EVALUATION OF EARLY MATURING MAIZE (*Zea mays* L.) HYBRIDS FOR MULTIPLE-STRESS TOLERANCE

BY

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ABSTRACT

Maize (*Zea mays* L.) is the most important cereal in Africa, but a number of constraints including biotic, abiotic and socio-economic factors affect its production. The abiotic factors such as drought, low nitrogen (N) and heat contribute to the low grain yield production, which creates a challenge that needs to be addressed by researchers. Thus, development and use of early maturing maize hybrids could help in stabilizing maize production. Early maturing maize hybrids help in reducing the growing period to escape some of the abiotic stresses that contains variability for high yield potential and adaptive traits. This study, therefore, was aimed at breeding and identifying early maturing maize hybrids cultivars that are tolerant to drought and low N stresses. Fifty early maturing maize hybrids including six commercial checks were evaluated under stress and non-stress environments during the 2016/17 maize growing season in South Africa. The objectives were (i) to estimate variance components, correlation and path coefficients among grain yield and secondary traits in early maturing maize hybrids across stress and non-stress environments and (ii) to evaluate genotype by environment interaction effects and stability for grain yield performance in early maturing maize hybrids across stress and non-stress environments.

To estimate the variance components, correlation and path coefficients among grain yield and secondary traits in early maturing maize hybrids across stress and non-stress environments, quantitative traits data including grain yield and its secondary components were recorded. Statistical analyses revealed that the effect of genotype, environment and genotype by environment interaction were significant ($P<0.01$) for all the traits. Hybrids CZH16084, CZH16064 and CZH16095 under managed drought, low N and optimum environments, respectively, were identified as the outstanding genotypes for grain yield and recommended for further testing, release and registration. High magnitude of phenotypic and genotypic coefficient of variation as well as high heritability were recorded for each single environment for anthesis days, silking days, ear height and plant height, suggesting that those traits interacted with the environment. Grain yield was positively correlated with anthesis days and ear height, field weight, grain moisture at Potchefstroom while at Lutzville and Cedara had negative correlation with those traits, suggesting that the genotypes differed significantly for most of the phenotypic traits. Path coefficient analyses revealed that anthesis days and anthesis-silking interval had positive direct effects while silking days, plant height and ear per plant had a negative direct effect on grain yield in all the environments. These traits are recommended for effective selection to the improvement of maize grain yield.

To evaluate genotype by environment interaction effects and stability for grain yield performance in early maturing maize hybrids across stress and non-stress environments, data collected from all environments which were Lutzville (managed drought), Potchefstroom (optimum), Cedara (optimum) and Cedara (low nitrogen) during the 2016/17 summer planting season, were subjected to ANOVA and GGE biplot analyses. Analysis of variance for individual environments showed that the genotype mean squares were significant at $P<0.01$. The ANOVA across environments showed that the genotype, environment and genotype by environment interaction mean squares were significant at $P<0.01$ for grain yield. From the GGE biplot analysis, the two principal components (PC1 and PC2) contributed 64.8% of the total variability due to genotypes plus genotype by environment interaction, with PC1 and PC2 accounting for 35.97% and 28.83%, respectively. The use of GGE biplot analyses provided a clear basis for determining the stability and performance of the 50 early maize hybrids and ranked them according to order. The best performing genotypes were G13 (CZH15448), G46 (CZH15574), G15 (local check 2), G33 (CZH16094), G7 (CZH16083), G20 (CZH16090) and G4 (CZH16089). The following hybrids were adapted to specific environments as follows: G26 (CZH16070), G34 (CZH16074), G9 (CZH15499) and G18(CZH16071) at Cedara (optimum) conditions; G46 (CZH15574), G40 (CZH16069) and G12 (CZH16080) excluding the checks G23 (local check 1) and G14 (SC301) at Potchefstroom (optimum); G22 (CZH16093), G6 (CZH15575), G49 (CZH16068) and G17 (CZH15600) excluding the check G15 (local check 2) at Cedara (low N) and G33 (CZH16094), G37 (CZH15184), G41 (CZH16082), G28 (CZH16076) and G8 (CZH16065) at Lutzville (managed drought). The GGE biplot analysis also identified nine stable and high yielding genotypes, which included G6 (CZH15575), G46 (CZH15574), G22 (CZH16093), G49 (CZH16068), G12 (CZH16080), G17 (CZH15600), G28 (CZH16076), G47 (CZH15452), and G8 (CZH16065). These genotypes will contribute to high maize yields and stable grain production in specific and across environments and are therefore, recommended for further testing and release.

DECLARATION

I, **Lucia Zinzi Ndlala**, declare that:

1. The research reported in this dissertation, except where otherwise indicated, is my original research.

2. This dissertation has not been submitted for any degree examination at any other university.

3. This dissertation does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted. Then:

   a. Their words have been re-written but the general information attributed to them has been referenced;

   b. Where their exact words have been used, then their writing has been placed in italics and inside quotation marks, and referenced.

4. This dissertation does not contain text, graphics or tables copied and pasted from the internet, unless specifically acknowledged, and the source being detailed in the dissertation and in the references sections.

Signed

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Lucia Zinzi Ndlala

As the candidate's supervisors, we agree to submission of this dissertation:

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“*Nothing is impossible if you believe and put more effort into it”*

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LIST OF ABBREVIATIONS

ANOVA	Analysis of variance
AEC	Average Environment Coordinate
ARC-GCI	Agricultural Research Council – Grain Crops Institute
CIMMYT	International Maize and Wheat Improvement Center
CV	Coefficient of Variation
DAFF	Department of Agriculture Forestry and fisheries
FAOSTAT	Food and Agriculture Organization of the United Nations Statistical Databases
GA	Genetic Advance
GAM	Genetic Advance Expressed as Percentage Of Mean
GEI	Genotype Environment Interaction
GCV	Genotypic Coefficient of Variation
GGE	Genotype, Genotype by Environment
GV	Genotypic Variance
H^2	Broad Sense Heritability
N	Nitrogen
PCA	Principal Component Analysis
PCV	Phenotypic coefficient of variation
PV	Phenotypic variance
SA	South Africa
SSA	Sub-Saharan Africa
USA	United States of America

CHAPTER ONE

General Introduction

1.1 Importance and origin of maize

Maize (*Zea mays* L.) is the most important food source in the world and is recorded to have originated from a wild grass called teosinte in Mexico around 7000 years ago. The Native Americans are believed to have domesticated and improved maize into a better source of food for human consumption (Ranum *et al.,* 2014). The crop was later distributed to the rest of the world as an improved cultivar. According to Meng and Ekboir (2001), maize is ranked as the second most important cereal after wheat around the world. In addition to high demand as food in Africa, maize is also fast becoming a very important agricultural export crop within the region (Asea, 2005). In South Africa (SA), demand for maize grain is forecasted to surpass that of wheat and rice by 2020, with about 14.5 million tonnes produced annually which is high in grain yield per unit area of land (FAO, 2017).

Maize is a versatile crop that is grown over a wide range of agro-climatic zones. It serves as a multi-purpose crop for food, medicinal purpose, animal feed, biofuel, and raw material in the synthesis of a broad range of industrial products (Zhou *et al.,* 2009). It is cultivated extensively in Africa mainly for its carbohydrate-rich kernel. Apart from being a source of food, maize also provides a supplementary source of income to farmers, especially rural women. Between now and 2050, in the developing world maize demand will double (Anley *et al*., 2013).

1.2 World maize production and climate change

Climate change and weather patterns pose many challenges to large-scale farmers and subsistence farmers. However, climate change scenario shows that agricultural production and the ability of many regions to achieve the necessary gains for future food security will be negatively affected (Lobell *et al.,* 2008). Climate change scenario for sub-Saharan Africa (SSA) includes high periodic seasons and extreme temperature events and intensity of drought and results in changing crop production (IPCC, 2007). Low yields are mostly linked with drought stress, low soil fertility (especially low N), weeds, pests and diseases, low fertiliser availability, low input usage and unsuitable seeds (Cairns *et al.,* 2013). Farmers will be tested for their resourcefulness and adaptation capacity since climate change is having an influence on the production and improvement of maize (Adger *et al.,* 2007).

Cultivars with increased tolerance to abiotic stresses including heat and drought stress will play an important role in adaptation to climate change (Easterling *et al*., 2007; Fedoroff *et al.,* 2010; Hellin *et al.,* 2012). Maize breeders have improved maize productivity through selection based on the phenotype. However, a greater understanding of the complex biology of quantitative traits and more evaluation of the broader genetic base of maize genotypes will be required (Ram, 2011). Global production of maize is currently at 1031.86 million tonnes, with the leading producer, the United States, producing 42% and Africa as a whole producing 6.5%. Africa imports 28% of the required maize from countries outside the continent (USDA, 2017). Table 1.1 shows the world production in 2016/17. Most maize production in Africa is rain-fed and the irregular rainfall can trigger shortages during occasional droughts (IITA, 2016).

Table 1-1 Top 10 maize producing countries in the world

Rank	**Country**	**Million metric tonnes**
1	United States	337.5
2	China	224.9
3	Brazil	83.0
4	India	42.3
5	Argentina	40.0
6	Ukraine	39.2
7	Mexico	32.6
8	Indonesia	19.0
9	France	17.1
10	South Africa	15.5

Source: US Grains Council 2017

Maize production over the years has been decreasing in all countries due to the catastrophic events such as prolonged drought and low nitrogen soils that have been happening, thereby creating new market for maize to be imported/exported to nearby countries. Some countries like China and the United States have not been significantly affected by the climatic changes so far and they continue to produce to meet market demands.

1.3 Maize production in South Africa

The crop estimates committee's figures indicated that in 2016/17 season, South Africa (SA) increased the area planted with 2,629 million ha maize by 27% to 2.46 million with a total production of 4,19 million tons under production compared to the previous season. In SA, maize consumption is about 10.5 million tonnes per year, therefore, any production above that would put the country in a good surplus position to produce more maize for export market (Hartigh, 2016). Figure 1-1 shows the distribution and production areas in SA that produced white maize harvested in 2015/16.

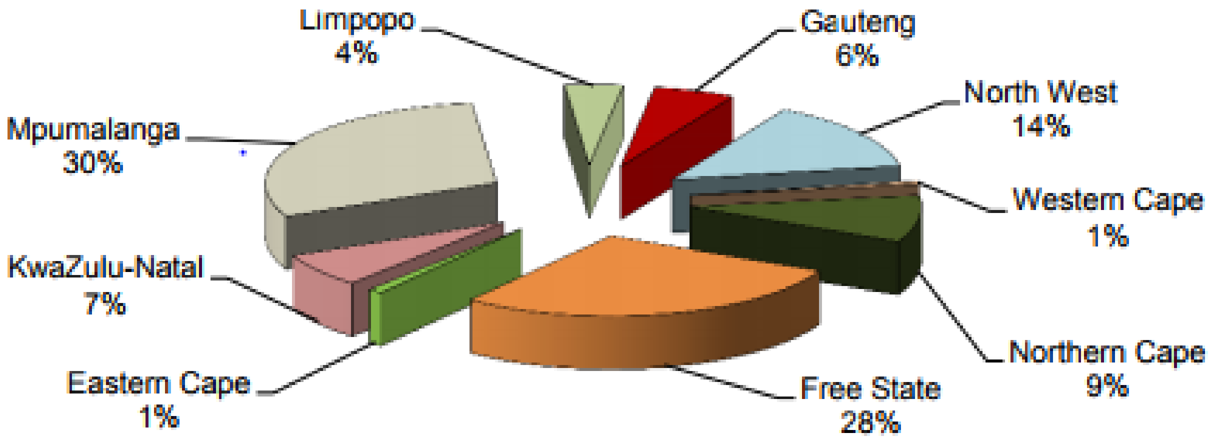

Figure 1-1 Distribution of maize production areas in South Africa

Source: DAFF, 2017

2015/16 estimates suggested that white maize production in SA was 3.254 million tonnes (31.3%) of 1.481 million tonnes less than the 4.735 million tonnes of 2015. Whereby, 2.948 million tonnes (or 47.5%) was less than the average of the five years, which was 6.201 million tonnes up to 2015. The estimated yield for white maize was 3.21 t ha^{-1}, compared to 3.27 t ha^{-1} the previous season. In the case of yellow maize, the production estimate for 2016 was 4.283 million tonnes (or 18.0%) of 936 900 tonnes less than the 5.220 million tonnes the previous season and 1.215 million tonnes (or 22.1%) less than the five-year average which was 5.498 million tonnes up to 2015. The estimated yield for yellow maize was 4.60 t ha^{-1}, compared to 4.33 t ha^{-1} in 2015 (DAFF, 2016).

Industrial consumption of maize consists mainly of ethanol, starch and fructose-glucose syrup production. Global consumption is projected to expand by 19 million tonnes (or by 7.3%), of which the expansion of ethanol accounts for only 4 million tonnes. SA industrial consumption may seem low at 6% of domestic consumption compared with the global average of 28%; however, one should take into account that SA does not produce maize-based ethanol or glucose fructose syrup, and that ethanol production in the US is so significant that it raises the global average. Excluding the US, the global average industrial consumption of maize is only 16%. Direct human consumption of maize typically accounts for just 11% of global maize consumption and is projected to only increase by 9 million tonnes (or by 9%) between 2013/14 and 2019/20 (IGC, 2014). Among the countries studied, food consumption of maize only played a significant role in SA and Mexico. According to reports by BFAP (2015), the role of food consumption in SA is expected, however, to reduce in future, as larger portions of maize production will be consumed by the animal feed sector as consumption patterns evolve to favour animal and wheat based products. Figure 1-2 shows the SA production and consumption of maize.

Figure 1-2 Southern Africa maize production and utilization (2005/06 - 2015/16)

Source: FAO/GIEW (2015)

According to the Bureau for Food and Agricultural policy baseline report for 2016-2025, area under white maize production in SA declined almost by 40% in 2015, because of drought in the western regions of the country where most of the white maize is produced on dry-land than other regions in the country. However, there was an increase in the maize production even though drought or climatic change had an impact on many crops (Hartigh, 2016).

Table 1-2 Cereal production in South Africa from 2012-2016 and its 2017 forecast

	2012-2016 Average	2016	2017 forecast	Change 2017/2016
		1000 tonnes		percent
Maize	11 803	8 214	14 500	77
Wheat	1 777	1 919	1 600	-17
Barley	310	354	334	-6
Others	226	163	205	26
Total	14 116	10 650	16 639	56

Source: FAO/GIEW country cereal balance sheets 2016/17

1.4 Constraints to maize production

Despite maize being the staple food diet for over 300 million people in Sub-Saharan Africa (SSA), its production is constrained by a number of biotic, abiotic and socio-economic factors causing variation in grain yield as compared to other regions (Olaoye, 2009). The biotic stresses include pest and diseases, while the abiotic stresses include drought, heat, waterlogging and low soil fertility (low N). Among the above-mentioned constraints, increasing drought incidences and infertile soils are the most limiting factors in maize production in SSA (Edmeades *et al.,* 2004). In most areas, including SA, drought and low soil fertility, especially nitrogen deficiency, frequently occur together. Drought that occurs shortly before flowering and grain filling can cause up to 37% crop loss and more (Bänziger *et al*., 1999), while soil nutrient depletion is a common consequence of most African agriculture (Smaling, 1993; Smaling *et al.,* 1997).

By 2050, it is estimated that demand for maize in the developing world would be almost double the current demand (Rosegrant *et al*., 2008). Thus with the current situation of production which is lagging far behind, estimates are not optimistic for the poor and marginal farm families. In addition, under the changing climate situation, there is a further threat to maize production in low and middle-income countries. Spatial analyses in recent years have consistently predicted an average of 10% or even more decline in maize yields by 2050 for SSA and Latin America mainly due to drought and low N (Lobell and Field, 2007; Thornton and Gerber, 2010). According to Food and Agriculture Organization of the United Nations (FAO, 2017), there was a 1.2 million tonnes reduction in maize harvest in 2017 and currently it stands at 2.593 million tonnes, which is 0.6% below the 2016 actual yield level attributed by drought and low N stress conditions.

Additional irrigation could potentially improve maize production in drought prone areas (Boyer and Westgate, 2004; FAO, 2006; Derera *et al.,* 2008; Nyombayire *et al.,* 2011). However, the majority of smallholder farmers cannot access irrigation due to various complications (Diallo *et al.,* 2001; Nyombayire *et al.,* 2011). Therefore, understanding the environmental conditions that contribute to drought tolerance and the expression of genetic variation for drought tolerance is critical to the success of any attempts to breeding for drought tolerance. Several scientists have studied the performance, adaptation and genetic variability in maize for grain yield and other secondary traits under drought stress and non-stress conditions to see the effect in terms of genotype with its environment and treatment interaction (Lafitte and Edmeades, 1994; Bänziger *et al.,* 1997; Duvick *et al.,* 2004; Edmeades *et al.,* 2006).

The second most important constraint is poor soil fertility, which includes micronutrient deficiency and low nutrient use efficiency. This is also ranked among the most important factors limiting crop productivity and yield stability in both high and low possible risk environments (Prasanna, 2013). Genetics and breeding alone cannot solve the complex challenge of enhancing productivity in smallholder farms, but there is a distinct need for effective complementation of improved maize cultivars by suitable conservation agriculture practices. Furthermore, agronomists and breeders have to work in collaboration to identify cultivars that respond best to such practices, and for generating a better understanding of the complex interactions between genotype, environment and management practices (Prasanna, 2013).

The major causes of low soil fertility are low application of external inputs, poor management practices, poor native soils and continuous cropping on the same piece of land without adequate use of fertiliser (Sanchez, 2010). This has resulted in the wide yield gap between research and smallholder farmers' yields. In most of the countries of the SSA region, the average maize yield is less than 1.0 t ha^{-1}, compared to yields of 10 t ha^{-1} or higher achieved by researchers. On average, the estimated annual loss of maize grain yield due to low N stress alone varies from 10-50% (Wolfe *et al.,* 1988; Logrono and Lothrop, 1997). Thus smallholder farmers, even those in well-watered areas, cannot realise the potential of enhanced germplasm mainly because of low and declining soil fertility.

Climate change is also worsening the frequency and intensity of drought and low soil fertility, further aggravating the challenges smallholder farmers face in SSA (Ertiro *et al.,* 2017). According to Nyombayire *et al.* (2011), only a few maize cultivars tolerate both drought and low nitrogen. Efforts to improve maize productivity have focused on producing high yielding and high input cultivars (Bänziger *et al*., 1997; Bänziger and Cooper, 2001; Nyombayire *et al.,* 2011), while smallholder farmers are faced with gradually degrading soil, decreasing crop yields, and limited access to commercial inputs. Therefore, there is an urgent need to provide the farmers with technologies that have significant returns and long-term sustainability. Poor seed selection and limited use of new improved commercial cultivars are among the reasons why farmers are not able to cope with the productivity demand (Okalebo *et al.,* 2006). Bolaños and Edmeades (1996) reported that breeding for maize cultivars with high and stable yields under drought conditions remains the most practical option to enhance maize productivity for many small-scale farmers. A better approach to helping subsistence farmers is thus selecting cultivars that are well adapted and stable under multiple stress environmental conditions, such as low nitrogen input levels and drought.

1.5 Statement of the Problem and justification

The demand for maize in SSA exceeds the production. Drought and low nitrogen are the major production constraints throughout the SSA countries, thus creating a need for high yielding, stable, low nitrogen and drought tolerant cultivars. The wide gap between potential and actual yields due to climate change effects suggests a need for new improved, high yielding and stable cultivars that are tolerant to multiple stresses for the smallholder farmers to reduce this gap. This study is therefore, undertaken to evaluate early maturing maize hybrids for grain yield under multiple stress environments. Hybrids have almost completely replaced the conventionally open-pollinated cultivars because of their potential for higher and more stable yields even under marginal environments (Schnable and Springer, 2013). Early maturing hybrid varieties play a major role in multiple stress tolerance through their ability to escape seasonal drought, which is currently prevalent due to climate change. Early maturing maize hybrids are, therefore, capable of contributing significantly to food security, especially in marginal rainfall areas (Badu-Apraku *et al.,* 2013; Oyekunle and Badu-Apraku, 2017). IITA (1992), Badu-Apraku *et al.* (2012) and Oyekunle and Badu-Apraku (2017) reported that early maturing and extra-early maturing genotypes afford farmers the chance to market the crop early as green maize at a first-rate price, as well as to use such genotypes for intercropping. Hence, breeding for earliness in maize offers a viable cropping mechanism towards addressing end-season drought among smallholder farmers who cannot afford irrigation technology.

The phenology of the crop to the pattern of water availability matches the selection for earliness. Since time from sowing to flowering and maturity are highly heritable traits, selection for earliness can easily be accomplished (Bänzinger *et al.,* 2000). As climate change is progressively leading to hotter and drier times, the effect of drought and low nitrogen constraints on yield and yield components will intensify. The key focus in breeding for multiple stress has been to expose the crop to stress at flowering and post-flowering stages of the crop. This is the stage when the crop is most susceptible to stress (Bänzinger *et al.,* 2000). Introgression of genes that are responsible for drought and low N in early maturing varieties may lead to the development of cultivars that are tolerant to multiples stress. The use of early maturing varieties tolerant to drought and low N provides opportunities to accelerate productivity of maize in SA. Therefore, it is important to use modern selection techniques such as molecular markers followed by multi-environment testing confirm consistence their performance in yields. In addition, deployment and distribution of drought, low nitrogen tolerant, high yielding, locally adapted early maturing maize hybrids cultivar can help in improving food security in Africa (Muhammad *et al.,* 2009). The goal of this study was achieved through identifying the best high yielding, stable and adapted maize genotypes that are recommended for further evaluation in other multi-environments to be registered and released to farmers.

1.6 Research goal and objectives

The goal was to evaluate early maturing maize hybrids under multiple stress environmental conditions for possible release in South Africa.

1.6.1 Objectives

The specific objectives of the study were as follows:

- To estimate variance components, correlation and path coefficients among yield and secondary traits in early maturing maize hybrids across stress and non-stress environments.

- To evaluate genotype by environment interaction and stability of grain yield in early maturing maize hybrids across stress and non-stress environments.

1.7 Structure of dissertation

This dissertation is structured as follows:

1. Chapter One: General introduction

2. Chapter Two: Literature review

3. Chapter Three: Variance components, correlation and path coefficients analyses in early maturing maize hybrids across stress and non-stress conditions

4. Chapter Four: Genotype by environment interaction and stability of early maturing maize hybrids across stress and non-stress environments

5. Chapter Five: General overview of the research findings

References

Adger, W. N., Agrawala, S., Mirza, M. M. Q., Conde, C., O'brien, K., Pulhin, J., Pulwarty, R., Smit, B. and Takahashi, K. 2007. Assessment of adaptation practices, management options, constraints and capacity. Climate Change. Impacts, Adaptation and Vulnerability. Contribution of Working Group II to the Forth Assessment Report of the Intergovernmental Panel on Climate Change,. In: Parry, M. L., Palutikof, J. P., Van Der Linden, P. J. and Hanson, C.E. (eds). Cambridge University Press, Cambridge, UK. pp 717-743.

Anley, W., Zeleke, H. and Dessalegn, Y. 2013. Genotype by environment interaction of maize (*Zea mays L.)* across North Western Ethiopia. Journal of Plant Breeding and Crop Science 5:171-181.

Asea, G. 2005. Genetic characterisation of partial resistance and comparative strategies for improvement of host resistance to multiple foliar pathogens of maize (PhD Thesis). Ohio State University, USA.

Badu-Apraku, B., Akinwale, R. O., Fakorede, M. A. B., Oyekunle, M. and Franco, J. 2012. Relative changes in genetic variability and correlations in early maturing maize population during recurrent selection. Theoretical and Applied Genetics 125:1289-1301.

Badu-Apraku, B., Yallou, C. G. and Oyekunle, M. 2013. Genetic gains from selection for grain yield and striga reistance in early maturing maize cultvars of three breeding periods under striga-infested and striga-free envvironments. Field Crops Research 147:54-67.

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

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

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

Bänzinger, M., Edmeades, G. O., Beck, D. and Bellon, M. 2000. Breeding for Drought and Nitrogen Stress Tolerance in Maize: From Theory to Practice. Mexico, D.F. CIMMYT. pp 9-75.

Bolaños, J. and Edmeades, G. O. 1996. The importance of the anthesis-silking interval in breeding for drought tolerance in tropical maize. Field Crops Research 48:65-80.

Boyer, J. and Westgate, M. E. 2004. Grain yields with limited water. Journal of experimental Botany 55:2385-2395.

BFAP. 2015. Adding value in the South African maize value chain. http://www.bfap.co.za/documents/research.pdf. Accessed 13 April 2017

Cairns, J., Hellin, J., Sonder, K., Araus, J., MacRobert, F. J., Thierfelder, C. and Prasanna, B. M. 2013. Adapting maize production to climate change in sub-Saharan Africa. Food and Security 5:345-360.

DAFF. 2016. Department of Agriculture, Forestry and Fisheries.Trends in the Agricultural Sector. pp.11-16.

Derera, J., Tongoona, P., Vivek, B. S. and Laing, M. D. 2008. Gene action controlling grain yield and secondary traits in southern African maize hybrids under drought and non-drought environments. Euphytica 162:411-422.

Diallo, A. O., Kikafunda, J., Legesse, W., Odongo, O., Mduruma, Z. O., Chivatsi, W. S., Friesen, D. K., Mugo, S. and Bänziger, M. 2001. Drought and low nitrogen tolerant hybrids for the moist mid-altitude ecology of Eastern Africa. Seventh Eastern and Southern Africa Regional Maize Conference. pp 206-212.

Duvick, D. N., Smith, J. S. C. and Cooper, M. 2004. Long-term selection in a commercial hybrid 557 maize breeding programme. Plant Breeding Reviews 24:109-151.

Easterling, W., Aggarwal, P., Batima, P., Brander, K., Erda, L., Howden, M., Kirilenko, A., Morton, J., Soussana, F., Schmidhuber, S. and Tubiello, F. W. 2007. Food, fibre and forest products. In: Parry, M. L., Palutikof, J. P., Van Linden, P. J. and Hansen C. E. (eds). Impacts, adaptation and vulnerability contribution of working group II to the fourth assessment report of the intergovernmental panel on climate change. Cambridge University Press, Cambridge, UK. pp 273-313.

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

Edmeades, G. O., Banziger, M., Campos, H. and Schussler, J. R. 2004. Improving drought tolerance in maize: a view from industry. Field Crops Research 90:19-34.

Ertiro, B., Beyene, Y., Das, B., Mugo, S., Olsen, M., Oikeh, S., Juma, C., Labuschagne, M. and Prasanna, B. 2017. Combining ability and testcross performance of drought-tolerant maize inbred lines under stress and non-stress environments in Kenya. Plant Breeding 136:197-205.

FAO. 2006. Demand for products of irrigated agriculture in sub-Saharan Africa. FAO, Rome, Italy.

FAO. 2015. Global Information And Early Warning System On Food and Agriculure (GIEWS). Special alert number 336. Southern Africa. pp 1-6 . http://www.fao.org/3/a-I5258e.pdf. Accessed 22 December 2016.

FAO. 2017. GIEWS country brief South Africa. FAO, Rome, Italy. pp 1-2. http://www.fao.org/giews/countrybrief/country.jsp?code=ZAF. Accessed 27 June 2018.

FAO. 2017. World food situation. FAO Cereal Supply and demand Brief. FAO, Rome, Italy. http://www.fao.org/worldfoodsituation/csdb/en/. Accessed 02 june 2017.

Fedoroff, N. V., Battisti, D. S., Beachy, R. N., Cooper, M., Fischhoff, D. A., Hodges, C. N., Knauf, V. C., Lobell, D. B., Mazur, B. J., Molden, D., Reynolds, C., Rosegrant, M. R., Sanchez, B. S. D., Vonshak, A. and Zhu, J. K. 2010. Radically Rethinking Agriculture For The 21st Century. Science Journal 327:833-834.

Hartigh, W. D. 2016. South Africa could become a net exporter of maize in 2017. https://www.farmersweekly.co.za/agri-news/south-africa/sa-could-become-a-net-exporter-of-maize-in-2017/. Accessed 30 April 2017.

Hellin, J., Shiferaw, B., Cairns, J., Reynolds, M., Ortiz-Monasterio, I. and Bänziger, M. 2012. Climate change and food security in the developing world: potential of maize and wheat research to expand options for adaptation and mitigation. Journal of Development and Agricultural Economics 4:311-321.

IGC. 2014. International Grains Council, Five-year Global Supply and Demand Projections. http://www.igc.int/en/downloads/grainsupdate/igc_5yrprojections2014.pd. Accessed 22 June 2016.

IITA. 1992. Sustainable food production in sub-Saharan Africa. I. IITA's contribution. IITA. Ibadan, Nigeria. pp 208.

IITA. 2016. Research to nourish Africa. http://blogs.iita.org/research/nourishing-africa /ensuring-food-security-in-africa-through-agricultural-research/ . Accessesd 19 March 2016

IPCC. 2007. Fourth assessment report: synthesis. http://www.ipcc.ch/pdf/assessment-report/ar4/syr/ar4_syr.pdf. Accessed 17 November 2007.

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

Lobell, D. B. and Field, C. B. 2007. Global scale climate-crop yield relationships and the impacts of recent warming. Environmental Research Letters 2:1-7.

Lobell, D. B., Burke, M. B., Tebaldi, C., Mastrandrea, M. D., Falcon, W. P and Naylor R. L. Prioritizing climate change adaptation needs for food security in 2030 Science 319: 607-610.

Logrono, M. and Lothrop, J. E. 1997. Impact of drought and low nitrogen on maize production in Asia. In: Edmeades, G. O. (ed). Developing drought- and low N-tolerant maize. CIMMYT/UNDP. Mexico, D. F. pp 39-43.

Meng, E. and Ekboir, J. 2001. Current and Future Trends in Maize Production and Trade. CIMMYT 1999–2000 World Maize Facts and Trends. In: Pingali, P.L. (ed.). Meeting World Maize Needs: Technological Opportunities and Priorities for the Public Sector. CIMMYT, Mexico. pp 35-44.

Muhammad, L., Mwabu, D., Mwangi, W. and La-Rovere, R. 2009. Community assessment of drought tolerant maize for Africa (DTMA) in Kenya. Nairobi, Kenya, CIMMYT. pp 1-20.

Nafziger, E. D. 2010. Growth and production of maize: mechanized cultivation. Encyclopedia of Life Support Systems. 1:2-5.

Nyombayire, A., Edema, R., Asea., G. and Gibson, P. 2011. Combining ability of maize inbred lines for performance under low nitrogen and drought stresses. African Crop Science Society 10:1-4.

Okalebo, J., Othieno, C. O., Woomer, P. L., Karanja, N. K., Semoka, J. M., Bekunda, M. A., Mugendi, D. N., Muasya, R. M., Bationo, A. and Mukhwana, E. J. 2006. Available technologies to replenish soil fertility in East Africa. Nutrient Cycling Agroecosystems 76:153-170.

