of OPV seeds for subsequent season plantings without much difference in grain yield. This is mainly due to the higher number of maize genotypes included in the formation of OPVs compared to the limited number of inbred lines involved in hybrids. Recycling of hybrid seeds will result in an immediate noticeable yield reduction in the first and second generations. Although, the amount of yield reduction depends on the type of hybrid used, higher yield loss is expected in single cross or other conventional hybrids than non conventional hybrids during recycling. Pixley and Bänziger (2001) reported a yield loss of 32% for elite conventional hybrids and 16 % for top cross hybrids by recycling seeds from the first generation of plants and 5% for OPVs by recycling seeds from the second generation of plants. Similar conclusion was reached by Morris *et al.* (1999) in their report on genetic change in farmer-recycled maize seed. Although some research has been reported on the performance of open pollinated QPM varieties from METs (Pixley and Bjarnason, 2002), the effect of recycling of QPM OPVs on grain yield is not well documented.

Table 5.38 shows the yield loss that occurred at the fourth generation of the OPVs. Based on the continuity of the genotypes in the successive trials seasons (2006-2008), the grain yield data of 19 QPM OPVs and the commercial check Katumani were compared for yield reduction. Each season the seed was produced by plant-to-plant (full-sib) hand pollination within the individual varieties to protect them from external pollen contamination. As a result, an average of 38% yield loss from the average of the three generation was recorded for the 20 OPVs at the fourth generation. The average yield loss for the 19 QPM-OPVs was 39% and for Katumani it was 32%. The maximum yield loss (46.5%) was recorded for entry 19 (POOL15QPM-SR-#-#) and the minimum yield loss (26%) for entry 7 (EEQPM-16-EA-#). Table 5.38 also indicates that the yield loss between the first generation and the fourth generation was almost 35%, a smaller variation than the combined results from the 27 sites obtained after three times of recycling (38%). This shows that recycling of OPVs for at least three generations, regardless of the number of environments, will give similar results (Table 5.38).

Table 5.38 Comparison of QPM OPVs and Katumani across generations for the assessment of yield loss due to recycling of OPV seed

Pedigree	Entry number	Mean grain yield (t ha^{-1}) for trial set A: Year 1 2006 (11 sites)	Mean grain yield (t ha^{-1}) for trial set A: Year 2 2007A (6 sites)	Mean grain yield (t ha^{-1}) for trial set B: Year 3 2007B (10 sites)	Mean grain yield (t ha^{-1}) for trial set B: Year 4 2008 (10 sites)	Mean grain yield (t ha^{-1}) years 1-3 (27 sites)	Yield loss between the 4th generation and the mean yield at the 3rd generation (%)	Yield loss after the 4th recycle of OPV seeds (i.e. between year one and year four) (%)
EEQPMOPV-1-EA-#	1	3.85	4.19	4.43	3.01	4.16	27.59	21.82
EEQPM-HT -#	2	3.96	4.96	3.96	2.57	4.29	40.14	35.10
EEQPM-6-EA -#	3	3.94	4.41	3.93	2.57	4.09	37.21	34.77
EEQPM-9-EA-#	4	4.05	4.44	4.24	2.72	4.24	35.90	32.84
EEQPM-8-EA-#	5	3.88	4.49	4.44	2.61	4.27	38.88	32.73
EEQPM-13-EA-#	6	4.23	4.45	4.13	2.77	4.27	35.13	34.52
EEQPM-16-EA-#	7	4.19	4.42	3.99	3.10	4.20	26.19	26.01
EEQPM-18-EA-#	8	4.02	5.29	5.23	2.69	4.85	44.50	33.08
EEQPM-29-EA-#	9	4.03	4.97	4.45	2.63	4.48	41.34	34.74
EEQPM-34-EA-#	10	4.23	4.18	4.61	2.77	4.34	36.18	34.52
EEQPM-36-EA-#	11	4.11	5.00	4.58	2.59	4.56	43.24	36.98
EEQPM-38-EA -#	12	4.09	4.28	4.68	2.35	4.35	45.98	42.54
EEQPM-45-EA -#	13	4.35	4.65	5.14	2.85	4.71	39.53	34.48
EEQPM-49-EA-#	14	4.02	4.75	4.00	2.95	4.26	30.70	26.62
EEQPM-21-EA-#	15	4.32	5.00	4.22	2.68	4.51	40.62	37.96
EEQPM-33-EA-#	16	4.05	4.44	4.44	2.61	4.31	39.44	35.56
EEQPM-42-EA-#	17	4.03	4.62	4.07	2.53	4.24	40.33	37.22
EEQPMS2-#-GEASP - 1-#	18	4.08	4.38	4.21	2.36	4.22	44.12	42.16
POOL15QPM-SR-#-#	19	4.42	4.95	4.88	2.54	4.75	46.53	42.53
Katumani (normal maize)	20	2.64	2.94	2.61	1.83	2.73	32.97	30.68
Mean		**4.02**	**4.54**	**4.31**	**2.64**	**4.29**	**38.33**	**34.49**

Although yield is the sum total effects of many biotic (pests and diseases) and abiotic (for example rain, temperature and soil) factors, recycling of OPV seeds was confirmed to cause significant yield reduction in the subsequent generations. Hence, it is advisable to maintain and refresh the seed stock of OPVs at least every three years to benefit from the genetic gain. Figure 5.23 graphically displays the yield performance of the 20 OPVs. Each line on the band shows the yield level of individual genotypes in each year. The mean yield reduction is shown at the fourth year where the band/rug plot shows a below 3.5 t ha^{-1} average yield level (Fig.5.23).

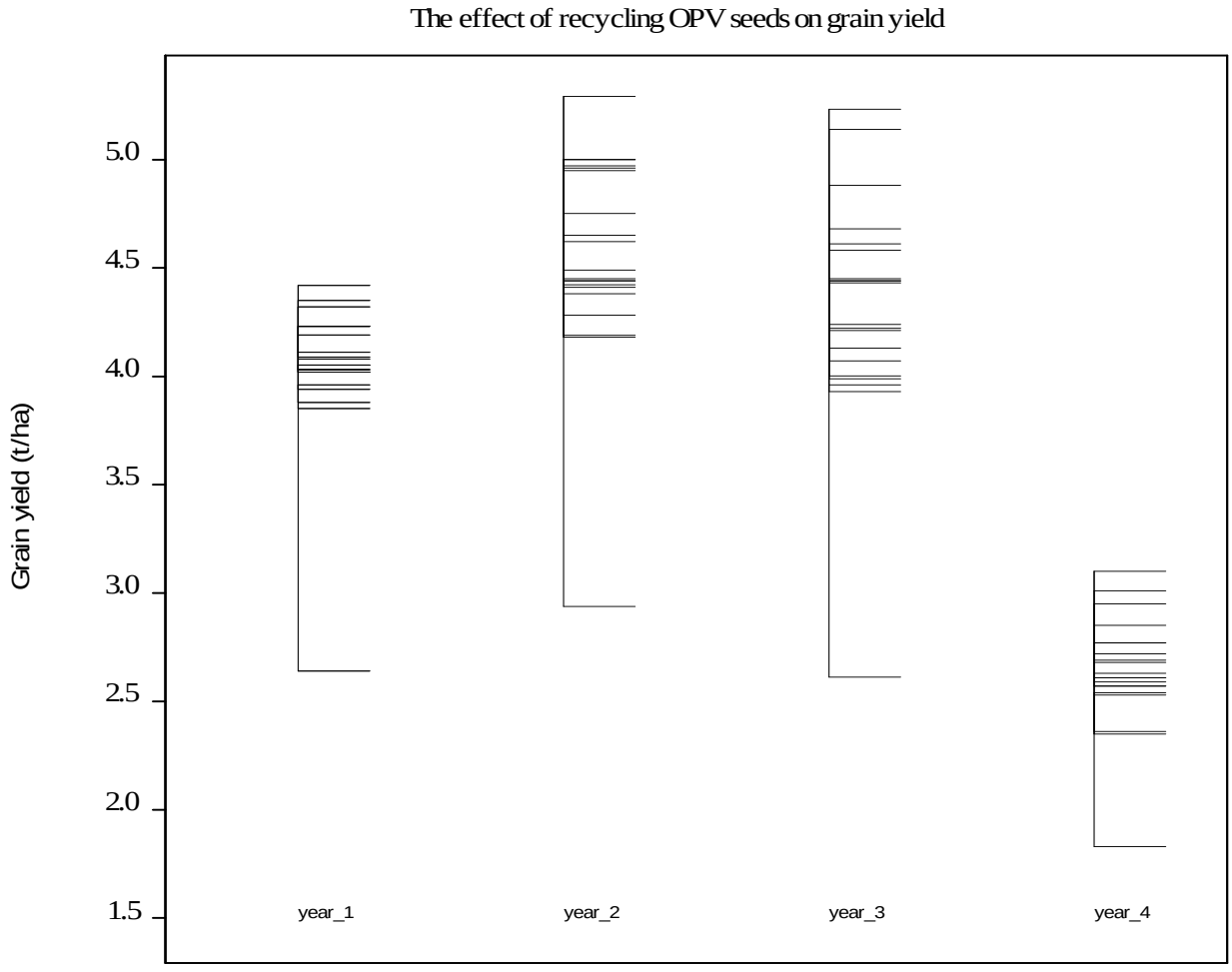

Figure 5.23 A graph (rug plot) showing the effect of recycling of OPV seeds on grain yield based on 20 OPVs (19 QPM and a normal check) evaluated for four seasons in ECA. The band show the yield level for each variety and the bottom log of the band shows the yield of the normal check (Katumani). The band at the fourth recycle indicated significant yield reduction.

5.5 Conclusions

Open pollinated varieties of QPM developed at CIMMYT Kenya were evaluated for their grain yield performance and days to anthesis under the diverse environments of ECA for four years. The evaluation was done in two sets of trials. The first set (set A) consisted of 21 varieties (19 QPM and two normal checks) and it was conducted during 2006 and 2007. The second set of trials (set B) was conducted during 2007 and 2008 and consisted of 39 varieties (37 QPM and two normal endosperm checks). The 19 QPM entries from the set A trials were also included in the set B trial and the remaining 18 QPM entries in the set B trial had a similar background to entries of set A except that they were developed through successive bulking of selected ears during the OPV formation.

