

**Genetic analysis of common bean (*Phaseolus vulgaris* L.) genotypes for  
tolerance to drought and heat stress in Zambia**

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**By**

**Nathan Phiri**

**BSc. Agric (Crop Science), University of Zambia, Zambia  
MSc. Crop Science, University of KwaZulu-Natal, Republic of South Africa**

**Submitted in partial fulfilment of the requirements for the degree of Doctor of  
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**African Centre for Crop Improvement,  
School of Agricultural, Earth & Environmental Sciences (SAEES)  
College of Agriculture, Engineering and Science  
University of KwaZulu-Natal  
Private Bag X01, Scottsville 3209  
Pietermaritzburg, Republic of South Africa**

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## Abstract

Common bean (*Phaseolus vulgaris* L.) is widely grown and consumed in Zambia but its production is limited by drought and high temperature stresses. In the country there is limited information on farmers' preferences and the genetics of drought and heat tolerance of common bean for breeding to enhance its production. Therefore, the objectives of this study were to: 1) determine farmers' selection criteria and preferences for common bean varieties, 2) evaluate the Zambian bean germplasm for drought and heat tolerance, and 3) determine the genetic effects and inheritance of drought and heat stress tolerance in Zambian common bean germplasm.

A participatory rural appraisal and survey studies established that the preferred bean varieties by the farmers in Siavonga (Lusitu) and Gwembe districts were of determinate bush type growth habit, red speckled seeds, large and elongated seed shape, early maturing, and prolific with high numbers of pods per plant. Lyambai, a red speckled seed variety, was chosen as their most preferred type meeting most of their selection criteria. It was also established that women were better able to distinguish between common bean varieties in terms of taste and cooking time than men. It was further established that the educated farmers based their variety selections on a background understanding of varietal characteristics.

A screening study involving 120 common bean genotypes identified LY4-4-4-B as the most drought tolerant genotype followed by LY1-2-B, ZM 3831, KAL-ZA, SCCI 13, ZM 4512-5 and LYA-ZA based on yield and yield related traits. Two genotypes, a mutant, LY4-4-4-B and a landrace, ZM 3831 were selected among the most drought tolerant genotypes for developing F1 populations used in the genetic study. This study also established that 100-seed weight was not affected by drought stress, probably due to the compensatory effects of reduced numbers of pods per plant and number of seeds per pod.

The evaluation of the 120 genotypes under elevated temperatures ( $>33^{\circ}\text{C}$ ) established that ZM 4143, ZM 4497, SCCI 4, KE 1, and ZM 07, were more tolerant to heat stress. ZM 4143 and ZM 4497 were further selected among the most heat tolerant genotypes for developing F1 populations used in the genetic study. The significant ( $P\leq 0.05$ ) GCA effects for 14 parental lines for yield, number of seeds  $\text{pod}^{-1}$ , and number of pods  $\text{plant}^{-1}$

indicated that additive gene effects were important in the inheritance of these traits under heat stress. The significant ( $P \leq 0.05$ ) and positive SCA effects for the  $F_2$  families of Kapisha X SEN 39, Kapisha X ZM 4497, Kalungu X SEN 39, and Lyambai X ZM 4143 were generated from parental lines with high and positive GCA values indicating their potential for further selection for high temperature tolerance from these populations.

Further genetic studies on drought tolerance for the 14 parents and the 48  $F_2$  populations established that ZM 4143 and ZM3831 were drought tolerant male parents with significant ( $P \leq 0.05$ ) and high positive GCA effects. The crosses with high SCA values for the  $F_2$  population emanating from Chambeshi X ZM 4143, Pan 148 X ZM 4143, Lyambai X SER 124, Chambeshi X ZM 3831, SCCI 2 X Ly 4 -4-4-B, ZM 05 X SER 124 and Lyambai and ZM 3831 had parents with high and positive GCA effects indicating potential for making further selections for drought tolerant genotypes. The high heritability estimate for yield of 60% found in drought stressed conditions also indicated that breeders can make progress in breeding for drought tolerance.

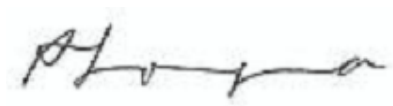
## Declaration

I, **Nathan Phiri**, declare that:

1. The research reported in this thesis, except where otherwise indicated, is my original research.
2. This thesis has not been submitted for any degree or examination at any other university.
3. This thesis does not contain other persons' data, graphs or other information, unless specifically acknowledged as being sourced from other persons.
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Signed..........Date.....  
**Nathan Phiri (Student)**

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

Signed:..........Date.....  
**Prof. Pangirayi Tongoona (Principal supervisor)**

Signed:.....Date.....  
**Prof. Rob Melis (Co-supervisor)**

Signed:..........Date.....  
**Dr. Githiri Mwangi (Co-supervisor)**

## **Dedication**

To my dear wife Christine, to our children Temwani, Nathan Jr. and Tasila, to mum and dad, and to my late brother, Lovemore for their sacrifice, perseverance, understanding, love and moral support

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## THESIS INTRODUCTION

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### 0.1. Background

The common bean (*Phaseolus vulgaris* L.) is an important pulse crop worldwide. The crop provides a cheap source of protein and fetch higher prices compared to cereals and has become a major source of farmer's incomes (Cortés et al., 2013). This crop is estimated production is about 23,816,123 t, covering a total of about 18 million ha, out of which 17 % are in Africa (Graham and Rannali, 1997; Wortmann et al., 1998;FAO, 2014). Common bean production fits in many farming systems, ranging from small-scale with limited technology in poor economies, to large scale farming systems with improved technology in developed economies. Most of the common bean production in Africa is dominated by resource poor small-scale farmers who grow the crop in various intercropping mixtures with cereals and other major crops (Adams et al., 1985; Wortmann et al., 1998). However, common bean yields realised in Africa are very low averaging below half a ton per hectare compared to those obtained in other regions of the world such as North America where yields reach about 1.5 ton per hectare (FAO, 2012). The low yields have been attributed to several biotic (pests and diseases) and abiotic factors (drought, heat and low soil fertility) (Thung, 1991; Giller et al., 1992).

The common bean is rich in protein and iron, making it an ideal crop to provide the much needed nourishment for the resource poor households (Bennink and Rondini, 2003). The crop has also been reported to contain medicinal qualities that are important to prevent cancer (Hangen and Bennink, 2003). Furthermore, it has been reported that the common bean contains favourable peptides which can be used to slow down the AIDS virus multiplication in HIV infected patients (Patrick and Ng, 2004; Wang and Ng, 2006; Wong et al., 2006).

The Republic of Zambia has a high prevalence of malnourished people (35-45% of population), which has been attributed to poor diets (Rogers, 1995). The total daily protein consumption per day is estimated at 48.1 g person<sup>-1</sup> day<sup>-1</sup> which is extremely low compared to other countries of the similar economic bracket in the region, such as Tanzania, whose daily protein consumption is higher (FAO, 2014). The government of Zambia has recognized the poor health status of most of its people and has included an

explicit goal in the agricultural policy which seeks to fight household food insecurity and reduce the malnutrition prevalence (Chizuni, 1994). The National Nutrition Policy in Zambia also recognizes the need to promote crop diversification to reduce malnutrition (GRZ, 2006). Common bean production has for along time been recognised as a cheap way of mitigating food insecurity and the malnutrition status of many poor families who cannot afford other expensive sources of protein in their diets (Schwartz and Corrales, 1989). The crop is becoming an increasingly important crop in the Zambian agriculture and ranks as the second most important food legume crop after groundnut, based on the area planted annually (Table 0.1).

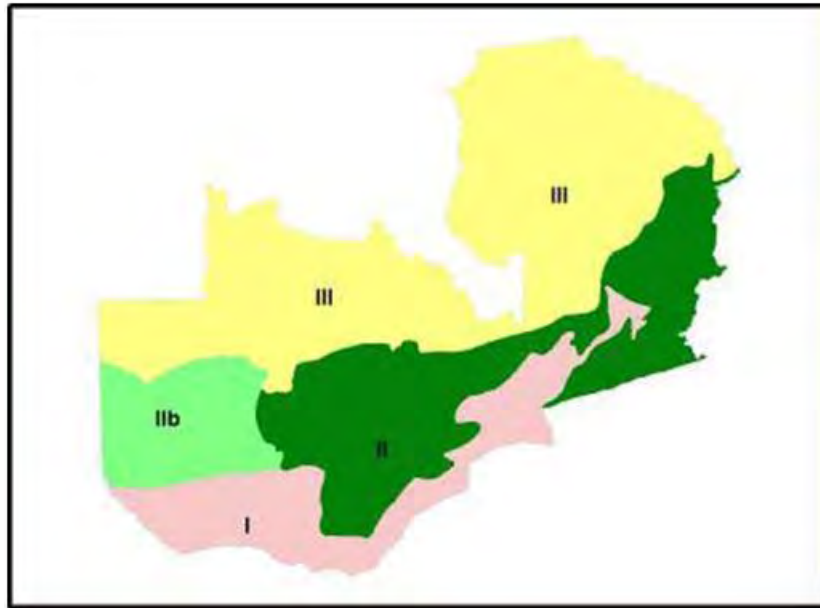
**Table 0. 1.** Hectarage and production estimates for selected food legume crops grown in Zambia over three agricultural seasons

Crop/Year	Area planted (ha)			Production(,000) kg ha <sup>-1</sup>			Average yield (kg ha <sup>-1</sup> )		
	2004/5	2005/6	2007/8	2004/5	2005/6	2007/8	2004/5	2005/6	2007/8
Cowpea	6 687	7 120	3 688	1 249	3 146	1 506	190	440	520
Common bean	50,496	54,532	59,590	23,098	27,697	44,464	460	510	670
Groundnut	161,962	144,250	144,200	74,218	84,010	70,527	460	580	660
Bambara nuts	3 407	2 387	2 204	1 237	1 593	2 513	360	670	840
Soybean	83 735	69 923	96 232	95 333	45 557	59 835	1 139	741	697

Source: Technical Compendium: Descriptive Agricultural Statistics and Analysis for Zambia, 2013

Common bean production in Zambia is predominantly rain fed. The crop is faced with serious negative impacts of the extreme climate events which are believed to be manifestations of the long term climate change (De Wit, 2006; UNFCCC, 2007). The climatic conditions in Zambia vary greatly as a result of variations in altitude, temperature, relative humidity, radiation and air masses which are highly influenced by the Inter-Tropical Convergence Zone (ITCZ). The climatic variations, especially in rainfall, have resulted in the country being sub-divided into three sub-regions namely, Regions I, II and III, (Figure 0.1) (Veldkamp et al., 1984). Zambia's rainfall patterns are very unreliable and poorly distributed, especially in Regions I and II which receive 400-800 mm and 800-1000 mm of rainfall annually, respectively (Veldkamp et al., 1984), and this has a negative impact on bean production (Sponchiado et al., 1989). Wortmann et al. (1998) estimated that on average, a ton per ha of potential common bean yield is lost in regions receiving

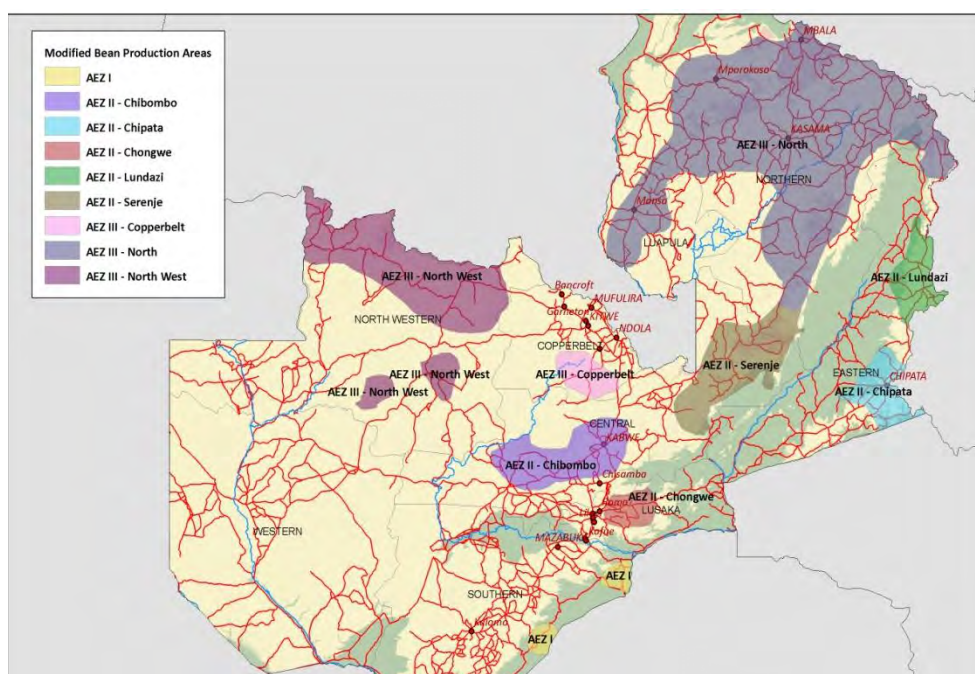
less than 300 mm of rain annually. These estimates are expected to be even higher for Southern Africa where the problem is compounded with extremely high temperatures (Boyer, 1982; Wortmann et al., 1998).



**Figure 0.1:** Agro-ecological regions of Zambia. Source: (Zambia Agricultural Research Insitute (ZARI), 2006)

Common bean yields in Zambia have remained low for a long time and currently are averaging between 460 and 670 kg ha<sup>-1</sup> on farmers' fields (Table 0.1). During the period 1991-2004 common bean yields shrank on average by 1.3% annually, while the area planted with the crop increased by 1.8% annually during the same period (Jayne et al., 2007).

Generally, the abiotic stresses contribute about 66.9% yield loss worldwide and this value seems to be increasing with time and affects the bean adoption and production distribution in the country (Wortmann et al., 1998). Common bean production is concentrated in Region III where rainfall and temperatures are not limiting (Figure 0.2). However, serious moisture stress has been limiting bean production in the southern parts of the country due to recurrent droughts and high temperatures.



**Figure 0.2:** Common bean spatial distribution in Zambia (Note: AEZ- Agro-ecological zones) (ZARI, 2006)

The most important abiotic stresses are drought and heat stress and the effects are manifested when the two stresses occurs at reproductive stage in beans (Ort and Long, 2003; Bates et al., 2008). Widely adaptable common bean varieties open up great opportunities for improving the livelihoods of farmers who currently occupy marginal pieces of land characterised by unfavourable weather patterns (Ramalho et al., 2009). Breeding crops for abiotic stresses has however received limited attention and has only recently been recognized as an option to minimize stress effects and found to be an economically viable tool for improvement of crop production in stressful environments (Blum, 1988). Studies related to heat tolerance are scarce in the literature. However, the few studies done have reported that the trait is inherited quantitatively and screening for heat tolerance is difficult. Some success has been achieved in the development of heat tolerant cultivars (Rosas et al., 2003; Beaver et al., 2008). There are large genotypes by environment (G X E) interactions in breeding for drought and heat tolerance and this poses difficulty in selecting an appropriate breeding method for the two traits. The genetic variability for resistance to abiotic stresses tends to be low and the heritability is also low with the G X E interaction having great influence on the phenotypic expression of the genotypes (Ramalho et al., 2009). However, selecting genotypes in environments that

experience frequent drought stress and high temperatures will remain an important research topic (Ehlers and Hall, 1998; UNFCCC, 2007; Williams et al., 2007). Genotypes achieving high yield under stress conditions have been considered tolerant (Fernandez, 1992). The use of yield to screen for drought tolerance is considered a difficult subject as yield is a complex trait that is controlled by many genes and need careful analysis in order to preclude other factors before making generalized conclusions.

Furthermore, there is still limited adoption of improved varieties, which is an indication of a disconnection between research and the small-holder farmers (DeVries and Toenniesen, 2001). Despite common bean's importance to the majority of the population in Zambia, its production continues to be too low to meet the food demand of the growing population and for export. This can be explained in part by low uptake of improved technology and limited use of farm inputs (Buruchara, 2007). The main reasons advanced for low adoption of varieties range from social to cultural beliefs of the farming communities (DeVries and Toenniesen, 2001). This has been confirmed for the common bean by Sperling et al. (2001) who reported that consumer preferences are important in developing common bean varieties which are likely to be adopted by small scale farmers. It has been emphasized that breeding should involve farmers in setting the breeding goals, variety design and development to enhance adoption of improved varieties by the farmers. According to Buruchara et al. (2011), many new agricultural technologies are currently available in Zambia, including improved common bean varieties production packages (e.g. fertilizers, and pesticides). Unfortunately, while available in principle, households' awareness of and access to these new technologies is distinctly limited in practice.

It has been estimated that about 40% of the common bean is grown under drought and relatively high temperatures particularly at low altitudes (Broughton et al., 2003). The majority of small-scale farmers in Africa depend on natural climatic conditions for their crop production (CIAT, 2005). These farmers are heavily constrained with financial resources and have no capacity to make investments into irrigation facilities or greenhouses unlike their counterparts in the commercial farming sector (CIAT, 2005). As a result, huge yield losses resulting from droughts and elevated temperatures are incurred in the low altitude areas. Farmers in most situations usually abandon the cultivation of improved varieties in preference for their own landraces, which have the

ability to adapt to various temperatures, rainfall, soil and other abiotic limitations (Mekbib, 2006). Although use of landraces ensures that farmers harvest something in times of harsh weather conditions, these genetic resources are inherently low yielding. Designed breeding provides an option to integrate important genes from farmers' germplasm with known improved cultivars to enhance productivity and serve the diverse needs of farmers.

## **0.2 Rationale of the study**

In Zambia, most breeding efforts have focused on breeding for disease tolerance for optimal environments. The varieties that have been developed have not been adopted because they lack farmer preferred traits. There is no published information available on breeding for heat and drought tolerance in common bean populations and integration of farmers' preferences for the common bean in Zambia. The scarcity of this information is a constraint to the development of drought and heat tolerant bean genotypes adapted to the low lying attitudes and also a limitation to increased farmer adoption of common bean varieties in the country. Knowledge on genetics of heat and drought tolerance in the common bean genotypes and farmer criteria for accepting varieties is therefore an invaluable resource in a breeding programme and hence, this study was conducted.

This study was designed with the following objectives:

1. To assess farmers preferences for bean varieties in the low altitudes areas in Zambia,
2. To identify drought tolerant common bean genotypes for use in breeding programmes and cultivation by farmers in the low altitudes in Zambia,
3. To evaluate and identify heat tolerant common bean genotypes in the Zambian landraces and determine the gene action, and
4. To determine the inheritance of yield and yield related traits under managed drought stressed conditions.

## **0.3. Organisation of thesis**

The thesis is written in the form of discrete research chapters, each following the format of a stand-alone research paper (whether or not the chapter has already been published). This is the dominant thesis format adopted by the University of KwaZulu-Natal, because it



facilitates the publishing of research out of the theses far more easily than the monograph form of thesis structure. As such, there is some unavoidable repetition of references and some introductory information between chapters.

The referencing system used in the chapters of this thesis is based on the “The American Society of Agronomy (ASA), Crop Science Society of America (CSSA), and Soil Science Society of America (SSSA) ***Publications Handbook and Style Manual***, referencing style,” and follows the specific style used in “Crop Science Journal”.

The outline of the thesis is therefore as follows:

1. Thesis Introduction
2. Chapter One: Literature review
3. Chapter Two: Farmers preferences and influencing factors for acceptance of common bean varieties in the low altitude areas of Zambia
4. Chapter Three: Evaluation of common bean genotypes for tolerance to drought stress
5. Chapter Four: Assessment of common bean landraces and genetic effects for high temperature tolerance under field conditions
6. Chapter Five: Genetic analysis of common bean for yield and yield components under managed drought stress conditions
7. Chapter Six: An overview , breeding implications and conclusions of the study

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# CHAPTER ONE

## Literature Review

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### 1.1 Introduction

The focus of this review is on the drought and heat stresses, the main yield reducing factors in common bean production, and its effects on the biological mechanisms. It highlights the common bean diversity, its origin and biology and spells out strategies for crop improvement in order to increase the bean yields under drought and heat stressed conditions. The common bean is sensitive to low moisture and heat stress, and their occurrence in combination does limit the spread of the crop to marginal climates (low altitudes), which are dominated by small-scale farmers. The review focuses on bean production constraints, genotype by environment effects on common bean breeding, methods on screening and breeding strategies for drought and heat tolerance in common beans. The farmer preferences for common bean varieties is also reviewed for purposes of setting the breeding goals.

### 1.2. Diversity, origin and taxonomy of common bean

The common bean (*Phaseolus vulgaris* L.) belongs to the family Leguminosae, subfamily Papilionoideae, tribe Phaseoleae and sub-tribe Phaseolinae (Debouck, 1999). It is a diploid with  $2n=2x=22$  chromosomes. The cultivated forms of the common bean are herbaceous annuals which are either determinate or indeterminate in growth habit. The common bean has a tap root system with adventitious roots that develop along the tap root which grows to about 10-15 cm in length (Duke, 1981). The common bean is a C3 crop and is poorly adapted to extremes of temperature compared to C4 plants. The crop is known to be highly polymorphic and has high variations in terms of growth habit, vegetative characters, flower colour and size, shape and colour of pods and seeds (Purseglove, 1968). The seed shape varies from round, elliptical, flattened or rounded and elongated with many different decorative colours. The seed mass ranges between 50 to 2000 mg seed<sup>-1</sup> (Debouck, 1991).

The origin of the common bean is controversial (Gentry, 1968; Kaplan, 1981). However, recent data from molecular markers and sequence information provide increasing molecular evidence for the Mesoamerican origin of common bean (Kwak and Gepts, 2009; Bitocchi et al., 2012). According to Gepts and Debouck (1991), the common bean

was domesticated in the highlands of Latin America. Two gene pools for the crop are recognized, the Mesoamerican and Andean (Gepts et al., 1986). These have further been divided into races namely, Mesoamerican, Durango, and Jalisco belonging to the Mesoamerica gene pool; and the Peru, Nueva Granada, and Chile races belonging to the Andean gene pool. The landraces belonging to the Andean gene pool have wide genetic variation in plant and grain morphology and are adaptable to a wide range of environments (Tohme et al., 1995). The Andean gene pool has also been established to reflect much of the human intervention through breeding and cultivation resulting into a narrow genetic base (Beebe et al., 2001). The landraces from the Mesoamerican group have been reported to contain greater variability than those from the Andean origin (Chiorato et al., 2007).

Most of the cultivars currently cultivated worldwide originate from two centres of domestication, the southern Andes and Mesoamerica (Gepts, 2001). The Centro Internacional de Agricultura Tropical (CIAT) maintains a large collection of both domesticated and wild forms of the common bean while a reference collection is maintained at the National Botanical Garden of Meise, in Belgium.

The common bean is a warm season crop which consists of several types based on growth habit and its flower biology has been well described by Debouck (1991). The crop is predominantly self-pollinated with less than one percent possibility of natural outcrossing (Brunner and Beaver, 1989). It exhibits two growth habits, determinate and indeterminate (Smoliak et al., 1990). Cultivars may be classified according to plant growth habits and described as follows: determinate habit, stem elongation ceases when the terminal flower racemes of the main stem or lateral branches have developed. With the indeterminate habit, flowering and pod filling will continue simultaneously or alternately as long as temperature and moisture availability permits growth to occur.

In addition to the distinction between determinate and indeterminate plant habits, four plant growth types have been identified. These are: Type I –determinate bush; Type II – upright short vine, narrow plant profile, three to four branches; Type III – indeterminate, prostrate vine; Type IV – indeterminate with strong climbing tendencies requiring trellis systems for optimal production. Kelly (2000) suggested that growth habit in beans can be used as a selection criterion for drought tolerance (Kelly, 2000). The expression of

genotypes in the growth habit was found to relate how genotypes differ in the root architecture. More branching shoots indicate a fibrous root system while less branching shoots may indicate less roots (Kelly and Miklas, 1998). While it is generally appreciated that early maturing genotypes would escape terminal drought, caution needs to be exercised, as early maturity may lower yields (Kelly and Miklas, 1998).

During emergence, the bean produces the hypocotyl arching from the soil with its large cotyledons suspended on the sides. The hypocotyl straightens after the cotyledons emerge from the soil forming the first unifoliate leaves and later grows trifoliate leaves that develop along the terminal and auxiliary buds. The crop also has perfect flowers that contain both the pistillate and the staminate parts. The flowers are set along the auxiliary and terminal racemes, which may be more than one in number. They contain ten stamens and one ovary. The bean produces three different colours of flowers, white, purple and pink. The biology of the common bean determines to a larger extent how the crop would adapt to drought and heat stress.

The genetic diversity of domesticated common beans is generally narrow as compared to wild forms (Koenig and Gepts, 1989; Chacon et al., 2005). The Andean gene pool is genetically narrower than the Middle American gene pool (Kwak and Gepts, 2009; Bitocchi et al., 2012). This is suggestive that limited progress would be made if crosses are made between the same gene pool. The common bean races have, however, made it easy to understand the genetic diversity and for use of the germplasm for crop improvement (Kelly et al., 1998). The interracial, intergene pool and even interspecific crosses of common bean with the wild forms of the *Phaseolus sp* have been exploited for bean improvement. For example, interracial crosses between races Durango and Mesoamerica have been useful in breeding for yield and drought resistance (Singh, 1995). However, this study has limitations to use these wild forms and therefore low progress would be expected.

### **1.3. Drought**

#### **1.3.1 Drought and its effects on common bean**

Drought stress is said to occur if there is insufficient moisture for normal plant growth and may occur at any stage in crop development. The topography and the type of soils can

also cause drought stress. Sloppy landscapes encourage water-run off while sandy soils do not hold water, hence causing water stress to plants (White and Singh, 1991). Two types of drought are recognized, agricultural drought and meteorological drought. Meteorologists define drought as the absence of rainfall for a long period of time causing moisture depletion in the soil and a decrease of water potential in plant tissue (Kramer, 1980).

For agricultural purposes, drought is defined as the inadequacy of water that is available to plants which could be as a result of having no rain or just non-availability of soil moisture in the soil. In agriculture, therefore, drought is a situation where soil moisture is limiting for normal plant growth caused by excessive water loss through evapotranspiration (Begg and Turner, 1976). Two types of droughts are known, intermittent and terminal drought (Acosta-Gallegos and Adams, 1991; Foster et al., 1995). Intermittent drought is due to climatic patterns of sporadic rainfall or inadequate irrigation during the growing season (Schneider et al., 1997a). In contrast, terminal drought occurs when plants suffer lack of water during later stages particularly at reproductive growth stage (Frahm et al., 2004). In many cases intermittent drought is usually experienced at high altitudes, whereas terminal drought is common at low altitudes. Intermittent droughts have been known to be difficult to manage while early maturing varieties have been used to manage terminal droughts (Chauhan et al., 2002).

The type of drought is very important for breeding since genotypic response and mechanisms to resist or tolerate terminal or intermittent drought differ in beans (Hall, 2001). It is therefore important that the type of drought stress the breeder imposes on the experiments resembles the type of drought stress that occurs in the target environment (White and Singh, 1991). Selection of genotypes may also be guided by the type of drought stress. Early maturing and determinate cultivars would be selected for areas affected by terminal drought because they would mature before the drought stress occurs while indeterminate and long season varieties would be selected and suitable for intermittent drought prone areas because they have the ability to recover after a long dry spell (Hall and Patel, 1985). Terminal drought has been known to affect the reproductive stages of the crop, especially during flowering and seed set (Nigam et al., 2002).



In general, low availability of moisture to the bean plant affects the metabolism of the plant during flowering time and pod-fill, as these are stages when drought causes the greatest yield reduction (Frahm et al., 2004a; Sponchiado et al., 1989). The traits that have been found to be important in both terminal and intermittent drought include earliness and early partitioning of photosynthates into reproductive structures for higher harvest index (Acosta-Gallegos and Adams, 1991; Foster et al., 1995). However, selection based on high harvest index has been criticized because breeders can only use yield after harvest in order to make selections based on yield and this could lead to discarding tolerant genotypes in an event that the genotypes differ in maturity dates and fail to yield (Gebeyehu, 2006). The crop cover in relation to leaf area was found to correlate with seed yield in both drought stressed and non-stressed conditions and is therefore important for measuring drought tolerance in common bean (Gebeyehu, 2006). The choice of traits to use in breeding for drought tolerance in common bean will depend on the type of drought the breeder is targeting (Beaver et al., 2003).

The extent to which drought affects the plants depends on the type and duration of the drought and the time it occurs. Intermittent droughts usually affect common bean by reducing yields through reduction of the leaf area (Maiti et al., 1996; Clarke and Dudley, 1981). The extent to which the leaf area reduction occurs depends on the individual genotypes. The reduced leaf area is usually associated with reduced evapotranspiration enabling genotypes to conserve and utilize the limited moisture in the soil effectively. Selection for drought tolerance based on leaf area is therefore possible, especially when genotypes are exposed to intermittent drought (Mohamed et al., 2002). Yield differences are said to be very visible when intermittent drought stress occurs at the initiation of meiosis (Westgate and Grant, 1989). Terminal drought on the other hand distinguishes genotypes on the basis of their ability to mobilize photosynthates into grain (Ludlow and Muchow, 1990). Bean genotypes tend to lose leaves during senescence in order to reduce the evapotranspiration and conserve moisture (Ramirez-Vallejo and Kelly, 1998).

The effect of drought depends upon the stage of crop development and the greatest impact occurs during the reproductive stage. The traits such as plant type, the root system and early flowering play a major role in adapting common bean to drought stress (Acosta-Gallegos et al., 1995). Early flowering is associated with partitioning of photosynthates into economic yield in common bean (Beaver and Rosas, 1998). The

early maturing genotypes are less likely to suffer terminal droughts as is the case with indeterminate late maturing genotypes (Kelly and Miklas, 1998). When conducting drought stress experiments, it has been suggested that grouping the genotypes according to their growth habit and maturity dates is of paramount importance in order to reduce the error in the experiments. Some reports have indicated that growth habit in beans can also influence its adaptation to drought stressed environments (Kelly, 2000).

### **1.3.2 Mechanisms of drought tolerance**

Plants have evolved different strategies to avoid deleterious effects of drought. These include escape, avoidance, and tolerance mechanisms (Levitt, 1972). Plants may combine various strategies to reduce damage associated with drought. The mechanisms of drought resistance are broadly grouped into three categories namely, drought avoidance, drought escape and drought tolerance (Levitt, 1972; Mittler et al., 2001).

#### **1.3.2.1 Drought escape**

Drought escape is usually manifested as early maturity and this involves quick plant development, early flowering and early maturity and is defined as the ability of the crop to complete its life cycle before drought sets in (Acosta-Gallegos et al., 1995; Foster et al., 1995). Times of flowering and early maturity are major traits associated with drought escape. However, earliness is usually associated with a yield penalty in most crops since higher yields generally require a longer growing period (White and Singh, 1991). In areas where terminal drought constrains production, a moderate shortening of vegetative growth period combined with a high growth rate might be advantageous. Agricultural practices that match crop growth with availability of soil moisture can significantly reduce yield losses. Another important mechanism that maintains crop productivity under terminal drought stress is associated with the efficiency of some genotypes in the partitioning of assimilates to developing fruits or seeds. This involves the plant's ability to store reserves in the shoot which are remobilized into the fruit or seed when the crop is exposed to drought stress. This response is common in cereals where stem and leaf reserves are used to support grain filling (Blum, 1996; 2005; Gebbing and Schnyder, 1999; Aggarwal and Sinha, 1984; Bruce et al., 2002), and in legumes where remobilization of assimilates from stems, leaves, and pod walls to the growing seed has been observed (Rodrigues et al., 1995; Chaves et al., 2002; Beebe et al., 2008). The

extent of assimilates partitioning depends on plant species, stage of crop development, duration of drought, and severity of drought (Farooq et al., 2009). The mobilization of photosynthates to the seed under terminal drought in common bean has been found to be an important trait in some landraces belonging to the Mesoamerica race (Rao, 2001).

#### **1.3.2.2 Drought avoidance**

Drought avoidance implies that a plant can maintain high water potential despite the limitation in the soil moisture levels. Genotypes avoid drought stress by maintaining relatively high tissue water potential, despite the low soil moisture condition. Such genotypes are usually characterized by an efficient deep, long and fibrous root system, reduced water loss through reduced leaf conductance, reduced absorption of radiation by leaf rolling, and reduced evapotranspiration surface (leaf area) (Mohamed et al., 2005; Wakrim et al., 2005).

Plants avoid drought by maximizing water uptake or limiting water loss and by retaining cellular hydration despite the reduction in water potential (Blum et al., 2005). Water uptake in deep soil layers is of particular importance in production areas where crops are grown on stored soil moisture. Soil water uptake depends on the degree of water loss throughout the shoot (Vadez et al., 2008) or water management by the shoot. Therefore, it is important to understand the root/shoot interactions in terms of plant water management as well as the combination of both shoot and root traits interactions with the environment (Vadez et al., 2008). For example, in lowland rice, it has been observed that water uptake by deep roots was consistent throughout stress periods in drought tolerant genotypes (Gowda et al., 2012). In legumes, the most critical component of drought avoidance was associated with conservative soil water use during early stages of development to allow a significant amount of water to remain for reproduction and pod filling (Devi et al., 2010; Sinclair et al., 2008; Zaman-Allah et al., 2011). Many studies have reported positive associations between yield and root depth under water deficits in cereal crops at grain filling stage (Bernier et al., 2007, 2009; Lopes and Reynolds, 2010; Manschadi et al., 2006). In other studies in some selected legumes such as common bean, chickpea, soybean and cowpea; root length density, maximum root depth, and fibrous root systems have been found to be associated with drought avoidance (Beebe et al., 2010; Gaur et al., 2008; Pantalone et al., 1996; Hall, 2012). However, studies indicate

that the root traits associated with drought stress in groundnut and pigeon pea are still unclear (Vadez et al., 2008).

On the other hand shoot drought avoidance mechanisms are mainly associated with stomatal closure to limit water loss through transpiration. The plants may also reduce light absorbance through leaf rolling, narrow leaf angles, shedding of older leaves, a dense trichome layer, leaf epicuticular wax, and lighter leaf color (Ehleringer and Cooper, 1992; Chaves et al., 2002; Srinivasan et al., 2008). This mechanism has however been unpopular for use in plant breeding due to the complexity of the mechanisms. The regulation of leaf water losses using various water saving traits as alluded to by most of the research work done towards ensuring seed development have been associated with drought tolerance in legumes (Sinclair et al., 2008; Zaman-Allah et al., 2011; Devi et al., 2010).

Drought avoidance through deep soil profile moisture extraction by use of deep and high root density have been reported to confer improved adaptation to drought stressed conditions (Sponchiado et al., 1989). Some photoperiod sensitive genotypes were found to use the phenotypic plasticity where genotypes of the same maturity groups are able to produce differently but are repeatable as a way of avoiding drought stress while some shorten their growing cycle even when planted late and are able to mobilise photosynthates and partition it to grain formation, increase of pod harvest index, pod partition index and leaf area index (Acosta-Gallegos et al., 1995;).

### **1.3.2.3 Drought tolerance**

Drought tolerance in legume crops has been characterized by restricting their transpiration rates to a certain level under extreme high temperature and high moisture deficit. It is recognised therefore that most legume plants manage themselves in moisture limited environments by reducing transpiration rate, a trait related to vapor pressure deficit. For instance, breeding for morphological traits related to limited water loss resulted in development of drought tolerant soybean with delayed wilting trait (Sinclair et al., 2008). In cereals (sorghum, rice, and maize), the stay green trait characterized by delayed leaf senescence during grain filling under water limited conditions is an important drought tolerance trait (Takeda and Matsuoka, 2008). Osmotic adjustment is another dehydration postponing trait that is expressed under soil drying conditions and this

involves the accumulation of a wide range of compatible solutes and ions such as soluble sugars, sugar alcohols, proline, glycinebetaine, organic acids, calcium, and potassium to maintain cell water balance (Blum, 2009; Blum et al., 2005; Farooq et al., 2009).

The osmotic adjustment maintains leaf turgor and improves the root capacity for water uptake (Blum, 2009). It is the ability for the crop to withstand low moisture levels while maintaining low tissue water potential. This enables the plants to withstand severe stress for a relatively long period of time. Drought tolerance therefore entails crop adaptation through sustained plant/cell function in a dehydrated state (Blum et al., 2005). This is done through specific mechanisms that may consist of accumulation of detoxifying and cell structure stabilizing components and various organelles including chloroplasts, mitochondria and peroxisomes which are key under drought stress (Farooq et al., 2009, Blum, 2005). Drought stress affects photosynthesis and plant growth and is usually associated with changes in the metabolism of sugars within the plant cells (Mwanamwenge et al., 1999).

The antioxidant enzymes in plants such as superoxide dismutase, glutathione reductase and ascorbate peroxidase remove toxic substances from the plants and therefore reduce damage to the plant tissue when plants are exposed to low moisture stress (Moore et al., 2009; Sofo et al., 2005). The plants also are able to produce stabilizing proteins during periods of drought stress (Kavar et al., 2008; Pinheiro et al., 2008). These proteins may accumulate in the stems and protect plants from serious damage from low moisture stress (Moore et al., 2009; Pinheiro et al., 2008). They are commonly referred to as late embryonic abundant (LEA) and have shown greater drought tolerance compared to the wild type in various crops (Xiao et al., 2005). Other types of proteins such as heat and cold shock proteins confer drought tolerance by acting as molecular chaperones that stabilize the mRNA which confers drought tolerance (Kavar et al., 2008; Pinheiro et al., 2008). The ability of plants to function well when exposed to low plant-water status and recover from dehydration is an important aspect of drought tolerance. The recovery in some crops has been shown to be a consistent and useful trait for selection to improve early drought adaptation where it is associated with secondary traits such as green leaf area or stem greenness (Kamoshita et al., 2004; Muchero et al., 2008). For instance some cowpea genotypes exhibit vegetative stage drought tolerance conferred by its capacity to recover from severe drought (Hall, 2004).

The responses of plants to tissue water-deficit determine their level of drought tolerance. The common bean like other related crop species employs a combination of these mechanisms to adapt to drought stressed conditions (Beebe et al., 2013). Many researchers have used and capitalised on these mechanisms, either separately or in combination, to develop common bean cultivars that would adapt to drought stress conditions (Amede et al., 2004; Beebe, 2012; Beebe et al., 2008; Rao, 2001).

### **1.3.3 Screening for drought tolerance**

The effect of soil moisture stress on common bean has been well explained in literature (Boutraa and Saunders, 2001). Different methods have been used to identify genotypes that are adaptable and productive in drought stressed conditions (Begg and Turner, 1976; Yadav and Bhatnagar, 2001; Raynolds et al., 2007). Mathematical models have been used to compare the change in yield between stressed and non-stressed conditions (Rosielle and Hamblin, 1981). However, bean breeders are more interested in selecting genotypes based on yield performance using indices other than drought tolerance *per se*. Drought tolerance in this case has been defined as relative yield of a genotype compared to other genotypes subjected to the same drought stress conditions, enabling the breeder to use various drought stress indices to distinguish genotypes (Ramirez-Vallejo and Kelly, 1998; Subbarao et al., 1995).

