VARIATION OF COMMON BEAN (*Phaseolus vulgaris* L.) GENOTYPES FOR WATER STRESS, ADAPTABILITY AND YIELD PERFORMANCE IN KAGERA REGION, NORTH – WESTERN, TANZANIA

JULIUS PETER MBIU

A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE IN CROP SCIENCE OF THE SOKOINE UNIVERSITY OF AGRICULTURE. MOROGORO, TANZANIA.

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GENERAL ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is the most important crop for the livelihoods of smallholder farmers in Tanzania; it is the most produced pulse by small-scale farmers for household consumption and earning income after selling surplus. Common beans are intercropped with maize or with permanent crops such as banana or coffee and some few farmers grow it as a sole crop. The objectives of this study were to assess the effects of water stress on seed yield of common bean under controlled environment; and determine the performance and adaptability of 16 genotypes at different agro-ecological environments in Kagera Region. Two experiments were conducted during the study; one was done in the screen-house and the other one was the field experiment. The screen house study on yield response to water regime revealed that genotypes DAB 582, SRC 59, IBWERA, DAB 602, SSIN 1240, Lyamungu 90, SMC 24, SMR 101, DAB 362 and JESCA were drought tolerant with lower and high value of the Drought Susceptibility Index (DSI) and Yield Stability Index (YSI) respectively. The analysis of variance of the Additive Main effects and Multiplicative Interaction (AMMI) model indicated that environments accounted for 56.9% of the total sum of square; genotypes effect explained 9.2% and the G x E interaction effect accounted 8.9% of the total sum of squares. According the results, the GGE biplot revealed that, the genotypes SSIN 1240, SAB 659 and DAB 219, SMR 101, SMC 162 and DAB 602 showed greater stability with the average closer to the overall average of the tested genotypes. Therefore, genotypes SMC 162, DAB 602, SSIN 1128, DAB 362 and SMR 101 were identified and recommended to be used in future breeding program as moisture stress tolerant, good seed yield and widely adapted in Kagera Region and similar agro ecologies.

DECLARATION

I, Julius Peter Mbiu do hereby declare to the Senate of Sokoine University of Agriculture that this dissertation is my own original work done within the period of registration and that it has neither been submitted nor being concurrently submitted in any other institution

……..…… ……

Julius Peter Mbiu Date

(MSc Student)

The above declaration is confirmed by;

……..…… ……

Prof. Susan Nchimbi-Msolla Date

(MSc. Supervisor)

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DEDICATION

To my dearly – loved WIFE TABITHA Peter Sizya has been wonderful counselor, comforter and care taker of our family even in my absence; I will continue loving you forevermore.

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LIST OF ABBREVIATIONS

%	Percent
˚C	Degree of Celsius
AEC	Average environment coordinate
AMMI	Additive Main effects and Multiplicative Interaction
CEC	Cation Exchange Capacity
CIAT	The International Center for Tropical Agriculture
DII	Drought Intensity Index
DNMRT	Duncan's New Multiple Range Test
DS	Drought Stress
DSI	Drought Susceptibility Index
DTI	Drought Tolerance Index
FAO	Food and Agriculture Organization
GEI	Genotype-Environment interaction
GGE –	Genotype main effects and genotype × environment interaction effects
GM	Geometric Mean
Ha	Hectare
HI	Harvest Index
ISSR	Interspecific Sample Sequence Repeat
K	Potassium
Kg	Kilogram
N	Nitrogen
NSPP	Number of Seed Per Pod
P	Phosphorus

PCA	Principal Components Analysis
pH	potential hydrogen concentration
PHI	Pod Harvest Index
PPI	Pod Partitioning Index
ppm	Part Per Million
PPP	Pod number Per Plant
PWP	Pod Wall Proportion
RCBD	Randomized Complete Block Design
RSR	Root Shoot Ratio
S.E	Standard Error
SUA	Sokoine University of Agriculture
SWPP	See Weight Per Plant
TARI	Tanzania Agricultural Research Institute
YRR	Yield Reduction Rate
YSI	Yield Stability Index
RW	Root Weight

CHAPTER ONE

1.0 INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important grain legume for human consumption as it plays a principal role in the livelihoods of smallholder farmers in Tanzania as food security crop and source of income. It provides an important source of protein (~22%), vitamins (folate), and minerals (Ca, Cu, Fe, Mg, Mn, Zn) for human diets, especially in developing countries (Beebe, 2012). It is the leading leguminous crop, accounting for 78% of land under legumes; contributing 38% of utilizable protein and 12-16% of daily calorific requirements for human nutrition (CIAT, 2008; Rugambisa, 1990). In eastern African countries, per capita consumption of bean is 50.45 kg per year (FAO 2004).

Common beans are traditionally a small farmer crop, often grown in complex farming systems in association or rotation with maize, sorghum, bananas, or other crops (Broughton *et al.,* 2003). Common bean production occupies about 800 000 hectares in Tanzania thus coming third as one of the largest cultivated crop after maize and cassava (Letaa *et al.,* 2014; Nyomora *et al.,* 2018). Common beans are the main grain legume crop grown in Tanzania, where they are often intercropped with maize. Cultivation of beans can be seen in most areas of Tanzania, but the crop does not tolerate prolonged periods without rainfall, and to obtain a reliable yield in the drier areas supplementary irrigation is required (Hillocks *et al.,* 2006).

Despite of being important crop as food and cash crop, in many areas, bean yields are still below the average (0.5 – 0.6 ton/ha) while the yield potential of improved bean varieties in Tanzania is 1.5 to 3.5 ton/ha using improved varieties and proper crop and land husbandry

(Kanyeka *et al.,* 2007). The main reasons for the low yield obtained by most smallholders are; poor seed quality, poor performance of the local landraces, mainly due to their susceptibility to pests and diseases, low soil fertility, poor crop management such as late weeding and currently drought (Hillocks *et al.,* 2006).

Approximately 60% of common beans production regions suffer serious from drought condition (CIAT, 1980). The rainfall received now is not as it used to be years ago, it is unreliable and poorly distributed. Of the various physiological problems limiting bean (*Phaseolus vulgaris* L.) production in developing countries, drought is rivaled in importance only by soil fertility problems. Most farmers have experienced serious drought in the last cropping seasons in most part of the country as a result of shortage of rainfall. According to TMA last season (2016/2017) Kagera received 200 mm of rainfall instead of average amount of 550 mm in *Vuli season* while Missenyi district received 93.8 mm instead of 400 mm in the same season. Therefore, it is high time to come up with common bean genotypes that will be tolerant to drought and widely adaptive which will make farmers get more yield from the bean crop than it is now due to unpredicted and poor distributed rainfall.

1.2 Objectives

1.2.1 Overall objective

Examine the level of drought tolerance, adaptability and yielding ability of common bean genotypes in Kagera Region agro – ecological system.

1.2.2 Specific objectives

i. To assess the effect of water stress on seed yield of 16 common bean genotypes under controlled environment.

ii. To determine the performance and adaptability of the 16 common bean genotypes at different agro-ecological environments in Kagera Region.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin of the Common Beans

Common bean (*Phaseolus vulgaris* L., Fabaceae) is an annual, diploid (2n=2x=22) species derived from wild ancestors distributed from northern Mexico to northwestern Argentina (Bornet *et al.,* 2003). Over a period of at least 7000 to 8000 years, the common bean has evolved from a wild – growing vine distributed in the highlands of Middle America and the Andes into a major leguminous food crop, grown worldwide in a broad range of environments and cropping systems(CIAT, 1991). During this period, which encompasses the initial domestication phase and subsequent evolution under cultivation, evolutionary forces – mutation, selection, migration and genetic drift – have acted on the raw material provided by wild –growing *P. vulgaris.* These forces have effected some striking changes in the common bean plant and have shaped the morphological, physiological and genetic characteristics of current common bean cultivar (CIAT, 1991).

Interspecific Sample Sequence Repeat (ISSR) markers resolved two major groups corresponding to the Andean and Mesoamerican gene pools of common bean. The major genepools in turn have been divided into races based on plant morphology, adaptation range and agronomic traits. The Middle American genepool was divided into the races Durango (prostrate bush types with medium-sized seed from dry highland Mexico), Jalisco (climbing beans from the moist highlands of central Mexico), and Mesoamerica (small seeded types), mostly bush habits, from lowland Central America and Mexico (Singh *et al.,* 1991).

2.2 Common Bean Production and Productivity

Total world production cannot be calculated with certainty due to confusion with other legumes in some of the data, but is between 11 and 12 million tons (FAO, 2006) and Tanzania is a major common beans producing country in East Africa (Fivawo and Nchimbi-Msolla, 2011) although according to official statistics, production per capita has almost halved in the last 20 years (Hillocks *et al.,* 2006). Common bean is grown in wetter and cool areas (Samwel, 2008), specifically, areas suitable for cultivation of beans are the northern zone (Arusha, Kilimanjaro, Manyara and Tanga Regions), eastern zone (Morogoro Region), southern highlands zone, western zone (Kigoma Region) and the north-western regions of Kagera and Mara around Lake Victoria. These common beans producing areas are characterized by altitude ranging from 1000 to 1500 m above sea level, with more than 400 mm of available soil moisture per growing season (Wortmann *et al.,* 1998). Although a mostly common bean is a subsistence crop in many areas of Tanzania, some regions such as Kilimanjaro and Arusha commercially produce the crop (Hillocks *et al.,* 2006).

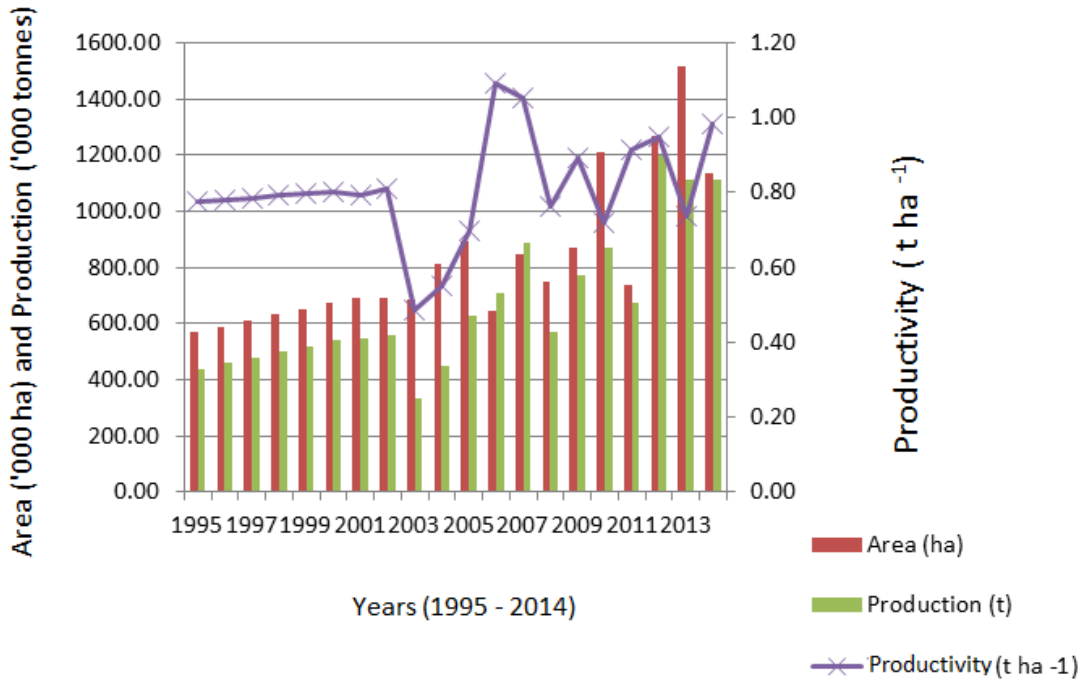

Figure 2.1: Common bean and production and productivity

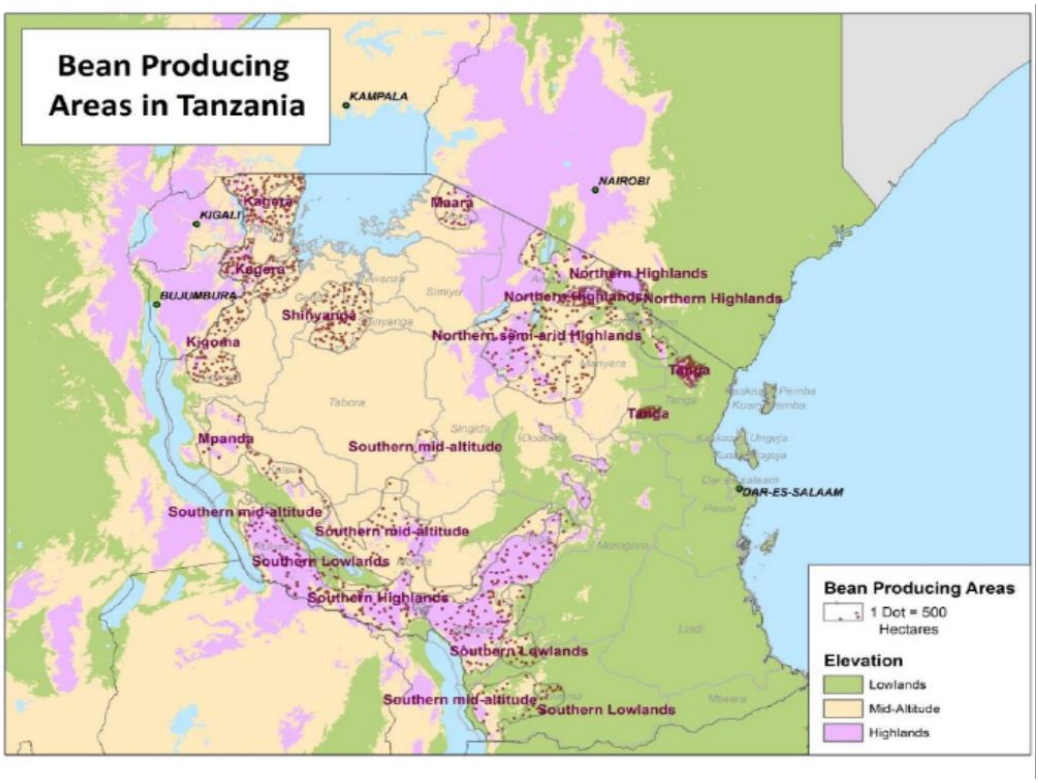

Figure 2.2: Map showing major beans producing areas (shaded) in Tanzania Source:

Binagwa *et al.* (2016)

Common bean is the most important pulse crop produced in Tanzania by small-scale farmers for household consumption, surplus of which is traded for cash (Mourice and Tryphone, 2012).

According to the Annual Agricultural Sample Survey report released by NBS (2017), Kigoma, Kagera and Manyara were the largest common bean producer in the country with the total harvested area of 87,589 ha, 88,672 ha and 93,030 ha respectively; Kigoma Region had the highest beans, with 71,812 tonnes (19.0 percent) and yield of 0.8 tonnes/ha, followed by Kagera (58,068 tonnes; 15.3 percent) with a yield of 0.6 tonnes/ha and Manyara (52,647 tonnes; 12.8 percent) with yield of 0.6 tonnes/ha. Lindi Region (0.2 tonnes; 0.01 percent) reported the lowest production.