Analysis of variance indicated significant and highly significant ($P \leq 0.05$ and $P \leq 0.01$) variability for grain yield and days to anthesis across all environments in 2006 and 2007. In all the environments the contribution of entries to the total variation was high for both grain yield and days to anthesis. However the percent contribution of entries to total variation was higher for days to anthesis than grain yield indicating that the influence of environmental factors was more pronounced on grain yield than days to anthesis.

The candidate QPM varieties out yielded the local checks in ten environments. In the remaining seven environments the various local checks out yielded the QPM candidates as well as the commercial standard check, Katumani (Table 5.8 and Table 5.9). The candidate QPM varieties out-yielded Katumani across the environments. Among the QPM candidates, V19 (POOL15QPM-SR-#-#) was best in more than one environment (at Embu in 2007 and at Kiboko in 2006 and 2007) with an average grain yield of 4.42 t ha^{-1} in 2006 and 4.95 t ha^{-1} in 2007. This indicates the potential for across environment suitability of the variety. Based on individual environments mean yield, the three highest yielding environments were: Kiboko-Kenya (8.70 t ha^{-1}), Embu-Kenya (8.27 t ha^{-1}) and Melkassa-Ethiopia (6.22 t ha^{-1}). Similarly the three lowest yielding environments were: Kakamega-Kenya (0.73 t ha^{-1}), Gandajika-DRC (2.04 t ha^{-1}) and Elgon Downs-Kenya (2.29 t ha^{-1}) (Tables 5.8 and 5.9). The yield differences among environments are a clear indication of the presence of significant cross over G x E interaction.

The commercial check variety, Katumani proved to be the earliest in male flowering in all the environments except at Kiboko in 2006 and Arusha in 2007 where local checks flowered earlier than Katumani. The mean days to anthesis for the 21 varieties in 2006 were 66.12 and for Katumani 58.61 and the mean days to anthesis for 2007 was 64.23 and for Katumani it was 58.27. Based on the mean days to anthesis of the 21 entries, the three earliest environments were: Wad Madani-Sudan (49.56 days), Gandajika-DRC (55.14 days) and Kiboko-Kenya (55.32 days). Similarly the environments with the most days to anthesis were: Selian-Tanzania (84.56 days), Arusha-Tanzania (81.81 days) and Elgon Downs-Kenya (81.22 days). This shows the extent of environmental influence (temperature and photoperiod) on the flowering time of the genotypes (Table 5.10 and Table 5.11).

Results of trial set B showed significant and highly significant ($P \leq 0.05$ and $P \leq 0.01$) variability for grain yield and days to anthesis across environments. The candidate QPM OPVs were superior in grain yield in nine environments out of ten during 2007. However the candidates were best in only four out of ten environments during 2008, probably an indication of declining grain yield of the QPM OPVs at the fourth generation of recycling. Yield reduction due to recycling may not be similar for the local checks as they differ from location to location and not similar in their genetic makeup as well (Tables 5.12 -5.17). The genotype contribution to total variation declined in 2008 as compared to the previous years and other environmental factors contributed more than 50% of the total sum of squares in four of the ten environments. The commercial check variety was the earliest flowering in all the environments except at Kakamega-Kenya and Mbulumblu-Tanzania where the QPM candidate varieties were earlier than Katumani during 2007. In 2008 Katumani was the earliest in eight out of 11 environments. The least days to anthesis was recorded at Mparambo-Burundi with a mean of 50.60 during 2008 while the maximum days to anthesis was recorded at Thika-Kenya (80.91 days) during 2007 (Tables 5.12 - 5.19).

The combined ANOVA of the two trial sets showed that the major contributor to the total variation was the environment (localities) for both grain yield and days to anthesis. From trial set A entry 19 (POOL15QPM-SR-#-#) was the highest yielder with an average of 4.61 t ha^{-1} while in trial Set B, entry 31 (EEQPM-45-EA -#-#) was the best with an average yield of 4.00 t ha^{-1}. The mean grain yield for trial set A was 4. 21 t ha^{-1} while that of trial set B was 3.48 t ha^{-1}. Based on the combined ANOVA for days to anthesis, Katumani was the earliest variety in both sets of trial with mean days to anthesis of 57 days in trial set A and 58.47 days in trial

set B. The latest flowering entry in trial set A was entry 19 (POOL15QPM-SR-#-#) with mean days to anthesis of 67.56 while in the trial set B it was entry 9 (EEQPMOPV--29-EA-B-B-#-#) with mean anthesis days of 69.2. The mean days to anthesis for trial set A was 64.22 days and for the trial set B, it was 66.30 days (Tables 5.21 - 5.31). Although the candidate varieties were classified as early maturing, there was a minimum of a week difference in male flowering with Katumani.

AMMI analysis of trial set A showed that environments explained 86.35% of the total grain yield variation followed by the G x E interaction (4.36%). The contribution of genotypes to the total variation was low (2.72%) as expected from METs. The first five IPCA axes were highly significant and explained 78.03% of the G x E interaction sum of squares for grain yield. For days to anthesis, environments explained 89.71% of the total variation followed by the genotypes (4.48%) and the interaction between the two (2.57%). The first four IPCA axes were significant and explained 76.23% of the G x E interaction.

Based on the AMMI model, the highest yielder was entry 19 (POOL15QPM-SR-#-#) followed by entry 15 (EEQPM-21-EA-#). Using the AMMI stability value (ASV) entry 7 (EEQPM-16-EA-#) was identified as the most stable with the smallest ASV followed by entry 17 (EEQPM-42-EA-#). The highest yield of entry 19 was an indication of its responsiveness to high yielding environments. The least stable and least responsive was entry 20 (Katumani) and this was clearly shown in the AMMI biplot (Fig.5.3). Similarly, the most responsive environments were KIB3 (Kiboko 1st season planting, 2007) followed by EMB2 (Embu-2007). These two environments were the most discriminating. The least responsive and least stable environment was KAK (Kakamega) and it was placed far from the centre of the biplot. Entry 19 was placed close to the highest yielding environment, Kib3 indicating its adaptation to that environment and entry 9 was found to be more responsive to Emb2. The environments Kib1 (Kiboko 1st season planting, 2006) and Kib2 (Kiboko 2nd season planting, 2006) were placed in the opposite direction of the biplot suggesting the existence of within season variation in the environment. The association among genotypes and environments and between genotypes and environments is elaborated in the various biplots (Fig.5.3 - 5.5).

Additive main effects and multiplicative interactive (AMMI) model analysis showed that entries 12, 15 and 18 were more stable in terms of days to anthesis than the other genotypes while entry 3 was the least stable. Entries with less days to anthesis showed below average

performance for grain yield. The average maximum difference in days to anthesis was ten days between entry 19 and entry 20, however the yield advantage of entry 19 was about 40%. Similarly, the gap between entry 20 and the mean days to anthesis was about a week; however, there was a 35% grain yield gap between entry 20 and the mean yield of the 20 genotypes. This shows the importance of variation in days to maturity on the final grain yield of early maturing tropical maize genotypes. The environments, Mel (Melkassa, Ethiopia) and Kib2 (Kiboko, Kenya-2nd season planting) were placed very close to each other and close to the origin of the biplot indicating their similarity and the relative stability of the environments in terms of days to anthesis. The close similarity between Melkassa and Kiboko further suggests that the two environments can serve equally for testing and exchange of germplasm and that result from one of the environments can be extrapolated to the other. The environments, Aru1 (Arusha, 2006) and Elgon Downs were the most discriminating due to the high mean days to anthesis and the fact that most of the genotypes showed no association with these environments. On the other hand, most of the genotypes showed closer association with Melkassa where mean days to anthesis was around 65 days. The association among genotypes and environments and between genotypes and environments regarding to days to anthesis is discussed in depth and also presented in the different biplots (Fig.5.6 - 5.9).

The genotypes and environments were also evaluated for stability and mega-environment analysis was conducted using the GGE model. The evaluation was done for grain yield and days to anthesis of the 38 genotypes included in trial set B (2007-2008). The high yielding and stable genotype based on proximity to the AEC was entry 31 followed by entries 2 and 11. The least stable and low yielding entry was 38 followed by entries 9 and 5 which were placed far from the AEC. Based on the days to anthesis, the late flowering genotypes were ranked as first and close to the AEC while the early flowering genotypes were far from the AEC (Fig. 5.11). Entries 37 and 9 were the late flowering genotypes while entries 38 (Katumani) and 1 were early flowering. The environment, Elgon Downs (Edo) was ranked first as genotypes took the most days to reach anthesis followed by Arusha (Aru), Thika (Thi) and Mosso (Mos). The lowest ranking environment was Mparambo (Mpa) where male flowering was early. The environments, Wad Madani (Wad), Rahad (Rah), Kimaeti (Kim) and Mparambo (Mpa) were ranked below the AEC meaning that days to flowering was below average an indication of early flowering. In contrast, days to flowering were average at Kakamega (Kak), Mbulumbulu (Mbu) and Melkassa (Mel) (Fig. 5.11).

The GGE biplot analysis for environmental association showed a close association between the environments, Mosso-Burundi (Mo) and Elgon Downs-Kenya (Ed) based on the grain yield performance of the 38 genotypes. Embu and Kakamega were considered as discriminating environments as Embu discriminated genotypes based on high yield and Kakakmega on low yield. SARI (Sa) was the least discriminating environment due to its short vector arm and was also a less informative environment based on grain yield performance of the QPM OPVs. There was a negative correlation between the environments of Weruweru (We) and Kimaeti (Km) an indication of strong crossover G x E interaction. The relatively short vector also indicates the non-informativeness of the environments as compared to others (Fig. 5.12).

The which-won-where pattern of the GGE biplot placed the 18 test environments in five sectors of the polygon. The highest yielding entry 31 was best for Mosso(Mo)-Burundi, Elgon Downs (Ed)- Kenya and SARI (Sa)-Tanzania. However, Entry 15 was identified as the best as it won in six environments for its superior grain yield performance (Fig. 5.13). The "which was the best for what?" pattern was indicated for days to anthesis. Entry 3 won at Wad Madani (Wad) for its highest days to anthesis (for being late in days to anthesis). Similarly, entry 37 won at Rahad (Ra), Mbulumbulu (Mb), Selian (Se) and SARI(Sa) for its long days to anthesis. Entry 1 was late in days to anthesis at Mparambao (Mp) while entry 9 was late in the rest of the environments (Fig. 5.14).