Olaoye, G. 2009. Evaluation of new generations of maize streak virus (MSV) resistant cultivar for grain yield, agronomic potential and adaptation to a southern Guinea Savanna ecology of Nigeria. Journal of Tropical Agriculture, Food, Environment and Extension 8:104-109.

Oyekunle, M. and Badu-Apraku, B. 2017. Agronomic perfomance of drought-tolerant maize hybrids in diverse environments of lowland tropics. Journal of Crop Improvement 31: 743-757.

Prasanna, B. M. 2013. Maize in the Developing World: Trends, Challenges, and Opportunities. Proceeding International Maize Conference. pp 26-36.

Ram, H. 2011. Crop Breeding and Biotechnology. Kalyani Publishers, Ludhiana, India. pp 733.

Ranum, P., Peña-Rosas, J. P. and Garcia-Casal, M. N. 2014. Global maize production, utilization, and consumption. Annals of the New York Academy of Science 1312:105-12.

Rosegrant, M. R., Msangi, S., Ringler. C., Sulser, T. B., Zhu, T. and Cline S. A. 2008. International model for policy analysis of agriculture commodities and trade (IMPACT): Model description. International food policy Institute, Washington, DC.: International Food Policy Research Institute.

Sanchez, P. A. 2010. Tripling crop yields in tropical Africa. Nature Geo-Science 3:299-300.

Schnable, P. S. and Springer, N. M. 2013. Progress towards understanding heterosis in crop plants. Annual Review of Plant Biology 64:71-88.

Smaling, E. M. A. 1993. The soil nutrient balance: an indicator of sustainable agriculture in sub-Sahara agriculture. In: Proceedings of the Fertiliser Society 340. pp 18.

Smaling, E. M. A., Nandwa, S. M. and Jansson, B. H. 1997. Soil fertility in Africa is at stake, In: Replenishing soil fertility in Africa. Special Publication. Soil Science Society of America, Madison, USA. pp 47-61.

Thornton, P. K. and Gerber, P. 2010. Climate change and the growth of livestock sector in developing countries. Mitigation and adaptation statergies for Global change. Global Environmental Change 15:169-184.

USDA. 2017. World corn production 2016/2017. https://www.worldcornproduction.com. Accessed 10 June 2017.

Wolfe, D. W., Henderson, D. W., Hsiao, T. C. and Alvio, A. 1988. Interactive water and nitrogen effects on maize. II. Photosynthetic decline and longevity of individual leaves. Agronomy Journal 80:865-870.

Zhou, S., Wei, F., Nguyen, J., Bechner, M., Potamousis, K. and Goldstein, S. E. A. 2009. A Single Molecule Scaffold for the Maize Genome. Peer-Reviewed Open-Access Journal of Genetics 5:1-3.

CHAPTER TWO

Literature Review

2.1 Introduction

This chapter reviews studies by other researchers on the development and improvement of early maturing maize hybrids under multiple stress conditions. The section also identifies the research gaps that exist and then presents the focus of the study conducted. The key areas reviewed are: botany of maize, taxonomy, conventional breeding, importance of early-maturing maize cultivars in sub-Saharan Africa (SSA), drought stress, low nitrogen stress, random and managed drought stress screening, secondary traits and grain yield, heritability and genetic components, correlations and path coefficient analysis, genotype by environment interaction, stability of yield and its components and the conclusion.

2.2 Botany of maize

Maize (*Zea mays* L.) is among the most human-modified crops on earth. Its ancestor is believed to be teosinte, a wild relative with a very small rachis that breaks at maturity to release 10 to 12 seeds enclosed in capsules (Nafziger, 2010). Selection over the years has produced a maize plant that can grow up to 5 m tall, with a rachis on a single branch that contains as many as 800 to 1,000 kernels covered by modified leaves (husks) that protect the kernels from desiccation. Maize would not exist in its current form had it not been selected and improved upon for years by scientists. Human intervention in the development of maize as a crop is assisted by the fact that maize is a monoecious crop, with separate staminate (the tassel) and pistilate (the ear) flower structures borne on the same plant. Both flowers are separated by a distance of one or more metres, and pollen must move this distance in order to effect pollination of the female flower. Pollen is disseminated by wind, making maize highly cross pollinated. At the same time, it is relatively easy to capture pollen from the tassel and to prevent pollination by covering the long pistils before they emerge. This helps in controlling pollination and enables the making of planned crosses between or within plants (Nafziger, 2010).

2.3 Taxonomy

Maize (*Zea mays* L., 2n = 2x = 20) belongs to the grass family Poaceae (Gramineae), which shares a classification with other important crops, such as wheat (*Triticum aestivum*), rice (*Oryza sativa*), oats (*Avena sativa*), sorghum (*Sorghum bicolor*), barley (*Hordeum vulgare*) and sugarcane (*Saccharum officinarum*). It is further organised as genus *Zea* that is native to

Mexico and Central America as a group of annual and perennial grasses. There are eight genera, of which five are from the Old World, from India through Southeastern Asia to Australia. Two other genera, *Euchlaena* and *Tripsacum*, occur in the American tropics. Both are closely related to maize and have contributed to its ancestry (Purseglove, 1976; Nafziger, 2010).

Tito *et al.* (1991) and Ellneskog-Staam *et al.* (2007) reviewed five *Zea mays* species, which comprises of 20 chromosomes. Additional to the simple A chromosome pair, Jones *et al*. (2008) revealed that maize has one or more extra chromosomes, called B chromosomes, during meiosis it never pairs with A chromosome. Maize and teosinte are usually classified as domestic and wild species, respectively. Teosinte, native to Mexico and Guatemala, has been found growing in the wild often whereby it crosses readily with cultivated maize and hybrids produced are fertile (Nafziger, 2010). The past extensive domestication has led to the co-existence of a wide variety of races, landraces, and improved cultivars that have been sustained by farmers and vastly enhanced professionally to create open pollinated cultivars (Paliwal, 2000).

2.4 Conventional breeding

Atlin and Lafitte (2002) indicated that conventional breeding is mainly focused on practical selection for grain yield. Under multiple stress conditions, this approach is far from being optimal since grain yield is a quantitative trait characterized by low heritability and high genotype x environment interaction (Babu *et al.,* 2003). Consequently, there is low genetic gain realised such that the use of secondary traits would assist to select for grain yield indirectly. According to Cattivelli *et al*. (2008), understanding of the physiological and molecular basis of maize may assist in targeting the key traits that reduce yield. Such methods complement conventional breeding programmes and accelerate yield improvement. The use of molecular biology to detect important gene structures and introgress quantitative trait loci (QTL) depends on the physiological processes (Araus *et al*., 2002; Kirigwi *et al.,* 2007).

It is difficult to screen for drought stress under natural environments because of the uneven and unpredictable drought response, while screening under managed stress environments and rainout shelters is more controllable. According to Venuprasad *et al.* (2007), selection response in the target population of environments under natural stress can be measured as linked response to selection in managed stress environment. On the other hand, classical breeding is a good method for enhancing drought tolerance, which depends on multi-location tests of progenies in environments representing a random selection of the variation in drought stress in the target conditions (Babu *et al*., 2003).

2.5 Importance of early maturing maize cultivars in SSA

Development of early maturing drought and low N stress tolerant maize germplasm is one of the important programmes that International Maize and Wheat Improvement Center (CIMMYT) is undertaking in order to alleviate hunger in sub-Saharan Africa (SSA). Early maturing maize hybrids are those characterized by shorter vegetative period and they are suitable for growth in areas with shorter growing seasons. Based on a study by CIMMYT-Zimbabwe (2000), early maturing maize hybrids are preferred for several reasons that include off-season planting in riverbeds and production during the secondary short rain season, which enables the planting of a full season maize crop or other crops in the following main season. In addition, they provide an early harvest during the main season to bridge the “hungry” season before harvest of full-season crop, which are important in areas where there are two growing seasons. The early maturing cultivars are also ideal for intercropping due to less and reduced moisture competition, soil nutrients and light than later maturing cultivars. In addition to providing flexibility in planting dates, it also enables multiple plantings in a season to extend the risk of losing a single particular crop to drought and late planting during delayed onset of rainfall.

South Africa faces a major challenge, as only 13% of its land is suitable for crop production. This challenge is exacerbated by low rainfall, which often results in drought. Drought leads to crop failure, unemployment, hunger, and poverty. Climate change is predicted to worsen the situation with rainfall that is more variable and above average temperatures. According to DAFF (2014), the release and deployment of maize varieties that are tolerant to low nitrogen and drought will help farmers to build resilient towards drought and low nitrogen incidences.

In South Africa, effort towards release and deployment of maize varieties that are tolerant to multiple stress has been enhanced through the Water Efficient Maize for Africa (WEMA) and Improved Maize for African Soils (IMAS) Projects. WEMA project is aimed at developing and deploying drought-tolerant maize hybrids royalty-free to smallholder farmers in SSA. The IMAS project is aimed at developing and deploying nitrogen-use efficient (fertilizer-friendly) conventional and genetic modified (GM) maize hybrids that give at least 25% yield advantage with the same amount of fertilizer application. Through the Agricultural Research Council-Grain Crop (ARC-GC) participation in these two projects, the first phase of drought tolerant maize varieties targeting the smallholder farmers has been released in South Africa (James, 2015). The Agricultural Research Council-Grain Crops (ARC-GC) plays a crucial role in conducting independent evaluation of maize cultivars from various seed companies in an effort to aid the farmers in selecting the best cultivar for every maize production region in South Africa.

2.6 Drought stress in maize

Drought or restricted water availability is the key factor that reduces crop production (Seghatoleslami *et al.,* 2008; Golbashy *et al.,* 2010). Drought has been a permanent constraint to agricultural production in many developing countries and seldom causes loss of agricultural production in the developed countries (Ceccarelli and Grando, 1996). Araus *et al.* (2003) suggested that yield was linked with water inputs under diverse water-stress conditions. Heisey and Edmeades (1999) predicted that 20-25% of the countries maize planted area is affected by drought in any given season throughout the year. Amongst the nine maize growing provinces in SA, the areas affected by drought and low N fall in Limpopo, Gauteng, Free State, Eastern Cape, Mpumalanga, North West, Western Cape and KwaZulu-Natal provinces (Radebe, 2013; ENCA, 2016).

Reduction in maize grain yield is mainly caused by drought, which varies from 10-76% depending on the strictness and time of incidence (Bolaños and Edmeades, 1996). Minimizing the ‘yield gap’ and increasing the yield stability under different stress conditions are of strategic importance in guaranteeing food for the future (Piepho, 2000). Thus, the best option for crop production, yield improvement and yield stability under drought stress conditions is to develop drought tolerant crop cultivars.

Various scientists have investigated the performance, adaptation and genetic variability in maize for grain yield and other agronomic traits under drought stress and non-stress conditions (Lafitte and Edmeades, 1994; Bänziger *et al*., 1997; Duvick *et al*., 2004; Edmeades *et al*., 2006). Vanshistha *et al.* (2013) reported that the presence of variability is important for the resistance of biotic and abiotic factors as well as wide adaptation for genotypes.

One key objective in a breeding programme is to choose the best genotypes under drought stress environments (Richards et al., 2002). This makes selection of plants for drought tolerance difficult as the breeding value and heritability of grain yield (a complex trait) decreases with increased stress intensity (Cooper *et al.,* 2006). Low heritability of drought tolerance and lack of effective selection methods limit improvement of tolerance of crop cultivars to environmental stress (Kirigwi *et al.,* 2004). Consequently, indirect selection of drought tolerance in maize can be successfully done using extremely heritable traits that link with drought tolerance such as anthesis-silking interval, ears per plant and senescence rate (Derera *et al*., 2008).

To estimate response of plant genotypes to drought stress, some selection indices based on mathematical relation between stress and non-stress conditions have been suggested (Rosielle and Hamblin, 1981; Clarke *et al*., 1992; Fernandez, 1992; Sio-Se *et al.,* 2006). For example, Fernandez (1992) classified plants according to their performance in stress and non-stress environments in four groups: group A-genotypes with good performance in both environments; group B-genotypes with good performance only in non-stress environments; group C-genotype with good performance in stress environments; and group D-genotype with weak performance in both environments. Shirinzadeh *et al.* (2009), on the other hand, established that stress tolerance index is a more effective index in detecting group A from other groups. Khalil *et al*. (2004) revealed that based on the geometric mean productivity and stress tolerant indices, selection of high yielding maize hybrids under stress and non-stress conditions could be possible. Therefore, improving maize yield stability in stress conditions requires identification of selection indices that are able to differentiate high yielding cultivars (Golbashy *et al.,* 2010).

2.7 Low nitrogen stress

Low nitrogen (N) is one of the main restrictive nutrient to maize production (Badu-Apraku *et al.,* 2010; Ismaila *et al*., 2010). In most of the developing countries of the world, maize is produced under conditions of low soil fertility (McCown *et al.,* 1992; Oikeh and Horst, 2001). Low N stress alone has been reported to reduce yield loss by 50% (Wolfe *et al.,* 1988). Kernel abortion in maize has been seen to be intensified by low N stress thereby leading to reduced grain number (Lemcoff and Loomis, 1986; Pearson and Jacobs, 1987; Uhart and Andrade, 1995a). Maize growth is affected by low N throughout its entire life cycle compared to drought that occurs at any particular period during the growth of the crop (Bänziger and Araus, 2007). Lafitte and Edmeades (1988) reported that N inaccessibility is predicted to be the main restrictive factor in more than 20% of arable land. Using inorganic fertiliser in SSA has resulted in the unavailability of fertiliser and ever-mounting cost. There are cultivars tolerant to low N which are efficient in exploiting available N, mostly because of their ability to efficiently utilise and absorb N in grain production (Lafitte and Edmeades, 1994).

Nitrogen deficiency in the soil is due to the rapidity by which it is taken up or lost from the soil through erosion, volatilization and leaching. A possible method to reduce N deficiency in soil is to reduce its demand by the crop in selection for low N tolerance (Smith, 1994; 1995). This method has brought about the improvement of maize inbred lines; open pollinated and hybrid cultivars, which are capable of using the available N in the soil. The improved cultivars should increase productivity in low N soils and reduce dependence on inorganic N fertilizer applications.

According to Lunze *et al.* (2007), the most reasonable agricultural practice for improving soil fertility remains the use of organic compost manure. This can be problematic to implement on a large scale because of inadequate amounts and poor quality of the existing organic resources on farms (Palm *et al.,* 1997). Combining with green manure enhances soil organic matter and can improve the soil's physical properties. Green manures also provide ground cover and preserve the soil against corrosion (Lal, 1991). It has been reported that besides providing nutrients for crop improvement, application of N may possibly lead to improved drought tolerance and enhance yield (Zaman and Das, 1991; Xu *et al.*, 2005).

Nitrogen (N) plays a critical part as an anti-oxidant protection enzyme and lipid peroxidation metabolism under multiple stress environments (Sun *et al*., 2001; Saneoka *et al*., 2004). There have been reports that N deficiency has negative effects on leaf expansion, emergence rate, radiation, interception radiation use efficiency and distributed between vegetative and reproductive organs (Uhart and Andrade, 1995a). Low N has also been implicated in the reduction of kernel number and number of ears (Lemcoff and Loomis, 1986; Pearson and Jacobs, 1987; Uhart and Andrade, 1995a, b: Monneveux *et al*., 2005). N deficiency has resulted in the extended anthesis-silking interval (Jacobs and Pearson, 1991) and accelerated senescence (Moll *et al*., 1994).

Breeding for tolerance to low N suggests the most comprehensive and sustainable method for improved maize yields in the SSA (Badu-Apraku *et al*., 2017). Enhancement for drought tolerance has resulted in specific adaptation and enhanced performance under low N conditions, suggesting that tolerance to either stress involves common adaptive mechanism (Banziger *et al*., 1999; Badu-Apraku *et al*., 2011; Badu-Apraku *et al*., 2015a). Therefore, it is important to increase adoption of a general method to identify genotypes or cultivars that are tolerant to a variety of stresses expected in the target environments instead of grouping the different stresses (Badu-Apraku *et al*., 2010). Numerous evaluation of hybrids developed in different areas under distinct N levels have been reported (Castleberry *et al*., 1984; Tollenaar *et al*., 1997; Sangoi *et al*., 2002; O'Neill *et al*., 2004).

Utilisation of secondary traits in the selection process has been repeatedly recommended (Lafitte *et al.,* 2003; Jearakongman, 2005; Kumar et al., 2007) as a result of low heritability estimates for grain yield under low N conditions. Secondary traits such anthesis-silking interval, leaf senescence and ears per plant have been suggested as ideal for selection when improving maize genotypes for low N environments (Bänziger and Lafitte, 1997; Bänzinger *et al*., 2000). Selection indices focused on these traits have been identified and these have significantly enhanced the selection efficacy under low N stress conditions (Bänziger and

Lafitte, 1997). Breeding for low N is much easier than for drought stress mostly because inaccessibility of N affects plant growth in a more even manner unlike drought periods that occur randomly (Bänziger *et al*., 2000). Screening germplasm under severe low N environments should be adequate to realize low N stress tolerance for different levels of N deficiency.

2.8 Random and managed drought stress screening trials

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 and Edmeades, 1993; Bänziger and Diallo, 2004; Muza *et al*., 2004). Hence, for maximum breeding progress, testing should be done in the environments that represent the target production environments (Allen, 1978). Edmeades *et al*. (2006) reported that the random nature of climate-related stresses and the inadequate number of testing sites have required the improvement and use of managed stress sites. Random drought stress trials are usually conducted in managed conditions furnished with irrigation facilities. To develop low N and drought tolerant genotypes for the region, selection is done by using three types of environments: low N stress, managed drought and recommended agronomic management or high rainfall conditions (optimum) (Edmeades *et al*., 2006).

Managed drought stress trials are done in the dry seasons when the temperature, day length, humidity and disease pressure may differ from the main growing season, while the managed low N are done in stress scenario occurring in the target environment (Weber et al., 2012). Under severe managed stress, irrigation is programmed such that drought stress matches with anthesis and silking. Application of irrigation should be uniform before onset of stress to obtain even stress levels in all genotypes, more constant plant performance and eventually improved breeding progress (Bänziger *et al*., 2000; Ndhlela, 2012).

Statistical analysis of grain yield under stress environments often shows non-significant differences or higher coefficients of variation than experiments performed under optimal environment (Bänziger and Cooper, 2001). This suggests that the error variance of grain yield does not reduce as much as the genetic variance when moving from high to low yielding environments (Bänziger and Lafitte, 1997).

2.9 Secondary traits and grain yield

Through abiotic stress conditions, grain yield and its yield components have been positively used to improve the genetic rate enhancement for maize populations. A suitable secondary component is genetically associated with grain yield under drought, highly heritable, stable and possible to measure and not associated with yield loss under ideal growing conditions (Edmeades *et al.,* 2001). Hence, since yield is a primary trait, it has revealed little success if any, in the selection of drought tolerant lines and hybrids. Grain yield as a primary trait can be characterised by low heritability under stress, low genetic variance and a high genotype by environment interaction while heritability of secondary traits rises under stress (Jackson *et al*., 1996; Bolaños and Edmeades,1996). Thus, secondary traits have helped in the advancement of breeding against drought stress. The manipulation of these highly heritable traits, which are associated with grain yield, presents a more effective option than direct selection of yield per se (Kashiani and Saleh, 2010).

The genetic associations among grain yield and secondary components can be used to help recover primary traits that have low heritability and are hard to measure under stress (Malosetti *et al*., 2008). Betran *et al*. (2003) reported that secondary components should be strongly correlated with grain yield both under stress and non-stress environments. Greater grain yield in inbred lines and hybrids are usually linked with shorter anthesis-silking intervals, earlier flowering, increased plant and ear height, increased ear per plant and increased shelling percentage under drought environments (Bänziger *et al*., 2002; Betran *et al*., 2003; Monneveux *et al*., 2008).

For the secondary component to be helpful in a breeding programme, it must conform to numerous requirements (Bänziger *et al*., 2000; Araus *et al*., 2002; Lafitte *et al*., 2003; Royo *et al*., 2005). According to Araus *et al*. (2002), firstly, secondary components must be genetically linked with grain yield under drought; secondly, the trait must be highly heritable than grain yield itself. This means that the environment should have less influence on it than grain yield and have less genotype by environment interaction (GEI). Thirdly, the trait must display genetic variability within the species. Fourthly, it must be stable, rapid, dependable and easy to measure. Fifth, for any breeding programme’s stress-prone environments, the secondary components should never be related with yield loss under the optimum growing conditions; and finally, the trait must be easily evaluated in individual plants or in very small plots. The use of secondary components in selection of drought tolerant cultivars is useful during inbred line enhancement with good performance for hybrid combination across drought stress levels (Betran *et al*., 2003).

2.10 Heritability and genetic components

Most of the characters of breeders’ interest are complex and polygenically controlled. A successful selection programme depends not only on heritability of desired characters but also on the information on association among various secondary yield components and their association with grain yield (Singh *et al*., 1995: Abdurakhmonov and Abdukarimov, 2008). Bello *et al*. (2012) defined heritability as a quantity of the phenotypic variance attributed to genetic causes and has predictive purposes in plant breeding. Heritability can be expressed into two senses, the narrow sense and the broad sense. Narrow sense heritability estimates are calculated as ratio of additive portion of the genetic variance to the phenotypic variance, while broad sense heritability estimates are calculated as the ratio of the total genetic variance to the phenotypic variance (Sujiprihati *et al*. 2003). High narrow sense heritability is associated with additive gene effects whereas low narrow sense heritability could be due to dominance and epistasis or great influence of the environment. Obilana and Fakorede (1981), earlier summarized procedures in heritability estimates into three; namely, regression of offspring on parent, variance component estimates and recurrent selection experiment. Whichever method a breeder decides to use does not really matter, rather, the predictive ability of the estimate in selecting genotypes for advancement makes it highly relevant in selection procedure (Olakojo and Olaoye, 2011).

Heritability provides information on the degree to which a specific morphogenetic trait can be passed on to continuous generations. Understanding of heritability effects the choice of selection processes used by the plant breeder to choose which selection procedures would be most valuable to develop the character, to predict gain from selection and to define the relative importance of genetic effects (Waqar-Ul-Haq *et al*., 2008, Laghari *et al*., 2010). Heritability in genetics indicates reliability of phenotypic value as a guide to breeding value (Falconer and Mackay, 1996). Highly heritable traits can be fixed with simple selection, which result in rapid advancement. However, genetic advanced is important when coupled with heritability (Najeeb *et al*., 2009).

High genetic advance combined with high heritability estimates suggests the most appropriate environments for selection (Bello *et al*., 2012). Ramanujam and Thirumalachar (1967) reported restriction in the narrow sense heritability estimates, which includes both additive and epistatic gene effects, and recommended that broad sense heritability estimated will be reliable if complemented by a high genetic advancement. Different researchers (Nelson and Somers, 1992; Rafaque *et al*., 2004) reported high heritability and high genetic advance for different yield regulating maize traits. Hence, understanding of these genetic parameters existing in different yield contributing traits and the comparative quantity of this genetic data in numerous measurable traits is a pre-requisite for effective crop enhancement. Bänziger *et al*. (2006) stated that to improve genetic gains from selection, careful management of multiple stress environments is very important to reduce environmental variance and increase heritability for stress tolerance plant characteristics.

2.11 Correlation and path coefficients analysis

Correlation and path coefficient analyses assist researchers to differentiate significant relationships amongst traits. According to Kusaksiz (2010) correlation and path coefficient analyses can assist in identifying certain components to be used in the enhancement of complex traits such as grain yield. The nature and the magnitude of variability present in genotypes can determine the effect of genetic enhancement of grain yield and yield component. The association between two variables, which can be directly observed, is termed as phenotypic correlation, whereas the inherent or heritable association is known as genotypic correlation. The correlation value suggests that only the nature and extent of linkage that exists amongst pairs of components. A character such as grain yield depends on numerous components that are jointly related, where true association exists amongst grain yield and secondary components, the whole network of cause and effects can be damaged by change in any one component. Ahmad and Saleem (2003) stated that correlation and path coefficient between grain yield and secondary components is important for selection of favourable plant types to achieve effective breeding programme. The aim of path coefficient analyses is to present an appropriate interpretation of correlation between variables, by creating cause and effect models (Solymanzadeh et al., 2007).

2.12 Genotype by environment interaction

Grain yield is a complex trait that is controlled by polygenes, which are significantly influenced by the environment. Genotype by environment interaction (GEI) is common under drought environments and makes breeding progress difficult as it is challenging to select the best performing and most stable genotypes. This, of course, decreases the selection progress (Yan and Hunt, 1998). The GEI may originate from environmental variation in the timing and severity of water deficits, genetic variation in flowering time, and nutrient deficiencies and toxicities whose existence and severity interact with water deficits (Bänziger and Cooper, 2001; Cooper *et al.,* 1999; Bänziger and Diallo, 2004). Smithson and Grisley (1992) reported that crops lack the wide environmental gene protection; therefore, for plant breeders, large GEI effects hinder breeding progress.

According to Beyene *et al.* (2011), tropical regions have witnessed great environmental fluctuations lately due to climate change. Genotype by environment interactions (GEIs) are as much a function of both the genotype and environment, which are only partly heritable (Hill, 1975). Several research studies have revealed that an appropriate understanding of the environmental and genetic factors causing the interaction as well as an evaluation of their significance in the relevant genotype by environment system could have a large impact on plant breeding (Magari and Kang, 1993).

There are various methods for assessing the performance of crosses and their genotypic interactions with the location according to Crossa and Cornelius (1997) and Eberhart and Russell (1966). These methods vary in the factors used in the assessment, the biometric procedures employed, and the analysis. The sites regression has been recommended as a suitable model for analysing multi environmental trials when large yield variation is due to environments (Crossa and Cornelius, 1997). The sites regression method provides a graphical display called genotype plus genotype x environment (GGE) interaction biplot that identifies cultivars that are superior in different environments. The performance of a genotype can differ among environments, and genotypes that are superior in one location may not be superior in other location due to GEI (Makumbi *et al.,* 2015).

2.13 Stability of yield and yield components

Stability in performance of a genotype for desirable attributes depends on the magnitude of genotype x environment interaction (GEI) over extensive range of environments with desirable attributes (Ahmad *et al.,* 1996; Lodhi *et al.,* 2015). Becker and Leon (1988) defined stability as the ability of the genotypes to be stable, both with high or low yield levels across different locations. On the other hand, adaptability refers to the change of a genotype to its environment, for example a genotype that produces high yields in specific location and poor yields in another (Balzarini et al., 2005, Kandus *et al.,* 2010). The stability of grain yield was statistically analysed through the evaluation of GEI in cultivar trials conducted in numerous locations of different crops (Crossa 1990; Piepho 1998; Lodhi *et al.,* 2015). The stability concept can be static or dynamic (Becker, 1981). Static stability is considered by stable genotype performance over different environmental circumstances, that is, the genotype is non-responsive to increased levels of inputs, while for dynamic stability, a genotype attains a constant high yield response to changes in the environment (Becker and Leon, 1988). Therefore, when considering yield stability of a certain genotype, we have to bear in mind that stability can be a consequence of various factors such as tolerance to drought or resistance to the most important diseases or pests (Babic *et al.,* 2010; 2013; Djurovic *et al.,* 2014).

Genotype stability for yield and agronomic performance is an essential breeding. Stability measures are based on either regression or principal component analyses (Bernado, 2002).

Some of the most common stability parameters include Finlay and Wilkinsons (1963) regression coefficient, Eberhart and Russell (1966) deviation from regression, Shukla (1972) stability variance, Kang (1993) yield stability parameter and Gauch (1992) the AMMI model. The adaptability of a genotype is frequently tested by the amount of its interaction with diverse locations. A cultivar is considered more adapted or stable if it has a high mean of grain yield with less degree of variation in yield ability for growing over several locations or even seasons (Amin *et al.,* 2005; Cehyan *et al.,* 2012). According to Kumari *et al.* (2014), stable genotypes are less influenced by GEI and have individual or population buffering mechanisms to make physiological adjustments to cope with physical, chemical and biological changes in the interaction of genetic and non-genetic development phases.

2.14 Conclusion

The review has shown that there is a huge gap between grain yield potential and the actual yield in the farmers' field, signifying the opportunities for breeders to bridge the gap. There is also a need for high yielding and stable maize cultivars to be used by farmers. Due to climate change, maize production environments have become limiting. Therefore, development and improvement of early maturing hybrids will ensure the availability of cultivars that perform well under multiple environmental stress conditions. Yield is the most important trait in maize and is influenced by multiple secondary components. Since yield is a complex trait with low heritability, use of secondary traits of high heritability and correlation with grain yield could help in selection of superior genotypes and accelerate breeding progress.

The review further showed that low soil fertility, especially N, plays a huge role in decreasing maize production in sub-Saharan Africa (SSA). The use of maize genotypes with improved N use efficiency suggests an essential yield benefit at insignificant additional cost to the farmers that will allow the farmers to accept them. Low N is a stress environment and its heritability decrease with increase in stress, making selection difficult. Drought is another important factor causing yield losses in SSA. Yield losses due to drought stress are major at flowering and grain filling stages due to reduced pollen-silk synchronisation and this further exacerbates poor ear and kernel development. It is suggested that grain yield can be improved by selecting for short anthesis-silking interval and high number of ears per plant under stress environments. In improving the seed quality there is need to bring in new technologies that will be adopted by farmers. This study, therefore, intended to bridge these research gaps by identifying, evaluating and registering new improved varieties under multiple stress conditions for farmers' sustainability in food security.

References

Abdurakhmonov, I., and Abdukarimov, A. 2008. Application of association mapping to understanding the genetic diversity of plant germplasm resources. International Journal of Plant Genomics 2008:1-18.

Agrama, H. 2006. Sequential path analysis of grain yield and it´s components in maize. Plant Breeding 115:343-346.

Ahmad, J., Choundhry, M. H., Salah-ud-Din, S., Ali, M. A. 1996. Stability for grain yield in wheat. Pakistan Journal of Botany 28:61-65.

Allen, F. L. 1978. Optimal environments for yield testing. Crop Science 18:747-751.

Amin, M., Mohammad, T., Khan, A. J., Irfaq, M., Ali, A. and Tahir, G. R. 2005. Yield stability of spring wheat (*Triticum aestivum* L.) in the North West Frontier Province, Pakistan. Songklanakarin. Journal Science Technology 27:1147-1150.

Araus, J. L., Slafer, G. A., Reynolds, M. P. and Royo, C. 2002. Plant breeding and water relations in C3 cereals: what should we Breeding for? Annals of Botany 89:925-940.

Araus, J. L., Villegas, D., Aparicio, N., Garcı`A Del Moral, L. F., El Hani-Rharrabti, Y., Ferrio, J. P. and Royo, C. 2003. Environmental factors determining carbon isotope discrimination and yield in durum wheat under Mediterranean conditions. Crop Science 43:170-80.

Ashley, J. 1999. Food crop and drought. CTA Macmillan Education Limited, London and Basingtoke. pp 133.