Seed yield has been reported as the most practical and appropriate way to screen for drought tolerance (Acosta-Gallegos and Adams, 1991; Terán and Singh, 2002a; White and Singh, 1991). In some cases drought tolerance is confounded with diseases. For example, drought tolerance may also confer resistance to fusarium and rhizoctonia root rots (Navarette-Maya et al., 2002b; Subbarao et al., 1995). Screening for drought tolerance takes into account the differences in genotype response mechanisms and yield under stressed and non-stressed conditions. Breeders have used several selection criteria to identify genotypes based on their performance in stress and non-stress environments (Fischer and Maurere, 1978; Rosielle and Hamblin, 1981; Fernandez, 1992). Drought indices which provide a measure of drought tolerance based on loss of yield under drought conditions in comparison to normal conditions have been used for screening drought tolerant genotypes (Mittler et al, 2001). Rosielle and Hamblin, (1981)

defined stress tolerance (TOL) as the differences in yield between the stress (Ys) and non-stress environments (Yp) and mean productivity (MP) as the average yield of Ys and Yp. Fischer and Maurer, (1978) proposed a stress susceptibility index (DSI) which measures the drought stress intensity. Fernandez (1992) proposed and stated that geometric mean productivity (GMP) can be used to determine relative performance of genotypes, since drought stress can vary in severity in field environments over years while stress tolerance index (STI) would be a useful tool for determining high yield and stress tolerance potential of genotypes. The stress tolerance index can be used to identify genotypes that produce high yield under both stress and non-stress conditions. Sio-se Mardeh et al. (2006) used drought tolerance indices in wheat and found that under moderate stress, MP, GMP and STI were more effective in identifying high yielding cultivars in both drought-stressed and non-stressed conditions. Under severe stress, none of the indices used were able to identify and group high yielding cultivars. Clarke et al. (1992) used SSI for evaluation of drought tolerance in wheat genotypes and found a year-to-year variation in DSI for genotypes and their ranking pattern. Guttieri et al. (2001) using the SSI criterion suggested that an SSI value more than 1 indicates above-average susceptibility while a value less than 1 indicates below-average susceptibility to drought stress. Fernandez (1992) proposed STI for identifying mungbean genotypes with high yield and stress tolerance potentials.

In general, selection for drought is done based on phenotypic traits (Acquaah, 2007) and among them, it is recommended that measurement of seed yield is the most efficient way of screening for drought tolerance (White and Singh, 1991). The selection based on geometric mean seed yields and the use of drought susceptibility index is an effective tool to choosing drought tolerant genotypes in beans (Ramirez-Vallejo and Kelly, 1998). In other studies, it was found that the use of indices such as Drought Tolerance Index, Pod Harvest Index and Pod Partitioning Index are important phenotypic traits reflecting greater potential for genotypes to remobilize photosynthates from vegetative plant parts to pods (Beebe et al., 2008). Various selection indices provide different dimensions on the details of selection and provide more information regarding the mechanism of tolerance towards drought. All the indices will therefore be used to explore the drought tolerance mechanisms in this study.

#### **1.3.4 Genetics of drought tolerance**

Drought tolerance is a complex trait and its inheritance is considered to be quantitative (Beebe et al., 2008; Blair et al., 2011). The inheritance of drought tolerance therefore requires specialized biometric methods to determine the gene action. However, many factors are known to confer drought tolerance and these may include morphological, physiological and chemical genotypic responses (Blum, 1988). The genetics of inheritance of tolerance to drought stress in common bean has been studied and reported by different researchers. Some of the key traits reported to be relevant in explaining the genetics of drought tolerance include seed mass, rooting pattern, partitioning of carbohydrate, flower and pod abortion, number of seeds per pod and number of pods per plant (Rao, 2001; Sponchiado et al., 1989).

Dominant gene effects have been reported to be predominant for the inheritance of drought tolerance in common bean (Hinkossa et al., 2013; Shahab et al., 2012). However, while it has been widely acknowledged that additive gene action is important for drought tolerance; non-additive gene action particularly epistatic gene effects have also been found to be significant for some traits (Shahab et al., 2012). The additive gene effects have been reported for number of seeds per pod and above ground biomass under stressed conditions (Hinkossa et al., 2013). The race Durango has been reported to contain drought tolerance genes and was recommended for genetic studies in drought tolerance (Frahm et al., 2004; Terán and Singh, 2002). The use in breeding for drought tolerance of the race Durango in combination with other races has proved to be a consistent source of drought tolerance for lowland tropics, indicating that polymorphism between races is adequate. Very little work has been done to determine the mechanisms of drought tolerance in legumes compared to cereal crops despite the fact that legumes have demonstrated an ability to grow in diverse and harsh environments (Turner et al., 2001). The screening of improved genotypes and landraces therefore provides great potential in identifying appropriate genotypes for adaptation to drought prone conditions.

#### **1.3.5 Breeding for drought tolerance**

Breeding progress in legumes for drought resistance has been slow due to the polygenic nature of drought resistance and due to the fact that breeding for drought resistance has relied on empirical selection for yield in target production zones. However, yield is a complex trait which is influenced by various factors with a high dependency on genotype



by environment interaction (Sinclair, 2011). Various secondary traits have been studied and used to select drought resistant genotypes. Among these, the most widely used traits in breeding have been traits related to phenology and adaptation. For example, selection for early maturing genotypes to escape terminal drought has led to drought tolerant chickpeas and this led to the expansion of the production area as well as the productivity of chickpeas (Gaur et al., 2008). Cowpea is recognized to be the most drought tolerant legume. The high leaf water status in cowpeas has been used to select genotypes for drought tolerance (Hall, 2012). A combination of vegetative drought resistance and earliness has been used to develop early maturing genotypes (Hall, 2012). Delayed senescence was also found useful to confer drought tolerance in cowpeas and this has been reported to combine very well with remobilization of stem reserves providing an opportunity for re-growth (Hall, 2012). Delayed wilting in soybean genotypes has been used to select drought tolerant genotypes (Sinclair et al., 2008).

Breeders have been able to exploit different mechanisms to develop improved cultivars that cope with drought stress. Most of the work done so far has been the identification of drought tolerant lines (White et al., 1994b). In breeding for drought tolerance, selection may be made for early maturing varieties that escape the stress, or make crosses between tolerant genotypes and susceptible ones in order to develop superior genotypes (Beebe et al., 2010). The Durango race has been identified as a potential donor for drought tolerance following intensive screening of large numbers of germplasm in different altitudes (Tohme et al., 1995). Using the race Durango, many breeding programmes have utilized intra-specific crosses to improve drought tolerance in susceptible genotypes of common bean genotypes (Beebe et al., 2008). Some inter-genepool crosses were also found to offer superior segregants for drought tolerance (Singh, 1995). Many drought tolerant cultivars have been reported to sustain their production through their favorable response in protecting reproductive traits (Beebe et al., 2008).

Genotypic differences in common bean for biomass partitioning are reflected through two key traits and these include: pod partitioning index and pod harvest index (Rao et al., 2004). Pod partitioning index is determined as the ratio of dry weight of pods at harvest to dry weight of total biomass at mid-pod fill expressed as a percentage while, pod harvest index is calculated as the ratio of dry weight of seed to dry weight of pod at harvest

expressed as a percentage. These two traits have been used to determine the physiological differences in the drought tolerance levels in common bean and measures the photosynthate accumulation and partitioning. The International Center for Tropical Agriculture has widely used bean genotypes with superior pod harvest index and pod partitioning index as selection criteria for genotypes that reflect a greater ability to mobilize photosynthates to grain under drought stress (Ramirez-Vallejo and Kelly, 1998). The selection based on high geometric mean seed yields and drought susceptibility index values were reported effective approaches to select for drought tolerance in beans (Ramirez-Vallejo and Kelly, 1998).

The crosses between the race Durango and Mesoamerican genotypes have been used in common bean breeding to develop drought tolerance (Singh et al., 1991; Frahm et al., 2004; Beebe et al., 2008; Singh et al., 2001; Singh, 2007). Breeding for drought tolerance has progressed using various selection criteria such as biomass accumulation, seed yield traits, and pod filling under drought stress and non-stress conditions (Schneider et al., 1997; Frahm et al., 2004; Beebe et al., 2008). Selection under both irrigation and drought stress allowed the selection of elite cultivars that maximize yield potential in stress-free environments but which also produce acceptable yields under drought stress. In addition, screening in both drought and non-stress conditions allowed breeders to quantify yield gap caused by drought conditions so that they can be able to select cultivars with minimal yield loss under water stress.

Generally, breeders and plant physiologists are in agreement to use root traits such as root depth, density, and biomass, to select for terminal drought avoidance (Gaur et al., 2008; White and Castillo, 1989, Beebe et al., 2010; Manavalan et al., 2009; Kumar et al., 2012; Khan et al., 2010). However, breeding for improved water uptake using root traits has been limited due to practical difficulties to take the measurements. In addition, root architectural differences have been observed (Ho et al., 2005). In spite of the challenges associated with breeding for root traits, the identification and use of QTLs associated with root traits for better water uptake would improve breeding efficiency for drought tolerance (Asfaw and Blair, 2012). These QTLs can facilitate the breeding for root traits in common bean irrespective of water conditions once confirmed. This may provide bean breeders with an opportunity to capitalize on marker assisted selection (MAS) for chromosomal

regions carrying these QTLs. Some traits such as deep rooting have been found useful for drought tolerance in common bean (Sponchiado et al., 1989).

Another avenue to improve legumes for drought tolerance is through genetic engineering (GE) to introduce genes from other species known to have drought tolerance attributes. Many transcription factors that regulate downstream genes involved in drought tolerance have been identified and cloned (Ko et al., 2006; Torres et al., 2006; Kavar et al., 2008; Haake et al., 2002; Rodriguez-Urbe and O'Connell, 2006). These genes could be targets for legume transformation in an effort to improve drought stress tolerance.

## **1.4 Heat stress**

### **1.4.1 Heat stress and its effects on common bean**

There is currently about 20% of common bean production that takes place in the low- and mid-altitudes areas at high temperatures in Sub-Saharan Africa (Wortmann et al., 1998). Heat stress effects tend to increase under limited soil moisture. It is said to occur when the temperatures are above optimum ranges for normal plant growth (usually 10-15°C above optimum) over a period of time. The optimum temperatures for growing common bean are between 15 and 23°C (Wortmann et al., 1998). Extremes of temperatures, high or low, cause damage to most legumes at various growth stages that may include vegetative and/or reproductive stages (Ismail et al., 2000). Heat stress usually occurs together with drought stress and has become a common phenomenon in most of tropical Africa. Heat stress that occurs during the reproductive stage of growth may result into total crop failure in common bean (McCarthy et al., 2001). The common bean is known to be a warm season crop, and suffers under extremely high temperatures (>30°C) stresses which cause flower abortion (Tischner et al., 2003). Flower abortion has serious implications on common bean yields. White and Izquierdo (1991) reported flower abortion levels of between 60-80% due to low moisture and high temperature stresses in common bean. However, studies specifically done to determine losses in common bean due to heat stress alone are scarce.

The effects of heat stress in common bean range from poor floral bud formation, flower drop to poor pod development. The heat affects the viability of pollen grains and anthers, thereby resulting in low pod setting (Khattak et al., 1998). High night temperatures have been reported to cause high flower abortion (Warrag and Hall, 1984). In other related

studies, high flower abortion has been reported in kidney beans and snap beans (Navarette-Maya et al., 2002; Shonnard and Gepts., 1994). The optimum temperature for pollen germination and tube growth depends on species and varies between cultivars (Loupassaki et al., 1997). However, no reports were found that establish the temperature threshold levels for pollen growth in common bean.

The plants' sensitivity and response to heat stress differs among the species and the genotypic constitution (Howarth, 2005). It is known that C4 plants have a higher temperature minimum than C3 plants due to the operation of a CO<sub>2</sub>-concentrating system that inhibits rubisco oxygenase activity (Berry and Bjorkman, 1980; Edwards and Walker, 1983). The C3 plants generally grow optimally and remain productive at temperatures between 20 and 30 °C (Larcher 1995), whereas, C4 and CAM plants generally have higher optimal temperatures (30 to 40 °C) (Larcher, 1995). Critical temperatures for thermal tolerance are often plastic within species (Froux et al., 2004, Nicotra et al., 2008). Recent comparative studies show plasticity, but few consistent differences among species from different environments in thermal tolerance of photosynthesis (Knight and Ackerly 2002; 2003). In C3 plants, where the common bean belongs, high temperatures affect the ratio of rubisco oxygenase:rubisco carboxylase activities (Britz and Kremer, 2002). As temperature increases, the ratio of dissolved O<sub>2</sub>/CO<sub>2</sub> and the specificity of rubisco for O<sub>2</sub> increase, thus favoring oxygenase activity inhibiting net photosynthesis (Monson et (Britz and Kremer, 2002).

Heat stress has been reported to influence the nutritional quality such as accumulation of phytosterols and tocopherols (collectively called tocots), which have health promoting effects in humans (Britz et al., 2007; Wolf et al., 1982). For example in soybeans, heat and drought may affect the presence of tocots (Britz and Kremer, 2002). Slight increases in temperature combined with extreme drought may cause a large increase in  $\alpha$ -tocopherol that is almost precisely matched by decreases in  $\delta$ -tocopherol and  $\gamma$ -tocopherol content (Tsukamoto et al., 1995; Caldwell et al., 2005). In soya beans, growth at high temperature and low moisture stress was found to influence the isoflavins content both positively and negatively (Tsukamoto et al., 1995; Caldwell et al., 2005).

#### **1.4.2 Genetics of heat tolerance**

The common bean is known to be highly sensitive to extremes of temperatures (low or high) and this has resulted into unstable yields in environments where high or low temperatures occur (Lynch, 2007). However, literature on the impact of temperature on common bean production is still limited. Gisela and Gepts (1994) reported the significance of additive and non-additive gene action in the inheritance of flower bud abortion and pod fill. Differential heat tolerance reactions were observed by Rainey and Griffiths (2005b), suggesting that they could be affected by non-allelic heat tolerance genes. Significant heterosis has been reported to be significant in common bean when exposed to heat stress indicating a possibility of high allelic interactions in the parents (Shonnard and Gepts, 1994). In related studies, heat tolerance was improved in cowpeas using pollen traits (Morfo and Hall, 1992). Susceptible cowpea genotypes to heat stress were found to produce sterile pollen while resistant genotypes produced fertile pollen (Singh et al., 1997). Some genotypes fail to dehisce with extreme drought and high temperature stress in cowpeas (Mutters and Hall, 1992). It was established that the genes controlling abortion of reproductive organs (flowers, buds and pods) in cowpeas was controlled by a single recessive gene (Rainey and Griffiths, 2005c). The genetics of heat tolerance seem to be better understood in cowpeas than in the common bean (Hall, 2004). However, the information could be used interchangeably as the two crops belong to the same family (Hall, 2004). In view of this, the reports indicating that a single recessive gene and some minor genes reported to enhance the ability of cowpea to set pods under heat stress could be relevant information for common bean selections in the F<sub>2</sub> generation (Rainey and Griffiths, 2005a). Similarly the additive and non-additive gene action reported in the inheritance of flower bud abortion and pod fill in common bean is useful information and could be explored in breeding for heat tolerance.

#### **1.4.3 Heat stress interaction with drought stress**

The occurrence of heat and drought stress at the same time affects the uptake and discharge of CO<sub>2</sub> in common bean (Yordanov et al., 1997). Heat and drought stresses have been reported to affect leaf growth in sorghum; cause low leaf water content in wheat (Chen et al., 1988); dehydrate plant tissues causing irreversible plant damage and eventually death of the plant (Bartels and Sunkar, 2005; Bray et al., 2000). To cope with

these constraints, plants induce complex modifications of both their physiological state and metabolic pathways, which are still not very clear.

## **1.5 Breeding for drought and heat tolerance**

### **1.5.1 Sources of tolerance for drought and heat**

Plant breeding is continually contributing to improving people's lives through release of new varieties. Breeding efforts to develop common bean genotypes that are tolerant to drought and heat stress, particularly in Africa, have been limited. Sources of resistance for drought (Beebe et al., 2008; Brick et al., 2001; Singh, 2001) and heat (Beaver et al., 2008; Rosas et al., 2003) have been reported. Most of these tolerant genotypes have been developed through screening of large numbers of bean collections. Very few sources of resistance have been identified among the African germplasm and no known sources of resistance have been identified in Zambia. Many researchers have reported variation for drought tolerance in seed yield in response to well-known disruption of reproductive processes in common bean (Rao, 2001; Rosales-Serna et al., 2004; Rosales-Serna et al., 2005; Singh, 2001; Terán and Singh, 2002a). Most of the genotypes identified as drought tolerant were found to be early maturing and basically utilized the escape mechanism to adapt to drought stressed conditions. Crosses between Durango and Mesoamerican genotypes have generated drought tolerant lines (Terán and Singh, 2002a).

Common bean landraces are also a good resource for resistance although their use has been limited. Farmers and local gene banks maintain large collections of cultivated common bean landraces which are often variable in appearance, adaptation and some of them are known by local names. Most of these landraces retain special attributes such as early maturity, and their adaptation to adverse weather patterns, and tolerance to biotic stresses (Harlan, 1992). These could therefore be exploited in breeding for drought tolerance by screening them to identify tolerant genotypes.

### **1.5.2 Breeding for heat tolerance in common beans and screening techniques**

Breeding crops for heat stress tolerance has received little attention and has only started to be recognized in recent years as an option to minimize the heat stress effects (Porch and Hall, 2013). Breeding for heat tolerance is based on clear understanding of the

physiology and genetic mechanisms in response to heat stress. The physiological response to heat stress is well documented but there is limited information on the genetics of heat tolerance. Heat tolerance is a quantitatively inherited trait which is polygenically controlled (Beaver et al., 2008). Despite the difficulties in screening for heat tolerance, some reports have indicated success in the development of heat tolerant cultivars (Beaver et al., 2008; Rosas et al., 2003).

Screening for heat tolerance in common bean has been difficult. However, based on the common bean physiology, some selections have been done. Few heat stress indices have been developed for the evaluation of high ambient temperature stress in plants. Some of the key indices used include the thermal stress index in cotton (Burke et al., 1990), which is based on selecting genotypes based on canopy and leaf temperature. Other indices that have been used to select heat tolerant genotypes include a number of yield-based stress indices such as geometric mean (GM) and the stress tolerance index (STI) (Fernandez, 1993). The stress tolerance index was developed to identify genotypes that perform well under both stress and non-stress conditions. Fisher and Maurer (1978) proposed the stress susceptibility index (SSI) and defined it as a ratio of genotypic performance under stress to non-stress conditions, adjusted for the intensity of each trial, and has been found to be correlated with yield and canopy temperature in wheat (Rashid et al., 1999). Both the GM and SSI have been applied in the selection of heat tolerant bean genotypes (Vallejo and Kelly, 1998).

## **1.6 Breeding methodology for drought and heat tolerance**

Various breeding methods have been used to breed for drought and heat tolerance in common bean. Several workers have used the pedigree method to breed common bean. However, the method has been criticized to be long and takes too much time to implement (Frahm et al., 2004b). Some studies have reported the use of single seed descent (SSD) which has been applied in the breeding of soybean. This method, though useful in maintaining variability (Kelly and Miklas, 1998), has not been applied often in common bean breeding because of the many traits to be considered in common bean selection as compared to soybeans where it has worked well. In order to alleviate the disadvantages of the SSD method, the use of gamete selection was proposed when dealing with multiple traits (Singh, 1994). Gamete selection allows an early evaluation of

promising genotypes and this enables the breeder to remove lines with less desired characteristics early enough thereby eliminating chances of wastage of resources. The method of gamete selection assumes multiple-parent crosses and simultaneous improvement of multiple traits. The parental population (male and/or female parents) should be heterozygous and that each zygotic seed results from a separate and independent fertilization event. This method can only be used when dealing with few populations since it is labor-intensive and therefore may prove irrelevant in screening for heat tolerance which requires that one deals with bigger populations (Singh, 1998).

Bulk selection breeding method has been used successfully on yield improvement and successes were recorded in early generations ( $F_3$  and  $F_4$ ) in common bean (Singh et al., 1999). Although recurrent selection would be more useful in population breeding techniques in the field and could be the best suited for quantitatively inherited characteristics such as drought and heat tolerance in bean, its application in self pollinated crop species is difficult. Some researchers have successfully achieved high yielding, adaptable and stable genotypes using recurrent selection (Garcia et al., 2003; Ranalli, 1996; Singh et al., 1999; Johnson and Gepts, 2002). Beebe et al. (2008) still recommended recurrent selection as an effective breeding strategy for drought and heat stresses.

Breeding for heat and drought tolerance has several limitations due to large effects of genotype by environment ( $G \times E$ ) interactions. Selection for drought and heat tolerance has been reported to be difficult because the drought stress may occur at different times, with different intensity modified by soil type and fertility (Rao, 2001). In the harsh environments in which the majority of smallholder farmers in developing countries grow crops, mechanisms of drought and heat tolerance are difficult to analyze because of the interaction of drought with other stress factors, such as high temperature, low soil fertility, and soil acidity. These factors pose difficulties in identifying an appropriate selection method for drought and heat tolerance. However, it has been cited that selecting genotypes in environments that experience frequent high temperatures may be useful (Ehlers and Hall, 1998). However, despite the growing evidence that selection under target environments enhances breeding gains for stress environments (Atlin and Frey, 1990; Bänziger et al., 1997; Ceccarelli et al., 1992), the difficulty of choosing appropriate selection environments, given a highly variable target environment, may limit the



identification of superior genotypes (Blum, 1979). Genotype by environment interactions may originate from environmental variation in the timing and severity of water deficits, genetic variation in flowering time, and nutrient deficiencies and toxicities whose occurrence and severity usually interact with water deficits (Banziger and Cooper, 2001; Cooper et al., 1999).

### **1.7 Participatory Variety selection and farmer variety preferences**

Participatory plant breeding (PPB) is the development of a plant breeding programme in which breeders may collaborate with farmers, marketers, processors and consumers or policy makers. Variety trials conducted on the research station are often managed very differently from farmer practices. For example, researchers apply more fertilizer, achieve more complete weed and pest control, and irrigate more frequently than farmers can. High-yielding varieties that perform well under these “high-input” conditions may not perform well under more stressful conditions faced by poor farmers who cannot spend much on purchased inputs or who lack the labor to completely control weeds.

Participatory plant breeding techniques have successfully been used to develop and increase adoption of common bean varieties to farmers (Danial et al., 2007). This approach allows the participation of farmers in the development of bean varieties which enhances the adoption rates (Sperling et al., 2001). The approaches and context in which farmers have been engaged to participate in common bean breeding have been well defined (Sperling et al., 2001). The specific bean trait combination of preferred colour and growth habit is possible to achieve through participatory plant breeding (Morris and Bellon, 2004). However, many selection criteria using participatory plant breeding may result in compromise between selection for meaningful genetic combinations and farmers preferred traits such as between yield and taste (Sperling et al., 2001). Participatory plant breeding has been used as a strategy for increased use of improved varieties (Brush, 2000) because it can be used to breed divergent cultivars for subtly different environments and for diverse end uses. The PPB can also add value to traditional landraces that would otherwise be lost from the system (Sthapit et al., 2001).

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## **CHAPTER TWO**

### **Farmers' preferences for common bean varieties and factors influencing their choices in the low altitudes in Zambia**

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#### **Abstract**

Breeding programmes have released many improved varieties of common bean but very low adoption of the improved varieties has been reported. The main reason behind the low adoption levels is that breeding programmes have done little to understand the incentives that govern varietal choices among small-holder farmers. Farmers' preferences for common bean varieties were investigated in two Zambian populations, in two districts, using formal surveys and focus group discussions (FGD). Results from the study indicated that small-holder farmers were willing to adopt common bean varieties that were adaptable to their environments. The adoption criteria set by the farmers were that they preferred a bush type growth habit, red speckled bean colour, large bean size and elongated shape, bean taste, early maturity and high number of pods per plant. Lyambai, a red speckled seed variety was chosen as their preferred type of bean meeting most of their selection criteria. Gender and formal education levels of the farmers were also found important and influenced farmers in making common bean adoption decisions.

## **2.1 Introduction**

The common bean is one of the most important food legumes in the low altitudes of Zambia as a source of cheap protein, mineral nutrients and vitamins (Musonda, 2008). The crop also serves as a source of cash for the poor rural populations. This crop supplements the nutrition status of the Tonga people, who are the major occupants of the Gwembe valley and who were displaced from the area that is now covered by Lake Kariba when the dam was built in the 1960s. Due to its relatively low altitude, the climate is mostly hot and dry, with average rainfall of about 600-700 mm per year. The livelihood pattern in this zone is small-scale subsistence agriculture and livestock rearing (Ndiyoyi and Phiri, 2010). The farmer's preferences for crop cultivars in this region are highly influenced by the weather patterns.

Formal crop breeding programmes have in many cases not benefited farmers. This has been attributed to a huge disparity between research priorities and farmer preferences (Devi and Singh, 2011). This is particularly the case for small-scale farmers in sub-Saharan Africa (SSA), especially Zambia where yield levels have remained low despite researchers releasing high yielding varieties (Sperling et al., 2001). There is general understanding that modern varieties have not addressed the farmers' preferences and this has resulted in low adoption rates of these varieties (DeVries, and Toenniessen, 2001). Breeders may emphasize yield and disease resistance, giving less (or no) weight to grain or straw quality, threshability, or other traits that may be important to farmers. Many agronomically superior varieties have failed because they were deficient in traits important to farmers, which were not considered by breeders (Sperling et al., 2001).

The common bean is among the crops with the lowest adoption rates for improved varieties in Zambia (Sperling et al., 2001). The low adoption has been attributed to failure by the varieties to meet farmers' preferences (Foolad and Bassari, 1983). A further complicating factor is that many improved varieties of common bean have been selected on the basis of their agronomic performance in on-station trials. Often, these trials are conducted under high management practices, which are very different from those of the small-scale farmers (Chirwa personal communication, 2010)

Farmer participation in the breeding of crop varieties for low-resource farmers has now been recognized as essential in a breeding programme as an excellent means of

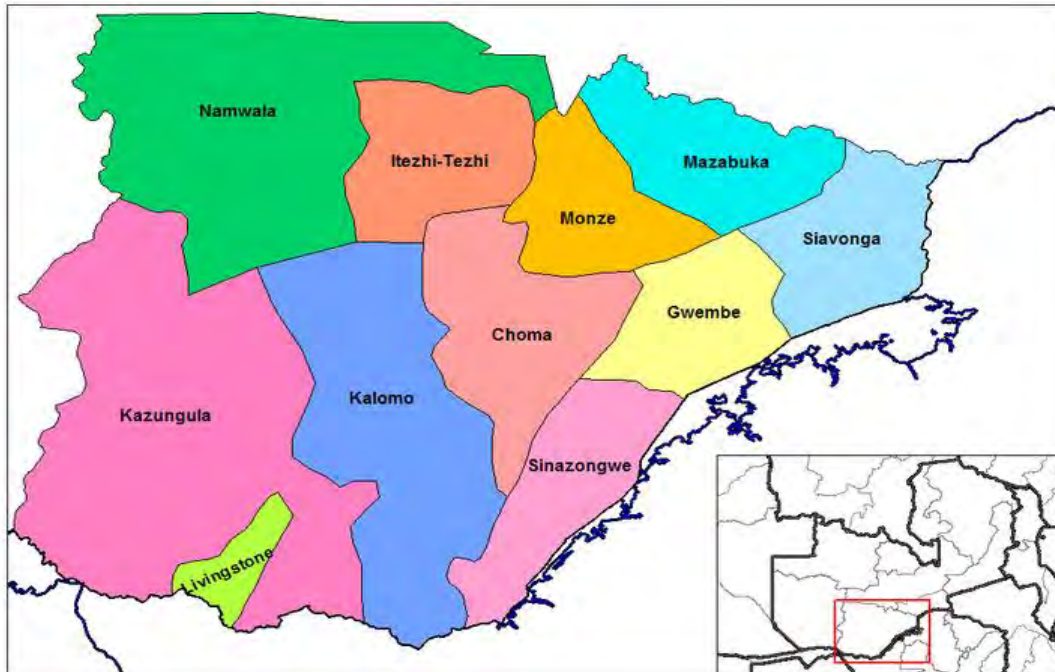
improving farmer acceptance and the adoption of improved varieties (Chirwa personal communication, 2010; Cokkizgin et al., 2013; Durson, 2007; Selehi et al., 2010). Owing to the nature of the common bean, it varies in colour, growth habit and taste, with varied consumer and farmer preferences (Idahosa and Alika, 2013). These preferences are more likely to be in new bean varieties if farmers participate in the research, and this will ensure increased adoption rates.

In light of the above background, this research was conducted to a) assess farmers' preferences for common bean varieties in the low altitude regions of Zambia, and b) identify and describe factors that influence the adoption and non-adoption of common bean varieties by these farmers.

## **2.2 Materials and methods**

### **2.2.1 Study sites**

The participatory study was conducted in two districts, namely, Siavonga and Gwembe districts (Figure 2.1) which are located approximately 140 and 180 km south and south west of Lusaka, the capital city of Zambia. The research focused on these two districts because they are both prone to droughts and high temperatures during the crop production seasons. According to CSO (2003), the population of Siavonga and Gwembe was 89,787 and 52,711 respectively and comprised 49% male and 51% female inhabitants in both districts. The districts vary in size and population density.



**Figure 2.1:** Map of Southern province showing the location of Siavonga and Gwembe districts Source:

[http://upload.wikimedia.org/wikipedia/commons/8/8c/Southern\\_Zambia\\_districts.png](http://upload.wikimedia.org/wikipedia/commons/8/8c/Southern_Zambia_districts.png)

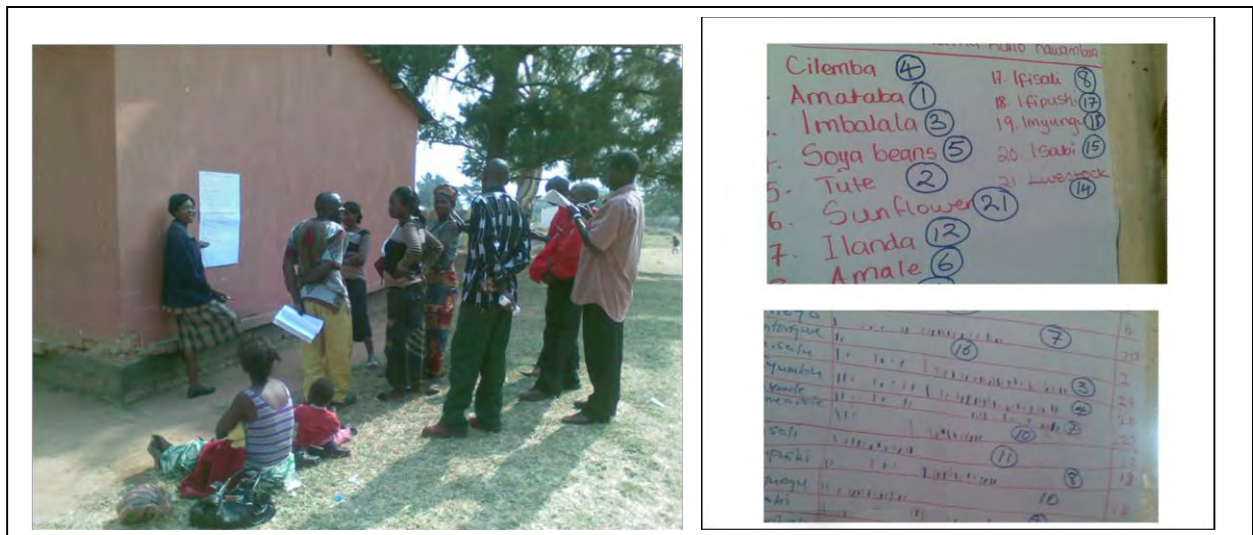
Most of the farmers in these two districts operate on a small-scale, occupying low farming potential, customary land under the control of traditional authorities (Central Statistical Office of Zambia, 2000). Siavonga and Gwembe lie within the tropical region with temperatures reaching above 30°C for most of the year. The districts receive the least rainfall in the country. This rainfall is usually erratic and the area is characterised by dry spells (Veldkamp et al., 1984; Zambia Agriculture Research Institute, 2006) but because of a lack of resources to invest in irrigation, farming in this area is predominately rain-fed. The growing season in the two districts is very short (between 60 – 90 days), from late November to early March. The districts lie along the Zambezi river basin which is low, flat, and widely embedded with brown red clay loams and highly prone to soil degradation. The two districts are occupied largely by the Tonga speaking community who are traditionally pastoralists but who grow crops for daily food needs, and whose maize diets are heavily supplemented by beans.

### 2.2.2 Data collection

The data was collected through two approaches; focus group discussions (FGDs) and a formal survey using a semi-structured questionnaire and structured questionnaire (Appendix 2.1 and 2.2).

### 2.2.3 Focus group discussions

The FGDs were held with four groups of farmers in December, 2010, in four selected camps; two groups came from each of the two districts, Siavonga and Gwembe (Figure 2.1). The agricultural camps are the smallest administrative units of the Ministry of Agriculture and Livestock for provision of extension services. In each of the selected camps, farmers were drawn from two different villages. These villages were selected on the basis of accessibility, and also because they practised bean growing. The identification of individual farmers was guided by key informants and the Ministry of Agriculture and livestock extension officers working in the selected areas. The sampling was done purposively as described by Ruane (2005) and Scheyvens and Storey (2003). This approach of sampling is designed to reach a desired target and was used to achieve a balance between women and men. The focus groups comprised 15 farmers each giving a total of 60 FGD participants. The discussions were open, with farmers using flip charts to summarise their discussions (Figure 2.2). The focus group discussions were held in different camps from those where the surveys by questionnaires were conducted to eliminate bias on answers from the farmers.



**Figure 2.2:** Farmers in focus group discussions, capturing main points on flip charts

Using the principles outlined by Grudens-Schuck (2003) and Grudens-Schuck et al. (2004), the composition of the groups was made with caution, with advice from the local extension agents, to ensure similarities in the general demographic data of the sampled households. The farmers' ages ranged between 40 and 60 years. Of the selected farmers, 40 were men while 20 were women and this also represented a balance of men to women ratios in the whole farming population of the districts. The discussions were moderated by the researcher to focus the discussions on what was being investigated and lead questions from the semi structured questionnaire were used to guide the discussions. Prior to these focus group meetings, the researcher met with extension officers and lead farmers to gain an insight into the communities' socio-economic characteristics in order to map the discussions to ensure accurate results.

The FGDs were held for a maximum of two hours at each site in order to limit prolonged discussions. The open-ended questions used were structured in such a way that they were more general at the beginning but later narrowed down to specific subjects. The farmers introduced themselves and ground rules were set in order to encourage openness in the discussions. The data were recorded on flip charts, together with moderator notes. The data from the FGDs were analysed through theme coding and qualitative data charts (Acosta-Gallegos et al., 1995; Halterlein et al., 1980). Valid themes were taken as those that were mentioned by two or more participants at least. Reviews of the discussions were done by a volunteer participant briefly going over the discussions to ensure the notes were accurate. During the FGDs, five released and already popular common bean varieties were used to identify seed characteristics that farmers would use in selecting their preferred varieties. The scores and ranking for seed traits were taken as a relative trait value on a scoring scale of 1 to 4 where 1 was highly preferred by the farmers while 4 was least preferred.

#### **2.2.4 Farmer survey and questionnaire administration**

The survey covered four agricultural camps in the two districts. Thus eight villages were included. The farmers were selected at random from entire village lists by the headmen who are the village administrative authorities. Enumeration was done with the assistance of local people who understood the local language and the farmers' culture. Grade 12 school-leavers in each area were recruited to work as enumerators. They were trained to conduct an interview and enter information in the questionnaires. The interviews were conducted in the Tonga language and enumerators entered the information in English

(Figure 2.3). In addition, general information on the sampled villages was collected from the village administrative authorities



**Figure 2.3:** Researcher conducting a farmer survey using a questionnaire

Five copies of the questionnaires were administered prior to the main survey as a preliminary test of the questionnaires, to train enumerators on data collection, and to check farmers' level of understanding of the questions. The necessary adjustments were made to the questionnaires based on the feedback from the preliminary test. The final questionnaire comprised of three major sections: questions relating to participant demographic and socio-economic factors; factors that influenced the decisions on choice of a variety by the members; and preferred crop traits.

#### **2.2.5 Data analysis**

The collected information was analysed using the statistical package for social scientists (SPSS) computer programme. A probit regression model was used to test the significance of the measured characters for farmers' preferences (Asante et al., 2013). The variables included in the analysis were chosen on the basis of the general economic theory on adoption (Comin and Hobijn, 2003). Under this model specification, a standard logistical distribution of the error terms is assumed. The standard logistical distribution has a mean equal to zero and a variance of  $\pi^2/3$  where  $\pi$  represents farmers' preferences and is symmetric around zero mean. This model further assumes that there is no correlation among the error terms and that it applies logistic regression, where farmers' decisions of choice are assumed to be dichotomous in nature. Contextual characteristics, such as district were included in the analysis, as they might have captured (though in a minor way), the agro-climatic differences, infrastructure variations,

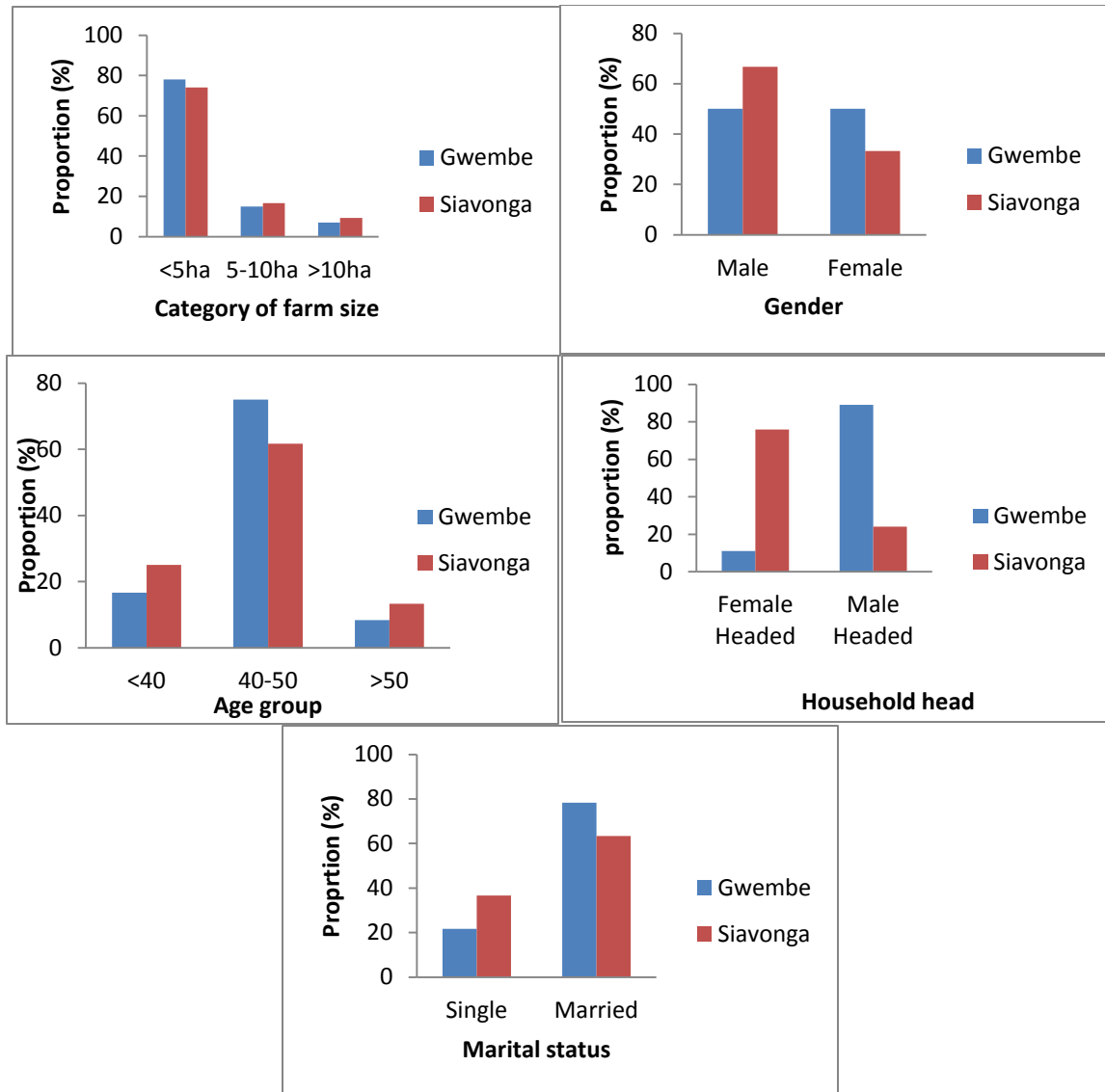


and district preferences. Farm attributes such as total land size and the major season for growing beans and farmer attributes, such as major source of income, age, education, and varietal preferences (farmers' preferred seed traits), were expected to influence farmer preferences and adoption of varieties.