Based on the grain yield performance of the 38 genotypes evaluated under 18 environments of ECA during 2007 and 2008, the GGE biplot identified five interlinked mega-environments. Based on days to anthesis, the test environments were grouped into four mega-environments. The mega-environment grouping based on grain yield was different from that based on days to anthesis. This is mainly because yield of a genotype is affected by many environmental factors other than flowering. The lower number of mega-environment groups based on days to anthesis also showed the similarity of the majority of the genotypes based on their response to flowering. The different mega-environments are discussed and depicted in the GGE biplots (Fig.5.15 and 5.16).

The GGE biplot identified the test environments of Embu, Mosso and Elgon Downs as the most discriminating because of the long projections from the biplot origin. Rahad and SARI were the most representative environments due to the small projection the from average

environment axis (AEA). However, these two environments were not discriminating, and as a result were not suitable for selecting genotypes with wider adaptation. Discriminating environments are good for selecting genotypes adapted to specific environments. Based on days to anthesis, the environments Mp, Wa, Ra and Km were the most discriminating in decreasing order. The rest of the environments generally showed their representativeness due to their overlapping proximity on to the AEA.

The GGE biplot also facilitates the identification of deal genotype and genotypes that are closer to the ideal genotype. Accordingly, entry 31 was the closest to the ideal genotype followed by entries 2 and 11. Comparison was also made between two specific genotypes to further identify environments that were suitable for individual genotypes. Furthermore, mono-plots were constructed based on environment and genotype centred data to examine in detail the performance of specific genotypes (environment-centred) and specific environments (genotype-centred) (Fig.5.17 - 5.22).

The yield of 20 OPVs (19 QPM and a normal check-Katumani) was analysed for the possible yield reduction at the fourth generation [during the years 2006, 2007(two seasons) and 2008)]. As a result, an average of 38% yield loss from the average of the three generation was recorded for the 20 OPVs at the fourth generation. The average yield loss for the 19 QPM-OPVs was 39% and for Katumani it was 32%. The maximum yield reduction (46.53%) was recorded for entry 19 (POOL15QPM-SR-#-#) and the minimum yield loss (26%) for entry 7 (EEQPM-16-EA-#). Although reduction in yield can be caused by many biotic and abiotic stresses, this study indicated the continued use of OPVs seeds more than three generation will cause significant yield reduction. Hence it is generally recommended to maintain the seeds of QPM-OPVs for a possible replacement after three recycling (Table 5.38 and Fig.5.23).

Generally, this study has confirmed the availability of superior QPM OPVs which are more appropriate than hybrids for resource-poor and farmers of marginal areas in ECA. The significant yield advantage of the candidate QPM varieties over the commercial check in nearly all environments of ECA will enhance adoption of the varieties in the region. The AMMI and GGE multivariate models identified superior genotypes and environments based on grain yield and days to anthesis. The models helped to identify stable genotypes for the traits in question and grouped the maize growing environments of ECA into mega-

environments based on grain yield performance and days to anthesis. This study also indicated the possibility of recycling QPM OPVs until the third generation without significant yield loss and recommends maintenance of varieties as well as use of fresh seeds after the third recycling. This study also stresses the importance of a functional maize seed system in ECA to enhance access and availability of QPM seeds particularly to small holder and resource poor farmers and the paramount need of stakeholders' collaboration to alleviate the deplorable trend of food and nutritional insecurity in the region and beyond.

5.6 References

Bänziger, M., and A.O. Diallo. 2004. Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference.5-11 February 2002. CIMMYT/KARI Nairobi, Kenya. pp.189-194.

Bjarnason, M., and S.K. Vasal. 1992. Breeding of quality protein maize (QPM). *Plant Breeding Review* 9:181-216.

Cordova, H.S., and S. Pandey. 1999. Stability and yield performance of high quality protein maize hybrids across 30 locations in the tropical mega-environment. In: Agronomy abstracts. p. 82. ASA, Madison, WI.

Craufurd, P.Q., and T.R. Wheeler. 2009. Climate change and the flowering time of annual crops. *Journal of Experimental Botany* 60:2529-2539.

Diallo, A.O., J. Kikafunda, L. Welde, O. Odongo, Z.O. Mduruma, W.S. Chivatsi, D.K.Friesen, S. Mugo, and M. Bänziger. 2004. Drought and low nitrogen tolerant hybrids for the moist mid altitude ecology of eastern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 206-212.

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

Erenstein, O., G.T. Kassie, A. Langyintuo, and W. Mwangi. 2011. Characterization of Maize Producing Households in Drought Prone Regions of Eastern Africa. CIMMYT Socio-Economics Working Paper 1. CIMMYT, Mexico, D.F.

FAOSTAT. 2010. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

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

Gauch, H.G., and R.W. Zobel. 1996. AMMI analyses of yield trials. In: M.S. Kang and H.G. Gauch (Eds.). Genotype by Environment Interaction. CRC, Boca Raton, Florida, USA. pp. 85-122.

GenStat. 2012. GenStat Fifteenth Edition, Statistical Software. Release 15.1.0.8035. GenStat, VSN International Ltd. Hertfordshire, HP1, 1ES, UK.

Hassan, R.M., M. Mekuria, and W. Mwangi. 2001. Maize breeding research in eastern and southern Africa: Current status and impacts of past investments made by public and private sectors 1966-1997. CIMMYT, Mexico, D.F., Mexico.

http://www. ggebiplot.com. Accessed Aug. 2012.

IFPRI. 2012. 2012 Global Hunger Index: Fact Sheet: Africa. International Food Policy Research Institute (IFPRI), Washington, DC.

Kang, M.S. 1993. Simultaneous selection for yield and stability in crop performance trials: Consequences for growers. *Agronomy Journal* 85:754-757.

Kikuchi, R., and H. Handa. 2009. Photoperiodic control of flowering in barley. *Breeding. Science* 59:546-552.

Koester, R.P., P.H. Sisco, and C.W. Stuber. 1993. Identification of quantitative trait loci controling days to flowering and plant height in two near isogenic lines of maize. *Crop Science* 33:1209-1216.

Kroonenberg, P.M. 1995. Introduction to biplots for G×E tables. Department of Mathematics, Research Report #51,University of Queensland, 22 .

Langyintuo, A.S., W. Mwangi, A.O. Diallo, J. MacRobert, J. Dixon, and M. Bänziger. 2010. Challenges of the maize seed industry in eastern and southern Africa: A compelling case for private-public intervention to promote growth. *Food Policy* 35:323-331.

MacRobert, J.F. 2009. Seed business management in Africa. CIMMYT, Harare, Zimbabwe.

Magorokosho, C., B. Vivek, and J. MacRobert. 2009. Characterization of maize germplasm grown in eastern and southern Africa: Results of the 2008 regional trials coordinated by CIMMYT. CIMMYT, Harare, Zimbabwe.

Magorokosho, C., B. Vivek, J. MacRobert, and A. Tarekegne. 2010. Characterization of maize germplasm grown in eastern and southern Africa: Results of the 2009 regional trials coordinated by CIMMYT. CIMMYT, Harare, Zimbabwe.

Makumbi, D. 2011. Results of the 2010 regional trials coordinated by CIMMYT-Kenya. CIMMYT, Nairobi, Kenya.

Mitchell, R., V. Mitchell, S. Driscioll, J. Franklin, and D. Lawlor. 1993. Effects of increased CO2 concentration and temperature on growth and yield of winter wheat at two levels of nitrogen application. *Plant, Cell and Environment* 16:521-529.

Morris, M.L., J. Risopoulos, and D.Beck. 1999. Genetic change in farmer-recycled maize seed: A review of the evidence.CIMMYT Economics Working Paper No.99-07, Mexcio DF.:CIMMYT.

Mugo, S.N., M.E. Smith, M. Bänziger, T.L. Setter, G.O. Edmeades, and A. Elings. 1998. Performance of Early Maturing Katumani and Kito Maize Composites Under Drought at the Seedling and Flowering. Stages *African Crop Science Journal* 6:329-344.

Nkonge, C., and M. Balance. 1982. A sensitive colorimetric procedure for nitrogen determination in Micro-Kjeldahl digests. *Journal of Agricultural and Food Chemistry* 30:416-420.

Patterson, H.D., and E.R. Williams. 1976. A new class of resolvable incomplete block designs. *Biometrika* 63: 83-89.

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

Pixley, K., and M. Bänziger. 2001. Open-pollinated maize varieties: A backward step or valuable option for farmers? Seventh Eastern and Southern Africa Regional Maize Conference. 11-15th February, 2001 CIMMYT.

Pixley, K.V., and M.S. Bjarnason. 1993. Combining ability for yield and protein quality among modified endosperm opaque-2 tropical maize inbreds. *Crop Science* 33:1229-1234.

Pixley, K.V., and M.S. Bjarnason. 2002. Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42:1882-1890.

Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Roberts, E.H., and R.J. Summerfield. 1987. Measurement and prediction of flowering in annual crops. In: J.G. Atherton (Ed.). Manipulation of flowering Butterworths, , London. pp. 17-50.

SAS Institute, Inc. 2003. SAS proprietary Software. SAS Institute, Inc, CARY, NC, Canada.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity* 29:237-245.

Smalberger, S., and A.S.du Toit. 2004. Identification of maize cultivars tolerant to low soil fertility in south Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 202-205.

Smale, M., D. Byerlee, and T. Jayne. 2011. Maize Revolutions in Sub-Saharan Africa. Policy Research Working Paper 5659. The World Bank- Development Research Group, Agriculture and Rural Development Team., Washington DC.

UNDP. 2011. Sustainability and Equity: A Better Future for All. Human Development Report 2011. UNDP, New York.

Vergara, N., H. Cordova, A. Ramirez, and O. Cano. 2000. Hybrid performance and combining ability of tropical quality protein maize inbred lines. In: Agronomy abstracts. ASA, Madison, WI. p.106.

Villegas, E. 1975. An integral system for chemical screening of quality protein maize. High quality protein maize. Proceedings of the CIMMYT-Purdue International Symposium on Protein Quality in Maize. El Batan, Mexico. pp. 330-336.

Vivek, B.S., and A. Pswarayi. 2008. Combining ability amongst CIMMYT's early maturing maize (*Zea mays* L.) germplasm under stress and non-stress conditions and identifications of testers. *Euphytica* 162:353-362.