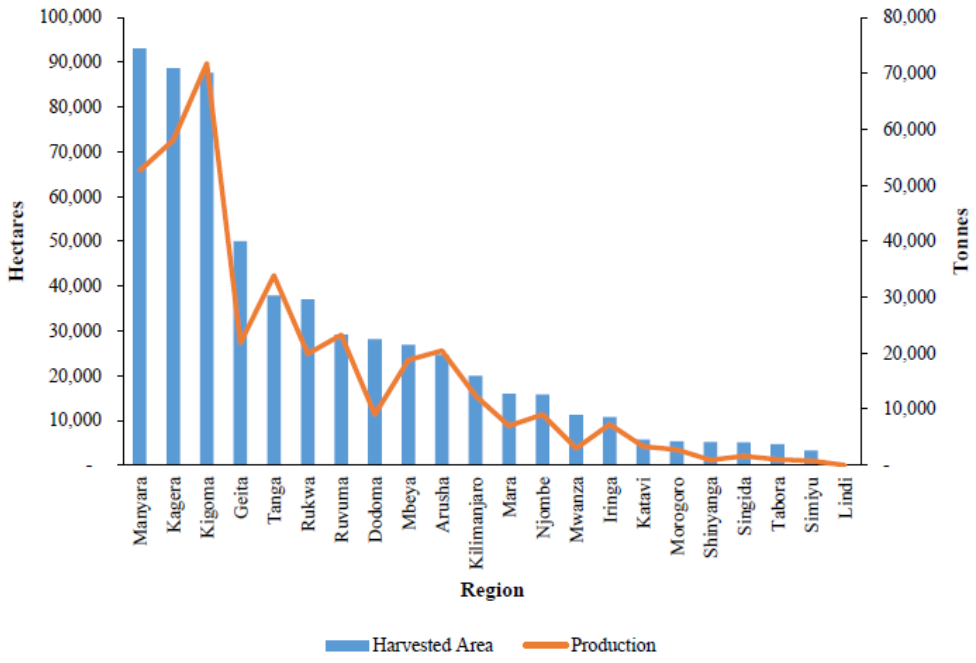

Figure 2.3: Harvested area (ha) and production of beans by Region, Tanzania Mainland 2016/17 (Source: NBS, 2017)

In Kagera region, a common bean is the dominant annual crop grown and it had a planted area 1.5 times greater than maize, which had the second largest planted area. The area under common beans cultivation constitutes 42 percent of the total area planted with other annual crops in the region. The largest area planted with common beans in the region was in Karagwe (52,054 ha, 34.5%). The average area planted per household in the region during the short rainy season was 0.36 ha (NBS, 2017).

2.3 Common Bean Production Constraints

Edaphic factors constrain bean production in most areas where this crop is grown (Graham, 2003). Its yield is quite low in developing as well as developed countries. Both biotic and abiotic constraints are responsible for this low yield. Low soil fertility is one of the most important yield-limiting factors in most of the bean-producing regions (Fageria, 2002).

Common beans are the main grain legume crop grown in Tanzania, where they are often intercropped with maize. Cultivation of common beans can be seen in most areas of Tanzania, but the crop does not tolerate prolonged periods without rainfall, and to obtain a reliable yield in the drier areas supplementary irrigation is required (Hillocks, 2006). Low yields are undoubtedly due in part to the direct effect of droughts, and in part to the fact that dry areas are also poverty hot spots where there is less capital investment (Beebe *et al.*, 2013).Whether in the form of droughts, floods, hurricanes or soil acidification, climate change impacts every level of food production and ultimately, the price instability of food (FAO, 2016). Drought acts in conjunction with biotic stresses, especially diseases and pests, and other abiotic stresses. Soil fertility related stresses, such as low soil P and N, soil acidity and the associated aluminium and manganese toxicity, are known to aggravate drought effects (Amede *et al.*, 2014).

2.4 Breeding for Drought Tolerance

Maintaining crop yields under adverse 'stress' environmental conditions is probably the major challenge facing modern agriculture. To meet this challenge, it is necessary to understand the contrasting adaptations mechanism of plants growing in stressed and unstressed conditions, and the compromises and trade-offs between them. The availability of crops with increased drought tolerance is then crucial for maintaining yield in areas where dry seasons are common. Thus, improvement in the drought resistance of cultivated species is a major objective of many breeding programmes (Carolina *et al.,* 2006). The use of genetic resources to respond to occurring and unpredictable climatic changes is one of the coping mechanisms for small scale farmers in Africa (Mukankusi *et al.,* 2015).

Drought stress linked with climate change is one of the major constraints faced by common bean farmers in Africa and elsewhere. Mitigating this constraint requires the selection of resilient varieties that withstand drought threats to common bean production. The effects of drought on common bean are dependent on the intensity, type and duration of the stress (Beebe *et al.,* 2013).

The rainfall related disturbance that has been noticed in recent decades are the consequence of climate change and with low fertility of the soils as the primary constraints that limit both the productivity and production of beans in the main production zones in Eastern, Central and Southern Africa (Beebe *et al*, 2008). Although conventional plant selection has been used to increase production yield and stress tolerance, drought tolerance selection based on phenotype is complicated by associated physiological, anatomical, cellular, biochemical, and molecular changes (Villordo-Pineda *et al.*, 2015).

2.5 Drought Stress

Drought stress is one of the premier limitations to global agricultural production due to the complexity of the water-limiting environment and changing climate. Drought acts in

conjunction with biotic stresses especially diseases and pests, and other abiotic stresses. Soil fertility related stresses, the most important being low soil P and N, soil acidity and the associated aluminium and manganese toxicity, are known to aggravate drought effects (Amede *et al.,* 2004).

Drought stress reduces leaf size, stems extension and root proliferation, disturbs plant water relations and reduces water-use efficiency. It reduces plant growth by affecting various physiological and biochemical processes, such as photosynthesis, respiration, translocation, ion uptake, carbohydrates, and nutrient metabolism and growth promoters (Tekle and Alemu, 2016).

In some cases, evaluations of specific symptoms are justified, e.g., leaf wilting, leaf orientation to avoid over-heating and flower drop, leaf malformation, and difficulty to pull out plants from the soil (CIAT, 1987).

2.6 The Mechanisms of Drought Resistance

The mechanisms of drought resistance of plants can be divided into four basic types: drought avoidance, drought tolerance, drought escape (Fang and Xiong, 2014; Beebe *et al.,* 2013).

2.6.1 Drought escape

Drought escape is defined as the ability of the crop to complete its life cycle before serious soil and crop water deficits develop. Drought escape allows plants to accelerate their cell cycle with an early flowering and maturity, and rapidly relocates metabolites to seed production (Beebe *et al.,* 2013) This mechanism matched with periods of soil moisture availability, where the growing season is shorter and terminal drought stress predominates,

developmental plasticity (variation in duration of growth period depending on the extent of water deficit) and remobilization of photosynthates to the grain (Beebe *et al.*, 2013; Araus *et al.*, 2002).

2.6.2 Drought avoidance

Drought avoidance is defined as the ability of the crop to maintain relatively high tissue water potential, despite a shortage of soil moisture. It is achieved through increased rooting depth, an efficient root system and increased hydraulic conductance, and by reduction of water loss through reduced leaf conductance, reduced absorption of radiation by leaf movement/rolling, and reduced evaporation surface (leaf area) (Beebe *et al.,* 2013).

2.6.3 Drought tolerance

Drought tolerance is defined as the ability to grow, flower and display economic yield under suboptimal water supply (Beck *et al.,* 2007). It is achieved through maintenance of turgor through osmotic adjustment (a process which induces solute accumulation in the cell), increase in cell elasticity and decrease in cell size, and desiccation tolerance by protoplasmic resistance (Beebe *et al.,* 2013).

Plants respond and adapt to and survive under drought stress by involving various morphological, physiological and biochemical processes at cell, tissue, organ and whole-plant levels, when activated at different stages of plant development (Tekle and Alemu, 2016; Beck *et al.*, 2007).

2.7 Screening Techniques

Lack of drought screening protocol in the past made it difficult to compare results from various sites. A useful way to evaluate the representativeness of sites is to implement

cluster analysis as suggested by White and Singh (1991). Sites that are very similar would appear in the same cluster (based on relative yield) and, thus, should be avoided since no new information is expected from the additional site. Grain yield formation in common beans is a more intricate process than in cereals in that the development of generative organs in beans is relatively gradual and could be prolonged if the external conditions, like water and nutrients, are readily available. Therefore, selection for drought resistance based on yield alone may not bring about the required genetic shift in specific physiological attributes, as the component of genetic variance is low when compared with environmental or genetic-environment-interaction variance under stress environments (Rosielle and Hamblin, 1981).

2.8 Rating Scale

CIAT has developed standard 1-9 rating scale for drought tolerance, where 1-3 is tolerant, 4-6 intermediate and 7-9 is susceptible. No better screening criteria than yield under drought have been found. Yield values in stress and control plots are used to calculate the geometric means. Stability analyses may be used where data from more than three or four trials with the same entries is available.

A standard scale for drought tolerance is not possible due to the great variation in the effects caused by drought (depending on climatic and soil conditions). The scales for vegetative adaptation and reproductive adaptation (in developmental stages R5 and R9) are normally used (CIAT, 1987). Amede *et al. (*2004) proposed traits to be integrated into bean breeding programmes as the drought resistance indicative traits, which are assessed in terms of potential contributions to productivity, survival under drought, stability across years, and practical usage of the trait under the existing laboratory and capacity conditions , as presented in Table 2.1.

Table 2.1: Potential indicators as identified based on sets of criteria for use in improving drought resistance in beans, (Source: Amede *et al.*, 2004)

Drought Resistance Indicator	**Correlation between the trait and drought resistances**	**Responds to changes in soil water status**	**Highly correlated to biomass production or grain yield**	**Easily measurable or observable**	**Of regional value for standard protocol**	**Total Sum**	Rank
Plant WP	3	3	2	1	3	12	9
Osmotic potential	3	3	2	3	3.5	14.5	1
RWC	3	3	3	3	2.25	14.25	2
RGR	3	3	2.5	3	2	13.5	8
Biomass	3	3	2	2.5	2	12.5	10
Vigour	3	3	3	3	3	15	4
Root depth	3	3	2	1	1	10	13
Root density	3	3	1	1	1	9	12
Pods/plant	2.5	2	3.5	3	3	14	6
Seeds/pod	1	1	3	3	2	10	10
Seed weight	1	1	1	3	1	7	14
Grain yield	2	2	3.5	3	3.5	14	4
Early maturity	3.5	2	3	3	3	14.5	2
Duration of flowering	2	3	2	3	3	13	7
Period of seed filling	2	2	3	3	2	12	9
Degree of translocation	2	2	3	3	2	12	9
Production efficiency	2	3	3	3	2	13	7
Sensitivity Index	3	2	2	3	3	13	7

Where; 0 = Irrelevant, 1 = medium, 3 = High, 3.5 = Very High, WP: Water potential, RWC: Relative water content, RGR: Relative growth rate

2.9 Measurement of Target Traits for Drought Experiment

Many drought adaptation traits, such as phenology, root size, and depth, hydraulic conductivity and storage reserves, are associated with plant development and structure, and are constitutive rather than stress-induced (Chaves *et al.*, 2003). Condon *et al.* (2004) suggested that the consequences of various plant traits and environmental conditions have to be evaluated in the specific field environments in which the crop is to be grown.

2.10 Drought Stress and Crop Yield

Since seed yield is the main economic trait in common bean, the most practical way to screen for drought tolerant genotypes is the quantification of seed production, expressed as mean seed yield (Terán and Singh, 2002). Consequently, there is an increasing need to improve drought tolerance in common bean cultivars, where adaptive mechanisms to cope with drought stress include traits such as root architecture, growth habit, maturity acceleration, early flowering, shoot biomass accumulation and efficient assimilate redistribution towards seeds, contributing to an increased harvest index (Terán and Singh, 2002; Rosales-Serna *et al.,* 2004).

Grain yield in beans is the product of number of plants (or fruitful axes) per unit area, number of pods per plant, number of seeds per pod and thousand seed weight. These yield factors are crucial for producing economic yield, and vary in time scale. Intermittent and terminal drought could dictate pod formation; seed setting and seed filling by altering the source-sink relationship by way of affecting assimilate production, translocation and partitioning (Amede *et al.,* 2004). Common bean plants exposed to water stress for days to weeks may develop long term physiological strategies such as altering the leaf area, modifying root to shoot ratio and the like. When available soil water is reduced, plants usually undergo three progressive stages of dehydration (Sinclair and Ludlow, 1986). Physiological/morphological mechanisms that may make the plant maintain tissue plant water potential and turgor that sustains assimilation, translocation and partitioning, are therefore of paramount importance (Amede *et al.,* 2004).

REFERENCES

Amede, T., Kimani, P., Ronno, W., Lunze, L. and Mbikay, N. (2004). Coping with Drought: Strategies to Improve Genetic Adaptation of Common bean to Drought Prone Regions of Africa. CIAT Occasional Publication Series, No. 38.

Araus, J. L., Slafer, G. A., Reynolds, M. P. and Royo, C. (2002). Plant breeding and drought in C3 cereals: what should we breed for? *Ann. Bot*. 89: 925–940.

Asrat, A. and Matthew, W. B. (2014). Quantification of drought tolerance in Ethiopian common bean varieties *Agricultural Sciences* Vol. 5, No. 2, 124-139 http://dx.doi.org/10.4236/as.2014.52016.

Assefa, T., Beebe, S. E., Rao, I. M., Cuasquer, J. B., Duque, M. C., Rivera, M. and Lucchin, M. (2013). Pod harvest index as a selection criterion to improve drought resistance in white pea bean. *Field Crops Research* 148: 24–33. https://doi.org/ 10.1016/j.fcr.2013.04.008.

Beck, E. H., Fettig, S., Knake, C., Hartig, K. and Bhattarai, T. (2007). Specific and unspecific responses of plants to cold and drought stress, *J. Biosci*. 32: 501–510.

Beebe, S. (2012). Common bean breeding in the tropics. *Plant Breed. Rev.* Vol. 36 36: 357–426.

Beebe, S. E., Idupulapati, M., Rao, C. C. and Miguel, G. (2008). Selection for Drought Resistance in Common Bean Also Improves Yield in Phosphorus Limited and Favorable Environments. *Crop Science* 48(2): 582-592. https://www.crops.org/ publications/cs/abstracts/48/2/582.

Beebe, S. E., Rao, I. M., Blair, M. W. and Acosta-Gallegos, J. A. (2013). Phenotyping common beans for adaptation to drought. *Frontiers in Physiology* 4: 1–20. https://doi.org/10.3389/fphys.2013.00035.

Binagwa, P., Kilango, M., Magdalena, W. and Rubyogo, J. C. (2016). Bean Research and Development in Tanzania (including bean biofortification). BNFB Inception meeting March 16-18th, 2016Kibo Hotel. Arusha, Tanzania.

Bornet, B., Balatti, P. A. and Branchard, M. (2003). Inter simple sequence repeat (ISSR) markers as a tool for the assessment of both genetic diversity and gene pool origin in common bean (Phaseolus vulgaris L .). *Euphytica* 1995: 297–301.

Broughton, W. J., Hernández, G., Blair, M., Beebe, S., Gepts, P. and Vanderleyden, J. (2003). Beans (*Phaseolus*spp.) – modelfood legumes. *PlantSoil* 252: 55–128.

Carolina, L., Mark, W., Juan, P., Martinez, D., Villegas, R., Meneses, E. H., Murchie, C. P., Bartolomeo, L., Paulo, V., Peter, H. and Manuel, P. (2006). Differential adaptation of two varieties of common bean to abiotic stress I. Effects of drought on yield and photosynthesis *Journal of Experimental Botany* Vol. 57, No. 3, pp. 685–697 doi:10.1093/jxb/erj062.

Catherine, J., Senkoro, G. J., Ley, A. E., Marandu, C. W., MuhamadiMzimbiri, J. M., Umbwe, S. R. and Lyimo, D. (2017). Optimizing Fertilizer Use within the Context of Integrated Soil Fertility Management in Tanzania. In: Fertilizer Use Optimization in Sub-Saharan Africa. Wortmann, C, S. and Sones, K. (eds). CAB International, Nairobi, Kenya. pp. 9–19.

Chaves, M. M., Pereira, J. S., Maroco, J., Rodrigues, M. L., Ricardo, C. P., Osoâ Rio, M. L., Carvalho, I., Faria, T. and Pinheiro, C. (2002). How plants cope with water

stress in the field. Photosynthesisi and growth. *Annals of Botany.* Vol 89: 907-916

CIAT (Centro Internacional de Agricultura Tropical) (1987).Standard system for the evaluation of bean germplams. Van Schoonhoven, A. and Pastor-Corrales, M. A. (compilers). Cali, Colombia. 54pp.

CIAT (Centro Internacional de Agricultura Tropical) (1991). Common beans : research for crop improvement. C.A.B. International in association with Centro Internacional de Agricultura Tropical. Retrieved from https://books. google.co.tz/books? id=CvcbUopfa54C&dq=ORIGIN+OF+COMMON+BEANS&lr=&source=gbs_ navlinks_s.