## **2.3 Results**

### **2.3.2 Demographic data**

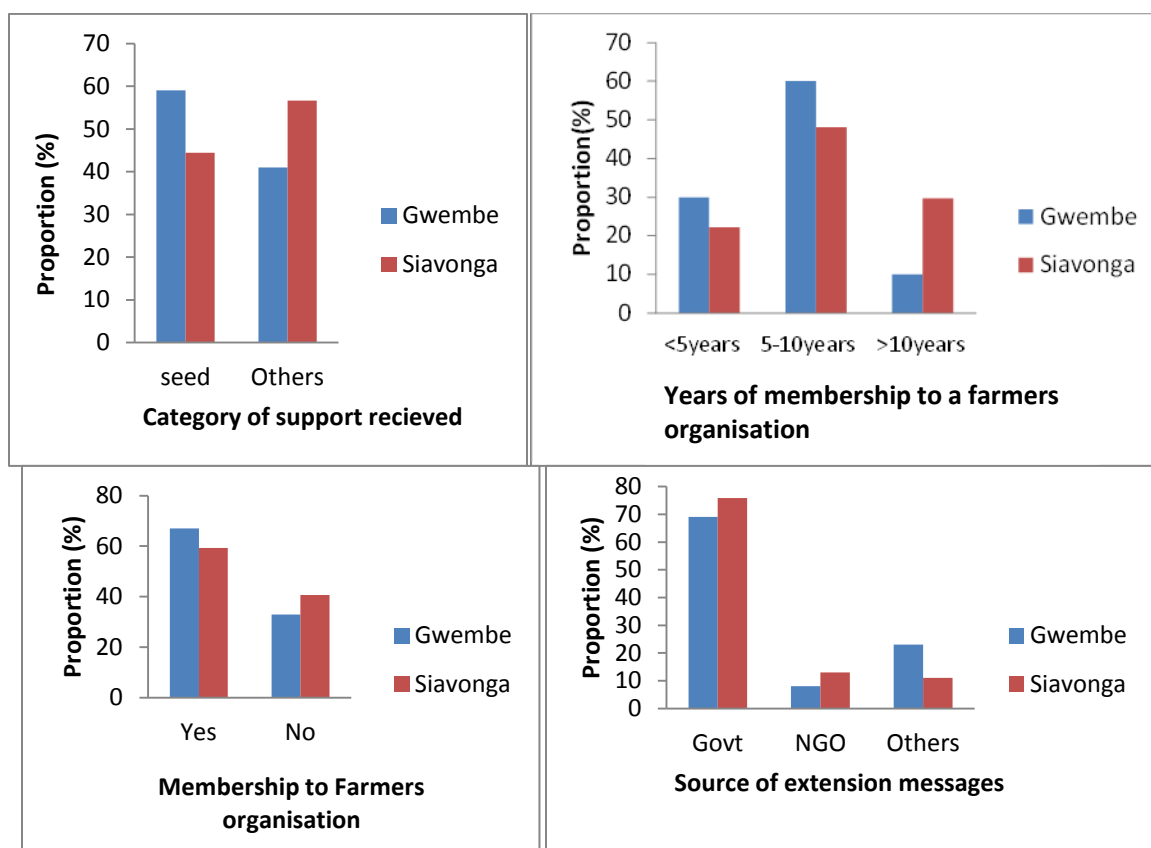
The demographic data for Siavonga and Gwembe exhibited similar trends (Figure 2.4). The age groups of the respondents ranged from those less than 40 years, between 40 and 50 years and those above 50 years (Figure 2.4). On average, 79% were male headed while only 21% were female headed households. Figure 2.4 provides demographic summaries for the interviewed households.



**Figure 2.4:** Demographic data description for Siavonga and Gwembe

### 2.3.3 Inherent factors influencing farmers choices for bean varieties

The general trends for factors influencing farmers' decisions were similar between the two districts (Figure 2.5). Most farmers (about 60%) indicated that they belonged to farmers' organisations (FO) from which they derived good support, including seed. It was also observed that the government extension service was the major source of extension messages in both districts. Most farmers in these districts confirmed that they owned less than 5 ha of land and thus qualified as small-scale based on the Zambian government classification.

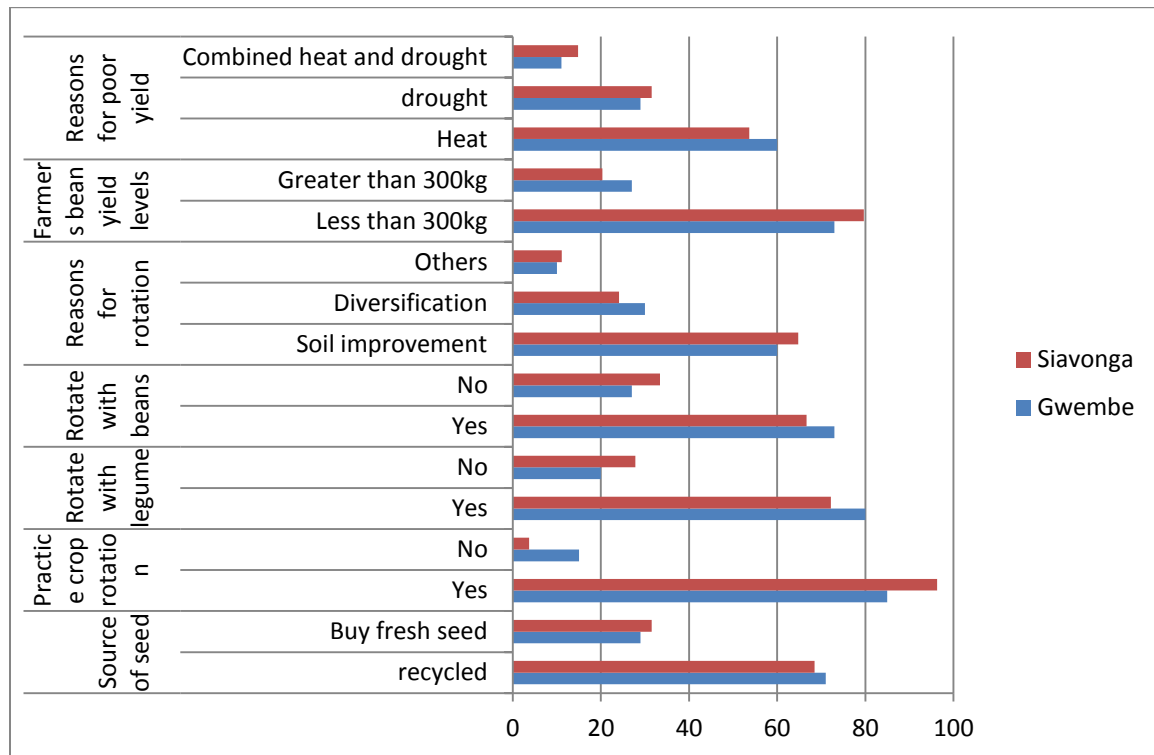


**Figure 2.5:** Factors influencing decisions on choices for common bean

#### 2.3.4 Farming systems used for bean cultivation influencing choices for common bean varieties

The crop factors influencing farmers' decisions showed similar trends with the demographic and other influencing factors (Figure 2.6). The seed used for common bean planting in both districts was mostly taken as part of harvest for grain, although a few farmers indicated that they bought seed from agro-dealers. Over 80% of the farmers practiced crop rotation and most of them rotated legumes with cereal crops. On average, 70% of the farmers who used legumes in crop rotation used beans indicating the significance of the common bean in the farmers' farming systems. The main reason given for rotating beans with cereals was to improve the soil fertility. However, bean yields in

both districts were reported to be poor, below 300 kg ha<sup>-1</sup>. High temperatures and drought were cited as the main factors that limited bean production in the two districts.



**Figure 2.6:** Production systems and constraints in bean production

### 2.3.5 Probit regression model for farmers' preferences

The results of the pooled regression coefficients for both districts are presented in Table 2.1 in a probit model. Gender and education levels were significant ( $P \leq 0.001$ ) from the demographic data category on bean adoption indicating its importance and its influence in the selection of varieties by the farmers.

The model shows that bean marketability, growth habit, time to maturity, number of pods per plant, seed colour and seed shape were significant in influencing farmers' choices of bean varieties. The farmers indicated they preferred elongated and curvy seed shape, red speckled seed coat, high yield with a high number of pods per plant, and early maturity. They also preferred the bush type of beans for ease of harvesting. Of the significant selection criteria, only education level (-0.005), and maturity dates (-0.106) had negative coefficients while the rest exhibited positive coefficients. Gender and source of

income for the farmers also significantly (highlighted in Table 2.1 at significance of  $P \leq 0.001$ ) influenced farmers' choices while the rest of the factors were not significant.

**Table 2.1:** Probit regression model: analysis of parameters measured in the two districts

Measured terms in the model	Model	Std. Error	t	Significance
(Constant)	-2.407	2.818	-0.854	0.933
<b>Gender</b>	<b>0.095</b>	<b>0.159</b>	<b>0.598</b>	<b>0.000</b>
District	0.899	0.591	1.521	0.785
Age	-0.015	0.134	-0.112	0.869
Household head	0.175	0.181	0.963	0.118
Marital status	-0.015	0.111	-0.138	0.973
<b>Education level</b>	<b>-0.005</b>	<b>0.121</b>	<b>-0.045</b>	<b>0.000</b>
<b>Major sources of income</b>	<b>0.073</b>	<b>0.354</b>	<b>0.207</b>	<b>0.000</b>
Member of farmers organisation	0.267	0.32	0.833	0.464
Period of membership	0.143	0.125	1.148	0.808
Support from organisation	-0.161	0.237	-0.678	0.441
Benefits from membership	-0.259	0.297	-0.87	0.610
Sources of extension messages	0.245	0.205	1.199	0.718
Size of farm	-0.021	0.153	-0.139	0.957
<b>Practice crop rotation</b>	<b>-0.037</b>	<b>0.36</b>	<b>-0.102</b>	<b>0.001</b>
Rotate with legume	0.122	0.321	0.38	0.700
Other crops rotated with beans	0.033	0.118	0.28	0.360
Reason for rotating with beans	-0.071	0.143	-0.497	0.747
Yield levels for beans	0.1	0.107	0.937	0.679
Reasons for poor yield	-0.008	0.103	-0.076	0.645
<b>Which beans sell better</b>	<b>0.093</b>	<b>0.136</b>	<b>0.682</b>	<b>0.000</b>
Source of seed	-0.064	0.211	-0.304	0.599
<b>Bean colour</b>	<b>0.106</b>	<b>0.213</b>	<b>0.497</b>	<b>0.000</b>
<b>Growth habit</b>	<b>0.502</b>	<b>0.173</b>	<b>2.894</b>	<b>0.000</b>
Yield	-0.412	0.331	-1.244	0.151
Drought tolerance	0.097	0.295	0.329	0.138
Heat tolerance	-0.297	0.254	-1.168	0.623
Cooking time	-0.138	0.286	-0.481	0.181
Taste	0.453	0.537	0.844	0.045
<b>Maturity</b>	<b>-0.106</b>	<b>0.849</b>	<b>-0.124</b>	<b>0.000</b>
Grain size	0.379	0.278	1.364	0.554
Shatter resistance	-0.1	0.273	-0.366	0.310
<b>Number of pods/plant</b>	<b>-0.067</b>	<b>0.61</b>	<b>-0.109</b>	<b>0.001</b>
Number of seeds/pod	-0.012	0.265	-0.044	0.102
Resistance to storage pests	-0.039	0.281	-0.14	0.238
<b>Seed shape</b>	<b>0.403</b>	<b>0.468</b>	<b>0.861</b>	<b>0.000</b>

**Note:** Bold terms in the model were significant at  $P \leq 0.001$

### 2.3.6 Correlation

The correlations measured among crop factors showed that grain size, heat tolerance, maturity, number of pods per plant, bean colour, drought tolerance and source of seed

were significantly ( $P \leq 0.01$ ) correlated with choices of varieties of beans (Table 2.2). There was general consistence of preference of choice from the correlation for common bean in both districts. The results also showed that farmers were more inclined to select bean varieties that would be more profitable because they depended on farming as their main source of income.

**Table 2.2:** Correlation coefficients for factors measured when correlated with farmer preferences

<b>Criteria</b>	<b>Correlation coefficients with bean varieties grown</b>
Grain size	-0.0805
Growth habit	0.5636**
Heat tolerance	0.0894**
Maturity	0.7033**
Number of pods plant <sup>-1</sup>	0.4629**
Number of seeds pod <sup>-1</sup>	-0.2224
Bean colour	0.0716**
Resistance to storage pests	0.1605
Seed shape	-0.5657
Source of seed	0.0148**
Taste	-0.2726
Yield	-0.1956
Cooking time	0.1819
Drought tolerance	0.2018**
Shatter resistance	-0.1383

\*\* = significance at 1%; the type of bean grown was correlated with each of the key selection criteria

## 2.4 Focus group discussions

### 2.4.1 Selection criteria and farmer preferences for cultivar traits

The selection criteria for bean varieties varied widely between districts, with the following key criteria included in the model: drought tolerance, heat tolerance, large seeds, bush type growth habits, early maturity, and a good yield (20-30 pods plant<sup>-1</sup>). However, farmers from Siavonga considered marketability as extra unique selection criteria while those from Gwembe considered cooking time. It was noticeable that, although men had more experience in the field, the women found it easier to evaluate and select, and rapidly saw differences between traits in the different bean materials. Their evaluations and selections were often more discriminating than those of the men.

#### 2.4.2 Ranking of seed related traits

The results from the FGDs (Figure 2.7) indicated that farmers preferred to eat beans compared to cowpeas despite challenges with its production. Table 2.3 summarises the outcome of the discussions on preferred variety attributes and traits.



**Figure 2.7:** Farmers discussing and taking note of the discussions on flip chart paper

While, the farmers were engaged in discussion, the notes from their discussions were translated into a 3 x 3 table matrix and summarised into three farmers selection criteria (Table 2.3). These notes largely informed farmer selection criteria for bean varieties and were used to compare them with the results of the survey.

**Table 2.3:** List of farmer preferred variety attributes and traits listed during focus group discussions in the two districts

Preference	Reason cited for preference	Farmer illustration and quotes on their preference
Highly preferred heat tolerant and high yield beans	Highly preferred owing to the high temperatures prevailing in the region.	<p>“It is hot here and beans does not grow at all”</p> <p>“Legumes do grow here. We only manage to grow sorghum better than other crops”</p> <p>“The temperatures are high and there is very little rain”</p> <p>“we do grow some beans during winter when temperatures are low and we supplement with irrigation since water for irrigation is abundant here”</p>
Least preferred small and dark coloured bean grains	Least preferred because they are not liked for eating – although they usually grow better in the valley	<p>“Small grain beans have no market”.</p> <p>“Dark beans make dark soup and are not appealing for consumption”.</p> <p>“Dark and small grain beans grow better in the valley”.</p>
Other preferred traits related to growth habit, size, taste, cooking time, and colour. Seed traits: large seed, red speckled beans	<p>Agronomic- bush type because it is early maturing and drought tolerant</p> <p>good taste and fast cooking</p>	<p>“We need bush type of beans because they mature early”</p> <p>“Reddish type makes good soup”</p> <p>“Like good taste and fast cooking beans”</p>

#### 2.4.3 Ranking of preferred seed traits by district and by bean type

The ranking of seed traits during the FGDs indicated that the farmers made choices based on seed shape, size, colour, texture, taste and aroma. The results of the ranking of bean traits by bean type in Siavonga showed that Lyambai, a large seeded red speckled bean was most preferred by the farmers over other types (Table 2.4). The rankings of the beans in Gwembe was however, largely uniform for all varieties (Table 2.5). Interestingly,



the ratings for all bean varieties were higher in Siavonga than in Gwembe. In addition to the traits listed in Table 2.4 and 2.5, the farmers also indicated their preferences for varieties that could withstand low moisture stress and high temperatures. The notes (Table 2.3) from the FGDs also showed that cooking time, yield, growth habit, drought tolerance, heat tolerance and seed size were the most important attributes that farmers considered. However, emphasis was also made during the FGDs on productivity traits such as number of pods per plant, high yielding and good pod filling (Table 2.4). Though farmers preferred Lyambai, a red speckled bean, they found it difficult to describe and interpret the colour. In Gwembe, the ranking shows that farmers would eat any type of beans among those presented to them.

**Table 2.4:** Scores for farmers' preferences for seed traits in Siavonga

Variety	Shape	Size	Colour	Texture	Taste	Aroma	Overall score	Rank
Lyambai	3	3	3	3	3	3	18	1
Chambeshi	2	2	2	4	4	3	17	2
Lukupa	2	2	2	4	3	3	16	3
Kabulangeti	2	2	2	3	3	3	15	4
Kalungu	3	2	1	3	3	3	15	4






**Note:** Overall variety assessment by farmers (Scoring criteria; 4=very good, 3=good, 2=fair, 1=bad) -

**Table 2.5:** Scores for farmers' preferences for seed traits in Gwembe

Variety	Shape	Size	Colour	Texture	Taste	Aroma	Overall score	Rank
Lyambai	2	2	2	2	2	2	12	1
Chambeshi	2	2	2	2	2	2	12	1
Lukupa	2	2	2	2	2	2	12	1
Kabulangeti	2	2	2	2	2	2	12	1
Kalungu	2	2	2	1	1	2	10	2

**Note:** Overall variety assessment by farmers (Scoring criterion; 4=very good, 3=good, 2=fair, 1=bad) -

The seed characteristics of the varieties used, Lyambai, Chambeshi, Lukupa, Kabulangeti, and Kalungu are provided in Figure 2.8. These five are currently released varieties used by the farmers in the two districts.

Variety	Important Variety Characteristics	Variety Appearance
Lyambai	Non-climber, Seed colour – red speckled Large seed size 82-90 days to maturity Potential yield – 1500kg ha <sup>-1</sup>	
Chambeshi	<ul style="list-style-type: none"> <li>• Non-climber</li> <li>• Seed colour – brownish speckled</li> <li>• Large seed size</li> <li>• 78-80 days to maturity</li> <li>• Potential yield – 1500kg ha<sup>-1</sup></li> </ul>	
Lukupu	<ul style="list-style-type: none"> <li>• Non-climber</li> <li>• Seed colour – tan</li> <li>• Large seed size</li> <li>• 78-80 days to maturity</li> <li>• Potential yield – 1500kg ha<sup>-1</sup></li> </ul>	
Kabulangeti	<ul style="list-style-type: none"> <li>• Climber</li> <li>• Seed colour – Purple mottled</li> <li>• Large seed size</li> <li>• 80-100 days to maturity</li> <li>• Potential yield – 1000kg ha<sup>-1</sup></li> </ul>	
Kalungu	<ul style="list-style-type: none"> <li>• Non-climber</li> <li>• Seed colour – white</li> <li>• Seed size – medium</li> <li>• 78 – 80 days to maturity</li> <li>• Potential yield – 1000 – 1500kg ha<sup>-1</sup></li> </ul>	

**Figure 2.8:** Important characteristics of bean varieties used in the research

## 2.5 Discussion

For ease in identifying farmers' preferences, this study grouped factors that may influence farmers' preferences into three broad categories: crop factors, inherent demographic

(internal factors), and influencing factors (external factors). A simple ordered probit model which produces coefficients (positive or negative) for variety attributes and other factors was used. The negative coefficients imply that the farmers would decrease their preference for the variety if appropriate farmer preferred traits are not integrated into the variety, while the positive values imply that the traits are more likely to enhance adoption of the varieties.

Results from this study indicated that farmers in the two districts considered yield related traits as very important crop factors in variety choices. Seed shape, growth habit, seed colour, early maturity, and number of pods per plant, were key criteria used for selecting common bean varieties.

According to the probit model, gender influenced farmers' choices. Common bean is traditionally considered a woman's crop if it is grown by women and meant for home consumption; thus decisions on these beans are made by women and choices take into consideration the entire family preferences. Men, on the other hand, considered mostly what the market preferred. This finding concurs with other similar studies on the adoption where gender was found to influence decisions on adoption of new varieties (Duvick, 1999; Robertson, 1966). The finding that age did not significantly influence farmers' choices for varieties according to the probit model is also consistent with similar studies conducted on the adoption of rice in Guinea (Katungi et al., 2009). The level of formal education did however, influence farmers' bean choices. Farmers who had formal education used their knowledge to read about and understand the traits of beans in making their choices. This finding contradicts research findings by Harper (2006) who claimed that education level was not a necessity in interpreting farmers' choices as most choices did not require a deep understanding but could be interpreted as being based on social values and community tastes. This finding is supported by other authors who established that the effect of education on the adoption of agricultural technologies related to the years farmers spent in formal schooling (Chaudhary et al., 2000; Lee and Parsons, 1968). However, this finding is not supported by other researchers working on adoption of other technologies who have argued that education did not have any influence on farmer choices (Harper, 2006).

The income levels of farmers significantly influenced the farmers' decisions on preferences. It was clear from the FGD that farmers with high levels of income made quick decisions and adopted varieties earlier than less wealthy farmers. Farmers who were engaged in fishing were a little wealthier than those who relied entirely on farming; they were able to make choices based on the fact that they could buffer their loss with income from fish sales if the variety they chose failed to perform.

The study also revealed that farmers would select bean varieties suitable for integration into their crop rotation activities and also those that sold at a better price on the market. The distance to these markets was therefore critical as concluded by Langyintuo and Mungoma (2008) in their research on maize variety adoption in Zambia.

Among crop related factors, bean colour, growth habit, taste, maturity, number of pods per plant and elongated kidney seed shape influenced farmer choices for common bean varieties. The farmers preferred red speckled large beans with good taste and early maturing. These six key crop characteristics were driven by the visual appeal, social factors, and farmer satisfaction and not necessarily by monetary considerations.

The FGDs identified high yield, early maturity, heat tolerance and drought tolerance as key factors for farmers' choices of varieties. Early maturity was considered an important criterion for two main reasons: It enabled the crop to escape drought and ensured early provision of food to the households to alleviate hunger. Taste was rated as an important trait although farmers considered it as an important factor only when they had adequate quantities of beans. Most households often grew less than they required for home consumption.

Most of the traits farmers use for their choices of bean varieties such as taste is usually ignored in conventional plant breeding because they are seen to compromise the progress to selection. As a result most of the varieties developed are less preferred and not adopted by the farmers.

## **2.6 Conclusions**

The research objective that guided this study was to determine farmers' preferences in order to increase common bean variety adoption in low altitude regions in Zambia. The

research provides insights into the farmers' preferences for common bean varieties and is unique in the sense that it is the first to be conducted with farmers in low altitudes of Zambia.

The research results reveal that the strongest predictors influencing the likelihood of common bean varieties being adopted by farmers were as follows: a bush type growth habit, a red speckled bean colour, a large bean size and shape, the taste of the bean to farmers, early maturity and high number of pods per plant. Taking this into account, the results further show that the farmers chose Lyambai during the FGD, as their best variety with key preferred characteristics such as red speckled seeds, large seeds, indeterminate growth habit and preferred taste although the rankings in Gwembe did not show any differences. This implies that new varieties with the genetic back ground of Lyambai were more likely to be adopted.

The research showed that other influencing factors, inherent in the population affected common bean adoption. These included some socio-economic factors such as income levels, education level, and the use of common bean in crop rotations, and demographic characteristics such as gender.

There are a number of breeding implications emanating from this research. The breeder has to take into consideration farmers' preferences and develop bean varieties that meet farmers' needs. The incorporation of farmers' preferences in the selection of bean varieties for the breeding process would increase the likelihood of adoption of the varieties.

In addition to identifying farmer preferences, consumer needs and preferences should also be studied to guide breeding. Failure to do this may hinder other important processing traits targeting different products made from bean which would make the bean marketable.

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**Appendix 2. 1:** Focus group discussion check list



**GPS Coordinate**(*latitude, longitude, altitude*)

**Number of farmers participating**

**Age categories**

**Date and Time of Meetings:**

**Participating villages**

**Location (Camp/Block)**

**District**

Total		Females		Males
18-25	26-35	36-45	46-60	Above 60
Date and Time of Meetings:				
Participating villages				
Location (Camp/Block)				
District				

## **Common Bean PRA Check-list, 2010**

1. List crops you grow in the area and rank them in order of importance
2. Production practices, yield levels, marketing issues, seed sources for common bean
3. What are the production constraints for beans
4. Is drought and heat one of the problems
5. Extent? Yield losses attributed to the heat and drought
6. How does drought and heat rate in comparison to other constraints in the area
7. How do farmers manage droughts and heat stress/coping strategies
8. List and rank the bean varieties grown in the area in terms of preferences by the farmers
9. Make preferences between traditional varieties versus improved varieties
10. Highlight farmer variety selection criteria
11. What are the preferred bean attributes farmers like most? List and rank them in order of importance
12. What is the awareness level of the existence of drought and heat tolerant varieties

**Appendix 2.2:** Questionnaire used for formal survey to collect bean preference data



**GPS Coordinate(*latitude, longitude, altitude*)**

--

**Common Bean Production Survey Questionnaire, 2010**

**Questionnaire/HH  
Number:**

**Date and Time of  
interview:**

**Name of Farmer:**

**Sex:**

**Village:**

**Camp/Block:**

**District/Province:**


## GENERAL INFORMATION

***[The respondent must be the head or de-facto head of the household]***

1. Name of respondent: \_\_\_\_\_
2. Gender of respondent: [1] Male [2] Female
3. Age of respondent (in years): [1] 18-25 [2] 26-35 [3] 36-45  
[4] 46-60
4. Is the respondent head of the household? [1] Yes [2] No

***If NO continue from Q14, BUT if YES, skip to Q9.***

5. Name of household (HH) head: \_\_\_\_\_
6. Gender of HH head: [1] Male [2] Female [3] N/A
7. Age of HH head (in years): [1] 18-25 [2] 26-35 [3] 36-45 [4] 46-60  
[5] above 60
8. Where is the household head? [1] Temporarily away from the house  
[2] Absent from home at least 6 months in a year
9. Who is the main decision maker on farming activities? [1] household head  
[2] Spouse [3] Children [4] Household head and spouse [4] Household  
head and children [5] Spouse and children [6] All members

***If household head is “TEMPORARILY AWAY FROM THE HOUSE” then  
RESPONDENT should provide answers for him/ her otherwise RESPONDENT  
should answer as the de-facto head of household***

10. Marital status of HH head: [1] Single [2] Married [3] Divorced [4] Separated  
[5] Widowed
11. Educational level of HH head: [1] Illiterate [2] Primary school. [3]  
Secondary school [4] Tertiary education (College & university) [5] Adult education

## HOUSEHOLD COMPOSITION AND INCOME

12. We are interested in knowing more about the composition of your **household** (all the people living in the same compound, eating from the same “pot” and working on the family farm)

Age group	Gender	Indicate type of off farm-income HH members is earning (Code below)	Number of months (in a year) available for farm work
Under 5 years	F= M=		
5-17	F= M=		
18-25	F= M=		
26-35	F= M=		
36-45	F= M=		
46-60	F= M=		
Above 60	F= M=		
		<b>1=Off farm employment 2=Trader 3=Non 4=Others (Specify).....</b>	

13. What are the sources of income for your household in 2005/06? (Tick appropriate)

Category	Category
Crops (grains/seeds) sales	Paid employment
Fruits and vegetables sales	Self employed
Livestock/fish sales	Remittances
Petty trading	Other (specify)

### ACCESS TO AGRIC EXTENSION (PUBLIC OR PRIVATE) SERVICES AND FARMER GROUPINGS

14. Do you belong to any farmers' associations/cooperatives in your Community?  
[1]=Yes [2] = NO

15. If YES, to Question 14 how many years have you been a member?

\_\_\_\_\_

16. During the 2009/10 cropping season did you attend **field days/demonstrations** organized by staff of the following organizations? [1] Government Agric extension staff  
[2] FoDiS project [4] Public research institutions [5] Private companies [3] NGOs, Specify..... [4] Others (specify).....

17. What are your frequent sources of extension messages?

[1] Agric extension staff [2] Extension bulletins [3] News paper [4] Radio

[5] Television [6] other (specify): \_\_\_\_\_

18. How many times did you interact with agricultural extension workers on crop production in 2009/10 season? [ 1] Once [2] 1-3times [3] more than 3 times

## PROBLEMS IN COMMON BEAN CROP PRODUCTION AND MARKETING

### CROP PRODUCTION

19. What is the total size of the farm land you have/own?

20. What crops do you grow on your farm (list all of them in the order of importance.

	Crops grown	Size of plot	Cropping pattern	Tenure system	Main water source?
		Unit of measure (specify).....			
Plot abandoned					
Plot under fallow					
Pasture land					
Tree crop plot					
Plot cropped (1)					
Plot cropped (2)					
Plot cropped (3)					
Plot cropped (4)					

		1=ha,2=acre, 3=lima	1=Pure stand 2=Intercrop ped 3=Other	Tenure codes 1= Own land 2= Land rented in 3= Land rented out 4= Sharecropped 5= Family land 6=Outright purchase 7=Communal 8=Other	Water sources 1=Rain 2=Irrigated 3=residual moisture
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21. Rank the three most important factors that determine how large your cultivated farm should be in any season (1 = most important, 3=less important)

- 1) Expected family labor availability      ---- 2) Cash availability to hire labor
- 3) Cash availability to purchase other inputs      ---- 4) Current grain prices
- 5) Expected grain prices after harvest      ---- 6) Food needs      ---- 7) Availability of seed      ---- 8) other:

22. What are the major problems with common bean production? Rank the following problems from 1 to 5 where 1 is no problem and 5 is a severe problem (tick where appropriate):

Problem	1 No problem	2	3	4	5 (Serious problem)
Uncertain climate (drought or heat)					
Livestock damage to common bean crops					
Inputs not available at affordable prices					
More work than the family can handle					
Insufficient cash and credit to finance inputs					
Insufficient technical advice when needed					
Insufficient information about alternative markets					
Lack of proper storage facilities					
Uncertain prices for beans sold locally					
Uncertain prices for beans sold to hawkers					
Farm is too small					
Limited local labour for hire					
Other: Please specify					

24. Has your household been affected by a serious shock\* in the last 10 years?

Specific shocks	Rank the five most serious shocks (1=most, 5=least important)	Indicate in which year it occurred out of the last 10	Has this risk/shock affected Common bean production directly? (1=Yes, 2=No)
Drought			
Heat			
Heat and drought			
Too much rain or flood			
Land slide			
Plant pests and diseases			
Destruction of crops by animals			
Dangerous weeds			
Large increases in input prices			
Large drop in crop prices			
Loss of farm land			
Burning of property (or arson)			
Birds			
Conflict			
Other _____			

\* An event that led to a serious reduction in the household's food security status resulting in a significant reduction in consumption

25. Approximately how many years do you crop your land before putting it to fallow?

\_\_\_\_\_

26. Approximately, how many years do you fallow a piece of land?

\_\_\_\_\_

27. Which crop(s) is/are grown following a fallow period?

1=Maize      2=Rice   3=Sorghum      4=Pearl millet                      5=Finger millet  
6=Cowpea

b=Common Beans      8=G'nuts      9=Cassava      10=Soybean                      11=Tree crop

12=N/A      13=Other(specify).....

## G. AGRICULTURAL MARKETING DECISIONS

28. How did you dispose off your beans harvested in the 2009/10 season?



	Quantity harvested	Quantity Consumed	Quantity Sold	Quantity Given out as gift	Quantity reserved as seed for next season	Quantity loss due to handling
Local bean variety						
Improved bean variety						

29. When do you sell your beans?

Time of the year	Quantity sold	Place of sale*	Av. Price per unit	Buyer**
Soon after harvest				
Six months after harvest				
Just before planting				

\*Places codes: [1] At home [2] In a market [3] Market  
cooperatives

\*\*Buyer codes: [1] Traders [2] Local community [3] Town/city consumers

30. We are interested in finding out your perceptions about output price (or marketing) risk

Bean category	Is the selling price for bean an important factor in determining how much of the crop you sell or not?  1. Yes 2. No	How will you change your beans sales if the selling prices are higher than normal?  1. Less 2. Same 3. More	How would your fertilizer and other input use change if the selling price was attractive for beans?  1. Increase 2. Same 3. Decrease	Would you acquire more credit if the selling price was attractive for beans?  1. Yes 2. No
Local variety				
Improved variety				

## SEED PROVISION

31. Provide a list of common bean varieties you grow on your farm (use codes provided where appropriate)

Variety	Category (local or improved)	Seed Source	When sourced	What are the attributes you like on the variety (Multiple answers accepted)
	Improved=1 Local = 2	Fellow farmers Seed company NGO/projects Research institute	Every season After 2 seasons After 5 seasons	Good colour Cooking time Taste Seed size Shape Early maturity Drought tolerant Heat tolerant Drought and heat tolerant Texture Aroma Others specify.....

32. If you use your own bean seed, provide the following:

Variety	Characteristics considered in selection

33. Which variety would you prefer growing during drought and hot seasons?

List.....  
.....  
.....  
.....

## CHAPTER THREE

### Evaluation of common bean genotypes for tolerance to drought stress

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#### Abstract

Drought stress is a limiting factor in common bean production in the low altitude areas of Zambia. The objective of this study was to identify drought tolerant genotypes for use in breeding programmes in order to develop appropriate varieties for cultivation by farmers in these regions. One hundred and twenty genotypes comprising landraces, mutants developed through UV mutagenesis and accessions obtained from the National Gene Bank, University of Zambia, farmers and other sources were evaluated under managed drought-stress (DS) and non-drought stressed (NDS) conditions for two growing seasons (2011-2012) in two locations. The genotypes were planted using alpha lattice design with two replications on two sites. Data on seed yield under DS and NDS were used to calculate drought tolerance indices. The indices including mean productivity (MP), geometric mean productivity (GMP), yield index (YI) and harmonic mean (HM) classified genotype LY4-4-4-B as the most drought tolerant followed by ZM 3831, ZM 4496, KAL–ZA and ZM 4512-5. LY4-4-4-B, a mutant of a released variety Lyambai could be further selected as a variety while the other genotypes identified had some undesirable seed colour for farmers and are therefore recommended for breeding drought tolerant genotypes. A biplot analysis grouped the four indices, MP, GMP, YI and HM together and confirmed their suitability for identifying high yielding bean genotypes under drought-stressed conditions. The study further established that the genotypes were efficient at photosynthate mobilisation and 100-seed mass was similar under DS and NDS conditions. Based on correlation analysis between yield in DS and NDS conditions, GMP, HM and STI supported Rank Sum in identifying genotypes with high yield under both stressed and non-stressed conditions and this was further confirmed by cluster analysis.

### 3.1 Introduction

The common bean (*Phaseolus vulgaris* L.) is an important food legume in Africa. The crop provides the much needed protein in the diets of many low income households (Broughton et al., 2003; Wortmann et al., 1998). Africa produces about 2 million tons of common bean annually on about 3.5 million ha (FAO, 2014) while, Zambia grows only about 60,000 ha under common bean annually. The crop ranks second to groundnut in Zambia among food legumes in terms of area under production; its importance can be reflected in the number of households growing and consuming it (Tembo and Sitko, 2013).

The common bean incurs high yield losses resulting from several biotic and abiotic stresses worldwide. Drought stress has been reported to be the worst among the abiotic stresses, causing yield losses of up to 60% in farmers' fields in sub-Saharan Africa (Barnabas et al., 2008; White and Singh, 1991). High common bean demand has caused an expansion of production into more marginal environments in sub-Saharan Africa where crop performance is often affected by even more extreme abiotic stresses, key of which has been severe drought (Porch et al., 2009).

The effects of droughts are complex, differing depending on the frequency with which the droughts occur, their duration, their intensity, and the stage of plant development at which they occur (Halterlein, 1983). The common bean is very sensitive to drought stress during the pre-flowering and flowering stages, when it causes excessive abortion of flowers, pods, and seed (Nielsen and Nelson, 1998; Ramirez-Vallejo and Kelly, 1998; Singh, 2007; Terán and Singh, 2002). The extent of the effects of drought stress in common bean is further compounded by high temperatures (Ramirez-Vallejo and Kelly, 1998). Research has shown, however, that drought stress can be mitigated by genetic improvement using the variability that exists within the common bean germplasm. The few market class varieties of common bean released and available in Zambia were bred mainly for the high agricultural potential regions and are limited for expansion to low potential regions (own observation). Landraces, therefore, offer a valuable resource for novel untapped genetic variation that should be explored to obtain more varieties for adaptation to low altitudes.

The performance of landraces in Zambia under drought stress has not, however, been studied and their genetic potential for the development of resistance to drought stress remains unknown.

In pursuit of the genetic resources for the drought stress resistance, it is important to note that genetic diversity changes with the continued biological evolution of crops under pressure from climatic pressure, disease, or human management. The study of landraces with respect to drought stress tolerance, therefore, has challenges of reliability resulting in few studies worldwide because of the difficulty in conducting such studies. However, a number of selection criteria have been used to select genotypes based on their performance in stress and non-stress environments (Fernandez, 1992; Fischer and Maurer, 1978; Rosielle and Hamblin, 1981).