Vivek, B.S., A.F. Krivanek, N. Palacios-Rojas, S. Twumasi-Afriye, and A.O.Diallo. 2008. Breeding Quality Protein Maize (QPM): Protocols for Developing QPM cultivars. CIMMYT, Mexico, D.F.

von Grebmer, K., R. Claudia, R. Mark W, O. Tolulope, W. Doris, F. Heidi, B. Ousmane, T. Maximo, Y. Yisehac, T. Jennifer, C. von Oppeln, and R. Claudia. 2012. 2012 Global Hunger Index: The Challenge of Hunger: Ensuring Sustainable Food Security Under Land, Water, and Energy Stresses. Welthungerhlife/International Food Policy Research Institute(IFPRI)/Concern Worldwide, Bonn,Washington DC, and Dublin.

Wallace, D.H., and W. Yan. 1998. Plant breeding and whole-system physiology. Improving adaptation, maturity and yield. CABI, Wallingford, UK.

Wheeler, T.R., G.R. Batts, R.H. Ellis, P. Hadley, and J.I.L. Morison. 1996. Growth and yield of winter wheat (*Triticum aestivum*) crops in response to CO_2 and temperature. *Journal of Agricultural Science, Cambridge* 127:37-48.

Xu, J., L. Yaxi, L. Jian, C. Moju, W. Jing, L. Hai, X. Yunbi, L. Yanli, P. Guangtang, and R. Tingzhao. 2012. The Genetic Architecture of Flowering Time and Photoperiod Sensitivity in Maize as Revealed by QTL Review and Meta Analysis. *Journal of Integrative Plant Biology* 54:358–373.

Yamada, Y. 1962. Genotype by environment interaction and genetic correlation of the same trait under different environments. *Japan Journal of Genetics* 37:498-509.

Yan, W. 2001. GGEbiplot – a Windows application for graphical analysis of multi-environment trial data and other types of two way data. *Agronomy Journal* 93:1111-1118.

Yan, W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agronomy Journal* 94:990-996.

Yan, W., and M.S. Kang. 2003. GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL.

Yan, W., and N.A. Tinker. 2006. Biplot analysis of multi-environment trial data: Principles and application. *Canadian Journal of Plant Science* 86:623-645.

Yan, W., L.A. Hunt, Q. Sheng, and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Science* 40:597-605.

CHAPTER 6

General conclusions and recommendations

Maize is among the leading cereal crops of the world together with rice and wheat (FAOSTAT, 2011). The global demand for maize is forecasted to be more than 50% and the demand for maize in SSA is projected to increase by 93% by the year 2020 from the base year of 1995 (CIMMYT, 2001). It is the primary food crop in SSA and it accounts for 53% of the total cereal area and 30-70% of total caloric consumption in ESA (Hassan et al., 2001; Diallo et al., 2004; Bänziger and Diallo, 2004; Smalberger and du Toit, 2004; FAOSTAT, 2010; Langyintuo et al., 2010). In ECA maize production is growing at a rate of 3% every year (Smale et al., 2011). Although maize is a dietary staple for millions of people in SSA, nutritionally it is deficient in two essential amino acids, lysine and tryptophan which cause malnutrition and attendant diseases in many parts of SSA.

Quality Protein Maize (QPM) is a result of several years of maize research which has led to an increased level of lysine and tryptophan and is believed to have the potential to alleviate the food and nutritional insecurity in SSA. However, the adoption of QPM in SSA depends on the competitiveness of QPM cultivars in grain yield and other agronomic traits with normal maize counterparts. Studies have demonstrated the superior performance of QPM compared to the best normal maize in many parts of the world. However, the effort in the development of high yielding and stable QPM varieties (hybrids and OPVs) adapted to the diverse environments (drought, low N and optimum) of SSA is the major bottleneck for the expansion of QPM in the region. Hence, this study was initiated to achieve the following objectives: (i) to evaluate the grain yield performance and stability of newly developed early maturing QPM hybrids under stress and non-stress environments of ESA (ii) to analyse mega-environments of SSA based on the primary and secondary traits of QPM (iii) to assess the adaptation pattern of QPM in SSA based on multivariate analysis techniques (iv) to identify and recommend best performing and widely adapted early maturing open pollinated QPM varieties for large scale production in the region and (v) to enhance the role of QPM in combating protein energy malnutrition and related diseases in SSA.

In this study 96 maize genotypes (95 QPM and one normal check) developed in CIMMYT Kenya were evaluated in 15 environments in ESA for grain yield during 2010 and 2011. The

combined ANOVA of grain yield across years and environments indicated that all the QPM entries out yielded the normal check hybrid (entry 96). Entry 40 was the most outstanding across all environments with an average grain yield of 4.57 t ha^{-1} followed by entry 37 (4.42 t ha^{-1}). The results of the combined ANOVA for specific environments which included eight optimum, four drought stress and three low N stress environments revealed that entry 55, entry 73 and entry 37 were the top yielding QPM hybrids under low N, drought and optimum environments with an average yield of 2.77 t ha^{-1}, 3.10 t ha^{-1} and 6.82 t ha^{-1} respectively. The superior performance of the QPM varieties suggests the need for their release and large scale production in the region.

The yield stability based on nine different parametric and non-parametric measures ranked the entries differently mainly due to the inclusion of extreme (stress) environments. Spearman's rank correlation coefficient identified significant and positive correlation among Eberhart and Russel (1966) deviation from regression, Wricke's (1962) ecovalence (W_i), Shukla's (1972) stability variance with no covariates, Shukla's (1972) stability variance with covariates, Nassar and Huehn's (1987) absolute rank difference and variance of ranks (S(1) and S(2)) and Purchase's (1997) AMMI stability value (ASV). There was a perfect correlation between Wricke's (1962) ecovalence and Shukla's (1972) stability variance with no covariates which indicates the similarity of the parameters in ranking the genotypes. Entry 80 was the most stable hybrid identified by Nassar and Hühn's (1987) absolute rank difference and variance of ranks [S (1) and S(2)] and by the parameters of Wricke's (1962) ecovalence (W_i) and Shukla's (1972) stability variance with no covariates. Based on mean grain yield and Linn and Binns's (1988) cultivar superiority measures, the most stable entry was entry 40. The difference in performance of the entries across the different environments indicated the need for the hybrids to be released for specific environments.

Multivariate analysis (AMMI and GGE) was used to examine the adaptation patterns of the 96 genotypes in 15 environments. The ANOVA of the AMMI model showed highly significant effects ($P \leq 0.001$) for environments, genotypes and G x E interaction. The environments main effect explained 76.88% of the total yield variation followed by the G x E interaction (12.44%). The genotypes explained only 3.35% of the variation, which is common expected when trials are conducted in very diverse environments. The most stable entry based on the AMMI model was entry 60 (G60) and the least stable was entry 37. However entry 37 was the highest yielding, indicating its responsiveness to favourable environments. Among

the 15 environments HREOP2 and HREOP1 (Harare-Zimbabwe, optimum environment) were the most responsive and discriminating environments and RATOP (Rattray-Arnold-Zimbabwe, optimum environment) was the most stable environment while AWAOP (Awassa-Ethiopia, optimum environment) was the most discriminating and the least representative environment.

The GGE biplot captured about 50% of the total variation of entries based on G x E interaction. In the delineation of mega-environments, the GGE biplot identified four broader groups within the 15 environments. The environments AWAOP, EMBOP, KAKOP, HREOP1, HREOP2, BAKOP and RATOP were classified under the same mega-environment indicating that genotypes which performed well in any of these locations is expected to do well in the others.

The comparison of AMMI and GGE biplot models revealed the merits and demerits of the two methods. AMMI2 was found to capture more of the variability due to G x E interaction than GGE2. The GGE2 biplot gives several options for easy visualisation and understanding of the complex multi-environment data sets than the different models of AMMI. Critics of biplot techniques in general warned against the over use and abuse of the method and recommended the application of other statistical procedures in taking decisions on genotype evaluation or selection. However, the application of AMMI and GGE biplot will remain useful for the foreseeable future.

Open pollinated QPM varieties are advantageous for resource poor farmers who can't afford purchasing hybrid seeds every year. In this study a total of 39 OPVs (37 QPM and two normal) were evaluated for grain yield and days to anthesis in two sets of trials under the optimum environments of ECA during 2006-2008. The results of the combined ANOVA for the trial set A that was evaluated in 17 optimum environments in ECA during 2006-2007 showed that entry 19 (POOL15QPM-SR-#-#) was the most outstanding with an average yield of 4.61 t ha^{-1}. In trial Set B, evaluated in 20 environments during 2007-2008, entry 31 (EEQPM-45-EA -#-#) was the most outstanding with an average yield of 4.00 t ha^{-1}. All the QPM OPVs out yielded the commercial non-QPM variety, Katumani in all 37 environments which is an indication of possible variety release in the region. Based on ANOVA of individual environments, the three highest yielding environments were: Kiboko-Kenya (8.70 t ha^{-1}), Embu-Kenya (8.27 t ha^{-1}) and Melkassa-Ethiopia (6.22 t ha^{-1}). On the other hand the

three lowest yielding environments were: Kakamega-Kenya (0.73 t ha^{-1}), Gandajika-DRC (2.04 t ha^{-1}) and Elgon Downs-Kenya (2.29 t ha^{-1}). These yield differences is an indication of high cross over G x E interaction.

Katumani was the earliest variety in terms of male flowering in all the environments with average days to anthesis of 57 in the first set of trials (2006-2007) and 58.5 in the second set (2007-2008). The earliest variety among the QPM candidates was entry 1 with average days to anthesis of 62.33 in the first set (2006-2007) and 63.70 in the second set (2007-2008). These results revealed the earliness of the candidate entries in maturity an indication of the importance of the trait for mitigating effects of climate change resulting in reduced rain fall and occurrence of drought in many parts of SSA. This study indicated that the entries possess better stability for days to anthesis than grain yield.

Yield stability, adaptation and mega-environment analysis were done using AMMI and GGE biplots. The results indicated that the QPM OPVs were more stable compared to the hybrids. This is in agreement with the results of Pixley and Bjarnason (2002) who reported that open pollinated cultivars are most stable followed by double-cross, three-way and single cross hybrids based on results of evaluation of different QPM cultivars in 13 locations in four continents. The most stable entries close to the average environment coordinate of the GGE biplot were entry 31 followed by entry 2 and entry 11. The GGE biplots also showed association among environments and genotypes and classified the environments into different mega-environments based on grain yield and days to anthesis of the entries. The results of this study also revealed that recycling of QPM OPVs will result in a significant yield reduction after the third generation. Hence, renewal of seed of QPM OPVs by farmers after three generations of recycling is strongly recommended.