CIAT (Centro International de Agricultura Tropical). 1980. Bean Program annual report 1979. Cali, Colombia. pp.111. In: *Common beans Research for crop improvement* edited by A. van Schoonhoven and O. Voysespp. 539pp.

Condon, A. G., Richards, R. A., Rebetzke, G. J. and Farquhar, G. D. (2004). Breeding for high water-use efficiency. *J. Exp. Bot.* 55, 2447–2460. doi: 10.1093/jxb/erh277.

Fageria, N. (2002). Nutrient management for sustainable dry bean production in the tropics. *Communications in Soil Science and Plant Analysis.* Vol. 33: 1537 - 1575.

Fang, Y. and Xiong, L. (2014), General mechanisms of drought response and their application in drought resistance improvement in plants. *Cellular and Molecular Life Sciences* 72(4): 673-689.

FAO (Food and Agriculture of the United Nations) (2016). Pulses and Climate Change.

FAO (Food and Agriculture of the United Nations) (2006). FAOSTAT: FAO Statistical Databases. Available on line at: http:// faostat.fao.org/

Fivawo, N. C. and Nchimbi-Msolla, S. (2011). The diversity of common bean landraces in Tanzania, *Tanzania Journal of Natural and Applied Sciences (TaJONAS)* 2(1): 337–351.

Graham, P. H., Rosas, J. C., Estevez de Jensen, C., Peralta, E., Tlusty, B., Acosta-Gallegos, J. and Arraes Pereira, P. A. (2003). Addressing Edaphic Constraints to Bean Production: The Bean/Cowpea CRSP Project In Perspective. *Field Crop Research* Vol. 82179 – 192.

Hillocks, R. J., Madata, C. S., Chirwa, R. and Euphytica (2006). Phaseolus Bean Improvement in Tanzania, 1959–2005. *Kluwer Academic Publishers* 150: 215-222. https://doi.org/10.1007/s10681-006-9112-9.

Jaspa, S. (2008). Identification of Drought tolerant Varieties of Common Bean (*Phaseolus vulgaris* L.) in Tanzania. A Dissertation for Award Degree of Master of Science in Crop Science of Sokoine University of Agriculture. Morogoro, Tanzania. 89pp.

Kanyeka, E., Kamala, R. and Richard, K. (2007). Improved agricultural technologies recommended in Tanzania. pp38-44.

Letaa, E., Kabungo, C., Katungi, E., Ojara, M. and Ndunguru, A. (2014). Farm level adoption and spatial diffusion of improved common bean varieties in southern highlands of Tanzania. Technical report 2012 – 2013. CIAT ARI Uyole, Tanzania.

Mourice, S. K. and Tryphone, G. M. (2012). Evaluation of common bean (Phaseolus vulgaris L.) genotypes for adaptation to low phosphorus. International Scholarly Research Network Agronomy. *ISRN Agronomy, Research Article*.

Mukankusi, C. M., Nkalubo, S., Katungi, E., Awio, B., Luyima, G., Radeny, M. and Kinyangi, J. (2015). Participatory Evaluation of Common Bean for Drought and Disease Resilience Traits in Uganda. CCAFS Working Paper no. 143. CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS). Copenhagen, Denmark. Available online at: [ww.ccafs.cgiar.org] site visited on 12/02/2019.

Nyomora, A. M. S., Katima, J. H. Y. and Ernest, B. (2018). Suitability of Constructed Wetland Treated Domestic Wastewater as Source of Irrigation Water and Nutrients on Common Beans (*Phaseolus Vulgaris*) Performance in Morogoro, Tanzania. *International Journal of Agriculture, Environment and Bioresearch* Vol. 3, No. 05

Rife, T. W. and Poland, J. A. (2014). Field Book: An open-source application for field data collection on Android. *Crop Sci.* 54(4): 1624-1627.

Rosales-Serna, R., Kohashi-Shibata, J., Acosta-Gallegos, J. A., Trejo-López, C., Ortiz-Cereceres, J. and Kelly, J. D. (2004). Biomass distribution, maturity acceleration and yield in drought – stressed common bean cultivars. *Field Crps Research* 85: 203-2011.

Rosielle, A. A. and Hamblin, J. (1981). Theoretical aspects of selection for yield in stress and non-stress environments. *Crop Sci.* 21: 943-946. In: Tilahun, A., Kimani, P., Ronno, W., Lunze, L. and Mbikay, N. (2004). Coping with Drought:

Strategies to Improve Genetic Adaptation of Common bean to Drought Prone Regions of Africa. CIAT Occasional Publication Series, No.38.

Rugambisa, J. (1990). Marketing of beans in SubSaharan Africa and impact of market on new cultivars.

Sinclair, T. R. and Ludlow, M. M. (1986). Influence of soil water supply on the plant water balance of four tropical grain legumes. *Aust. J. Plant Physiol.* 13: 329-341.

Singh, S. P., Gepts, P. and Debouck, D. G. (1991). Races of common bean (*Phaseolus vulgaris*, Fabaceae). *Econ. Bot.* 45: 379–396.

Tekle, A. T. and Melkam, A. A. (2016). Drought Tolerance Mechanisms in Field Crops World Journal of Biology and Medical Sciences Published by *Society for Advancement of Science* Vol. 3(2): 15-39.

Terán, H. and Singh, S. P. (2002). Selection for drought resistance in early generations of common beans populations. *Can. J. Plant Sci.* 82: 491–497.

Thung, M. and Rao, I. M. (1999). Integrated management of abiotic stresses. In Asrat Asfaw and Matthew W. Blair (2014. Quantification of drought tolerance in Ethiopian common bean varieties *Agricultural Sciences* 7 Vol.5, No.2, 124-139 http://dx.doi.org/10.4236/as.2014.52016.

Villordo-Pineda, E., González-Chavira, M. M., Giraldo-Carbajo, P., Acosta-Gallegos, J. A. and Caballero-Pérez, J. (2015). Identification of novel drought-tolerant-associated SNPs in common bean (*Phaseolus vulgaris*). *Frontier in Plant Science*. 6: 546-556. doi: 10.3389/fpls.2015.00546.

White, J. W. and Singh, S. P. (1991). Sources and inheritance of earliness in tropically adapted indeterminate common bean. *Euphytica* 55: 15–19.

Wortmann, C. S., Kirkby, R. A., Eledu, C. A. and Allen, D. J. (1998). Atlas of common bean (*Phaseolus vulgaris* L.) production in Africa. CIAT, Cali, Colombia.

CHAPTER THREE

3.0 ASSESSMENT OF THE EFFECTS OF WATER STRESS ON SEED YIELD OF COMMON BEAN GENOTYPES

3.1 Abstract

Drought stress is among the most important abiotic factors that contribute to the significant yield reduction of common bean (*Phaseolus vulgaris* L.) in Tanzania. Due to unreliable and poor distribution of rainfall, a drought tolerance has become the important trait in common bean growing areas. The main objective of this study was to evaluate 16 common bean genotypes for drought tolerance under three moisture regimes and identify genotypes with specific traits that improved tolerance to drought among 16 lines developed that could be recommended for released and become useful parents in the breeding programs. The experiment was conducted in Maruku, Bukoba under screen – house conditions. Genotypes with greater potential to drought tolerances were identified during the experiment. The two – factors experiment was used in this study in randomized complete block design layout in split – plot arrangement with three replications. The main – plot factor was water level/regimes with three levels (75 ml, 200 ml and 400 ml of water) and sub – plot factor was common bean genotypes with 16 levels. Based on the drought stress indices which includes drought tolerance index (DTI) and Harvest Index (HI), SMC 162, DAB 602, SSIN 1128, DAB 378, DAB 362 and SMR 101 performed better than other tested genotypes. Also, the results showed that genotypes DAB 582, SRC 59, DAB 602, SSIN 1240, SMC 24, SMR 101 and DAB 362 were drought tolerant with lower and high value of the DSI and YSI respectively. Therefore, the later genotypes can be used in the future breeding programs as the parent for drought tolerances and also can used as a new varieties by farmers after one or two more evaluation in the same environment.

3.2 Introduction

Common beans (*Phaseolus vulgaris* L.) is an important crop in Tanzania grown, by a wide range of farming communities (Kilasi, 2010), which has great potential for improving human nutrition due to its high protein content (Manjeru *et al.* 2007), it provides about 38% of utilizable protein and 12- 16% of daily calorific requirements (CIAT, 2008).

Given the high consumption rates of water by agriculture, constraints on water resources can be mitigated through the genetic improvement of drought stress (DS) tolerance in crop species (Porch *et al*. 2009).

Germplasm development has resulted in the release of a number of lines tolerant to DS and has led to a better understanding of the genetics of this trait. Drought tolerance, measured as seed yield, is an additive and quantitative trait with significant interaction with the environment (White *et al.,* 1994). The combination of traits associated with drought tolerance from both gene pools can result in significant gains in seed yield in drought-prone environments (Beebe *et al.* 2008). The presence of large amounts of genetic variability for drought tolerance is fundamental since it allows the selection of the best varieties for breeding programs (Gustavo *et al.,* 2003).

Improved photosynthate acquisition, accumulation, and then remobilization have been observed as important mechanisms for adaptation to drought stress (Asfaw *et al.,* 2012), which is considered one of the most important causes of yield reductions (Gustavo *et al.*, 2003). Better remobilization of photosynthates to grain production is needed for the success of superior genotypes under stress (Polania *et al.,* 2017).

Due to the importance of reproductive development in the DS response, higher water requirements during reproductive development, and the occurrence of terminal DS in production areas worldwide, germplasm evaluation in common bean is commonly

conducted through the application of DS between pre-flowering and physiological maturity (Porch *et al.*, 2009).

Drought susceptibility index (DSI) was found to be the most reliable index to identify drought tolerant genotypes, while drought intensity index (DII) and stability index (SI) were better suited to identifying intensity of drought at a location and grouping of drought tolerant genotypes, respectively (Kilasi, 2010). The genotypes that had DSI value lower than unit were selected as drought tolerant genotypes and those whose DSI values were higher than one, were selected as drought sensitive genotypes (Salyula, 2013).

Two dry matter partitioning indices have been shown to be relevant to improved drought resistance: pod partitioning index (PPI) which indicates the extent of mobilization of assimilates from the vegetative structures to pod formation, and pod harvest index (PHI) which indicates the extent of mobilization of assimilates from the pod wall to grain formation (Rao *et al.*, 2013). Drought stress also caused poor pod-partitioning and harvest index as shown by the other indices and traits evaluated at harvest (Asfaw and Blair, 2014).

Pod harvest Index (PHI) reflects plant efficiency in partition of photosynthates from vegetative shoot structures to pods and from pod wall to grain, which varies with the genotypes and is affected by drought (Beebe *et al.*, 2009).The ability of genotypes to partition the stored vegetative biomass to reproductive organs to a large extent determines sink establishment and economic yield under drought stress (Chaves *et al.*,2002) which reduce biomass and seed yield, harvest index, and seed weight (Muñoz-Perea *et al.*, 2006).

The main objective of this study was to evaluate 13 genotypes with specific traits that have been improved for tolerance to drought some of which could be recommended for release or useful parents in the breeding programs.

3.3 Material and Method

3.3.1 Experimental Site and Materials

The study was conducted in screen house for two consecutive seasons; October – January 2017/2018 and February – May 2018 at TARI Maruku station which is located in Bukoba District, Kagera Region. During the experimental period, the minimum, mean and maximum temperatures were 14 °C, 22 °C and 31 °C respectively.

A total of 16 common bean genotypes, 13 genotypes were introduced from the International Center for Tropical Agriculture, CIAT, two released varieties (Lyamungu 90 and JESCA as drought check) and one landrace (Ibwera as local check) were used in the experiment. The main characteristics of these genotypes are described in Table 3.1. The genotypes had different plant growth habit, seed sizes, seed color and seed color patterns.

Table 3.1: Characteristics of the common bean genotypes used under experimentation

Genotype	Seed size	SCP[1]	SCS[2]	SBS[3]	GH
DAB 378	Large	R	2	3	Type I
DAB 219	Large	M	6	2	Type I
DAB 291	Large	M	6	3	Type I
SAB 659	Large	M	6	1	Type I
SCR 59	Medium	O	6	1	Type II
SSIN 1128	Medium	O	2	1	Type III
SSIN 1240	Medium	M	6	1	Type III
IBWERA	Medium	R	2	1	Type I
JESCA	Large	O	2	1	Type I
Lyamungu 90	Large	M	2	2	Type I
SMC 162	Medium	O	1	1	Type II
SMC 24	Medium	O	1	2	Type III
SMR 101	Large	O	1	1	Type I
DAB 602	Large	M	2	1	Type I
DAB 582	Large	R	2	1	Type I
DAB 362	Large	R	2	3	Type I

GH, Growth habit

1 Seed color Pattern: O – No pattern, M – Mottled, R – Striped, J – speckle, P – pinto, B – bicolor,

2 Seed color Scale: 1 – white, 2 – Cream-beige, 3 – yellow, 4 – brown maroon, 5 – pink, 6 – Red

3 Seed Brilliance Scale: 1 – Dull, 2 – Semi-Shine, 3 – Shiny (CIAT, 1987).

3.3.2 Experimental design and layout

The two – factors experiment was used in this study in randomized complete block design layout in split – plot arrangement with three replications. The main – plot factor was water level/regimes with three levels (75 ml, 200 ml and 400 ml of water) and sub – plot factor was common bean genotypes with 16 levels.

3.3.3 Soil Preparation

After sieving the soil was steam boiled at 100 ^{o}C for three hour as a treatment measure against soil borne pathogens. Treated soil mixture containing forest soil, sand and farm yard manure in ratio of 1:1:1 was filled in the plastic pot. Each pot was filled with 5 kg of air – dried soil and watered to field capacity.

3.3.4 Planting and water Treatment

Four seeds were sown in each pot and later on were thinned to two seedlings per pot one week after germination. All pots were well watered equally to field in order to establish the trial until plants had three trifoliate leaves when the water stress treatments were imposed. There were three levels of water treatment as follows 75 ml, 200 ml and 400 ml of water was applied for treatment I (T1), II (T2) and III (T3) respectively, water was monitored using a tensiometer and applied to the soil at the top of the pot, the treatment III was considered as control.

3.3.5 Data collection

Days to flowering and days to maturity were recorded as the number of days from planting to when 50% of plants in a pot had at least one open flower and when 75% of plants in a pot had at least 90% of their pods dried, respectively (Rezene *et al.*, 2012).

The destructive sampling was done at mid-pod filling and harvest. At mid – pod filling, plant of each genotype from each pot was selected for destructive sampling from both moisture stressed and no stress treatments (Polania *et al.*, 2016).Selected plant was cut to soil – surface level in the pot and then plants were separated into leaves (without petioles), stems and the remaining (pods and reproductive structures) plant parts. Those plant parts were oven dried for 48 hrs at 80˚C and after drying of the samples, dry weight of each sample was measured using electronic weighing balance to determine total dry matter production and dry matter distribution in different plant parts (leaf biomass, stem biomass and pod biomass)(Asfaw and Blair, 2014). These data were used to determine dry matter partitioning indices: Pod partitioning index (PPI), pod harvest index (PHI) and pod harvest index (PHI).

At the time of harvest; data recorded during the harvest were dry weights of stem biomass, pod biomass, seed biomass, number of pods per plant, dry weight of pod wall biomass (pod without seeds), seed number per pod, seed number per plant.

Each plant was harvested from each pot depending on the time of attaining allowed moisture content for harvest. Plant were cut and dry weights of stem, pod, seed, and pod wall, seed number per plant (SPP) and pod number per plant (PPP) were recorded.

The severity of drought stress on plant traits, the Drought Intensity Index (DII) was calculated as $DII = 1 - X_{ds}/X_{ns}$, where X_{ds} and X_{ns} are the mean yield of all genotypes under Drought Stress (DS) and Non-Stress (NS) environments, respectively. Drought susceptibility index (DSI) for each genotype was calculated as follows:

$DSI = (1 - Y_{ds}/Y_{ns})/DII$

Where Y_{ds} and Y_{ns} are mean yields of a given genotype under DS and NS conditions, respectively (Fischer and Maurer 1978).

DSI and DII were derived from the grain yield data under the three moisture regime treatments (Kilasi, 2010).

Drought tolerance index: was calculated by the formula given by Fischer and Maurer (1978).