As tools for selecting desired drought resistant materials, scientists have used drought tolerance indices that provide a measure of drought response based on loss of yield under drought when compared to normal conditions (Mittler et al., 2001). Some of these tolerance indices include a stress tolerance index (STI), a stress susceptibility index (SSI), a tolerance index (TOL), harmonic mean (HM), geometric mean productivity (GMP), mean productivity (MP), a yield index (YI), a yield stability index (YSI), and a sensitive drought index (SDI). These indices have been mathematically defined: TOL and GMP by Rosielle and Hamblin (1981); SSI by Fischer and Maurer (1978); and GMP and STI by Fernandez (1992). The STI out of the listed indices is designed to identify genotypes that produce high yield under both stress and non-stress conditions because the genotypes identified by the use of this index will have higher stress tolerance (Fernandez, 1992). These indices measure different parameters and provide a complete picture of the behavior of the genotypes when exposed to drought stress. The use of all the indices therefore provides complete understanding of the germplasm collection by studying their stability and tolerance mechanisms.

The research reported on here was therefore designed to build on research conducted elsewhere on drought tolerance in the common bean. It was expected to generate new information on the adaptability of Zambian common bean germplasm to low lying altitudes in the southern parts of the country. The specific objective of this study was to assess the performance of common bean genotypes in Zambia under drought stress.

## 3.2 Materials and methods

### 3.2.1 Plant material

A collection of 120 genotypes was assembled from the University of Zambia, the National Gene Bank, small-scale farmers in the low altitude areas of Zambia and others (Table 3.1). The detailed list of the genotypes and general phenotypic description of the genotypes is presented in Appendix 3.1. The landraces from the genebank and farmers had not been characterized before and there was no information available about their performance in different agro-ecologies. The larger portion (about 52%) of the collected germplasm was gene bank accessions. However, the elite genotypes and the mutants had limited agronomic information but had not been studied for drought stress. Most mutants were generated from released varieties such as Lyambai, and Solwezi beans.

**Table 3.1:** Composition of the collected common bean germplasm assembled from the National Gene Bank, Farmers, University of Zambia, seed companies and Zambia Agriculture Research Institute

Source	Number of lines	Description/Type
University of Zambia	18	Mutants
National Gene Bank/Farmers	94	Landraces
Seed companies	3	Elite cultivars
Legumes Research Team (ZARI)	5	Elite Cultivars
<b>Total collections</b>	<b>120</b>	

### 3.2.2 Experimental sites

The experiments were conducted at two sites namely Mount Makulu in Chilanga and the National Agricultural Irrigation Research Station, commonly referred to as Nanga, in Mazabuka. Mount Makulu is located in Lusaka at latitude 15°13.10'S, longitude 28°14.93'E, and at 1206 m above sea level. The soils at this site are chromemi-hapliclicixols with fine sandy loam to clay characteristics. The soil pH is around 5.8. The site receives between 800 and 1000 mm of rainfall from November to April with mean relative humidity of 69.8%. The site experiences, on average, three ten-day drought

spells during each crop season, spread between planting time, vegetative stages and flowering time (Veldkamp et al., 1984).

The other site, Nanga, is located in Mazabuka, Southern Province, at latitude 15°46'S, longitude 27° 55' E and an altitude of 1190 m above sea level. The soils at this site are reddish clays, deep, well-structured, and well-drained with a sandy clay top soil. The soil pH ranges from 5.5 to 6.0. The mean annual rainfall received at this site is about 850 mm during the period November to March, with an average humidity of about 54.8%. Temperatures vary from freezing point in July to about 38°C in October. This site also experiences about three ten-day drought spells each season spread across the crop growing season from planting to flowering stage. The chosen sites do not fall in the dryer regions of the Zambia but were chosen for their suitability to control drought stress artificially. However, the sites had favourable weather conditions and soil for the imposing of artificially managed drought stress. The managed drought stress experiments were conducted during the dry season from the end of July to the end of October at both locations; this allowed for the imposition of the drought stress treatments at the flowering stage.

### **3.2.3 Experimental layout, trial management, data collection and computation of indices**

The germplasm were pre-assessed and found to be of similar maturity groups but of different growth habits including climbers, semi-dwarf, and dwarf plants. The trials were planted at the end of July each year to allow the bean genotypes to grow to maturity by early October. During these months, the two sites are dry and temperatures lie between 20 and 30°C which are favourable for common bean growth. They were laid out in a 10 X 12 alpha lattice, incomplete block design, with two replications over the two years, 2011 and 2012. Thirty (30) seeds were sown in single rows, 5 m in length, at an inter- and intra-row spacing of 75 cm and 15 cm.

Compound D fertilizer (N = 10%, P = 20%, K = 10%) at the rate of 200 kg ha<sup>-1</sup> was applied as recommended to all the plots at planting time. During growth, optimal and recommended management practices of weeding and pest control were used. Drought stress was imposed on the experiments following the methodology described by Teran and Singh (2002). Line-source sprinkler irrigation was used to irrigate both stressed (DS)

and non-stressed (NDS) plots during the seedling stage. At 50% flowering, irrigation was withdrawn for about three weeks from the DS treatment, while irrigation was maintained at the NDS treatments. Climatic conditions at both sites were recorded using HOBO U12 data loggers (Make - U12-001 manufactured by Onset-USA).

Data on seed yield, one hundred seed mass (HSW), number of pods per plant (NPP) and number of seeds per pod (NSP) were collected during the growing season and were measured as follows:.

- I. **Days to 50% flowering (DAF)** – This was taken as the number of days from 50% seedling emergence to the date when the genotype reached 50% flowering.
- II. **Days to physiological maturity (DPM)** – This was taken as the number of days from 50% seedling emergence to the date when 50% of the plants showed senescence and pods turned brown.
- III. **Leaf area retention (LAR)** - The leaf area retention was taken as the difference of the percentage leaf cover between the leaf area at 50% flowering and leaf area three weeks after 50% flowering.
- IV. **Yield** – Grain yield was obtained after hand harvesting and was taken as whole plot harvests, shelled bean. The grain masses were adjusted to 12.5% moisture content. The grain yield was determined and expressed as ton per hectare.
- V. **Hundred seed mass (HSW)** – This was taken as the weight of 100 grains counted individually and weighed.

Across the sites, data on genotypic mean yield in DS and NDS plots was used to calculate various indices: STI, MP, YI, YSI, SSI, SDI, and GMP in order to identify the best index for identifying high yielding genotypes under drought stress conditions. The STI, MP, and GMP have been suggested as the best criteria for selecting high yielding genotypes for both stressed and non-stressed environments (Nazari and Pakniyat, 2010). The indices were calculated as follows:

1.  $STI = (Y_p + Y_s) / (\bar{Y}_p)^2$ ; the genotypes with high STI values are tolerant to drought stress (Fernandez, 1992).
2.  $YI = Y_s / \bar{Y}_p$ ; the genotypes with high YI values are suitable for drought stress environments (Gavuzzi et al., 1997; Lin et al., 1986).



3.  $MP = \frac{Y_p + Y_s}{2}$ ; the genotypes with high values of the MP are more desirable (Rosielle and Hamblin, 1981).
4.  $GMP = \sqrt{(Y_s)(Y_p)}$ ; the genotypes with a high value of the GMP are desirable for drought stressed environments (Schneider et al. 1997).
5.  $YSI = Y_p/Y_s$ ; the genotypes with high YSI values are considered as stable genotypes under stress and non-stressed conditions (Gavuzzi et al., 1997; Lin et al., 1986).
6.  $SSI = (1 - Y_s/Y_p) / (1 - (\bar{Y}_s)/(\bar{Y}_p))$ , where,  $1 - (\bar{Y}_s)/(\bar{Y}_p)$  is the stress intensity; the genotypes with SSI values less than 1 are more tolerant to drought stress conditions (Fischer and Maurer., 1978).
7.  $HM = (2((Y_p)/(Y_s)) / (Y_s + Y_p))$ ; the genotypes with high HM values are considered more desirable for drought stressed conditions (Chakherchaman et al., 2009).
8. Mean rank (MR) = is the average of the ranks and is given by  $\sum R/n$ , R= ranks and n=number of indices summed together.
9. RS (Rank sum) = Rank mean (R) + Standard deviation of rank (SDR) (Farshadfar and Elyasi, 2012).

In the above formulae,  $Y_s$  refers to yield under stress,  $Y_p$  is yield under non-stress,  $\bar{Y}_s$  is mean yield in stress and  $\bar{Y}_p$  is mean yield in non-stressed conditions measured for each genotypes. The stress intensity was also determined for the drought stressed experiments using the equation;  $SI = 1 - (Y_s/Y_p)$ , where  $Y_s$ =mean total yield in stress conditions and  $Y_p$  = mean total yield in normal conditions (Fenandez, 1992).

### 3.2.4 Monitoring soil moisture content on the drought stressed plots

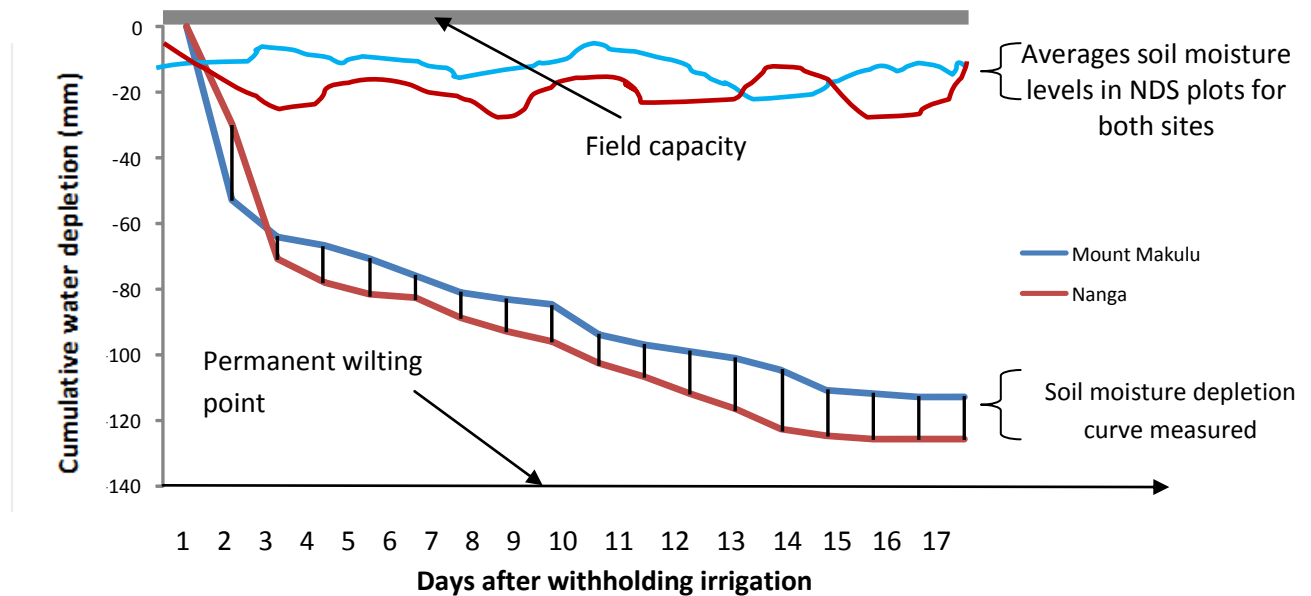
Soil moisture was monitored using the gravimetric method through daily collection of soil samples from the date of withdrawing irrigation water for about 17 days (Figure 3.1). Soil samples were collected from drought stressed plots at different depths (0 to 90 cm below soil surface) as shown in Figure 3.1 and taken to Mount Makulu soil testing laboratory for analysis.



**Figure 3. 11** Soil sample collection from drought stressed and drought stressed plots at Mount Makulu and Nanga

The soil samples were collected from each plot to ensure the results represented the trial. These samples were submitted to the Zambia Agricultural Research Institute (ZARI) for analysis; the results obtained were used to calculate various parameters of the moisture content of the soils. .

The soil field capacity was determined by applying water to a depth of 1 m until the soil profile was saturated. This was determined through digging a soil profile after applying water. The plot was then covered with black polythene sheets to stop evaporation. The soil moisture content was determined at 24 h intervals until the differences between measurements were almost negligible; this was taken as the field capacity (ZARI soil analysis results). The permanent wilting point was also determined when the depletion became almost parallel to the X-axis (Figure 3.2). This, by interpretation, was about 15 bars and the soil moisture content had dropped to about 15 to 20% moisture content; that is, it was not available to the plant in the root zone (Odendo et al., 2002) and the results of the soil depletion curve are as presented in Figure 3.2.



**Figure 3.2:** Average water depletion curve from the root zone after withdrawing water

### 3.2.5 Statistical data analysis

The data collected were subjected to the analysis of variance (ANOVA) for various agronomic traits recorded to obtain mean sum of squares and the residual, according to Steele and Torrie (1980).

A mean rank for each genotype was calculated by taking the average of the total ranking of the indices. The biplot analysis was performed for ranking the genotypes and to describe the nature of the relationships that existed between grain yield and the drought screening indices for the 12 selected drought tolerant genotypes in order to avoid overcrowding of the plot (Figure 3.3). Principal components of the original data set, consisting of  $n$  measurements on  $p$  variables, were reduced to one consisting of  $n$  measurements on  $k$  principal components. The biplot display of principal component analysis was used to identify suitable stress tolerance indices, and stress tolerant and high-yielding genotypes. Analysis of principal components often reveals relationships that were not previously suspected and thereby allows more detailed interpretations (Johnson and Wichern, 1996). The genotypes could be categorised into four groups based on their performance in stress and non-stress environments; genotypes suitable for both stress and non-stress environments, those suitable for non-stress environments; genotypes suitable for stress environments; and genotypes not suitable for either stress or non-stress environments.

### 3.3 Results

#### 3.3.1 Across site analysis of variance

The results of the analysis of variance for the pooled results across the sites (Nanga and Mount Makulu) and years (2011 and 2012) indicated genotypic differences which were significant for yield ( $P \leq 0.05$ ) and for NPP and LAR ( $P \leq 0.01$ ) (Table 3.2). The main effects for water treatment were significant for NPP and DAF ( $P \leq 0.05$ ) and for yield, HSW, NSP and LAR ( $P \leq 0.01$ ) (Table 3.2). Site effects were significant for yield and NPP ( $P \leq 0.01$ ); for HSW and HSP ( $P \leq 0.001$ ) and; for DAF ( $P \leq 0.05$ ). The year effects were significant for yield ( $P \leq 0.01$ ) and for HSW, NPP and LAR ( $P \leq 0.001$ ). The genotype by water treatment effect was significant for HSW ( $P \leq 0.01$ ) only. The genotypes by site interactions were significant for HSW, NPP and LAR ( $P \leq 0.01$ ), while the water treatment by site interaction was significant for yield and LAR ( $P \leq 0.01$ ) and for HSW and NPP ( $P \leq 0.05$ ). Site by year interactions were significant for yield, HSW, NSP, NPP and DAF ( $P \leq 0.01$ ). Genotypes by water treatment and site interactions were not significant for the traits measured, while genotypes by water treatment by year interactions were only significant for NPP ( $P \leq 0.01$ ). Genotype by site by year interactions was significant for NPP and LAR ( $P \leq 0.01$ ). The four way interaction between genotypes, water treatment, site and year was not significant for all the traits. The significant differences between means are only discussed for the three way interactions, two way interactions and main effects for which results were significant.

**Table 3.2:** Across site and season mean squares for yield and selected agronomic traits

Source	df	LAR	DAF	NPP	NSP	Yield	HSW
Genotype	119	82.71**	97.52	1138.3**	8240	1.992*	41.38
Water trt	1	21.14**	39.23*	385.6*	5528**	72**	15.03*
Site	1	14.27	505.05*	5421**	110549***	58.748**	46487.75***
Year	1	9476.66***	323.25	56222.6***	16148	12.493**	131050***
Genotype. Water trt	119	38.39	99.19	197.1	7687	1.988	31.19**
Genotype.Site	119	779**	91.89	1316.7**	8290	2.135	44.71**
Water trt.Site	1	733.03**	93.97	2.1*	521	13.658**	13.31*
Genotype.Year	119	78.41**	96.56	576.8*	8100	2.01	38.63
Water trt.Year	1	587.32**	116.38	1191.4**	3213	1.574	2102
Site.Year	1	115.19	4559**	58942**	33625***	26.917	22308.86***
Genotype. Water trt.Site	119	47.7	95.9	222.6	7896	1.901	32.39
Genotype. Water trt.Year	119	36.83	95.12	538.7**	7890	1.984	32.33
Genotype.Site.Year	119	57.45**	97.05	462.2**	7999	2.063	31.63*
Water trt.Site.Year	1	1475.85**	5.27	-	33283***	003	28127
Genotype. Water trt.Site.Year	119	35.92	94.64	-	7742	1.94	32.61
Residual	930	41.47	98.95	318	7396	2.035	34.68
CV (%)		36.8	18.2	16.7	22.0	21.3	38.1

**Note:** Water trt = water level (drought stressed vs non drought stressed); LAR = leaf area retention ; DAF = days to 50% flowering; NPP = number of pods per plant; NSP = number of seeds per pod; HSW = hundred seed mass; df = degrees of freedom; \* = significant at 5%; \*\* = significant at 1%; \*\*\* = significant at 0.1%

### **3.3.2 Genotypic response of agronomic traits to drought stress**

The main site effects were significant for HSW and NSP ( $P \leq 0.001$ ); significant for yield and NPP ( $P \leq 0.01$ ) and; significant) for DAF ( $P \leq 0.05$ ), (Table 3.2). The genotypic mean performance of the 12 highest ranked genotypes based on selection indices under DS and NDS and corresponding percentage trait reduction for LAR, NPP, NSP, DAF, and HSW, are presented in Tables 3.3 and 3.4 for both sites. Drought stress generally decreased LAR, NPP, DAF and NSP. Based on the selection indices, the 12 highest ranked genotypes at Mount Makulu expressed between 0.30% and 50.00% loss for DAF, 0.23% and 1.75% for NPP, 0.25% and 5.17% for LAR, 3.70% and 38.07% for NSP, and 0.23% and 21.93% for HSW (Table 3.3 ).

The lowest yielding genotypes lost between 53.00% and 66.25% for DAF, 37.10% and 50.06% for NPP, 45.24% and 75.14% for LAR, 1.96% and 20.44% for NSP and 21.14% and 50.59% for HSW. The lowest yielding genotypes generally yielded the least under drought stressed conditions implying that they were susceptible to drought stressed conditions.

At Nanga, the 12 high yielding genotypes recorded reductions between 0 to 0.71% for DAF, 1.41 to 25.00% for NPP, 0.05 to 17.33% for LAR, 6.45 to 37.91% for NSP and 1.12 to 1.33% for HSW (Table 3.4). The lowest yielding genotypes on the other hand had a trait reduction between 3.17 and 13.88% for DAF, 54.12 and 68.49% for NPP, 54.4 and 72.22% for NSP, 56.54 and 93.84% for LAR, and 22.94 and 95.81% for HSW.

**Table 3.3:** Percentage reduction in selected trait performance for 12 highest and 12 lowest yielding genotypes at Mount Makulu under drought stressed and non-stressed plots

Genotype	DAF			NPP			LAR			NSP			HSW		
	NS	NDS	% Rd	NS	NDS	%Rd	NS	NDS	%Rd	NS	NDS	%Rd	NS	NDS	%Rd
SCCI 8	53.75	53.59	0.30	22.05	22.00	0.23	39.60	39.50	0.25	6.75	6.50	3.70	22.05	22.00	0.23
SCCI 3	51.25	51.00	0.49	23.00	22.88	0.52	57.50	57.30	0.35	6.90	6.50	5.80	23.00	22.88	0.52
LY4-4-4-B	51.50	51.25	0.49	18.75	18.63	0.64	27.80	27.70	0.36	7.70	6.36	17.40	18.75	18.63	0.64
SCCI 4	50.50	25.25	50.00	28.50	28.25	0.88	52.50	52.30	0.38	7.60	5.56	26.84	28.50	28.25	0.88
ZM3831	48.00	47.75	0.52	26.00	25.75	0.96	45.20	45.00	0.44	7.60	5.43	28.55	26.00	25.75	0.96
SCCI 7	48.50	48.25	0.52	23.75	23.50	1.05	43.80	43.60	0.46	7.70	5.45	29.22	23.75	23.50	1.05
LY1-2-B	56.00	55.56	0.79	23.75	23.49	1.09	37.50	37.30	0.53	5.27	3.70	29.79	23.75	23.49	1.09
ZM4512-5	47.75	47.25	1.05	22.25	22.00	1.12	18.50	18.40	0.54	8.70	5.98	31.26	22.25	22.00	1.12
KAL-ZA	54.00	53.25	1.39	24.00	23.70	1.25	35.00	34.80	0.57	8.40	5.45	35.12	24.00	23.70	1.25
SCCI 13	48.25	47.50	1.55	22.55	22.25	1.33	52.80	52.50	0.57	7.10	4.55	35.92	22.55	22.25	1.33
ZM4496	53.59	52.75	1.57	21.00	20.69	1.48	58.00	55.00	5.17	8.60	5.40	37.21	26.90	21.00	21.93
LYA-ZA	48.84	48.00	1.72	22.25	21.86	1.75	49.10	48.80	0.61	8.80	5.45	38.07	22.25	21.86	1.75
ZM3681	53.75	45.50	15.35	42.25	26.25	37.87	42.00	23.00	45.24	6.40	5.80	9.38	42.25	26.25	37.87
ZM3624	54.00	45.50	15.74	34.50	21.38	38.03	58.60	31.50	46.25	5.30	5.09	3.96	34.50	21.38	38.03
ZM4302	54.00	45.25	16.20	39.50	23.88	39.54	65.20	32.20	50.61	6.60	5.79	12.27	39.50	23.88	39.54
ZM4144	57.50	42.00	26.96	45.00	26.50	41.11	33.00	15.80	52.12	6.90	5.97	13.48	45.00	26.50	41.11
ZM3636	55.00	45.50	17.27	39.75	23.19	41.66	37.90	17.80	53.03	7.70	6.44	16.36	39.75	23.19	41.66
ZM4490	54.50	44.75	17.89	34.75	20.25	41.73	33.80	15.20	55.03	9.00	7.16	20.44	34.75	20.25	41.73
ZM4520	59.25	48.25	18.57	41.63	22.50	45.95	47.50	20.00	57.89	6.30	5.53	12.22	41.63	22.50	45.95
ZM6713	55.25	44.25	19.91	39.50	20.80	47.34	32.30	13.00	59.75	4.60	4.51	1.96	39.50	20.80	47.34
NP5	53.00	41.50	21.70	52.19	27.25	47.79	45.50	17.50	61.54	5.60	5.07	9.46	52.19	27.25	47.79
ZM3203-3	56.00	43.00	23.21	43.25	22.25	48.55	27.50	9.10	66.91	5.60	5.06	9.64	43.25	22.25	48.55
ZM4511	58.41	44.75	23.39	50.06	25.00	50.06	24.60	6.50	73.58	7.30	6.04	17.26	50.06	25.00	50.59
KAB-ZA	66.25	46.25	30.19	32.94	20.70	37.16	35.40	8.80	75.14	6.40	5.44	15.00	32.59	25.70	21.14
<b>Grand mean</b>	32.85	32.32	1.62	16.22	12.86	19.61	52.87	36.56	29.03	5.78	4.42	10.46	35.07	24.76	28.24
<b>LSD</b>	3.30	2.80		1.93	2.10		5.20	3.80		1.12	1.80		8.70	6.30	
<b>CV</b>		1.30			9.20			3.00			9.30			12.00	

Note: HSW = hundred seed mass; NSP = number of seeds per pod; NPP = number of pods per plant; LAR = leaf area in retention; DAF = Days to 50% flowering; %Rd = percentage reductions; NS = non –drought stressed; NDS = drought stressed. The dotted line separates high yielding from low yielding

**Table 3.4:** Percentage reduction in selected trait performance for 12 highest and lowest yielding genotypes at Nanga under drought stressed and non-stressed conditions

Genotype	DAF			NPP			LAR			NSP			HSW		
	NS	NDS	% Rd	NS	NDS	%Rd	NS	NDS	%Rd	NS	NDS	%Rd	NS	DS	%Rd
SCCI 8	32.50	32.50	0.00	28.00	21.00	25.00	42.02	42.00	0.05	5.45	4.44	18.58	45.30	44.79	1.12
SCCI 3	32.00	32.00	0.00	35.50	35.00	1.41	53.35	53.25	0.19	5.8	5.17	10.92	39.50	39.03	1.19
LY4-4-4-B	36.95	36.94	0.03	34.80	34.30	1.44	47.12	47.00	0.25	5.09	4.63	9.14	41.10	40.59	1.23
SCCI 4	33.04	32.98	0.18	14.80	14.50	2.03	37.39	37.29	0.27	5.79	5.42	6.45	50.30	49.68	1.23
ZM3831	32.25	32.15	0.31	35.00	33.80	3.43	37.12	37.00	0.32	5.97	5.25	12.06	32.50	32.09	1.25
SCCI 7	32.10	31.98	0.37	35.00	29.30	16.29	37.50	31.00	17.33	6.44	4.19	34.98	30.50	30.12	1.25
LY1-2-B	37.75	37.50	0.66	28.80	27.50	4.51	36.87	36.10	2.09	7.16	4.50	37.15	55.70	55.00	1.25
ZM4512-5	38.00	37.75	0.66	33.00	31.50	4.55	47.50	46.38	2.36	5.53	4.56	17.50	39.40	38.91	1.25
KAL-ZA	36.75	36.50	0.68	31.30	29.80	4.79	46.13	44.98	2.49	5.56	4.51	18.92	40.40	39.89	1.26
SCCI 13	36.50	36.25	0.68	28.00	22.00	21.43	73.58	71.63	2.65	6.50	5.07	22.00	25.30	24.97	1.30
ZM4496	35.00	34.75	0.71	36.00	34.00	5.56	64.34	62.37	3.06	5.06	4.25	16.01	32.30	31.88	1.30
LYA-ZA	35.25	35.00	0.71	33.80	31.80	5.92	53.96	52.00	3.63	6.04	3.75	37.91	45.30	44.70	1.33
ZM3681	31.50	30.50	3.17	38.80	17.80	54.12	93.77	47.50	49.34	5.44	3.31	39.11	55.70	42.92	22.94
ZM3624	38.25	37.00	3.27	31.00	13.80	55.48	53.63	21.98	59.02	4.67	3.50	25.05	39.40	29.91	24.08
ZM4302	30.25	29.25	3.31	94.40	41.50	56.04	69.19	28.25	59.17	5.64	3.88	31.29	40.40	30.32	24.95
ZM4144	33.73	32.60	3.35	22.00	9.50	56.82	87.03	33.75	61.22	5.74	3.81	33.58	25.30	18.96	25.05
ZM3636	32.77	31.65	3.42	26.50	11.00	58.49	58.75	21.11	64.07	6.31	4.25	32.65	32.30	24.05	25.54
ZM4490	32.25	31.00	3.88	23.50	9.50	59.57	68.90	25.00	63.72	5.25	4.38	16.67	45.60	32.11	29.58
ZM4520	39.85	38.25	4.02	11.00	3.80	65.45	66.79	19.37	71.00	6.29	5.56	11.62	39.50	27.67	29.96
ZM6713	33.00	31.50	4.55	42.00	14.00	66.67	58.25	13.92	76.10	5.45	4.56	16.28	37.80	24.62	34.87
NP5	33.00	31.50	4.55	28.30	9.00	68.20	64.12	15.19	76.31	5.8	5.13	11.64	37.20	23.37	37.17
ZM3203-3	33.75	31.75	5.93	45.80	14.50	68.34	55.75	11.48	79.41	4.47	4.25	4.92	45.60	23.93	47.52
ZM4511	32.75	28.75	12.21	36.50	11.50	68.49	38.00	7.55	80.13	5.02	3.75	25.30	39.50	19.04	51.79
KAB-ZA	31.35	27.00	13.88	37.80	15.00	60.32	43.00	2.65	93.84	5.13	3.31	35.43	37.80	37.74	0.16
Grand mean	32.85	32.32	1.62	16.22	12.86	19.61	52.87	36.56	29.03	5.78	4.42	10.46	35.07	24.76	28.24
LSD	3.30	2.80	1.93	2.10	2.10	5.20	3.80			1.12	1.80		8.70	6.30	
CV		1.30			9.20		3.00				9.30			12.00	

Note: HSW = Hundred seed mass; NSP = number of seeds per pod; NPP = number of pods per plant; LAR = Leaf area in retention; DAF = Days to 50% flowering; % Rd = Percentage reductions; NS = Non-drought stressed; NDS = Drought stressed. The dotted line separates high yielding from low yielding genotypes

### **3.3.3 Comparison and selection of genotypes based on tolerance indices and yield**

Water stress generally reduced yield of bean genotypes in DS conditions as compared to NDS conditions. Based on the stress tolerance indices, MP, STI, GMP and HM ranked the genotypes similarly while YI and SSI ranked the genotypes similarly as well with relatively low ranks ranging between 3 and 30 (Table 3.5). The genotypes SCCI 13, Ly4-4-4-B, SCCI 2, ZM 3831, Ly1-2-B, ZM 4512, ZM 4512-5, Kal-Za, LYA-ZA, LY2-7-B, ZM 3683 and ZM 4496 (described in appendix 3.1) were found to be highly drought tolerant based on the low standard deviations of the means and Rank Sums. Yield Index and SSI ranking was also similar in ranking to MP, STI, GMP and HM. The Rank Sum for the best 12 genotypes ranged between 15.48 and 32.56. Among them LY4-4-4-B was the highest ranked genotype. The indices largely used yield to identify drought tolerant genotypes.

According to STI, MP and GMP values, the 12 genotypes namely SCCI 3, SCC I3, SCC I4, SCCI 7, ZM 3831, ZM 4512-5, SCCI 9, LY1-7-B, KAL-ZA, ZM 4496 and LY1-2-B were identified as drought tolerant genotypes. The indices recorded for the 12 highest ranked genotypes on the basis of the three indices were higher than the rest of the genotypes (Appendix 2). The relatively high values for the indices MP, GMP, YI and HM are desirable for selecting high yielding genotypes for drought stressed conditions.

The genotypes SCCI 12, ZM 3683, Ly 2-2-B, ZM 4296, ZM 07, ZM 3202, NP 6, Kaba-Za, ZM 4482, ZM 3749, ZM 4491, and ZM 3624 were ranked high on YSI indicating they were stable in both DS and NDS environments. Further analysis by calculating the individual ranking of each genotype for each index, mean ranking showed that Ly 1-2-B, ZM 01, ZM 4496, Ly 1-7-B, Kal-Za, SCCI 9, ZM4512-5, ZM 3831, SCCI 7, SCCI 4, Ly4-4-4-B, SCCI 8 and SCCI 3 had high mean rankings (Table 3.5).

The ranking based on individual indices are detailed in Appendix 3.2. The selection based on individual indices were and to a lesser extent not completely consistent despite the fact that some genotypes were consistently ranked in the top 12 and bottom 12.



**Table 3.5:** Twelve high ranked and 12 lowest ranked genotypes based on yield in drought stressed plots across sites and across years with corresponding selection indices, ranks(R) and Rank sum

Genotype	Yp	R	Ys	R	MP	R	GMP	R	STI	R	YI	R	YI	R	YSI	R	SSI	R	HM	R	Mean Rank	Sdev	RS
LY4-4-4-B	0.833	5	0.779	3	0.806	4	0.806	4	0.029	4	1.679	3	1.998	3	0.935	32	-0.679	3	0.805	4	6.5	8.98	15.48
LY1-2-B	0.682	17	0.658	7	0.670	12	0.670	11	0.020	11	1.419	7	1.688	7	0.966	23	-0.419	7	0.670	10	11.2	5.22	16.42
ZM3831	0.723	10	0.671	5	0.697	6	0.697	6	0.022	6	1.446	5	1.721	5	0.928	34	-0.446	5	0.696	6	8.8	8.98	17.78
KAL-ZA	0.702	13	0.650	9	0.676	10	0.675	10	0.021	10	1.401	9	1.667	9	0.927	35	-0.401	9	0.675	9	12.3	8.07	20.37
SCCI 13	0.692	14	0.647	10	0.670	13	0.669	13	0.020	13	1.394	10	1.659	10	0.935	33	-0.394	10	0.669	11	13.7	6.96	20.66
ZM4512-5	0.726	9	0.654	8	0.690	7	0.689	7	0.022	7	1.409	8	1.676	8	0.901	43	-0.409	8	0.688	7	11.2	11.19	22.39
LYA-ZA	0.690	15	0.631	12	0.660	15	0.660	14	0.020	14	1.359	12	1.617	12	0.914	38	-0.359	12	0.659	14	15.8	7.90	23.70
ZM4496	0.703	12	0.637	11	0.670	11	0.669	12	0.020	12	1.373	11	1.634	11	0.906	42	-0.373	11	0.669	12	14.5	9.68	24.18
LY2-7-B	0.641	22	0.591	15	0.616	19	0.615	19	0.017	19	1.273	15	1.515	15	0.922	36	-0.273	15	0.615	18	19.3	6.34	25.64
ZM3683	0.546	36	0.572	20	0.559	23	0.559	23	0.014	23	1.233	20	1.467	20	1.048	14	-0.233	20	0.559	23	22.2	5.57	27.77
SCCI 2	0.529	38	0.507	26	0.518	31	0.518	29	0.012	29	1.093	26	1.301	26	0.958	27	-0.093	26	0.518	27	28.5	3.75	32.25
ZM4512	0.520	40	0.518	25	0.519	30	0.519	28	0.012	28	1.117	25	1.329	25	0.997	18	-0.117	25	0.519	26	27	5.56	32.56
NP5	0.267	108	0.152	117	0.209	115	0.201	116	0.002	116	0.327	117	0.389	117	0.568	116	0.673	117	0.193	116	115.5	2.72	118.22
ZM3788-2	0.264	109	0.259	94	0.262	105	0.262	105	0.003	105	0.559	94	0.665	94	0.983	21	0.441	94	0.262	104	92.5	25.81	118.31
ZM3203-3	0.232	114	0.116	118	0.174	118	0.164	118	0.001	118	0.250	118	0.298	118	0.500	119	0.750	118	0.155	118	117.7	1.34	119.04
KAB-ZA	0.158	119	0.098	120	0.128	119	0.124	119	0.001	119	0.211	120	0.251	120	0.620	115	0.789	120	0.121	119	119	1.49	120.49
ZM3636	0.249	111	0.199	113	0.224	113	0.223	113	0.002	113	0.429	113	0.511	113	0.801	75	0.571	113	0.221	113	109	11.96	120.96
ZM4830	0.263	110	0.234	106	0.249	109	0.248	109	0.003	109	0.505	106	0.601	106	0.891	45	0.495	106	0.248	108	101.4	19.88	121.28
ZM4490	0.237	112	0.197	114	0.217	114	0.216	114	0.002	114	0.425	114	0.506	114	0.832	68	0.575	114	0.216	114	109.2	14.49	123.69
ZM4491	0.223	115	0.254	99	0.239	111	0.238	111	0.003	111	0.547	99	0.651	99	1.137	9	0.453	99	0.238	111	96.4	31.38	127.78
ZM3681	0.237	113	0.229	109	0.233	112	0.233	112	0.002	112	0.492	109	0.586	109	0.966	24	0.508	109	0.232	112	102.1	27.49	129.59
ZM4511	0.126	120	0.114	119	0.120	120	0.120	120	0.001	120	0.246	119	0.292	119	0.908	41	0.754	119	0.120	120	111.7	24.85	136.55
ZM3624	0.179	117	0.227	110	0.203	116	0.201	115	0.002	115	0.489	110	0.582	110	1.270	3	0.511	110	0.200	115	102.1	34.94	137.04
ZM6713	0.178	118	0.178	116	0.178	117	0.178	117	0.001	117	0.384	116	0.457	116	1.005	16	0.616	116	0.178	117	106.6	31.84	138.44
Mean	0.46		0.39		0.42		0.85		0.84		0.85		0.16		0.14		0.42		0.46				

Note: Yp=yield under non drought stressed conditions; Ys =yield under drought stressed conditions; HM = hamonic mean, MP=mean productivity; STI = stress tolerance index; SSI=stress susceptibility index; GMP=geometric mean productivity; SDI=susceptibility drought index; YI=Yield index; YSI=yield stability index; R=rank; Mean ranking is calculated as an average of the rankings for each of the indices; RS=Rank sum (Rank sum (RS)= Rank mean ( R ) + Standard deviation of rank (SDR) (Farshadfar and Elyasi, 2012), Sdev (R) = standard deviation of the ranks.

#### **3.3.4 Genotype ranking based on the rank sum**

The ranking based on rank sum which takes into consideration the deviation observed in each index and, this based on the mean rank and standard deviation of the ranks, identified LY 4-4-4-B, ZM3831, ZM4512-5, KAL-ZA and ZM4496 as most drought tolerant genotypes and identified ZM3203-3, KAB-ZA, NP5, ZM3624 and ZM6713 as most sensitive genotypes (Table 3.5). The Rank Sum for the highest yielding genotypes ranged between 15.48 and 32.56 while the lowest yielding genotypes had mean ranking between 118 and 138. Fifty two genotypes had yields above the mean ( $390 \text{ kg ha}^{-1}$ ) in DS plots while the rest (68) showed yields below the mean performance (Appendix 3.2). This translates to the fact that 43.0% of the genotypes yielded normally above the trial mean.

#### **3.3.5 Yield response of the genotypes to drought stress on yield**

The yield loss for most of the highly ranked genotypes based on the selection indices was less than 10% except for SCCI 8, SCCI 3, SCCI 4 and SCCI 7 which recorded yield reductions of 29.6%, 25.0%, 29.5% and 28.8% respectively. The 12 lowest ranked genotypes based on the selection indices had yield losses ranging between 0.5% and 50.0%. Most of the genotypes ranked least by the selection indices had yield reductions of between 16.8% and 50.0% except for ZM 3681, ZM 6713, and ZM 4511 that recorded relatively low yield reductions of 3.4%, 0.5% and 9.2% respectively.

#### **3.3.6 Correlations between yield and selected agronomical traits under drought stress**

The results of the correlations between yield in DS plots and measured traits are presented in Table 3.6. Significant positive correlations were recorded in DS conditions between yield and HSW ( $r = 0.689$ ,  $P \leq 0.01$ ), and NPP ( $r = 0.82$ ,  $P \leq 0.01$ ). The correlations between yield under stressed plots with HSW ( $r = 0.689$ ), LAR ( $r = -0.81$ ), NPP ( $r = 0.82$ ) and NSP ( $r = 0.75$ ) were significant ( $P \leq 0.01$ ). However the results indicated that yield and LAR were negatively correlated with yield while LAR ( $r = -0.81$ ,  $P \leq 0.01$ ), and with NSP ( $r = -0.75$ ,  $P \leq 0.01$ ) positively correlated with yield under DS conditions. The correlation between HSW and NPP was significant and positive ( $r = 0.64$ ,  $P \leq 0.01$ ). Similarly, NSP was positively correlated with NPP ( $r = 0.474$ ,  $P \leq 0.05$ ). There was also

significant ( $r=0.64$ ,  $P\leq 0.01$ ) and positive correlation between HSW and NPP. The DAF was significantly correlated with HSW, LAR, NPP ( $P\leq 0.01$ ) and with NSP ( $P\leq 0.05$ ).