Based on the results of this study, it is recommended that the best performing QPM hybrids and OPVs should be released in different countries of SSA for large scale production. The seeds of promising QPM hybrids and OPVs need to be increased in CIMMYT for distribution to national programmes for further testing and validation in specific ecologies in the respective countries. The AMMI and GGE biplots were found to be effective in identifying potential cultivars from the multi environment data set. The evaluation of germplasm in stress environments (drought, low-N) will help to develop QPM cultivars with wider adaptation. The best performing early maturing QPM OPVs from this study will contribute to the effort

of developing climate resilient varieties which in turn mitigate the effect of climate change. The existence of functional systems in the development and deployment of improved QPM varieties in SSA will facilitate access and availability of seeds particularly among resource poor farmers and help to curb the deplorable trend of food and nutritional insecurity.

6.1 References

Bänziger, M., and A.O. Diallo. 2004. Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference.5-11 February 2002. CIMMYT/KARI Nairobi, Kenya. pp.189-194.

CIMMYT. 2001. 2000/2001 World maize facts and trends. Mexico D.F.

Diallo, A.O., J. Kikafunda, L. Welde, O. Odongo, Z.O. Mduruma, W.S. Chivatsi, D.K.Friesen, S. Mugo, and M. Bänziger. 2004. Drought and low nitrogen tolerant hybrids for the moist mid altitude ecology of eastern Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 206-212.

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

FAOSTAT. 2010. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

FAOSTAT. 2011. Statistical Database of the Food and Agriculture Organization of the United Nations. [Online] http://www.fao.org

Hassan, R.M., M. Mekuria, and W. Mwangi. 2001. Maize breeding research in eastern and southern Africa: Current status and impacts of past investments made by public and private sectors 1966-1997. CIMMYT, Mexico, D.F.

Langyintuo, A.S., W. Mwangi, A.O. Diallo, J. MacRobert, J. Dixon, and M. Bänziger. 2010. Challenges of the maize seed industry in eastern and southern Africa: A compelling case for private-public intervention to promote growth. *Food Policy* 35:323-331.

Lin, C.S., and M.R. Binns. 1988. A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Sciences* 68:193-198.

Nassar, R., and M. Huehn. 1987. Studies in estimation of phenotypic stability: Test of significance for non-parametric measures of phenotypic stability. *Biometrics* 43:45-53.

Pixley, K.V., and M.S. Bjarnason. 2002. Stability of grain yield, endosperm modification, and protein quality of hybrid and open-pollinated quality protein maize cultivars. *Crop Science* 42:1882-1890.

Purchase, J.L. 1997. Parametric analysis to describe G x E interaction and yield stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfontein, South Africa.

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity* 29:237-245.

Smalberger, S., and A.S. du Toit. 2004. Identification of maize cultivars tolerant to low soil fertility in south Africa. In: D.K. Friesen and A.F.E. Palmer (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. 5-11 February 2002, CIMMYT/KARI, Nairobi, Kenya. pp. 202-205.

Smale, M., D. Byerlee, and T. Jayne. 2011. Maize Revolutions in Sub-Saharan Africa. Policy Research Working Paper 5659. The World Bank- Development Research Group, Agriculture and Rural Development Team., Washington DC.

Wricke, G. 1962. Über eine Method zur Erfassung der Ökologischen Streuberite in Feldversuchen. *Z. Pflanzenzüchtg* 47:92-96.

SUMMARY

Quality protein maize (QPM) which is nutritionally enhanced, has the potential to alleviate malnutrition and related diseases in communities where maize is a dietary staple and often the only source of proteins. The wide dissemination and utilisation of QPM in Africa depends on the competitiveness of cultivars for grain yield and other agronomic traits compared to normal maize. This study was conducted to (i) evaluate the grain yield performance and stability of newly developed early maturing QPM hybrids under stress and non-stress environments of ESA (ii) analyse mega-environments of SSA based on the primary and secondary traits of QPM (iii) asses the adaptation pattern of QPM in SSA based on multivariate analysis techniques (iv) identify and recommend best performing and widely adapted early maturing open pollinated QPM varieties for large scale production in the region and (v) enhance the role of QPM in combating protein energy malnutrition and attendant diseases in SSA.

The result of the evaluation of 96 single cross hybrids (95 QPM and one normal maize) for grain yield and stability showed that the candidate varieties out yielded the normal check based on combined ANOVA across 15 environments. Nine parametric and non-parametric measures were used to analyse grain yield stability. The parameters ranked the entries differently mainly due to the inclusion of extreme (stress) environments in the analysis and the less stable nature of single cross hybrids. Most of the stability parameters were significantly and positively correlated.

AMMI and GGE biplots were effective for the analysis of the multi environment data set. The models were used to identify stable genotypes, discriminating environments and adaptation patterns of the entries in ESA. Entries 40 and 37 were the highest yielding while entry 60 was the most stable. The optimum environments in Harare, Zimbabwe were the most discriminating and representative. Mega-environment analysis using the GGE biplot grouped the environments into four groups, with each having more than one site except Chisumbanje, Zimbabwe which was identified as a separate mega-environment. AMMI2 explained 60% of the G x E interaction which was higher than the GGE2 (50%) which in turn was higher than the AMMI1 (35.73%) model. The GGE biplot options allow better visualisation of the complex multi-environment data than the AMMI model.

Candidate QPM OPVs out yielded the normal maize commercial variety, Katumani in 37 environments of ECA based on two sets of trials conducted during 2006-2008. However, Katumani was earliest maturing in all the environments. The environments were grouped into different mega-environments based on grain yield and days to anthesis. The classification of environments into similar mega-environments will facilitate germplasm exchange among environments and will assist the large scale production of QPM in similar environments. It was found that recycling of QPM OPVs for more than three years or seasons will result in significant yield reduction. Hence, seeds should be renewed after three generations of recycling.

Although this study should significantly contribute to the role of QPM in reducing malnutrition and related diseases in SSA through best performing genotypes, the fast-track deployment of QPM in the region, however, depends upon the presence of a functional maize seed system. A viable maize seed system will improve access and availability of QPM seeds, particularly OPV seeds, to resource poor farmers who are the most vulnerable to food and nutritional insecurity. Future research can also deal with the effect of diverse growing conditions of SSA on the nutritional quality of QPM and how farmers can maintain the seed and protein quality of OPVs.

Key words: QPM, grain yield, stability analysis, AMMI and GGE, G x E interaction, mega-environment analysis and sub-Saharan Africa.

OPSOMMING

Kwaliteit proteïen mielies (QPM) wat verhoogde voedingswaarde het, het die potensiaal om wanvoeding en verwante siektes in gemeenskappe uit te wis waar mielies die stapel voedsel en dikwels die enigse bron van proteïen is. Die wye verspreiding en gebruik van QPM in Afrika hang af van hoe kompeterend QPM is in terme van opbrengs en ander agronomiese eienskappe teenoor gewone mielies. Hierdie studie is gedoen om (i) graanopbrengs en stabiliteit van nuut ontwikkelde vroeg ryp QPM basters onder stremmings en optimale toestande in oostelike en suidelike Afrika te bepaal (ii) om mega-omgewings van SSA te bepaal vanaf primêre en sekondêre eienskappe van QPM (iii) om die aanpassingspatrone van QPM in sub Sahara Afrika (SSA) te bepaal volgens multivariaat analise tegnieke (iv) om die bes produserende en aangepaste oop bestuifde QPM variëteite te identifiseer vir grootskaalse produksie in die area en (v) om die rol van QPM in die stryd teen proteïen wanvoeding en verwante siektes in SSA te vergroot.

Die evaluasie van 96 enkelkruis basters (95 QPM en een normale baster) vir graanopbrengs het getoon dat die kandidaat variëteite hoër opbrengs as die normale baster gehad het in die ANOVA van 15 omgewings. Nege parametriese en nie-parametriese stabiliteitsmetings is gebruik om stabiliteit te bepaal. Die parameters het die inskrywings in verskillende volgordes geplaas hoofsaaklike a.g.v. die insluiting van ekstreme (stres) omgewings in die analise en die onstabiele karakter van enkelkruis basters. Meeste van die stabiliteitsparameters was betekenisvol positief gekorreleer.

AMMI en GGE modelle was effektief vir die analise van die multi-omgewing datastel. Die modelle is gebruik om stabiele genotipes, diskriminerende omgewings en aanpassingspatrone van die inskrywings in oostelike en suidelike Afrika te bepaal. Inskrywings 40 en 37 het die hoogste opbrengs gegee, en inskrywing 60 was die mees stabiel. Die optimum omgewings by Harare-Zimbabwe was die mees diskriminerend en verteenwoordigend. Mega-omgewing analise met die GGE model het die omgewings in vier verdeel, elk met meer as een lokaliteit, behalwe Chisumbanje, Zimbabwe wat as ‘n aparte mega-omgewing gekategoriseer is. AMMI2 het 60% van die G x E interaksie verklaar wat hoër was as GGE2 (50%) wat weer hoër was as die AMMI1 (35.73%) model. Die GGE biplot opsie laat beter visualisering van komplekse multi-omgewing data toe as die AMMI model.

Kandidaat QPM OPVs het hoër opbrengste gehad as die gewone kommersiële mielie variëteit, Katumani in 37 omgewings in oostelike en sentraal Afrika, gebasseer op twee stelle proewe wat uitgevoer is in 2006-2008. Katumani was egter die vroegste ryp in al die omgewings. Die omgewings is gegroepeer in verskillende mega-omgewings gebasseer op graanopbrengs en dae tot blom. Die klassifikasie van omgewings in soortgelyke mega-omgewings sal kiemplasma uitruiling tussen omgewings fasiliteer en sal bydra tot grootskaalse produksie van QPM in soortgelyke omgewings. Daar is gevind dat die hersirkulering van QPM OPVs vir meer as drie jaar of seisoene betekenisvolle afname in opbrengs sal veroorsaak. Daarom moet saad met vars saad vervang word teen die vierde generasie.