Drought tolerance index = $\frac{\textbf{Grain yield under stress}}{\textbf{Grain yield under normal irrigation}}$…… Equation 1

Under such conditions common bean genotypes with higher mean yields in NS and DS environments and lower DSI values are desirable (Terán and Singh, 2002).

The geometric mean (GM), harvest index (HI), pod harvest index (PHI), pod wall biomass proportion (PWBP), pod partitioning index (PPI) were determined as described by Beebe *et al.* (2013).

i. Geometric mean Productivity (GMP)

   GMP = (Yns × Yds) 1/2 where ns is non-stress and ds is drought stress.

ii. Mean productivity (MP) = $(Y_{DS} + Y_{NS})/2$, where NS is non stress and DS is drought stress.

iii. Harvest index (HI): seed biomass dry weight at harvest / total shoot biomass dry weight at mid – pod filling × 100.

iv. Pod harvest index (PHI): the PHI for each genotype is determined by seed biomass dry weight at harvest / pod biomass dry weight at harvest × 100.

v. Pod wall biomass proportion (PWP) (%): pod wall biomass dry weight at harvest / pod biomass dry weight at harvest × 100.

vi. Pod partitioning index: pod (PPI) biomass dry weight (without seeds) at harvest/total shoot biomass dry weight at mid – pod filling × 100.

vii. Yield Stability Index (YSi); Grain yield under drought stress /grain yield under non-stress

viii. Percentage Yield reduction rate (YRR) was determined using formulae described by Fischer and Maurer (1978). YRR due to drought stress was calculated as [(mean value non-stress traits) - (mean value of drought stress trait)]/mean value of non-stress (Rezene *et al.,* 2012).

3.3.4 Data analysis

Analysis of variance of the variables was done using GenStat Discovery Version edition 13 Computer program and means separation test was done using a Duncan Multiple Range Test (DMRT). Relationships between selected parameters were determined using the Pearson‘s simple correlation test.

3.4 Results and Discussion

3.4.1 Analysis of variances

Analysis of variances for treatments was highly significantly (Table 3.2). However, for genotypes all traits showed significant variation except pod wall proportion. The genotype x treatment had not brought any significant differences on RW and NPPP at 0.05 level of significant.

Table 3.2: Analysis of variance

TRAIT	PPP	SPP	EY	TSB	PBM	PWB	RL	RW	PWP	PPI	RSR
T	**	**	**	**	**	**	**	**	**	**	**
G	**	**	**	**	**	**	**	**	ns	**	**
G x T	ns	**	**	**	**	**	**	ns	*	**	*
CV%	4.0	16.6	15.9	12.8	15.0	14.6	3.8	14.2	4.0	5.7	20.3
S.E	0.2	1.2	0.3	1.2	0.8	0.5	0.3	0.2	1.9	2.9	2.65

T: Treatment, G: Genotype, G x T: Genotype X Treatment Interaction, EY: Economic Yield Biomass (g plant^{-1}), TSB: Total Stem Biomass, PBM: Pod Biomass (g plant $^{-1}$), PWB: Pod Wall Biomass (g plant $^{-1}$g), SB: Seed Biomass (g plant $^{-1}$), RL: Root Length (cm), RW: Root Biomass (g plant $^{-1}$), PPP: Pod Per Plant, SPP: Seed Per Pod, PWP: Pod Wall Proportion, PPI: Pod Partition Index, RSR: Root Shoot Ratio

*significant at P≤ 0.05: ** significant at P≤ 0.01, ns: not significant

As it was reported by Kilasi (2010) that DSI was found to be the most reliable index to identify drought tolerant genotypes. The genotypes that had DSI value lower than 1 were selected as drought tolerant genotypes and those whose DSI values higher than a unit, were selected as drought sensitive genotypes (Salyula, 2013). Based on the DSI, results revealed that genotype DAB 582, SCR 59, IBWERA (local) and DAB 602 performed better because they had lower values of DSI which were – 0.99, 0.00, 0.07 and 0.08 respectively, while genotypes DAB 219, DAB 291, SSIN 1128 and SAB 659 were the least performers based on the DSI which were 1.4, 1.4, 1.7 and 2.2 respectively as shown in the Table 3.3.

Based on the mean productivity of the tested genotypes, SMC 162, SSIN 1128, DAB 602 and DAB 378 were the genotypes which had higher yield compared with other with the mean productivity of 5.2, 5.1, 4.5 and 4.3 g plant$^{-1,}$ while SAB 659, DAB 291, SMC 24 and Lyamungu 90 were the genotypes with lower yield with mean productivity of 1.97, 1.38, 1.27 and 1.10 respectively.

Furthermore, the genotypes responded differently to the level of moisture stress imposed during the experiment, based on the percentage yield reduction rate (YRR) The genotypes which had low value of YRR were DAB 582, SCR 59, IBWERA, and DAB 602 which had values of -45, 0.00, 3.19 and 3.82 respectively. This means these genotypes were drought tolerant while the last four genotypes which had higher YRR.

(DAB 291, DAB 219, SSIN 1128 and SAB 659) were drought sensitive with the values of 61.7, 61.7, 74.8 and 100.00 respectively. The genotypes with low values of the YRR were the ones with the high values of yield stability index (YSI) as shown in Table 3.3.

Table 3.3: Grain Yield and Selection indices for drought tolerance in response to grain yield under stress (T1) and non-moisture stress (T3) conditions of the 16 tested common bean genotypes

	Grain Yield (g/plant)										
Genotype	**T2**	**T3**	**HI**	**PHI**	**DSI**	**DTI**	**MP**	**GMP**	**YRR**	**YSI**	**PPI**
DAB 219	1.5	3.8	4.2	33.6	1.4	0.4	2.7	2.4	61.7	0.4	70.2
DAB 291	0.8	2.0	2.5	36.3	1.4	0.1	1.4	1.2	61.7	0.4	64.4
DAB 362	2.9	5.2	9.4	30.3	1.0	1.0	4.0	3.9	44.9	0.6	65.8
DAB 378	2.5	6.4	10.4	43.2	1.3	1.1	4.5	4.0	60.9	0.4	73.2
DAB 582	3.0	2.1	3.4	35.5	-1.0	0.4	2.5	2.5	-45.1	1.5	67.3
DAB 602	4.2	4.4	8.5	27.8	0.1	1.3	4.3	4.3	3.8	1.0	65.5
IBWERA	2.0	2.1	10.9	46.7	0.1	0.3	2.1	2.1	3.2	1.0	77.4
JESCA	2.1	3.8	6.9	29.5	1.0	0.6	3.0	2.8	44.7	0.6	68.2
LYAMUNGU 90	0.9	1.3	5.9	54.1	0.6	0.1	1.1	1.1	26.4	0.7	59.2
SAB 659	0.0	3.9	4.5	19.5	2.2	0.0	2.0	0.0	100.0	0.0	69.5
SCR 59	2.1	2.1	8.6	43.5	0.0	0.3	2.1	2.1	0.0	1.0	71.0
SMC 162	3.1	7.3	11.1	43.1	1.2	1.6	5.2	4.8	56.9	0.4	66.1
SMC 24	1.0	1.5	1.8	20.1	0.7	0.1	1.3	1.2	31.1	0.7	36.5
SMR 101	2.6	4.3	9.9	45.5	0.9	0.8	3.5	3.4	38.8	0.6	67.6
SSIN 1128	2.0	8.1	13.9	48.0	1.6	1.1	5.1	4.1	74.8	0.3	64.9
SSIN 1240	2.3	2.7	4.9	43.9	0.4	0.4	2.5	2.5	17.1	0.8	62.2

DSI: Drought Susceptibility Index, DTI: Drought Tolerance Index, MP: Mean Productivity, T1=Moisture stressed treatment, T3 = Non –moisture stressed treatment, GMP: Geometric Mean Productivity, YRR: Yield Reduction Rate %, YSI: Yield Stability Index.

3.4.2 Association among traits

All observed traits were positively correlated to each other as shown in the Table 3.4. The SWPP of the tested genotypes under moisture stress (T2) had shown a highly positive correlation with TPW (r = 0.99) and TSW (r = 0.87) while in non-moisture stress (T3), the association of the SWPP and TSW was increased by 0.11 to r = 0.98. This revealed that during the moisture stress the association of seed weight and total shoot weight is decreased to make sure that photosynthetic materials were relocated to economic part of the plant during moisture stress. This indicates their potential use in the selection of

genotypes yielding well under drought stress, the results of this study is also in line with that of Darkwa *et al.* (2016).

The NSPP was highly positively correlated with RL (r = 0.62) and RW (r = 0.59) in the moisture stress condition but in non-moisture stress condition, the association of NSPP with RL was decreased by 0.20 to r = 0.42 with no significance while its association with RW was increased to r = 0.63. This means that during the non-moisture stress condition plant gets enough water therefore there were no need to extending root length for water extraction. Exposure to drought affects total biomass and seed yield, photosynthates translocation and partitioning, root length and mass.

Table 3.4: Correlation among seven indices with respect to grain yield of the 16tested common bean genotypes performances at moisture stress (T2) and non-moisture stress (T3) regimes

	Grain Yield								
	Stress (T2)	**Non – Stress (T3)**	**PPI**	**PHI**	**HI**	**DSI**	**DTI**	**MP**	**GMP**
T2	-								
T3	0.2 ns	-							
PPI	0.3 *	0.1 ns	-						
PHI	0.2 *	0.0	0.1 ns	-					
HI	0.2 *	0.6 **	0.3 *	0.36 *	-				
DSI	0.2 ns	0.3 *	0.1 ns	0.0	0.0	-			
DTI	0.6 ***	0.7 ***	0.2 ns	0.0	0.5 *	0.0	-		
MP	0.5 *	0.9 ***	0.1 ns	0.0	0.6 **	0.0	0.9 ***	-	
GMP	0.8 ***	0.6 *	0.4 *	0.1 ns	0.5 *	0.0	0.9 ***	0.8 ***	-

PPI: Pod Partition Index, PHI: Pod Harvest Index, HI: Harvest Index, DSI: Drought Susceptibility Index, DTI: Drought Tolerance Index, MP: Mean Productivity, GMP: Geometric Mean Productivity

*significant at P≤ 0.05: ** significant at P≤ 0.01, ns: not significant.

The study revealed a positive and significant correlation between grain yield and dry matter partition indices (PPI, PHI, and HI) (Table 3.5). This positive relationship indicates that genotypes with higher values of grain yield under drought stress are physiologically responsive to drought stress by partitioning and trans-locating its photosynthetes to economic part of the plant (pods and seeds). Other studies have suggested that the drought resistance in common bean is associated with a more efficient dry matter partitioning to pod formation and grain production (Polania *et al.,* 2016).

In this regards, PHI could serve as a useful selection criterion for improving drought resistance because of its simplicity in measurement and its significant correlation with grain yield under both irrigated and drought conditions (Assefa*et al.,* 2013).

The genotypes Lyamungu 90, SSIN 1128, IBWERA SMR 101, SSIN 1240 were superior in their ability to partition greater proportion of biomass to pod with grain yield of 0.9, 2.0, 2.0, 2.6 and 2.3 g/plant respectively in drought stress environment while genotypes IBWERA, DAB 378, SCR 59, DAB 219 and SAB 659 were superior in partition its biomass to grain production after being exposed to moisture stress environment (Table 3.3).

As shown in the Table 3.4, NPP, PWW, NSPP, SWPP and TPW were highly positive and significantly correlated to each other in both moisture stress (T2) and non-moisture stress (T3) environment. Also the results revealed that the RW had a positive and significant association with most of the traits except TPW in non-moisture stress but it was observed that RW had positive and significant association with NSPP only in moisture stress environment.

Root length (RL) had a positive significant effect on NSPP in moisture stress environment while had no significant in non-moisture stress environment. This means that during the moisture stress, plants had potential to extend its tap roots deeper to extract more water from the soil, the previous study by Ndimbo *et al.* (2015) reported the same result.

Table 3.5: Pearson's correlation coefficients, r, of the grain yield and other traits of the tested 16 genotypes under moisture stress (T2) (lower diagonal) and non-stress (T3) (upper diagonal) conditions

Trait	NPP	PWW	NSPP	SWPP	TPW	SW	RL	RW	TSW
NPP	-	0.79**	0.97**	0.86**	0.82**	0.31^{ns}	0.39 ^{ns}	0.60*	0.84**
PWW	0.80**	-	0.75**	0.98**	0.99**	0.20^{ns}	0.13 ^{ns}	0.50*	0.97**
NSPP	0.86**	0.77**	-	0.83**	0.78**	0.31^{ns}	0.42 ^{ns}	0.63**	0.80**
SWPP	0.78**	0.96**	0.76**	-	0.99**	0.23^{ns}	0.16 ^{ns}	0.51*	0.98**
TPW	0.79**	0.99**	0.77**	0.99**	-	0.21^{ns}	0.14 ^{ns}	0.51*	0.98**
SW	0.07 ^{ns}	0.25 ^{ns}	0.11^{ns}	0.19 ^{ns}	0.22 ^{ns}	-	0.00 ^{ns}	0.03 ^{ns}	0.40 ^{ns}
RL	0.41^{ns}	0.42 ^{ns}	0.62**	0.31 ^{ns}	0.38 ^{ns}	0.42^{ns}	-	0.69**	0.13 ^{ns}
RW	0.45 ^{ns}	0.28 ^{ns}	0.59*	0.32 ^{ns}	0.29 ^{ns}	0.13^{ns}	0.69**	-	0.49 ^{ns}
T SW	0.66 ^{ns}	0.90**	0.64**	0.87**	0.89**	0.61**	0.49 ^{ns}	0.30 ^{ns}	-

NPP: Number of pod per plant, PWW: Pod wall weight (without seeds), NSPP: Number of seeds per plant, SWPP: Seed weight per plant, TPW: Total pod weight, SW: Stem weight, RL: Root length (Tap root), RW: Root weight, TSW: Total shoot weight.

*significant at P≤ 0.05: ** significant at P≤ 0.01: ns: not significant

Table 3.6: Average, minimum, maximum and percentage reduced of four selected traits 16 common bean genotypes at three different moisture regime levels

Trait	Average			Minimum			Maximum			Percentage Reduced	
	T1	T2	T3	T1	T2	T3	T1	T2	T3	T1	T2
Economic yield (EY)	0.50	2.07	3.81	0.00	0.60	1.27	1.13	4.20	8.07	86.88	45.67
Number of pod per plant (PPP)	1.08	5.19	8.19	0.00	1.50	2.00	3.33	8.67	13.00	86.81	36.63
Number of seed per pod (SPP)	1.40	3.42	4.63	0.00	1.00	3.00	3.00	5.00	6.00	69.76	26.13
Root length (RL)	4.73	12.43	11.94	0.00	7.30	8.17	12.00	18.17	20.17	60.39	-4.10

T1: Treatment 1, T2: Treatment 2, T3: Treatment 3.

The yield and yield components economic yield (EY), number of pod per plant (PPP), number of seeds per pod (SPP) together with root length were used to assess the responses of the genotypes to different levels of the water regime. The genotypes responded differently against moisture levels. The T 1 reduced economic yield, number of pod per plant, number of seed per pod and root length of the genotypes by 86.88%, 86.81%, 81.00% and 60.39% respectively, while T 2 had reduction of the same by 45%, 36.63%, 41.25% and -4.10% of the reduces economic yield, number of pod per plant, number of seed per pod and root length respectively as shown on Table 3.6. Also the study revealed a negative reduction of the root length under moisture stress due to the fact that when plant exposed to stress environment extend it tap root deeper in the lower horizon to extract more water (Table 3.6).

The reduction in economic yield of the genotypes after they were imposed to moisture stress was associated with the decrease in photosynthate assimilation and poor carbohydrate partitioning to the developing grain while reduction in number of pods per plant in drought – stress as compared with the non-stress condition. This may have been due to a reduction in flower fertilization under drought-stress conditions. Ambachew *et al.*

(2016) suggests that common bean responds to drought stress by increasing root growth. Yield-component traits are generally good indicators of overall drought stress (Ambachew *et al.*, 2016). This study revealed the significant reductions of the number of PPP and SPP under moisture stress in similar manner as reported by Ambachew *et al.* (2016), Asfaw and Blair (2014), Lizana *et al.* (2006).