**Table 3.6:** Correlation between yield and selected agronomic traits under drought stress

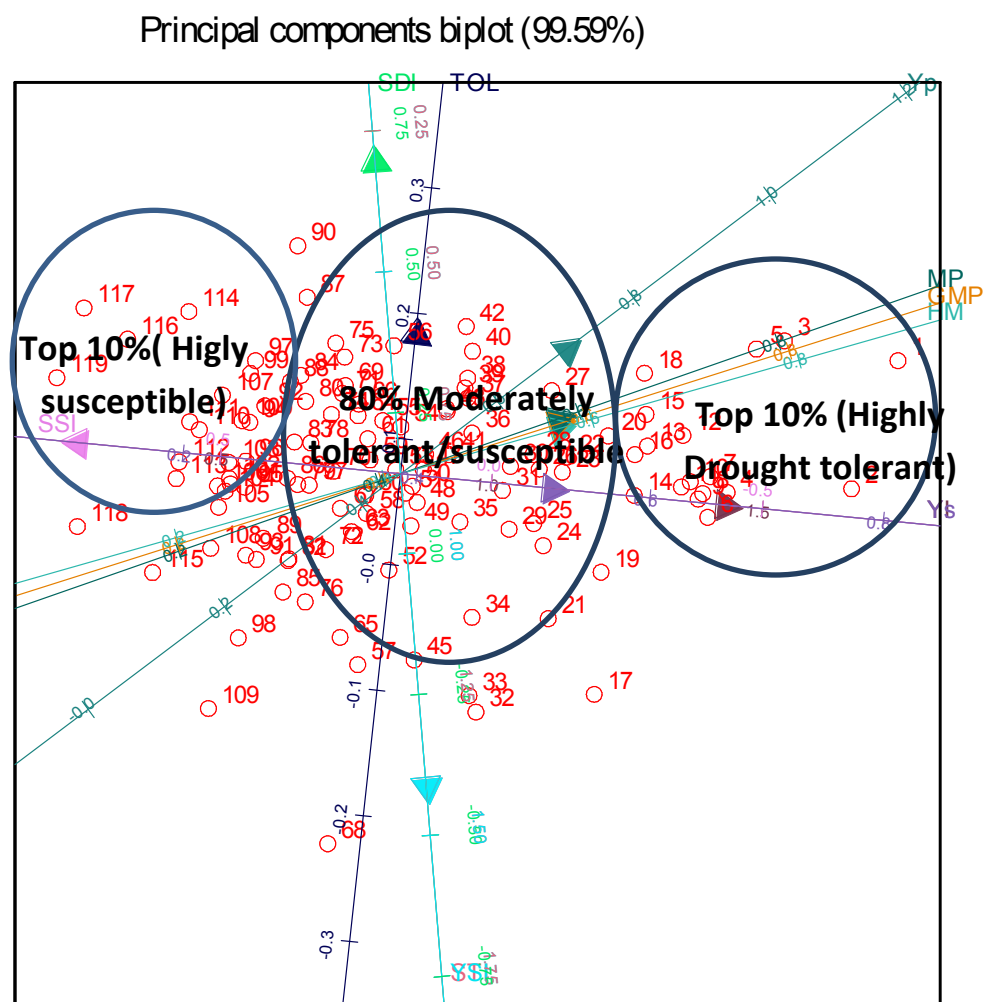
	DAF	HSW	LAR	NPP	NSP	Yield
DAF	1					
HSW	0.72**	1				
LAR	0.55**	-0.48	1			
NPP	0.84**	0.64**	0.85**	1		
NSP	-0.46*	0.155	0.925**	0.474*	1	
Yield	-0.27	0.689**	-0.81**	0.82**	0.75**	1

**Note:** HSW = Hundred seed mass; NSP = Number of seeds per pod; NPP = Number of pods per plant; LAR = Leaf area in retention; DAF = Days to 50% flowering

### 3.3.7 Principal component analysis

The biplot analysis (Figure 3.3) described the relationships that existed between grain yield and the screening indices in accounting for general trends in the behavior of the 120 genotypes when exposed to drought stress. The first principal component (PC-1) accounted for 75.9% of the variation while the second principal component (PC-2) accounted for only 23.7%. Hundred seed mass contributed the most (99.9%) to PC-1. From the biplot (Figure 3.3), it can be observed that most of the genotypes (about 80%) were more concentrated to the middle of the biplot implying that they were moderately susceptible or tolerant. The genotypes denoted by the numbers 1 to 10 are lying on the right side of the biplot forming another cluster of the genotypes identified as highly drought tolerant comprising SCCI 4, SCCI 7 ZM 3831, ZM 4512-5, Ly1-2-B, ZM 4512-5, LyA-ZA, ZM 4496, SCCI 3, Ly4-4-4-B and SCCI 2. The genotypes denoted by the numbers 110 to 120 represent the genotypes that have been classified as highly susceptible to drought by the indices.

This cluster of genotypes forms the bulk of the germplasm and it agrees with the 80.0% majority identified as moderately tolerant to susceptible by the principal component analysis (Figure 3.3). These results are in line with the description of the indices and their relationships. The SSI values recorded for the top 12 ranked genotypes were less than 1 denoting more drought tolerant genotypes when compared with the rest of the genotypes.



**Figure 3.3:** Biplot display of the 120 genotypes across all environments. The biplot shows the first two principal components for the 120 selected genotypes based on selection indices

### 3.4 Discussion

The results of the analysis of variance (Table 3.2) showed significant differences in terms of all traits under drought stress condition. The results showed significant differences in terms of all traits for LAR, HSW, DAF, NPP, NSP and yield. This indicates that the magnitude of differences between cultivars was sufficient for selection for drought resistance. The results revealed that water decreased the grain yield of all cultivars significantly. Similar observations have been reported in wheat (Farshadfar, 2012). Significant variability was observed on the basis of yield and yield components,

providing a good starting point in the development of improved varieties that are tolerant to drought stress. About 40% of the genotypes screened under drought stress yielded above the trial mean which could classify them as relatively tolerant to drought stress. This result is also presented graphically in the biplot analysis (Figure 3.3). This result implies that breeding for drought tolerance would generally successfully use of the local germplasm. The clear distinction between high yielding and low yielding genotypes when screened under drought stress is a good indicator that shows diversity for drought tolerance. Drought affected average yield at both sites. The results also indicated this group of genotypes had flowered earlier and yielded above the mean when exposed to drought stress when compared to non-drought stress conditions.

The mean NPP was reduced as a result of drought stress. The high yielding genotypes generally had low pod reduction indicating the possible ability of the genotypes to mobilise photosynthates from vegetative parts to developing pods when exposed to drought stress. There was a positive and significant correlation between NPP and yield under drought. It would therefore be implied that drought tolerant genotypes were possibly using their ability to remobilize photosynthates to adapt to drought stressed conditions and achieve some yield. The drought tolerant genotypes showed minimal reduction in leaf area. Out of the 12 highest yielding under drought stress, about 10 were landraces. Among the notable genotypes, is Lyambai, which had the ability to yield high under DS and was also preferred by the farmers as shown earlier in a PRA study reported in this thesis. The mutants of Lyambai such as LYA-ZA, LY4-4-4-B and LY 1- 2-B could be released as cultivars. However, it needs to be noted that most of these high yielding genotypes had many undesirable characteristics such as small seeds, and dark colours.

There were no significant differences in HSW between genotypes under drought stress. This finding contradicts the findings made by Munroz-Perea *et al.* (2006) who found significant differences in seed mass between drought stressed and non- stressed conditions which could be attributed to the differences in the germplasm used. The yield components, number of pods per plant and number of seeds per pod were both reduced by drought stress and would have contributed to yield reduction.

The ranking of the genotypes at the two sites showed a mixed pattern. However, although the ranking differed, genotypes in the top 12 maintained their superiority in terms of yield while the bottom 12 also maintained their lower ranking. These results show that the rank order of the genotypes for yield, NPP, and HSW between seasons, sites, and water treatments was consistent for high yielding genotypes. This translates to the fact that 40% of the genotypes yielded normally above the trial mean.

The significant and negative correlations between yield and LAR and with NSP implies that genotypes that had fewer seeds per pod and low leaf area retention had more grain yield and would be desirable for selecting in drought stressed conditions. This may imply that genotypes with fewer numbers of seeds per pod concentrated all their photosynthates into the few seeds set in each pod. Furthermore, the genotypes that had low leaf area retention probably conserved most of the photosynthetic products and partitioned them to seed development other than supporting vegetative growth resulting into slightly higher yield. The selection for low number of seeds per pod and low leaf area retention under drought stress would therefore be desirable in common bean to achieve relatively high yields. The biplot analysis on the mean ranking and correlation matrix showed that the first PCA explained most of the variation between yield and drought tolerance indices. The genotypes lying near and around zero were considered high yielding and stable in both DS and NDS conditions and correlated with high MP, GMP and HM values supporting the findings of Farshadfar et al. (2012). The breeders use principal component analysis to describe a pattern to complement other methods of grouping genotypes. The main advantage of principal component is that the statistics are well assigned to each particular group of genotypes (Khodadadi et al., 2011).

The GMP, MP, YI, HM discriminated the genotypes into classes based on their adaptation to drought stress (Table 3.6). The high values for GMP, MP, YI and HM are desirable for high yielding genotypes in drought stressed environments. SCCI 8, SCCI 3, LY4-4-4-B, SCCI 4, ZM 3831, SCCI 7, LY1-2-B, ZM 4512-5, KAL-ZA, SCCI 13, ZM 4496 and LYA-ZA were ranked in the top 12 high yielding genotypes by these indices indicating that they were high yielding and suitable for DS environments. ZM3681, ZM 3624, ZM 4302, ZM 4144, ZM 3636, ZM 4490, ZM 4520, ZM6713, ZM 3203-3, ZM 4511, NP5 and KAB-ZA on the other hand were ranked as lowest yielding in the bottom 12.

This result is confirmation of the appropriateness of the indices in identifying high yielding common bean genotypes for DS environments.

The more sensitive genotypes (ZM3681, ZM 3624, ZM 4302, ZM 4144, ZM 3636, ZM 4490, ZM 4520, ZM 6713, ZM 3203-3, ZM 4511, NP5 and KAB-ZA) comprised landraces and these expressed severe depression in trait expression while the less sensitive genotypes (SCCI 8, SCCI 3, LY4-4-4-B, SCCI 4, ZM 3831, SCCI 7, LY1-2-B, ZM 4512-5, KAL-ZA, SCCI 13, ZM 4496 and LYA-ZA) expressed less trait depression. This difference could be seen in the extent of trait reductions for NPP, LAR and NSP for each of the genotypes when contrasted between the 12 highest and 12 lowest yielding genotypes. The differences are attributed to the differences in the genetic makeup and their adaptation ability. The genotypes identified as drought tolerant in this study seemingly used different adaptation mechanisms and were all selected based on yield potential. For instance, Ly4-4-4-B had higher yield than the drought sensitive genotypes like KAB-ZA based on the three traits (NPP, NSP and LAR). However, it needs to be noted that drought tolerance is not a single trait but rather the sum of the different mechanisms that occur in the plant. It was observed that low NSP and high NPP resulted in high yield and this may imply that the fewer the seeds in a pod the better as they would grow to maturity. This may relate to the ability of the genotypes to mobilize photosynthates. The property of genotypes to mobilise photosynthates when exposed to drought stress has also been reported by Klaedtke et al. (2012) but was not tested in this study. However, potential yield provides the most effective way for selecting drought tolerant genotypes and worth testing to confirm if applicable in this case.

The various methods of determining drought tolerance in the genotypes namely, rank sum, mean rank, correlation, and biplots were consistent in ranking drought tolerant genotypes, though with very minor and insignificant variation. This confirms information already published that selection for drought tolerance should be based on tolerance indices for yield under stressed and non-stressed conditions. The GMP, MP, YI and HM though showing variations were useful in identifying high yielding genotypes adaptable to both drought stressed and non-drought stressed conditions. The results agree with separate and similar observations made by Fernandez (1992) and Mohammadi et al. (2010). These results show the consistency of performance of the genotypes under drought stress and non-drought stress conditions. The genotypes with high values of stress tolerance (STI), geometric mean productivity, and mean productivity (MP) can be

selected as tolerant genotypes to water stress. The estimates of indicators of drought tolerance (Table 3.5) indicated that the identification of drought-tolerant cultivars was contradictory based on a single criterion. To determine the most desirable drought tolerant cultivar according to all the indices rank and mean rank of all drought tolerance criteria were calculated and the most desirable drought tolerant cultivars were identified based on these two criteria. The ranking based on one index has been criticised as it has been established that in many cases, the indices contradict each other. Thus each index provides different order of tolerance when considered individually (Ashraf et al., 2015). Therefore the use of rank sum gives a good statistical ranking and removes bias due to error. In consideration to all indices, LY4-4-4-B, LY1-2-B, ZM3831, KAL-ZA, ZM4512-5, ZM4496 and SCCI 13 showed the best mean rank and low rank sum in water deficit stress condition, hence they were identified as the most drought tolerant cultivars which are in agreement with most indices.

### **3.5 Conclusion**

According to the results collected in this research, genotypic differences were evident. The genotypes could be grouped into three categories, those that were highly drought tolerant lying in the top 10% of the 120 genotypes screened, moderately susceptible or tolerant comprising about 80% and most susceptible lying at the bottom 10%. Overall about 40% of the 120 genotypes yielded above the mean.

Selecting the top five genotypes of the 120 genotypes and based on the rank sum, LY4-4-4-B, LY1-2-B, ZM3831, KAL-ZA, and ZM4512-5, as highly tolerant to drought. LY4-4-4-B is a mutant derived from a released cultivar, LYA – ZA (Lyambai), while, KAL- ZA is a released cultivar, and ZM 3831 and ZM 4512-5 are landraces. The landraces were small seeded, reddish brown in colour and appeared less attractive for human consumption based on results of the PRA work. The mutants retained the background of red speckled and the original size and colour as Lyambai from which they were derived. These could be released as cultivars with further selection. The released cultivars on the other hand provided more choices for use in breeding programmes as a sources of tolerance to drought stress.



The local landraces have shown a lot of undesirable characteristics in terms of seed size and seed color. From the results of this study, these landraces would require to be improved upon. The recommendation would be, to breed for large seed size and red speckled seed colour in the selected landraces to make them acceptable by the farmers while maintaining their levels of drought tolerance.

This study also established that HSW mass was not affected by stress and was similar both in DS and NDS conditions. All the tested genotypes showed reduced number of days to flowering when grown under drought stress.

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### Appendix 3.1: List of germplasm used, the source and phenotypic characteristics

No.	Germplasm	Category	Source	Seed Colour	Seed shape	Growth habit	Flower colour standard	Plant growth type	HSW
1	KE 5	Landrace	National gene bank (Zambia)	red	Kidney	III	1	2	35.6
2	KE 1	Landrace	National gene bank (Zambia)	white	Kidney	I	1	1	24.3
3	KE 3	Landrace	National gene bank (Zambia)	brown	Kidney	III	1	2	25.8
4	KE 2	Landrace	National gene bank (Zambia)	brownish	Kidney	I	2	1	16.5
5	KE 4	Landrace	National gene bank (Zambia)	brownish	Kidney	I	2	1	14.3
6	ZM 4497	Landrace	National gene bank (Zambia)	white	Kidney	III	1	2	20.1
7	ZM3200	Landrace	National gene bank (Zambia)	red	Kidney	I	1	1	40
8	ZM 4143	Landrace	National gene bank (Zambia)	red	Kidney	III	1	2	35.6
9	ZM 4512-3	Landrace	National gene bank (Zambia)	red	cuboid	I	2	1	39.4
10	ZM 4830	Landrace	National gene bank (Zambia)	white	oval	IV	1	2	32.8
11	ZM 4144	Landrace	National gene bank (Zambia)	brownish	Kidney	IV	1	2	25.1
12	ZM 4296	Landrace	National gene bank (Zambia)	bicolour	oval	IV	2	2	14.8
13	ZM 4520	Landrace	National gene bank (Zambia)	bicolour	oval	III	2	2	21.2
14	ZM 07	Landrace	National gene bank (Zambia)	white	oval	I	1	2	29.7
15	ZM 4303	Landrace	National gene bank (Zambia)	brown	oval	III	1	1	25.6
16	ZM 6713	Landrace	National gene bank (Zambia)	brownish	oval	I	2	1	27.9
17	ZM 4489	Landrace	National gene bank (Zambia)	brownish	oval	I	2	1	20.8
18	ZM 3730	Landrace	National gene bank (Zambia)	white	oval	III	2	1	32
19	ZM 4488	Landrace	National gene bank (Zambia)	red	oval	I	2	1	29.6
20	ZM 3831	Landrace	National gene bank (Zambia)	red	oval	I	2	1	33.4
21	ZM 3788	Landrace	National gene bank (Zambia)	red	oval	I	3	1	29.4
22	ZM 04	Landrace	National gene bank (Zambia)	white	cuboid	I	2	2	22.2
23	ZM 4833	Landrace	National gene bank (Zambia)	brownish	cuboid	I	2	1	37.2
24	ZM 4831	Landrace	National gene bank (Zambia)	bicolour	cuboid	I	2	1	15.7
25	ZM 3636	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	2	2	35.2
26	ZM 3688	Landrace	National gene bank (Zambia)	brownish	Kidney	I	1	1	27.9
27	ZM 5128	Landrace	National gene bank (Zambia)	brownish	Kidney	III	2	2	46.8
28	ZM 02	Landrace	National gene bank (Zambia)	white	Kidney	III	2	2	28
29	ZM 3793	Landrace	National gene bank (Zambia)	red	Kidney	I	1	1	11.5
30	ZM 4840	Landrace	National gene bank (Zambia)	red	cuboid	III	2	2	10.8
31	ZM 4829	Landrace	National gene bank (Zambia)	red	oval	IV	1	2	23

32	ZM 4289	Landrace	National gene bank (Zambia)	white	Kidney	III	2	2	28.2
33	ZM 4516	Landrace	National gene bank (Zambia)	brownish	oval	IV	2	2	7.8
34	ZM 4490	Landrace	National gene bank (Zambia)	bicolour	oval	I	1	1	29.8
35	ZM 4482	Landrace	National gene bank (Zambia)	bicolour	oval	I	1	1	17.8
36	ZM 03	Landrace	National gene bank (Zambia)	white	oval	*	1	2	25.5
37	ZM 6612	Landrace	National gene bank (Zambia)	brown	oval	IV	1	2	28.5
38	SCCI 6	Landrace	National gene bank (Zambia)	brownish	oval	III	1	2	5.3
39	ZM 3696	Landrace	National gene bank (Zambia)	brownish	oval	III	1	2	16.4
40	ZM 4836	Landrace	National gene bank (Zambia)	white	oval	III	2	1	20.5
41	ZM 6602	Landrace	National gene bank (Zambia)	red	oval	III	2	2	23.5
42	ZM 3202	Landrace	National gene bank (Zambia)	red	oval	IV	2	2	23.8
43	ZM 6604	Landrace	National gene bank (Zambia)	red	cuboid	III	3	2	27.1
44	ZM 3694	Landrace	National gene bank (Zambia)	white	cuboid	I	2	2	19.7
45	ZM 6603	Landrace	National gene bank (Zambia)	brownish	cuboid	III	2	2	27.9
46	ZM 4514	Landrace	National gene bank (Zambia)	bicolour	Kidney	III	1,2	2	28.2
47	ZM 4302	Landrace	National gene bank (Zambia)	brownish	Kidney	III	2	2	20.4
48	ZM 3624	Landrace	National gene bank (Zambia)	white	cuboid	III	1	2	25.2
49	ZM 3203	Landrace	National gene bank (Zambia)	red	oval	I	2	2	30.3
50	ZM 4483	Landrace	National gene bank (Zambia)	red	Kidney	IV	1	2	40.6
51	SCCI 3	Landrace	National gene bank (Zambia)	red	oval	III	2	2	18.3
52	ZM 3831-4	Landrace	National gene bank (Zambia)	white	oval	III	2	2	23.1
53	ZM 4491	Landrace	National gene bank (Zambia)	brownish	oval	IV	1	2	13.5
54	ZM 4496	Landrace	National gene bank (Zambia)	bicolour	oval	*	2	2	31.6
55	ZM 3200	Landrace	National gene bank (Zambia)	bicolour	oval	I	2	2	31
56	ZM 3677	Landrace	National gene bank (Zambia)	brownish	oval	III	4	2	34.2
57	SCCI 12	Landrace	National gene bank (Zambia)	brownish	oval	III	2	2	23.2
58	ZM 3681-2	Landrace	National gene bank (Zambia)	white	oval	IV	2	2	27.5
59	SZ3	Landrace	National gene bank (Zambia)	red	oval	III	1	1	9.3
60	ZM 3683	Landrace	National gene bank (Zambia)	red	oval	IV	4	2	21.9
61	ZM 05	Landrace	National gene bank (Zambia)	red	cuboid	III	3	2	30.6
62	ZM 5136	Landrace	National gene bank (Zambia)	white	cuboid	III	2	2	33.1
63	ZM 4508	Landrace	National gene bank (Zambia)	brownish	cuboid	III	2	2	32.5
64	ZM 5127	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	1	2	16.9
65	ZM 4512-4	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	1	2	19.1

66	ZM 6601	Landrace	National gene bank (Zambia)	white	Kidney	IV	2	2	10.5
67	ZM 4524	Landrace	National gene bank (Zambia)	brown	Kidney	III	2	2	33.7
68	ZM 4305	Landrace	National gene bank (Zambia)	brownish	Kidney	IV	2	2	13
69	ZM 4525	Landrace	National gene bank (Zambia)	red	Kidney	III	2	2	28.9
70	ZM 4502	Landrace	National gene bank (Zambia)	red	Kidney	III	4	2	29
71	ZM 4294	Landrace	National gene bank (Zambia)	white	Kidney	I	1	1	14.2
72	ZM 06	Landrace	National gene bank (Zambia)	brownish	Kidney	III	4	2	30.6
73	ZM 3749	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	2	2	29.6
74	ZM 3838	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	2	2	21.8
75	ZM 4512	Landrace	National gene bank (Zambia)	white	Kidney	IV	2	2	17.6
76	ZM 3206	Landrace	National gene bank (Zambia)	brown	Kidney	IV	2	2	26.5
77	ZM 4479	Landrace	National gene bank (Zambia)	brownish	Kidney	III	1	2	29.4
78	ZM 4512-2	Landrace	National gene bank (Zambia)	brownish	Kidney	III	2	2	34.1
79	ZM 4298	Landrace	National gene bank (Zambia)	white	Kidney	III	1	2	18.1
80	SCCI 1	Landrace	National gene bank (Zambia)	red	Kidney	IV	4	2	20.5
81	ZM3681	Landrace	National gene bank (Zambia)	red	Kidney	III	1	2	28.6
82	ZM 4478	Landrace	National gene bank (Zambia)	red	Kidney	III	2	2	38
83	SCCI 9	Landrace	National gene bank (Zambia)	white	Kidney	III	2	2	27.2
84	SCCI 5	Landrace	National gene bank (Zambia)	brownish	Kidney	III	2	2	5.2
85	SCCI 7	Landrace	National gene bank (Zambia)	bicolour	Kidney	IV	1	2	20.8
86	SCCI 13	Landrace	National gene bank (Zambia)	bicolour	Kidney	III	4	2	39.1
87	SCCI-5	Landrace	National gene bank (Zambia)	brownish	Kidney	III	2	2	20.5
88	SCCI 10	Landrace	National gene bank (Zambia)	brownish	Kidney	III	1	2	23.7
89	SCCI 11	Landrace	National gene bank (Zambia)	white	Kidney	III	1	2	30
90	SCCI 11	Landrace	National gene bank (Zambia)	red	Kidney	I	1	1	18.8
91	SCCI 2	Landrace	National gene bank (Zambia)	red	Kidney	IV	1	2	40.6
92	SCCI 4	Landrace	National gene bank (Zambia)	red	Kidney	III	2	2	26
93	SCCI 8	Landrace	National gene bank (Zambia)	white	Kidney	I	2	1	38
94	KAB-ZA	Landrace	National gene bank (Zambia)	brownish	Kidney	III	1	2	21.7
95	MEX 54	Kenyan bean	Seed Company	red	cuboid	III	1	2	14.4
96	G10909	Kenyan bean	Seed Company	red	cuboid	III	4	2	26.5
97	GADRA	RSA cultivar	Seed Company	sugar bean	Kidney	III	2	2	20.1
98	SCCI/LYA	Mutant	UNZA	brownish	Kidney	III	2	2	28.6
99	KABA-ZA	Mutant	UNZA	brownish	Kidney	IV	4	2	38
100	LY2-7-B	Mutant	UNZA	brownish	Kidney	III	1	2	27.2
101	LY2-3-B	Mutant	UNZA	brownish	Kidney	III	2	2	5.2

102	LY2-8-B	Mutant	UNZA	brownish	Kidney	III	2	2	20.8
103	LY4-4-B	Mutant	UNZA	brownish	Kidney	*	2	2	39.1
104	LY1-2-B	Mutant	UNZA	brownish	Kidney	III	2	2	20.5
105	LY2-2-B	Mutant	UNZA	brownish	Kidney	III	4	2	23.7
106	SZ-4-B-B	Mutant	UNZA	red speckled	Kidney	IV	2	2	30
107	SZ31BB1	Mutant	UNZA	red speckled	Kidney	III	2	2	18.8
108	SZ33BB2	Mutant	UNZA	red speckled	Kidney	III	2	2	40.6
109	SZ7-4-B-B	Mutant	UNZA	red speckled	Kidney	III	1	2	26
110	LY1-7-B	Mutant	UNZA	brownish	Kidney	III	1	2	38
111	SZ33BB1	Mutant	UNZA	red speckled	Kidney	IV	2	2	30
112	SZ9-B-B-B2	Mutant	UNZA	red speckled	Kidney	III	4	2	18.8
113	SZ32BB1	Mutant	UNZA	red speckled	Kidney	III	1	2	40.6
114	LY-UNZA	Mutant	UNZA	brownish	Kidney	III	1	2	26
115	CAR	Mutant	UNZA		Kidney	III	2	2	38
116	LYA-ZA	Released cultivar	ZARI	Red speckled	Kidney	III	2	2	21.7
117	CHAM-ZA	Released cultivar	ZARI	brownish	Kidney	III	3	2	14.4
118	KAL-ZA	Released cultivar	ZARI	white	cuboid	III	2	2	26.5
119	LUK-ZA	Released cultivar	ZARI	tan	cuboid	III	1	2	20.1
120	LWA-ZA	Released cultivar	ZARI	whittish	Kidney	III	2	2	30

**Note:** UNZA=University of Zambia, ZARI=Zambia Agriculture Research Institute



### Appendix 3.2: List of all the genotypes ranked by Rank Sum

Genotype	Yp	R	Ys	R	MP	R	GMP	R	STI	R	YI	R	YI	R	YSI	R	SSI	R	HM	R	Mean Rank (X)	Sdev	RS
LY4-4-4-B	0.833	5	0.779	3	0.806	4	0.806	4	0.029	4	1.679	3	1.998	3	0.935	32	-0.679	3	0.805	4	6.5	8.98	15.48
LY1-2-B	0.682	17	0.658	7	0.670	12	0.670	11	0.020	11	1.419	7	1.688	7	0.966	23	-0.419	7	0.670	10	11.2	5.22	16.42
ZM3831	0.723	10	0.671	5	0.697	6	0.697	6	0.022	6	1.446	5	1.721	5	0.928	34	-0.446	5	0.696	6	8.8	8.98	17.78
KAL-ZA	0.702	13	0.650	9	0.676	10	0.675	10	0.021	10	1.401	9	1.667	9	0.927	35	-0.401	9	0.675	9	12.3	8.07	20.37
SCCI 13	0.692	14	0.647	10	0.670	13	0.669	13	0.020	13	1.394	10	1.659	10	0.935	33	-0.394	10	0.669	11	13.7	6.96	20.66
ZM4512-5	0.726	9	0.654	8	0.690	7	0.689	7	0.022	7	1.409	8	1.676	8	0.901	43	-0.409	8	0.688	7	11.2	11.19	22.39
LYA-ZA	0.690	15	0.631	12	0.660	15	0.660	14	0.020	14	1.359	12	1.617	12	0.914	38	-0.359	12	0.659	14	15.8	7.90	23.70
ZM4496	0.703	12	0.637	11	0.670	11	0.669	12	0.020	12	1.373	11	1.634	11	0.906	42	-0.373	11	0.669	12	14.5	9.68	24.18
LY2-7-B	0.641	22	0.591	15	0.616	19	0.615	19	0.017	19	1.273	15	1.515	15	0.922	36	-0.273	15	0.615	18	19.3	6.34	25.64
ZM3683	0.546	36	0.572	20	0.559	23	0.559	23	0.014	23	1.233	20	1.467	20	1.048	14	-0.233	20	0.559	23	22.2	5.57	27.77
SCCI 2	0.529	38	0.507	26	0.518	31	0.518	29	0.012	29	1.093	26	1.301	26	0.958	27	-0.093	26	0.518	27	28.5	3.75	32.25
ZM4512	0.520	40	0.518	25	0.519	30	0.519	28	0.012	28	1.117	25	1.329	25	0.997	18	-0.117	25	0.519	26	27	5.56	32.56
KE 2	0.683	16	0.585	17	0.634	17	0.632	17	0.018	17	1.260	17	1.500	17	0.856	56	-0.260	17	0.630	17	20.8	12.37	33.17
SCCI 9	0.748	7	0.623	13	0.686	8	0.683	8	0.021	8	1.342	13	1.596	13	0.832	67	-0.342	13	0.680	8	15.8	18.18	33.98
KE 5	0.601	25	0.525	24	0.563	22	0.562	22	0.014	22	1.132	24	1.347	24	0.875	49	-0.132	24	0.560	22	25.8	8.23	34.03
CHAM-ZA	0.704	11	0.594	14	0.649	16	0.647	16	0.019	16	1.280	14	1.524	14	0.844	63	-0.280	14	0.645	16	19.4	15.40	34.80
ZM4483	0.583	30	0.505	27	0.544	26	0.543	24	0.013	24	1.089	27	1.296	27	0.867	50	-0.089	27	0.541	24	28.6	7.75	36.35
SCCI 3	1.050	2	0.788	2	0.919	2	0.910	2	0.038	2	1.698	2	2.021	2	0.750	86	-0.698	2	0.901	2	10.4	26.56	36.96
SZ3	0.619	23	0.527	23	0.573	21	0.571	21	0.015	21	1.135	23	1.351	23	0.851	59	-0.135	23	0.569	21	25.8	11.71	37.51
SCCI 5	0.531	37	0.477	32	0.504	35	0.503	35	0.011	35	1.027	32	1.222	32	0.898	44	-0.027	32	0.502	33	34.7	3.71	38.41
SCCI 12	0.457	55	0.577	18	0.517	32	0.514	31	0.012	31	1.244	18	1.481	18	1.262	4	-0.244	18	0.510	31	25.6	13.70	39.30
ZM4525	0.504	43	0.487	30	0.495	38	0.495	38	0.011	38	1.049	30	1.248	30	0.965	25	-0.049	30	0.495	37	33.9	5.61	39.51
KAP-ZA	0.559	32	0.480	31	0.520	29	0.518	30	0.012	30	1.034	31	1.231	31	0.859	54	-0.034	31	0.517	28	32.7	7.57	40.27
ZM 01	0.740	8	0.587	16	0.663	14	0.659	15	0.020	15	1.265	16	1.505	16	0.794	77	-0.265	16	0.655	15	20.8	19.89	40.69
LY2-2-B	0.471	51	0.530	22	0.500	36	0.499	36	0.011	36	1.142	22	1.358	22	1.125	10	-0.142	22	0.499	36	29.3	11.72	41.02
KE 4	0.680	18	0.559	21	0.619	18	0.616	18	0.017	18	1.204	21	1.433	21	0.822	72	-0.204	21	0.613	19	24.7	16.68	41.38
LY-UNZA	0.591	27	0.498	29	0.545	25	0.542	25	0.013	25	1.073	29	1.276	29	0.842	65	-0.073	29	0.540	25	30.8	12.16	42.96
SCCI 8	1.134	1	0.798	1	0.966	1	0.951	1	0.041	1	1.719	1	2.046	1	0.704	103	-0.719	1	0.937	1	11.2	32.26	43.46
SCCI 7	0.934	4	0.665	6	0.800	5	0.788	5	0.028	5	1.434	6	1.706	6	0.712	99	-0.434	6	0.777	5	14.7	29.63	44.33
SCCI 4	0.974	3	0.687	4	0.830	3	0.818	3	0.030	3	1.480	4	1.761	4	0.705	102	-0.480	4	0.805	3	13.3	31.17	44.47
ZM3200	0.468	52	0.443	36	0.455	43	0.455	42	0.009	42	0.955	36	1.136	36	0.947	31	0.045	36	0.455	42	39.6	5.85	45.45
LY1-7-B	0.790	6	0.577	19	0.684	9	0.675	9	0.021	9	1.244	19	1.480	19	0.730	94	-0.244	19	0.667	13	21.6	25.95	47.55
ZM4298	0.477	48	0.406	48	0.441	45	0.440	45	0.009	45	0.875	48	1.041	48	0.852	57	0.125	48	0.438	45	47.7	3.59	51.29
ZM4840	0.678	19	0.503	28	0.591	20	0.584	20	0.016	20	1.084	28	1.290	28	0.742	90	-0.084	28	0.578	20	30.1	21.44	51.54
ZM4831	0.453	56	0.399	51	0.426	49	0.425	48	0.008	48	0.859	51	1.022	51	0.879	48	0.141	51	0.424	48	50.1	2.51	52.61
ZM 04	0.513	41	0.426	42	0.470	41	0.468	41	0.010	41	0.918	42	1.093	42	0.830	69	0.082	42	0.466	41	44.2	8.73	52.93
SCCI/LYA	0.555	33	0.443	37	0.499	37	0.496	37	0.011	37	0.954	37	1.136	37	0.798	76	0.046	37	0.493	38	40.6	12.51	53.11
SZ3-1-B-B	0.445	59	0.404	49	0.425	50	0.424	49	0.008	49	0.871	49	1.036	49	0.908	40	0.129	49	0.424	49	49.2	4.49	53.69
ZM3202	0.413	67	0.462	35	0.438	46	0.437	46	0.009	46	0.995	35	1.184	35	1.117	11	0.005	35	0.436	46	40.2	14.20	54.40
ZM6602	0.442	60	0.394	52	0.418	53	0.417	51	0.008	51	0.848	52	1.009	52	0.890	46	0.152	52	0.416	50	51.9	3.45	55.35
ZM6604	0.492	46	0.406	47	0.449	44	0.447	44	0.009	44	0.876	47	1.042	47	0.827	71	0.124	47	0.445	43	48	8.23	56.23
SCCI 11	0.451	57	0.383	54	0.417	54	0.415	52	0.008	52	0.825	54	0.982	54	0.849	61	0.175	54	0.414	52	54.4	2.76	57.16

Genotype	Yp	R	Ys	R	MP	R	GMP	R	STI	R	YI	R	YI	R	YSI	R	SSI	R	HM	R	Mean Rank (X)	Sdev	RS
KE 1	0.587	28	0.434	38	0.510	34	0.505	34	0.012	34	0.935	38	1.113	38	0.739	91	0.065	38	0.499	35	40.8	17.91	58.71
ZM 02	0.553	35	0.419	44	0.486	40	0.481	40	0.011	40	0.903	44	1.074	44	0.758	83	0.097	44	0.477	40	45.4	13.53	58.93
SZ9-B-B-B2	0.555	34	0.418	45	0.486	39	0.481	39	0.011	39	0.900	45	1.072	45	0.754	84	0.100	45	0.477	39	45.4	14.08	59.48
ZM6601	0.423	64	0.401	50	0.412	58	0.412	55	0.008	55	0.864	50	1.028	50	0.948	30	0.136	50	0.412	53	51.5	8.80	60.30
ZM4516	0.595	26	0.430	40	0.512	33	0.506	33	0.012	33	0.927	40	1.103	40	0.723	96	0.073	40	0.499	34	41.5	19.70	61.20
ZM4833	0.609	24	0.431	39	0.520	28	0.512	32	0.012	32	0.928	39	1.104	39	0.708	101	0.072	39	0.504	32	40.5	21.89	62.39
ZM 07	0.368	78	0.464	34	0.416	55	0.413	54	0.008	54	0.999	34	1.188	34	1.259	5	0.001	34	0.410	55	43.7	19.77	63.47
ZM4296	0.365	82	0.471	33	0.418	52	0.414	53	0.008	53	1.014	33	1.207	33	1.290	2	-0.014	33	0.411	54	42.8	21.09	63.89
SZ31BB1	0.493	45	0.382	55	0.437	47	0.434	47	0.009	47	0.824	55	0.980	55	0.776	81	0.176	55	0.430	47	53.4	10.57	63.97
ZM4524	0.645	21	0.430	41	0.538	27	0.527	27	0.013	27	0.926	41	1.102	41	0.666	108	0.074	41	0.516	30	40.4	24.93	65.33
LY2-3-B	0.435	62	0.360	60	0.397	64	0.395	63	0.007	63	0.775	60	0.923	60	0.828	70	0.225	60	0.394	60	62.2	3.16	65.36
ZM3688	0.480	47	0.366	56	0.423	51	0.419	50	0.008	50	0.789	56	0.939	56	0.763	82	0.211	56	0.415	51	55.5	9.87	65.37
SCCI 1	0.670	20	0.420	43	0.545	24	0.530	26	0.013	26	0.905	43	1.077	43	0.627	113	0.095	43	0.516	29	41	26.92	67.92
ZM 06	0.450	58	0.356	62	0.403	62	0.400	59	0.007	59	0.766	62	0.912	62	0.791	78	0.234	62	0.397	57	62.1	5.92	68.02
ZM3788	0.404	68	0.359	61	0.382	66	0.381	66	0.007	66	0.774	61	0.921	61	0.889	47	0.226	61	0.380	64	62.1	5.93	68.03
ZM4488	0.392	70	0.362	59	0.377	70	0.377	69	0.006	69	0.779	59	0.927	59	0.921	37	0.221	59	0.376	67	61.8	10.06	71.86
SCCI 6	0.460	54	0.345	65	0.402	63	0.398	60	0.007	60	0.743	65	0.885	65	0.750	85	0.257	65	0.394	59	64.1	8.18	72.28
ZM 05	0.391	71	0.330	71	0.361	72	0.359	71	0.006	71	0.710	71	0.845	71	0.842	64	0.290	71	0.358	73	70.6	2.41	73.01
ZM4305	0.376	74	0.385	53	0.380	67	0.380	67	0.007	67	0.830	53	0.987	53	1.025	15	0.170	53	0.380	65	56.7	16.60	73.30
ZM4508	0.471	50	0.344	67	0.408	59	0.403	57	0.007	57	0.742	67	0.883	67	0.731	93	0.258	67	0.398	56	64	11.83	75.83
KE 3	0.568	31	0.365	57	0.467	42	0.455	43	0.009	43	0.786	57	0.935	57	0.642	111	0.214	57	0.444	44	54.2	21.86	76.06
KABA-ZA	0.346	85	0.412	46	0.379	68	0.378	68	0.006	68	0.888	46	1.057	46	1.190	7	0.112	46	0.376	66	54.6	21.48	76.08
SZ33BB2	0.434	63	0.323	75	0.378	69	0.374	70	0.006	70	0.695	75	0.827	75	0.743	88	0.305	75	0.370	69	72.9	6.59	79.49
ZM4836	0.366	80	0.351	63	0.359	74	0.359	72	0.006	72	0.757	63	0.901	63	0.959	26	0.243	63	0.359	71	64.7	14.82	79.52
ZM3831-4	0.368	79	0.350	64	0.359	75	0.359	73	0.006	73	0.754	64	0.897	64	0.952	29	0.246	64	0.358	72	65.7	14.02	79.72
NP8	0.391	72	0.308	79	0.349	78	0.347	77	0.005	77	0.664	79	0.790	79	0.789	79	0.336	79	0.345	77	77.6	2.17	79.77
SCCI 10	0.373	77	0.339	68	0.356	76	0.355	75	0.006	75	0.730	68	0.868	68	0.909	39	0.270	68	0.355	74	68.8	11.12	79.92
LUK-ZA	0.464	53	0.329	72	0.397	65	0.391	64	0.007	64	0.710	72	0.844	72	0.710	100	0.290	72	0.385	63	69.7	12.25	81.95
CAR	0.475	49	0.331	70	0.403	61	0.396	62	0.007	62	0.713	70	0.848	70	0.697	104	0.287	70	0.390	62	68	14.26	82.26
ZM5128	0.375	75	0.295	84	0.335	79	0.332	80	0.005	80	0.635	84	0.755	84	0.785	80	0.365	84	0.330	81	81.1	2.96	84.06
ZM4514	0.359	83	0.310	78	0.335	80	0.334	79	0.005	79	0.669	78	0.796	78	0.863	51	0.331	78	0.333	79	76.3	9.02	85.32
ZM5127	0.502	44	0.326	74	0.414	56	0.405	56	0.007	56	0.703	74	0.837	74	0.650	110	0.297	74	0.396	58	67.6	18.30	85.90
ZM 03	0.419	66	0.300	81	0.359	73	0.354	76	0.006	76	0.646	81	0.769	81	0.716	98	0.354	81	0.350	76	78.9	8.23	87.13
ZM3730	0.349	84	0.300	80	0.325	84	0.324	83	0.005	83	0.647	80	0.770	80	0.861	53	0.353	80	0.323	83	79	9.30	88.30
ZM4289	0.507	42	0.317	76	0.412	57	0.401	58	0.007	58	0.683	76	0.813	76	0.625	114	0.317	76	0.390	61	69.4	19.43	88.83
ZM4482	0.303	92	0.362	58	0.332	81	0.331	82	0.005	82	0.779	58	0.927	58	1.196	6	0.221	58	0.329	82	65.7	24.77	90.47
ZM4489	0.335	90	0.329	73	0.332	82	0.332	81	0.005	81	0.708	73	0.843	73	0.981	22	0.292	73	0.332	80	72.8	18.70	91.50
LY4-4-B	0.344	87	0.291	87	0.317	88	0.316	86	0.005	86	0.628	87	0.747	87	0.848	62	0.372	87	0.315	85	84.2	7.84	92.04
LY2-8-B	0.437	61	0.293	85	0.365	71	0.358	74	0.006	74	0.632	85	0.752	85	0.671	107	0.368	85	0.351	75	80.2	12.33	92.53
ZM3749	0.302	93	0.345	66	0.323	85	0.322	84	0.005	84	0.743	66	0.884	66	1.144	8	0.257	66	0.322	84	70.2	24.15	94.35
SZ32BB1	0.420	65	0.285	89	0.352	77	0.346	78	0.005	78	0.615	89	0.732	89	0.680	106	0.385	89	0.340	78	83.8	11.06	94.86
ZM6603	0.345	86	0.256	95	0.300	90	0.297	91	0.004	91	0.551	95	0.656	95	0.743	89	0.449	95	0.294	92	91.9	3.11	95.01
ZM3838	0.373	76	0.267	93	0.320	86	0.315	87	0.005	87	0.575	93	0.685	93	0.716	97	0.425	93	0.311	87	89.2	5.94	95.14
ZM4829	0.527	39	0.287	88	0.407	60	0.389	65	0.007	65	0.618	88	0.736	88	0.545	117	0.382	88	0.372	68	76.6	21.56	98.16