Alhoewel hierdie studie betekenisvol behoort by te dra tot die rol van QPM om verminderde wanvoeding en verwante siektes in SSA te weeg te bring deur beter presterende QPM genotipes vry te stel, sal die vinnige verspreiding van QPM in die streek afhang van ‘n funksionele mieliesaad sisteem. ‘n Lewensvatbare saadsisteem sal toegang en beskikbaarheid van QPM saad, veral OPV saad, vir hulpbronarm boere verhoog wat die mees sensitief is vir voedsel en voedings insekuriteit. Die verbetering van die sisteem waar verbeterde QPM variëteite miljoene boere in SSA kan bereik, is noodsaaklik. Toekomstige navorsing kan ook kyk na die effek van diverse produksietoestande in SSA op voedingswaarde van QPM en hoe boere saad en proteïen kwaliteit van OPVs kan onderhou.

Sleutelwoordes: QPM, graanopbrengs, stabiliteitsanalise, AMMI en GGE, G x E interaksie, mega-omgewing analise en sub-Sahara Afrika.

Appendix 1 Grain yield performance (t ha^{-1}) of 96 QPM hybrids tested across six environments in ESA, 2010

	Environments											
	HREOP1		RATOP		BKOPT		HRELN1		BKOLN		CHIDT1	
Rank	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
1	52	9.12	46	6.10	96	9.28	40	2.32	15	4.93	23	4.77
2	4	8.87	96	5.75	40	8.03	16	2.32	22	4.74	73	4.50
3	43	8.71	82	5.68	45	7.83	96	2.32	29	4.70	29	4.04
4	37	8.59	92	5.60	59	7.45	87	2.28	64	4.65	16	3.90
5	6	8.28	47	5.56	15	7.28	55	2.26	48	4.51	22	3.90
6	45	8.21	76	5.54	55	7.13	26	2.24	37	4.38	27	3.80
7	46	8.19	52	5.47	49	7.00	79	2.20	55	4.35	58	3.73
8	10	8.10	10	5.47	4	6.92	85	2.12	75	4.29	60	3.71
9	87	7.89	33	5.46	48	6.85	67	2.12	4	4.20	61	3.69
10	40	7.88	60	5.42	60	6.67	93	2.10	35	4.17	40	3.67
11	12	7.84	15	5.36	37	6.37	73	2.09	92	4.14	8	3.66
12	8	7.83	64	5.35	70	6.37	88	1.95	56	4.14	67	3.65
13	54	7.80	12	5.31	12	6.28	17	1.93	45	4.03	12	3.65
14	53	7.79	84	5.28	17	6.27	86	1.91	49	3.99	92	3.61
15	48	7.63	37	5.18	16	6.27	12	1.91	96	3.98	33	3.60
16	7	7.55	43	5.08	69	6.25	39	1.91	54	3.93	11	3.58
17	82	7.52	91	5.08	63	6.23	54	1.90	91	3.93	86	3.53
18	1	7.50	7	5.04	54	6.20	18	1.84	51	3.86	19	3.53
19	42	7.46	4	5.02	52	6.19	51	1.84	73	3.83	94	3.49
20	55	7.35	49	5.01	38	6.18	47	1.82	69	3.82	59	3.48
21	51	7.27	13	5.01	91	6.18	61	1.69	40	3.80	14	3.48
22	49	7.24	57	5.01	67	6.16	22	1.68	47	3.70	79	3.45
23	73	7.20	54	5.01	29	6.15	46	1.66	12	3.62	13	3.41
24	39	7.17	5	4.98	51	6.12	52	1.66	60	3.62	10	3.38
25	16	7.16	2	4.97	5	6.10	23	1.65	14	3.61	88	3.38
26	77	7.15	48	4.90	17	3.34	66	1.65	77	7.15	17	3.34
27	3	7.13	45	4.88	36	3.31	24	1.62	3	7.13	36	3.31
28	41	7.13	30	4.88	2	3.30	6	1.62	41	7.13	2	3.30
29	44	7.07	62	4.87	15	3.23	21	1.60	44	7.07	15	3.23
30	72	7.06	9	4.86	68	3.23	41	1.60	72	7.06	68	3.23
31	84	7.03	40	4.82	48	3.22	76	1.60	84	7.03	48	3.22
32	22	6.88	93	4.82	87	3.21	37	1.58	22	6.88	87	3.21

Appendix 1 Continued….

Rank	Environments											
	HREOP1		RATOP		BKOPT		HRELN1		BKOLN		CHIDT1	
	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
33	2	6.80	78	4.82	20	5.90	29	1.57	38	3.44	18	3.20
34	64	6.76	26	4.79	26	5.86	82	1.55	76	3.44	76	3.16
35	24	6.75	70	4.76	1	5.80	64	1.52	19	3.44	52	3.15
36	50	6.75	32	4.76	62	5.80	42	1.52	13	3.42	78	3.14
37	69	6.73	1	4.75	3	5.80	15	1.51	16	3.42	69	3.13
38	92	6.64	24	4.70	27	5.78	13	1.51	2	3.41	51	3.07
39	67	6.63	55	4.68	8	5.77	31	1.49	27	3.33	63	3.07
40	15	6.63	41	4.68	57	5.76	92	1.46	61	3.31	53	3.03
41	75	6.63	25	4.68	41	5.71	69	1.46	70	3.29	70	3.03
42	60	6.58	67	4.64	30	5.70	11	1.46	50	3.27	66	3.02
43	14	6.52	51	4.61	6	5.69	35	1.46	85	3.26	82	3.01
44	13	6.49	3	4.60	92	5.69	48	1.46	71	3.25	25	2.99
45	33	6.48	39	4.59	24	5.66	49	1.41	95	3.20	28	2.98
46	57	6.44	53	4.55	10	5.64	4	1.40	62	3.15	85	2.94
47	21	6.44	44	4.54	44	5.48	90	1.40	17	3.13	50	2.93
48	30	6.43	77	4.53	28	5.46	89	1.40	8	3.12	75	2.93
49	38	6.38	95	4.53	76	5.43	7	1.38	10	3.10	65	2.93
50	9	6.38	90	4.50	46	5.37	25	1.32	72	3.09	64	2.91
51	5	6.37	63	4.50	77	5.36	10	1.30	86	3.07	56	2.90
52	78	6.35	88	4.50	80	5.35	95	1.30	88	3.06	39	2.89
53	76	6.32	73	4.44	22	5.32	50	1.30	24	3.04	93	2.88
54	70	6.26	87	4.44	53	5.29	56	1.25	84	3.01	80	2.84
55	95	6.22	56	4.40	42	5.29	78	1.24	9	2.99	5	2.79
56	18	6.14	6	4.38	18	5.28	53	1.24	5	2.97	91	2.78
57	94	6.09	81	4.34	84	5.25	43	1.19	21	2.97	90	2.74
58	26	6.08	85	4.32	81	5.23	34	1.18	33	2.95	47	2.72
59	63	6.08	8	4.31	56	5.21	20	1.18	34	2.85	72	2.71
60	89	6.02	58	4.30	21	5.18	62	1.16	44	2.84	49	2.71
61	11	5.97	29	4.29	58	5.12	27	1.15	1	2.84	77	2.69
62	66	5.95	11	4.24	23	5.11	5	1.15	65	2.83	84	2.69
63	20	5.82	79	4.20	64	5.11	44	1.13	43	2.82	89	2.69
64	88	5.75	42	4.16	31	5.08	33	1.13	59	2.79	71	2.68

Appendix 1 Continued….

	Environments											
	HREOP1		RATOP		BKOPT		HRELN1		BKOLN		CHIDT1	
Rank	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
65	32	5.74	83	4.14	73	5.01	71	1.10	20	2.79	7	2.67
66	27	5.74	50	4.13	2	4.99	94	1.08	77	2.78	43	2.67
67	29	5.74	14	4.13	71	4.96	59	1.05	80	2.78	1	2.66
68	86	5.74	65	4.11	85	4.91	14	1.00	18	2.78	4	2.65
69	74	5.73	21	4.08	72	4.91	91	0.97	90	2.72	26	2.62
70	91	5.67	80	4.06	68	4.90	63	0.93	6	2.71	41	2.62
71	59	5.65	34	4.04	11	4.89	60	0.93	52	2.70	44	2.59
72	58	5.56	22	4.03	39	4.86	3	0.91	26	2.68	45	2.59
73	85	5.51	16	3.95	7	4.80	70	0.91	7	2.62	74	2.57
74	83	5.48	94	3.89	61	4.75	57	0.89	94	2.58	62	2.55
75	28	5.47	66	3.88	43	4.73	38	0.88	87	2.54	24	2.55
76	96	5.45	75	3.87	66	4.69	32	0.85	31	2.54	83	2.48
77	47	5.43	59	3.84	93	4.66	8	0.83	83	2.53	42	2.45
78	80	5.41	19	3.84	25	4.65	2	0.83	78	2.52	54	2.43
79	34	5.40	72	3.82	82	4.60	9	0.83	32	2.51	55	2.38
80	56	5.37	38	3.79	89	4.59	68	0.82	57	2.49	3	2.38
81	62	5.35	86	3.77	79	4.48	72	0.78	41	2.48	30	2.34
82	19	5.30	68	3.76	94	4.35	65	0.77	28	2.48	46	2.30
83	90	5.29	74	3.74	88	4.33	77	0.77	74	2.42	81	2.22
84	25	5.25	17	3.67	83	4.32	80	0.77	39	2.42	9	2.20
85	79	5.07	35	3.58	13	4.29	75	0.77	79	2.42	32	2.17
86	93	5.01	69	3.54	65	4.27	36	0.75	93	2.40	34	2.12
87	81	5.00	71	3.49	78	4.22	84	0.75	36	2.32	31	2.12
88	61	4.98	31	3.29	33	4.22	28	0.75	46	2.30	38	2.10
89	71	4.96	61	3.27	90	4.14	74	0.74	81	2.18	57	2.09
90	65	4.96	27	3.15	34	4.14	81	0.71	25	2.16	21	2.09
91	23	4.89	89	3.08	74	4.00	30	0.69	58	2.14	20	2.05
92	35	4.86	36	3.06	86	3.98	58	0.66	42	2.12	6	2.04
93	68	4.76	23	3.02	9	3.72	19	0.64	82	2.02	96	1.91
94	17	4.66	20	2.99	14	3.50	45	0.58	89	1.94	37	1.88
95	36	4.63	28	2.94	95	3.42	83	0.55	11	1.86	95	1.82
96	31	4.63	18	2.66	36	2.96	1	0.49	3	1.80	35	1.71
Mean	**6.45**		**4.46**		**5.48**		**1.36**		**3.18**		**2.94**	
Max	**9.12**		**6.10**		**9.28**		**2.32**		**4.93**		**4.77**	
Min	**4.63**		**2.66**		**2.96**		**0.49**		**1.80**		**1.71**	
LSD $_{0.05}$	**0.56**		**1.47**		**1.31**		**0.81**		**0.63**		**0.73**	
CV %	**4.29**		**16.64**		**12.03**		**29.85**		**9.93**		**12.79**	