Table 3.7: Mean economic yield (g/plant) of the 16 tested genotypes under three moisture regime treatments

	Yield (g plant $^{-1}$)				RSR		PWP%			PPI	PHI	
Genotype	**T1**	**T2**	**T3**	**Mean**	**T2**	**T3**	**T2**	**T3**	**T2**	**T3**	**T2**	**T3**
DAB 219	0.0	1.5	3.8	1.8	7.5	8.7	61.8	60.7	37.7	70.2	56.3	44.6
DAB 291	0.7	0.8	2.0	1.2	12.7	15.3	40.7	60.3	47.9	64.4	37.3	50.0
DAB 362	0.0	2.9	5.2	2.7	6.4	10.0	59.7	61.2	74.5	65.8	47.8	43.0
DAB 378	0.9	2.5	6.4	3.3	18.5	10.1	53.8	64.3	64.6	73.2	55.9	39.0
DAB 582	0.3	3.0	2.1	1.8	4.4	25.8	38.9	60.8	43.2	67.3	31.3	50.5
DAB 602	0.0	4.2	4.4	2.9	6.4	9.9	62.6	63.0	63.1	65.5	42.1	41.4
IBWERA	0.5	2.0	2.1	1.5	15.4	17.5	65.0	61.9	57.8	77.4	52.3	50.8
JESCA	0.0	2.1	3.8	2.0	9.5	11.0	66.0	61.1	73.3	68.2	44.2	44.3
LYAMUNGU 90	1.0	0.9	1.3	1.1	36.7	22.4	62.4	62.2	72.7	59.2	57.7	50.3
SAB 659	0.2	0.0	3.9	1.4	0.0	9.3	0.0	62.0	0.0	69.5	0.0	43.1
SCR 59	0.9	2.1	2.1	1.7	32.0	32.1	61.1	65.5	67.0	71.0	50.0	43.9
SMC 162	1.1	3.1	7.3	3.8	16.3	7.4	57.1	57.2	67.2	66.1	50.1	45.8
SMC 24	0.0	1.0	1.5	0.8	13.0	7.5	45.9	42.0	45.3	36.5	29.8	30.6
SMR 101	1.1	2.6	4.3	2.7	25.7	14.5	58.6	57.4	73.6	67.6	51.1	47.7
SSIN 1128	1.1	2.0	8.1	3.7	22.5	10.2	63.3	59.5	60.5	64.9	45.9	43.7
SSIN 1240	0.1	2.3	2.7	1.7	34.8	13.3	54.7	60.3	72.2	62.2	60.7	48.7
AVERAGE	0.5	2.1	3.8	2.1	16.4	14.1	53.2	59.9	57.5	65.6	44.5	44.8

RSR: Root – Shoot ratio, PWP: Pod wall proportion, PPI: Pod partition index, T1: Treatment 1, T2: Treatment 2, T3: Treatment 3.

The average yield effects of all tested genotypes were 0.5 and 2.06 g plant $^{-1}$ for treatment 1 and treatment 2 respectively (Table 3.7) which give a yield reduction rate of 86.88% 45.67% respectively, while the non-stress treatment had an average yield of 3.81 g plant $^{-1}$.The study revealed two genotypes DAB 582 and SCR 59 were able to increase their yield by 45.1% under moisture stress (T2) and maintaining the yield regardless of the stress respectively. DAB 582 performed well under moisture stress due to its ability to reduced root to shoot ratio and pod wall proportional by 83% and 36.0% respectively. Genotype SAB 659 did not perform well at all in moisture stress (T2) because all plants wilted.

The effects of moisture stress on dry matter distribution

Two dry matter partitioning indices have been shown to be relevant to improved drought resistance: pod partitioning index (PPI) which indicates the extent of mobilization of assimilates from the vegetative structures to pod formation (Rao *et al.,* 2013). The study revealed that the dry matter distribution of the 16 genotypes responded significantly to the moisture stress. Drought stress caused the significant reduction of the average pod partitioning index by 8 % from 65.56 in no stress treatment (T3) to 57.55 in stress treatment (T2) (Table 3.7).

Root shoot ratio (w/w)

The ratio of the root biomass and the total shoot biomass revealed that DAB 582, DAB 362, DAB 602 and DAB 219 genotypes had lower ratio when subjected to the moisture stress (T2) compared with other genotypes with the average scores of 4.36%, 6.4%, 6.44% and 7.54% respectively while Lyamungu 90, SCR 59, SMR 101, DAB 378 had higher ratios of 36.68, 31.97, 25.74 and 18.51 respectively (Table 3.7). In non-moisture stress treatment (T3), SMC 162, SMC 24, DAB 219 and DAB 659 were the first four genotypes which had lower ratio of the root to shoot biomass with the values of 7.42%, 7.51%,

8.67% and 9.26% respectively. While SCR 59, DAB 582, Lyamungu 90 and IBWERA genotypes had higher percent of the root biomass to total shoot biomass.

Pod wall proportion

Pod wall proportions, (PWP) of the tested genotypes also differed significantly with respect to the moisture stress treatments. It was observed that the average pod wall proportion of the tested genotypes dropped from 59.94% in no stress treatment to 53.20% in stress II treatment.

The study also revealed that DAB 582, DAB 291, SMC 24 and DAB 378 were the genotypes that had lower contribution to pod wall biomass when subjected to the moisture stress (T2) compared with other tested genotypes with 38.9, 40.7, 45.9 and 53.83% of the pod wall biomass in the pod biomass respectively. While the last four genotypes JESCA, IBWERA, DAB 602, Lyamungu 90 had higher contribution of the pod wall biomass to the pod biomass of 65.97%, 64.96%, 62.60% and 62.43% respectively.

In the non-moisture stress treatment (T3), the SMC 24 had lower contribution of the pod wall biomass of 41.97% to the pod biomass compared with other genotypes as shown in Table 3.4.

Pod partitioning Index

The pod dry matter partition index revealed that DAB 362, SMR 101, JESCA and Lyamungu 90 were the genotypes which had higher PPI values of 74.48%, 73.59%, 73.28% and 72.73% respectively for the T 2 but in T 3, IBWERA, DAB 378, SCR 59 and DAB 219 had performed better than other genotypes with values of 77.4%, 73.2, 71.0 and 70.2 as shown in Table 3.4. This means that the earlier genotypes have got high ability of reallocating its resource (photosynthates) to the pod when gets stressed but under non – stress environment the very same genotypes have low their PPI compared to later

genotypes. This revealed that DAB 362, SMR 101, JESCA and Lyamungu 90 are the better genotypes to be grown in drought prone environments.

3.4.3 Effect of drought stress on seed yield and yield components

Figure 3.1 reveals that in treatment 1, genotypes SMC 162, SSIN 1128, SMR 101 and Lyamungu 90 were the ones which performed best among the tested genotypes with the mean economic yield of 1.13, 1.13, 1.07 and 1.00 g plant^{-1} respectively, while in the treatment 3 genotypes DAB 602, SMC 162, DAB 582, DAB 362 and SMR 101 performed better than others with the mean yield of 4.37, 3.13, 3.00, 2.88 and 2.63 g plant $^{-1}$. For the case of treatment 3, the mean performances of the genotypes SSIN 1128, SMC 162, DAB 378, DAB 362 and DAB 602 were higher compared with others which were 8.07, 7.27, 6.4, 5.2, 4.37 g plant $^{-1}$.

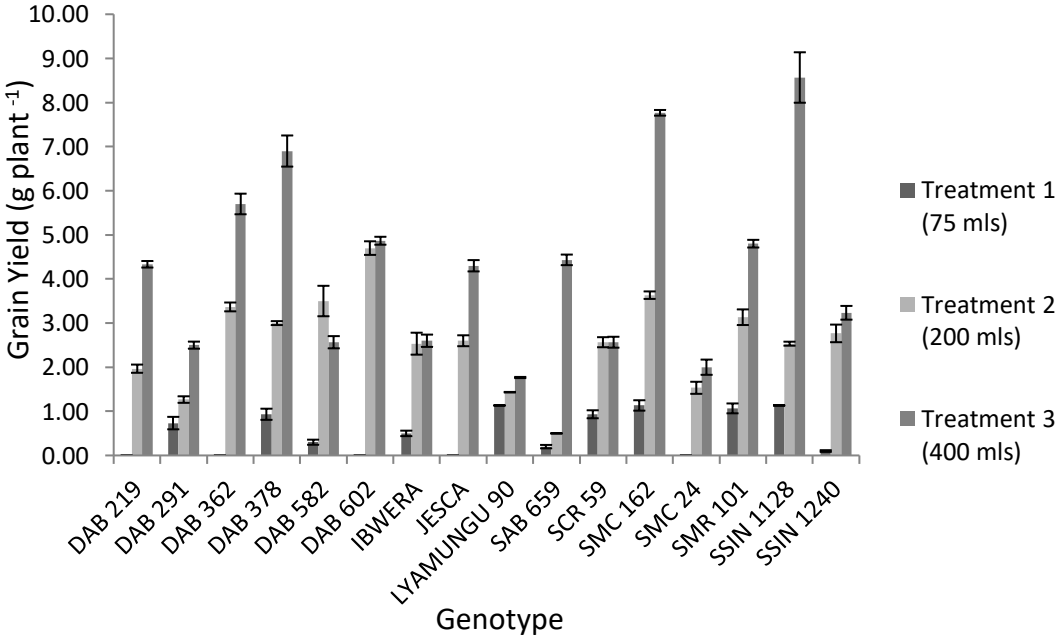

Figure 3.1: Mean economic yield of the 16 tested genotypes under different moisture regime treatments

However, DAB 582 was performed well under drought stress (3.0 g/plant) compared to its performance in non – moisture stress condition (2.1 g/plant), this is associated with its

ability to remobilize photosynthates to grain development during stress. Genotypes SSIN 1128 and SMC 162 had performed better under non-moisture stress condition compared with others but were highly sensitive to moisture stress as it reduced its seed yields were reduced by 74.8% and 56.9% respectively under moisture stress (T2) which was different to other genotypes such as DAB 602, DAB 362 which reduced its yield by 3.8% and 44.9% respectively under the same condition.

Also the results revealed that genotype DAB 582 performed better under moisture stress (T2) by increased yield of 45.1%. These genotypes were able to remobilize the photosynthates to economic part of the plant while the genotype SCR 59 stabilized its yield regardless of the moisture stress condition (Table 3.3).

3.5 Conclusion

The current study revealed that there was a positive and significant association between the grain yield of the tested genotypes and the dry matter partitioning indices; PPI, PHI, HI, and DTI in moisture stress environment, this meant during the drought stress plants had ability to partitioned its photosynthates from the vegetative structures to pods and grain production.

It was also observed that there were a positive association (r = 0.62 **) of the tap root length and the number of seeds per pod during the moisture stress environment. Genotypes SMC 162, DAB 602, SSIN 1128, DAB 378, DAB 362 and SMR 101 had expressed their superiority in tolerating moisture stress with higher values of HI and DTI.Harvest index (HI) has proved to be an important trait to breeders in identifying genotypes that are adapted to drought stress through better photosynthates mobilization.

REFERENCES

Acosta-Gallegos, J. A. and Adams, M. W. (1991). Plants traits and yield stability of common bean (*Phaseolus vulgaris*) cultivars under drought stress. *Journal of Agricultural Science* 117: 213–219.

Ambachew, D. F., Mekbib, A., Asfaw, S. E. and Beebe, M. W. B. (2015). Trait associations in common bean genotypes grown under drought stress and field infestation by BSM bean fly, *Crop J*. 3: 305–316.

Asfaw, A. and Matthew, W. B. (2014). Quantification of Drought Tolerance in Ethiopian Common Bean Varieties. *Agricultural Sciences* 5(2): 124–39.

Asfaw, A., Matthew, W. B. and Struik, P. C. (2012). Multienvironment Quantitative Trait Loci Analysis for Photosynthate Acquisition, Accumulation, and Remobilization Traits in Common Bean Under Drought Stress. *Genes|Genomes|Genetics* 2(5): 579–95. http://g3journal. org/ lookup/doi/10. 1534/g3.112.002303.

Assefa, T., Beebe, S., Rao, I. M., Cuasquer, J., Duque, M. C. and Rivera, M. (2013). Pod harvest index as a selection criterion to improve drought resistance in white pea bean. *Field Crop Res.* 148: 24–33.doi:10.1016/j.fcr.2013.04.008.

Beebe, S. E., Idupulapati, M. R., César, C. and Miguel, G. (2008). Selection for Drought Resistance in Common Bean Also Improves Yield in Phosphorus Limited and Favorable Environments. *Crop Science* 48(2): 582-593. https://www.crops.org/ publications/cs/abstracts/48/2/582.

Beebe, S. E., Idupulapati, M. R., Matthew, W. B. and Jorge, A. A. (2013). Phenotyping

Common Beans for Adaptation to Drought *Frontiers in Physiology* 4: 1–20. http://www.ncbi .nlm.nih.gov/ pubmed/ 23507928.

CIAT (Centro International de Agricultura Tropical) (1980). Bean Program annual report 1979. Cali, Colombia. p.111. In: *Common beans Research for crop improvement* edited by A. van Schoonhoven and O. Voysespp 539pp.

Darkwa, K., Ambachew, D., Mohammed, H., Asrat A. and Matthew, W. B. (2016). Evaluation of Common Bean (*Phaseolus Vulgaris* L.) Genotypes for Drought Stress Adaptation in Ethiopia. *The Crop Journal* 4(5): 367–76. http://www.sciencedirect. com/science/article/ pii/S2214514116300617.

Fischer, R. A. and Maurer, R. (1978). Drought resistance in spring wheat cultivars: I. Grain yield re- sponses. *Aust. J. Agric. Res*. 29: 897-912.

Gustavo, M. S., Saulo de Tarso, A., Carlos, D. G. and Ferraz de Oliveira, R. (2003). Drought stability in different common bean (*Phaseolus Vulgaris* L.) genotypes. *Crop Breeding and Applied Biotechnology* 3: 203–208. http://www.esalq. usp.br/lepse/imgs/conteudo_ thumb/Drought-stability-in-different- ommon-bean-Phaseolus-vulgaris-L---genotypes-.pdf.

Lizana, C. (2006). Differential Adaptation of Two Varieties of Common Bean to Abiotic Stress I. Effects of Drought on Yield and Photosynthesis. *Journal of Experimental Botany 57*(3):685–97. Retrieved December 13, 2016 (http://www.ncbi.nlm.nih.gov/pubmed/16415330).

Manjeru, P., Madanzi, T., Makeredza, B., Nciizah, A., and Sithole M. (2007). Effects of Water Stress at Different Growth Stages on Components and Grain Yield of Common Bean (*Phaseolus Vulgaris* L.).*Crop Science* 8: 299–303.

Mary, A., Ndimbo, S. and Nchimbi-Msolla, E. S. (2015. Effects of moisture stress levels at different growth stages on nodulation and nitrogen fixation in common bean (*Phaseolus vulgaris* L.) genotype. *Asian Journal of Agriculture and Rural Development* 5(8): 187-201. DOI: 10.18488/journal.1005/2015.5.8/1005.8. 187.201.

Muñoz-Perea, C. G. (2006). Selection for Drought Resistance in Dry Bean Landraces and Cultivars. *Crop Science* 46(5): 2111. [https://www.crops .org/publications/ cs/abstracts/ 46/ 5/2111] site visited on 10/08/2018.

Newton, L. K. (2010). Comparison of selection indices for tolerance to water stress in common beans (*Phaseolusvulgaris* L.) for the dry environment of Tanzania. 78pp.

Polania, J. (2017). Shoot and Root Traits Contribute to Drought Resistance in Recombinant Inbred Lines of MD 23–24 × SEA 5 of Common Bean. *Frontiers in Plant Science.*

Polania, J. A., Charlotte, P., Stephen, B. and Idupulapati, M. R. (2016). Effective Use of Water and Increased Dry Matter Partitioned to Grain Contribute to Yield of Common Bean Improved for Drought Resistance. *Frontiers in Plant Science* 7:1–10. [http://journal.frontiersin. org/Article/ 10.3389/fpls. 2016.00660/ abstract] site visited on 04/07/2018.

Porch, T. G., Ramirez, V. H., Santana, D. and Harmsen, E. W. (2009). Evaluation of common bean for drought tolerance in Juana Diaz, Puerto Rico. *Journal of Agronomy and Crop Science* 195(5): 328–334. https:// doi.org/ 10.1111/j.1439-037X.2009.00375.x.