Aslam, M., Khan, I. A., Saleem, M. and Ali, Z. 2006. Assessment of water stress tolerance in different maize accessions at germination and early growth stage. Pakistan Journal of Botany 38:1571-1579.

Atlin, G. N. and Lafitte, H. R. 2002. Marker-assisted breeding versus direct selection for drought tolerance in rice. In: Saxena N. P., O'Toole J. C (eds). Field screening for drought tolerance in crop plants with emphasis on rice, Proc. InternationalWorkshop on Field Screening for Drought Tolerance in Rice, 11-14 Dec 2000. ICRISAT, Patancheru, India, and The Rockefeller Foundation, New York. pp 208.

Babić, V., Babić, M., Ivanović,M., Kraljević-Balalić, M. and Dimitrijević, M. 2010. Understanding and utilization of genotype-by-environment interaction in maize Breeding. Genetika 42: 79-90.

Babu, R. C., Nguyen, B. D., Chamarerk, V. P., Shanmugasundaram, P., Chezhian, P., Jeyaprakash, S. K., Ganesh, A., Palcham, Y. S., Sadasivam, S., Sarkarung, S., Wade, L. J. and Nguyen, H. T. 2003. Genetic analysis of drought resistance in rice by molecular markers. Crop Science 43:1457-1469.

Badu-Apraku, B. and Oyekunle, M. 2012. Genetic analysis of grain yield and other traits of extra early yellow maize inbreds and hybrids perfomance under contrasting environments. Field Crops Research 129:99-110.

Badu-Apraku, B., Fakorede, M. A. B., Oyekunle, M. and Akinwale, R. O. 2015a. Genetic gains in grain yield under nitrogen stress following three decades of breeding for dought tolerance and striga resistanein early maturing maize. Journal of Agricultural Science 59:49-57.

Badu-Apraku, B., Menker, A., Ajala, S. O., Akinwale, R. O., Oyekunle, M. and Obeng-Antwi, K. 2010. Perfomance of tropical early maturing maize cultuvars in multiple stress environments. Canadian Journal of Plant Science 90:831-852.

Badu-Apraku, B., Oyekunle, M., Akinwale, R. O. and Lum, A. F. 2011. Combining ability of early maturing white maize inbreds under stress and non stress environment. Agronomy Journal 103:544-557.

Badu-Apraku, B., Yallou, C. G., Obeng-Antwi, K., Talabi, A. O., Annor, B., Oyekunle, M., Akaogu, I. C. and Aderounmu, M. 2017. Yield gains in extra-early maize cultivars of three Breeding eras under mutliple environments. Agrononmy Journal 109:1-14.

Balzarini, M., Bruno, C. and Arroyo, A. 2005. Análisis de ensayos agrícolas multi-ambientales: Ejemplos con Info-Gen. Fac. de Cs. Agropec. U.N.C., Argentina. pp 141.

Bänziger, M. and Araus, J. 2007. Recent advances in Breeding maize for drought and salinity stress tolerance. In*:* Jenks M.A. and Jain S. M. (eds). Advances in molecular breeding toward drought and salt tolerant crops, Springer, Dordrecht. pp 587-601.

Bänziger, M. and Cooper, M. 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 Diallo, A. O. 2004. Progress in developing drought and N stress tolerant maize cultivar for eastern and southern Africa. In: Friesen, D. K. and Palmer, A. F.E. (eds). Intergrated approach to higher maize productivity in the new millenium, 5-11 February 2002. Nairobi, Kenya, CIMMYT/KARI.

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

Banziger, M., Edemeades, G. O. and Lafitte, R. 1999. selection for drought tolerance increase maize yields across a range of nitrogen levels. Crop Science 39:1035-1040.

Bänziger, M., Edmeades, G. O. and Lafitte, H. R. 2002. Physiological mechanisms contributing to the increased N stress tolerance of tropical maize selected for drought tolerance. Field Crops Research 75:223-233.

Bänziger, M., Edmeades, G. O., Beck, D. and Bellon., M. 2000. Breeding for Drought and Nitrogen Stress Tolerance in Maize. From theory practice. Crop Science 39:1035-1040.

Bänziger, M., Mickelson, H. R. and Peña-Valdivia, C. B. 1997. Developing Drought- and Low N-Tolerant Maize. Proceedings of a Symposium, 25-29 March 1996, CIMMYT, El Batán, Mexico. Mexico, D.F. CIMMYT.

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

Baurear, I., Drinić, S. M., Filipović, M. and Kronstantinov, K. 2005. Genetic characterization of early maturing maize hybrids (*Zea mays L.)* obtained by protein and RAPD markers. Genetika 37:235-243.

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

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

Bello, O. B., Azeez M. A., Mahmud, J., Afolabi, M. S., Ige, S. A. and Abdulmaliq, S. Y. 2012. Evaluation of grain yield and agronomic characteristics in drought-tolerant maize cultivar belonging to two maturing groups. Journal of Agricultural Science 2:70-74.

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

Betran, F.J., Beck, D., Bänziger, M. and Edmeades, G. O. 2003. Secondary Traits in Parental Inbreds and Hybrids Under Stress and Non-Stress Environments in Tropical Maize. Journal of Field Crops Research 83:51-65.

Beyene, Y. S., Mugo, C., Mutinda, T. T., Karaya, H., Ajanga, S., Shuma, J., Tende, R. and Kega, V. 2011. Genotype by environment interactions and yield stability of stem borer resistant maize hybrids in Kenya. African Journal of Biotechnology 10:4752-4758.

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

Bolaños, J. and Edmeades, G. O. 1996. The importance of the anthesis-silking interval in breeding for drought tolerance in tropical maize. Field Crops Research 48:65-80.

Borra´S, L., Westgate, M. E., Juan, P. A., and Echarte, L. 2007. Coupling time to silking with plant growth rate in maize. Field Crops Research 102:73-85.

Bruce, W. B., Edmeades, G. O. and Barker, T. C. 2002. Molecular and physiological approaches to maize improvement for drought tolerance. Journal of Experimental Botany 53:13-25.

Buckler, E. S. and Stevens, N. M. 2005. Maize Origins, Domestication, and Selection. pp 67-90

Castleberry, R.M., Crum, C.W., and Krull, C.F. 1984. Genetic yield improvement of U.S. maize cultivars under varying fertility and climatic environment. Crop Science 24:33-36.

Cattivelli, L., Rizza, F., Badeck, F. W., Mazzucotelli, E., Mastrangelo, A. M., Francia, E., Mare`, C., Tondelli, A. and Stanca, A. M. 2008. Drought tolerance improvement in crop plants: An integrated view from breeding to genomics. Field Crops Research 105:1-14.

Ceccarelli, S., and Grando, S. 1996. Drought as a challenge for the plant breeder. Plant Growth Regulation 20:149-155.

Ceyhan, E., Kahraman, A., Ates, M. K. and Karadas, S. 2012. Stability analysis on seed yield and its components in pea. Belgium Journal of Agricultural Science 18:905-911.

CIMMYT- Zimbabwe. 2000. Research highlights. CIMMYT, Harare, Zimbabwe.

Clarke, J. M., Depauw, R. M. and Townley-Smith, T. F. 1992. Evaluation of methods for quantification of drought tolerance in wheat. Crop Science 32:423-428.

Cooper, M., Padlich, D. W. and Fukai, S. 1999. Combining information from multi-environment trials and molecular markers to select adaptive traits for yield improvement of rice in water-limited environments. In: Ito, O., O'Toole, J. and Hardy, B. (eds.). Genetic improvement of rice for water-limited environments. IRRI Makati City.

Cooper, M., Van Eeuwijk, F. A., Chapman, S. C., Podlich, D. W. and Loffler, P. 2006. Genotype by- environment interactions under water-limited conditions. In: Ribaut, J. M. E. (eds). Drought Adaptation in Cereals. Haworth Press, Inc. pp 51-96.

Crossa, J. 1990. Statistical analysis of multi-location trials. Advanced Agronomy 44:55-85

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

DAFF. 2014. Department of Agriculture, Forestry and Fisheries.Trends in the Agricultural Sector. pp.9-14.

Darrah, L. L., Mccullen, M. D. and Zuber, M. S. 2003. Breeding, Genetics, and Seed Corn Production. Chapter 2. In: White, P. J. and Johnson, L. A. (eds). Corn: chemistry and technology, Edition 2nd. American Association of Cereal Chemists, Inc. St. Paul, Minnesota, USA.

Derera, J., Tongoona, P., Vivek, B. S. and Laing, M. D. 2008. Gene action controlling grain yield and secondary traits in southern African maize hybrids under drought and non drought environments. Euphytica 162:411-422.

Djurović, D. S., Madić, M. R., Bokan, N. R., Stevović, V., Tomić, D. D. and Tanasković, T.S. 2014. Stability Parameters for Grain Yield and its Component Traits in Maize Hybrids of Different FAO Maturity Groups. Journal of Central European Agriculture 15:199-212.

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

Duvick, D. N., Smith, J. S. C. and Cooper, M. 2004. Long-term selection in a commercial hybrid maize breeding programme. Plant Breeding Review 24:109-152.

Eberhart, S. A. and Russell, W. A. 1966. Stability parameters for comparing cultivar. Crop Science 6:36-40.

Edmeades, G. O. and Mcmaster, G. S. 2004. Genomics and the physiologist: bridging the gap between genes and crop response. Field Crops Research 90:5-18.

Edmeades, G. O., Banziger, M., Campos, R. M. and Schussler, J. 2006. Improving tolerance to abiotic stresses in staple crop: A random or planned process?. In: K.R Lamkey and M.Lee (eds). The Arnel R. Hallauer International sympossium. Blackwell, Ames, IA. Plant Breeding. pp 293-309.

Edmeades, G. O., Bolanos, J., Chapman, S. C., Lafitte, H. R. and Banziger, M. 1999. Selection improves drought tolerance in tropical maize populations: I. Gains in biomass,grain yield, and harvest index. Crop Science 39:1306-1315.

Edmeades, G. O., Cooper, M., Lafitte, R., Zinselmeier, C., Ribaut, J. M., Habben, J. E., Löffler, C. and Bänziger, M. 2001. Abiotic stresses and staple crops. Proceedings of the Third International Crop Science Congress, 18–23 August 2000. Hamburg, Germany. CABI (in press).

ENCA. 2016. Water update: national water levels dangerously low. www.enca.com. Accessed 31 October 2016.

Fernandez, G. C. J. 1992. Effective selection criteria for assessing stress tolerance. In: Kuo, C. G. E. (ed). Proceedings of the International Symposium on Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress. Tainan, Taiwan.

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

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

Gauch, Jr. H. G. 1992. Statistical analysis for regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, The Netherlands.

Golbashy, M., Ebrahimi, M., Khorasani, S. K., and Choukan, R. 2010. Evaluation of drought tolerance of some maize (*Zea mays* L.) hybrids in Iran. African Journal of Agricultural. Research 5:2714-2719.

Heisey, P. W. and Edmeades, G. O. 1999. Maize Production in Drought Stressed Environments: Technical Options and Research Resource Allocation. Part 1 of CIMMYT 1997/1998 World Facts and Trends; Maize Production in Drought Stressed Environments.

Hill, J. 1975. Genotype by environment interaction: A challenge for plant breeding. Journal of Agricultural Science 85:477-493.

Ismaila, U., Gana, A. S., Tswanya, N. M. and Dogara, D. 2010. Cereals production in Nigeria: Problems, constraints and opportunities for betterment. African Journal Agricultural Research 5:1341-1350.

Jackson, P., Robertson, M., Cooper, M. and Hammer, G. 1996. The role of physiological understanding in plant breeding; from a Breeding perspective. Field Crops Research 49:11-37.

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

James, M. 2015. Low-cost drought and low nitrogen tolerance maize hybrids for food security in South Africa. htt://www.grainsa.co.za/low-cost-drought-and-nitrogen-tolerant-maize-hybrids-for-food-security-in-South-Africa. Accessed 22 March 2015.

Jamshidian, P., Golparvar, A. R., Naderi, M. R. and Darkhal, H. 2013. Phenotypic correlations and path analysis between ear yield and other associated characters in corn hybrids (*Zea mays* L.). International Journal of Farming and Allied Sciences 2:1273-1276.

Jearakongman, S., 2005. Validation and discovery of quantitative trait loci for drought tolerance in backcross introgression lines in Rice (*Oryza sativa* L.) Cultivar IR64. PhD Thesis. Kasetsart University. pp 95.

Jones, R. N., Viegas, W. and and Houben, A. 2008. A Century of B Chromosomes in Plants: So What?. Annals of Botany 101:767-775.

Kandus, M., Almorza, D., Ronceros, R. B. and Salerno, J. C. 2010. Statistical models for evaluating the genotype-environment interaction in maize (*Zea mays L.).* International Journal of Experimental Botany 79: 39-46.

Kang, M. S. 1993. Simultaneous selection for yield and stability in crop performance trials: Consequences for growers. Agronomy Journal 85:754-757.

Kashiani, P. and Saleh, G. 2010. Estimation of genetic correlations on sweet corn inbred lines using SAS Mixed Model. American Journal of Agricultural Biology Science *5*:309-314.

Kassa, Y., Asea, G., Demissew, A. K., Ligeyo, D., Demewoz, N., Saina, E., Sserumaga, J. P., Twumais-Afriyie, S., Opio, F., Rwomushana, I., Gelase, N., Gudeta, N., Wondimu, F., Solomon, A., Habtamu, Z., Andualem, W. B. A., Habte, J. and Muduruma, Z. 2012. Stability in performance of normal and nutritionally enhanced highland maize hybrid genotypes in Eastern Africa. Asian Journal of Plant Science12:51-60.

Khalil, H. E., Nawar, A. I. and Kamel, A. S. 2004. Response of sunflower to multiseasonal crop sequences under different regimes of NPK fertilization. Alexandria Journal of Agricultural Research 99:13-23.

Kirigwi F. M., Van Ginkel, M., Trethowan, R., Sears, R. G., Rajaram, S. and Paulsen, G. M. 2004. Evaluation of selection strategies for wheat adaptation across water regimes. Euphytica 135:361-371.

Kirigwi, F. M., Van Ginkel, M., Brown-Guedira, G., Gill, B. S., Paulsen, G. M., and Fritz, A. K. 2007. Markers associated with a QTL for grain yield in wheat under drought. Molecular Breeding 20:401-413.

Kumar, R., Venuprasad, R., Atlin, G.N., 2007. Genetic analysis of rainfed lowland rice drought tolerance under naturally-occurring stress in eastern India: heritability and QTL effects. Field Crops Research 103 42-52.

Kumari, V., Tyagi, B. S., Verma, A. and Sharma, I. 2014. Stability analysis for grain yield and its components under different moisture regimes in bread wheat (*Triticum aestivum*). Journal of Agricultural Science 84:931-936

Lafitte, H. R. and Edmeades, G. O. 1988. An update on selection under stress: Selection Criteria. Second Eastern, Central and Southern African Regional Maize Workshop. Harare, Zimbabwe: The College Press.

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

Lafitte, R., Blum, A., Atlin, G., Fischer, K. S. and Hardy, B. 2003. In: Breeding Rice for Drought-Prone Environments., (eds). The International Rice Research Institute, Los Bolaños. pp. 14-22.

Laghari, K. A., Sial, M. A., Afzal Arain, M. A., Mirbahar, A. A., Pirzada, A. J., Dahot, M. U. and Mangrio, S. M. 2010. Heritability studies ofyield and yield associated traits in bread wheat. Pakistan Journal of Botany 42:111-115.

Lee, E. A. and Tollenaar, M. 2007. Physiological basis of successful breeding strategies for maize grain yield. Crop Science 47:202-215.

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

Lodhi, R. D., Prasad, L. C., Bornare, S. S., Madakemohekar, A. H. and Prasada, R. 2015. Stability analysis of yield and its component traits of barley (*Hordeuin vulgare L.*) genotypes in multi-environmnet trials in the North Eastern plains of India. Society for the Advancement of Breeding Researches in Asia and Oceania. Journal of Breeding and Genetics 47:143-159.

Löffler, C. M., Wei, J., Fast, T., Gogerty, J., Langton, S., Bergman, M., Merrill, B. and Cooper, M. 2005. Classification of maize environments using crop simulation and geographic information systems. Crop Science 45:1708-1716.

Lunze, L., Kimani, P. M., Ngatoluwa, R., Rabary, B., Rachier, G. O., Ugen, M. M., Ruganza, V. and Awad-Elkarim, E. E. 2007. Bean improvement for low soil adaptation in Eastern and central Africa. In: Bationo A, Waswa B, Kihara J, Kimetu J (eds). Advances in integrated soil fertility management in Sub-Saharan Africa: Challenges and opportunities, Springer, The Netherlands. pp 324-332..

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

Makumbi, D., Diallo, A., Kanampiu, K., Mugo, S. and Karaya, H. 2015. Agronomic performance and genotype x environment interaction of herbicide-resistant maize cultivar in Eastern Africa. Crop Science 55:540-555.

Malosetti, M., Ribaut, J. M., Vargas, M., Crossa, J. and Van Eeuwijk, F. A. 2008. A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize (*Zea mays L*.). Euphytica 161:241-257.

Mccown, R. L., Wafula, B. M. and Keating, B. A. 1992. Prospects for improving maize productivity through response farming In: Probert, M. E., (ed). A search for strategies for suistainable dryland cropping in semi-arid eastern Kenya. pp 138.

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

Monneveux, P., Sanchez, C. and Tiessen, A. 2008. Future progress in drought tolerance in maize needs new secondary traits and cross combinations. Journal of Agricultural Science 146:1-14.

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

Moola, S. 2010. African green revolution drought tolerant maize scam. ACB briefing paper no.12

Nafziger, E. D. 2010. Growth and production of maize: mechanized cultivation. Encyclopedia of Life Support Systems. 1:1-12.

Najeeb, S., Rather, A. G., Parray, G. A., Sheikh, F. A. and Razvi, S. M. 2009. Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under high altitude temperate ecology of Kashmir. Maize Genetics Cooperation Newsletter. Maize Genetics Cooperation Newsletter. 83:1-8.

Ndhlela, T. 2012. Improved strategies for yield potential, disease resistance and drought tolerance in zimbabwean maize inbred lines. PhD, University of the Free State.

Nelson, D. W. and Sommers, L. E. 1992. Total organic carbon and organic matter. In: Methods of soil analysis, Miller, A. L. *et al*., (eds.). 2nd edn, Part 2, Agronomy Monograph, 27, ASA, Madison, Wisconsin, USA. pp 539-580.

Nemati, A., Sedghi, M., Sharifi, R. S. and Seiedi, M. N. 2009. Investigation of Correlation between Traits and Path Analysis of Corn (*Zea mays* L.) Grain Yield at the Climate of Ardabil Region (Northwest Iran). Notulae Botanicae Horti Agrobotanici Cluj-Napoca 37:194-198

Ober, E. S., Clark, C. J. A., Le Bloa, M., Royal, A., Jaggard, K. W. and Pidgeon, J. D. 2004. Assessing the genetic resources to improve drought tolerance in sugar beet: agronomic traits of diverse genotypes under droughted and irrigated conditions. Field Crops Research 90:213-234.

Obilana, A. T. and Fakorede, M. A. B. 1981. Heriability: A treaties. Samaru Journal of Agricultural Research 1:72-82.

Oikeh, S. O. and Horst, W. J. 2001. Agro-physiological responses of tropical maize cultivars to nitrogen fertilization in the moist savanna of West Africa in plant nutrition. Fourteenth International Plant Nutrition Colloquium. Hannover, Germany: Kluwer Academic publishers.

Olakojo, S. A. and Olaoye, G. 2011. Correlation and heritability estimates of maize agronomic traits for yield improvement and *Striga asiatica* (L.) Kuntze tolerance. African Journal of Plant Science 5:365-369.

O'neill, P. M., Shanahan, J. F., Schepers, J. S. and Caldwell, B. 2004. Agronomic responses of corn hybrids from different eras to deficit and adequate levels of water and nitrogen. Agronomy Journal 96:1660-1667.

Paliwal, R. L. 2000. Genetic Resources. In: R. L Paliwal, G Granados, H. R Lafitte, A. D Vlollc, eds. Tropical Maize: Improvement and Production. Food and Agriculture Organization of the United Nations Rome. African Crop Science Journal 6:329-324.

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

Piepho, H. P. 1998. Methods for comparing the grain yield stability of cropping systems-a review. Journal of Agronomy and Crop Science 180:193-213.

Piepho, H. P. 2000. A mixture-model approach to mapping quantitative trait loci in barley on the basis of multiple environment data. Genetics. pp 156.

Purseglove, J. W. 1976. *Voandezia subterranea* (L.) Thouras. A tropical crop. Dicotyledons. English Language book society/ Longman. pp 329-32.

Radebe, M. P. 2013. The sustainability of soil fertilitilization on small scale farmers in the Estcourt area of KwaZulu-Natal province, in South Africa. pp18-20.

Rafaque, M., Hussain, A., Manhmood, T., Alvi, A. W., and Alvi, M. B. 2004. Heritability and inter section ship among grain yeld and yield components in maize (*Zea mays L.)* inbred lines. International Journal of Agriculture and Biology 6:1113-1114.

Ramanujam, S. and Thirumalachar, D. K. 1967. Genetic variability of certain characters in red pepper (*Capsicum annum*). Mysore Journal of Agricultural Science 1:30-36.

Rather, A. G., Bhatt, M. A. and Zagar, M. A. 2003. Genetic variation in maize (Zea mays L.) population in high altitude temperate conditions in Kashmir. Indian Journal of Agricultural Science 79:179-180.

Reynolds, C. 2015. Drought delays 2015/16 corn planting SA. USDA: Foerign agriculture services. Commodity intelligence report.

Richards, A. R., Rebetzke, G. J., Condom, A. G. and Van Herwaarden, A. F. 2002. Breeding opportunitities for increasing the efficiency of water use and crop yield in temperate cereals. Crop Science 42:111-121.

Rosielle, A. A., and Hamblin, J. 1981. Theoretical aspects of selection for yield in stress and nonstress environment. Crop Science 21:943-946.

Royo, C., Garc´Ia Del Moral, L. F., Slafer, G., Nachit, M. N. and Araus, J. L. 2005. Selection tools for improving yield-associated physiological traits. In: Durum Wheat Breeding: Current Approaches and Future Strategies. pp. 563-598.

Sadra, V.O. and Milroy, S. P. 1996. Soil water thresholds for the response of leaf expansion and gas exchange: A review. Field Crops Research 47:253-266.

Saneoka, H., Moghaieb, R. E. A., Premachangra, G. S. and Fujita, K. 2004. Nitrogen nutrition and water stress effects on cell membrane stability and leaf water relations in Agrostis polustris. Experimental Botany 52:131-138.

Sangoi, L., Graceietti, M. A., Rampazzo, C., and Bianchetti, P. 2002. Response of brazilian maize hybrids from different eras to change in plant density. Field Crops Research 79:39-51.

Seghatoleslami, M. J., Kafi, M. and Majidi, E. 2008. Effect of drought stress at different growth stage on yield and water use efficiency of five proso millet (*Panicum Miliaceum L.)* genotypes. Pakistan Journal of Botany 40:1427-1432.

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

Shirinzadeh, A., Zarghami, R. and Shiri, M.R. 2009. Evaluation of drought tolerance in late and medium maize hybrids-using stress tolerance indices, Iran. Crop Science 10:416-427.

Shukla, G. K. 1972. Some Statistical Aspects of Partitioning Genotype-Environmental Components of Variability. Heredity 29:237-245.

Singh, N. P., Singh, P. and Kumar, M. 1995. Genetic variability and analysis of yield component in linseed germplasm. Annual Agricultural Research India.16:164-169.

Sio-Se, M. A., Ahmadi, A., Poustini, K. and Mohammadi, V. 2006. Evaluation of drought tolerance indices under various environmental conditions. Field Crops Research 98:222-229.

Sleper, D. A. and Poehlman, J. M. 2006. Breeding Field Crops. Fifth edition, 2121 State Avenue, Ames, Iowa 50014, Blackwell Publishing Professional.

Smith, B. D. 1994-95. The origins of agriculture in the Americas. Evolutionary Anthropology 3:174-184.

Smithson, J. B. and Grisley, W. 1992. First African Bean Yield and Adaptation Nursery (AFBYAN I): Part II. Performance across Environments. Occasion publication series. No. 3B. CIAT, Dar es Salaam Tanzania.

Sujiprihati, S., Saleh, G. B., and Ali, E. S. 2003. Heritability, performance and correlation studies on single cross hybrids of tropical maize. Asian Journal Plant Science 2:51-57.

Sun, Q., Liang, Z. S., Wang, L. W., Li, X. J. and Zhang, F. S. 2001. Effects of mechanism lipid peroxidation and photosynthesis rate on water stress under different nitrogen levels in maize. Acta Agriculture. Boreal-Occident sin. 1:7-10.

Tollenaar, M., Aguilera, A. and Nissanka, S. P. 1997. Grain yield is reduced more weed interference in an old than in a new maize hybrid. Agronomy Journal 89:239-246.

Tyagi, S. D. and Khan, M. H. 2010. Studies on genetic variability and interrelationship among the different traits in Microsperma lentil (*Lens culinaris* Medik*).* Journal of Agriculture, Biotechonlogy and Sustainable Devevelopment 2:15-20.

Uhart, S. A., and Andrade, F. H. 1995a. Nitrogen deficiency in maize: I. Effects on crop growth, development, dry matter partitioning and kernel set. Crop Science 35:1367-1383.

Uhart, S. A., and Andrade, F. H. 1995b. Nitrogen deficiency in Maize II. Carbon-Nitrogen interaction effects on kernel number and grain yield. Crop Science 35:1384-1389.

USDA. 2017. World corn production 2016/2017. https://www.worldcornproduction.com.

Venuprasad, R., Lafitte, H. R. and Atlin, G. N. 2007. Response to direct selection for grain yield under drought stress in rice. Crop Science 47:285-293.

Waqar-Ul-Haq, M., Malik, F., Rashid, M., Munir, M. and Akram, Z. 2008. Evaluation and estimation of heritability and genetic advancement for yield related attributes in wheat lines. Pakistan Journal of Botany 40:1699-1702.

Weber, V. S., Melchinger, A. E., Magorokosho, C., Makumbi, D., Bänziger, M. and Atlin, G. N. 2012. Efficiency of Managed-Stress Screening of Elite Maize Hybrids under Drought and Low Nitrogen for Yield under Rainfed Conditions in Southern Africa. Crop Science 52:1011-1019

Wolfe, D. W., Henderson, D. W., Hsiao, T. C. and Alvio, A. 1988. Interactive water and nitrogen effects on maize. II. Photosynthetic decline and longevity of individual leaves. Agronomy Journal 80:865- 870.

Yan, W. and Hunt, L. A. 1998. Genotype by environment interaction and crop yield. Plant Breeding Review 16:135-178.

Zaman, A. and Das, P. K. 1991. Effect of irrigation and nitrogen on yield and quality of safflower. Indian Journal of Agronomy 36:177-179.

Zheng, H. J., Wu, A. Z., Zheng, C. C., Wang, Y. F., Cai, R., Shen, X. F., Xu, R. R., Liu, P., Kong, L. J. and Dong, S. T. 2009. QTL mapping of maize (*Zea mays*) stay-green traits and their relationship to yield. Plant Breeding 128:54-62.

Zhu, Q., Schmidt, J. P., Lin, H. S., Sripada, R. P., 2009. Hydropedological processes and their implications for nitrogen availability to corn. Geoderma 154:111-122.

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

CHAPTER THREE

Variance Components, Correlation and Path Coefficient Analysis in Early Maturing Maize Hybrids across Stress and Non-Stress Environments

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ABSTRACT

Development of early maturing maize hybrids is a strategy for adapting maize to the gradually shortening rainy season, so that it can tolerate and escape drought stress that often occurs during grain filling stage late in the growing season. This study was carried out to estimate variance components and to investigate correlation and path coefficients among traits in early maturing maize hybrids across three locations in South Africa, *viz.* Lutzville (managed drought), Cedara (low N) and Potchefstroom (optimum) in the 2016/17 summer season. Fifty early maturing hybrids comprising of 44 experimental hybrids and 6 commercial checks were laid out in a 10 x 5 alpha (0.1) lattice design with two replications in each environment. The effect of genotype, environment and genotype by environment interaction were significant ($P \leq 0.01$) for all the traits. Hybrids CZH16084, CZH16064 and CZH16095 under managed drought, low N and optimum environments, respectively, were identified as the outstanding genotypes for grain yield and recommended for further testing, release and registration. High magnitude of phenotypic and genotypic coefficient of variation as well as high heritability were recorded for each single environment for anthesis days, silking days, ear height and plant height, suggesting that those traits interacted with the environment. Grain yield was positively correlated with anthesis days and ear height, field weight, grain moisture at Potchefstroom while at Lutzville and Cedara had negative correlation with those traits, suggesting that the genotypes differed significantly for most of the phenotypic traits. Path coefficient analyses revealed that anthesis days and anthesis-silking interval had positive direct effects while silking days, plant height and ear per plant had a negative direct effect on grain yield in all the environments. These traits are recommended for effective selection to the improvement of maize grain yield.

Keywords: Early maturing, Genetic advance, Grain yield, Heritability, Maize (*Zea mays* L.) hybrids, Secondary traits

3.1 Introduction

Maize (*Zea mays* L.) is an important staple food crop in Africa that has high potential for production and productivity. It also plays an important role in the world economy and is a valuable ingredient in a large proportion of manufactured items worldwide (Alvi *et al.,* 2003). Maize hybrids have been commercially exploited in different leading maize-producing countries because they have a greater genetic potential compared to synthetic and composite cultivars (Kinfe and Tsehaye, 2015). Adoption of improved technologies is thus important to maximize yields. For example, early maize cultivars can avoid the effect of reduced moisture supply during flowering resulting in a reduction of farmers' risk in drought-prone ecological zone (Hussain *et al.,* 2011; Bello *et al.,* 2012). In addition, the early maturing maize hybrids offer flexibility of planting dates, which enables multiple plantings during the season to spread the risk of losing a single crop to drought. Furthermore, late planting can be done when rainfall is delayed and terminal drought can be avoided (CIMMYT, 2000; Bello *et al*., 2012).

Variance components and heritability estimates have been extensively used by plant breeders in selection of promising genotypes and in prediction of percentage heritability of desirable components (Morakinyo, 1996; Anderson *et al.,* 1991; Olakojo and Olaoye, 2011). The genetic improvement of yield and its components depends on the nature and magnitude of variability present in the genotypes. Most of the characters of breeders' interest are complex and polygenically controlled (Bekele and Rao, 2014). Knowledge on heritability influences the choice of breeding strategy that can be used by plant breeders to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Waq-Ul-Haq *et al.,* 2008; Laghari *et al* 2010). The most important function of heritability in genetic studies of quantitative traits is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay 1996; Bello *et al.,* 2012). The higher the genetic variability the more will be the opportunities for improvement through appropriate selection procedures. Genetic parameters such as genotypic and phenotypic coefficient variability, heritability and genetic advance provide precise estimates of genetic variation of quantitative traits (Yadav and Dalal 1972; Vejay *et al.,* 1975; Khorgade and Pillai, 1994; Khan *et al.,* 1998; Khan *et al.,* 2000; Muhammed *et al.,* 2003).