Appendix 2 Grain yield performance (t ha^{-1}) of 96 QPM hybrids tested across nine environments in ESA, 2011

	Environments																	
	HRELN2		HREOP2		CHIDT2		CHSDT		EMBOP		KAKOP		KBODT		MLKOP		AWAOP	
Rank	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
1	51	2.16	37	8.68	94	2.02	31	2.44	40	8.84	42	6.64	22	4.66	41	7.06	37	7.62
2	54	1.90	43	8.24	52	1.98	84	2.13	37	8.32	95	6.26	10	4.33	92	6.82	55	7.62
3	22	1.82	12	8.06	68	1.91	33	2.04	41	7.98	96	6.10	25	4.31	60	6.76	54	6.73
4	53	1.69	3	8.05	18	1.91	4	2.00	54	7.65	45	5.97	73	4.22	63	6.64	46	6.60
5	55	1.69	10	7.85	33	1.90	66	1.98	96	7.40	9	5.95	63	4.16	58	6.55	15	6.48
6	67	1.68	52	7.79	64	1.87	7	1.90	48	7.40	10	5.91	78	4.07	38	6.48	61	6.35
7	89	1.57	40	7.73	73	1.87	24	1.88	51	7.33	51	5.86	43	3.92	8	6.41	3	6.35
8	84	1.55	92	7.73	92	1.86	46	1.87	45	7.31	15	5.82	88	3.77	57	6.36	91	6.35
9	82	1.55	82	7.71	60	1.84	56	1.84	4	7.05	4	5.80	60	3.62	76	6.25	95	6.35
10	68	1.54	54	7.69	56	1.84	73	1.81	27	6.96	38	5.78	82	3.55	49	6.18	96	6.22
11	25	1.52	6	7.67	23	1.82	65	1.77	13	6.88	3	5.57	86	3.53	56	6.14	40	6.10
12	46	1.46	84	7.40	90	1.80	14	1.75	18	6.87	21	5.54	8	3.46	94	6.13	26	5.97
13	75	1.43	4	7.33	70	1.80	38	1.73	50	6.83	32	5.48	52	3.36	64	6.13	53	5.97
14	49	1.41	8	7.31	40	1.80	89	1.71	29	6.68	1	5.47	87	3.30	55	6.00	52	5.59
15	48	1.40	45	7.29	57	1.77	26	1.69	5	6.67	24	5.45	62	3.26	50	5.96	38	5.46
16	44	1.40	62	7.28	7	1.76	63	1.69	82	6.64	39	5.45	15	3.26	15	5.91	60	5.46
17	83	1.38	2	7.22	65	1.76	34	1.66	25	6.64	50	5.37	30	3.15	44	5.80	79	5.46
18	24	1.38	39	7.22	67	1.74	28	1.64	91	6.60	40	5.33	20	3.02	10	5.72	2	5.33
19	52	1.33	1	7.11	44	1.71	90	1.62	76	6.59	55	5.30	21	2.93	21	5.70	25	5.21
20	16	1.30	7	7.09	71	1.71	43	1.61	42	6.57	46	5.30	96	2.93	62	5.59	84	5.08
21	93	1.27	66	7.08	48	1.70	69	1.60	9	6.55	48	5.27	67	2.91	47	5.56	33	5.08
22	10	1.25	51	7.07	74	1.70	76	1.58	38	6.55	37	5.25	42	2.90	12	5.56	50	5.08
23	90	1.25	41	7.00	22	1.70	11	1.57	1	6.49	54	5.22	38	2.90	72	5.53	87	5.08
24	88	1.22	22	6.99	61	1.69	55	1.56	31	6.46	47	5.18	51	2.88	40	5.51	76	5.08
25	66	1.21	32	6.98	41	1.69	44	1.56	63	6.46	56	5.17	28	2.87	5	5.45	63	5.08
26	63	1.19	69	6.90	77	1.68	8	1.56	62	6.45	41	5.16	24	2.83	77	5.31	94	5.08
27	1	1.16	42	6.85	82	1.66	50	1.56	85	6.41	43	5.13	76	2.81	30	5.28	70	5.08
28	23	1.15	5	6.85	78	1.62	68	1.55	35	6.39	84	5.08	91	2.81	84	5.26	62	5.08
29	79	1.13	46	6.83	53	1.60	70	1.55	49	6.39	20	4.94	48	2.77	43	5.25	65	4.95
30	86	1.13	48	6.82	63	1.59	23	1.55	58	6.38	66	4.90	23	2.77	42	5.25	45	4.95
31	50	1.11	60	6.80	81	1.56	67	1.51	7	6.36	16	4.88	85	2.76	85	5.23	18	4.95
32	42	1.11	49	6.78	80	1.56	72	1.50	43	6.35	12	4.84	94	2.73	13	5.20	44	4.83
33	37	1.10	91	6.75	31	1.55	78	1.50	10	6.31	83	4.80	80	2.70	70	5.13	13	4.83

Appendix 2 Continued…

Rank	Environments																	
	HRELN2		HREOP2		CHIDT2		CHSDT		EMBOP		KAKOP		KBODT		MLKOP		AWAOP	
	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
34	62	1.08	50	6.70	69	1.55	12	1.47	52	6.30	62	4.72	83	2.69	3	5.06	24	4.83
35	92	1.07	55	6.68	13	1.55	13	1.47	71	6.30	7	4.66	79	2.69	48	5.01	10	4.83
36	12	1.05	21	6.59	43	1.55	91	1.46	3	6.28	52	4.64	57	2.69	87	4.99	42	4.83
37	40	1.04	27	6.56	30	1.51	15	1.44	57	6.26	94	4.62	58	2.68	6	4.93	27	4.70
38	6	1.04	89	6.51	47	1.51	83	1.44	20	6.23	18	4.61	6	2.67	88	4.92	81	4.57
39	78	1.02	9	6.49	79	1.50	6	1.39	32	6.20	53	4.61	1	2.66	20	4.91	43	4.57
40	21	0.99	73	6.48	17	1.47	1	1.39	14	6.17	60	4.60	56	2.66	78	4.86	59	4.57
41	87	0.99	63	6.46	10	1.46	39	1.39	55	6.13	25	4.60	33	2.56	35	4.85	73	4.44
42	26	0.99	88	6.42	62	1.45	19	1.38	21	6.13	92	4.55	29	2.48	65	4.82	41	4.44
43	95	0.97	57	6.42	20	1.44	45	1.37	56	6.13	22	4.48	41	2.48	22	4.80	5	4.44
44	81	0.96	87	6.38	58	1.43	17	1.36	95	6.09	2	4.45	45	2.48	67	4.77	39	4.44
45	39	0.94	64	6.38	15	1.40	75	1.34	47	6.07	93	4.45	70	2.46	9	4.76	49	4.44
46	14	0.94	59	6.34	50	1.40	41	1.34	77	6.02	26	4.42	64	2.44	24	4.69	85	4.44
47	43	0.93	96	6.32	35	1.37	49	1.32	8	6.00	85	4.42	90	2.41	61	4.68	89	4.44
48	34	0.93	75	6.31	19	1.36	88	1.31	75	6.00	67	4.41	31	2.37	52	4.60	19	4.32
49	85	0.91	24	6.24	55	1.36	77	1.31	60	6.00	44	4.40	11	2.33	18	4.59	35	4.32
50	94	0.91	35	6.24	96	1.35	86	1.29	34	6.00	11	4.38	84	2.32	39	4.59	75	4.32
51	15	0.89	72	6.18	72	1.33	25	1.27	33	5.95	75	4.37	17	2.31	37	4.58	1	4.32
52	18	0.89	30	6.16	76	1.32	79	1.23	2	5.91	64	4.33	92	2.27	29	4.56	22	4.19
53	27	0.88	80	6.15	16	1.31	35	1.22	81	5.91	87	4.32	65	2.24	90	4.55	29	4.19
54	73	0.86	67	6.11	87	1.30	60	1.22	16	5.89	63	4.32	19	2.17	46	4.54	31	4.06
55	17	0.86	44	6.02	91	1.28	52	1.21	44	5.88	13	4.28	72	2.13	96	4.53	6	3.94
56	91	0.86	33	5.98	25	1.25	36	1.21	24	5.86	30	4.26	7	2.12	81	4.50	16	3.81
57	56	0.86	47	5.95	45	1.23	21	1.19	6	5.84	5	4.20	89	2.10	32	4.47	48	3.81
58	74	0.86	58	5.95	84	1.22	58	1.17	39	5.84	82	4.19	18	2.00	74	4.44	36	3.81
59	9	0.85	38	5.95	6	1.22	82	1.16	66	5.83	72	4.09	69	1.99	51	4.44	80	3.81
60	96	0.85	29	5.91	93	1.21	51	1.16	59	5.76	80	4.08	36	1.96	54	4.44	58	3.81
61	11	0.83	85	5.88	34	1.21	20	1.16	69	5.76	68	4.02	16	1.94	80	4.35	71	3.81
62	3	0.82	26	5.86	29	1.15	48	1.15	84	5.76	19	4.00	49	1.90	91	4.32	47	3.81
63	19	0.82	28	5.86	75	1.14	61	1.13	74	5.70	59	3.97	66	1.89	27	4.32	12	3.68
64	60	0.80	13	5.82	83	1.14	53	1.10	15	5.66	73	3.96	14	1.86	82	4.29	72	3.68
65	7	0.78	15	5.75	11	1.13	81	1.09	26	5.65	89	3.95	81	1.85	86	4.21	7	3.68