Ramírez-Builes, V. H. (2007). Plant-water relationships for several common bean genotypes (*Phaseolus vulgaris* L.) with and without drought stress conditions. A Thesis for the Degree Award of Master Science in Agronomy at University of Puert. [http://academic.uprm.edu/ hdc/documents/ Victor_ Ramirez_Builes_ Thesis. pdf] site visited on 10/08/2018.

Rao, I. M., Beebe, S., Polania, J., Ricaurte, J., Cajiao, C. and Garcia, R (2013). Can tepary bean be a model for improvement of drought resistance in common bean? *Afr. Crop Sci. J*. 21: 265–281.

Rezene, Y., Gebeyehu, S. and Zelleke, H. (2012). Morpho-Physiological Response to Post-Flowering Drought Stress in Small Red Seeded Common Bean (Phaseolus Vulgaris L.) Genotypes. *Journal of Plant Studies* 2(1).

Salyula, P. K. (2013). Physiological Responses of Common Bean (*Phaseolus Vulgaris* L.) Genotypes to Water Stress.1–91. [http://dspace. unza.zm:8080/jspui/handle/ 123456789/3430] site visited on 10/08/2018.

Sani, M. R., Ganjeali, A., Lahouti, M., Mousa, S. and Kouhi, M. (2018). Morphological and Physiological Responses of Two Common Bean Cultivars to Drought Stress. [https:// jispp. iut.ac. ir/article-1-843-en.pdf] site visited on 10/08/2018.

Terán, H. and Singh, S. (2002). Selection for drought resistance in early generations of common bean populations. *Canadian Journal of Plant Science* 82: 491-497.

White, J. W., Ochoa, R., Ibarra, P. F. and Singh, S. P. (1994). Inheritance of seed yield, maturity and seed weight of common bean (*Phaseolus vulgaris*) under semi-arid rainfed conditions. *J. Agric. Sci*. 122: 265–273.

CHAPTER FOUR

4.0 PERFORMANCE AND ADAPTABILITY OF 16 COMMON BEAN GENOTYPES AT DIFFERENT AGRO-ECOLOGICAL ENVIRONMENTSIN KAGERA REGION IN TANZANIA

4.1 Abstract

Sixteen common beans (*Phaseolus vulgaris* L.) genotypes were used to study the genotype by environment interaction and grain yield stability in three Districts of Kagera Region, North – western Tanzania. A randomized complete block design was used with three replicates and plot size of 3.0 m by 1.5 m. Data on yield were analyzed using additive main effects and multiplicative interaction (AMMI) model and genotype plus genotype by environment interaction. In addition GGE biplot model was used to display graphical representation of the yield data using GenStat software v.13, and the yield stability index (YSi). The analysis of variance of the AMMI model indicated that environments accounted for 56.9% of the total sum of square; genotypes effect explained 9.2% and the G x E interaction effect accounted 8.9% of the total sum of squares for the 16 genotypes tested across three environments and were all significant ($P < 0.01$). The average grain yield were 2.7 t ha^{-1}, 1.38 t ha^{-1} and 1.20 t ha^{-1} for Karagwe, Bukoba and Muleba respectively. According to the results, the GGE biplot revealed that, the genotypes SSIN 1240, SAB 659 and DAB 219, SMR 101, SMC 162 and DAB 602 showed greater stability with the average closer to the overall average of the tested genotypes. Therefore, they are recommended to be used as varieties or parents for further improvement of available cultivars. Genotypes that performed well in specific environments were also identified and those could be recommended for direct use or be improved for these areas.

4.2 Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the major sources of dietary proteins, vitamins, and minerals to millions of resource-poor farmers, particularly in developing countries (Broughton *et al.,* 2003). Beans are the main grain legume crop grown in Tanzania, where they are often intercropped with maize. Cultivation of beans can be seen in most areas of Tanzania (Hillocks *et al.,* 2006).

In agricultural experimentation, a large number of genotypes are normally tested over a wide range of environments (locations, years, growing seasons, etc) (Bondari, 2002). Due to the variation of the climate, soil properties and the inherent potential of genotypes, crop yield may vary from one environment to another as a result of interaction between the environment and genotypes. The presence of a genotype x environment interaction automatically implies that the behavior of the genotypes depend upon the particular environment in which they are evaluated (Nchimbi-Msolla and Tryphone, 2010). Therefore, it was important to study the genotype and environment interaction of the genotypes in order to identify high-yielding and stable cultivars, discriminating and representative test environments (Yan, 2001).

The presence of the GxE interaction indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment (Falconer and Mackay, 1996).

The genotype x environment interaction for certain bean characteristics, such as yield, may hinder cultivar recommendation for large geographical areas (Araújo *et al.*, 2003). The selection of genotypes to maximize yield when genotype rank changes occur across environments is complicated because of the complexity of genotype responses (Silveira *et al.*, 2013).

A recently developed graphical data summary, called Genotypes main effects and Genotype x environment interaction effects (GGE) biplot, can aid in data exploration. GGE biplot is a Windows application that performs biplot analysis of two-way data that assume an entry × tester structure. A multi – environment trial data set, in which cultivars and environments are testers, was used to demonstrate the functions of GGE biplot (Yan, 2001). These include but are not limited to: (i) ranking the cultivars based on their performance in any given environment, (ii) ranking the environments based on the relative performance of any given cultivar, (iii) comparing the performance of any pair of cultivars in different environments, (iv) identifying the best cultivar in each environment, (v) grouping the environments based on the best cultivars, (vi) evaluating the cultivars based on both average yield and stability, (vii) evaluating the environments based on both discriminating ability and representativeness, and (viii) visualizing all of these aspects for a subset of the data by removing some of the cultivars or environments. GGE biplot has been applied to visual analysis of genotype × environment data, genotype × trait data, genotype × marker data, and diallel cross data (Yan, 2001). GGE biplot identifies G x E interaction patterns of data and clearly shows which variety performs best in which environments and thus facilitates mega – environment identification (Gurmu, 2017; Yan, 2001; Yan and Rajean, 2002; Yan and Kang., 2003).

Therefore, there is need for understanding the nature of G x E interaction, quantifying its magnitude and identifying stable and widely adapted common bean genotypes before release (Gurmu, 2017).

G x E due to different responses of genotypes in diverse environments, makes choosing the superior genotypes difficult in plant breeding programmes. Traditionally, plant breeders tend to select genotypes that show stable performance as defined by minimal G x E effects across a number of locations and/or years (Akinwale *et al.*, 2011). The term

stability is sometimes used to characterize a genotype which shows a relatively constant yield independent of changing environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable (Kundy and Mkamilo, 2014).

The current study was conducted to evaluate the G x E interaction for the plant yield of common bean genotypes in Kagera Region, in order to identify stable high yielding and stable genotypes.

4.3 Material and Method

4.3.1 Experimental sites and Materials used for the study

The study was conducted during 2017/2018 cropping season in three different agro ecological sites of Kagera Region which includes Bukoba, Karagwe and Muleba Districts figure 4.1 with their characteristics outlined in Table 4.1.

Table 4.1: Characteristics of the experimental sites

	Location		
	Bukoba	**Muleba**	**Karagwe**
Altitude (masl)	1349	1153	1160
Latitude	01°25'1"	01°37' 27.1"	01°18.027'
Longitude	031°46' 41"	031°37' 13.1"	031°21.494'
Soil Type	Sandy clay loam	Sand Clay Loam	Loamy Sand
pH (H_2O)	5.26	5.42	5.87
N Total (%)	0.24	0.18	0.17
P (mg/kg) Bray 1	17.90	19.20	23.40
Organic Carbon (%)	2.39	2.34	2.41
Mg (meq/100 g soil)	0.12	0.14	0.36
Ca (meq/100 g soil)	0.66	0.78	2.04
EC (mS/cm)	0.33	0.28	0.30
CEC	3.10	3.80	5.20
Agro – ecological zone	High rainfall	Medium rainfall	Low rainfall

Where farmers grow common beans as food and commercial crop as well. A total of 16 common bean genotypes, (13 introduced genotypes from the International Center for Tropical Agriculture CIAT, two released varieties (Lyamungu 90 and JESCA as control) and one landrace (Ibwera as local check)) were used during the experimentation across three environments. The list of these genotypes is presented in Table 4.2.

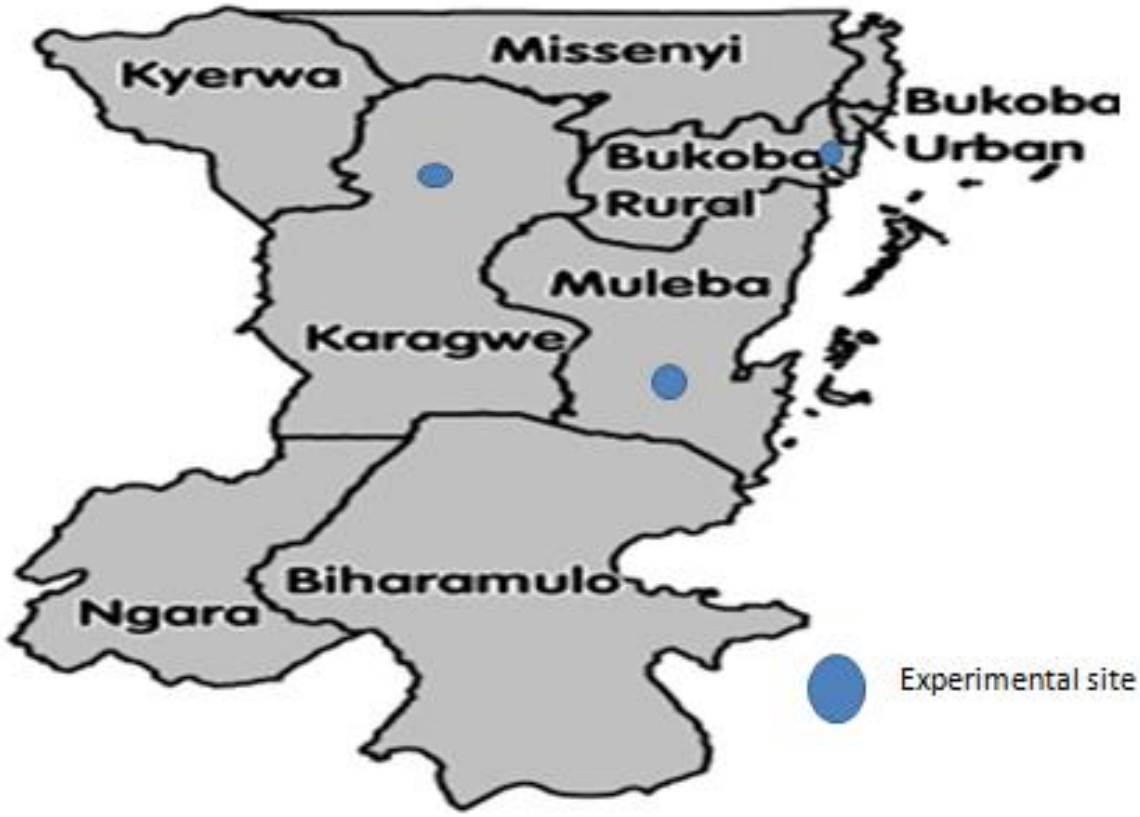

Figure 4.1: Map showing experimental sites in Kagera region

Table 4.2: Characteristics of the common bean genotypes used under experimentation

Genotype	Seed size	PSC [1]	SCP [2]	SCB [3]	GH
DAB 378	Large	R	2	3	Type I
DAB 219	Large	M	6	2	Type I
DAB 291	Large	M	6	3	Type I
SAB 659	Large	M	6	1	Type I
SCR 59	Medium	O	6		Type II
SSIN 1128	Medium	O	2	1	Type III
SSIN 1240	Medium	M	6	1	Type III
IBWERA	Medium	R	2	1	Type I
JESCA	Large	O	2	1	Type I
Lyamungu 90	Large	M	2	2	Type I
SMC 162	Medium	O	1	1	Type II
SMC 24	Medium	O	1	2	Type III
SMR 101	Large	O	1	1	Type I
DAB 602	Large	M	2	1	Type I
DAB 582	Large	R	2	1	Type I
DAB 362	Large	R	2	3	Type I

GH, Growth habit
1 T Seed color Pattern: O – No pattern, M – Mottled, R – Striped, J – Speckle, P – Pinto, B – Bicolor,
2 Seed color Scale: 1 – White, 2 – Cream-beige, 3 – Yellow, 4 – Brown maroon, 5 – Pink, 6 – Red
3 Seed Brilliance Scale: 1 – Dull, 2 – Semi-Shine, 3 – Shiny (CIAT, 1987).

4.3.2 Experimental design and field layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) arranged in a split plot layout with three replications at each site (Table 4.1).

Two factors were used; the first was location (the main factor), three Districts of Kagera Region (Bukoba, Karagwe and Muleba) with different agro climate was involved during the experiment (Table 4.1). The second factor was genotypes (the sub factor): sixteen common bean genotypes used in the experiment.

The experimental unit size was 3 x 1.5 m, consisting of four rows at spacing of 50 cm between rows and 20 cm in rows. Two seeds were planted per hill were planted. Hand –

hoe weeding and Fertilizer application were done twice when beans had one trifoliate leaf and before flowering. Fertilizer used was NPK: 20:10:10 at recommended rate of 100 kg/ha. All recommended agronomic practices for common bean productions were followed.

Statistical Model

$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + c_{ik} + e_{ijk}$ …….….. Equation 2

Where

μ is a population mean.

α_i is the main effect of location (A).

β_j is a main effect of genotypes (B)

$(\alpha\beta)_{ij}$ is the interaction effect of A and B

c_{ik} is the plot error distribution, k = 1, 2.

e_{ijk} is the sub – plot error distribution, k = 1, 2.

4.3.3 Data collection

4.3.3.1 Days to 50% flowering (DF)

This was measured in days-after-planting and coinciding with the initiation of developmental stage R6 when 50% of the plants have one or more flowers (CIAT, 1987).

4.3.3.2 Days to physiological maturity (DPM)

This was measured in days-after-planting and coinciding with the initiation of developmental stage R9 when 50% of the plants have reached physiological maturity and changing pod color from green to yellowish (CIAT, 1987).

4.3.3.3 Number of pods/plant

Number of pods per plant were recorded from ten plant selected randomly in the net plot and the average of the plot was calculated (CIAT, 1987).

4.3.3.4 Number of seeds/pod

The number of seed per pod was recorded from ten randomly selected pods in the net plot and the average of the plot was calculated (CIAT, 1987).

4.3.3.5 Seeds Size

Seed size is expressed as the weight in grams of 100 randomly chosen seeds and categorized as follows; Small: Less than 25 g, Medium: 25 g to 40 g, Large: More than 40 g (CIAT, 1987).

4.3.3.6 Grain yield (kg/ha)

Harvesting was done for two middle rows of each plot and grain yield was adjusted by converting plot yield (at 14% moisture content) to seed yield per hectare (Kadhem and Baktash, 2016).

4.3.4 Statistical analysis

4.3.4.1 The additive main effect and multiplicative interaction analysis

The data for grain yield were pooled to perform the analysis of variance across the environment. Since the pooled analysis of variance considers only the main effects, the additive main effect and multiplicative interaction model (AMMI) was computed using Genstat software.

The AMMI analysis is a combination of analysis of variance (ANOVA) and principal component analysis (PCA) in which the sources of variability in genotype by environment interaction are partitioned by PCA (Marjanović-Jeromela, 2011).

The main idea of the AMMI models is: (i) first apply the additive of the variance model (ANOVA) to a two-way table and (ii) secondly apply the multiplicative principal component analysis (PCA) model to the residual from the additive model (Gauch, 1992). The AMMI model with multiplicative terms can be written as:

$Y_{ij} = \mu + G_i + E_j + \Sigma_{k=1}\lambda_k\gamma_{ik}\,\alpha_{jk} + \rho_{ij} + \varepsilon_{ij}$ .....Equation 3

Where: Yij is the yield of genotype i in environment j;

μ Grand mean;

G_i the genotype means deviations (the genotype means minus the grand mean);

E_j the environment mean deviations;

λ_k the singular value for the PCA axis k; γ_{ik} and $\gamma_{ik}\,\alpha_{jk}$ are the genotype and environment PCA scores for PCA axis k; K is the number of PCA axes (Kadhem and Baktash, 2016).