Genotype	Yp	R	Ys	R	MP	R	GMP	R	STI	R	YI	R	YI	R	YSI	R	SSI	R	HM	R	Mean Rank (X)	Sdev	RS
ZM3694	0.338	88	0.249	101	0.294	93	0.290	93	0.004	93	0.537	101	0.639	101	0.738	92	0.463	101	0.287	93	95.6	4.88	100.48
ZM3696	0.315	91	0.255	97	0.285	95	0.284	95	0.004	95	0.550	97	0.655	97	0.811	73	0.450	97	0.282	95	93.2	7.33	100.53
NP6	0.291	98	0.313	77	0.302	89	0.302	89	0.004	89	0.674	77	0.802	77	1.075	12	0.326	77	0.302	89	77.4	24.13	101.53
ZM4478	0.583	29	0.270	91	0.427	48	0.397	61	0.007	61	0.582	91	0.693	91	0.463	120	0.418	91	0.369	70	75.3	26.48	101.78
MEX 54	0.299	94	0.297	82	0.298	91	0.298	90	0.004	90	0.640	82	0.762	82	0.994	19	0.360	82	0.298	90	80.2	21.99	102.19
NP3	0.400	69	0.255	98	0.328	83	0.319	85	0.005	85	0.549	98	0.653	98	0.637	112	0.451	98	0.311	86	91.2	11.93	103.13
G10909	0.384	73	0.252	100	0.318	87	0.311	88	0.004	88	0.543	100	0.646	100	0.657	109	0.457	100	0.304	88	93.3	10.34	103.64
ZM3206	0.297	97	0.296	83	0.297	92	0.297	92	0.004	92	0.638	83	0.759	83	0.997	17	0.362	83	0.297	91	81.3	23.17	104.47
ZM5136	0.298	95	0.256	96	0.277	100	0.276	98	0.003	98	0.551	96	0.656	96	0.858	55	0.449	96	0.275	97	92.7	13.33	106.03
ZM3793	0.336	89	0.231	108	0.283	96	0.279	97	0.004	97	0.498	108	0.593	108	0.689	105	0.502	108	0.274	98	101.4	6.83	108.23
ZM4497	0.297	96	0.241	104	0.269	102	0.268	102	0.003	102	0.519	104	0.618	104	0.810	74	0.481	104	0.266	100	99.2	9.20	108.40
ZM3677	0.287	101	0.274	90	0.280	98	0.280	96	0.004	96	0.590	90	0.702	90	0.953	28	0.410	90	0.280	96	87.5	21.28	108.78
ZM4303	0.278	104	0.293	86	0.285	94	0.285	94	0.004	94	0.631	86	0.751	86	1.055	13	0.369	86	0.285	94	83.7	25.51	109.21
ZM4479	0.289	99	0.242	103	0.266	103	0.264	103	0.003	103	0.522	103	0.622	103	0.840	66	0.478	103	0.263	102	98.8	11.59	110.39
NP4	0.219	116	0.336	69	0.277	99	0.271	99	0.003	99	0.723	69	0.861	69	1.534	1	0.277	69	0.265	101	79.1	32.55	111.65
ZM4294	0.286	102	0.243	102	0.265	104	0.264	104	0.003	104	0.524	102	0.624	102	0.850	60	0.476	102	0.263	103	98.5	13.56	112.06
ZM4302	0.288	100	0.215	111	0.251	108	0.249	108	0.003	108	0.463	111	0.551	111	0.746	87	0.537	111	0.246	109	106.4	7.57	113.97
ZM4144	0.283	103	0.206	112	0.244	110	0.241	110	0.003	110	0.445	112	0.529	112	0.730	95	0.555	112	0.238	110	108.6	5.48	114.08
ZM6612	0.271	107	0.269	92	0.270	101	0.270	100	0.003	100	0.579	92	0.688	92	0.992	20	0.421	92	0.270	99	89.5	24.95	114.45
ZM4502	0.278	104	0.239	105	0.258	106	0.258	106	0.003	106	0.515	105	0.613	105	0.862	52	0.485	105	0.257	105	99.9	16.84	116.74
ZM4143	0.273	106	0.233	107	0.253	107	0.252	107	0.003	107	0.501	107	0.596	107	0.851	58	0.499	107	0.251	107	102	15.46	117.46
ZM4520	0.366	81	0.197	115	0.281	97	0.268	101	0.003	101	0.424	115	0.504	115	0.537	118	0.576	115	0.256	106	106.4	11.65	118.05
NP5	0.267	108	0.152	117	0.209	115	0.201	116	0.002	116	0.327	117	0.389	117	0.568	116	0.673	117	0.193	116	115.5	2.72	118.22
ZM3788-2	0.264	109	0.259	94	0.262	105	0.262	105	0.003	105	0.559	94	0.665	94	0.983	21	0.441	94	0.262	104	92.5	25.81	118.31
ZM3203-3	0.232	114	0.116	118	0.174	118	0.164	118	0.001	118	0.250	118	0.298	118	0.500	119	0.750	118	0.155	118	117.7	1.34	119.04
KAB-ZA	0.158	119	0.098	120	0.128	119	0.124	119	0.001	119	0.211	120	0.251	120	0.620	115	0.789	120	0.121	119	119	1.49	120.49
ZM3636	0.249	111	0.199	113	0.224	113	0.223	113	0.002	113	0.429	113	0.511	113	0.801	75	0.571	113	0.221	113	109	11.96	120.96
ZM4830	0.263	110	0.234	106	0.249	109	0.248	109	0.003	109	0.505	106	0.601	106	0.891	45	0.495	106	0.248	108	101.4	19.88	121.28
ZM4490	0.237	112	0.197	114	0.217	114	0.216	114	0.002	114	0.425	114	0.506	114	0.832	68	0.575	114	0.216	114	109.2	14.49	123.69
ZM4491	0.223	115	0.254	99	0.239	111	0.238	111	0.003	111	0.547	99	0.651	99	1.137	9	0.453	99	0.238	111	96.4	31.38	127.78
ZM3681	0.237	113	0.229	109	0.233	112	0.233	112	0.002	112	0.492	109	0.586	109	0.966	24	0.508	109	0.232	112	102.1	27.49	129.59
ZM4511	0.126	120	0.114	119	0.120	120	0.120	120	0.001	120	0.246	119	0.292	119	0.908	41	0.754	119	0.120	120	111.7	24.85	136.55
ZM3624	0.179	117	0.227	110	0.203	116	0.201	115	0.002	115	0.489	110	0.582	110	1.270	3	0.511	110	0.200	115	102.1	34.94	137.04
ZM6713	0.178	118	0.178	116	0.178	117	0.178	117	0.001	117	0.384	116	0.457	116	1.005	16	0.616	116	0.178	117	106.6	31.84	138.44

Note: Yp=yield under non drought stressed conditions; Ys =yield under drought stressed conditions; HM = hamonic mean, MP=mean productivity; STI = stress tolerance index; SSI=stress susceptibility index; GMP=geometric mean productivity; SDI=susceptibility drought index; YI=Yield index; YSI=yield stability index; R=rank; Mean ranking is calculated as an average of the rankings for each of the indices; RS=Rank sum (Rank sum (RS)= Rank mean ( R ) + Standard deviation of rank (SDR) (Farshadfar and Elyasi, 2012), Sdev (R) = standard deviation of the ranks.

## CHAPTER FOUR

### Heat stress tolerance and its genetic basis in common bean

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#### Abstract

Common bean production has expanded to lowland regions of Zambia where high temperatures are prevalent during the cropping season. This study was undertaken to identify heat tolerant genotypes through selection at the pod filling stage and to determine the genetics of the heat tolerance trait. The experiments were conducted in the field at Lusitu and Nanga over two seasons where supplementary irrigation could be applied when needed. One hundred and twenty landraces were evaluated in an alpha lattice design with two replications. A second experiment comprised of 48  $F_2$  populations derived from crosses of eight female by six male using NCD II mating was also planted at the same site to study the gene action for heat tolerance. The trials were sown in early August in order for the seed development and pod filling stages to coincide with the period when temperatures are above 33°C to induce heat stress. The genotypes ZM 4143, ZM 4497, SCCI 4, KE 1 and ZM 07, were found to be the highest yielding genotypes under high temperatures. ZM 4497 was found to be genetically superior for tolerance to heat stress and recommended as a donor parent in breeding for heat tolerance. Significant GCA mean squares for yield, number of seeds per pod and number of pods per plant were detected implying that additive gene effects were important for the expression of heat tolerance in common bean. The female parents ZM 05, Chambeshi, Pan 148 and SCCI 2, and the male parent ZM 4143 recorded high GCA effects for yield and therefore good for use in generating segregating populations for high temperature stress tolerance.

#### 4.1 Introduction

The common bean (*Phaseolus vulgaris* L.) is a good source of cheap protein especially in Africa (FAO, 2009). It is one of the five cultivated species from the genus *Phaseolus* and currently ranks first among the legumes in human diets especially for the poor (Broughton et al., 2003; Singh, 1999). In sub-Saharan Africa, the common bean is grown both for food and for cash (Broughton et al., 2003). It is also important in crop rotations with cereals and contributes to enhanced soil fertility (Peoples and Craswell, 1992; Ledgard and Giller, 1995; Mafongoya and Bationo, 2006)

In recent years, the demand for the common bean has been steadily increasing in sub-Saharan Africa. The rise in demand has been attributed to the rise in population and intra-regional trade. Despite the increasing demand for the common bean, production has remained low, more especially in the low lying regions where temperatures are high (Graham and Rannali, 1997). Elevated temperatures (>30°C during the day and >20°C at night) in the summer lead to low yields in common bean emanating from flower and pod abortion (Nakano et al., 1998).

The common bean is known to be sensitive to high temperatures which affect most of the reproductive processes (Konsens et al., 1991). Poor fertilization due to high temperature stress can also cause low yield as the common bean pollen is very sensitive to heat stress (Halterlein et al., 1980). Despite the well documented effects of heat stress on the common bean, literature on the genetics of heat tolerance is still scanty. Quantitative inheritance with large environmental interference has been suggested in pod set and seed set in bean (Dickson and Petzoldt, 1989).

In Zambia, the common bean is grown in the northern parts of the country where climatic conditions are favorable (Zambia Agriculture Research Institute, 2012). The climatic conditions are not favorable for most of the southern parts of the country (Zambia Agriculture Research Institute, 2012). High temperatures (>30°C) and low moisture stresses cause flower and pod abortion and reduce yields of common bean (Baligar and Jones, 1997). For example, White and Izquierdo (1991) reported flower abortion levels of 60-80% in the common bean due to high temperatures.

Common bean landraces are an important genetic resource that are commonly grown by small scale farmers and preferred because of their adaptability, quality (taste and

appearance), but they are generally low yielding (Debouck et al., 1993; Gepts and Bliss, 1986). Despite the low yields, the landraces cannot be neglected as they possess important traits such as early maturity (Beebe et al., 2000; Harlan, 1992).

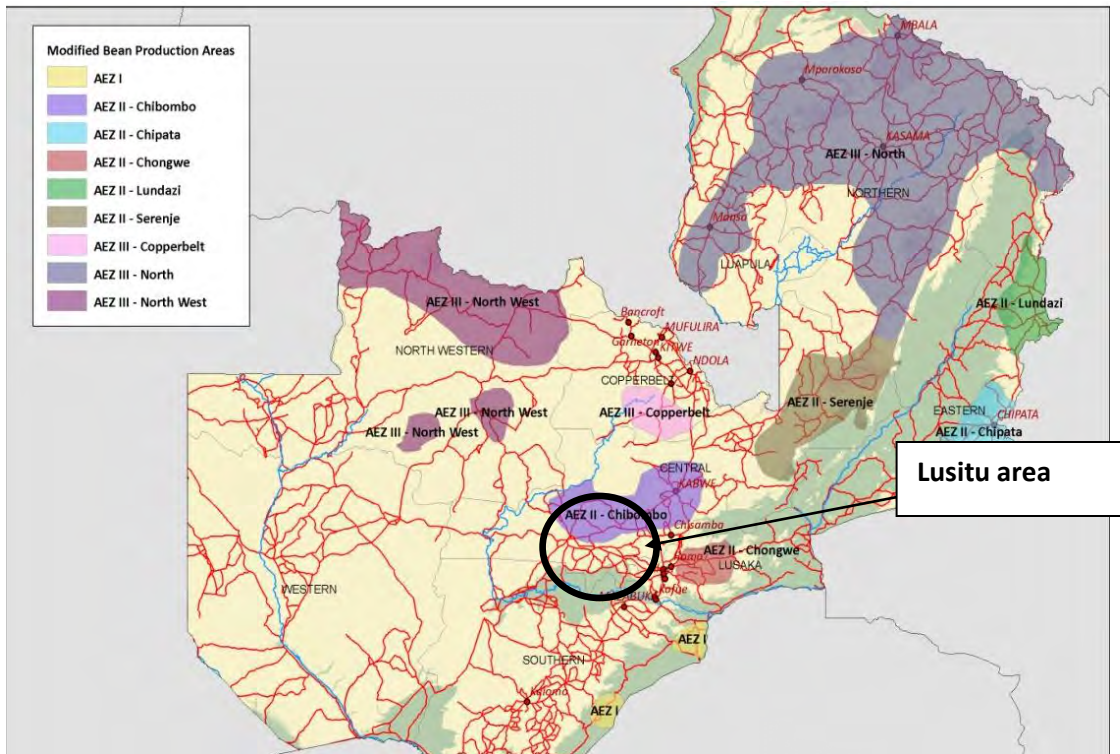
In order to enhance common bean production in hot environments in Zambia, the landraces need to be studied. This study was therefore designed to identify genotypes that would perform well under elevated temperatures and determine the genetic effects for heat tolerance.

## **4.2 Materials and methods**

### **4.2.1 Experimental materials and site**

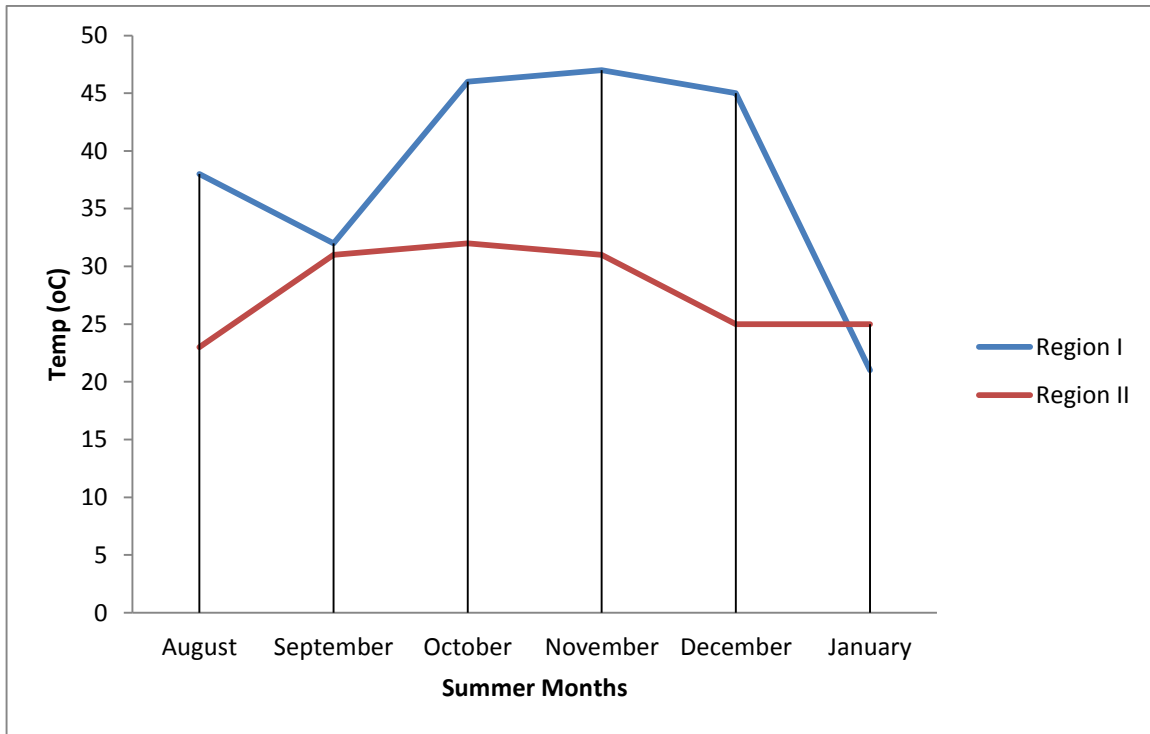
The materials used in this study were as outlined in 3.2.1 in Chapter 3 of this thesis.

The study was conducted at Lusitu in Siavonga district located in Region I of Zambia. Region I receive the least rainfall (less than 400 mm) in the country and is characterised by high summer temperatures. Figure 4.1 shows the location of Lusitu in Siavonga and the current spatial distribution of common bean production in Zambia.



**Figure 4.1:** Map of Zambia showing the location of Lusitu and spatial distribution of common bean production. AEZ stand for Agro-ecological Zone.

Lusitu lies between latitude 16.13°S and longitude 28.83°E in the south of the country. The soils at Lusitu are sandy loam and have a pH of about 7.5. Lusitu has an elevation of 480 m above sea level. This site was chosen because it lies in Region I where the temperatures are persistently high (>33°C) during most of the summer months (October to January) when compared with region II during the same period of time (Figure 4.2).

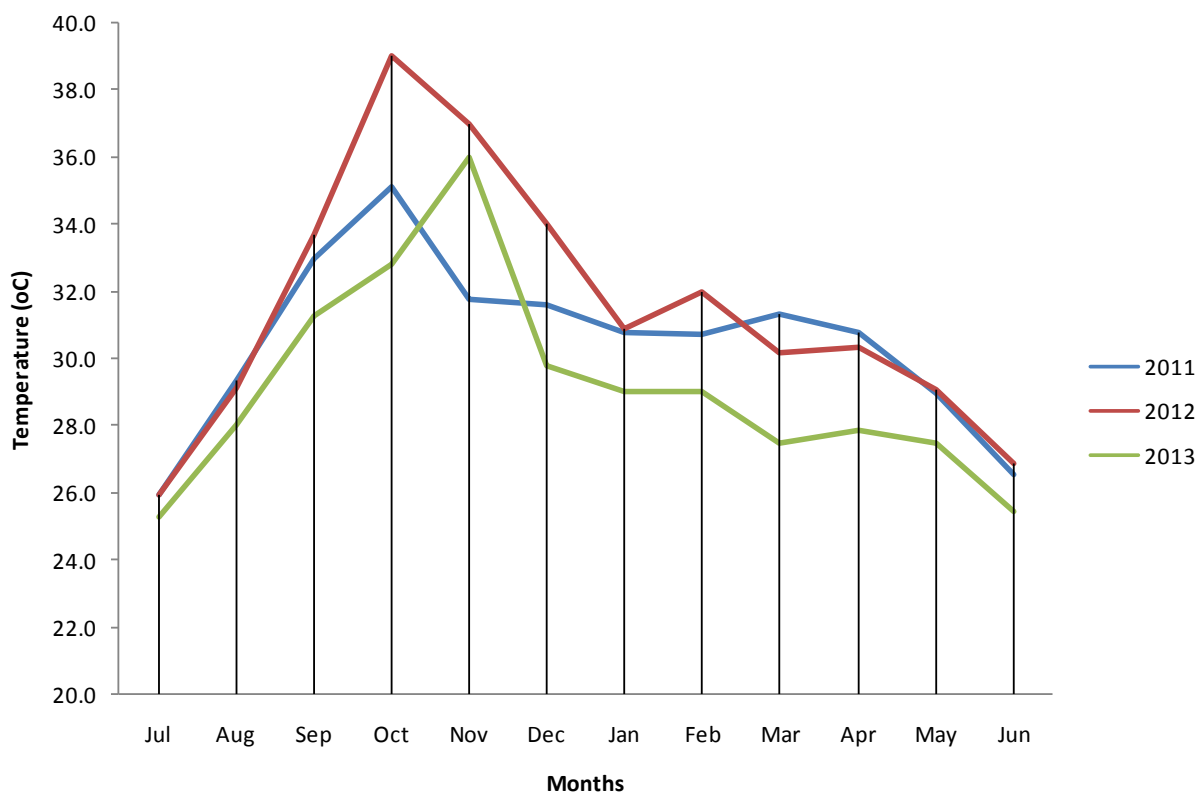


**Figure 4.2:** Average annual temperatures for region I and region II

#### 4.2.2 Weather conditions during the growing season

Temperature data (Figure 4.3) was recorded at regular intervals during the two years using the Hobo U12 of data loggers (Make - U12-001 manufactured by Onset-USA). The monthly average air temperatures at Lusitu ranged between 25 and 39°C from the date of sowing to harvesting (Figure 4.3). High temperatures ( $> 33^{\circ}\text{C}$ ) occurred at six weeks (September-October) after planting and coincided with the time when the crops were at the vegetative to the flowering stages. Water was provided as and when required to ensure it was not limiting.





**Figure 4.3:** Mean temperatures recorded during the cropping seasons over the three years (2011, 2012 and 2013)

#### 4.2.3 Experiment 1: screening of common bean genotypes for heat tolerance

A collection of 120 genotypes was assembled and evaluated under field conditions in Lusitu in 2011 and 2012 as outlined in 3.2.1 in Chapter three and further elaborated in Table 3.1.

The planting layout was similar to that used in Chapter 3 (refer to 3.2.1). The trials were planted in mid-August to synchronise the flowering with the occurrence of high temperatures in the month of October. Supplementary irrigation was provided through flood irrigation when needed. Thirty seeds were sown in single rows 5 m in length, at inter- and intra- row spacing of 75 cm x 15 cm. During the growing season, data were recorded on the following:

- i. **Days to 50% flowering (DAF)** – This was taken as the number of days from 50% seedling emergence to the date when the genotype reached 50% flowering.
- ii. **Days to physiological maturity (DPM)** – This was taken as number of days from 50% seedling emergence to the date when 50% of the plants showed senescence and pods turned brown.
- iii. **Leaf area retention (LAR)** - The leaf area retention was taken as the difference in percentage leaf cover between the leaf area at 50% flowering and leaf area three weeks after 50% flowering.
- iv. **Yield** – Yield was taken as whole plot harvest, shelled bean seeds adjusted to 12.5% moisture content. The grain mass was adjusted to 12.5% moisture content using the following formula:  $Y(M2) = \{(100 - M1)/(100-M2)\} \times Y (M1)$ ; where  $Y(M2)$  = mass of grain at 12.5% moisture content,  $Y (M1)$  = mass of grain at actual moisture content,  $M1$  = actual moisture content and  $M2$  = expected moisture percentage. The grain yield (GY) was determined and expressed as tonnes per hectare ( $t\ ha^{-1}$ ).
- v. **Hundred seed mass (HSW)** – This was taken as the weight of 100 grains counted individually and weighed.

Compound D (Composition N = 10, P= 20 and K=10) fertilizer at the rate of  $200\ kg\ ha^{-1}$  was applied at planting time. Recommended management practices of weeding and pest control were practised during crop growth.

#### 4.2.4 Experiment 2: Genetic study

This study was conducted using 48  $F_2$  populations developed between the eight selected female parents with six male parents in a North Carolina design II mating scheme as described in Chapter 3. The eight female parents were elite and popular genotypes among the farmers as described in Figure 2.8 in chapter 2 of this thesis. The male parents on the other hand were selected from the genotype screened for heat tolerance in an earlier study, and some were provided by CIAT and University of Zambia.

ZM 4143, ZM 3831, ZM 4497, SER 124, SEN 39 and LY 4-4-B were used as male parents in the crosses. Genotypes ZM 4143, ZM 3831 and ZM 4497 were medium seeded and selected from the landraces screened for high temperatures. The three genotypes are small seeded and have dark seed coats. Genotypes SER 124 and SEN 39 were provided by CIAT as heat tolerant genotypes and were all red and small seeded

while LY 4-4-B was developed through mutagenesis by the University of Zambia from Lyambai variety, a released large seeded red speckled bean. The mutant was screened along with other 119 genotypes and was found to be heat tolerant. North Carolina design II was used to develop the  $F_1$  populations. The parents were planted in pots in the screen house and cross-pollinated to give the  $F_1$  seed. The  $F_{1s}$  were grown in pots and self-pollinated to generate the  $F_2$  populations. A total of 48  $F_2$  populations, 14 parental lines and two checks (from CIAT) were planted in an 8 x 8 alpha lattice design with two replications. The seeds were sown at the beginning of August, 2011. Each plot consisted of two rows of 30 seeds per plot planted at a spacing of 75 cm between rows and 25 cm between plants. The trial was managed following normal recommended agronomic practices for beans.

Individual plant measurements were taken for 30 plants in each plot to obtain data on yield, HSW, NSP, DAF, and NPP and were recorded as described in section 4.2.2 of this chapter. In addition, flower abortion was taken as the difference between the average numbers of flowers recorded when the crop reached 50% flowering and the harvested mature pods. Each plant was tagged to ensure the same plants were used to count the number of flowers at 50% flowering and the number of mature pods. The data was analysed as an RCBD as there were no differences in the results after analyzing it as an alpha lattice design. The genetic analysis was done using the line by tester proc ANOVA SAS software.

### 4.3 Results

#### 4.3.1 Experiment 1: Analysis of variance

Results of the analysis of variance (ANOVA) for selected agronomic traits are given in Table 4.2 while the results on the genotype performance for all the 120 genotypes are presented in Appendix 4.1.

**Table 4.2:** Mean squares for yield and selected agronomic traits recorded for 120 genotypes grown in Lusitu, Zambia in 2011 and 2012

Source	df	LAR	DAF	NPP	NSP	PM	Yield	HSW
Year	1	654.70	36.94**	35.39	1 3052**	32.86*	0.399	43.30
Genotype	119	15 0551.50*	44, 286.88*	931931.50**	63.8793**	0.8**	134.5512**	55684.72
Genotype X Year	119	603.80	42.74**	39.66	1.2785	15.09	0.3597	41.75
Error	196	520.00	25.70	33.87	0.8364	12.12	102.7297	69.64

**Note:** LAR = leaf area retention; DAF = days to 50% flowering; PM = physiological maturity; NPP = number of pods per plant; NSP = number of seeds per pod; and HSW = hundred seed weight; \* = significance at  $P \leq 0.05$ ; \*\* = significance at  $P \leq 0.01$

#### **4.3.3 Yield and its correlation to yield components**

The mean square for genotype performance was significant for yield ( $P \leq 0.01$ ) (Table 4.2). There was no significant genotype by year interaction for yield, PM, NSP, NPP, LAR and HSW ( $P \leq 0.001$ ). Hundred seed mass was significant for genotype by year interaction ( $P \leq 0.001$ ). None of the elite market class genotypes in Zambia were ranked in the top 12 high yielding genotypes when exposed to heat stressed conditions. The 12 highest ranked genotypes based on yield comprised mostly landraces and mutants (Table 4.3). ZM 4497 recorded the highest yield ( $0.78 \text{ Mt ha}^{-1}$ ) under high temperature stress. (Table 4.3). The 12 highest and 12 lowest yielding genotypes showed mixed patterns in terms of ranking for PM, NSP, NPP, LAR, and DAF. Yield was correlated with other traits including the yield components and the results of the correlations are presented in Table 4.4. Significant variation for yield components was observed among the genotypes at high temperatures. Fifty nine out of the 120 genotypes screened under high temperatures yielded above the overall mean of  $0.318 \text{ t ha}^{-1}$  (appendix 4.1).

**Table 4.3:** Trait mean performance for the 12 highest and 12 lowest ranked genotypes grown during the 2011 and 2012 season

Genotypes	LAR	R	DAF	R	PM	R	NPP	R	NSP	R	Yield	R
ZM 4497	11.4	79	44.1	84	91.0	26	9.5	52	5.3	66	0.780	1
ZM3200	29.5	1	45.6	103	92.0	41	6.8	110	5.1	55	0.687	2
LY2-3-B	16.8	26	41.0	16	101.3	114	8.6	80	5.7	101	0.631	3
SCCI 2	6.8	111	44.9	93	98.9	107	8.5	83	5.7	102	0.627	4
SZ-4-B-B	3.0	118	44.4	89	101.4	115	10.4	30	4.5	14	0.624	5
SCCI 4	5.8	112	39.4	3	90.3	16	10.2	36	6.3	113	0.603	6
KE 5	12.8	63	41.5	27	94.6	76	9.7	47	4.5	6	0.592	7
ZM 4143	14.4	47	41.9	39	99.5	108	7.8	94	5.1	59	0.570	8
ZM 4512-3	6.9	110	41.4	24	94.0	68	9.4	56	5.7	97	0.563	9
MEX 54	4.9	114	41.4	23	101.2	113	6.0	116	5.1	53	0.543	10
KE 1	12.1	70	42.5	57	93.7	62	7.3	104	5.7	99	0.535	11
KAB-ZA	9.9	97	48.1	114	91.6	37	10.2	37	4.8	31	0.533	12
ZM 4512	21.3	11	37.9	2	93.6	60	11.6	13	5.3	69	0.140	109
SZ32BB1	19.8	16	42.8	63	96.7	99	8.9	70	4.7	26	0.135	110
ZM 3206	17.7	24	39.6	4	91.1	27	11.8	10	5.1	52	0.133	111
ZM 4479	25.6	6	45.0	98	90.3	15	13.3	5	4.6	20	0.121	112
ZM 4512-2	22.6	10	43.3	71	94.3	71	3.1	120	4.5	9	0.092	113
ZM 4298	14.2	49	41.6	28	90.4	20	5.4	119	5.3	74	0.069	114
SCCI 11	27.5	4	39.8	5	97.6	101	10.3	33	5.2	61	0.043	115
SCCI 11	15.6	34	53.9	120	102.4	117	8.9	67	6.0	110	0.041	116
LY-UNZA	14.6	45	47.1	111	95.6	84	8.2	87	5.0	50	0.040	117
SCCI 1	15.3	40	41.6	29	93.3	55	9.1	62	5.3	67	0.040	118
ZM3681	11.4	82	42.9	64	90.3	17	13.1	6	3.3	1	0.035	119
ZM 4478	10.7	91	41.8	32	89.7	11	6.3	113	4.5	7	0.008	120
<b>Mean</b>	<b>13.9</b>		<b>43.3</b>		<b>94.3</b>		<b>9.4</b>		<b>5.3</b>		<b>0.318</b>	
<b>LSD</b>	<b>3.0</b>		<b>1.1</b>		<b>5.3</b>		<b>2.6</b>		<b>0.8</b>		<b>0.130</b>	
<b>CV (%)</b>	<b>4.1</b>		<b>3.7</b>		<b>3.0</b>		<b>1.7</b>		<b>5.7</b>		<b>18.5</b>	

**Note:** LAR = leaf area retention; DAF = days to 50% flowering;; PM = physiological maturity; NPP = number of pods per plant; NSP = number of seeds per pod; R = Ranking

All the correlations between yield and yield components (HSW, NPP and NSP) were significant ( $P \leq 0.05$ ). The correlation coefficient with HSW with yield was significant and negative ( $P \leq 0.05$ ,  $r = -0.648$ ) (Table 4.4). The correlation coefficients ( $r = 0.637$  for DAF;  $r = 0.345$  for NSP) were significant and relatively strong and positive with yield (Table 4.4).

**Table 4.4:** Correlation between yield and yield traits

	LAR	DAF	PM	NPP	NSP	HSW	Yield
<b>LAR</b>	1						
<b>DAF</b>	0.372**	1					
<b>PM</b>	0.318**	0.101***	1				
<b>NPP</b>	-0.277**	-0.265**	-0.173**	1			
<b>NSP</b>	-0.161**	-0.288**	0.063	0.162**	1		
<b>HSW</b>	-0.443**	-0.690*	-0.086	-0.582**	0.309**	1	
<b>Yield</b>	0.289**	0.637**	-0.057	0.189**	0.345**	-0.648**	1

**Note:** LAR = leaf area retention; DAF = days to 50% flowering, PM = physiological maturity; NPP = number of pods per plant; NSP = number of seeds per pod; HSW = hundred seed mass

#### 4.3.4 Physiological maturity (PM)

Highly significant differences were detected for PM ( $P \leq 0.01$ ) (Table 4.2). No significant differences were detected for the year (seasons) and genotype by year interactions. Of the 12 highest yielding genotypes, ZM 4497, ZM 3200, ZM 4512-3, KE 1, KAB ZA and SCCI matured earlier when compared to the mean while others matured above the mean (Table 4.3). The days to physiological maturity for the top 12 highest yielding genotypes ranged between 91.0 and 101.4 days (Table 4.3). Most of the 12 lowest yielding genotypes matured below the mean. The difference between the earliest to mature and the latest was about 21 days.

The mean number of days to physiological maturity was 94.3 and 68 genotypes (56%) of the 120 matured earlier than the mean. Out of the 12 highest yielding genotypes, ZM 3200 (92), SCCI 4 (90.3), ZM 4497 (91), KE 1(93.7), ZM 4512-3 (94), ZM 6602 (93.2), KAB-ZA (91.6) matured earlier than the mean PM while the rest of the high yielding genotypes comprising; MEX 54 (101.2), Ly2-3-B (101.3), SZ4-B-B (101.4), SCCI 2 (98.9), ZM 4143 (99.5), and KE 5 ( 94.6), reached their PM above the mean (Table 4.4).

The genotypes SCCI 11 (102.4), G10909 (95.1), SZ 32BB1 (96.7), Ly-Unza (95.6), ZM4512-2 (94.3), ZM 4512 (93.6) and SCCI 1(93.3) were among the 12 low yielding genotypes and reached their PM later above the mean. ZM 4478 (89.7), ZM 4479 (90.3), ZM 3681 (90.3), ZM 4298 (90.4) and ZM 3206 (91.1) on the other hand though low yielding, matured earlier than the mean PM (Table 4.2).

The correlation between yield and PM was negative and not significant (Table 4.4) Gadra was the earliest to maturity at 87.3 days while KE 2 was the latest to maturity at

108.8 days (Appendix 4.1). The highest yielding genotype, ZM 4497 took 91 days to physiological maturity and was ranked among the early maturing genotypes. The lowest yielding genotype took 93.3 days to physiological maturity.

#### **4.3.5 Number of seeds per pod (NSP)**

Highly significant differences were detected for genotypes and year ( $P \leq 0.01$ ) (Table 4.2). Large differences between numbers of seeds per pod were detected between the seasons. The mean number of seeds per pod was 5.27. Sixty five out of the 120 genotypes representing 54% recorded NSP values greater than the mean.

The results showed a mixed picture on the number of seeds per pod for the 12 highest yielding genotypes (Table 4.3). Out of the 12 high yielding genotypes, the following genotypes recorded low numbers of seeds per pod as presented in parenthesis; KE 5 (4.5), SZ 4-B-B (4.5), KAB-ZA (4.8), ZM 6602 (4.8), MEX 54 (5.1), ZM 3200 (5.1) and ZM 4143 (5.1) (Table 4.4.). SCCI 4 (6.3), SCCI (5.7), LY2-3-B (5.7), KE 1 (5.7), ZM 4512-3 (5.7) and ZM 4497 (5.3) were among the 12 highest yielding genotypes and also recorded high numbers of pods greater than the mean.