A successful selection programme depends not only on heritability of desirable traits but also on the information on association among various yield component characters with grain yield (Abduraqkhmonov and Abdukarimov, 2008; Singh *et al.* 1995; Bekele and Rao, 2014). The success of the genetic breeding programme lies in the availability of the genetic variability for desirable traits. Genetic resources through global exploration, introduction, characterization and evaluation provides a strong base for development of elite cultivars by various improvement methods (Paul *et al.,* 2015). Therefore, knowledge of the nature of genetic variability and interrelationship among grain yield and its components would facilitate the improvement of these traits.

Correlation coefficient analyses helps researchers to distinguish significant relationships between traits. However, correlation analysis provides only limited information as it disregards the complex interrelationships that exists amongst the traits. Accordingly, correlation coefficient analysis should be used with caution in making decisions regarding indirect selection (Kang, 1994; Board *et al.,* 1997; Paul *et al.,* 2015). In order to understand how changes made by selection in one trait may influence changes in others, genetic relationships among important traits should be considered in exploiting genetic populations through breeding and directed selection (Tyagi and Khan 2010; Knife and Tsehaye, 2015). Path coefficient analysis is an important statistical tool that indicates which variable (cause) exerts influence on other variables (effects) while recognising the impact of multi collinearity, unlike correlation which measures the mutual association without considering causation (Akanda, 1996; Hailu et al., 2016). Therefore, the objective of the present study was to estimate variance components, correlation and path coefficients among yield and secondary traits in early maturing maize hybrids across stress and non-stress environments.

3.2 Materials and Methods

3.2.1 Germplasm

Fifty early maturing maize hybrids were planted during the 2016/17 summer season. They consisted of 44 elite experimental hybrids developed by CIMMYT-Zimbabwe under the Water Efficient Maize for Africa (WEMA) project, three commercial hybrid checks from SeedCo, one from Pannar and two from ARC-GCI (Table 3-1).

Table 3-1 List of maize hybrids used in the study and their sources

Hybrid code	Hybrid name	Source
G1	CZH16087	CIMMYT-Zimbabwe
G2	CZH16077	CIMMYT-Zimbabwe
G3	CZH16081	CIMMYT-Zimbabwe
G4	CZH16089	CIMMYT-Zimbabwe
G5	CZH16084	CIMMYT-Zimbabwe

Hybrid code	Hybrid name	Source
G6	CZH15575	CIMMYT-Zimbabwe
G7	CZH16083	CIMMYT-Zimbabwe
G8	CZH16065	CIMMYT-Zimbabwe
G9	CZH15499	CIMMYT-Zimbabwe
G10	CZH16086	CIMMYT-Zimbabwe
G11	CZH16085	CIMMYT-Zimbabwe
G12	CZH16080	CIMMYT-Zimbabwe
G13	CZH15448	CIMMYT-Zimbabwe
G14	SC301	SeedCo
G15	Local check 2	ARC-GCI
G16	CZH16066	CIMMYT-Zimbabwe
G17	CZH15600	CIMMYT-Zimbabwe
G18	CZH16071	CIMMYT-Zimbabwe
G19	CZH16091	CIMMYT-Zimbabwe
G20	CZH16090	CIMMYT-Zimbabwe
G21	CZH16073	CIMMYT-Zimbabwe
G22	CZH16093	CIMMYT-Zimbabwe
G23	Local check 1	ARC-GCI
G24	CZH16092	CIMMYT-Zimbabwe
G25	CZH1258	CIMMYT-Zimbabwe
G26	CZH16070	CIMMYT-Zimbabwe
G27	SC513	SeedCo
G28	CZH16076	CIMMYT-Zimbabwe
G29	CZH16095	CIMMYT-Zimbabwe
G30	CZH16072	CIMMYT-Zimbabwe
G31	CZH16064	CIMMYT-Zimbabwe
G32	CZH15189	CIMMYT-Zimbabwe
G33	CZH16094	CIMMYT-Zimbabwe
G34	CZH16074	CIMMYT-Zimbabwe
G35	SC403	SeedCo
G36	CZH16096	CIMMYT-Zimbabwe
G37	CZH15184	CIMMYT-Zimbabwe
G38	CZH16067	CIMMYT-Zimbabwe
G39	CZH16063	CIMMYT-Zimbabwe
G40	CZH16069	CIMMYT-Zimbabwe
G41	CZH16082	CIMMYT-Zimbabwe
G42	CZH16078	CIMMYT-Zimbabwe
G43	CZH1261	CIMMYT-Zimbabwe
G44	CZH16088	CIMMYT-Zimbabwe
G45	CZH16079	CIMMYT-Zimbabwe
G46	CZH15574	CIMMYT-Zimbabwe
G47	CZH15452	CIMMYT-Zimbabwe
G48	PAN 413	PANNAR
G49	CZH16068	CIMMYT-Zimbabwe
G50	CZH16075	CIMMYT-Zimbabwe

3.2.2 Experimental sites

The hybrids were evaluated at three locations, *viz*. Potchefstroom (ARC-GCI) in North West Province, Cedara in KwaZulu-Natal Province and Lutzville in Western Cape Province in South Africa during the 2016/17 summer season. Table 3-2 shows the coordinates, environmental conditions and soil information for each environment. The distribution of the monthly rainfall and average temperatures for all the locations are shown in Figures 3-1, 3-2 and 3-3. At Lutzville, managed drought were imposed by stopping irrigation two weeks before flowering and then resuming irrigation two weeks after flowering. Low N environments were developed by depleting the soil of nitrogen to a yield potential of less than 60%.

Table 3-2 Geographical coordinates and environmental conditions of study sites

Location	**Latitude**	**Longitude**	**Altitude (m)**	**Total season rainfall (mm)**	**Temperature range Min-Max (^{0}C)**	**Soil type/texture**
Potchefstroom (Optimum)	26^0.7361'S	27^0.0755'E	1349	439	12.3-26.9	Spodosols, sandy-loam
Cedara (Low N)	-29^0.5419'S	30^0.2650'E	1068	561	10.8-25.1	Vertisols, clay-loam
Lutzville (Managed drought)	-31.5854'S	18.3803'E	18	30	11.5-28.9	Spodosols, sandy

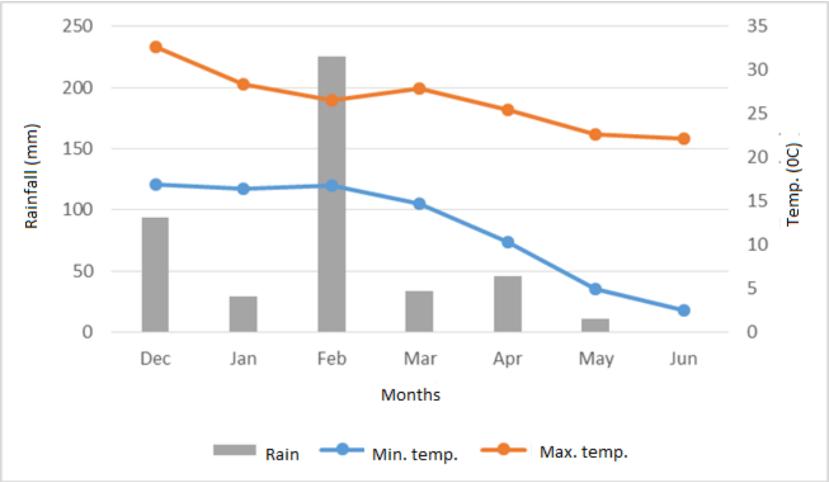

Figure 3-1 Total monthly rainfall and total monthly average temperature for the 2016/17 growing season at Potchefstroom (Optimum)

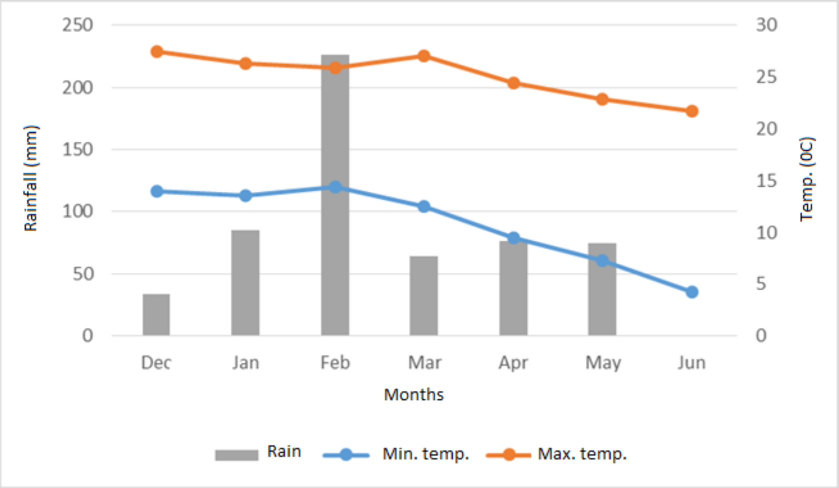

Figure 3-2 Total monthly rainfall and total monthly average temperature for the 2016/17 growing season at Cedara (low N)

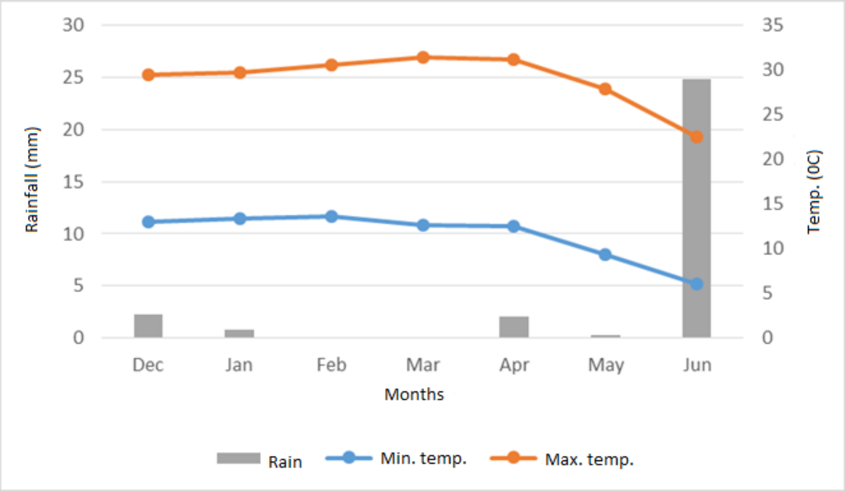

Figure 3-3 Total monthly rainfall and total monthly average temperature for the 2016/17 growing season at Lutzville (Managed drought)

3.3 Field trial design and management

The fifty hybrids were laid out in a 10 x 5 alpha (0.1) lattice design with two replicates and five entries in each of the 10 incomplete blocks, under each environment. Each entry was planted in two-row plots. The rows were 5 m long and plants were spaced 0.25 m apart within the row and 0.75 m between rows to give a plant population of approximately 53 000 plant ha^{-1}. There were two border rows on each side of the block to reduce border effects.

Under optimum environment (Potchefstroom), water was applied throughout the growing season. Managed drought stress environment (Lutz Ville), irrigation water was withheld 10 days prior to flowering stage and during grain filling stage that lasted until harvest without any irrigation. The optimum and managed drought environments, fertiliser was applied as basal at planting in the form of compound (N.P.K) 2:3:2 at 250 kg ha^{-1} (56 kg N ha^{-1}, 83 kg P ha^{-1} and 111 kg K ha^{-1}). Under low N (Cedara) the soil was depleted of N with soil analysis taken. Fertiliser was applied at four weeks after crop emergence in the form of Lime Ammonium Nitrate (LAN, 28% N) at a rate of 250 kg ha^{-1}. Basal fertiliser was applied as super phosphate (P_2O_5) at 25 kg ha^{-1} and potassium chloride (K_2Cl) at 25 kg ha^{-1}. Standard cultural practices for maize were followed including hand weeding, rouging off-types, use of herbicides and insecticides at each environment.

3.4 Data collection

The following traits were measured following standard procedures used at CIMMYT (Magorokosho *et al*., 2009):

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a) **Days to anthesis (AD)**: number of days after planting when 50% of the plants per plot shed pollen.
b) **Days to silking (SD)**: number of days after planting when 50% of the plants per plot showed silks.
c) **Anthesis-silking interval (ASI)**: determined as the difference between days to silking and anthesis.
d) **Plant height (PH)**: determined by measuring 10 representative plants, in cm, from the base of the plant to the insertion point of the first tassel branch of the same plant.
e) **Ear height (EH)**: determined by measuring, 10 representative plants, in cm, from the base of the plant to the insertion of the top ear of the same plant.
f) **Grain moisture (GM)**: measured (by a moisture meter) as percentage water content of grain at harvest.
g) **Field weight (FW):** measured as the weight of the ears per plot taken directly after harvest, after removal of husks, but before shelling.
h) **Grain weight (GW):** this was the weight of the grain per plot after shelling.
i) **Grain yield (GY):** this was calculated using the grain weight adjusted to 12.5% moisture content.

j) **Ears per plant (EPP):** this is the total number of ears in a plot divided by the total number of plants in the plot at harvesting time.

3.5 Statistical Analyses

3.5.1 Analysis of variance

Data was subjected to analysis of variance (ANOVA) using GenStat software 14th edition (Payne *et al*. 2009). The following statistical models was used for the single site analysis:

$$Y_{ijk} = \mu + H_i + r_j + B_{K(j)} + \varepsilon_{ijk}$$

Where, Y_{ijkl} = main effect; μ = overall mean or grand mean; H_i = the effect of the i th hybrid and l=1,2,3…50; r_j = number of replications and j=1,2; $B_{k(j)}$= estimate of the incomplete block within replication and k=1,2; and ε_{ijk} = overall random error.

The following statistical model was used for the combined analysis:

$$Y_{ijkl} = \mu + r_j + B_K + S_l + SH_{il} + \varepsilon_{ijkl}$$

Where, Y_{ijkl} = main effect; μ= overall mean or grand mean; r_j = effect of number of replications; $B_{k=}$ effect of the kth block nested in jth replication and k=1,2,3…10, while j=1,2; S_l =the effect of the l^{th} environment and l =1,2,3; H_i = the effect of the i^{th} hybrid and i =1,2,3…50; SH_{il} = interaction effect of the i^{th} hybrid and l^{th} environment and ε_{ijkl} = random error. The hybrids means were ranked according to yield, which was the principal selection criterion at all sites.

3.5.2 Estimation of heritability and genetic advance

3.5.2.1 Estimating variance component

Variance components were estimated using PROC MIXED (Method=REML) of SAS version 9.3 (SAS Institute, 2010). The environment was considered as fixed while the genotypes were regarded as random. Genotypic (σ_g^2) and error (σ_e^2) variances were obtained directly from the

PROC MIXED output. Using these variance components, phenotypic variance (σ_p^2) was calculated as follows in a single environment:

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

3.5.2.2 Phenotypic and genotypic coefficient of variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated for all the quantitative traits according to Singh and Chaudhary (2004), using the formulae:

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma_p^2}}{mean} \times 100$ and

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{mean} \times 100$

Where, σ_p^2= phenotypic variance, σ_g^2= genotypic variance and mean = grand mean of the trait.

3.5.2.3 Heritability

Broad sense heritability was calculated as the proportion of the genotypic variance to the total phenotypic variance. Broad sense heritability across environments were calculated as follows (Hallauer and Miranda, 1988):

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2} \times 100$$

Where, σ_g^2= genotypic variance and σ_e^2 = error variance, respectively.

3.5.2.4 Genetic advance

Genetic advance was calculated for each trait using the following formula (Singh and Chaudhary, 2004) for combined data:

GA = $K * \sigma_P^2 * H^2$

Where, GA = genetic advance, K = standardised selection differential at 5% selection intensity (2.063), σ_p = phenotypic standard deviation of base population and H^2 = the heritability of the trait under selection.

Genetic advance as percentage of the mean (GAM) was calculated as follows:

$$GAM\% = \frac{GA}{mean} \times 100$$

Where, GAM% = genetic advance as a percentage of the mean and mean = grand mean of the trait in the unselected population.

3.5.2.5 Correlation analyses

Simple Pearson phenotypic correlation was calculated using genotype means of traits data from all sites using the IBM SPSS version 25 software (SPSS, 2014), as follows:

$$r_p = \frac{\mathrm{cov}(x, y)}{\sqrt{(\mathrm{var}(x) \times \mathrm{var}(y))}}$$

Where, r_p = phenotypic correlation; $\mathrm{cov}(x, y)$ = phenotypic covariance of traits x and y; and $\sqrt{\mathrm{var}(x)}$ = square root of the phenotypic covariance of trait x and $\sqrt{\mathrm{var}(y)}$ square root of the phenotypic covariance of trait y.

3.5.2.6 Path coefficient analyses

Path coefficient was calculated using Microsoft Office Excel software by taking the Pearson phenotypic correlation data to determine the contribution (direct and indirect) of each variable to the total effect as suggested by Akintunde (2012). The following equation was used to calculate the path coefficient:

$$y = a + b_1 X_1 + b_2 X_2 + b_3 X_3 + U$$

Where, y = single response variable (grain yield) and $a+b_1X_1+b_2X_2+b_3X_3+U$ = variables from correlation data with the assumptions that values of variables are random, normally distributed and that the causal variables are independently contributing to the dependent variable (grain yield).

3.6 Results

3.6.1 Single environment analysis

The single analysis of variance (ANOVA) on the three environments for all traits are presented in Table 3-3. At Lutz Ville (managed drought), the mean squares for replication were significant ($P \leq 0.01$) for anthesis-silking interval and ear height, while it was non-significant with anthesis days, ears per plant, field weight, grain moisture, grain weight, grain yield, plant height and silking days. The replication by incomplete block mean squares were significant ($P<0.01$) for ear height and ear per plant. The genotype mean squares were significant ($P<0.01$) for ear height and silking days.

At Cedara (low N), the mean squares for replication were significant ($P \leq 0.01$) for grain weight, grain yield and plant height, while it was non-significant with anthesis days, anthesis-silking interval, ear height, ears per plant, field weight, grain moisture and silking days. The replication by incomplete block mean squares were significant ($P<0.01$) for ear height, ear per plant, field weight, grain moisture, grain weight, grain yield and silking days. The genotype mean squares were non-significant ($P<0.01$) for ear per plant.

At Potchefstroom (Optimum) the mean squares for replication were significant ($P \leq 0.01$) for anthesis days, ear height, field weight, grain weight, grain yield and silking days, while it was non-significant with anthesis-silking interval, ears per plant, grain moisture and plant height. The replication by incomplete block mean squares were significant ($P<0.01$) for field weight, grain weight, grain yield, plant height and silking days, while non-significant for anthesis-silking interval, ear height and ear per plant. The genotype mean squares were significant ($P<0.01$) for anthesis-silking interval, ear height and ear per plant.

The combined analysis of variance across the three environments for all traits is presented in Table 3-4. The mean squares for genotype were highly significant ($P \leq 0.001$) for anthesis days, anthesis-silking interval, ear height, ear per plant, field weight, grain moisture, grain weight, plant height and silking days. The mean squares for environment were very highly significant ($P \leq 0.001$) for all the traits. The genotype-by-environment interaction mean squares were very highly significant for all the traits at $P \leq 0.001$ except from grain moisture, which was significant at $P \leq 0.01$.

Table 3-3 Mean squares analysis of variance of 50 early maturing maize hybrids for grain yield and secondary traits evaluated at three environments

Lutzville (managed drought)											
Sources	**DF**	**AD**	**ASI**	**EH**	**EPP**	**FW**	**GM**	**GW**	**GY**	**PH**	**SD**
Rep	1	204.49	0.16*	445.21**	0.00ns	0.12ns	0.27ns	0.08ns	0.19ns	70.56	193.21ns
Rep*Incomplete block	8	104.14	0.48	158.17*	0.052*	1.13	0.94	0.64	1.69	160.6	100.51
Genotype	49	47.59	0.94	177.65**	0.12	1.13	2.26	0.68	1.83	183.73	50.03**
Residual	41	16.05	0.05	74.15	0.02	0.17	0.18	0.06	0.16	87.51	16.35
Total	99	40.68	0.53	135.92	0.07	0.72	1.27	0.41	1.11	140.87	41.61

Cedara (low N)											
Sources	**DF**	**AD**	**ASI**	**EH**	**EPP**	**FW**	**GM**	**GW**	**GY**	**PH**	**SD**
Rep	1	5.76ns	0.04ns	196.00ns	0.01ns	0.39ns	0.04ns	0.37*	1.08*	816.10*	6.76ns
Rep*Incomplete block	8	26.34	0.17	378.1***	0.03*	0.3207*	0.51***	0.14*	0.60***	738.60	25.16***
Genotype	49	39.09	0.35	302.20	0.02ns	0.60	2.32	0.41	1.30	625.30	41.04
Residual	41	6.20	0.04	102.30	0.015	0.16	0.13	0.07	0.20	146.10	6.02
Total	99	24.10	0.20	224.50	0.019	0.39	1.24	0.25	0.79	437.90	24.91

Potchefstroom (optimum)											
Sources	**DF**	**AD**	**ASI**	**EH**	**EPP**	**FW**	**GM**	**GW**	**GY**	**PH**	**SD**
Rep	1	16.00*	0.16ns	1479.70*	0.028ns	8.09**	0.93ns	2.82***	7.02**	402.70ns	12.96*
Rep*Incomplete block	8	3.90	0.56n.s	582.70n.s	0.02ns	1.74*	1.37	0.85**	2.25**	586.40**	5.48*
Genotype	49	10.78	0.70***	692.50*	0.02*	2.69	2.35	1.36	3.63	802.50	10.50
Residual	41	2.21	0.34	358.50	0.01	0.81	0.31	0.24	0.65	165.30	2.33
Total	99	6.73	0.54	553.20	0.02	1.89	1.41	0.87	2.32	517.10	6.74

DF=degree of freedom, AD= anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, FW=field weight, GM=grain moisture, grain weight, GY= grain yield, PH=plant height, silking days. *, **, **** indicate level of significance of the data is at P=0.1, 0.01 and 0.001. ns indicates non-significant at 5% probability level.

Table 3-4 Mean squares combined analysis of variance of 50 early maturing maize hybrids for grain yield and secondary traits evaluated across three enviroment

Source	**DF**	**Anthesis days**	**Anthesis-silking interval**	**Ears height**	**Ear per plant**	**Field weight**	**Grain moisture**	**Grain weight**	**Grain yield**	**Plant height**	**Silking days**
Rep	1	84.27***	0.33n.s	1766.60***	0.02n.s	3.17n.s	0.02n.s	1.35***	3.63***	1086.8n.s	74.0n.s
Rep.IB	8	41.99***	0.49***	427.30**	0.03n.s	0.46n.s	1.13***	0.41***	0.98ns	569.3***	37.25***
Genotype	49	65.35***	0.88***	605.00***	0.07***	1.82***	2.82***	1.01***	2.90***	836.0***	66.6***
ENV	2	9136.72***	30.41***	56568.10***	5.98***	939.70***	87.42***	624.87***	1717.14***	142606.9***	8213.7***
Genotype.ENV	98	21.04***	0.60***	310.40***	0.05***	1.47***	2.16**	0.80***	2.16***	421.0***	22.42***
Residual	141	9.89	0.16	179.20	0.02	0.40	0.21	0.13	0.36	144.6	10.07
Total	299	84.79	0.62	681.10	0.08	7.28	1.88	4.69	12.88	1315.9	79.2

*, **, ***, indicate level of significance of the data at P≤0.05, P≤0.01 and P≤0.001, respectively. n.s indicate non-significant at 5% probability level., DF=degree of freedom, Rep.IB= Rep*Incomplete block

3.6.2 Genotype performance by single environment

Means for the hybrids in respect of grain yield and secondary traits are presented in Table 3-5 and the means of the other traits are in Appendix 1. Entry effects for grain yield, anthesis-silking interval, ear height, plant height and ear per plant were highly significant across managed drought, low N and optimum. Grain yield of commercial hybrid checks ranged from 1.45 t ha^{-1} (G14) to 3.4 t ha^{-1} (G15) under managed drought, while for low N it ranged from 2.10 t ha^{-1} (G23) to 4.30 t ha^{-1} (G27) and for optimum it ranged from 7.70 t ha^{-1} (G48) to 12.35 t ha-1 (G14). The following checks; G15 under managed drought, G27 under low N, and G14 under optimum environments, were ranked as the top-yielding hybrid checks (Table 3-6). The top yielding experimental hybrids, G17 under Lutz Ville (managed drought), G47 under Cedara (low N) and G5 under Potchefstroom (optimum), were ranked above the hybrid checks G15, G27 and G14, respectively. The environments were ranked in terms of their mean grain yielding potential as follows: optimum> low N> managed drought. Mean anthesis-silking interval was significant for all the genotypes, and ranged from 0.50-2.00; 0.50-1.00 and 1.50-3.50 under managed drought, low N and optimum, respectively. The shortest ear height was for G50 (97 cm) under managed drought, G16 and G43 (61 cm) under low N and G30 (99 cm) under optimum, while plant height ranged from 197 cm (G47), 206 cm (G22) and 279 cm (G25) under managed drought, low N and optimum, respectively. Ears per plant was lowest for G1 under managed drought, G13 under low N and under optimum was G13 and G31 with values of 0.25, 0.70 and 0.90 respectively. The coefficient of variation (CV) for most of the traits was significantly low in all the environments while anthesis-silking interval had the highest CV (30.65) under managed drought. Mean grain yield for top performing early maturing hybrids and checks with significant levels under each environment are presented in Table 3-5. The hybrid with the highest mean grain yield under managed drought was G29, under low N was G27 (check) and optimum was G5 with 5.0, 4.3 and 14.3 t ha^{-1}, respectively. Among the maize hybrids evaluated in each environment, bolded checks in Table 3-5 denotes that they demonstrated similar performance with the early maturing maize hybrids that were evaluated.

Table 3-5 Mean perfomance of genotypes for each environmet

Traits	**GY (tha^{-1})**			**ASI (days)**			**EH (cm)**			**PH (cm)**			**EPP**		
	Lutz	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G1	1.30	1.55	8.95	1.00	1.00	1.50	121.00	85.00	141.00	178.00	167.00	273.00	0.25	0.90	1.00
G2	3.20	1.40	9.55	2.00	1.00	2.50	115.00	80.00	118.00	174.00	157.00	235.00	0.85	1.10	1.35
G3	2.20	1.10	7.85	2.00	0.00	2.50	124.00	71.00	114.00	189.00	156.00	207.00	0.45	0.95	1.05
G4	3.40	2.20	9.10	0.50	1.00	2.00	135.00	83.00	128.00	189.00	157.00	231.00	1.15	0.85	1.00
G5	2.20	1.70	14.30	2.00	1.00	3.00	118.00	96.00	129.00	171.00	175.00	228.00	0.60	1.05	1.30
G6	2.85	2.10	11.85	1.00	1.00	1.50	123.00	80.00	108.00	181.00	169.00	218.00	0.65	0.90	1.05
G7	4.90	3.05	11.80	2.00	1.00	2.50	113.00	91.00	106.00	180.00	178.00	206.00	0.60	1.05	1.10
G8	1.15	1.50	8.75	2.00	1.00	2.00	117.00	67.00	140.00	187.00	150.00	251.00	0.35	0.95	1.20
G9	3.55	2.30	10.50	2.00	0.50	2.00	115.00	93.00	140.00	166.00	176.00	235.00	1.15	0.90	1.30
G10	2.15	2.40	9.25	1.00	1.00	2.50	103.00	87.00	138.00	173.00	181.00	259.00	0.60	1.00	1.10
G11	1.25	1.70	9.50	2.00	1.00	1.50	135.00	67.00	117.00	192.00	151.00	225.00	0.35	0.75	1.05
G12	1.15	2.15	9.75	2.00	0.00	2.00	107.00	88.00	135.00	156.00	171.00	244.00	0.65	1.00	1.20
G13	2.20	0.65	9.95	1.00	1.00	1.50	129.00	74.00	135.00	171.00	147.00	240.00	0.60	0.70	0.90
G14	1.45	2.55	12.35	0.50	1.00	2.50	128.00	95.00	137.00	184.00	187.00	263.00	0.35	0.90	1.05
G15	3.40	3.30	11.60	1.00	1.00	2.00	103.00	92.00	141.00	170.00	178.00	214.00	0.75	0.90	1.15
G16	2.35	3.75	11.05	0.00	0.00	1.50	121.00	61.00	116.00	170.00	145.00	225.00	0.65	1.05	1.10
G17	4.85	1.45	8.85	1.00	1.00	2.00	115.00	65.00	115.00	161.00	140.00	224.00	0.55	0.90	1.00
G18	3.70	2.05	9.55	1.00	1.00	2.00	124.00	70.00	109.00	170.00	156.00	201.00	1.20	1.00	1.10
G19	2.50	3.15	7.80	2.00	1.00	2.00	124.00	83.00	119.00	178.00	168.00	240.00	0.45	0.95	1.05
G20	2.30	2.20	8.40	2.00	2.00	3.00	116.00	98.00	123.00	179.00	186.00	229.00	0.50	0.90	1.00
G21	3.70	2.55	9.10	2.00	1.00	2.00	115.00	88.00	123.00	176.00	187.00	244.00	0.95	0.95	1.20
G22	1.30	2.60	10.30	1.00	1.00	1.50	133.00	126.00	151.00	166.00	206.00	247.00	0.50	0.95	1.15
G23	1.75	2.10	8.35	0.00	1.00	0.50	124.00	84.00	123.00	167.00	167.00	214.00	0.70	0.80	1.10
G24	2.05	2.25	10.05	2.00	1.00	2.50	127.00	86.00	134.00	175.00	139.00	253.00	0.45	1.05	1.05
G25	1.60	2.60	9.50	2.00	0.50	1.00	128.00	108.00	165.00	188.00	193.00	279.00	0.45	0.90	1.00