The AMMI model was used to identify genotypes(s) which are adapted in different environment.

The AMMI's stability values (ASV) were computed using equation 3 as described by Purchase *et al.* (1997).

$$\mathbf{ASV} = \sqrt{\left(\left[\left(\frac{SSIPCA1}{SSIPCA2}\right)(IPCA1SCORE)\right]^2\right) + ((IPCASCORE2)^2)}$$ **...Equation 4**

Where SSIPCA1/SSIPCA2 is the weight given to the IPCA1 value by dividing the IPCA1 SS by the IPCA1 SS; and the IPCA1 and IPCA2 scores are the genotypic scores in the AMMI model (Rad *et al.,* 2013).

4.3.4.2 Genotype and genotype by environment (GGE) – Biplot Analysis

The GGE biplot methodology was used to analyze the multi – location genotype yield trial data to evaluate the grain yield stability and identify superior genotypes using the GenStat v.13 software.

GGE biplot analysis was also used to generate graphs for: (i) comparing environments to the ideal environment; (ii) the "which-won-where" pattern; (iii) environment vectors. The angles between environment vectors were used to judge correlations (similarities/ dissimilarities) between pairs of environments (Yan and Kang, 2003).

4.4 Results and Discussion

4.4.1 Analysis of variance

The single site analysis of variances (Table 4.3) revealed the high significance differences among genotypes in each tested environment but the results shows variability of the genotype rank form one environment to another. This justified the conduction of a more refined analysis so as to increase the efficiency of the selection of the cultivars. In this sense, AMMI analysis represents a potential tool that can be used to deepen the understanding of factors involved in the manifestation of the G × E interaction (Silveira *et al.*, 2013).

The analysis of variance of the AMMI model indicated that environments accounted for 56.9% of the total sum of square; genotypes effect explained 9.2% and the G x E interaction effect accounted 8.9% for the 16 genotypes tested across three environments (Table 4.3) and were all significant ($P < 0.01$). A large SS for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation (Silveira *et al.*, 2013) in genotype grain yield. This means

that there were large environmental effects on the genotypes performance across the environments than the interaction between the genotypes and the environment.

Table 4.3: Summary of analysis of variance and partitioning of the G X E interaction using AMMI method

		Means squares of individual analysis of variance by location			Combined Analysis of variance				
Source of variation	**df**	**L1**	**L2**	**L3**	**Source**	**df**	**SS**	**MS**	**%SS**
Replication	2	0.55	0.28	0.64	Genotypes	15	10.49	0.7**	9.22
Genotype	15	3.29**	10*	7.38**	Location	2	64.80	32.40**	56.94
Error	30	2.91	9	4.3	Interactions (GxL)	30	10.18	0.34**	8.94
Mean (t ha^{-1})		1.38	2.7	1.20	IPCA 1	16	6.20	0.39*	5.45
CV%		9.5	3.4	11.8	IPCA 2	14	3.98	0.28*	3.5
S.E		0.13	0.09	0.14	Error	96	18.16	0.19	15.96

L1 = Bukoba, L2 = Karagwe, L3 = Muleba ** = significant at 1%, * = significant at 5% level, df = Degree of freedom, SS = Sum of Square, MS = Mean sum of Square, %SS = percentage sum of square

4.4.2 Mean performance of the genotypes in each and across environments

The mean grain yields of the genotypes are presented in the Table 4.4. Karagwe site (L2) was the best environment for common bean production that gave the average grain yield of 2.7 t ha^{-1}, followed by Bukoba which gave 1.38 t ha^{-1} and Muleba become the least with an average production of 1.20 t ha^{-1}(Table 4.4). In Karagwe, plant responded vigorously and most of the genotypes yielded more than 2 t ha^{-1} with high scores of the plant vigor of scale 1 and 2 to most of the tested genotypes, while in Muleba which is the least site in the performances of the genotypes was poor with some of the genotypes scoring plant vigor of scale 3 (good) and 5 (intermediate) for plant vigor according to CIAT, 1987.

4.4.3 AMMI's stability values (ASV)

The ASV is the distance from zero in a two dimensional scatter gram of interaction principal component analysis axis 1 (IPCA1) scores against IPCA2 scores. Since the IPCA1 score contributes more to GE sum of scores, it has to be weighted by the

proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 total GE sum of squares.

Table 4.4: The mean genotype yield (t h^{-1}) AMMI stability value of the 16 genotypes tested across three environments

Genotype	L1	L2	L3	MEAN	IPCA1	IPCA2	ASV
SSIN 1240	1.4	2.8	1.1	1.7	0.12	0.02	0.19
SAB 659	1.4	2.8	1.5	1.9	-0.15	0.04	0.23
DAB 219	2.0	3.1	1.4	2.2	0.16	-0.14	0.29
LYAMUNGU 90	1.0	2.7	1.2	1.7	-0.11	0.26	0.31
IBWERA	1.2	2.1	0.9	1.4	-0.09	-0.29	0.32
JESCA	1.4	2.7	1.5	1.9	-0.21	-0.03	0.32
SMC 162	1.7	2.4	1.1	1.7	0.03	-0.45	0.45
DAB 602	1.3	2.7	1.6	1.9	-0.28	0.08	0.45
SMR101	1.2	3.3	1.4	1.9	0.07	0.47	0.48
DAB 378	1.0	1.5	0.3	0.9	0.01	-0.50	0.50
SCR59	1.4	2.9	0.9	1.7	0.32	0.07	0.51
DAB 362	1.3	3.4	1.1	1.9	0.30	0.43	0.64
SSIN 1128	1.6	3.1	0.9	1.9	0.42	0.09	0.66
DAB 582	1.2	2.8	1.9	2.0	-0.48	0.22	0.78
SMC24	1.8	2.9	0.8	1.8	0.49	-0.21	0.79
DAB 291	1.1	2.2	1.7	1.7	-0.63	-0.08	0.98
Mean	1.4	2.7	1.2	1.8			

L1= Bukoba, L2= Karagwe, L3= Muleba

From the calculation of equation 1, genotypes SSIN 1240, SAB 659, DAB 219 and Lyamungu 90 had shown higher adaptive capacity compared with others genotypes due to their lower AMMI stability values as shown in the Table 4.4. As described by Kadhem and Baktash (2016); Al-Naggar *et al.* (2018) genotype with least ASV and IPCA scores (either negative or positive) are considered as the most stable while the genotypes SSIN 1128, DAB 582, SMC24 and DAB 291 had shown lesser adaptive capacity.

Some of the genotypes may perform better in one environment but the some genotype performs less in the other environment. For instance, the genotype DAB 362 ranked

number one in performance with average yield of 3.363 t ha^{-1} in Karagwe site but it did less in other two environments like – wise DAB 219 ranked number one in Bukoba and in Karagwe ranked number four but in Muleba it did not appeared in top four genotypes (Tables 12 and 13).

Table 4.5: First four AMMI genotypes selections per environment

Environment	Mean	Score	1	2	3	4
KARAGWE	2.70	0.589	DAB 362	SMR101	SSIN 1128	DAB 219
BUKOBA	1.38	0.381	DAB 219	SMC24	SMC 162	SSIN 1128
MULEBA	1.20	-0.971	DAB 582	DAB 291	DAB 602	JESCA

As stated by Kadhem and Baktash (2016) the best genotype needs to combine good grain yield and stable performance across a range of production environments. In this study only two genotypes DAB 219 and SSIN 1128 appeared to perform well in Karagwe and Bukoba sites. This was happened despite the facts that the environments were divers and caused for a great variation in grain yield which is a quantitative trait. Therefore, the environmental factors are crucial determinant of yield expression (Kadhem and Baktash, 2016). However, the AMMI stability values revealed that SSIN 1240, SAB 659, DAB 219 were the most stable genotypes across three tested environments above checks which were Lyamungu 90, JESCA (released varieties) and Ibwera (landrace). Among them, DAB 219 (arranged in increasing order of stability) had environment average yield of 2.169 t ha^{-1} higher than any tested genotypes (Table 4.4), while the first two more stable genotypes SSIN 1240, SAB 659 had environmental average yield of 1.737 t ha^{-1} and 1.892 t ha^{-1} respectively.

4.4.4 Genotype plus genotype by environment (GGE) biplot

In biplot the differences among genotypes in terms of direction and magnitude along the X-axis (yield) and Y axis (IPCA 1 scores) are important (Kadhem and Baktash, 2016). In

the biplot display, genotypes or environments that appear almost on a perpendicular line of the graph had similar mean yields and those that fall almost on a horizontal line had similar interaction (Alberts, 2004). Genotypes or environments on the right side of the midpoint of the perpendicular line have higher yields than those on the left side. The score and sign of IPCA1 reflect the magnitude of the contribution of both genotypes and environments to GEI, where values closer to the origin of the axis (IPCA1) provide a smaller contribution to the interaction than those that are further away (characteristic of stability), whereas higher score (absolute value) considered as unstable and specific adapted to certain environment (Gollob, 1968; Silveira *et al.*, 2013). The characterization of each promising lines (genotypes) to mean grain yield and contribution to GEI by mean of IPCA1 (Alberts, 2004) and based on these attributes, our study indicates that genotypes SMR 101, DAB 362, SSIN 1128, SMC 24 and DAB 219 were specifically adapted to Karagwe which was the high yielding environment as shown in Figure 4.3.

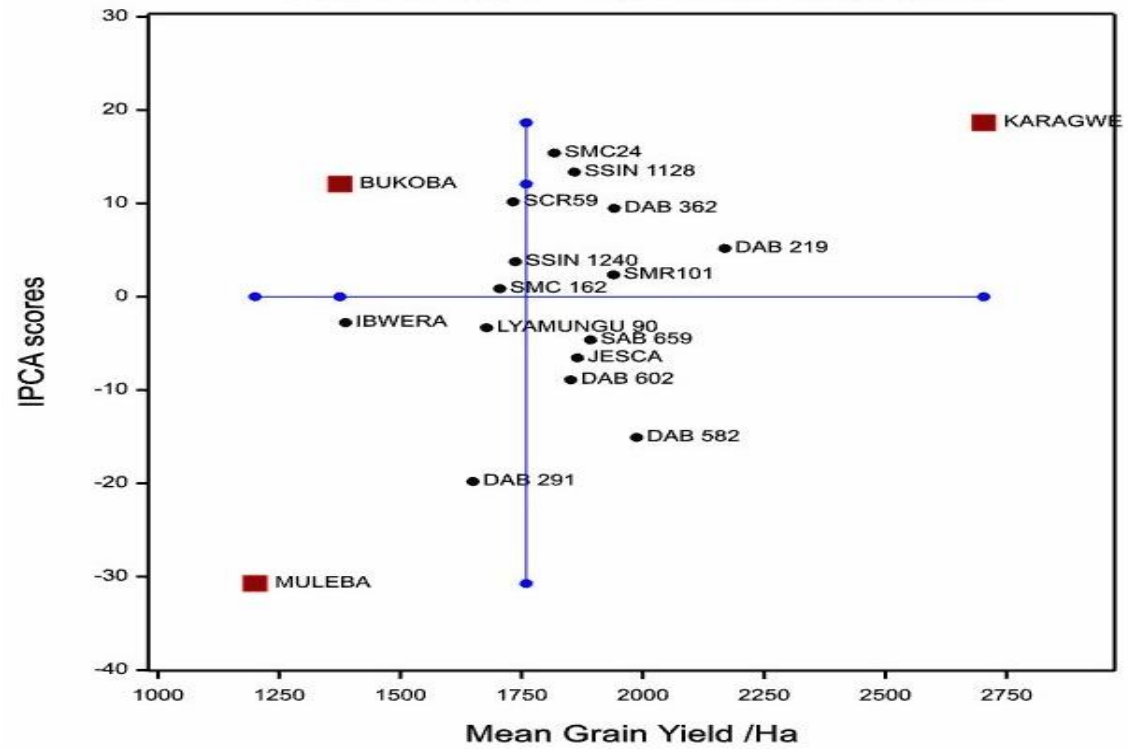

Figure 4.2: The biplot of 16 genotypes and environment IPCA score against means

The genotypes SSIN 1240, SAB 659 and DAB 219, SMR 101, SMC 162, IBWERA, Lyamungu 90, JESCA and DAB 602 showed greater stability with the average closer to the overall average of the tested genotypes. However, genotypes SSIN 1240, SMC 162, IBWERA and Lyamungu90 were identified to be adapted to low yielding environment since they appeared on the left side of the mid – point representing grand mean in Figure 4.2.

The GGE analysis was performed on the average grain yield of the 16 common beans genotypes tested in three different sites. The results showed that the GGE biplot explained 89.5% of the genotype main effects and the Genotype by Environment interaction. The primary (PC1) and Secondary (PC2) components explained 59.8% and 29.8% of the genotypes main effects and G x E interaction respectively (Figure 4.3).

The genotypic PC1 scores greater than zero classified the high yielding genotypes while PC1 scores less than zero identified low yielding genotypes, unlike genotypic PC1, genotypic PC2, scores near zero showed stable genotypes whereas large PC2 scores discriminated the unstable ones (Jalata, 2011).

The plot of PCA1 vs. PCA 2 revealed that SSIN 1240, SAB 659, DAB 219 and Lyamungu 90 were the most stable genotypes due to the fact that, they were found closer or at a lesser distance from the center of the biplot when compared with other genotypes, while SSIN 1128, DAB 582, SMC24 and DAB 291 were considered as most unstable genotypes among all other tested genotypes across three environments as shown in the Figure 4.3. The similar result was also reported by Kadhem and Baktash (2016).

The GGE biplot was also used to show the association among the tested environment. Figure 4.3 show that Karagwe and Muleba exhibits longer vectors compared with Bukoba. This contributed more to the environment sum of square as also indicated in the ANOVA Table 4.3. Genotypes and environments positioned close to each other in the biplot have positive associations, thus these enable the creation of agronomic zones with relative ease (Silveira *et al.*, 2013). In the current study, the polygon view of GGE biplot for grain yield indicates the best genotype(s) for each environment(s).

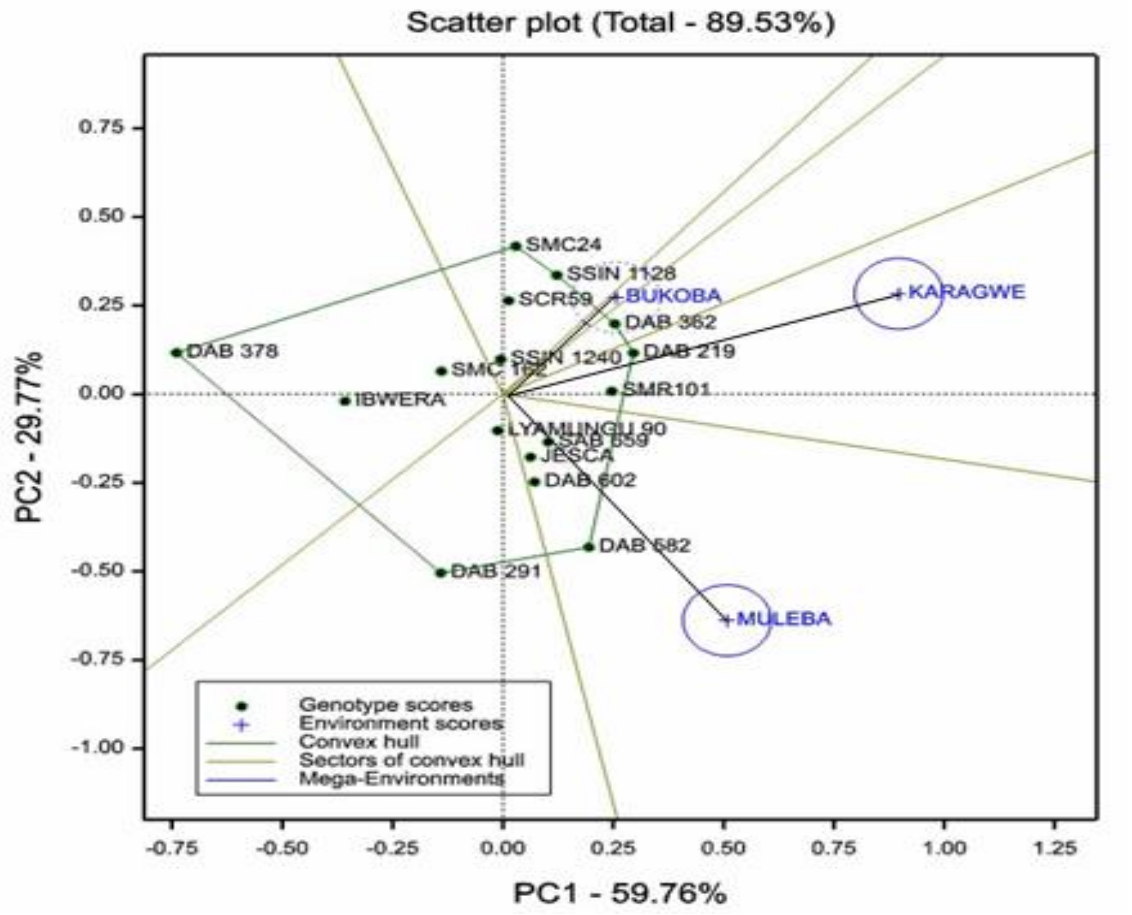

Figure 4.3: GGE biplot showing the two main axes of interaction (PCA1 vs. PCA2) in 16 genotypes across three locations

The vector view of GGE – biplot (Figure 4.3) provides a succinct summary of the interrelationships among the environments. All environments were positive correlated

because all angles among them were smaller than 90^0 (Rad *et al.*, 2013). The correlation between Karagwe and Bukoba is stronger than that of Muleba and either of the other two locations. The results suggest that indirect selection for grain yield can be practical across the tested environment. This means that adaptable genotypes in Karagwe may also show a similar respond in Bukoba and less response in Muleba.