The correlation coefficient ( $r = 0.345$ ) between yield and NSP was positive and significant ( $P \leq 0.05$ ). The correlation coefficients between NSP and other traits were significant ( $P \leq 0.05$ ) and positive for NPP ( $r = 0.162$ ) and HSW ( $r = 0.309$ ) and; significant and negative for DAF ( $r = -0.288$ ) and LAR ( $r = -0.161$ ) (Table 4.4)

#### **4.3.6 Number of pods per plant (NPP)**

The main effects of genotype were highly significant ( $P \leq 0.01$ ) for number of pods per plant (NPP) (Table 4.2). The genotype and year were not significantly ( $P > 0.05$ ) different for NPP (Table 4.2). The 12 highest ranked genotypes recorded relatively high numbers of pods per plant. Forty six (46%) of the 120 genotypes screened recorded NPP above the mean of 9.35 (Appendix 4.1). Of the 12 highest ranked genotypes, SZ4-B-B, SCCI 4, KAB-ZA, KE 5, ZM 4497 and ZM 4512-3 recorded high NPP while ZM 6602, LY2-3-B, SCCI 2, ZM 4143, KE 1, ZM 3200 and MEX 54 recorded low NPP (Table 4.4). Among the lowest ranked genotypes, ZM 4479, ZM 3681, ZM 3206, ZM 4512, G 10909 and SCCI 11 recorded NPP values above the mean of 9.35 while SCCI 11, SZ32BB1, LY-UNZA, ZM 4478, ZM 4298 and ZM 4512-2 recorded NPP values lower than the mean.

The correlation between NPP and seed yield was significant and positive ( $r=0.189$ ,  $P\leq 0.05$ ) (Table 4.5). ZM 4497, the highest ranked genotype recorded 9.5 pods per plant which was not different from the mean (9.35) for the 120 genotypes (Table 4.4). The lowest yielding genotype, ZM 4478, recorded 9.1 pods per plant and this was also not different from the mean (9.35) for the 120 genotypes screen (Table 4.4). ZM 4512-2 was amongst the lowest (3.1) in terms of number of pods per plant while the highest was ZM 06 with 20.3 pods per plant.

#### **4.3.7 Leaf area retention (LAR)**

There were significant differences between genotypes for LAR ( $P\leq 0.05$ ) (Table 4.2). The interaction between genotype and year was not significant. The 12 highest yielding genotypes recorded LAR values between 3 and 29.5% while the lowest yielding genotypes recorded between 10.5 and 27.5% (Table 4.3). The mean LAR for the 120 genotypes was 13.9%. ZM 4497 retained fewer leaves (11.4%) after the three weeks stress period and was quite comparable with lowest yielding genotype, ZM 4478 with 10.7%. Fifty one genotypes (representing 42% of the 120) recorded LAR values greater than the mean.

Out of the 12 highest yielding genotypes, ZM 3200 (29.5%), ZM 6602 (23.2%), LY2-3-B (16.8%) and ZM 4143 (14.4%) recorded high LAR values greater than the trial mean while SZ-4-B-B (3%), MEX 54 (4.2%), SCCI 4 (5.8%), SCCI 2 (6.8%), ZM 4512-3 (6.9%), KAB-ZA (9.9%), ZM 4497 (11.4%), KE1 (12.1%) and KE 5 (12.8) recorded lower LAR than the mean. The highest ranked 12 genotypes comprised those that recorded high LAR values {SCCI 11 (27.5%), ZM 4479, ZM 4512-2 (22.6%), ZM 4512 (21.3%), SZ32BB1 (19.8%), ZM 3206 (17.7%), SCCI 11 (15.6%), SCCI 1 (15.3%), LYA-UNZA (14.6%), ZM 4298 (14.2%)}, and those that recorded low LAR values lower than the mean { ZM 4478 (10.7%), G10909 (10.7%) and ZM 3681 (11.4%)}, (Table 4.4). The highest yielding genotype ZM 4497 recorded LAR retention level of 11.4% while the lowest yielding genotype recorded 15.3% for LAR.

The correlations between LAR with seed yield ( $r=0.289$ ) and PM ( $r=0.318$ ) were positive and significant while the correlations between LAR with NSP ( $r=-0.161$ ) and NPP ( $r=-0.277$ ) were negative and significant ( $P\leq 0.05$ ).



#### **4.3.8 Days to 50% flowering (DAF)**

Mean squares for the number of days to 50% flowering were significantly different for genotypes, year and for their interaction (Table 4.2). The 12 genotypes that flowered early ranged between 36.6 to 40.8 days after 50% field emergence while the 12 genotypes that flowered latest ranged between 46.0 and 48.8 days from 50% field emergence (Appendix 4.1).

Out of the 12 lowest yielding genotypes, ZM 4512(36.6), ZM 3206 (39.6), SCCI 11 (39.8), ZM 4298 (41.6), SCCI (41.6), ZM 4478 (41.8), SZ32BB1 (42.8), ZM 3681(42.9) and ZM 4512-2 (43.3) recorded DAF lower than the mean while SCCI 11 (53.9), LY-UNZA (47.1), G10909 (45.3) and ZM 4479 (45) recorded DAF higher than the mean. Of the 12 highest yielding, SCCI 4 (39.4), LY2-3-B (41), MEX 54 (41.4), ZM 4512-3 (41.4), KE 5 (41.5) and ZM 4143 (41.9) recorded low number of DAF while KAB-ZA (48.1), ZM 6602 (47.6), ZM 3200 (45.6), SCCI 2 (44.9), SZ4BB1 (44.4) and ZM 4497 (44.1) recorded high numbers of DAF. The earliest genotype to reach 50% flowering was ZM 4512 and flowered at 36.6 days while the latest to flower was SCCI 9 which flowered at 48.5 days (Table 4.4). The mean flowering days for the 120 genotypes was 43.3 days.

#### **4.3.9 Hundred seed mass**

The mean squares for the year, genotype and their interaction were not significant for 100 seed mass (HSW) ( $P \leq 0.05$ ). The correlation between HSW and yield and with PM was also not significant. However, significant ( $P \leq 0.05$ ) and negative correlation coefficients between HSW with LAR ( $r = -0.443$ ), NPP ( $r = -0.582$ ) and DAF ( $r = -0.690$ ) were detected.

### **4.4 Experiment 2: Genetic study**

#### **4.4.1 Analysis of variance**

The results of the analysis of variance for GCA effects and SCA effects are presented in Table 4.5. The analysis of variance showed significant GCA effects for females for yield, NSP, and NPP ( $P \leq 0.01$ ) and highly significant for flower abortion ( $P \leq 0.001$ ). The GCA effects for male were significant ( $P \leq 0.01$ ) for NSP, yield, and flower abortion and highly significant for NPP ( $P \leq 0.001$ ). Specific combining ability effects were highly significant effects for yield ( $P \leq 0.001$ ), and flower abortion, and significant for NSP ( $P \leq 0.01$ ), and

were not significant for NPP ( $P \leq 0.01$ ). The GCA mean squares were predominant over the SCA mean squares for yield, NPP and flower abortion (Table 4.5). However, the opposite was observed for NSP. The  $GCA_m$  mean square was higher than  $GCA_f$  and SCA effects.

**Table 4.5:** Mean squares for genetic effects for common bean in the  $F_2$  populations

Source	DF	Yield	NSP	NPP	Flower abortion
Rep	1	113161.46	2769.57	189.10	360.55
$GCA_F$	7	212907.80**	1403.30**	305.24**	526.04***
$GCA_M$	5	146821.62**	2588.84**	199.32***	790.65**
$SCA_{F \times M}$	48	102523.68***	4249.35**	144.58	491.07***
Error	43	81322.70	921.74	161.85	393.71

**Note:** PM = physiological maturity; NSP = number of seeds per pod; NPP = number of pods per plant; LAR = leaf area retention; D50F = days to 50% flowering; \*\*=significant at  $P \leq 0.01$ ; \*\*\*=significant at  $P \leq 0.001$

#### 4.4.3 GCA and SCA effects for yield and yield components

The GCA effects for both female and male parents for yield, number of seeds per pod, number of pods per plant and flower abortion is presented in Table 4.6. The female lines ZM 05, Chambeshi, Pan 148, and SCCI 2 recorded positive GCA effects for yield while Kabulngeti, Kalungu, Kapisha and Lyambai showed negative GCA effects for yield. All the female lines except Chambeshi and Lyambai which had negative GCA effects for NSP, showed positive GCA effects for number of seeds per pod. The genotypes Pan 148 and Kapisha had positive GCA effects for number of pods per plant. All the male lines recorded positive GCA effects for yield, while the GCA effects for number of pods per plant and number of seeds per pod showed a mixed outlook with both negative and positive GCA effects recorded for some parents. All the female parents except Kabulngeti and Kalungu recorded positive GCA effects for flower abortion (Table 4.5). Male parents ZM 4143 and SER 124 recorded negative GCA effects for flower abortion while the remaining male parents recorded positive GCA effects for this trait.

**Table 4.6:** General combining ability effects for yield and agronomic traits

<b>Female lines</b>	<b>Flower abortion</b>	<b>NPP</b>	<b>NSP</b>	<b>Yield</b>
ZM 05	3.5	-9.01	0.03	201.6
Chambeshi	9.2	-2.29	-0.03	38.1
Pan 148	7.6	17.71	0.076	163.03
Kabulangeti	-5.1	-4.88	1.18	-182.1
Kalungu	-2.1	-1.54	1.30	-180.4
Lyambai	4.7	-9.01	-1.75	-101.71
Kapisha	6.1	7.514	0.90	-301.88
SCCI 2	10.2	-8.29	2.02	240.55
<b>Male lines</b>				
ZM 4143	-6.1	5.29	0.29	1.23
ZM 4497	12.9	10.04	-0.12	314.88
SER 124	-7.4	12.38	0.31	357.88
Ly4-4-4-B	6.5	-6.71	-0.11	228.25
ZM 3831 )	4.7	-10.13	-0.47	171.25
SEN 39	1,8	6.38	0.37	265.06

Note: NSP = NPP = Number of pods per plant; Number of seeds per pod

The male genotypes ZM 4497 and SER124 recorded the highest positive GCA effects for yield and number of pods per plant, while ZM 4143 had the lowest positive GCA effects for yield (Table 4.7). ZM 05 and SCCI 2 recorded the highest positive GCA estimates among the female lines for yield while Kapisha recorded the lowest negative GCA value. SEN 39 recorded the highest GCA value for NSP among the male lines while SCCI 2 recorded the highest GCA value among the female genotypes. The lowest GCA values for NSP were recorded for ZM 3831 amongst the male parents and Lyambai amongst the female genotypes. SER 124 and ZM 4143 recorded the lowest GCA values for flower abortion amongst the male genotypes while Kabulangeti and Kalungu recorded the lowest amongst the female genotypes. ZM 4497 recorded the highest GCA value for flower abortion among the male lines while SCCI 2 recorded the highest GCA value for flower abortion among the female lines.

The SCA effects were significant for yield ( $P \leq 0.01$ ), NSP ( $P \leq 0.05$ ) and flower abortion ( $P \leq 0.01$ ). The SCA effects though significant were inferior to GCA effects. However, even though the SCA effects were significant for the three traits, they are not critical as they cannot be fixed in common bean which is self-pollinating.

## **4.5 Discussion**

### **4.5.1 Experiment 1 – Screening for heat stress**

The mean monthly temperature values recorded were high during the months of September, October and November in both seasons. The maximum temperature that occurred between vegetative and flowering stages was 33°C in September, 38°C in October, and 37°C in November, which exceeded the critical upper limit for beans. The average temperatures required for normal common bean growth is 20 - 25°C (Rainey and Griffiths, 2005b; Wantanbe, 1953), an indication that the site was heat stressed for beans.

The absence of the interactions between season and genotype for yield, PM, NSP, LAR and HSW suggests that the order for ranking of the genotypes for these traits was the same in both years. This may further suggests that the genotype performance can be determined over one season in Lusitu. However, it is important to note that the intensity of heat stress varies greatly and this assumption would entirely depend on the stress levels and the durations. The results showed that it was possible to distinguish genotypes between those that were tolerant to high temperature stress and those that were not on the basis of yield and the yield components such as NSP and NPP. This finding concurs with that reported by Fernandez (1992) and Kristin et al. (1997) who alluded to the fact that yield and its components were good measures of heat and drought tolerance.

Yield has always been used as a key trait and very often ranked the highest in variety selection by the farmers (PRA own work, 2013). From the results of this research, the correlation coefficients between yield and its components were significant. Hundred seed mass, number of pods per plant, NSP and LAR were positively correlated to yield. However, even though the correlations indicated these positive associations the genotypes showed a mixed pattern. For example, some genotypes such as KE 5, SZ 4-B-B, KAB-ZA, ZM 6642, MEX 54, ZM 3200 and ZM 4143 were high yielding but recorded low NSP. Some of genotypes could be having compensating effects for high yield through having many pods per plant and a heavier seed. This is shown by the positive correlation between NSP and NPP. This group of genotypes could be selected for tolerance to drought stress on the basis of NPP. Some genotypes however recorded high yield and high NSP. These genotypes could be compensating for high yields on the

basis of having many seeds in a pod. This is generally accepted and agrees with reports by many authors.

Some high yielding genotypes such as ZM 4497, KE 1, ZM 4512-3, ZM 6602 and KAB-ZA were found to reach PM early in less than the mean of 94.29 days while some reached PM later than the mean. This result shows the wide genetic variation from which selections could be made. For instance, selection for high yielding genotypes and early maturity would be ideal for developing genotypes that may escape high temperatures. Some of the genotypes that reached 50% flowering early reached their PM late. This is an indication that the genotypes had prolonged seed set and maturity periods. This could imply that the genotypes were slow at grain filling.

The correlation between yield and NSP ( $r=0.345^{**}$ ) was positive and significant. Some high yielding genotypes such as ZM 6642, MEX 54, ZM 3200 and ZM 4143 recorded fewer pods. This result could imply that this group of genotypes compensated on their yield by having heavier seeds. The high yielding genotypes with more pods such as SCCI 4, ZM 4512-3 and ZM 4497 also recorded more NPP. This could imply that this group of genotypes achieved their yield by having more NSP and more NPP. Therefore high NSP contributed to high yield.

Knowledge of the relationship between yield and its yield components under high temperature stress is important in plant breeding. Therefore the simple correlations between these traits and yield would contribute to great understanding on the selection for high temperature stress. The results of this study have shown that there were positive correlations between NSP and NPP with yield. However, the relationship between NPP and yield was shown to be weaker than what has been reported by other authors (Duarte and Adams, 1972; Westerman and Croathers, 1977; Prakash and Ram, 1981; Yorgancilar et al., 2003). This variation in the genotypes provides more selection opportunities in breeding for heat tolerance. Ideally, based on the positive correlation between yield and NSP, it would be advantageous to select genotypes that are high yielding and have high NSP. The poor yielding cultivars in this study were late maturing and had low number of pods per plant. These results are similar to those of Masaya and White (1991) who reported excessive flower abortion due to high temperatures. It has been well and widely accepted that bean plants are generally sensitive to high

temperatures which may lead to high flower drop (Rainey and Griffiths, 2005b). The general indication that numbers of days to physiological maturity, numbers of pods per plant and number of seeds per pod affect yield as observed by the correlation coefficients, is expected and is similar to the results reported by several other researchers (Porch and Jahn, 2001; Prasad et al., 2002).

The genotypes identified as high yielding in Lusitu offer a great opportunity for developing heat tolerant genotypes suitable for hot, low altitude regions in Zambia and other parts of the world with similar weather conditions. SCCI 4, KAB-ZA, KE 5 and ZM 4512-3, which were among the high yielding genotypes had high NPP, low LAR, few DAF and few days to maturity. These traits could be used therefore in combination with the selection high yielding genotypes but early maturing. The individual traits could also be used singularly to select high yielding genotypes. These results are however not conclusive as the heat stress was not quantified and there was no control experiment since heat is difficult to control in the field. The root systems and canopy temperatures were also not studied and could have contributed to the differences in performances expressed by the genotypes.

The extreme ranges between the highest yielding and the lowest yielding genotypes shows that there is adequate variation in the germplasm for heat tolerance and good genetic progress can be made towards breeding for heat tolerance.

#### **4.5.2 Experiment 2 - Genetic study**

The analysis of variance results indicated highly significant ( $P \leq 0.01$ ) GCA effects for yield, NSP, NPP and flower abortion (Table 4.5) and this is supported by other studies (Rainey and Griffiths, 2005c). These findings are a clear indication that additive genetic effects were important for yield, NSP and NPP. The SCA effects were significant for yield, NSP and flower abortion at  $P \leq 0.01$  implying the importance of non-additive genetic effects for the expression of the characters influencing heat tolerance (Table 4.5). The positive and highly significant GCA effects for yield, NSP, NPP and negative GCA effects for flower abortion are a good indicator that good progress can be made in breeding for heat tolerance. However, very few genotypes expressed desirable negative GCA effects for flower abortion. Rainey and Griffiths (2005b) also found significant GCA effects for NSP and NPP.

The estimates of GCA effects for yield, NSP, NPP and flower abortion are presented in Table 4.6. The female parental lines ZM 05, Chambeshi, Pan 148 and SCCI 2 with positive GCA effects for yield indicate that they are good combiners and yielded above the mean. The male parents all recorded positive GCA effects. These seemingly have favorable alleles for yield with additive effects. This may imply therefore that these female parents when crossed with male parents with positive GCA effects would be good for the generation of segregating populations with high mean yield from which better combinations can be selected.

On the contrary, the positive GCA effects for flower abortion for most female lines except for Kabulangeti and Kalungu implies that, despite the fact that they could be good parents for yield, they are prone to negative effects of heat stress. This implies that Kalungu and Kabulangeti would be the best parents to select for low flower abortion. The male lines ZM 4143 and SER 124 with negative GCA effects for flower abortion and positive GCA effects for yield would be the best suited to develop segregating populations from which selection could be done for heat stress tolerance. Among them is a line used as a check from CIAT, SER 124. ZM 05, Chambeshi, Pan 148 and SCCI 2 with high and positive GCA effects would be appropriate to cross with male parents with negative GCA effects for flower abortion.

According to Griffing (1956), parents which present the highest GCA estimates should generate a population with a higher mean yield. However, in the process of choosing parents, the highest GCA for yield alone is not sufficient for this choice, since, if the parents are susceptible to flower abortion, and genetically similar, the population may have a reduced chance to select improved lines. From the results of this study therefore, the genotypes with relatively good level of flower abortion (low) would be more suitable for developing segregating populations. However, realising that most female parents were quite susceptible to flower abortion, but high yielding, crosses between the female parental lines with high GCA effects and male parents with negative GCA effects for flower abortion would be recommended for developing segregating populations from which high yielding heat tolerant genotypes could be selected.

ZM 4497 had the highest positive GCA effect for yield. Its combination with other lines gave high and positive SCA values. This could imply that ZM 4497 was a good combiner. The parental lines that recorded high and positive GCA effects and produced crosses with positive SCA effects such as ZM 4497 and ZM 05 may indicate that both additive and non-additive gene effects were important. However, it can be concluded that the GCA effects and the SCA effects for such parents and crosses had the same effect towards one direction to increase yield. Among the high yielding genotypes, Ly4-4-B had high and positive GCA values but gave negative SCA values implying that non-additive gene action was important when in combination with other parental lines. These F<sub>2</sub> populations may therefore not give meaningful segregants for further selection. It may also imply that the two parents involved in such a cross were very closely related and not meaningful to cross.

#### **4.6 Conclusion**

On the basis of results from this study it was concluded that:

- Out of the 120 genotypes screened for heat tolerance, about 5-10% yielded above the trial mean indicating the genotypes could be possessing the genes for tolerance to heat stress.
- Among parental genotypes used, female parents with positive GCA effects for yield ZM 05, Chambeshi, Pan 148 and SCCI 2 would be appropriate for use in combination with male parental lines ZM 4143 and SER 124 with negative GCA effects for flower abortion to generate segregating populations from which heat tolerant genotypes could be derived. ZM 4143 recorded high SCA values in combination with some female parents implying that they are good combiners.
- Genotypes ZM 4143, ZM 4497, SCCI 4, KE 1, and ZM 07, were the most heat tolerant and can therefore be used as sources of resistance to heat tolerance in breeding programmes. These comprise two landraces (ZM 4143, ZM 4497), and three cultivars (SCCI 4, KE 1 and ZM 07) that were still undergoing official variety release trials.



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**Appendix 4.1: Genotype performance over the two year under high (>33°C) temperatures**

Genotypes	Yield	R	PM	R	NSP	R	NPP	R	LAR	R	D50E	R	D50F	R	Mean R
ZM 4497	0.780	1	91.0	26	5.3	66	9.5	52	11.4	79	9.5	83	44.1	84	56
ZM3200	0.687	2	92.0	41	5.1	55	6.8	110	29.5	1	10.3	114	45.6	103	61
LY2-3-B	0.631	3	101.3	114	5.7	101	8.6	80	16.8	26	8.7	32	41.0	16	53
SCCI 2	0.627	4	98.9	107	5.7	102	8.5	83	6.8	111	9.8	100	44.9	93	86
SZ-4-B-B	0.624	5	101.4	115	4.5	14	10.4	30	3.0	118	8.6	24	44.4	89	56
SCCI 4	0.603	6	90.3	16	6.3	113	10.2	36	5.8	112	8.6	25	39.4	3	44
KE 5	0.592	7	94.6	76	4.5	6	9.7	47	12.8	63	8.6	23	41.5	27	36
ZM 4143	0.570	8	99.5	108	5.1	59	7.8	94	14.4	47	10.2	113	41.9	39	67
ZM 4512-3	0.563	9	94.0	68	5.7	97	9.4	56	6.9	110	10.6	118	41.4	24	69
MEX 54	0.543	10	101.2	113	5.1	53	6.0	116	4.9	114	10.0	111	41.4	23	77
KE 1	0.535	11	93.7	62	5.7	99	7.3	104	12.1	70	8.6	22	42.5	57	61
KAB-ZA	0.533	12	91.6	37	4.8	31	10.2	37	9.9	97	9.0	54	48.1	114	55
ZM 4830	0.519	13	94.7	79	5.4	81	8.9	65	13.1	59	9.4	80	41.1	19	57
ZM 4144	0.506	14	95.9	87	5.7	98	8.1	88	11.0	86	9.5	96	43.7	77	78
ZM 4296	0.495	15	91.2	29	6.0	109	10.1	38	16.7	27	9.0	59	42.0	42	46
ZM 4520	0.492	16	90.2	14	5.6	92	11.8	11	11.4	80	9.5	82	46.2	107	57
SZ31BB1	0.491	17	94.4	73	3.7	2	12.4	8	5.8	113	8.1	4	43.9	82	43
KABA-ZA	0.490	18	91.5	33	4.5	7	8.9	69	13.9	51	8.9	47	40.3	8	33
SCCI 7	0.490	19	100.9	112	4.6	17	11.0	22	15.6	35	8.7	27	51.7	118	50
ZM 07	0.483	20	91.7	38	6.2	112	9.4	54	12.0	73	8.9	43	43.1	66	58
ZM 4303	0.466	21	94.9	80	5.5	91	5.5	118	7.5	107	10.3	116	46.3	108	92
SCCI 8	0.459	22	100.6	111	5.1	58	9.6	51	7.5	106	9.3	74	36.6	1	60
ZM 6713	0.447	23	95.7	86	6.4	116	8.3	86	3.9	116	8.7	30	41.9	39	71
ZM 4489	0.443	24	90.5	22	5.5	88	10.3	34	15.7	32	8.5	15	39.9	6	32
ZM 3730	0.437	25	94.6	76	4.6	16	9.2	59	24.1	7	9.8	101	42.1	44	47
ZM 4488	0.433	26	91.4	32	5.8	103	11.3	18	27.1	5	8.6	26	42.0	43	36
ZM 3831	0.421	27	98.3	104	5.3	76	9.9	43	11.3	84	8.7	29	42.5	53	59
ZM 3788	0.418	28	91.3	31	5.8	105	11.6	15	13.6	56	9.4	75	42.4	51	52
ZM 04	0.416	29	90.4	19	4.9	42	10.0	41	10.2	94	10.0	103	41.9	35	52
SZ33BB2	0.414	30	90.7	25	4.8	30	8.9	67	12.8	62	9.5	87	43.7	78	54
ZM 4833	0.413	31	96.5	96	4.9	38	8.7	74	10.7	89	9.0	60	46.0	105	70
LY2-8-B	0.408	32	96.5	97	5.8	104	9.4	53	12.3	67	8.5	19	41.7	31	58
ZM 4831	0.404	33	91.2	30	5.5	89	8.6	77	9.4	101	9.0	56	42.5	53	63
LY4-4-B	0.397	34	96.3	93	4.6	18	7.4	103	14.9	43	8.7	34	41.9	36	52
SCCI 13	0.386	35	100.0	110	4.4	5	8.1	90	14.6	46	9.7	98	44.7	91	68
LY1-2-B	0.385	36	92.2	42	5.4	83	6.9	109	10.9	87	9.4	77	40.6	10	63
ZM 3636	0.385	37	92.3	45	4.9	36	8.8	71	15.5	36	9.4	78	42.6	61	52
ZM 3688	0.384	38	92.4	47	5.1	54	8.7	73	15.8	31	9.0	51	48.6	116	59
SZ7-4-B-B	0.381	39	0.0	1	5.1	55	11.5	16	20.6	14	10.3	115	43.9	80	46
ZM 5128	0.377	40	94.2	69	5.6	96	6.0	115	11.8	74	9.5	87	42.5	53	76
ZM 02	0.376	41	88.7	5	5.4	78	9.2	60	10.0	96	10.0	106	40.5	9	56
ZM 3793	0.367	42	89.5	7	5.6	95	6.2	114	12.9	61	9.3	72	40.7	11	57
ZM 4840	0.366	43	94.3	70	6.4	114	9.8	46	8.9	105	8.5	15	40.9	14	58
KE 3	0.355	44	0.0	1	6.4	117	7.2	106	19.1	19	8.4	9	45.9	104	57
ZM 4829	0.354	45	93.4	57	5.3	72	9.4	54	9.6	100	8.9	49	44.1	85	66
ZM 4289	0.350	46	90.6	23	7.2	119	7.5	99	11.5	78	9.4	76	42.1	44	69
ZM 4516	0.349	47	93.9	66	5.5	86	7.2	105	11.6	76	8.7	31	45.0	98	73
ZM 4490	0.342	48	93.4	59	4.7	25	8.1	88	12.5	65	9.5	92	43.5	72	64
KE 2	0.341	49	108.8	120	5.0	45	10.1	39	19.0	20	9.0	50	52.0	119	63
ZM 4482	0.340	50	96.3	91	5.1	60	9.8	44	7.1	109	9.5	95	43.5	74	75
ZM 03	0.340	51	92.9	52	4.5	11	7.5	99	10.9	87	8.6	21	43.6	75	57
LYA-ZA	0.339	52	92.7	51	5.0	46	9.3	57	9.8	98	9.0	61	43.2	69	62
ZM 6612	0.334	53	94.4	72	4.7	23	12.1	9	15.7	32	9.2	68	43.0	65	46
SCCI 6	0.332	54	91.8	39	4.5	14	8.6	77	3.3	117	8.7	35	41.9	36	53
SCCI-5	0.331	55	93.8	64	4.7	26	8.0	91	28.0	2	8.9	48	40.8	12	43
ZM 3696	0.330	56	93.8	65	5.3	73	9.7	49	13.7	54	9.5	85	44.7	92	68
LY1-7-B	0.322	57	93.4	58	5.4	82	10.8	24	7.4	108	8.9	45	44.1	86	66
ZM 4836	0.319	58	92.4	46	4.8	29	7.6	97	11.4	81	8.9	41	42.6	60	59
KE 4	0.319	59	93.8	63	4.1	3	8.8	72	10.1	95	8.9	42	45.1	101	62
ZM 6602	0.312	60	93.2	54	4.8	32	8.9	66	23.2	9	10.4	117	47.6	112	64
ZM 3202	0.311	61	96.1	90	4.6	20	11.3	17	11.3	83	8.1	6	42.5	56	48
LY2-7-B	0.303	62	95.9	87	5.0	44	10.5	28	21.2	12	9.1	62	44.9	97	56
ZM 6604	0.303	63	92.6	49	5.3	69	10.5	29	15.2	41	9.8	102	41.3	21	53
ZM 3694	0.301	64	102.6	118	6.0	108	9.7	48	11.6	76	9.0	52	45.0	100	81
ZM 6603	0.301	65	94.6	75	4.9	33	9.7	50	19.8	17	9.5	91	42.3	49	54

SCCI 9	0.298	66	101.8	116	5.7	99	10.4	31	11.0	85	9.0	56	48.5	115	81
ZM 4514	0.297	67	98.1	102	5.3	69	11.1	21	14.9	44	8.8	38	40.1	7	50
ZM 4302	0.295	68	94.6	74	5.4	79	9.1	63	13.2	57	9.0	58	44.9	96	71
ZM 3624	0.287	69	99.8	109	5.6	92	8.6	76	17.2	25	8.5	13	43.5	72	65
SCCI 5	0.281	70	95.2	82	4.7	22	9.3	58	13.2	58	10.0	109	41.1	17	59
ZM 3203	0.277	71	96.4	95	5.2	65	8.6	79	9.3	103	10.0	104	41.5	25	77
ZM 4483	0.276	72	91.8	39	5.5	85	5.8	117	12.0	71	9.5	87	46.5	109	83
GADRA	0.273	73	87.3	4	5.0	49	14.4	4	4.2	115	9.0	52	42.6	58	51
SCCI 3	0.270	74	90.1	13	5.4	80	9.9	42	16.3	29	9.0	55	40.8	13	44
SCCI/LYA	0.269	75	95.6	85	4.9	40	9.2	61	15.4	39	8.5	10	43.1	66	54
ZM 3831-4	0.269	76	89.6	9	6.7	118	8.4	85	10.3	93	9.1	66	43.9	81	75
ZM 4491	0.265	77	98.4	106	4.9	35	12.7	7	-0.8	120	9.6	97	40.9	14	65
CAR	0.262	78	93.3	56	5.5	90	10.5	27	12.0	72	8.9	44	47.7	113	69
ZM 4496	0.262	79	91.5	34	5.9	106	16.7	2	9.3	102	9.3	70	42.3	50	63
SZ33BB1	0.260	80	0.0	1	5.3	68	10.2	35	1.7	119	7.7	1	44.9	94	57
ZM 3200	0.259	81	97.5	100	4.9	37	7.7	95	16.0	30	10.0	107	44.6	90	77
ZM 3677	0.259	82	93.1	53	4.9	34	8.0	92	15.5	37	8.5	18	41.8	32	50
SCCI 12	0.249	83	96.3	91	5.5	87	8.5	84	9.6	99	8.5	15	41.5	26	69
ZM 3681-2	0.242	84	98.1	103	5.0	47	8.7	75	19.6	18	9.5	84	42.7	62	68
CHAM-ZA	0.239	85	90.6	24	4.5	10	10.8	25	13.1	60	9.5	87	41.9	36	47
SZ3	0.236	86	92.2	44	5.0	43	6.7	112	14.0	50	8.8	37	43.8	79	64
ZM 3683	0.236	87	94.0	67	5.3	74	10.0	40	12.4	66	8.5	14	43.7	76	61
ZM 05	0.235	88	92.7	50	5.4	84	6.8	110	12.2	69	9.5	81	46.7	110	85
ZM 5136	0.232	89	92.2	42	5.2	62	15.5	3	10.4	92	8.8	40	42.1	44	53
KAL-ZA	0.230	90	89.6	10	5.1	51	9.8	45	9.2	104	10.9	119	44.2	87	72
ZM 4508	0.227	91	91.5	34	5.2	63	10.4	32	20.3	15	9.3	73	41.1	18	47
ZM 5127	0.225	92	94.7	78	5.2	64	10.6	26	14.2	48	9.1	65	42.5	52	61
ZM 4512-4	0.221	93	96.3	94	4.5	13	7.7	96	20.7	13	10.0	108	41.2	20	62
ZM 6601	0.220	94	90.5	21	4.9	41	8.5	82	13.7	52	9.7	99	44.9	94	69
ZM 4524	0.220	95	89.4	6	6.4	114	7.6	98	18.0	23	9.1	63	41.9	41	63
ZM 4305	0.216	96	91.6	36	4.6	19	7.9	93	23.3	8	8.7	27	44.0	83	52
ZM 4525	0.215	97	91.1	28	4.9	39	9.1	64	12.7	64	8.8	36	42.1	44	53
LUK-ZA	0.213	98	96.1	89	13.8	120	11.3	19	27.7	3	8.2	7	42.2	48	55
ZM 4502	0.204	99	89.6	8	4.7	28	6.9	108	12.2	68	10.0	105	41.3	22	63
SZ9-B-B-B2	0.186	100	98.3	104	5.4	77	7.5	101	18.1	22	8.2	8	43.2	70	69
ZM 4294	0.180	101	95.4	83	5.1	57	11.7	12	13.7	54	9.1	67	44.3	88	66
SCCI 10	0.180	102	107.6	119	5.0	47	11.1	20	18.5	21	9.2	69	46.2	106	69
LY2-2-B	0.178	103	93.6	61	5.9	107	8.6	80	15.5	37	8.5	20	43.1	66	68
ZM 06	0.177	104	92.6	48	4.2	4	20.3	1	11.8	75	8.5	10	41.8	32	39
ZM 3749	0.174	105	89.7	11	4.5	11	7.5	101	13.7	53	9.5	86	41.6	30	57
ZM 3838	0.157	106	90.3	17	4.7	24	11.6	14	16.3	28	10.1	112	42.6	58	51
LWA-ZA	0.148	107	96.6	98	6.0	111	7.2	107	15.2	41	8.8	39	49.3	117	89
G10909	0.144	108	95.1	81	5.6	94	10.8	23	10.7	90	9.5	93	45.3	102	84
ZM 4512	0.140	109	93.6	60	5.3	69	11.6	13	21.3	11	8.0	3	37.9	2	38
SZ32BB1	0.135	110	96.7	99	4.7	26	8.9	70	19.8	16	8.9	46	42.8	63	61
ZM 3206	0.133	111	91.1	27	5.1	52	11.8	10	17.7	24	8.5	10	39.6	4	34
ZM 4479	0.121	112	90.3	15	4.6	20	13.3	5	25.6	6	8.7	32	45.0	98	41
ZM 4512-2	0.092	113	94.3	71	4.5	9	3.1	120	22.6	10	8.1	5	43.3	71	57
ZM 4298	0.069	114	90.4	20	5.3	74	5.4	119	14.2	49	9.3	71	41.6	28	68
SCCI 11	0.043	115	97.6	101	5.2	61	10.3	33	27.5	4	10.9	120	39.8	5	63
SCCI 11	0.041	116	102.4	117	6.0	110	8.9	67	15.6	34	9.1	63	53.9	120	90
LY-UNZA	0.040	117	95.6	84	5.0	50	8.2	87	14.6	45	9.4	79	47.1	111	82
SCCI 1	0.040	118	93.3	55	5.3	67	9.1	62	15.3	40	10.0	109	41.6	29	69
ZM3681	0.035	119	90.3	17	3.3	1	13.1	6	11.4	82	8.0	2	42.9	64	42
ZM 4478	0.008	120	89.7	11	4.5	7	6.3	113	10.7	91	9.5	93	41.8	32	67
Mean	0.318		94.29		5.27		9.35		13.88		9.1394		43.30		
LSD	0.130		5.32		0.76		2.6		3.0		0.67		1.1		
CV	1.3		3		5.7		1.7		4.1		2.6		3.7		

Note: PM = physiological maturity; NSP = number of seeds per pod; NPP = number of pods per plant; LAR = leaf area retention; D50E=days to 50% flowering; D50F = days to 50% flowering; R = Ranking

## CHAPTER FIVE

### **Genetic analysis of common bean (*Phaseolus vulgaris* L.) for yield and yield components under managed drought stress conditions**

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#### **Abstract**

Many of the world's common bean (*Phaseolus vulgaris* L.) growing regions are prone to either intermittent or terminal drought stress, making drought the primary cause of yield loss under farmers' field conditions. The aim of the study was to assess the inheritance of yield and yield related traits under moisture stress conditions among Zambian grown common bean genotypes. Sixty four (64) genotypes comprising of 14 parental lines, two checks and 48 F<sub>2</sub> populations were grown in an 8 x 8 alpha-lattice design with two replications at two sites, Nanga and Mount Makulu under managed drought conditions during 2013 in Zambia. Significant differences were recorded among the genotypes for yield and number of seeds per pod. General combining ability effects (GCA) and specific combining ability (SCA) effects were significant for the two traits under managed drought stress conditions implying that both additive and non-additive gene effects were important in their inheritance. ZM 4497 and Ly4-4-4-B were found to be the most drought tolerant male parents with positive GCA effects and their F<sub>2</sub> combinations were in the top 10 highest yielding F<sub>2</sub> populations for SCA effects for yield. The heritability estimate for yield was 60% which implied that progress can be made during selection for yield.

## 5.1 Introduction

The common bean (*Phaseolus vulgaris* L.) is an important food legume in sub-Saharan Africa. In Zambia the crop is popular as a source of protein among low income households (Kimani, 1999). It supplements the cereal based diets in Zambia with the much needed protein (Ribeiro et al., 2005). The common bean ranks second after groundnuts based on area under production in Zambia (Food and Agriculture Organisation, 2012). Many farmers including those in drought prone regions prefer growing beans because of the ability of the crop to grow to maturity in a short period of time (Legesse et al., 2006). Despite its importance in human diets, yield levels have remained low due to a number of abiotic and biotic stresses. Among the major abiotic factors are the increasing droughts and a rise in temperatures emanating from climate change which are major threats to crop production worldwide (McCarthy et al., 2001). This is also anticipated to significantly affect common bean production (Katungi et al., 2009). It is estimated that yield losses of up to about 40% will be experienced due to droughts and high temperatures (Wang et al., 2006).

Many scientists have used plant breeding to develop crops for drought prone areas and for regions of high temperatures as a key solution towards improving bean production in the low altitudes. It has widely been proposed that any meaningful breeding programmes should evaluate the breeding value of prospective parental lines to be used for developing new, locally or extensively adapted common bean varieties (Lee and Parsons, 1968; Robertson, 1966).

Drought tolerance has been reported to be a physiologically complex trait that must be expressed in terms of increased grain yield under field conditions. Its inheritance is considered to be a quantitative complex trait with low heritability for which no appropriate selection criteria have been developed (Schneider et al., 1997, Blair *et al.*, 2010). It is also widely acknowledged that drought tolerance is a difficult trait because the drought stress can present itself at different times, with different intensities which could be modified by soil type (Rao, 2001). The mechanisms of drought tolerance are difficult to analyze because of the interaction of drought with other stress factors, such as high temperature, low soil fertility, and soil acidity. Drought tolerance is therefore susceptible to genotype  $\times$  environment (G $\times$ E) interactions.