Traits	GY (tha^{-1})			ASI (days)			EH (cm)			PH (cm)			EPP		
	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch
Genotype	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT
G26	2.20	2.65	8.85	0.50	0.50	1.00	127.00	96.00	115.00	186.00	183.00	233.00	0.60	1.35	1.20
G27	3.25	4.30	9.55	2.00	1.00	1.00	116.00	88.00	115.00	181.00	175.00	235.00	0.70	0.95	1.05
G28	1.50	2.20	11.20	2.00	1.00	2.00	125.00	73.00	131.00	184.00	160.00	260.00	0.45	0.85	1.05
G29	5.00	1.80	8.85	1.00	1.00	2.00	107.00	91.00	119.00	181.00	175.00	230.00	0.45	0.85	1.00
G30	2.15	2.70	7.60	2.00	1.00	1.50	118.00	64.00	99.00	169.00	137.00	202.00	0.55	0.80	0.95
G31	3.90	4.05	8.00	1.00	1.00	2.00	105.00	75.00	127.00	159.00	165.00	242.00	0.40	1.00	0.90
G32	1.65	2.40	8.35	2.00	1.00	1.50	133.00	115.00	154.00	195.00	199.00	258.00	0.55	1.15	1.15
G33	1.40	2.40	9.70	1.00	0.00	2.50	128.00	82.00	128.00	181.00	163.00	233.00	0.35	1.00	1.25
G34	1.50	0.60	9.20	1.00	0.00	2.50	117.00	80.00	141.00	176.00	169.00	253.00	0.35	0.80	1.00
G35	1.80	3.45	10.95	2.50	1.00	2.00	108.00	76.00	126.00	185.00	162.00	241.00	0.50	1.05	1.15
G36	3.65	3.55	10.00	2.00	1.00	2.00	117.00	76.00	128.00	195.00	171.00	229.000	0.55	1.00	1.00
G37	2.15	2.05	9.60	1.00	1.00	1.00	110.00	79.00	128.00	185.00	165.00	240.00	0.50	0.95	1.00
G38	3.25	1.65	6.95	1.00	1.00	1.00	115.00	77.00	101.00	175.00	160.00	200.00	0.65	0.75	1.00
G39	3.25	1.50	8.70	1.00	1.00	2.00	146.00	77.00	142.00	189.00	162.00	270.00	0.60	0.85	1.00
G40	2.15	2.40	9.15	0.50	0.00	1.50	125.00	79.00	112.00	170.00	167.00	230.00	1.45	1.05	0.95
G41	3.55	3.00	11.65	2.00	0.00	3.00	111.00	78.00	124.00	186.00	163.00	229.00	0.45	1.05	1.15
G42	1.35	3.55	9.60	1.00	1.00	1.50	116.00	91.00	141.00	186.00	181.00	247.00	0.45	0.85	1.15
G43	2.35	2.25	9.15	1.00	1.00	1.50	116.00	61.00	102.00	180.00	99.00	203.00	0.50	0.85	1.10
G44	2.60	3.15	10.80	0.00	1.00	2.50	123.00	95.00	145.00	187.00	185.00	264.00	0.50	0.85	1.00
G45	1.90	1.95	9.55	2.00	1.00	2.00	128.00	70.00	150.00	184.00	141.00	269.00	0.65	0.85	1.00
G46	1.90	2.90	8.45	2.00	1.00	2.50	119.00	89.00	135.00	159.00	184.00	255.00	1.20	0.95	1.05
G47	3.30	3.80	11.65	2.00	0.00	2.00	116.00	103.00	114.00	197.00	192.00	234.00	0.60	1.00	1.20
G48	3.20	3.15	7.70	0.50	0.00	1.00	130.00	87.00	211.00	180.00	162.00	246.00	0.40	0.90	0.95
G49	2.25	3.15	8.70	2.00	1.00	2.50	106.00	90.00	152.00	195.00	188.00	271.00	0.45	1.00	1.05
G50	1.60	2.30	10.20	3.00	0.50	1.50	97.00	90.00	112.00	175.00	163.00	218.00	0.55	0.85	1.10
Min	1.15	0.60	6.95	0.00	0.00	0.50	97.00	61.00	99.00	156.00	99.00	200.00	0.25	0.70	0.90
Max	5.00	4.30	14.30	3.00	2.00	3.00	146.00	126.00	211.00	197.00	206.00	279.00	1.45	1.35	1.35

Traits	**GY (tha^{-1})**			**ASI (days)**			**EH (cm)**			**PH (cm)**			**EPP**		
	Lutz	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
Mean	2.51	2.43	9.64	1.42	0.80	1.90	119.00	84.00	129.00	178.00	167.00	237.00	0.60	0.94	1.08
CV (%)	8.36	18.38	16.17	30.65	23.87	16.21	14.69	12.08	7.22	5.42	7.25	5.24	10.62	12.88	25.42
S.E.	0.81	0.45	0.40	0.58	0.19	0.23	18.93	10.11	8.61	12.86	12.09	9.36	0.11	0.12	0.15
LSD(0.05)	1.63	0.89	0.82	1.18	0.38	0.46	38.24	20.43	17.39	25.96	24.41	18.89	0.23	0.24	0.31
P-value	<.001	<.001	<.001	0.009	<.001	<.001	0.016	<.001	0.002	<.001	<.001	0.008	0.049	0.106	<.001

GY=Grain yield, ASI=Anthesis-silking interval, EH=Ear height, PH=Plant height, EPP=Ear per plant, Lutz=Lutzville, Ced=Cedara, Potch=Potchfestroom, Opt=optimum, LN=low Nitrogen, MD=Managed drought

Table 3-6 Mean grain yield for top perfoming hybrids and checks under each environment (ranked by grain yield)

Mean Grain Yield (tha^{-1})					
Genotype	**Lutz Ville (Managed drought)**	**Genotype**	**Cedara (Low Nitrogen)**	**Genotype**	**Potchefstroom (Optimum)**
G29	5.00	**G27**	4.30	G5	14.30
G7	4.90	G31	4.05	**G14**	12.35
G17	4.85	G47	3.80	G6	11.85
G31	3.90	G16	3.75	G7	11.80
G21	3.70	G36	3.55	G41	11.65
G18	3.70	G42	3.55	G47	11.65
G36	3.65	G35	3.45	**G15**	11.60
G9	3.55	**G15**	3.30	G28	11.20
G41	3.55	G19	3.15	G16	11.05
G4	3.40	G44	3.15	**G35**	10.95
Min	1.15		0.60		6.95
Max	5.00		4.30		14.3
Mean	2.51		2.43		9.64
CV (%)	8.36		18.38		16.17
S.E.	0.81		0.45		0.40
LSD$_{(0.05)}$	1.63		0.89		0.82
P-value	<.001		<.001		<.001

3.6.3 Heritability and genetic parameters for each single environment

Substantial differences in heritability values for the different traits are presented in Table 3-7, 3-8 and 3-9. The heritability (%) was categorised as low, moderate and high, similar to that of Robinson *et al.* (1949) as follows: 0-0.30 = low; 0.30-0.60 = moderate and >0.60 = high. The study revealed the whole range of low to high heritability estimates. At Lutzville (managed drought) broad sense heritability ranged from 0 to 79% (Table 3-7). High broad sense heritability was exhibited by grain moisture, grain yield, grain weight, anthesis days and silking days, while field weight and ear height had moderate heritability. Anthesis-silking interval, plant height and ear per plant exhibited low heritability. Genetic advance as a percentage of mean ranged from 56 to 87%, with plant height displaying the lowest and grain yield the highest. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. Genotypic coefficient of variation ranged from 0.48 to 12.50, while PCV ranged from 1.42 to 14.46.

At Cedara (low N) broad sense heritability ranged from 26 to 100% (Table 3-8). High broad sense heritability was exhibited by plant height, grain moisture, silking days, anthesis days, grain weight and grain yield, while ear height and field weight revealed moderate heritability. Anthesis-silking interval and ear per plant exhibited low heritability. Genetic advance as a percentage of mean ranged from 10 to 76%, with anthesis days displaying the lowest and anthesis-silking interval the lowest. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. Genotypic coefficient of variation ranged from 2.82 to 12.18, while PCV ranged from 3.12 to 15.55.

At Potchefstroom (optimum) broad sense heritability ranged from 39 to 90% (Table 3-9). High broad sense heritability was exhibited by Anthesis-silking interval, field weight, grain weight, grain moisture, grain yield and ear per plant only. Whereas, anthesis days, silking days, ear height and plant height recorded moderate heritability. No other trait exhibited low heritability. Genetic advance as a percentage of mean ranged from 9.0 to 97.0%, with plant height displaying the lowest and grain weight the highest. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. Genotypic coefficient of variation ranged from 2.69 to 8.57, while PCV ranged from 3.12 to 13.08.

Table 3-7 Estimates of heritability and genetic parameters for grain yield and secondary traits for the 50 early maturing maize hybrids at Lutzville (managed drought)

Traits	σ_g^2	σ_e^2	σ_p^2	**H^2**	**GCV**	**Mean**	**PCV**	**GA**	**%GA**
AD	4.47	2.16	6.63	0.67	2.33	82.20	2.84	4.35	5.30
SD	4.33	2.35	6.67	0.65	2.28	83.36	2.83	4.28	5.14
ASI	0.14	0.40	0.54	0.26	3.55	1.09	7.02	0.76	69.95
PH	0.40	166.59	166.99	0.00	0.48	177.00	9.71	1.30	0.74
EH	0.64	126.32	111.96	0.01	0.85	88.63	11.24	1.65	1.86
FW	1.06	0.77	1.83	0.58	6.17	2.77	8.12	2.12	76.39
GW	0.64	0.21	0.85	0.75	5.80	1.89	6.71	1.64	86.96
GM	1.11	0.30	1.41	0.79	2.94	12.89	3.31	2.17	16.85
GY	0.70	0.57	2.27	0.75	12.50	1.08	14.46	2.68	47.41
EPP	0.00	0.02	0.02	0.14	0.53	0.92	1.42	0.10	11.33

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, FW=Field weight, GM=Grain moisture, GW=Grain weight, GY=Grain yield, PH=Plant height, SD=Silking days, σ_g^2 = genotypic variance, σ_e^2 = error variance, σ_p^2 = phenotypic variance, H2=broad sense heritability, GCV=genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GA=genetic advance, GAM%= genetic advance as percent of the mean

Table 3-8 Estimates of heritability and genetic parameters for grain yield and secondary traits for the 50 early maturing maize hybrids at Cedara (low N)

Traits	σ_g^2	σ_e^2	σ_p^2	H^2	GCV	Mean	PCV	GA	%GA
AD	17.16	6.37	23.53	0.73	4.57	82.20	5.35	8.53	10.38
SD	18.12	6.23	24.35	0.74	4.66	83.36	5.40	8.77	10.52
ASI	0.16	0.40	0.56	0.29	3.88	1.09	7.19	0.83	76.56
PH	262.72	0.04	262.76	1.00	12.18	177.00	12.18	33.39	18.86
EH	118.10	96.19	214.29	0.55	11.54	88.63	15.55	22.39	25.26
FW	0.22	0.17	0.39	0.57	2.82	2.77	3.73	0.97	34.94
GW	0.18	0.07	0.25	0.73	3.09	1.89	3.60	0.88	46.31
GM	1.13	0.12	1.25	0.90	2.96	12.89	3.12	2.19	16.98
GY	0.58	0.20	0.77	0.75	5.26	2.08	6.09	1.57	75.10
EPP	0.01	0.01	0.02	0.26	0.75	0.92	1.47	0.15	16.20

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, FW=Field weight, GM=Grain moisture, GW=Grain weight, GY=Grain yield, PH=Plant height, SD=Silking days, σ_g^2 = genotypic variance, σ_e^2 = error variance, σ_p^2 = phenotypic variance, H^2=broad sense heritability, GCV=genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GA=genetic advance, GAM%= genetic advance as percent of the mean

Table 3-9 Estimates of heritability and genetic parameters for grain yield and secondary traits for the 50 early maturing maize hybrids at Potchfestroom (optimum)

Traits	σ_g^2	σ_e^2	σ_p^2	H^2	GCV	Mean	PCV	GA	%GA
AD	18.88	15.48	34.36	0.55	4.89	78.81	6.60	8.95	11.36
SD	19.90	15.89	35.79	0.56	4.96	80.78	6.66	9.19	11.38
ASI	0.48	0.06	0.53	0.90	4.91	1.97	5.19	1.42	72.12
PH	55.43	84.99	140.42	0.39	5.88	160.30	9.36	15.34	9.57
EH	55.38	73.45	128.83	0.43	8.57	75.34	13.08	15.33	20.35
FW	0.56	0.17	0.73	0.77	4.75	2.50	5.40	1.55	61.84
GW	0.34	0.07	0.41	0.84	4.41	1.76	4.83	1.21	68.47
GM	1.10	0.18	1.28	0.86	2.90	13.08	3.12	2.16	16.53
GY	0.93	0.17	1.11	0.84	6.77	2.03	7.38	1.99	97.90
EPP	0.05	0.02	0.07	0.70	2.96	0.59	3.54	0.47	79.48

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, FW=Field weight, GM=Grain moisture, GW=Grain weight, GY=Grain yield, PH=Plant height, SD=Silking days, σ_g^2 = genotypic variance, σ_e^2 = error variance, σ_p^2 = phenotypic variance, H^2=broad sense heritability, GCV=genotypic coefficient of variation, PCV= phenotypic coefficient of variation, GA=genetic advance, GAM%= genetic advance as percent of the mean

3.6.5 Correlation between yield and secondary traits for each single environment

Phenotypic correlations between yield and secondary traits for each environment were determined and they indicated significant associations among the agronomic traits (Table 3-10, 3-11 and 3-12). At Lutzville (Managed drought) it was observed that anthesis days and ear height showed significant but negative correlations (r = -0.372** and -0.317* respectively) with grain yield. Anthesis-silking days, ear per plant and field weight showed significant positive significant and positive correlation (r=0.815**, 0.874** and 0.969** respectively). There were highly significant and positive correlations between the following pairs of traits: anthesis days and ear height (r=0.917**); anthesis-silking interval and ear per plant (r = 0.933**); anthesis-silking interval and field weight (r=0.877**); ear per plant and field weight (0.945*); anthesis days and grain moisture (r=0.889**); ear height and grain moisture (r = 0.56**); anthesis-silking interval and grain yield (r=0.815**); ear per plant and grain yield (r=0.874**); plant height and anthesis days (r=0.943**); ear height and plant height (r=0.944**); grain moisture and plant height (r=0.903**) anthesis days and silking days (r = 0.999**); ear height and silking days (r = 0.913**); grain moisture and silking days (r=0.888). There were highly significant and negative correlations between the following pairs of traits: anthesis days and anthesis-silking days (r=-0.425**); anthesis days and ear per plant (r=-0.530**); anthesis days and field weight (r=-0.451**); anthesis-silking days and ear height (r=-0.443**); anthesis-silking days and grain moisture (r=-0.334**); anthesis-silking days and plant height (r=-0.433**); anthesis-silking days and silking days (r=-0.414**); ear height and ear plant per (r=-0.504**); ear height and field weight (r=-0.391**); ear per plant and grain moisture (r=-0.416**); ear per plant and plant height (r=-0.549**); ear per plant and silking days (r=-0.531**); field weight and grain moisture (r=-0.295*) field weight and plant height (r=-0.436**) and field weight and silking days (r=-0.453**).

At Cedara (low N) (Table 3-11) it was observed that anthesis days showed significant but negative correlations (r = -0.400**) with grain yield. Anthesis-silking days, ear per plant and field weight showed significant positive significant and positive correlation (r=0.917**, 0.939** and 0.975** respectively). There were highly significant and positive correlations between the following pairs of traits: anthesis days and ear height (r=0.33**); anthesis days and grain moisture (r=0.885**); anthesis days and plant height (0.943**); anthesis days and silking days (r=1.000**); anthesis-silking interval and ear per plant (r = 0.986**); anthesis-silking interval and field weight (r=0.963**); ear height and grain moisture (r=0723**); ear height and plant height (r=0.937**); ear height and silking days (r=0.734**); ear per plant and field weight (r=0.982**); grain moisture and silking days (R=0.886**); plant height and silking days (r = 0.850**); ear height and silking days (r = 0.913**); grain moisture and silking days (r=0.888).

There were highly significant and negative correlations between the following pairs of traits: anthesis days and anthesis-silking days (r=-0.516**); anthesis days and ear per plant (r=-0.480**); anthesis days and field weight (r=-0.462**); anthesis-silking days and ear height (r=-0375**); anthesis-silking days and grain moisture (r=-0.379**); anthesis-silking days and plant height (r=-0.461**); anthesis-silking days and silking days (r=-0.513**); ear height and ear plant per (r=-0.332*); ear height and field weight (r=-0.280*); ear per plant and grain moisture (r=-0.339*); ear per plant and plant height (r=-0.415**); ear per plant and silking days (r=-0.479**); field weight and grain moisture (r=-0.324*); field weight and plant height (r=-0.366**); field weight and silking days (r=-0.462**); grain yield and plant height (r=-0.270*) and grain yield and silking days (r=-0.399**).

At Potchefstroom (optimum) (Table 3-12) it was observed that anthesis days, ear height, field weight and grain moisture showed highly significant but positive correlations (r = 0.622**, 0.576**, 0.779** and 0.687** respectively) with grain yield. There were highly significant and positive correlations between the following pairs of traits: anthesis days and ear height (r=0.709**); anthesis days and field weight (r=0.298**); anthesis days and grain moisture (r=0.910**); anthesis days and plant height (r=0.948**); anthesis days and silking days (r=0.999**); anthesis-silking interval and ear per plant (r = 0.986**); anthesis-silking interval and field weight (r=0.470**); ear height and field weight (r=0.329**); ear height and grain moisture (r=0.688**); ear height and plant height (r=0.794); ear height and silking days (r=0.707**); ear per plant and field weight (r=0.449***); field weight and grain moisture (r=0.428**); field weight and plant height (r=0.301*); field weight and silking days (r=0.305*); grain moisture and plant height (r=0.854**); grain moisture and silking days (r=0.906**); grain yield and plant height (R=0.624**); grain yield and silking days (r = 0.628**); and plant height and silking days (r = 0.948**).The following pairs showed significant but negative correlations anthesis days and ear height (r=-0.512**); anthesis days and ear per plant (r=-0.455**); anthesis-silking interval and ear height (r=-0.2766*); anthesis-silking interval and grain moisture (r=-0.356); anthesis-silking interval and plant height (r=-0.480**); anthesis-silking interval and silking days.(r=-0.508**); ear per plant and grain moisture(r=-0.279*); ear per plant and plant height (r=-0.431) and plant height and silking days (r=-0.445**).

Table 3-10 Pearson correlation coefficients for grain yield and secondary traits at Lutz ville (managed drought)

Traits	ASI	EH	EPP	FW	GM	GY	PH	SD
AD	-.425**	.917**	-.530**	-.451**	.889**	-.372**	.943**	.999**
ASI		-.443**	.933**	.877**	-.334*	.815**	-.433**	-.414**
EH			-.504**	-.391**	.856**	-.317*	.944**	.913**
EPP				.945**	-.416**	.874**	-.549**	-.531**
FW					-.295*	.969**	-.436**	-.453**
GM						-0.202	.903**	.888**
GY							-.340*	-.373**
PH								.944**

*,**. Correlation is significant at P≤ 0.05 and P≤0.01 level, respectively.AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, GY=Grain yield, PH=Plant height, SD=Silking days

Table 3-11 Pearson correlation coefficients for grain yield and secondary traits at Cedara (low N)

Traits	ASI	EH	EPP	FW	GM	GY	PH	SD
AD	-.516**	.733**	-.480**	-.462**	.885**	-.400**	.850**	1.000**
ASI		-.375**	.986**	.963**	-.379**	.917**	-.461**	-.513**
EH			-.332*	-.280*	.723**	-0.194	.937**	.734**
EPP				.982**	-.339*	.939**	-.415**	-.479**
FW					-.324*	.975**	-.366**	-.462**
GM						-0.262	.796**	.886**
GY							-.270*	-.399**
PH								.850**

*,**. Correlation is significant at P≤ 0.05 and P≤0.01 level, respectively.AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, GY=Grain yield, PH=Plant height, SD=Silking days

Table 3-12 Pearson correlation coefficients for grain yield and secondary traits at Potchfestroom (optimum)

Traits	ASI	EH	EPP	FW	GM	GY	PH	SD
AD	-.512**	.709**	-.445**	.298*	.910**	.622**	.948**	.999**
ASI		-.276*	.986**	.470**	-.356**	0.028	-.480**	-.508**
EH			-0.218	.329*	.686**	.576**	.794**	.707**
EPP				.499**	-.279*	0.075	-.431**	-.445**
FW					.428**	.779**	.301*	.305*
GM						.687**	.854**	.906**
GY							.624**	.628**
PH								.948**

*,**. Correlation is significant at P≤ 0.05 and P≤0.01 level, respectively.AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, GY=Grain yield, PH=Plant height, SD=Silking days

3.6.6 Path coefficient analysis for single environment

Path coefficient analysis was studied at phenotypic level considering grain yield as dependent character for each environment. The phenotypic direct and indirect effect of yield-related traits are presented in Table 3-13, 3-14 and 3-15. At Lutzville (managed drought) the path coefficient analysis revealed that anthesis day, anthesis-silking interval, ear height and grain moisture had positive direct effects on grain yield. A negative direct effect was contributed by field weight (-0.109), plant height (-0.129), ear per plant (-0.890) and silking days (-1.724). The direct contribution of anthesis days to grain yield of maize was 1.711, while the highest indirect contribution through ear per plant and ear height were 0.472 and 0.109 respectively; giving a total contribution of -0.372**. Direct contribution of anthesis-silking interval to grain was 0.177 whereas indirect contribution was through silking days and plant height were 0.714 and 0.056, respectively; giving a total contribution of 0.815**.

At Cedara (low N) the path coefficient analysis revealed that anthesis days, anthesis-silking interval, grain moisture, ear height, plant height and field weight had positive direct effects on grain yield. A negative direct effect was contributed by ear per plant (-0.916) and silking days (-7.631). The direct contribution of anthesis days to grain yield of maize was 7.544, while the highest indirect contribution through ear per plant and grain moisture were 0.472 and 0.075 respectively; giving a total contribution of -0.400**. Direct contribution of anthesis-silking interval to grain was 0.587 whereas indirect contribution was through silking days and field weight were 3.915 and 0.012 respectively; giving a total contribution of 0.917**.

At Potchefstroom (optimum), the path coefficient analysis revealed that anthesis days, silking days, ear height, anthesis-silking interval and field weight had positive direct effects on grain yield. A negative direct effect was contributed by plant height (-0.100), grain moisture (-0.144) and ear per plant (-0.358). The direct contribution of anthesis days to grain yield of maize was 0.106, while the highest indirect contribution through ear per plant and silking days were 0.159 and 0.105 respectively; giving a total contribution of 0.622**. Direct contribution of silking days to grain was 0.105 whereas indirect contribution was through ear per plant and anthesis days were 0.159 and 0.106, respectively; giving a total contribution of 0.628**.

Table 3-13 The direct (diagonal) and indirect (out diagonal) contribution of maize yield traits on grain yield at Lutz ville (managed drought)

Traits	AD	ASI	EH	EPP	FW	GM	PH	SD	Total correlation to GY
AD	**1.711**	-0.075	0.109	0.472	0.049	0.017	-0.122	-1.722	-0.372**
ASI	-0.727	**0.177**	-0.053	-0.830	-0.096	-0.006	0.056	0.714	0.815**
EH	1.569	-0.079	**0.119**	0.448	0.043	0.016	-0.122	-1.574	-0.317*
EPP	-0.907	0.165	-0.060	**-0.890**	-0.103	-0.008	0.071	0.915	0.874**
FW	-0.772	0.155	-0.046	-0.784	**-0.109**	-0.006	0.056	0.781	0.969**
GM	1.521	-0.059	0.102	0.345	0.028	**0.019**	-0.117	-1.531	-0.202
PH	1.613	-0.077	0.112	0.456	0.042	-0.006	**-0.129**	-1.627	-0.340*
SD	1.709	-0.073	0.108	0.441	0.043	-0.006	0.053	**-1.724**	-0.373**

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, PH=Plant height, SD=Silking days, GY=Grain yield

Table 3-14 The direct (diagonal) and indirect (out diagonal) contribution of maize yield traits on grain yield at Cedara (low N)

Traits	AD	ASI	EH	EPP	FW	GM	PH	SD	Total correlation to GY
AD	**7.544**	-0.303	0.051	0.440	-0.006	0.075	0.055	-7.631	-0.400**
ASI	-3.892	**0.587**	-0.026	-0.904	0.012	-0.032	-0.030	3.915	0.917**
EH	5.529	-0.220	**0.070**	0.304	-0.003	0.062	0.060	-5.601	-0.194
EPP	-3.621	0.579	-0.023	**-0.916**	0.012	-0.029	-0.027	3.655	0.939**
FW	-3.485	0.565	-0.020	-0.900	**0.012**	-0.028	-0.024	3.526	0.975**
GM	6.676	-0.223	0.051	0.311	-0.004	**0.085**	0.051	-6.761	-0.262
PH	6.412	-0.271	0.066	0.380	-0.004	0.068	**0.064**	-6.486	-0.270*
SD	7.544	-0.301	0.051	0.439	-0.006	0.076	0.055	**-7.631**	-0.399**

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, PH=Plant height, SD=Silking days, GY=Grain yield

Table 3-15 The direct (diagonal) and indirect (out diagonal) contribution of maize yield traits on grain yield at Potchfestroom (Optimum)

Traits	AD	ASI	EH	EPP	FW	GM	PH	SD	Total correlation to GY
AD	**0.106**	-0.024	0.050	0.159	0.002	-0.131	-0.095	0.105	0.622**
ASI	-0.054	**0.047**	-0.019	-0.353	0.003	0.051	0.048	-0.053	0.028
EH	0.075	-0.013	**0.071**	0.078	0.002	-0.099	-0.079	0.074	0.576**
EPP	-0.047	0.047	-0.015	**-0.358**	0.003	0.040	0.043	-0.047	0.075
FW	0.032	0.022	0.023	-0.179	**0.006**	-0.062	-0.030	0.032	.779**
GM	0.097	-0.017	0.048	0.100	0.003	**-0.144**	-0.085	0.095	0.687**
PH	0.101	-0.023	0.056	0.154	0.002	-0.123	**-0.100**	0.099	0.624**
SD	0.106	-0.024	0.050	0.159	0.002	-0.131	-0.095	**0.105**	0.628**

AD=Anthesis days, ASI=Anthesis-silking interval, EH=Ear height, EPP=Ears per plant, GM=Grain moisture, PH=Plant height, SD=Silking days, GY=Grain yield

3.7 Discussion

3.7.1 Analysis of variance and genotype performance for grain yield and secondary traits

Grain yield varied significantly among the hybrids in all the environments. The combined analysis of variance across the three sites in the study revealed that genotype, environment and genotype by environment interaction were significant for all the traits amongst the genotypes. The results are in agreement with Saikia and Sharma (2000) who reported significant genotype and environment effect and GEI for all traits. This suggests that there is genetic variability amongst the traits for the maize hybrids. Genetic variability provides a good opportunity for yield improvement, which means effective selection is attainable. The presence of significant genotype by environment interaction indicates that the genotypes responded differently to changes in environment. These differences could be attributed to the variation in climatic factors in the test environments. This are similar findings done by Bello and Olaoye (2009), Aly *et al.,* (2011) and Abdel-Moneam *et al.,* (2014) reported that the significant mean squares observed for all traits indicate that the experimental growing conditions are different. The error variance of the mean for all the traits was significant. This might be a result of the minimum number of replications and data from the sites used in estimating the components of variance for all the traits. The variability observed for grain yield as a quantitative inherited trait was high among the genotypes implying that there are opportunities for selection in the genotypes for enhancement of grain yield. This variability could be heritable and exploited in the process of selection in the breeding programme. Similar results were recorded by other researchers (Ackura *et al*., 2005; Acura and Kaya, 2008; Asfaw, 2008; Dagne, 2008; Solomon *et al*., 2008; Abdurhaman, 2009; and Muluken, 2009).

The mean grain yield of hybrids ranged from 1.45-3.4 t ha^{-1}, 2.1-4.31 t ha^{-1} and 7.7-12.0 t ha^{-1} under managed drought, low N and optimum, respectively. The results of the mean grain yield under managed drought and low N were similar to Bolaños and Edmeades (1996) Pswarayi and Vivek (2008), Nyombayire *et al*. (2011) and Ertiro *et al.* (2017) reported that yield reduction is between 20-30% under well-watered conditions, while in low N the is 50% grain yield reduction and in drought conditions is about 50-60%. This implies that large part of yield potential is not realised in many genotypes when evaluated under multiple stress environments. Since the top three hybrids (G5, G31, and G29) could withstand the multiple stress and out-yielded the commercial checks, it is, therefore, ideal that these hybrids be tested for stability across environments. Further, yield improvements to match the three hybrids would be achieved by improving ears per plant of these promising top yielding hybrids.

Low N environments had the lowest mean grain yield and significant reductions in plant and ear height. This confirms that reductions in plant and ear height are related with yield reductions especially under stress environments. The effect of drought and low N stress on plant height is in agreement with previous studies done by Ertiro *et al.,* (2017), respectively reported 1% and 40% reductions due to drought and low N. Mean grain yield for top performing genotypes which were ranked as best therefore can be used to improve tolerance to both drought and low N stress, since they contribute greatly to higher yields and to stress tolerance.

3.7.4 Heritability and genetic parameters for each single environment

The genotypic variances for each environments`(managed drought, low N and optimum) under grain yield were reduced due to the multiple stress effect. Similarly, genotypic variance for the other traits was reduced with increasing stress. These traits showed an almost similar trend in mean grain yield. Many researchers have reported that genotypic variance for grain yield in stress environments is generally lower than in non-stress environments (Al-Naggar et al., 2009; Al-Naggar et al., 2011; Garg et al., 2017). Therefore, it is important to consider using secondary traits to indirectly select for grain yield under multiple stress.

High broad sense heritability coupled with high genetic advance was observed for most of the traits in each environment suggesting that some of the secondary traits were least influenced by environmental effects. Similar results were reported by other researchers (Nelson and Somers, 1992; Rafique *et al.,* 2004; Kashiani *et al.,* 2008; Wannows *et al.,* 2010) that anthesis days, grain yield and silking days' traits had higher values of heritability than maize grain yield. Moderate heritability was observed for plant height, ear height, anthesis-silking interval and ear per plant while low broad sense heritability estimates were observed for grain moisture, grain yield and field weight. The implication is that those traits with moderate heritability can readily respond to selection while for those with low heritability, selection need to be delayed. The results in the present study showed that multiple stresses in combination influenced the magnitude of variances for each trait. Genotypic, error variances and heritability should be used together in predicting the ultimate effect for selecting superior varieties (Muchie and Fentie, 2016). Therefore, attention must be taken while breeding for this complex trait as it is considerably influenced by environmental factors.

Estimate of heritability for secondary traits varied significantly between the environments indicating the role of genotype by environment effects for conditioning these traits. This implies that there was large genetic variation in each environment. These results are in contrast with Aminu and Izge (2012) who reported moderate heritability of some traits. Although high genetic variation was observed at each environment, the results imply that secondary traits are highly influenced by the environment as revealed by very low heritability at other environments. This suggests that some other trait might not respond to selection in some environments. These results are in line with the findings of Lorenzana and Bernardo (2008). Shahrokhi and Ebrahimi (2013) and Ullah *et al*. (2013) have reported low, medium and high estimates of heritability in different plant traits in different environments and working with different genotypes. Higher and relatively moderate broad sense heritability of the traits revealed that variations were transmissible and potential for developing high yielding varieties through selection of desirable plants.

Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone (Singh, 2000). Days to silking and plant height observed in the present study were similar to those obtained in a study by Mahmood *et al*. (2004). The moderate broad sense heritability for plant and ear height in this study for each environment suggests that the actual heritability estimates might be lower (Falconer and Mackay 1996), which may lead to low genetic gain when selecting for these traits. For a trait measured from the same genotype in different environments, indirect selection can be applied given information on the heritability and the genetic correlation for the secondary trait in the environments (Makumbi *et al.,* 2015). Low to moderate broad sense heritability estimates for the traits that were observed in this study maybe due to the environmental influence and the multiple stresses.

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are not only useful for comparing the relative amount of phenotypic and genetic variation among different traits but also for estimating the scope for improvement by selection. The reliability of the parameters to be selected for a breeding programme, among other factors, is dependent on the magnitude of its coefficient of variation especially GCV. However, the difference between genotypic and phenotypic coefficient of variation indicates the presence of environmental influence (Bello *et al.,* 2012). The PCV were slightly higher than the GCV in some of the traits. High value of PCV and GCV was observed in ear height, plant height, grain yield, anthesis-silking interval, silking days, anthesis days and field weight in each environment implying that there is sufficient scope for their improvement through selection. The results are similar to the research findings of Nelson and Somers (1992), Rafique *et al.* (2004), Rafiq *et al.* (2010), Singh *et al.* (2003), Abirami *et al.* (2005) and Vashistha *et al.* (2013). This implies that selection based on the phenotype would be more reliable thus resulting in genetic enhancement of the traits.

Low values of PCV and GCV were observed for days to anthesis, ear per plant, grain moisture, grain weight and field weight at each environment suggesting that there was low variability among the traits. The results are similar to the study done by Shoran and Tandon (1995), Hossain and Joarder (2006), Bello *et al*. (2012) and Rahman *et al*. (2014). Hence, selection for the low heritable traits results in limited possibility for improvement.

3.7.5 Correlation between grain yield and secondary traits for each single environment

At Lutzville (Managed drought), it was observed that anthesis days, ear height, plant height and silking days showed significant but negative correlations with grain yield. At Cedara (low N) it was observed that anthesis days and plant height, silking days showed significant but negative correlations with grain yield. The results are also in line with Akbar *et al.* (2008) and Bocanski *et al.* (2009) reported that anthesis days, ear height, plant height and silking days showed significant but negative correlations with grain yield. At Potchefstroom (optimum) it was observed that anthesis day, ear height, field weight and grain moisture showed highly significant but positive correlations with grain yield. This implies that increasing expression of these traits can positively influence grain yield. The results for Potchefstroom are in line with the work done by Selvaraj and Nagarajan (2011) who reported that plant height, ear height and grain weight showed significant positive association with yield. The difference between the results is mainly due to difference in genotypes used and the environments. Hence, there is need to evaluate genotypes under different environments to determine the effects of genotype by environment on the correlation between yields and secondary traits. Anthesis date, silking days, ear height and plant height showed significant and negative correlation with yield at Lutzville and Cedara. These results show that a negative correlation on the anthesis days is favoured to obtain early maturing hybrids and that directing these traits would be effective for indirect selection of grain yield. These results are similar with Selvaraj and Nagarajan (2011) who reported that anthesis days and silking days showed positive non-significant association with grain yield.

In plant breeding, correlation coefficient analysis measures the mutual relationship between various plant traits and determines the component characters that can be used in the selection for genetic improvement in yield (Hossain and Joarder, 1987). Generally, positive correlation of grain yield with other yield related traits indicates that plant breeders can use these traits as indicators in predicting grain yield. When two traits correlate, selecting for one would ensure selection for the other trait. Knife and Tsehaye (2015) reported that effective selection based on anthesis days, plant and ear height, ear per plant, anthesis- silking interval, grain moisture, silking days and ear diameter is possible, which is similar to the research finding of this study in each environment. A significant and positive correlation of anthesis days, ear height, field weight and grain moisture at Potchefstroom reported in this study is consistent with the findings by Bänziger *et al*. (1997) and Gissa (2008).

3.7.6 Path coefficient analysis for each single environment

Path coefficient analysis was used to partition the relationships between secondary traits and grain yield into direct and indirect effects. The estimation of correlation indicates only the extent and nature of association between grain yield and its attributes but does not show the direct and indirect effect of different yield traits on grain yield. Grain yield is dependent on anthesis days, silking days, anthesis-silking interval, plant height, ear height and ear per plant, which are mutually associated and in turn impair the true link existing between a component and grain yield. According to Singh-Jakhar *et al.* (2017), a change in one component is likely to disturb the whole network of cause and effect. Thus, each component has two paths of action viz., the direct influence on grain, indirect effect through components, which are not revealed from correlation studies. Muhammad et al. (2008) reported that ear per plant, plant height, ear height, anthesis days and silking days exerted positive direct effect on grain yield per plant. The present study reveal that the was significant amount of variability in each environment for all the traits and that they should be taken into consideration for selection of these traits as they showed positive significant association with grain yield.

At Lutzville (managed drought) the path coefficient analysis revealed that anthesis day, anthesis-silking interval, ear height and grain moisture had positive direct effects on grain yield. While negative direct effect was contributed by field weight, plant height, ear per plant and silking days. Rafiq *et al.* (2010) and knife and Tsehaye (2015) have earlier reported similar results in maize. At Cedara (low N) the path coefficient analysis revealed that anthesis days, anthesis-silking interval, grain moisture, ear height, plant height and field weight had positive direct effects on grain yield. While negative, direct effect was contributed by ear per plant and silking days. The results were well supported by similar finding results by knife and Tsehaye (2015).

At Potchefstroom (optimum), the path coefficient analysis revealed that anthesis days, silking days, ear height, anthesis-silking interval and field weight had positive direct effects on grain yield. While negative direct effect was contributed by plant height, grain moisture and ear per plant. These findings are in agreement with those from Geeth and Jayaraman (2000), Muhammad et al. (2003), Vijayabharathi et al. (2009), Bello et al. (2010), Dipika *et al.* (2014) and Sridhar et al. (2016) that positive direct and indirect effects of a trait on grain yield make it possible for its exploitation in selection under specific conditions. Grain yield is influenced by many independent traits and understanding the nature and magnitude of the association of these traits with grain yield and among themselves is vital for effective selection for grain yield.

3.8 Conclusion

Results from this study showed high genetic variability amongst the experimental hybrids and thus the possibility of selecting good early maturing hybrids for grain yield and other agronomic traits under managed drought, low N and optimum stress conditions is possible. Low to moderate heritability estimates were realised in each environment due to the contribution of the genotype by environment interaction and error variances, which lowered the estimates. High heritability estimates observed coupled with high genetic advance for anthesis days, ear height, plant height and silking days indicated that genetic variation was higher than the environmental variation in the study. This implies that phenotypic selection for these traits could be effective. Grain yield was positively correlated with anthesis days, silking days, anthesis-silking interval, plant height, ear height, grain moisture, field weight and ear per plant that are important yield components in maize. Thus, these traits are very important components of grain yield and should be used in the selection process to improving maize grain yield. Path coefficient analysis revealed that in each environment, some traits like anthesis days, silking days, ear height, anthesis-silking interval, grain moisture and field weight had positive direct effect on grain yield while few traits such as plant height and ear per plant had negative direct effect on grain yield. Any increase in one of those traits will results in overall increase in the yield.

This study concludes that effective selection for superior genotypes is possible considering direct selection of the traits that contribute to grain yield improvement. Preference for selection must be given to low N and optimum screening results than to managed drought screening results, which may be more effective in eliminating genotypes that perform very poorly under drought stress. Under managed drought environment, the best performing genotypes were G29 (CZH16095), G7 (CZH16083), G17 (CZH15600), G31 (CZH16064), G21 (CZH16073), G18 (CZH16071), G36 (CZH16096), G9 (CZH15499), and G41 (CZH16082). Under low N, G27 (SC513), G31 (CZH16064), G47 (CZH15452), G16 (CZH16066), G36 (CZH16096), G42 (CZH16078), G35 (SC403), **G15** (local check 2), G19 (CZH16091) and G44 (CZH16088) emerged as the best. Under optimum environment, G5 (CZH16084), **G14** (SC301), G6 (CZH15575), G7 (CZH16083), G41 (CZH16082), G47 (CZH15452), **G15** (local check 2), G28 (CZH16076), G16 (CZH16066) and G35 (SC403) were the best performers. Therefore, these selected best performing hybrids under each stress and non-stress conditions excluding the checks are recommended for further evaluation and testing in advanced multi-environmental trials.

References

Abdel-Moneam, M. A., Sultan, M. S. Sadek, S. E. and Shalof, M. S. 2014. Estimation of heterosis and genetic parameters for yield and yield components in maize using the diallel cross method. Asian Journal of Crop Science 6:101-111.

Abdurakhmonov, B. Y. and Abdukarimov, A. 2008. Application of association mapping to understanding the genetic diversity of plant germplasm resources. International Journal of Plant and Genomics 2008:1-8.

Abdurhaman, B. 2009. Genotype by environment interaction and yield stability of maize genotypes evaluated in Ethopia. MSc Thesis, Department of Plant Science/Plant Breeding. University of the Free State Bloemfontein, South Africa.

Abira, S., Vanniarajan, C. and Armugachamy, S. 2005. Genetic variability studies in (*Zea mays* L.) germplasm. Plant archieve 5:105-108.

Acura, M. and Kaya Y. 2008. Non-parametric stability methods for interpreting genotypes (*Triticum aestivum* L.). Genetics and Molecular Biology 31:906-913.

Adu, G. B., Akromah, R., Abdulai, M. S., Obeng-Antwi, K., Alidu, H. and Tengan, K. M. L. 2016. Traits association for improvement of extra-early maturing maize hybrids evaluated in the forest and transitional zones of Ghana. Australian Journal of Crop Science 10:1127-1135.

Akbar, M., Shakoor M. S., Husein A. and Sarwar, M. 2008. Evolution of Maize 3-Way Crosses through Genetic Variability, Broad Sense Heritability, Characters Association and Path Analysis. Journal of Agriculture Research 46:39-45.

Akcura, M.Y.,Kaya, Y. and Taner, S. 2005. Genotype by environment interaction and phenotypic stability analysis for grain yield of durum wheat in the Central Anatolian region. Turkey Journal of Agriculture 29:369-375.

Akintunde, A.N. 2012. Path Analysis Step by Step Using Excel. Journal of Technology and Science Technology 1:9-15.

Al-Tabbal, J. A. and Al-Fraihat, A. H. 2012. Genetic Variation, Heritability, Phenotypic and Genotypic Correlation Studies for Yield and Yield Components in Promising Barley Genotypes. Journal of Agricultural Science 4:193-210.

Al-Naggar, A. M. M., Shabana, R., Mahmoud, A. A., Abdel El-Azeem, M. E. M. and Shaboon S. A. M. 2009 Recurrent selection for drought tolerance improves maize productivity under low-N conditions. Egyptian Journal of Plant Reaserch Breeding 13:53-70.

Al-Naggar, A. M. M., Soliman, M. S. and Hashimi, M. N. 2011. Tolerance to drought at flowering stage of 28 maize hybrids and populations. Egyptian Journal of Plant Breeding 15:67-87.

Alvi, B. M. M., Rafique, M., Tariq, S., Hussain, A., Mahmood, T., and Sarwar, M. 2003. Character association and path coefficient analysis of grain yield and its components in maize (*Zea mays* L.). Pakistan Journal of Biological Science 6:136-138.

Aly, R. S. H., Metwali, E. M. R. and Mousa, S. T. M. 2011. Combining ability of maize (*Zea mays* L.) inbred lines for grain yield and some agronomic traits using topcross mating design. Global Journal of Molecular Science 6:1-8.

Aminu, D. and Izge, A. 2012. Heritability and Correlation Estimates in Maize (*Zea mays* L.) under Drought Conditions in Northern Guinea and Sudan Savannas of Nigeria. World Journal of Agricultural Sciences 8:598-602.

Anderson, W. F., Holbrook, C. C. and Wynne, J. C. 1991. Heritability and early-generation selection for resistance to early and late leafspot in peanut. Crop Science 31:588-593.

Asfaw, A. 2008. Assessment of yield stability in sorghum using univariant and multivariant statistical approaches. Hereditas 145:28-37.

Atlin, G. N. and Frey, K. J. 1990. Selecting oat lines for yield in low productivity environments. Crop Science 30:556-561.

Banziger, M., Edmeades, G. O. and Quarrie, S. 1997. Drought stress at seedling stage: Are there genetic solutions? In: Edmeades, G.O., M. Banziger, H. R. Mickelson and C.B. Pena-Valvidia (eds). Developing Drought and Low N Tolerant Maize. Proceedings of a Symposium, March 25-29, 1997, CIMMYT, El Batan, Mexico, D.F. pp 348-354.

Bekelo, A. and Rao, T. N. 2014. Estimates of heritability, genetic advance and correlation study for grain yield and its attributes in maize (*Zea mays* L.). Journal of Plant Science 2:1-4.

Bello, O. and Olaoye, G. 2009. Combining ability for maize grain yield and other agronomic characters in a typical southern guinea savanna ecology of Nigeria. African Journal of Biotechnology 8: 2518-2522.

Bello, O. B., Abdulmaliq, S. Y., Afolabi, M. S. and Ige, S. A. 2010. Correlation and path coefficient analysis of yield and agronomic characters among open-pollinated maize cultivar and their F1 hybrids in a diallel cross. African Journal of Biology 9:2633-2639.

Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmaliq, S. Y. and Mahamood, J. 2012. Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). International Journal of Plant Research 2:138-145.

Board, J. E., Kang, M. S. and Harville, B. G. 1997. Path analyses identify indirect selection criteria for yield of late-planted soybean. Crop Science 37:879-884.

Bocanski, J., Sreckov, Z. and Nastasic, A. 2009. Genetic and Phenotypic Relationship between Grain Yiled and Components of Grain Yiled of Maize (*Zea mays* L.). Genetika 41:145-154.

CIMMYT. 2000. CIMMYT-Zimbabwe: 2000 Research highlights. Harare, Zimbabwe.

Dagne, W. 2008. Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. Phillosophiae Doctor Department of Plant Science. University of the Free State, Bloemfontein, South Africa.

Dipika, S. M., Srikant, V. and Gedion, J. S. 2014. Inter-relationship and coefficeint analysis for different physiological and yiled contributing traits in maize. Annals of Plant and Soil Research 16:35-40

Ertiro, B., Beyene, Y., Das, B., Mugo, S., Olsen, M., Oikeh, S., Juma, C., Labuschagne, M. and Prasanna, B. 2017. Combining ability and testcross performance of drought-tolerant maize inbred lines under stress and non-stress environments in Kenya. Plant Breeding 136:197-205.

Falconer, D. and Mackay, T. 1996. Introduction to Quantitative Genetics. Longman, London.

Garg, H. S., Kumari, P., Bhattacharya, C., Panja, S. and Kumar, R. 2017. Genetic parameters estimation for yield and yield related traits in rice (*Oryza sativa* L.) with drought tolence traits under stress condition. Journal of crop and weed 13:83-88.

Geeth, K. and Jayaraman, N. 2000. Path analysis in maize (*Zea mays* L.). Agriculture Science Digest 20:60-61.

Gissa, D. W., Zelleke, H., Abakemal, D., Hussien, T. and Singh, H. 2008. The combining ability of maize inbred lines for grain yield and reaction to grey leaf spot disease. East African Journal of Science 2:135-145.

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, Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein, South Africa.

Hallauer, A. R. and Miranda, J. B. 1988. Quantitative Genetics in Maize Breeding. Second edition. Iowa State University Press, Ames, Iowa.

Hossain, M. S. and Joarder, O. I. 2006. Genetic variability, correlation and path analysis in some quantitative traits in wheat. Bangladesh Journal of Crop Science 17:1-6.

Hussain, N., Khan, M. Y. and Baloch, M. S. 2011. Screening of maize cultivar for grain yield at Dera Ismail Khan. Journal of Animal and Plant Science 21:626-628.

Kang, M. S. 1994. Applied Quantitative Genetics. M.S. Kang Publishers, Baton Rouge.

Kashiani, P., Saleh , G., Abdullah, S. N., and Abdullah, N. A. P. 2008. Performance, heritability correlation studies on sweet corn inbred lines. Proceedings of the 10th Symposium of the Malaysian Society of Applied Biology, 6-8 November 2008, Malaysia. pp 48-49.

Khan, N. I., Iqbal, N. and Fazal, S. 2000. Factor analysis of seed yield in linseed. Pakistan Journal of Biological Science 3:328-329.

Khan, N. I., Din, F., Naseerrullah, M. and Shahid, M. T. H. 1998. Genetic variability and association of traits in linseed (*Linum usitatissimum* L.). Journal of Agricultural Research 36:83-87.

Khorgade, P. W. and Pillai, B. 1994. Genetic variability studies in linseed. Agriculture Science Digest 14:54-56.

Knife, H. and Tsehaye, Y. 2015. Studies of heritability, genetic parameters, correlation and path coefficient in elite maize hybrids. Academic Research Journal 3:296-303.

Laghari, K. A, Sial, M. A., Arain, M. A., Mirbahar, A. A., Pirzada, A. J., Dahot, M. U. and Mangrio, S. M. 2010. Heritability studies of yield and yield associated traits in bread wheat. Pakistan Journal of Botany 42:111-115.

Lorenzana, R. E. and Bernardo, R. 2008. Genetic Correlation between Corn Performance in Organic and Conventional Production Systems. Crop Science 48:903-910.

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

Mahmood, Z., Malik, Z. R., Akhtar, R. and Rafique, T. 2004. Heritability and genetic advance estimates from maize genotypes in Shishi Lusht, a Valley of Krankurm. International Journal of Agricultural Biology 6:790-791.

Makumbi, D., Diallo, A., Kanampiu, K., Mugo, S. and Karaya, H. 2015. Agronomic performance and genotype by interaction of herbicides-resistance maize cultivar in eastern Africa. Crop Science 55:540-555

Morakinyo, J. A. 1996. Heritability, Correlation and expected responses to selection of some yield components in grain sorghum (*Sorghum bicolor* L. Moench). Niger Journal of Genetics 11:48-54.

Muchie, A. and Fentie, D. 2016. Performance Evaluation of Maize Hybrids (*Zea mays* L.) in Bahir Dar Zuria District, North Western Ethiopia, Department of natural sciences, Addis Zemen Preparatory school, Addis Zemen Ethiopia. International Research Journal of Agricultural and Soil Science 3:37-43.

Muhammad, B. A., Tariq, M., Nwara,M., Muhammad, L., Muhammad, S. and Jafar, S. 2003. Linseed Improvement Through Genetic Variability, Correlation and Path Coefficient Analysis. International Journal of Agricultural Biology 5:303-305.

Muhammad, B. A., Muhammad, R., Muhammad, S. T, Amerr, H., Tariq, M. and Muhammad, S. 2003. Character association and path coefficient analysis of grain yield and yield components in maize (*Zea mays L.*). Pakistan Journal of Biological Science 6:136-138.

Muhammad, B. A., Shakoor, M. S., Amber, H. and Muhammad, S. 2008. Evaluation of maize three way cross through genetic variability brod sense heritability, character association and path analysis. Journal of Agriculture Research Lahore 46:399-415.

Muluken, B. 2009. Analysis and correlation of stability parameters in malting barley. African Crop Science Journal 17:145-153

Nelson, D. W. and Somers, L. E. 1992. Total carbon, total organic carbon and organic matter. Methods of soil analysis, Part 2, 2nd ed. Agronomy Monograph, 27, ASA, Madison, Wisconsin. USA. pp 539-580.

Nyombayire, A., Edema, R., Asea., G. and Gibson, P. 2011. Combining ability of maize inbred lines for performance under low nitrogen and drought stresses. African Crop Science Society 10:1-4.

Olakojo, S. A. and Olaoye, G. 2011. Correlation and heritbaility estimates of maize agronomic traits for yield improvement and *Striga asiatica* [(L.) Kuntze] tolerance. African Journal of Plant Science 5:365-369.

Paul, S., Bhateria, S. and Kumar, A. 2015. Genetic variability and interrelationship of seed yield and yield components in linseed (*Linum usitatissimum* L.). Crop Science 47:375-383.

Payne, R. W., Murray, D. A., Harding, S.A., Baird, D. B. and Soutar, D. M. 2009. GenStat for Windows (12th ed.) Introduction. VSN International, Hemel Hempstead.

Prakash, V. 2006. Genetic divergence and correlation analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Crop Improvement 33:175-180.

Rafiq, C.M., Rafique, M., Hussain, A. and Altaf, M. 2010. Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). Agricultural Research 48:35-38.

Rafique, M., Hussain, A., Manmood, T., Alvi, A. W. and Alvi, B. 2004. Heritability and interrelationships among grain yield and yield components in maize (*Zea mays* L.). International Journal of Agricultural Biology 6:1113-1114.

Rahman, M. S., Hossain, M. S., Islam, M.S., Shoma, J. F. and Ali, L. 2014. Genetic variability correlation and path analysis for some quantintative traits in wheat. Eco-friendly Agriculture Journal 7:158-162.

Robinson, H. F., Comstock, R. E and Harvey, R. H. 1949. Estimation of heritability and the degree of dominance in corn. Agronomy Journal 41:353-359.

SAS Institute Inc. 2010. SAS/STAT® 9.3 User's Guide . Cary, NC: SAS Institute Inc.

Selvaraj, C. and Nagarajan, P. 2011. Interrelationship and Path-Coefficient Studies for Qualitative Traits, Grain Yield and Other Yield Attributes among Maize (Zea Mays L.). Journal of Plant Breeding and Genetics 10:56-63.

Shahrokhi, M. and Ebrahimi S. K. A. 2013. Study of Genetic Components in Various Maize (Zea Mays L.) Traits, Using Generation Mean Analysis Method. International Journal of Agronomy and Plant Production 4:405-412.

Shoran, J. and Tandon, J. P. 1995. Genetic divergence in winter wheat (*Triticum aestivum* L.). Indian Journal of Genetics 55:406-409.

Singh, B. 2000. Plant Breeding: principles and methods 6th ed. Kalyani Publishers, New Delhi.

Singh, G., Singh, M. and Dhiman K. P. 1995. Genetic analysis of maize (Zea mays L.) in Sikkim. Indian Journal of Agricultural Science 65:293-249.

Singh, P., Dass, S., Kumar, Y. and Dutt, J. Y. 2003. Variability studies for grain yield and component triats in maize (*Zea mays* L.). Annals Agricultural Biological Research 8:29-31.

Singh, R. K. and Chaudhary, B. D. 2004. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India.

Singh-Jakhar, D., Singh, R. and Kumar, A. 2017. Studies on Path Coefficient Analysis in Maize (*Zea mays* L.) for Grain Yield and Its Attributes. International Journal of Current Microbiology and Applied Science 6:2851-2856.

Solomon, A., Mandefro, N. and Habtamu, Z. 2008. Genotype-environment interaction and stability analysis for grain yield of maize (*Zea mays* L.) in Ethiopia. Asian Journal of Plant Sciences 2:163-169.

SPSS. 2014. Statistics for Windows, version 25 (SPSS Inc., Chicago, Ilinois., USA). http://www-01.ibm.com/support/docview.wss?uid=swg21476197.

Sridhar, M., Muralikrishna, K. Sultana, R. and Bhave, M. H. V. 2016. Character association and path analysis for grain yield and yield component traits in popcorn (*Zea mays* var. *everta* Sturt.). International Journal of Agricultaral Science and Research 6:145-150.

Tyagi, A., Pokhariyal, G. and Odongo, O. 1998. Correlation and path coeffiencient analysis for yield components and maturity traits in maize. Maydica 33:109-119.

Tyagi, S. D. and Khan, M. H. 2010. Studies on genetic variability and interrelationships among the different traits in microsperma lentil (*Lens culinaris* Medik.). Bulgarian Journal of Agricultural Science 16:30-35.

Ud-Din. N., Carver, B.F. and Clutter, A.C. 1992. Genetic analysis and selection for wheat yield in drought stressed and irrigated environments. Euphytica 62:89-96.

Ullah, K., Noor M. and Iqbal M. 2013. Heritability Estimates and Yield Performance of Half Sib Families Derived from Maize Variety Sarhad White. Sarhad Journal of Agriculture 29:29-32

Vashistha, A., Dixit, N. N., Dipika, S., Sharma, K. and Marker, S. 2013. Studies on heritability and genetic advance estimates in maize genotypes. Bioscience Discovery 4:165-168.

Vejay, K., Rao, S. V. and Mansinklal, S. W. 1975. Study of variability and character association analysis in linseed (*Linum usitatissimum* L.). Mysore Journal of Agriculture 9: 236-245.

Vijayabharathi, A., Anandakumar, C. R. and Gnanamalar, R. P. 2009. Analysis of correlations and path effects for popping expansion in popcorn (*Zea mays* var. *everta* Sturt*.).* Journal of Plant Breeding 1:60-64.

Wannows, A. A., Azzam, H. K. and Al-Ahmad, S. A. 2010. Genetic variances, heritability, correlation, and path coefficient anlysis in yellow maize crosses (*Zea mays* L.). Agriculture and Biology Journal of North America 1:630-637.

Waqar-Ul-Haq, M., Malik, F., Rashid, M. Munir, M. And Akram, Z. 2008. Evaluation and estimation of heritability and genetic advancement for yield related attributes in Wheat Lines. Pakistan Journal of Botany 40:1699-1702.

Yadav, T. P. and Dalal, T. L.1972. Genetic variability and correlation studies in linseed (*Linum usitatissimum* L.). Punjab Agricultural University Journal of Research 11:35-39.

CHAPTER FOUR

Genotype by Environment Interaction and Stability of Early Maturing Maize (*Zea Mays* L.) Hybrids across Stress and Non-Stress Environments

ABSTRACT

The study of genotype by environment interaction and stability of grain yield across stress and non-stress conditions was carried out on 50 early maturing maize hybrids. The plant materials included 44 experimental hybrids from CIMMYT-Zimbabwe and 6 commercial checks from the region. The experiment was conducted under low N, managed drought and two optimum environments around South Africa during the 2016-2017 planting season, using a 10 x 5 (0.1) alpha lattice design with two replications. Analysis of variance at all individual environments showed that the genotype mean squares were significant ($P<0.01$). The analysis of variance across environments showed that the genotype, environment and genotype by environment interaction mean squares were highly significant ($P<0.01$) for grain yield. The contribution of the genotype, environment and genotype by environment interaction to grain yield variation was about 6.36, 77.96 and 11.81%, respectively. The genotype and genotype by environment interaction were partitioned using the GGE biplot model, where PC1 and PC2 accounted for 35.97 and 28.83% of variability, respectively. The following hybrids were highly adapted to the respective environments: CZH15448, CZH16073, CZH16074, CZH15499, and CZH15452 under optimum conditions at Cedara; CZH15574, CZH16069 excluding the checks, local check 1 (WE3128) and SC301, and CZH16080 under optimum conditions at Potchefstroom; CZH16093, CZH15575, CZH16068 and CZH15600 excluding the local check 2 (WE4145) under low N at Cedara; and CZH16094, CZH15184, CZH16082, CZH16076 and CZH16065 under managed drought at Lutzville. The GGE biplot analysis identified nine genotypes CZH15575, CZH15574, CZH16093, CZH16069, CZH16068, CZH15600, CZH16080, CZH15452 and CZH16076 as the best performing and stable across environments. These hybrids would contribute to high maize yields and stable grain production in specific or across environments.

Keywords: Drought, Early maturing, GGE biplots, Grain Yield, Low N.

4.1 Introduction

Maize (*Zea mays*) crop in Africa is the most important staple food source with high potential for productivity and production. Global ecological and demographic revolution introduced the maize crop in Africa during the 15th century (McCann, 2005). According to Badu-Apraku *et al.* (2010), maize production has gone down to 7% in the last decade due to increasing population. The existing local cultivars grown by African farmers are the product of natural out-crossing and farmers' selection to fit in the different farming systems (Menkir *et al.*, 2008) and meet various climatic conditions (Sanou *et al.*, 1997; Menkir *et al.*, 2008). These local maize cultivars provide good sources of germplasm to breed for broad adaptation to demanding growing environments (Framkel *et al.*, 1998; Menkir *et al.*, 2008).

Climate change is currently the world's greatest challenge, which increases biotic, abiotic and socio-economic factors that have adverse effect on yield of many crops. Banks (2015) stated that expansion of irrigation in developing countries is limited due to the large number of farmers requiring water supply. Using genetics to enhance drought, low N tolerance and offer grain yield stability is an important part in stabilising global production. Sustainable genetic improvement of maize can be achieved through selection of low N and drought tolerance alleles. Ceccarelli *et al.* (1992) and Menkir *et al.* (2008) reported that farmers' local varieties can be valuable sources of distinctive physiological traits and alleles for adaptation to drought tolerance, which are not present in the current improved early maturing maize cultivars.

Improved maize hybrids and landraces display a broad range of sensitivity to drought stress which is ideal for further evaluation (Blum *et al.*, 1991; Denčić *et al.*, 2000; Menkir and Akintunde, 2001; Menkir *et al.*, 2009). Improvement for drought tolerance can also bring about specific adaptation and superior performance under low N conditions, signifying that tolerance to either stress involves a common adaptive mechanism (Bänziger *et al.*, 1999; Badu-Apraku *et al.*, 2010). Badu-Apraku *et al.* (2010) stated that under field conditions, drought and low N can occur concurrently, which leaves a devastating effect to crop production. Through recognition of the significant influence of the multiple stress conditions, CIMMYT-Zimbabwe has developed maize source populations and hybrids that combine earliness or extra-earliness with multiple stress tolerance. Multi-environments evaluation is necessary to estimate the importance of genotype by environment interaction and to identify genotypes that have broad adaptation and those that have specific adaptation. Gauch and Zobel (1996; 1997) defined a mega-environment as a portion of a crop species' growing region with a homogenous environment in which some genotypes perform similarly. Setimela *et al.* (2007) used the maize multi-environment trials data set by CIMMYT-Zimbabwe and agro-climatic data to identify maize mega-environments for sub-Saharan Africa including West Central Africa.

The multi-environmental trials usually show significant genotype by environment interactions due to the response of cultivars to different growing conditions (Badu-Apraku et al., 2010; Workie *et al.* 2013). This has justified extensive testing of hybrids in multiple environments over several years to support decisions on cultivar recommendations. Genotype by environment interaction reduces the correlation between the phenotypic and genotypic values (Comstock and Moll, 1963; Akcura *et al.* 2005; Badu-Apraku *et al.*, 2011) and obscures the selection of the best genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Epinat-Le Signor *et al.* (2001) reported that identification of a combination of genotypic traits expressivity contributing to genotype by environment interaction for grain yield facilitates the biological explanation of the results of genotype by environment interaction analysis and identification of superior, stable hybrids and inbred lines for hybrid production and development of synthetics.