Appendix 2 Continued

Rank	Environments																	
	HRELN2		HREOP2		CHIDT2		CHSDT		EMBOP		KAKOP		KBODT		MLKOP		AWAOP	
	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield	Entry	Yield
66	70	0.78	77	5.62	66	1.11	80	1.09	22	5.64	35	3.94	35	1.85	19	4.20	32	3.56
67	5	0.77	19	5.55	28	1.11	9	1.06	12	5.62	33	3.87	75	1.82	4	4.19	74	3.56
68	76	0.77	86	5.50	88	1.10	10	1.05	46	5.56	6	3.87	9	1.82	31	4.18	78	3.56
69	2	0.75	76	5.45	12	1.09	64	1.04	87	5.51	86	3.85	2	1.79	69	4.17	69	3.56
70	29	0.72	78	5.44	27	1.06	27	1.01	72	5.50	77	3.82	27	1.79	45	4.10	77	3.56
71	45	0.71	93	5.33	24	1.04	3	0.99	93	5.41	57	3.81	93	1.79	7	4.09	93	3.56
72	64	0.71	68	5.25	5	1.04	94	0.97	61	5.40	49	3.80	74	1.77	79	4.04	68	3.56
73	4	0.71	81	5.11	89	1.01	87	0.97	92	5.40	14	3.77	44	1.77	23	4.03	11	3.43
74	80	0.69	70	5.11	21	1.01	74	0.92	19	5.33	23	3.75	68	1.77	75	3.96	4	3.18
75	20	0.69	90	4.98	46	0.99	95	0.92	30	5.33	58	3.72	53	1.77	25	3.95	66	3.18
76	32	0.67	79	4.94	8	0.96	62	0.90	88	5.27	34	3.69	50	1.76	73	3.95	92	3.18
77	33	0.63	25	4.91	86	0.93	85	0.90	70	5.24	76	3.64	61	1.76	17	3.90	30	3.18
78	77	0.63	83	4.89	51	0.91	71	0.89	73	5.23	27	3.62	77	1.75	53	3.85	9	3.18
79	47	0.61	71	4.82	59	0.89	2	0.89	64	5.22	81	3.60	26	1.75	28	3.75	67	3.18
80	28	0.60	34	4.78	32	0.89	16	0.89	78	5.17	17	3.58	46	1.75	83	3.73	88	3.05
81	35	0.58	11	4.69	1	0.85	47	0.88	80	5.16	29	3.54	32	1.75	33	3.69	20	3.05
82	13	0.55	65	4.68	37	0.83	5	0.88	53	5.16	91	3.52	5	1.74	68	3.62	83	3.05
83	41	0.53	56	4.52	85	0.83	30	0.86	11	5.10	61	3.51	12	1.74	2	3.60	21	2.92
84	58	0.53	36	4.49	49	0.82	57	0.85	23	5.07	88	3.38	55	1.74	93	3.54	56	2.79
85	59	0.49	16	4.48	26	0.75	92	0.82	89	5.06	70	3.35	13	1.74	16	3.52	51	2.79
86	30	0.49	14	4.39	4	0.73	37	0.82	67	5.04	28	3.32	59	1.73	34	3.48	82	2.67
87	65	0.47	20	4.38	14	0.71	93	0.77	36	4.97	8	3.31	34	1.72	89	3.34	34	2.54
88	72	0.45	94	4.38	9	0.67	54	0.77	94	4.93	69	3.31	71	1.71	36	3.32	86	2.54
89	8	0.45	31	4.36	2	0.67	59	0.75	17	4.85	74	3.26	54	1.71	26	3.30	64	2.54
90	71	0.44	53	4.33	54	0.63	32	0.70	90	4.84	90	3.23	3	1.63	66	3.23	28	2.54
91	57	0.42	61	4.31	38	0.60	96	0.69	65	4.80	65	3.21	47	1.58	71	3.21	17	2.54
92	69	0.35	95	4.29	36	0.59	29	0.67	28	4.77	36	2.90	40	1.34	1	3.19	23	2.54
93	36	0.33	74	4.27	39	0.50	18	0.64	86	4.47	79	2.47	4	1.30	59	2.80	14	2.29
94	61	0.25	23	4.07	42	0.33	42	0.64	83	4.37	31	2.28	39	1.22	14	2.45	8	1.91
95	31	0.19	17	3.51	3	0.31	22	0.42	68	4.16	71	2.18	37	1.07	11	2.22	57	1.40
96	38	0.13	18	3.47	95	0.16	40	0.32	79	3.66	78	2.12	95	0.82	95	2.00	90	1.27
Mean	**0.97**		**6.12**		**1.31**		**1.29**		**5.99**		**4.42**		**2.44**		**4.72**		**4.30**	
Max	**2.16**		**8.68**		**2.02**		**2.44**		**8.84**		**6.64**		**4.66**		**7.06**		**7.62**	
Min	**0.13**		**3.47**		**0.16**		**0.32**		**3.66**		**2.12**		**0.82**		**2.00**		**1.27**	
LSD $_{0.05}$	**0.77**		**1.36**		**0.65**		**0.81**		**1.34**		**0.89**		**1.41**		**1.56**		**2.36**	
CV %	**40.07**		**11.12**		**37.22**		**31.52**		**11.19**		**10.11**		**29.05**		**16.54**		**27.57**	

Appendix 3 Grain yield performance (t ha^{-1}) of 96 QPM hybrids tested across 15 environments in ESA, 2010-2011

Rank	Trial years					
	2010		2011		2010-2011	
	Entry	Yield	Entry	Yield	Entry	Yield
1	40	5.09	10	4.30	40	4.57
2	4	4.84	37	4.25	37	4.42
3	15	4.82	55	4.23	55	4.42
4	96	4.78	40	4.22	10	4.38
5	12	4.77	41	4.19	15	4.37
6	48	4.76	63	4.18	52	4.34
7	52	4.72	43	4.17	96	4.34
8	55	4.69	60	4.12	60	4.27
9	45	4.69	52	4.09	54	4.27
10	37	4.66	54	4.08	48	4.26
11	49	4.56	15	4.07	45	4.23
12	54	4.54	96	4.04	43	4.18
13	92	4.52	84	3.98	63	4.13
14	73	4.51	62	3.98	41	4.13
15	16	4.50	50	3.97	12	4.12
16	10	4.50	38	3.95	51	4.09
17	60	4.49	45	3.93	4	4.09
18	51	4.46	48	3.92	22	4.08
19	67	4.46	42	3.90	92	4.06
20	22	4.43	3	3.89	46	4.06
21	29	4.41	46	3.88	49	4.03
22	87	4.38	22	3.86	50	4.02
23	64	4.38	51	3.84	73	3.99
24	46	4.32	24	3.80	84	3.99
25	8	4.25	91	3.77	87	3.94
26	76	4.25	92	3.74	76	3.93
27	53	4.22	25	3.74	62	3.91
28	47	4.21	76	3.72	91	3.90
29	43	4.20	82	3.71	24	3.90
30	69	4.16	44	3.71	38	3.89
31	6	4.12	12	3.68	42	3.87
32	70	4.10	49	3.67	67	3.87
33	91	4.10	21	3.67	82	3.85

Appendix 3 continued…

Rank	Trial years					
	2010		2011		2010-2011	
	Entry	Yield	Entry	Yield	Entry	Yield
34	50	4.08	87	3.65	3	3.84
35	75	4.08	73	3.65	6	3.82
36	82	4.06	1	3.63	44	3.80
37	5	4.06	6	3.62	64	3.80
38	63	4.06	7	3.61	8	3.79
39	24	4.05	13	3.59	1	3.78
40	2	4.05	4	3.59	7	3.77
41	26	4.05	58	3.58	13	3.76
42	59	4.04	5	3.56	47	3.76
43	41	4.04	56	3.55	5	3.76
44	13	4.02	85	3.53	29	3.76
45	7	4.01	94	3.53	33	3.70
46	1	4.00	33	3.52	53	3.70
47	84	4.00	39	3.51	39	3.69
48	33	3.97	8	3.49	21	3.69
49	39	3.97	67	3.48	56	3.68
50	44	3.94	9	3.48	75	3.68
51	30	3.93	47	3.46	70	3.67
52	77	3.88	27	3.43	16	3.67
53	56	3.88	35	3.42	2	3.66
54	85	3.84	75	3.41	85	3.66
55	17	3.83	32	3.41	25	3.65
56	42	3.83	64	3.41	26	3.64
57	88	3.83	2	3.40	69	3.61
58	27	3.83	70	3.39	27	3.59
59	23	3.82	88	3.38	30	3.59
60	62	3.81	66	3.38	58	3.58
61	38	3.80	72	3.38	88	3.56
62	19	3.79	26	3.38	94	3.55
63	57	3.78	30	3.36	66	3.54
64	66	3.77	53	3.34	77	3.53
65	3	3.77	57	3.33	72	3.52
66	72	3.73	18	3.33	32	3.52

Appendix 3 continued…

	Trial years					
	2010		2011		2010-2011	
Rank	Entry	Yield	Entry	Yield	Entry	Yield
67	21	3.73	29	3.32	57	3.51
68	78	3.71	20	3.31	35	3.50
69	14	3.71	89	3.30	9	3.49
70	32	3.68	77	3.30	19	3.46
71	86	3.67	80	3.29	18	3.46
72	11	3.67	78	3.26	78	3.44
73	18	3.65	69	3.24	59	3.44
74	93	3.65	81	3.24	80	3.39
75	79	3.63	19	3.24	61	3.39
76	35	3.63	61	3.23	20	3.37
77	61	3.61	65	3.19	23	3.31
78	58	3.59	16	3.11	86	3.30
79	94	3.58	31	3.10	89	3.29
80	80	3.54	95	3.10	93	3.28
81	25	3.51	83	3.05	79	3.26
82	9	3.50	86	3.05	81	3.26
83	68	3.48	68	3.04	65	3.24
84	90	3.46	93	3.04	95	3.22
85	20	3.45	59	3.03	68	3.22
86	95	3.41	79	3.01	11	3.18
87	71	3.41	23	2.97	17	3.16
88	28	3.35	74	2.94	31	3.14
89	65	3.31	28	2.94	83	3.13
90	34	3.29	34	2.89	90	3.12
91	89	3.29	90	2.89	14	3.10
92	81	3.28	11	2.85	28	3.10
93	83	3.25	71	2.78	34	3.05
94	74	3.20	17	2.71	74	3.04
95	31	3.19	14	2.70	71	3.03
96	36	2.84	36	2.62	36	2.71
Mean	**3.98**		**3.51**		**3.70**	
Max	**5.09**		**4.30**		**4.57**	
Min	**2.84**		**2.62**		**2.71**	
LSD $_{0.05}$	**0.45**		**0.41**		**0.21**	
CV %	**14.15**		**18.04**		**11.11**	