The GGE biplot was also used to draw the polygon for G × E interaction effect from which different interpretations can be derived. The polygon is formed by connecting the markers of the genotypes that were further away from the biplot origin such that all other genotypes were contained in the polygon as shown in Figure 4.3. The polygon view of a biplot is the best way to visualize the patterns of interaction between genotypes and environments, and to effectively interpret a biplot (Shiri, 2013). In Figure 4.4, the genotypes SMC 24, SSIN 1128, DAB 362, DAB 219, DAB 582, DAB 291 and DAB 378 were the best or poorest genotypes because they are located on the vertex of a polygon (Hagos and Abay, 2013).

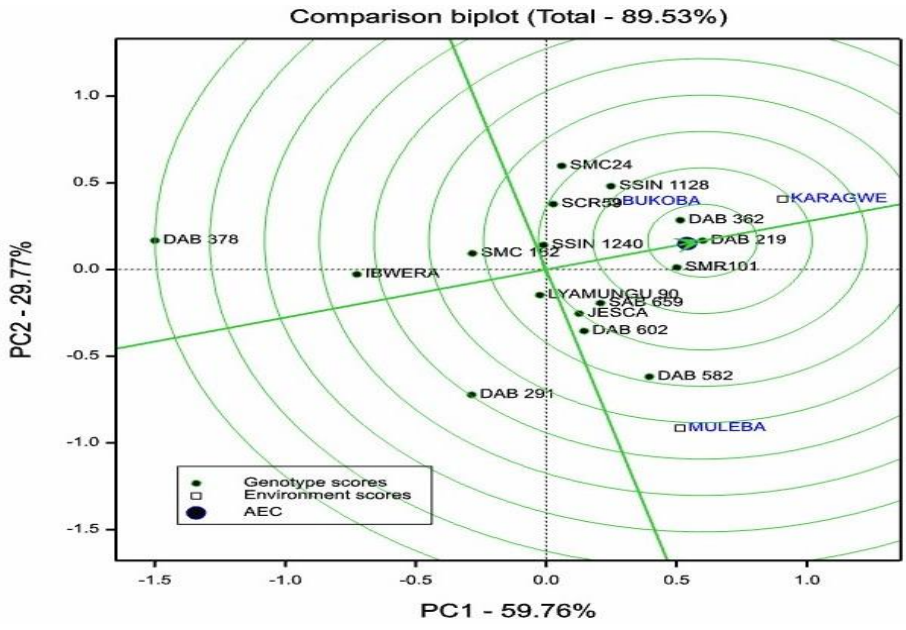

Figure 4.4: GGE – biplot based on environment – focused scaling for comparing the environments with the ideal environment

An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the centre, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan *et al.,* 2000; Yan and Rajcan, 2003). Figure 4.4 shows that Karagwe was an ideal test environment in terms of being the most representative of the overall environment.

The graphical representation of the means performances of the genotypes per location indicated that, Karagwe is better performing environment (Figure 4.5). However, the vector of GGE – biplot shows interrelation among tested environment in which all three environment were positively correlated and the GGE – biplot, for comparing environments with ideal environment, positioned Karagwe site at the center of the concentric circles (Figure 4.4). As stated by Silveira *et al.* (2013) genotypes and environments positioned close to each other in the biplot have positive associations, thus these enable the creation of agronomic zones with relative ease. Both the genotype and the environment determine the phenotype of an individual. The effects of these two factors, however, are not always additive because of the interaction between them. The large G x E variation usually impairs the accuracy of yield estimation and reduces the relationship between genotypic and phenotypic values (Ssemakula and Dixon, 2007).

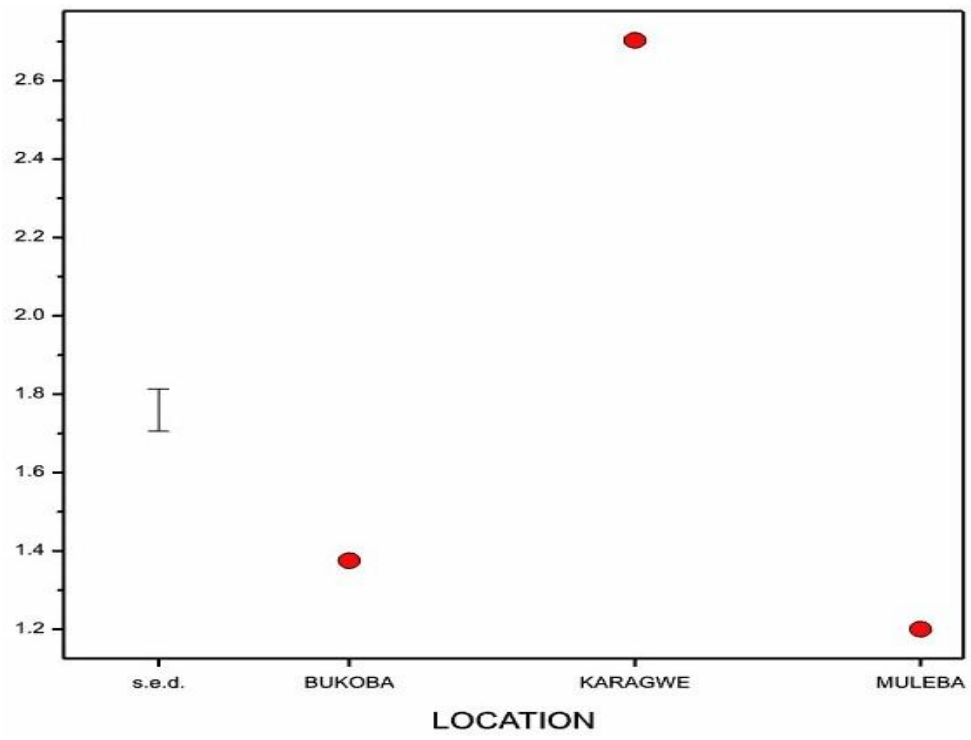

Figure 4.5: Genotypes grain mean yield per location

4.5 Conclusion

The result of this study indicates the significant genotypes environment interaction in grain yield across the tested environments. This means that each genotype responded differently when exposed to different location due to variations in climate and edaphic factors. It was difficult to identify genotype which was superior for all tested environment.

Therefore, based on GGE and AMMI multivariate analyses which performed evaluation of genotypes adaptability/stability across the tested sites, recommendations for specific environment can be made for example genotypes DAB 362, and SMR 101 could be recommended to be used in Karagwe. While genotypes SMC 24, SMC 162 and SSIN 1128 could be used in Bukoba, likewise genotypes DAB 582, DAB 602 and DAB 291 could be used in Muleba. SSIN 1128 and DAB 219 could be grown in Karagwe as well as in Bukoba.

CHAPTER FIVE

5.0 CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusion

The results of this study showed that the grain yield performances of the 16 tested common bean genotypes was highly influenced by environment. Genotypes SMC 162, DAB 602, SSIN 1128, DAB 378, DAB 362 and SMR 101 had expressed their superiority in tolerating moisture stress with higher values of HI and DTI. The HI has proved to be an important trait to breeders in identifying genotypes that are adapted to drought stress through better photosynthates mobilization. These genotypes were able to mobilize the assimilated carbon for the production of pods and grains, evidenced by the high harvest index. Also the capacity of root traits to explore limited water and their ability to dynamically respond to soil-water deficit are also being investigated as indicators for drought stress tolerance.

Based on GGE and AMMI multivariate analyses which performed evaluation of genotypes adaptability/stability across the tested sites, genotypes DAB 362, SMR 101 and SSIN 1128 could be recommended to be used in Karagwe. While genotypes SMC 24, SMC 162 and SSIN 1128 could be used in Bukoba, likewise genotypes DAB 582, DAB 602 and DAB 291 could be used in Muleba. DAB 219 could be grown in Karagwe as well as in Bukoba.

Therefore, genotypes SMC 162, DAB 602, SSIN 1128, DAB 362 and SMR 101 were identified as the possible candidates to be used for future breeding program as good seed yield parent

5.2 Recommendations

The following are recommended for future studies:

1) Considering the high influence of the environment in grain yield, further testing in other locations and seasons should be implemented.
2) The QTL Analysis should also be conducted for future study in order to understand the genetic point of view of the genotypes with respect to drought stress tolerance.
3) The superiority of the drought tolerant genotypes should be harnessed into local varieties that are performing better as they are not drought tolerance at all

REFERENCES

Akinwale, M. G., Akinyele, B. O., Odiyi A. C. and Dixon, A. G. O. (2011). Genotype X Environment Interaction and Yield Performance of 43 Improved Cassava (*Manihot esculenta* Crantz) Genotypes at Three Agro-climatic Zones in Nigeria. *British Biotechnology Journal* 1(3): 68-84.

Alberts, M. (2004). A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials. Thesis Plant Sciences (Plant Breeding) at the University of the Free State. University of the Free State. Retrieved from [http://citeseerx.ist.psu.edu/viewdoc/ download ?doi= 10.1.1.462. 1429&rep = rep1&type=pdf] site visited on 12/05/2018.

Al-Naggar, A. M., El-Salam, R., Asran, M. and Yaseen, W. Y. (2018). Yield Adaptability and Stability of Grain Sorghum Genotypes across Different Yield Adaptability and Stability of Grain Sorghum Genotypes across Different Environments in Egypt using AMMI and GGE-biplot Models. *Annual Research and Review in Biology* 23(3): 1–16. https://doi.org/ 10.9734/ARRB/2018/39491.

Araújo, R., De, Miglioranza, É., Montalvan, R., Destro, D. and Celeste, M. (2003). Genotype x environment interaction effects on the iron content of common bean grains. *Crop Breeding and Applied Biotechnology* 3(4): 269–273.

Bondari, K. (2002). Statistical Analysis of Genotype X Environment Interaction in Agricultural Research. Experimental Statistics, Coastal Plain Station, University of Georgia. pp1–6.

Broughton, W. J., Hernández, G., Blair, M., Beebe, S., Gepts, P. and Vanderleyden, J. (2003).Beans (Phaseolus spp.) – model food legumes.*Plant and Soil* 252(1): 55–128. https://doi.org/10.1023/A:1024146710611.

CIAT (The International Center for Tropical Agriculture) (1987). Standard system for the evaluation of bean germplasm.

Falconer, D. S. and Mackay, T. F. C. (1996). *Introduction to Quantitative Genetics.* 4ed. London: Longman Scientific and Technical, Essex, England. 374pp.

Gauch, H. G., J. (1992). Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs. 280. Retrieved from [https:// www.cabdirect.org/ cabdirect/abstract/19931643324] site visited on 12/05/2018.

Gollob, H. F. (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika* 33(1): 73–115. https://doi.org/ 10.1007/BF02289676.

Gurmu, F. (2017). Stability Analysis of Fresh Root Yield of Sweet potato in Southern Ethiopia using GGE. *International Journal of Pure Agricultural Advances* 1: 1–9. https://doi.org/10.20448/813.11.1.9.

Hagos, H. G. and Abay, F. (2013). AMMI and GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia. *Journal of Plant Breeding and Genetics* 01: 12–18.

Jalata, Z. (2011). GGE-biplot Analysis of Multi-environment Yield Trials of Barley (*Hordeium vulgare* L.) Genotypes in South eastern Ethiopia

Highlands.*International Journal of Plant Breeding and Genetics* 5(1): 59–75. https://doi.org/10.3923/ijpbg.2011.59.75.

Kadhem, F. and Baktash, F. Y. (2016). AMMI ANALYSIS OF ADAPTABILITY AND YIELD STABILITY OF PROMISING. *The Iraqi Sciences, Agricultural Issue* 47: 35–43.

Kundy, A. C. and Mkamilo, G. S. (2014). Genotype x Environment Interaction and Stability Analysis for Yield and its Components in Selected Cassava (*Manihot esculenta*) Genotypes in Southern Tanzania. *Journal of Biology, Agriculture and Healthcare* 4(19): 29–40.

Marjanović-Jeromela, A, Nagl, N, Gvozdanović-Varga, J, Hristov, N, Kondić-Špika, A, Vasić, M. and Marinković, R. (2011). Genotype by environment interaction for seed yield per plant in rapeseed using AMMI model. *Pesquisa Agropecuaria Brasileira* 46: 174-181.

Nchimbi-Msolla, S. and Tryphone, G. M. (2010). The Effects of the Environment on Iron and Zinc Concentrations and Performance of Common Bean (*Phaseolus vulgaris* L.) genotypes. *Asian Journal of Plant Sciences* 9(8): 455–462. https://doi.org/10.3923/ajps.2010.455.462.

Purchase, J. L. (1997). Parametric analysis to describe Genotype x environment interaction and yield stability in winter wheat. Ph.D. Thesis, for Award Degree of Doctorate at University of the Free State, Bloemfontein, South Africa. 176pp.

Rad, M. R. N., Kadir, M. A., Rafii, M. Y., Jaafar, H. Z. E. and Naghavi, M. R. (2013). Genotype × environment interaction by AMMI and GGE biplot analysis in three

consecutive generations of wheat (*Triticumaestivum*) under normal and drought stress conditions. *Australian Journal of Crop Science* 7(7): 956–961.

Shiri, M. (2013). Grain yield stability analysis of maize (*Zea mays* L.) hybrids under different drought stress conditions using GGE biplot analysis. *Crop Breeding Journal* 3(2): 107–112.

Silveira, L. C. I., da, Kist, V., Paula, T. O. M., de, Barbosa, M. H. P., Peternelli, L. A. and Daros, E. (2013). AMMI analysis to evaluate the adaptability and phenotypic stability of sugarcane genotypes. *Scientia Agricola* 70(1): 27–32. https://doi.org/10.1590/S0103-90162013000100005.

Ssemakula, G. and Dixon, A. (2007). Genotype X environment interaction, stability and agronomic performance of carotenoid-rich cassava clones. *Scientific Research and Essay* 2: 390-399.

Yan, W. (2001). GGEbiplot—A Windows Application for Graphical Analysis of Multienvironment Trial Data and Other Types of Two-Way Data. *Agronomy Journal* 93(5): 1111-1126. https://doi.org/ 10.2134/agronj2001.9351111 xs.

Yan, W. and Kang, M. S. (2003). *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists CRC Press*, Boca Raton, FL, USA. 288pp.

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

Yan, W., Hunt, A., Sheng, L., Qinglai, S., Zlavnics, Z. (2000). Cultivar Evaluation and Mega-Environment Investigation Based on the GGE Biplot. *Crop Science* 40:1-12.