The GGE biplot methodology proposed by Yan *et al.* (2000) is a great statistical tool to analyse and identify the best performing cultivars in any given environment. This tool is also most suitable for each cultivar assessment of any pair of hybrids in individual environments and combination of hybrids stability and yield under different environments. It provides an opportunity for differentiation of the best hybrids for each environment and mega-environments, and gives information on the discriminating ability and representativeness of the environments (Yan et al. 2000). Therefore, the objective of this study was to evaluate 50 early maturing maize hybrids for genotype by environment interaction and yield stability across stress and non-stress environments.

4.2 Materials and Methods

4.2.1 Germplasm

Germplasm and list of hybrids used and their sources are as presented in section 3.2.1.

4.2.2 Experimental sites

Experimental sites and characterization of environmental conditions are as presented in section 3.2.2.

4.3 Field trial design and management

Field trial design and management are as presented in section 3.3.

4.4 Data collection

Data were collected for grain yield (GY) on per plot basis in all the environments. The weight of grain per plot after shelling was determined and used to calculate GY per hectare adjusted to 12.5% moisture content, as follows:

$$GY = GW \times \frac{100 - MC}{100 - 12.5} \times \frac{1000}{Plotarea}$$

Where, GW = grain weight after shelling, MC = grain moisture content of the shelled grain.

4.5 Statistical Analyses

4.5.1 Analysis of variance

To determine the effects of genotype by environment interaction for grain yield, the data were first subjected to analysis of variance using GenStat software 14th edition (Payne *et al.* 2009). Analyses were done for across and individual environments to test the levels of significance (Table 4-1 and 4-2).

The following ANOVA model was used for the combined analysis across environments:

$$Y_{ijkl} = \mu + r_j + B_K + S_l + H_i + SH_{il} + \varepsilon_{ijkl}$$

Where; Y_{ijkl} = main effect; μ = overall mean or grand mean; r_j = number of replications; B_k = effect of the kth block nested in jth replication and k = 1,2,3…10, while j = 1,2; S_l = the effect the l^{th} environment and l =1,2,3,4; H_i = the effect of the i^{th} hybrid and i=1,2,3…50; SH_{il} = interaction effect of the i^{th} hybrid and l^{th} environment, and ε_{ijkl} = random error. The hybrid means were ranked according to yield, which was the principal selection criterion at all sites.

The following model for single site ANOVA was used.

$$Y_{ijk} = \mu + H_i + r_j + B_{K(j)} + \varepsilon_{ijk}$$

Where; Y_{ijk} = the individual observation in each plot; μ = grand mean for each variable; H_i = the effect of the i th hybrid and i =1,2,3…50; r_j = 2 number of replications and j = 1,2; $B_{k(j)}$ = estimate of the incomplete block within replication and k = 1,2; and ε_{ijk} = overall random error effect.

4.5.2 GGE biplot analysis

The GGE biplot analysis was performed using R statistical package GEAR R version 4.0 (Pacheco *et al*., 2015). It was used to generate graphs showing (i) "which-won- where", (ii) discriminative versus representative and (iii) means versus stability (Yan and Kang, 2003). The GGE biplot represents the first two principal components (PC1 and PC2, referred as primary and secondary effects, respectively) derived from subjecting environment centered yield data (yield variation due to GGE), to singular value de-composition (Yan *et al.,* 2000).

The following model for GGE biplot was used:

$$\frac{Y_{ij-}Y_j}{S_j} = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where, Y_{ij} = the average yield of genotype i = in the environment; Y_j = the average yield across all genotypes in environment j; S_j = the standard deviation in environment j; λ_1 and λ_2 = the singular values for PC1 and PC2; ξ_{i1} and ξ_{i2} = PC1 and PC2 scores, for genotype i ; η_{j1} and η_{j2} = PC1 and PC2 scores, for environment j; and ε_{ij} = the residual of model associated with the genotype i in the environment j. The data were not transformed but standardised and environmental centered.

4.6 Results

4.6.1 Agronomic performance for grain yield

Analysis of variance for agronomic performance for individual and across environments detected highly significant (P≤0.01) differences among the experimental hybrids and checks for grain yield (Tables 4-1 and 4-2). Across environments, ANOVA also revealed highly significant (P≤0.01) effects of environments and genotype by environment interaction (Table 4-1). The contribution of the genotype, environment and genotype by environment interaction to grain yield variation was about 6.36, 77.96 and 11.81%, respectively

Table 4-1 Combined ANOVA for effects of genotype, and genotype by environment on maize grain yield across four environments

Source of variation	DF	Sum of Squares	Mean Square	SST%
Replication	1	1.38	1.38**	0.03
Replication*Incomplete block	8	33.58	4.20**	0.75
Genotype	49	285.89	5.83**	6.36
ENV	3	3505.67	1168.56**	77.96
Genotype*Environment	147	531.21	3.61**	11.81
Residual	191	138.80	0.73	3.09
Total	399	4496.53	11.27	

DF=degree of freedom, SST%= percentage sum of squares total, **, indicate level of significance of the data is P=0.01.

Table 4-2 ANOVA for grain yield in each environment

Source of variation	DF	Cedara (Low N)	Cedara (Opt)	Lutzville (MD)	Potchefstroom (Opt)
Replication	1	0.98ns	0.90ns	0.15ns	7.29 **
Replication*Incomplete block	8	0.60**	17.91**	1.69**	2.31**
Genotype	49	1.29**	7.39**	1.82**	3.63**
Residual	41	0.20	1.67	0.17	0.63
Total	99	0.78	5.80	1.11	2.32

DF=degree of freedom, OPT=optimum, LN=low nitrogen, MD=managed drought, ** indicate level of significance of the data at P=0.01. ns indicates non-significant at 5% probability level.

4.6.2 Genotype performance

The mean grain yield of the hybrids are represented in Table 4-3 for each environment and across environments. Observed grain yield means ranged from 3.39-7.13 t ha^{-1} across the environmental conditions. Individual grain yield means for each environment ranged from 0.60-4.3, 0.85-10.3, 1.30-5, to 6.95-14.3 t ha^{-1} under Cedara (Low N), Cedara (Optimum), Lutzville (Managed drought) and Potchefstroom (Optimum), respectively. The best performing hybrids for are underlined and bolded according to the mean grain yield of the environment represented in the Table 4-3.

Table 4-3 Mean grain yields (t ha-1) of 50 early maturing hybrids at individual environments and across four environments in 2016/17

	Environments				**Mean GY across environments**
Genotype	**Cedara (Low N)**	**Cedara (Opt)**	**Lutzville (MD)**	**Potchefstroom (Opt)**	
G1	1.55	7.50	1.30	8.95	4.83
G2	2.15	6.75	1.15	9.75	4.95
G3	2.10	4.85	1.75	8.35	4.26
G4	0.60	6.50	1.50	9.20	4.45
G5	1.95	7.15	1.90	9.55	5.14
G6	3.80	7.45	3.30	11.65	**6.55**
G7	3.15	1.80	3.20	7.70	3.96
G8	3.15	6.25	2.25	8.70	5.09
G9	2.30	7.80	1.60	10.20	5.48
G10	1.40	7.70	3.20	9.55	5.46
G11	1.10	4.90	2.20	7.85	4.01
G12	2.20	9.90	3.40	9.10	6.15
G13	1.70	6.60	2.20	**14.30**	**6.20**
G14	2.10	5.95	2.85	11.85	5.69
G15	3.05	8.50	4.90	11.80	**7.06**
G16	1.50	4.00	1.15	8.75	3.85
G17	2.30	6.10	3.55	10.50	5.61
G18	2.40	8.20	2.15	9.25	5.50
G19	1.70	1.10	1.25	9.50	3.39
G20	0.65	0.85	2.20	9.95	3.41
G21	2.55	7.30	1.45	12.35	5.91
G22	3.30	5.20	3.40	11.60	5.88
G23	3.75	8.95	2.35	11.05	**6.53**
G24	1.45	4.50	4.85	8.85	4.91
G25	2.05	3.90	3.70	9.55	4.80

	Environments				**Mean GY across environments**
Genotype	**Cedara (Low N)**	**Cedara (Opt)**	**Lutzville (MD)**	**Potchefstroom (Opt)**	
G26	3.15	3.75	2.50	7.80	4.30
G27	2.20	3.90	2.30	8.40	4.20
G28	2.55	5.95	3.70	9.10	5.33
G29	2.60	4.65	1.30	10.30	4.71
G30	2.25	6.60	2.05	10.05	5.24
G31	2.60	3.95	1.60	9.50	4.41
G32	2.65	7.25	2.20	8.85	5.24
G33	**4.30**	1.65	3.25	9.55	4.69
G34	2.20	6.90	1.50	11.2	5.45
G35	1.80	3.20	**5.00**	8.85	4.71
G36	2.70	3.65	2.15	7.60	4.03
G37	4.05	5.80	3.90	8.00	5.44
G38	2.40	5.70	1.65	8.35	4.53
G39	2.40	6.25	1.40	9.70	4.94
G40	3.45	9.30	1.80	10.95	**6.38**
G41	3.55	1.05	3.65	10.00	4.56
G42	2.05	6.55	2.15	9.60	5.09
G43	1.65	6.25	3.25	6.95	4.53
G44	1.50	4.85	3.25	8.70	4.58
G45	2.40	6.95	2.15	9.15	5.16
G46	3.00	**10.3**	3.55	**11.65**	**7.13**
G47	3.55	7.52	1.35	9.60	5.50
G48	2.25	5.90	2.35	9.15	4.91
G49	3.15	6.85	2.60	10.8	5.85
G50	2.90	7.25	1.90	8.45	5.13
Mean	2.43	5.83	2.51	9.64	
Maximum	4.30	10.30	5.00	14.30	
Minimum	0.10	0.30	0.80	6.70	
%CV	18.58	22.12	16.53	8.25	
SE	0.45	1.29	0.41	0.79	
L.S.D	0.91	2.61	0.84	1.61	
F pr	<.001	<.001	<.001	<.001	

4.6.3 The GGE biplot analysis

The results are presented in three sections: the first represents “which won where” identifying the best genotype for each environment; second section represents the discriminative and representative of genotypes among environments; the last section shows the genotype performance and their stability.

4.6.3.1 ‘Which-won-where’ biplot

The GGE biplot analysis was used to identify the best hybrids at each environment and to assess their stability. The biplot analysis gave a good visual assessment of genotype by environment interaction which explained 64.80% (PC1=35.97and PC2=28.83%) of the total variation for grain yield across the test environments (Figure 4-1). Based on the environments used in this study, the results revealed four sectors with each environment falling in a different sector and thus showing different winning genotypes for each environment (Figure 4-1). The winning genotypes are located at the vertices of the polygon. The vertex genotypes were G15, G33, G7, G20, G4, G13 and G46 (Figure 4-1) in different sectors. At Cedara (Opt) genotype G13; Potchefstroom (Opt) genotype G46; Cedara (Low N) genotype G15 and Lutzville (MD) genotype G33 were the winning genotypes. Genotypes G7, G20 and G4 were poorest in all the four environments.

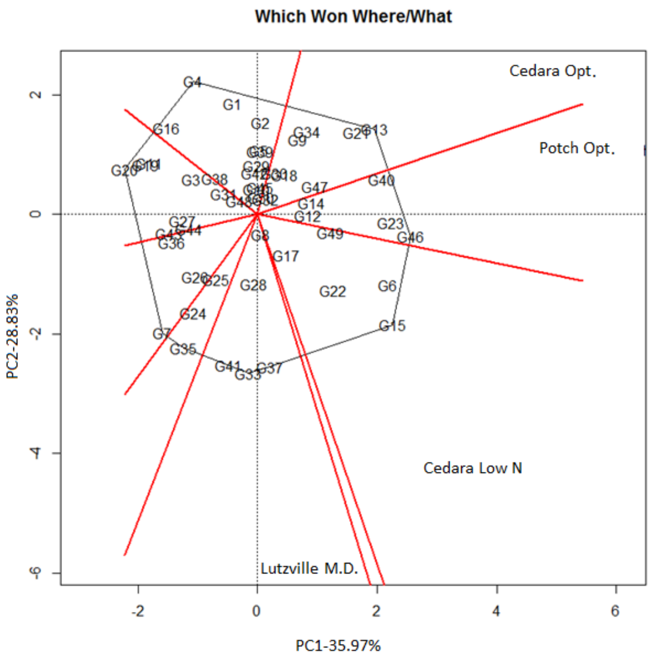

Figure 4-1 A polygon view of the GGE Bi-plot showing the "which-won-where" using standardised data of 50 early maturing hybrids across four environments

4.6.3.2 Discriminative versus representative

Environment vectors were drawn from biplot origin to connect the environment markers (Figure 4-2). The correlation between environments is determined by the angle between their environment vectors (<90^0 - high correlation, = 90^0 - no correlation and >90^0 - negative correlation) as described by Yan and Holland (2010). The optimum environments Cedara (Optimum) and Potchefstroom (Optimum) were highly correlated with an acute angle between them, while Cedara (Low N) and Lutzville (managed drought) were highly correlated. In terms of discriminating ability (informative), the longer the environment vector from the biplot origin to the environment marker, the more discriminating it is of the genotypes. Lutzville (Managed drought) had the longest vector, thus highly discriminating of the genotypes. The other three environments Cedara (Low N), Cedara (Optimum) and Potchefstroom (Optimum) were more or less the same in terms of discriminating ability, all with relatively long vectors from the biplot origin. The distance between two environments measures their similarity or dissimilarity in discriminating the genotypes (Yan and Tinker, 2006). Cedara (Optimum) and Potchefstroom (Optimum) had the least distance between, while the greatest distance was observed between Cedara (Optimum) and Lutzville (Managed drought). The distance between Lutzville (managed drought) and Cedara (Low N) was shorter than the distance between Cedara (Low N) and both optimum environments (Cedara (Optimum) and Potchefstroom (Optimum)). For representativeness of the environments, an Average-Environment Axis (AEA, or average-tester-axis) was added. The average environment is represented by the small circle at the end of the arrow and has the average coordinates of all test environments, while the AEA is the line that passes through the average environment and the biplot origin. A test environment that has a smaller angle with the AEA is more representative of other test environments. Thus, Cedara (optimum)> Potchefstroom (Optimum)>Cedara (low N) were the most representative whereas Lutzville (MD) was the least representative.

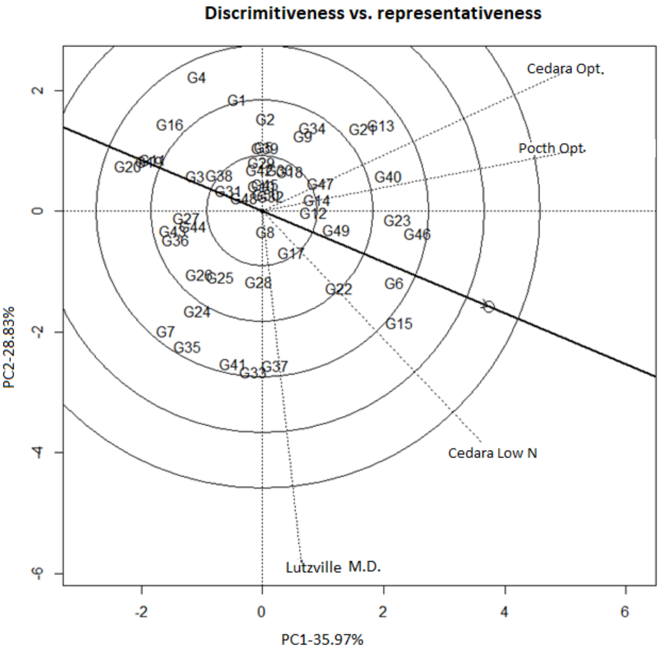

Figure 4-2 Ranking of environments based on discriminating ability and representativeness GGE biplot of grain yield for 50 early maturing maize hybrids evaluated across four environments in 2016/17

4.6.3.3 Means versus stability

The mean versus stability view biplot (Figure 4-3) was used to assess performance and stability of the 50 genotypes across the four environments. The axis of the average environment coordinates (AEC) abscissa, or the average environment axis, is the single-arrowed line that passes through the biplot origin and average environment, which is at the center of the small circle. The hybrids were ranked along the average environment axis, with the arrow pointing to a greater value based on the mean performance across all environments. G15 and G46 were the best performing genotypes for mean yield while G6, G49 and G12 were the most stable but G6 had a higher mean yield than G49 and G12. The top ten ranking genotypes in terms of mean yield were G15, G46, G6, G23, G40, G13, G21, G22, G49 and G47 while for stability (according to their projection onto the average environment axis) the top nine stable genotypes were G49, G6, G12, G8, G17, G46, G23, G47 and G22 (Figure 4-6). The checks were G15, G23 and G14.

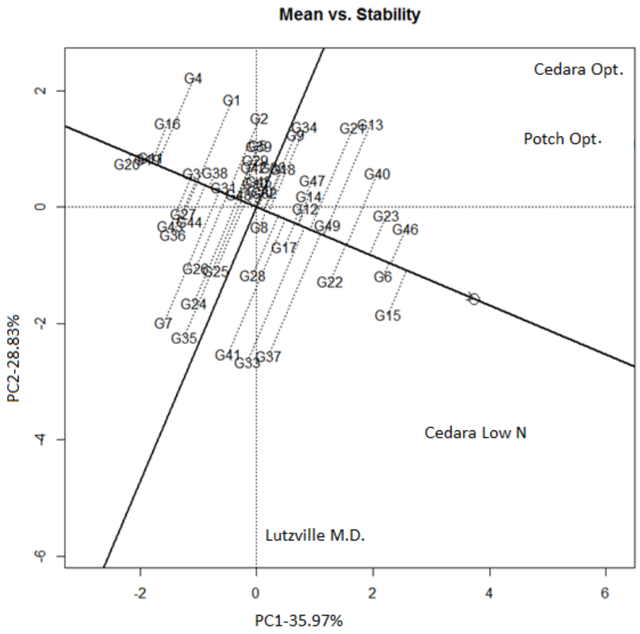

Figure 4-3 The mean vs stability view of the GGE biplot of grain yield for 50 early maturing hybrids evaluated across four environments in 2016/17

4.7 Discussion

4.7.1 Agronomic performance for grain yield

The highly significant (P<0.01) environmental mean squares for grain yield indicated that the environments contributed significantly to the total variation observed in the hybrid performance. The ANOVA for grain yield revealed that genotype, environment and genotype by environment interaction accounted for 6.36, 11.81 and 77.96% of the total sum of squares, respectively. According to Yan and Kang (2003), the environment contributes more to variation in multi-environment trials, but it is regarded as irrelevant for genotype evaluation to identify superior genotypes and to determine mega-environments in a targeted region. This is the reason that environment is removed from the phenotypic data observed in GGE biplot analysis and the focus is on genotype and genotype by environment interaction effect, which are relevant for genotype evaluation (Yan and Kang, 2003; Fan *et al.,* 2007; Solonechnyi *et al.,* 2015). This highly significant genotype, genotypes by environment interaction for grain yield under the individual and across all environments confirmed the differences among the environments in terms of the stresses and the weather variation the genotypes were exposed to, resulting in the different performance of the genotypes. The best basis for selection is the mean grain yield and stability of the genotypes in the environments. Comstock and Moll (1963) reported that the presence of genotype by environment interaction complicates the selection process as it reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values. One check which has been bolded out yielded the tested maize hybrids in Cedara under optimum. Maize genotypes performance in each environment were as follows: Cedara (low N) G33, G49, G37; Cedara (Optimum) G18, **G23**, G32, G10, G1; Lutzville (Managed drought) G24, G37, G28, G10; and Potchefstroom (Optimum) G13, G21, G46, G6, G49.

4.7.3 The GGE biplot analysis

The GGE biplot was constructed by using GEA-R statistical tool that had the first two principal components PC1 (35.97%) and PC2 (28.83%) gave a total variation of 64.8% for grain yield across the test environments. Yan (2000), Yan *et al*. (2007), Yan (2014) and Solonechnyi *et al*. (2015) stated that the GGE biplot graphically displays genotype plus genotype by environmental interaction of the multi-environmental trial data in a way that facilitates visual genotype evaluation and the mega-environment identification.

4.7.3.1 Which-won-where biplot

The GGE biplot analysis was used to identify the best hybrids in each environment and assess their stability, and the biplot accounted for 64.8% of total variation across environments (Figure 4-1). The biplot indicated the best performing hybrids for each environment and the groups of environments. The rays divided the polygon view into nine sections with the four environments appearing in four sectors. Thus, based on the result there could be four mega environments present, each with its own winning genotype. This also shows presence of crossover GEI. It is also possible to group the environments into two mega environments based on their similarities with mega environment one comprising of Cedara (optimum) and Potchefstroom (optimum) and mega environment two comprising of Cedara (low N) and Lutzville (managed drought). The vertex genotypes were G13 (CZH15448), G46 (CZH15574), G15 (local check 2), G33 (CZH16094), G7 (CZH16083), G20 (CZH16090) and G4 (CZH16089). Yan *et al.* (2000) pointed out that the vertex genotypes in each sector represent the highest yielding genotypes in the environments that fell within that particular sector. Thus, G13 at Cedara (optimum), G46 at Potchefstroom (optimum), G15 at Cedara (low N) and G33 Lutzville (managed drought) were the highest yielding hybrids. Genotypes G4, G20 and G7 did not have any environments falling in the sectors where they were located, suggesting that they were low yielding genotypes in some or all the environments. The following hybrids were adapted to specific environments: G26 (CZH16070), G34 (CZH16074), G9 (CZH15499) and G18(CZH16071) at Cedara (optimum); G46 (CZH15574), G40 (CZH16069) and G12

(CZH16080) excluding the checks G23 (local check 1) and G14 (SC301) at Potchefstroom (optimum); G22 (CZH16093), G6 (CZH15575), G49 (CZH16068) and G17 (CZH15600) excluding the check G15 (local check 2) at Cedara (low N) and G33 (CZH16094), G37 (CZH15184), G41 (CZH16082), G28 (CZH16076) and G8 (CZH16065) at Lutzville (managed drought). While the other hybrids were located within, the polygon and most of them near the plot origin suggesting that they are more adapted to low yielding environments than the vertex hybrids. According to a study done by Solonechinyi *et al*. (2015) the results, findings were the same. That means that the yield capacity of this genotype was the highest in the particular environment. Sserumaga *et al.,* (2015) reported similar findings that different altitudes were distinct from the test environments. Genotypes within the polygon, especially those located near the point of origin are less responsive than the vertex genotypes (Yan *et al*., 2000) which is similar to the study.

4.7.3.2 Discriminating versus representative

To show the discriminating ability and representativeness of the trial environments, environmental vectors are drawn from the biplot origin to connect the environment markers. All the environments had a positive PC1 score suggesting good discriminating ability. The cosine of an angle between environment vector were used for evaluating the correlation between them; the smaller the angle between environment vectors the larger the correlation between them (Yan and Holland, 2010; Solonechnyi *et al*., 2015). Thus the angle between the four environments in the study was less than 90^0 suggesting that there was high correlation between them. The length of the vector from the biplot origin to the environment marker approximates the standard deviation of the test environment. According to Yan *et al*. (2010), shorter environmental vectors indicate the specific environments are not strongly correlated with the environments with the longer vectors and that they were probably not strongly correlated with one another either. A long environment vector represented a good discriminating ability for a given environment. A discriminant test environment accurately resolves genotype differences, thereby having better capability versus the environments with low discriminating capability and lack of representativeness, which might give misleading results. Similar research finding were done by Abakemal *et al.* (2016) suggesting that a lack of discriminating power of the environments is generally attributed to unfavourable seasonal conditions and therefore, genotypic differences based on short environmental vectors may not be reliable. In this study, it was observed that the least discriminating environments, which had shorter vectors and located closer to the biplot origin, were mainly stress environments, including low N and managed drought stress, which is similar to the research finding of Yan et al., (2007). It is therefore impossible to obtain adequate information on the differences in the performance of all genotypes within these environments. Based on the study, Lutzville (Managed drought) had the longest vector, which had the most discriminating on the genotype (G33, G37, G28 and G8) than Cedara (low N), Potchefstroom (Optimum) and Cedara (Optimum) which had the lowest discriminating power. Respectively, there was a strong correlation between Cedara (Optimum) and Potchefstroom (Optimum). The environments could be ranked as follows in terms of their discriminating ability: Lutzville (managed drought)>Cedara (low N)>Potchefstroom (optimum)>Cedara (optimum). According to Yan and Kang (2003), environments with long vectors and small angles with the AEC abscissa are more representative of mega environments and are ideal for testing and selecting superior genotypes. In this study, the most representative environments were Potchefstroom (optimum) and Cedara (low N). The biplot measures representativeness of the environments by identifying an average environment and using it as a reference for comparison. According to Solonechnyi *et al*. (2015), a test environment with a small angle to average environment coordinate is the most representative related to the test environment. The ideal environment is the most discriminating for the genotypes and yet representative of the other test environments. Thus, in this study, Potchefstroom (Optimum) and Cedara (low N) were the most desirable for selecting the genotypes, hence the best environments for genetic differentiation of experimental hybrids.

4.7.3.4 Mean versus stability

The GGE biplot ranks genotypes by their mean yield capacity and stability in a number of environments. The average tester coordinates x-axis (ATC) or the performance line passes through the biplot origin with an arrow indicating the positive end of the axis and ranks genotypes according to performance. Thus, the average environment coordinate (AEC) is represented by a small circle that is defined by the average PC1 and PC2 scores of all environments. According to Yan *et al*., (2007) and Makumbi *et al.,* (2015) reported that the axis of the AEC that passes through the biplot origin is perpendicular to the AEC abscissa. The mean yield capacity of the genotypes is estimated by the projection of their markers to the average tester coordinates x-axis. The closer the genotype to the circle indicates higher mean grain yield. Genotype G15 (local check 2) had highest mean grain yield and G19 (CZH16091) had lowest mean grain yield. An ideal genotype should have both high mean grain yield and high stability within a mega environment (Yan and Tanker 2006; Makumbi *et al.,* 2015; Sserumaga *et al.,* 2015; Solonechnyi *et al.,* 2015).

Nine stable and high yielding hybrids were identified as follows: G6 (CZH15575), G46 (CZH15574), G22 (CZH16093), G49 (CZH16068), G12 (CZH16080), G17 (CZH15600), G28

(CZH16076), G47 (CZH15452), and G8 (CZH16065) because of their short projection onto the AEC excluding the local checks G15 (local check 2), G23 (local check 1) and G14 (SC301). Hybrid G19 had low grain yield (3.39tha^{-1}) and high stability while G48 had the averaged grain yield (4.91tha^{-1}) and low stability. Hence, in breeding perspective hybrids G19 and G48 are not desirable for selection because farmers are looking for stable and high yielding hybrids. Generally, hybrid G6 with acceptable stability and good yield is the best genotype characterized by its projection against the y-axis, hence the more projection of the hybrid the more stable the hybrid, which is line with the work of Yan *et al.* (2007).

4.8 Conclusion

Analyses of variance across environments for grain yield revealed that genotype by environment interaction played an important part in the selection of the best genotype in terms of stability and high grain yield. The study on mean performance and stability identified nine maize hybrids with high mean grain yield and stability across environments, suggesting that these varieties would contribute to high maize grain yields under multiple stress environments. The GGE biplot approach could help breeders to make rational decision on which hybrids should be recommended for broader or specific adaptation. The GGE biplot analysis provided a clear basis for determining the stability and performance of the 50 early maturing maize hybrids and their rank. The vertex genotypes were G13 (CZH15448), G46 (CZH15574), G15 (local check 2), G33 (CZH16094), G7 (CZH16083), G20 (CZH16090) and G4 (CZH16089). The following hybrids were specific adapted to the respective environmental sectors: G26 (CZH16070), G34 (CZH16074), G9 (CZH15499) and G18(CZH16071) at Cedara (optimum) conditions; G46 (CZH15574), G40 (CZH16069) and G12 (CZH16080) excluding the checks G23 (local check 1) and G14 (SC301) at Potchefstroom (optimum); G22 (CZH16093), G6 (CZH15575), G49 (CZH16068) and G17 (CZH15600) excluding the check G15 (local check 2) at Cedara (low N) and G33 (CZH16094), G37 (CZH15184), G41 (CZH16082), G28 (CZH16076) and G8 (CZH16065) at Lutzville (managed drought). The GGE biplot analysis also revealed that nine stable and high yielding were identified as follows: G6 (CZH15575), G46 (CZH15574), G22 (CZH16093), G49 (CZH16068), G12 (CZH16080), G17(CZH15600), G28(CZH16076), G47(CZH15452), and G8(CZH16065) because of their short projection onto the AEC coordinate excluding the local checks G15 (local check 2), G23 (local check 1) and G14(SC301).These hybrids can contribute to high maize grain yields and stable grain production in specific or across the environments.

References

Abakemal, D., H. Shimelis, and J. Derera. 2016. Genotype-by-environment interaction and yield stability of quality protein maize hybrids developed from tropical highland adapted inbred lines. Euphytica 209: 757-769.

Akcura, M., Yaya, Y. and Taner, S. 2005. Genotype by environment interaction and phenotypic stability analysis for grain yield of durum wheat in the Central Anatolian region. Turkey Journal of Agriculture 29:369-375.

Badu-Apraku, B. 2007. Genetic variances and correlations in an early tropical white maize population after three cycles of recurrent selection for Striga resistance. Maydica 52: 205-217.

Badu-Apraku, B. and Oyekunle, M. 2012. Genetic analysis of grain yield and other traits of extra-early yellow maize inbreds and hybrids perfomance under contrasting environments. Field Crops Research 29:99-110.

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

Badu-Apraku, B., Akinwale, R. O. and Fakorede, M. A. B. 2010. Selection of early maturing maize inbred lines for hybrid production using multiple traits under *Striga*-infested and *Striga*-free environments. Maydica 55:261-274.

Badu-Apraku, B., Fajemisin, J. M. and Diallo, A. O. 1995. The performance of early and extra-early cultivar across environments in West and Central Africa. In: Contributing to Food Self-Sufficiency: Maize Research and Development in West and Central Africa. Badu-Apraku, B. A., Ouedraogo, M. O. and Quin, M. (eds). Proceedings of a Regional Maize Workshop, 29 May-2 June, 1995. IITA, Cotonou, Benin Republic.

Badu-Apraku, B., Fakorede, M. A. B. and Lum, A. F. 2008. S1 family selection in early maturing maize population in Striga-infested and Striga-free environments. Crop Science 48:1984-1994.

Badu-Apraku, B., Fakorede, M. A. B., Lum, A. F. and Akinwale, R. 2009. Improvement of yield and other traits of extra-early maize under stress and non-stress environments. Agronomy Journal 101:381-389.

Badu-Apraku, B., Oyekunle, M., Akinwale, R. O. and Lum, A. F. 2011. Combining ability of early maturing white maize inbreds under stress and non-stress environments. Agronomy Journal 103:544-557.

Banks, W. 2005. Agriculture Investment Sourcebank. Agriculture and Rural Development. World Bank, Washington DC.

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

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

Betran, F. J., Beck, D., Bänziger, M. and Edmeades, G. O. 2003. Secondary traits in parental inbreds and hybrids under stress and non-stress environments in tropical maize. Field Crops Research 83:51-65

Blum, A. and Sullivan, C. Y. 1986. The comparative drought resistance of landraces of sorghum and millet from dry and humid regions. Annals of Botany 57:835–846.

Blum, A., Golan, G. and Mayer, J. 1991. Progress achieved by breeding open-pollinated cultivars as compared with landraces of sorghum. Journal of Agricultural Science 117:307–312.

Boshev, D., Jankulovska, M., Ivanovska, S., Jankuloski, L., Kuzmanovska, B. and Tanaskovic, V. 2014. Evaluation of maize hybrids for grain yield stability under rainfed and irrigated conditions using GGE Bi-plot analysis. Journal of Agricultural Science 20:1320-1325.

Ceccarelli, S. and Grando, S. 1989. Efficiency of empirical selection under stress conditions in barley. Journal of Genetics and Plant Breeding 43:25-31.

Ceccarelli, S., Grando, S. and Hamblin, J. 1992. Relationship between barley yields measured in low-and high-yielding environments. Euphytica 64:49-58.

Comstock, R. E. and Moll, P. H. 1963. Genotype-environment interaction. In*:* Proceeding of the Symposium on Statistical Genetics and Plant Breeding. NAS-NRC Publication, Washington DC, USA.

Dehghani, H., Sabaghnia, N. and Moghaddam, M. 2009. Interpretation of genotype by environment interaction for late maize hybrids grain yield using a Bi-plot method. Turkey Journal Agriculture and Forestry 33:139-148.

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

Ebdon, J. S. and Gauch, J. H. G. 2002. Additive main effect and multiplicative interaction analysis of national turf grass perfomance trials: Interpretation of genotype x environment interaction. Crop Science 42:489-496.

Epinat-Le Signor, C., Lorgeou, J., Denis, J. B., Bonhomme, R., Carolo, P. and Charcosset, A. 2001. Interpretaion of genotype x environment interactions for early maize hybrids over 12 years. Crop Science 41:663-669.

Fakorede, M. A. B. and Adeyemo, M. O. 1986. Genotype environment components of variance for three types of maize cultivar in the rainforest zone of S.W. Nigeria. Nigeria Journal of Agronomy 1:43-46.

Fan, X. M., Kang, M. S., Chen, H., Zhang, Y., Tan, J. and Xu, C. 2007. Yield stability of maize hybrids evaluated in multi-environment trials in Yunnan, China. Agronomy Journal 99:220-228.

Framkel, O. H., Brown, A. H. D. and Burdon, J. J. 1998. The Conservation of Plant Biodiversity. 2nd ed. Cambridge University Press, Cambridge, New York

Gauch, H. G. and Zobel, R. W. 1996. Optimal replication in selection experiments. Crop Science 36:838-843.

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

IITA. 2016. Research to nourish Africa. http://blogs.iita.org//research/transforming-iita-to-nourish-africa. Accessed Accessed 17 May 2018.

Kaya, Y., Ackura, M. and Taner, S. 2006. GGE Bi-plot analysis of multi-environment yield trials in bread wheat. Turkey Journal of Agriculture 62:199-246.

Koroma, M. S., Swaray, M., Akromah, R. and Obeng-Antwi, K. 2017. Genotype x environment interaction and stability of extra-early maize hybrids (*Zea mays* L.) for yield evaluated under irrigation. International Journal of Environmental Agriculture and Biotechnology 2:2573-2578.

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

Makumbi, D., Diallo, A., Kanampiu, K., Mugo, S. and Karaya, H. 2015. Agronomic performance and genotype x environment interaction of herbicide-resistant maize cultivar in Eastern Africa. Crop Science 55:540-555.

Malla, S., Ibrahim, A. H. M., Little, R., Kalsbeck, S., Glover, K. D. and Ren, C. 2010. Comparison of shifted multiplicative model, rank correlation and Bi-plot analysis for clustering winter wheat production environments. Euphytica 174:357-370.

McCann, J. C. 2005. Maize and Grace: Africa's Encounter with a New World Crop. Howard University Press, Washington DC, USA.

Menkir, A. and Akintunde, A. O. 2001. Evaluation of the performance of maize hybrids, improved open-pollinated and farmers' local cultivar under well-watered and drought stress conditions. Maydica 46:227-238.

Menkir, A., Badu-Apraku, B., Ajala, S. O., Kamara, A. and Ndiaye, A. 2008. Response of early maturing maize landraces and improved cultivar to moisture deficit and sufficient water supply. Plant Genetic Resources: Charact Utilization 7:205-215.

Nesmith, D. S. and Ritchie, J. T. 1992. Effect of soil water-defecits during tassel emergence on development and yield components of maize (*Zea mays* L.). Field Crops Research 28:251-256.

Oikeh, S. O. and Horst, W. J. 2001. Agro-physiological responses of tropical maize hybrids to nitrogen fertilization in the moist savanna of West Africa. In: Horst, J. E. (ed.). Plant-nutrition, food security and sustainability of agro-ecosystems. Kluwer Academic Publication, Dordrecht, the Netherlands. pp 804-805.

Pacheco, A., Vargas, M., Alvarado, G., Rodríguez, F., López, M., Crossa, J. and Burgueño, J. 2015. GEA-R (Genotype x Environment Analysis with R for Windows). Version 4.0.

http://www.oracle.com/technetwork/java/javase/terms/license/index.html. Developed by CIMMYT.

Payne, R. W., Murray, D. A., Harding, S. A., Baird, D. B. and Soutar, D. M. 2009. GenStat for Windows (12th ed.) Introduction. VSN International, Hemel Hempstead.

Sanou, J., Gouesnard, B. and Charrier, A. 1997. Isozyme variability in West African Maize hybrids (*Zea mays L.).* Maydica 42:1-11.

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

Solonechnyi, P., Vasko, N., Naumov, A., Solonechnyi, O., Vazhenina, O., Bondareva, O. and Logvinenko, Y. 2015. GGE Bi-plot analysis of genotype by environment interaction of spring barley cultivar. Zemdirbyste-Agriculture 102:431-436.

Sserumaga, J. P., Oikeh, S. O., Mugo, S., Asea, G, Otim, M., Beyene, Y., Abalo, G. and Kikafunda, J. 2015. Genotype by environment interactions and agronomic performance of doubled haploids testcross maize (*Zea mays L*.) hybrids. Euphytica 207:1-13.

Tonk, F. A., Ilker E. and Tosun, M. 2011. Evaluation of genotype by environment interaction in maize hybrids using GGE Bi-plot analysis. Crop Breeeding and Applied Biotechnology 11:1-9.

Workie. A., Habtamu, Z. and Yigzaw, D. 2013. Genotype by environment of maize (Zea mays L.) across North Western Ethopia. Journal of Plant Breeding and Crop Science 59:171-181

Yan, W. 2014. Crop variety trials: Data management and analysis. John Wiley and Sons, London?, UK.pp 360.

Yan, W. and Fregeau-Reid, J. 2008. Breeding line selection based on the multiple traits. Crop Science 48:417-423.

Yan, W. and Hollard, J.B. 2010. A heritability-adjusted GGE Bi-plot for test environment evaluation. Euphytica 171:355-369.

Yan, W. and Kang, M. S. 2003. GGE Bi-plot Analysis: A graphical tool for breeders, geneticists and agronomists. CRC Press, Boca Raton, Florida., USA. pp 288.

Yan, W. and L.A. Hunt, 2001. Interpretation of genotype x environment interaction for winter wheat yield in Ontario. Crop Science 41:19-25.

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

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

Yan, W., Kang, M. S., Ma, B., Woods, S. and Cornelius, L.P. 2007. GGE Bi-plot vs. AMMI analysis of genotype by environment data. Crop Science 47:643-655.

CHAPTER FIVE

Overview of the Research Findings

5.1 Introduction and objectives of the study

Maize is an important staple food crop in Africa, which has high potential for production and productivity. It is a versatile crop, which can be grown over a range of agro-climatic zones and has become very important in the agricultural export crop industry. The crop is affected by socio-economic, biotic and abiotic factors that decrease grain yield production. The abiotic stresses include drought, low N, heat and waterlogging which can occur concurrently in an environment. This chapter outlines the findings of the study conducted on 50 early maturing maize hybrids under multiple stresses at Potchefstroom, Cedara and Lutzville. The objectives, summary of the research findings and recommendations are highlighted.

The objectives of the study were:

- To estimate variance components, correlation and path coefficient analysis in early maturing maize hybrids across stress and non-stress environments.

- To evaluate genotype by environment interaction and stability of early maturing maize hybrids across stress and non-stress environments.

5.2 Summary of the research findings

Variance Components, Correlation and Path Coefficient Analysis in Early Maturing Maize Hybrids across stress and non-stress environments

- The analysis of variance revealed highly significant ($P<0.01$) differences among the experimental hybrids for all the traits studied in each environments
- The mean performance results of all traits studied across environments revealed that some of the experimental hybrids performed better than the local checks
- High broad sense heritability estimates at Lutzville (Managed drought) revealed that grain moisture, grain yield, grain weight, anthesis days and silking days, while field weight and ear height had moderate heritability. Anthesis-silking interval, plant height and ear per plant exhibited low heritability

- High broad sense heritability at Cedara (low N) revealed that plant height, grain moisture, silking days, anthesis days, grain weight and grain yield, while ear height and field weight revealed moderate heritability. Anthesis-silking interval and ear per plant exhibited low heritability
- High broad sense heritability at Potchefstroom (optimum) revealed that anthesis-silking interval, field weight, grain weight, grain moisture, grain yield and ear per plant only. Whereas, anthesis days, silking days, ear height and plant height recorded moderate heritability
- Genetic advance in all the three environments were coupled with high-low phenotypic and genotypic coefficient variation
- The correlation coefficient analysis at Lutzville (Managed drought) revealed that grain yield was negatively correlated with anthesis days and ear height, field weight, grain weight and ears per plant while anthesis-silking days, ear per plant and field weight showed significant positive significant and positive correlation
- The correlation coefficient analysis at Cedara (low N) revealed that grain yield was negatively correlated with anthesis days while anthesis-silking days, ear per plant and field weight showed significant positive significant and positive correlation
- The correlation coefficient analysis at Potchefstroom (optimum) revealed that grain yield was positively correlated with anthesis days and ear height, field weight, grain moisture showed significant positive significant and positive correlation
- The path coefficient analysis at Lutzville (managed drought) revealed anthesis days, anthesis-silking interval, ear height and grain moisture had positive direct effects on grain yield had positive direct effect on grain yield while field weight, plant height, ear per plant and silking days had negative direct effect on grain yield selection
- The path coefficient analysis at Cedara (low N) revealed anthesis days, anthesis-silking interval, grain moisture, ear height, plant height and field weight had positive direct effects on grain yield while ear per plant and silking days had negative direct effect on grain yield selection
- The path coefficient analysis at Potchefstroom (optimum) revealed anthesis days, silking days, ear height, anthesis-silking interval and field weight had positive direct effects on grain yield while plant height, grain moisture and ear per plant had negative direct effect on grain yield selection
- This implies that these traits should be considered for effective selection for grain yield improvement in each single environment

Genotype by environment interaction and stability of early maturing maize (*Zea mays L.*) hybrids across stress and non-stress environments

- The ANOVA for grain yield revealed that genotype, environment and genotype by environment interaction were highly significant ($P<0.01$) for all the traits across environments
- The contribution of the genotype, environment and genotype by environment interaction to grain yield variation was about 6.36, 77.96 and 11.81%, respectively
- The two principal components (PC1 and PC2) obtained in the GGE Bi-plot accounted for 35.97% and 28.83% variability for grain yield, respectively
- Which-won-where revealed four mega-environments with possible classification into only two mega environments and crossover interaction. Different winning experimental hybrids (vertex genotypes) across the environments were identified. The environments within the mega environment one were Cedara (optimum) and Potchefstroom (optimum). The environments for mega environment two were Cedara (low N) and Lutzville (managed drought). The vertex genotypes were G13 (CZH15448), G46 (CZH15574), G15 (local check 2), G33 (CZH16094), G7 (CZH16083), G20 (CZH16090) and G4 (CZH16089)
- Discriminativeness versus representativeness biplot revealed that Lutzville (managed drought) had the longest vector, which had the most discriminating power while Cedara (low N), Potchefstroom (Optimum) and Cedara (Optimum) had the lowest discriminating power and the angle between the environments were less than 90^0 which are ideal for selecting the best genotype
- The mean versus stability biplot revealed that the nine stable and high yielding hybrids were identified as follows: G6 (CZH15575), G46 (CZH15574), G22 (CZH16093), G49 (CZH16068), G12 (CZH16080), G17(CZH15600), G28 (CZH16076), G47 (CZH15452), and G8 (CZH16065) because of their short projection onto the AEC coordinate excluding the local checks G15 (local check 2), G23 (local check 1) and G14 (SC301). These genotypes are recommended for further testing for possible release and registration

5.3 General implications and the way forward

The following implications and future directions were identified:

- Coefficients of variation for the quantitative traits for maize revealed that significant variation exists for all the traits. Selection can be made among these traits for further improvement of the crop.

- Low heritability and low genetic advance for most traits indicated the presence of non-additive genes in the traits and suggested non-reliability of traits for improvement through selection of the traits.

- Mean performance in respect to grain yield and secondary traits studied across environments revealed that some experimental hybrids performed better depending on the environmental conditions.

5.4 Conclusion and recommendations

The main objective of the study was to evaluate 50 early maturing maize hybrids for multiple stress tolerance. Among the experimental hybrids evaluated, most had desirable agronomic characteristics for the purpose of selection for grain yield improvement. In general, the study identified valuable experimental hybrids that were stable and high yielding which can be recommended for further evaluation in multi-environmental trials for possible release in specific or broad agro-ecological regions of South Africa.

APPENDIX 1

Appendix 1 Mean performance of genotypes for each site

Traits	**GY (th^{-1})**			**AD (days)**			**SD (days)**			**ASI (days)**			**EH (cm)**		
	Lutz	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G1	1.30	1.55	8.95	93.00	95.00	76.50	94.00	96.00	78.00	1.00	1.00	1.50	121	85	141
G2	3.20	1.40	9.55	85.50	98.00	76.00	87.50	99.00	78.50	2.00	1.00	2.50	115	80	118
G3	2.20	1.10	7.85	89.50	92.50	75.00	91.50	92.50	77.50	2.00	0.00	2.50	124	71	114
G4	3.40	2.20	9.10	92.00	96.00	73.00	92.50	97.00	75.00	0.50	1.00	2.00	135	83	128
G5	2.20	1.70	14.30	85.50	93.00	72.50	87.50	94.00	75.50	2.00	1.00	3.00	118	96	129
G6	2.85	2.10	11.85	74.00	91.50	70.00	75.00	92.50	71.50	1.00	1.00	1.50	123	80	108
G7	4.90	3.05	11.80	90.50	89.00	70.00	92.50	90.00	72.50	2.00	1.00	2.50	113	91	106
G8	1.15	1.50	8.75	92.50	96.50	72.00	94.50	97.50	74.00	2.00	1.00	2.00	117	67	140
G9	3.55	2.30	10.50	84.00	86.00	71.50	86.00	86.50	73.50	2.00	0.50	2.00	115	93	140
G10	2.15	2.40	9.25	90.50	93.50	73.50	91.50	94.50	76.00	1.00	1.00	2.50	103	87	138
G11	1.25	1.70	9.50	90.50	96.00	72.00	92.50	97.00	73.50	2.00	1.00	1.50	135	67	117
G12	1.15	2.15	9.75	90.50	92.00	76.00	92.50	92.00	78.00	2.00	0.00	2.00	107	88	135
G13	2.20	0.65	9.95	95.00	93.00	78.50	96.00	94.00	80.00	1.00	1.00	1.50	129	74	135
G14	1.45	2.55	12.35	90.50	92.50	74.50	91.00	93.50	77.00	0.50	1.00	2.50	128	95	137
G15	3.40	3.30	11.60	91.00	90.00	73.00	92.00	91.00	75.00	1.00	1.00	2.00	103	92	141
G16	2.35	3.75	11.05	79.00	86.00	70.50	79.00	86.00	72.00	0.00	0.00	1.50	121	61	116
G17	4.85	1.45	8.85	91.00	97.00	72.50	92.00	98.00	74.50	1.00	1.00	2.00	115	65	115
G18	3.70	2.05	9.55	73.50	85.00	70.00	74.50	86.00	72.00	1.00	1.00	2.00	124	70	109
G19	2.50	3.15	7.80	90.00	96.50	73.50	92.00	97.50	75.50	2.00	1.00	2.00	124	83	119
G20	2.30	2.20	8.40	80.50	85.00	68.00	82.50	87.00	71.00	2.00	2.00	3.00	116	98	123
G21	3.70	2.55	9.10	84.00	87.50	72.00	86.00	88.50	74.00	2.00	1.00	2.00	115	88	123
G22	1.30	2.60	10.30	92.50	94.50	76.50	93.50	95.50	78.00	1.00	1.00	1.50	133	126	151

Traits	**GY (th^{-1})**			**AD (days)**			**SD (days)**			**ASI (days)**			**EH (cm)**		
	Lutz	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**	**Lutz**	**Ced**	**Potch**
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G23	1.75	2.10	8.35	93.00	85.00	77.00	93.00	86.00	77.50	0.00	1.00	0.50	124	84	123
G24	2.05	2.25	10.05	89.00	85.00	75.00	91.00	86.00	77.50	2.00	1.00	2.50	127	86	134
G25	1.60	2.60	9.50	92.5	92.00	74.50	94.50	92.50	75.50	2.00	0.50	1.00	128	108	165
G26	2.20	2.65	8.85	88.00	80.00	71.50	88.50	80.50	72.50	0.50	0.50	1.00	127	96	115
G27	3.25	4.30	9.55	90.00	96.00	73.50	92.00	97.00	74.50	2.00	1.00	1.00	116	88	115
G28	1.50	2.20	11.20	91.00	93.50	72.50	93.00	94.50	74.50	2.00	1.00	2.00	125	73	131
G29	5.00	1.80	8.85	74.50	87.00	72.00	75.50	88.00	74.00	1.00	1.00	2.00	107	91	119
G30	2.15	2.70	7.60	92.50	87.50	70.50	94.50	88.50	72.00	2.00	1.00	1.50	118	64	99
G31	3.90	4.05	8.00	85.50	89.00	75.00	86.50	90.00	77.00	1.00	1.00	2.00	105	75	127
G32	1.65	2.40	8.35	92.00	93.00	76.00	94.00	94.00	77.50	2.00	1.00	1.50	133	115	154
G33	1.40	2.40	9.70	91.00	88.00	73.00	92.00	88.00	75.50	1.00	0.00	2.50	128	82	128
G34	1.50	0.60	9.20	92.50	95.50	75.50	93.50	95.50	78.00	1.00	0.00	2.50	117	80	141
G35	1.80	3.45	10.95	91.50	92.50	73.50	94.00	93.50	75.50	2.50	1.00	2.00	108	76	126
G36	3.65	3.55	10.00	90.50	80.50	74.50	92.50	81.50	76.50	2.00	1.00	2.00	117	76	128
G37	2.15	2.05	9.60	88.50	93.50	76.00	89.50	94.50	77.00	1.00	1.00	1.00	110	79	128
G38	3.25	1.65	6.95	74.00	87.00	71.00	75.00	88.00	72.00	1.00	1.00	1.00	115	77	101
G39	3.25	1.50	8.70	89.50	98.00	75.00	90.50	99.00	77.00	1.00	1.00	2.00	146	77	142
G40	2.15	2.40	9.15	92.00	92.00	71.00	92.50	92.00	72.50	0.50	0.00	1.50	125	79	112
G41	3.55	3.00	11.65	86.50	87.50	70.50	88.50	87.50	73.50	2.00	0.00	3.00	111	78	124
G42	1.35	3.55	9.60	93.00	95.50	74.00	94.00	96.50	75.50	1.00	1.00	1.50	116	91	141
G43	2.35	2.25	9.15	86.00	92.00	71.00	87.00	93.00	72.50	1.00	1.00	1.50	116	61	102
G44	2.60	3.15	10.80	91.00	97.00	75.50	9100	98.00	78.00	0.00	1.00	2.50	123	95	145
G45	1.90	1.95	9.55	93.50	96.00	76.00	95.50	97.00	78.00	2.00	1.00	2.00	128	70	150
G46	1.90	2.90	8.45	91.00	92.50	75.50	93.00	93.50	78.00	2.00	1.00	2.50	119	89	135
G47	3.30	3.80	11.65	82.00	86.00	71.00	84.00	86.00	73.00	2.00	0.00	2.00	116	103	114
G48	3.20	3.15	7.70	91.00	90.00	76.50	91.50	90.00	77.50	0.50	0.00	1.00	130	87	211

Traits	GY (th^{-1})			AD (days)			SD (days)			ASI (days)			EH (cm)		
	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G49	2.25	3.15	8.70	93.00	9600	75.50	95.00	97.00	78.00	2.00	1.00	2.50	106	90	152
G50	1.60	2.30	10.20	84.00	88.50	70.50	87.00	89.00	72.00	3.00	0.50	1.50	97	90	112
Min	1.15	0.60	6.95	73.50	80.00	68.00	74.50	80.50	71.00	0.00	0.00	0.50	97	61	99
Max	5.00	4.30	14.30	95.00	98.00	78.50	96.00	99.00	80.00	3.00	2.00	3.00	146	126	211
Mean	2.51	2.43	9.64	88.27	91.24	73.40	89.69	92.04	75.30	1.42	0.80	1.90	119	84	129
CV (%)	8.36	18.38	16.17	2.02	2.73	4.54	2.03	2.67	4.51	30.65	23.87	16.21	14.69	12.08	7.22
S.E.	0.81	0.45	0.4	1.48	2.49	4.01	1.53	2.45	4.04	0.58	0.19	0.23	18.93	10.11	8.61
LSD(0.05)	1.63	0.89	0.82	3	5.03	8.09	3.08	4.96	8.17	1.18	0.38	0.46	38.24	20.43	17.39
P-value	<.001	<.001	<.001	<.001	<.001	<.001	0.016	<.001	0.002	0.009	<.001	<.001	0.016	<.001	0.002

GY= grain yield, ASI=Anthesis-silking interval, EH=Ear height, PH=plant height, EPP=Ears per plant, OPT=optimum, LN=low nitrogen, MD=managed drought, Potch= Potchefstroom, Ced= Cedara, Lutz= Lutzville

Continuetion of traits

Traits	PH (cm)			EPP			FW (kgh^{-1})			GM			GW (kgh^{-1})		
	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G1	178	167	273	0.25	0.90	1.00	1.35	1.25	5.85	12.70	14.45	13.35	0.80	0.95	5.43
G2	174	157	235	0.85	1.10	1.35	3.50	1.35	8.88	13.50	10.05	13.25	1.95	0.95	5.79
G3	189	156	207	0.45	0.95	1.05	2.20	0.95	7.42	12.00	12.25	13.35	1.30	0.65	4.76
G4	189	157	231	1.15	0.85	1.00	2.50	1.65	4.74	13.35	12.45	12.35	2.05	1.30	5.45
G5	171	175	228	0.60	1.05	1.30	1.60	2.65	10.14	12.45	12.70	14.70	1.35	1.00	8.79
G6	181	169	218	0.65	0.90	1.05	2.55	1.65	9.34	13.15	12.65	13.10	1.75	1.25	7.17
G7	180	178	206	0.6	1.05	1.10	4.20	2.20	9.26	12.65	10.65	14.80	2.95	1.80	7.28
G8	187	150	251	0.35	0.95	1.20	0.90	1.25	6.83	14.60	12.50	12.05	0.70	0.90	5.22
G9	166	176	235	1.15	0.90	1.30	2.50	1.60	7.15	14.40	11.35	12.20	2.15	1.40	6.30

Traits	PH (cm)			EPP			FW (kgh^{-1})			GM			GW (kgh^{-1})		
	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch
Genotype	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT	MD	LN	OPT
G10	173	181	259	0.60	1.00	1.10	1.95	1.85	6.31	14.30	10.50	11.80	1.30	1.40	5.49
G11	192	151	225	0.35	0.75	1.05	1.50	1.30	6.51	15.25	12.45	13.55	0.80	1.00	5.78
G12	156	171	244	0.65	1.00	1.20	0.90	1.65	7.83	13.40	12.80	12.95	0.70	1.30	5.90
G13	171	147	240	0.60	0.70	0.90	1.50	0.65	7.07	12.80	12.10	14.35	1.30	0.40	6.10
G14	184	187	263	0.35	0.90	1.05	1.10	2.10	8.23	13.20	11.20	13.55	0.90	1.50	7.48
G15	170	178	214	0.75	0.90	1.15	2.65	2.55	9.12	15.10	10.40	13.45	2.10	1.95	7.04
G16	170	145	225	0.65	1.05	1.10	2.30	3.00	6.84	11.75	10.30	13.40	1.40	2.20	6.70
G17	161	140	224	0.55	0.90	1.00	3.20	1.35	9.10	13.70	11.50	12.05	2.95	0.85	5.27
G18	170	156	201	1.20	1.00	1.10	4.20	1.45	7.60	13.35	10.75	14.3	2.25	1.20	5.85
G19	178	168	240	0.45	0.95	1.05	1.95	2.15	6.33	12.95	10.40	11.75	1.55	1.85	4.64
G20	179	186	229	0.50	0.90	1.00	1.60	1.65	6.30	12.25	10.55	12.55	1.40	1.30	5.04
G21	176	187	244	0.95	0.95	1.20	2.65	2.05	6.45	12.85	12.70	12.05	2.25	1.55	5.44
G22	166	206	247	0.50	0.95	1.15	1.50	2.35	7.60	12.55	13.40	14.65	0.80	1.65	6.35
G23	167	167	214	0.70	0.80	1.10	1.50	1.65	6.29	13.50	12.85	13.55	1.10	1.30	5.06
G24	175	139	253	0.45	1.05	1.05	1.55	2.35	8.15	12.50	12.35	12.55	1.25	1.35	6.04
G25	188	193	279	0.45	0.90	1.00	1.25	1.95	7.78	12.95	11.85	14.80	0.95	1.55	5.87
G26	186	183	233	0.60	1.35	1.20	1.95	2.50	7.48	16.50	12.65	15.25	1.40	1.60	5.49
G27	181	175	235	0.70	0.95	1.05	3.00	3.15	5.23	12.60	11.25	13.20	1.95	2.55	5.78
G28	184	160	260	0.45	0.85	1.05	1.10	1.75	8.62	12.95	14.55	12.05	0.90	1.35	6.66
G29	181	175	230	0.45	0.85	1.00	3.30	1.30	6.50	13.60	10.55	10.50	3.05	1.05	5.19
G30	169	137	202	0.55	0.80	0.95	1.60	2.30	5.42	13.60	12.55	14.35	1.30	1.60	4.67
G31	159	165	242	0.40	1.00	0.90	3.35	2.40	6.37	14.50	12.30	14.15	2.40	2.40	4.88
G32	195	199	258	0.55	1.15	1.15	1.20	1.80	7.24	13.65	12.25	14.20	1.00	1.45	5.13
G33	181	163	233	0.35	1.00	1.25	1.05	1.85	7.86	13.40	10.70	12.35	0.85	1.40	5.82
G34	176	169	253	0.35	0.80	1.00	1.55	2.05	7.59	15.55	10.50	13.35	0.95	1.55	5.56
G35	185	162	241	0.50	1.05	1.15	1.35	2.55	7.42	14.70	12.40	14.45	1.10	2.10	6.73

Traits	PH (cm)			EPP			FW (kgh^{-1})			GM			GW (kgh^{-1})		
	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch	Lutz	Ced	Potch
Genotype	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**	**MD**	**LN**	**OPT**
G36	195	171	229	0.55	1.00	1.00	2.30	2.65	7.28	14.50	12.55	12.65	2.25	2.15	6.02
G37	185	165	240	0.50	0.95	1.00	1.70	1.50	7.00	12.40	12.30	11.45	1.30	1.25	5.69
G38	175	160	200	0.65	0.75	1.00	2.40	1.15	5.59	16.85	12.50	12.30	2.05	1.00	4.14
G39	189	162	270	0.60	0.85	1.00	2.55	1.10	5.26	13.60	10.40	12.45	2.00	0.85	5.23
G40	170	167	230	1.45	1.05	0.95	1.65	1.85	5.97	14.40	12.30	14.75	1.35	1.45	5.66
G41	186	163	229	0.45	1.05	1.15	2.45	2.35	8.57	12.55	10.35	10.45	2.15	1.80	6.83
G42	186	181	247	0.45	0.85	1.15	1.00	2.60	7.44	12.55	11.55	14.30	0.80	2.10	5.88
G43	180	99	203	0.50	0.85	1.10	2.25	1.80	6.70	13.70	12.65	13.40	1.45	1.40	5.80
G44	187	185	264	0.50	0.85	1.00	2.20	2.25	8.66	12.95	10.25	13.30	1.60	1.85	6.53
G45	184	141	269	0.65	0.85	1.00	1.85	1.85	8.21	13.20	12.15	14.50	1.15	1.15	5.84
G46	159	184	255	1.20	0.95	1.05	1.35	2.20	7.91	14.35	11.25	13.90	1.15	1.75	5.15
G47	197	192	234	0.60	1.00	1.20	2.35	2.75	8.69	14.65	12.55	12.05	2.05	2.30	6.95
G48	180	162	246	0.40	0.90	0.95	2.30	2.45	6.22	14.45	10.65	13.85	1.95	1.85	4.68
G49	195	188	271	0.45	1.00	1.05	1.90	2.25	7.37	14.35	12.45	12.55	1.40	1.85	5.24
G50	175	163	218	0.55	0.85	1.10	1.35	1.65	6.98	14.45	12.75	13.00	1.00	1.35	6.17
Min	156	99	200	0.25	0.70	0.90	0.90	0.65	4.74	11.75	10.05	10.45	0.70	0.40	4.14
Max	197	206	279	1.45	1.35	1.35	4.2	3.15	10.14	16.85	14.55	15.25	3.05	2.55	8.79
Mean	178	167	237	0.6	0.94	1.08	2.03	1.93	7.29	13.62	11.83	13.18	1.53	1.47	5.83
CV (%)	5.42	7.25	5.24	10.62	12.88	25.42	12.36	20.54	20.44	4.2	3.01	3.1	8.37	17.79	16.14
S.E.	12.86	12.09	9.36	0.11	0.12	0.15	0	0.39	0.41	0.55	0.36	0.42	0.49	0.26	0.25
LSD(0.05)	25.96	24.41	18.89	0.23	0.24	0.31	1.82	0.8	0.83	0.12	0.72	0.85	0.98	0.53	0.49
P-value	<.001	<.001	0.008	0.049	0.106	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001

GY= grain yield, ASI=Anthesis-silking interval, EH=Ear height, PH=plant height, EPP=Ears per plant, OPT=optimum, LN=low nitrogen, MD=managed drought, Potch= Potchefstroom, Ced= Cedara, Lutz= Lutzville