The traits associated with tolerance to drought in common bean have been identified and they include deep and balanced root systems that extract water from deep soil profiles, days to flowering and to physiological maturity, biomass accumulation, number of pods per plant, number of seeds per pod, harvest index, pod harvest index, 100-seed mass, yield, and yield based indices (White and Castillo, 1985; Acosta-Gallegos and Shibata, 1989; Schneider et al., 1997; Ramirez-Vallejo and Kelly, 1998; Frahm et al., 2004; Rosales-Serna et al., 2004; Beebe et al., 2008). However, the underlying genetic basis of most of these traits remains to be understood. It has been reported that yield losses occur under drought stress during reproductive development in common bean (Halterlein et al., 1980).

Common bean cultivars have been found to respond differently to drought stress under field conditions and this is due to differences in genotypes. The traits reported to be valuable in drought tolerance are earliness and yield components such as number of seeds per pod, and number of pods per plant which are key components of yield (Acosta-Gallegos and Shibata, 1989). Many inter-racial and inter-gene pool combinations have also shown favorable responses to drought tolerance in common bean (Schneider et al., 1997). The days to flowering and days to physiological maturity have been reported to have negative relationships with grain yield under drought stress and that there is adequate variation for these traits to distinguish genotypes for drought tolerance. Other reports show that number of days to physiological maturity is positively associated with the number of pods per plant, number seeds per pod, hundred seed mass, and yield (Acosta-Gallegos et al., 1995; Porfirio and James, 1998). Some reports have suggested that among the common bean genotypes, shorter duration to podding or flowering for determinate genotypes are usually early maturing and results in a higher number of pods per plant (Porfirio and James, 1998).

Making significant genetic gain for adaptation to drought stress in breeding requires a better understanding of the nature and level of drought tolerance in the current varieties used in each country and sources of resistance. This study therefore focused on determining the nature and levels of drought tolerance of selected Zambian bean genotypes. The specific objective was to estimate the genetic parameters for yield and yield components under managed drought stress conditions in order to determine the breeding value of selected genotypes for use in the development of drought tolerant common bean genotypes. .

## **5.2 Materials and methods**

### **5.2.1 Germplasm**

Eight female and six male parents were used in this experiment in the generation of experimental crosses. The females used were all genotypes well adapted to bean production regions with preferred grain types by the farmers and consumers while the male parents were selected from landraces through a comprehensive screening experiment and others were materials obtained from Centro Internacional de Agricultura Tropical (CIAT). The eight female parents and six male parents were inter-mated using the North Carolina Design II scheme as described by (Comstock and Robinson, 1948) to generate 48  $F_1$  crosses. The crossed seed ( $F_1$ ) were sown in pots placed in the screen house. The  $F_1$  plants were advanced to the  $F_2$  generation.

### **5.2.2 Study locations**

The test materials ( $F_2$  populations and the parental genotypes) were planted at two locations, Mount Makulu and Nanga. Mount Makulu is at latitude  $15^{\circ}13.10'$ , longitude  $28^{\circ}14.93'$  and at an altitude of 1200 m above sea level (Veldkamp et al., 1984; ZARI, 2006). This site receives rainfall of up to 1000 mm per annum. Nanga on the other hand lies at a latitude of  $15^{\circ}32.87'$  and longitude of  $27^{\circ}32.93'$ . The site is situated at an altitude of 1190 m above sea level. Nanga also receives rainfall up to 1000 mm annually (Veldkamp et al., 1984; ZARI, 2006). The detailed description of the geographical and climatic conditions including the types of soils is presented in Table 5.1. The two sites are similar in general weather characteristics but differ in the soil types. The soils at Nanga are slightly sandier than the soils at Mount Makulu implying that water is likely to drain more quickly at Nanga than at Mount Makulu.

The experiments were planted in March, 2013, towards the end of the rainy season in order to take advantage of the last rains for early seedling germination and growth. The dry season begins from mid April to October each year and there is no possibility of any kind of precipitation after the last rains. This ensured adequate control of irrigation.



**Table 5.1:** Geographical and climatic site descriptions of the experimental sites

<b>Environmental characteristics</b>	<b>Mount Makulu</b>	<b>Nanga NIRS</b>
Latitude (South)	15°13.10'	15°32.87'
Longitude (East)	28°14.93'	27 °10.93'
Altitude (meters above sea level)	1206.00	1190.00
Relative humidity (%)	69.40	54.80
Annual rainfall (mm)	800-1000	800-1000
Soil type	Chromi-haplic lixisols	Vertisols
Soil characteristics	Fine loam to clay	Sandy clay
Soil pH	5.8	5.2

Sources: Mateological department; Mt. Makulu Research Station

The two sites were also well equipped with irrigation facilities in order to conduct the experiments under managed drought conditions.

### **5.2.3 Experimental design and crop management**

The 64 entries (14 parental lines, two checks and 48 F<sub>2</sub> populations) were planted in an alpha-lattice design in two replications. Thirty seeds were sown in two rows of 5 m in length at a spacing of 75 cm by 30 cm in between rows and in between plants respectively. Compound D fertilizer (NPK), of the composition 10:20:10 at a recommended rate of 200 kg N ha<sup>-1</sup> was applied at planting time as basal dressing. Supplementary irrigation was applied on the experiments optimally until the crops reached 50% flowering after which water was withdrawn from evaluation of the genotypes under drought stressed conditions while irrigation was continued for the non-stressed experiments. Weeding was done manually at all sites. Pests and disease control were done through spraying appropriate pesticides and fungicides.

### **5.2.4 Data collection and data analysis**

Data was collected from the whole plot on seed yield, 100 seed mass, days to 50% flowering, and days to maturity during crop growth. Other secondary data parameters on; number of days to 50% flowering, number of pods per plant, and number of seeds per pod were recorded as follows. Data on DAF, DPM, LAR, yield and HSW was collected as described in 3.2.3 in chapter three. In addition to the data collection description provided under 3.2.3, PM and flower abortion as described below:

- **Days to physiological maturity (PM)** – number of days from 50% seedling emergence to 50% physiological maturity and plant senescence.
- **Flower abortion (FA)** – was taken as the difference between the number of flowers counted at 50% flowering and the number of mature pods.
- The computation for Bakers ratio was done using the formula,  $\text{bakers ratio} = \frac{2\text{MSGCA}}{2\text{MSGCA} + \text{MSSCA}}$ , where MSGCA= mean square for GCA and MSSCA is the mean square for SCA

For each measurement, 30 single plants were measured and recorded to determine the frequencies and distributions since these were segregating populations.

The SAS statistical general linear models as random model for all terms were used for the analysis of variance (ANOVA) (SAS Institute, 2002).. The variations due to the offspring were broken into females, males, interaction between females and males and their interaction with the environment (Hallauer and Miranda, 1988). The expected mean squares from the ANOVA provided the GCA and SCA variances for parental lines and crosses respectively. The variances for males and females were depicted as  $\text{GCA}_m$  and  $\text{GCA}_f$  respectively while those for the interactions between female and male crosses were depicted as  $\text{SCA}_{fm}$

The ANOVA for each environment and combined ANOVA were computed using the PROC MIXED procedure of SAS (SAS Institute, 2002). The SAS programme for the line x tester analysis was used to compute the GCA and SCA effects following the procedure presented by (Singh and Chaudhary, 1977). The data on measured traits of segregating populations, parents and controls was analyzed according to the statistical model:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + rk + e_{ijk}$$

Where:

$Y_{ijk}$  = mean value of a character measured on cross  $i \times j$  in  $k$ th replication  
 $g_i$  = GCA effect of  $i^{\text{th}}$  parent;  $g_j$  = GCA effect of the parent  $j$ ;  $s_{ij}$  = SCA effect of cross  $i \times j$ ;  $rk$  = replication effect;  $e_{ijk}$  = environmental effect peculiar to  $(ijk)^{\text{th}}$  individual;  $\mu$  = population mean effect;

The GCA effects were calculated as follows:

Females:  $g_i = x_{i...}/tr - y_{...}/lrt$

Males:  $g_j = x_{.j.}/lr - x_{...}/ltr$

#### Estimation of SCA effects:

$s_{ij} = x_{ij.}/r - x_{i...}/tr - x_{.j.}/lr - x_{...}/ltr$

Where: l = number of females; t = number of males; r = number of replications

#### Estimation of standard errors:

S.E. (GCA for females) =  $(Me/r \times t)^{1/2}$ ; S.E. (GCA for males) =  $(Me/r \times l)^{1/2}$ ; S.E.

(SCA effects) =  $(Me/r)^{1/2}$ ; S.E. ( $g_i - g_j$ ) female =  $(2Me/r \times t)^{1/2}$ ; S.E. ( $g_i - g_j$ ) male =

$(2Me/r \times l)^{1/2}$ ; S.E. ( $s_{ij} - s_{kl}$ ) =  $(2Me/r)^{1/2}$

The outline of the expected mean squares is as presented in Table 5.2:

**Table 5.2:** Estimated mean squares for the analysis

Source	df	Expected Mean square
Rep	r-1	
Site	s-1	$MS_s$
GCA <sub>Male</sub>	m-1	$MS_m$
GCA <sub>Female</sub>	f-1	$MS_f$
SCA = Male x female	(m-1)(f-1)	$MS_{(m-1)(f-1)}$
Site x GCA <sub>Male</sub>	S(m-1)	$MS_{S(m-1)}$
Site x GCA <sub>Female</sub>	S(f-1)	$MS_{S(f-1)}$
Site x SCA = Male x female	S(m-1)(f-1)	$MS_{S(m-1)(f-1)}$
Error	Smf(r-1)	$MS_{error}$

## 5.3 Results

### 5.3.1 Analysis of variance and $F_2$ genotypic mean performance under drought stress

The combined ANOVA across the water stress conditions revealed different levels of significance for the mean squares for all the traits measured. The ANOVA of the parental genotypes are presented in Table 5.3. The main site effects were highly significant ( $P \leq 0.001$ ) for yield and significant ( $P \leq 0.01$ ) for DAF, FA, NPP and HSW. The main site effects,  $GCA_f$ ,  $GCA_m$ ,  $SCA_{f \times m}$ ,  $Site \times GCA_f$ ,  $site \times GCA_m$  and overall interaction ( $site \times female \times male$ ) were highly significant ( $P \leq 0.01$ ) for yield. Mean squares for GCA effects for males were significant for yield, number of seeds per pod, flower abortion, and number of pods per plant while the GCA effects for females were significant for yield, and number of seeds per pod (Table 5.3). The  $GCA_f$  were significant for FA ( $P \leq 0.05$ ) and highly significant for NSP ( $P \leq 0.01$ ). The  $GCA_f$  by site mean squares were highly

significant for yield, NSP and NPP ( $P \leq 0.01$ ) and significant for FA ( $P \leq 0.05$ ). The  $GCA_m$  by site was highly significant for yield ( $P \leq 0.01$ ). The SCA mean squares were significant for yield ( $P \leq 0.01$ ); for NSP, DAF and flower abortion ( $P \leq 0.05$ ). The overall interactions (site by female by male) were highly significant for yield, FA ( $P \leq 0.01$ ), and NPP.

**Table 5.3:** Mean squares for variance components for yield and related traits under drought stress

Source	DF	Yield	NSP	DAF	FA	NPP	HSW
Rep							
Site	1	15561228.97***	253.28	1442.41**	1167.21**	16213.66**	27726.75**
$GCA_F$	7	247051.83**	2982.86**	19.32	261.86*	1686.84	7410.92
$GCA_M$	5	312450.36**	219.66*	21.77	193.43**	2474.58**	2403.21
$SCA_{F \times M}$	35	135446.23**	428.89*	24.88*	195.87*	4691.81	6076.62
Site* $GCA_F$	30	242539.97**	6171.87**	32.10	283.74*	2175.52**	7582.26
Site* $GCA_M$	26	294822.00**	180.12	14.20	193.24	2234.50	4565.95
Site*Female*Male	70	150609.72**	376.23	16.80	209.08**	3226.36**	7555.04
Error		623.44	101.21	29.00	88.10	548.99	911.70
Bakers ratio		0.81	0.88	0.62	0.70	0.47	0.62
<b>Broad Sense Heritability</b>		<b>0.60</b>	<b>0.33</b>	<b>0.42</b>	<b>0.49</b>	<b>0.38</b>	<b>0.42</b>

Note: NSP-number of seeds per pod; DAF – days to 50% flowering; FA – flower abortion; NPP – number of pods per plant; HSW – hundred seed weight

The Baker's ratio ranged between 0.47 for NPP to 0.88 for NSP. This is an indication that the GCA effects were predominant over the SCA effects. NPP had the lowest Baker's ratio of 0.47, HSW and DAF had 0.62, FA had 0.70, Yield had 0.81 and NSP had 0.88.

### 5.3.2 General combining ability for grain yield across sites, under stressed environments

The  $GCA_f$  effects for grain yield were significant for the across site analysis ( $P \leq 0.05$ ) (Table 5.4). The GCA mean squares were predominant over the SCA mean squares for all traits except for yield as seen by the Bakers Ratio. The genotypes ZM 05, Chambeshi, Lyambai and SCCI-2 showed positive GCA effects for yield across the sites. Pan 148, Lyambai and SCCI-2 had positive GCA effects for stressed environments at Mount Makulu (Table 5.4). The GCA effects at Nanga were positive for ZM 05, Chambeshi, Pan 148 and Lyambai (Table 5.4).

**Table 5.4:** General combining ability effects for yield across sites under drought stress of the male and female parents

Genotype	Nanga	Mt. Makulu	Across drought sites
<b>GCA effects – Female</b>			
ZM 05	51.29*	-52.07**	135.43**
Chambeshi	108.04**	-3.16	94.25*
Pan 148	125.38**	49.34**	-33.92*
Kabulangeti	-60.71*	-78.82	-56.94*
Kalungu	-107.13**	-32.41**	-103.64**
Lyambai	69.38	35.01	29.43*
Kapisha	-37.88	-36.57**	-95.95*
SCCI-2	-148.38**	118.68*	31.33*
<b>GCA effects – Male</b>			
ZM 4143	1.23	-91.51	-146.56*
ZM 4497	314.88**	345.06*	591.41*
SER 124	357.88**	329.19*	526.03*
Ly4-4-4-B	228.25	332.75*	487.20*
ZM 3831	171.25*	363.19*	459.31*
SEN 39	265.06**	277.94*	506.13*
<b>*Significant at <math>P \leq 0.05</math>, **Significant at <math>P \leq 0.01</math></b>			

The GCA effects for the male parents across drought stressed environments and for each site are presented in Table 5.4. All the male parents except ZM 4143 had significant and positive GCA effects across sites for yield ( $P \leq 0.05$ ). The GCA effects for male parents were also all positive at Mount Makulu and Nanga except ZM 4143 which showed a negative value at the former site (Table 5.3). However, the GCA estimates for ZM 4143 though positive at Nanga was very low. ZM 4497, SER 124, Ly4-4-4-B, ZM 3831 and SEN 39 had high and positive GCA effects for yield, while ZM 4142 had very low GCA effects. ZM 4497 had the highest GCA effect for grain yield across all sites (Table 5.4). SER 124 had the highest GCA estimate at the non-stressed environment, while ZM 3831 and ZM 4497 had the highest GCA estimates under stress conditions at Mt. Makulu and Nanga respectively (Table 5.4). The male line with the highest GCA value for grain yield across the environments was ZM 4497. Positive GCA effects are desirable for grain yield.

### 5.3.3 Specific combining ability and mean performance of $F_2$ populations for grain yield across sites, under drought stress conditions

Specific combining ability effects were significant for yield at all the testing sites and across the three sites ( $P \leq 0.05$ ). However, SCA effects are not fixable in common bean hence not important and can therefore be ignored. The mean performance for grain yield

ranked on the basis of across sites under drought stressed conditions is presented in Appendix 5.1. The 10 highest yielding populations that performed well above the overall mean (273.58kg ha<sup>-1</sup>) across sites are 4, 35, 61, 14, 5, 48, 45, 12, 34, and 8, and their parents had high and positive GCA values. The F<sub>2</sub> combinations were derived from the combinations of Chambeshi, Pan 148, ZM 05, Lyambai, SER 124, ZM 3831, LY 4-4-4-B, SCCI-2, and SEN 39 which recorded high positive GCA effects for yield. However, ZM4143 recorded the lowest positive GCA effect for male.

#### 5.3.4 Correlations among grain yield and related traits under drought stress

The correlation coefficients were significant ( $P \leq 0.01$ ) between yield and NPP ( $r=0.61$ ), and significant ( $P \leq 0.05$ ) for FA ( $r=0.29$ ) (Table 5.5). The relationships were in the positive direction but not very strong for all the correlations between yield and measured traits. Days to 50% flowering was significant ( $P \leq 0.01$ ) and negatively correlated with HSW ( $r=-0.65$ ) and FA ( $r=-0.61$ ) while it was significant ( $P \leq 0.05$ ) and positive with NPP ( $r=0.43$ ) and NSP ( $r=0.46$ ). The correlations were also highly significant ( $P \leq 0.01$ ) between NPP and FA ( $r=0.79$ ).

**Table 5.5:** Correlation coefficients between grain yield under stressed conditions and selected measured traits

DAF	1					
FA	-0.61**	1				
NPP	0.43*	0.79**	1			
NSP	0.46*	0.13	0.16	1		
Yield	0.27	0.29*	0.61**	0.15	1	
HSW	-0.65**	0.54*	0.16	-0.048	0.18	1
	DAF	FA	NPP	NSP	Yield	HSW

Note: DAF – days to 50% flowering; FA – flower abortion; NPP – number of pods per plant; NSP- number of seeds per pod; HSW – hundred seed mass; \*Significant at  $P \leq 0.05$ ; \*\*significant at  $P \leq 0.01$

#### 5.3.7 Phenotypic variability of the parents and the derived lines

Significant differences ( $P \leq 0.05$ ) were observed among the F<sub>2</sub> populations and between parents for most traits measured in both drought stress and non-stress environments at both locations. The F<sub>2</sub> population distributions were continuous for all traits, suggesting quantitative inheritance in all cases and both in drought stress and non-stress

environments (Figure 5.1). The mean performance for the  $F_2$  and the parental genotypes for selected crosses that gave the highest SCA values are presented in Table 5.6.

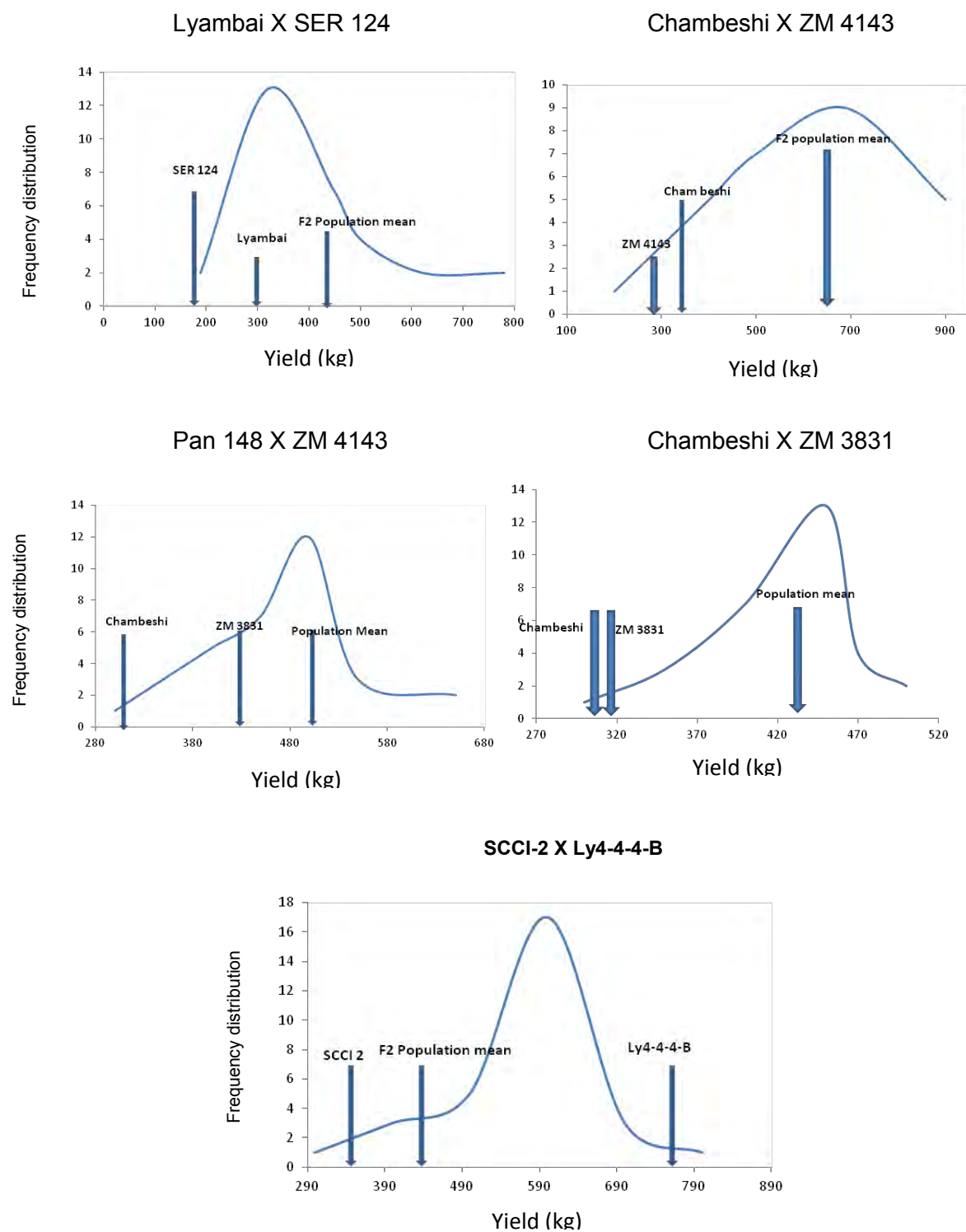
**Table 5.6:** The mean values of traits measured in drought-stressed conditions at Nanga and Mount Makulu during the year 2011 and 2012 for some selected parental lines and corresponding  $F_2$  populations

<b>1. Lyambai X SER 124</b>					
<b>Trait</b>	<b>Parents</b>		<b><math>F_2</math> population</b>		<b>P value</b>
	<b>P1</b>	<b>P2</b>	<b>Mean</b>	<b>Range (<math>F_2</math>)</b>	
Yield (kg)	321.25	199.50	446.50	188-780	$\leq 0.001$
Number of days to maturity	45.75	36.00	49.50	33-64	$\leq 0.001$
Number of seeds per pod	4.13	1.80	4.75	1.1-7.2	$\leq 0.001$
Number of pods per plant	10.05	11.60	12.20	0.6-34	$\leq 0.001$
One hundred seed mass	46.00	31.50	42.50	25-51	$\leq 0.001$
<b>2. Chambeshi X ZM 4143</b>					
<b>Trait</b>	<b>Parents</b>		<b><math>F_2</math> population</b>		<b>P value</b>
	<b>P1</b>	<b>P2</b>	<b>Mean</b>	<b>Range (<math>F_2</math>)</b>	
Yield (kg)	300.28	294.50	688.67	201-890	$\leq 0.001$
Number of days to maturity	42.00	42.00	47.0	40-55	$\leq 0.001$
Number of seeds per pod	5.63	4.25	4.83	4.2-7	$\leq 0.001$
Number of pods per plant	16.10	14.50	13.27	11-16.9	$\leq 0.001$
One hundred seed mass	45.50	38.75	41.33	42-49	$\leq 0.001$
<b>3. Pan 148 X ZM 4143</b>					
<b>Trait</b>	<b>Parents</b>		<b><math>F_2</math> population</b>		<b>P value</b>
	<b>P1</b>	<b>P2</b>	<b>Mean</b>	<b>Range (<math>F_2</math>)</b>	
Yield (kg)	408.00	294.5	525.50	300-651	$\leq 0.001$
Number of days to maturity	45.75	42.00	47.75	36-52	$\leq 0.001$
Number of seeds per pod	4.31	4.25	5.50	3.9-5	$\leq 0.001$
Number of pods per plant	11.80	14.50	9.40	7.6-16	$\leq 0.001$
One hundred seed mass	49.00	38.75	49.0	33-54	$\leq 0.001$
<b>4. Chambeshi X ZM 3831</b>					
<b>Trait</b>	<b>Parents</b>		<b><math>F_2</math> population</b>		<b>P value</b>
	<b>P1</b>	<b>P2</b>	<b>Mean</b>	<b>Range (<math>F_2</math>)</b>	
Yield (kg)	300.28	310.75	434.25	260-470	$\leq 0.001$
Number of days to maturity	42.00	48.00	48	36-60	$\leq 0.001$
Number of seeds per pod	5.63	5.00	5.38	3.9-5.7	$\leq 0.001$
Number of pods per plant	16.10	16.10	23.5	14-27	$\leq 0.001$
One hundred seed mass	45.50	47.50	43.25	40-51	$\leq 0.001$
<b>5. SCCI-2 X Ly4-4-4-B</b>					
<b>Trait</b>	<b>Parents</b>		<b><math>F_2</math> population</b>		<b>P value</b>
	<b>P1</b>	<b>P2</b>	<b>Mean <math>F_2</math></b>	<b>Range (<math>F_2</math>)</b>	
Yield (kg)	324.75	757.67	406	301-790	$\leq 0.001$
Number of days to maturity	44.75	43.33	44.75	42-47	$\leq 0.001$
Number of seeds per pod	3.88	5.42	3.75	3.0-6.3	$\leq 0.001$
Number of pods per plant	19.70	12.20	17.45	12.1-27	$\leq 0.001$
One hundred seed mass	49.00	55.33	50.00	44-58	$\leq 0.001$

The drought-tolerant paternal line, LY 4-4-4-B, out-yielded both drought tolerant and susceptible genotypes. Hundred seed mass has been reported in other studies as being a response mechanism to drought stress and uses photosynthetic remobilization. However, hundred seed mass was not significant ruling out the possibility of the genotypes remobilizing the photosynthates into seed ( $P \leq 0.05$ ).

The drought tolerant control genotype SER 124 was inconsistent in performance, sometimes being found to be better or and other times worse than other parental lines for many of the traits. The  $F_2$  population distributions were continuous for all traits, suggesting quantitative inheritance (Figure 5.1). From the parental means and  $F_2$  means, it was observed that there was transgressive segregation among the  $F_2$  populations for all the traits measured. This transgressive segregation was found both in positive and negative directions.





**Figure 5.1:** F<sub>2</sub> frequency distribution for yield

## 5.4 Discussion

The parents exhibited different results with respect to levels of GCA effects which is an indication that there was adequate additive genetic variance which can be exploited during selection. The mean squares due to GCA were significant for yield and number of seeds per pod and similar results were exhibited for SCA mean squares. General combining ability effects are associated with additive gene action while SCA effects are associated with non-additive gene action. Significant GCA and SCA effects for traits such as grain yield implies that both additive and non-additive gene effects were important in the inheritance of yield parameters and number of seeds per pod. However, the additive gene effects were more important going by the Baker's ratios. However, SCA effects for NPP were more important than GCA effects but not important in beans. The predominance of the additive gene effects suggests that the best progeny might be derived from crosses with genotypes having the greatest positive GCA values as suggested by Arunga et al. (2010). Generally, it would imply that selection for yield would be achieved easily and fast from segregating generations of such parents. These results are in agreement with those reported in common bean (Hinkossa et al., 2013; Idahosa and Alike, 2013; Islam et al., 2006). However, these results differ from those reported by Cruz et al. (2004) and Vidigal et al. (2008) who reported high significant SCA effects for yield under drought stress. This difference could be attributed to the differences in the germplasm used and the environments used.

Chambeshi, Pan 148, ZM 05, Lyambai, SER 124, ZM 3831, LY 4-4-4-B, SCCI-2, and SEN 39 showed that they were good general combiners for most traits as they showed maximum GCA effects. Moreover, they had the highest *per se* performance and showed the maximum cross mean performances. This result is in good agreement with related previous studies on yield and NPP in common beans although on different types of bean collections (Foolad and Bassiri, 1983; Rainey and Griffith, 2005b). NPP is one of the principal yield components in common bean (Dursun, 2007; Selehi et al., 2010; Cokkizgin et al., 2013). Hence, these parents could be considered as good parents for future hybridization programmes with a major aim of improving yield under drought stress. Lyambai X SER 124 generated negative SCA effects despite the parents recording high GCA effects. This may indicate that the two parents are closely related. Such crosses would imply that their combination may not be of value for drought tolerance.

The significant and positive GCA effects and high Baker's ratio for NSP across the environments imply that the additive gene action was important in its inheritance. Apart from Kabulangeti and Kalungu whose  $F_2$  combinations showed negative SCA values, the results generally indicate that additive gene action was preponderant for NSP. Lyambai had good combinations with all the male parents for NSP based on positive SCA effects recorded. The NSP could therefore be used as an indirect trait when breeding for drought tolerance and this finding agrees with those reported in other studies on common bean (Foolad and Bassari, 1983; Rainey and Griffiths, 2005a). This trait has been reported as one of the key traits determining yield in common bean (Cokkizgin et al., 2013; Durson, 2007; Selehi et al., 2010).

Both gene effects (additive and non-additive) were involved in the determination of yield and number of seeds per pod. However, it is critical to consider the GCA effects when developing common bean varieties suitable for drought prone environments since SCA effects are not useful in beans where a pure line is the variety rather than hybrid. The selection and crossing criteria should be to get one parent with high significant GCA effect and carefully choosing the other parent to ensure the results are not negative as exhibited by Ly4-4-4-B which had the highest GCA effects performance as a pure line but produced the worst  $F_2$  populations. This implies unpredictable progress in breeding and this genotype needs to be avoided in hybridization. However, targeting both parents with high positive GCA for yield could produce high yielding bean genotypes with desired traits as recommended by Arunga et al. (2010). Genotypes should be selected based on positive GCA effects for yield to obtain a reliable result (Narro et al., 2003).

Highly significant and positive correlation coefficients between grain yield and the measured traits were found in this research. The high and positive correlation coefficient of 0.61 for number of pods per plant with yield indicates the usefulness of the trait to yield although the analysis of variance did not show significant results for number of seeds per pod. The number of pods per plant would be an ideal secondary trait to be considered in the selection of drought tolerant genotypes in common beans although it is tedious to implement. Selection based on yield would therefore be recommended. The significant environmental effects of yield suggest that more sites need to be used for selecting for high grain yield.

Many plant breeders have used variance components and heritability estimates in the selection of promising genotypes and prediction of desirable traits (Morakinyo, 1986). The broad sense heritability estimates for yield in this study are an indication that it is controlled by additive genes. The 60% heritability estimate (Table 5.3) for grain yield would be adequate to make progress in breeding for drought tolerance in common bean. However, the magnitudes of heritability estimates are products of the population being tested, environments within which the testing is done and traits being measured (Falconer and Mackey, 1986). It should, therefore, be understood that heritability values reported for a given trait, are specific to the population in question (Hallauer and Miranda, 1981). The heritability estimates for the other traits such as NSP, DAF, FA, NPP and HSW were low as expected for drought tolerance because inheritance for drought tolerance is considered as polygenic (Table 5.3). However, the low Baker's ratio value and the importance of broad sense heritability relative to narrow sense heritability emphasized the preponderant role of non-additive gene action in controlling the drought tolerance in common bean for NPP.

Flower abortion showed unique response to drought tolerance. The mean square for  $GCA_m$  was significant while that for  $GCA_f$  was not. This result shows that non-additive gene action may be controlling the inheritance for flower abortion. This result may imply that the parental lines used for this study did not contain resistance genes for flower abortion. This result is in agreement with research results reported by Khattack et al. (2006) who failed to secure tolerant genotypes for flower abortion. This may therefore imply that large numbers of genotypes need to be screened as the genes for flower abortion may be rare.

The leaf area retention was reduced due to drought probably as mechanism to conserve moisture. These results suggest that severe drought during the active growth stages in common bean might have deleterious effects on yield through reduced leaf area. This is important since the plants may not have sufficient time to invest in an increase in leaf mass after an extended period of drought. Instead they might directly enter the reproductive period without sufficient biomass reserves for optimum yield. This could be disastrous for bean genotypes with determinate growth habit which may not be able to initiate a second flush of pod setting when the vegetative growth period has passed.

This study amplified understanding of the mechanisms and genetics of drought tolerance. The principal achievement was to analyze three different categories of drought tolerance mechanisms namely drought escape, drought avoidance and drought tolerance. From the results, and using data on flowering and days to maturity, it could be assumed that some genotypes flowered early and matured early in an effort to escape drought. The harvest index, which reflects the differences in the photosynthate partitioning process, could not be used however as the genotypes lost leaves to a great extent making it practically difficult to quantify. The number of days to flowering and days to physiological maturity would be the most useful traits to select genotypes that would use an escape mechanism. The remobilisation of photosynthates from vegetative plant structures to the pod wall and from pod wall to the final grain yield is an important mechanism in drought adaptation for common bean more especially for indeterminate genotypes which retained higher leaf area under drought stress. It is interesting to see where leaf area retention provides functional relationship with yield. In this regard, the traits related with photosynthate accumulation and partitioning such as leaf area retention were important and need to be investigated further.

The response to drought stress by the yield components particularly number of seeds per pod and number of pods per plant had positive relationship with grain yield under drought stressed environments. Some genotypes were able to produce pods along with fresh flush of leaves after three weeks of imposing drought stress.

The transgressive segregation observed with the measured traits such as yield, number of pods per plant and number of seeds per pod (Figure 14), was important for these populations and is of interest in applying selections for drought improvement in common bean. Higher yield, higher number of pods per plant and higher number of seeds for pod could therefore used directly to select genotypes adaptable to drought stressed environments. The better performance of the  $F_2$  population showing transgressive segregation provides a great opportunity for selecting high yielding genotypes that would be tolerant to drought stress.

## 5.5 Conclusions

This study focused on the genetics of inheritance to drought tolerance for selected traits in common bean. Significant GCA and SCA mean squares showed the importance of both additive and non-additive gene effects for yield. The Baker's ratio results showed that additive gene effects were more important than non-additive gene effects for all traits suggesting that selection would be effective during breeding. The high heritability of 60% for yield further confirms the importance of additive gene effects for drought tolerance in common beans.

Ly 4-4-4-B and ZM 4497 were found to be tolerant genotypes to drought stress based on high and positive GCA effects and selection could be made to release them as varieties.

The parents in  $F_2$  combination for the crosses 4, 35, 61, 14, 5, 48 and 45 were found to have high GCA effects and they performed above the check varieties from CIAT under drought stress. These parents could therefore be used in developing drought tolerant genotypes. This will require further exploration by selecting from the  $F_2$  populations in subsequent generations. The moderately high heritability for yield would guarantee quick progress. NSP can also be used as an indirect trait for improving yield.

Transgressive segregation was also found among the  $F_2$  populations for drought tolerance indicating the possibility of making appropriate choices from segregating populations for the generation of adaptable genotypes for yield and other traits under drought stressed conditions.

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**Appendix 5.1: Mean performance for yield and related traits for 14 parental lines, two checks and 48 F<sub>2</sub> populations under drought stress**

S.No.	Entry	Category	Fem	Male	D50F	NF50F	NPPI	NSP	HSW	Yield (across sites) (Kg)
1	32	Male parent	Ly4-4-4-B	Ly4-4-4-B	43.33	43.00	12.20	5.42	55.33	757.67
2	4	Cross	Chambeshi	ZM 4143 (H)	47.00	28.60	13.27	4.83	41.33	688.67
3	35	Cross	Pan 148	ZM 4143 (H)	47.75	34.60	9.40	5.50	49.00	525.50
4	50	Female parent	ZM 05	ZM 05	44.75	31.85	6.50	5.00	49.75	469.75
5	61	Cross	Lyambai	SER 124	49.50	37.70	12.20	4.75	42.50	446.50
6	14	Cross	Chambeshi	ZM 3831 (D)	48.00	35.65	23.50	5.38	43.25	434.25
7	27	Female parent	Pan 148	Pan 148	45.75	30.25	11.80	4.31	49.00	408.00
8	5	Cross	SCCI-2	Ly4-4-4-B (D)	44.75	30.55	17.45	3.75	50.00	406.00
9	3	Male parent	ZM 4497 (H)	ZM 4497 (H)	46.00	29.95	16.45	4.75	44.00	404.25
10	48	Cross	ZM 05	SER 124	44.75	35.75	11.85	5.00	49.25	395.00
11	45	Cross	Lyambai	ZM 3831 (D)	47.75	35.35	11.45	4.31	36.00	363.75
12	56	Check	SXB 413	SXB 413	49.00	37.20	5.30	5.25	45.50	363.50
13	12	Cross	Pan 148	ZM 3831 (D)	44.33	37.53	14.47	5.08	43.33	350.67
14	34	Cross	ZM 05	SEN 39	30.00	28.70	14.60	6.25	32.00	341.50
15	8	Cross	SCCI-2	SER 124	44.75	36.60	21.40	5.06	45.50	331.75
16	31	Female parent	SCCI-2	SCCI-2	44.75	43.35	19.70	3.88	49.00	324.75
17	44	Cross	Lyambai	ZM 4497 (H)	46.75	29.55	8.05	4.94	38.25	323.00
18	58	Female parent	Lyambai	Lyambai	45.75	33.05	10.05	4.13	46.00	321.25
19	41	Cross	Chambeshi	Ly4-4-4-B (D)	48.00	36.10	10.00	4.94	47.50	319.75
20	33	Cross	ZM 05	Ly4-4-4-B (D)	42.00	35.35	15.60	4.31	40.25	319.25
21	11	Cross	Pan 148	SEN 39	47.75	48.45	13.15	4.69	48.25	315.25
22	49	Male parent	ZM 3831 (D)	ZM 3831 (D)	48.00	32.35	16.10	5.00	47.50	310.75
23	22	Cross	SCCI-2	ZM 4143 (H)	43.67	28.40	25.20	4.58	47.67	309.00
24	19	Cross	Kabulangeti	SER 124	36.25	28.15	14.70	9.38	32.75	308.50
25	24	Cross	ZM 05	ZM 4497 (H)	44.75	33.30	11.20	4.88	50.50	307.50
26	40	Female parent	Chambeshi	Chambeshi	42.00	36.00	16.10	5.63	45.50	300.28
27	2	Cross	Kapisha	ZM 4497 (H)	48.25	27.95	11.20	4.88	40.50	299.00
28	39	Cross	Pan 148	SER 124	43.67	32.53	12.67	4.25	37.00	295.00
29	18	Male parent	ZM 4143 (H)	ZM 4143 (H)	45.25	30.60	14.50	4.25	38.75	294.50
30	42	Cross	Kabulangeti	ZM 4497 (H)	45.50	40.25	7.95	4.94	40.25	281.50
31	1	Cross	ZM 05	ZM 4143 (H)	45.00	29.60	10.80	4.92	48.67	279.33
32	17	Female parent	Kalungu	Kalungu	46.50	32.25	18.00	4.50	47.50	270.00
33	55	Male parent	SEN 39	SEN 39	42.00	26.65	9.75	7.69	55.50	263.25
34	29	Cross	Pan 148	ZM 4497 (H)	35.75	27.95	105.45	70.63	36.75	260.75
35	23	Cross	Lyambai	SEN 39	48.25	36.80	10.15	4.44	48.50	239.75
36	6	Cross	ZM 05	ZM 3831 (D)	44.75	44.70	15.75	6.10	48.00	237.25
37	25	Cross	Chambeshi	ZM 4497 (H)	47.75	37.60	56.60	5.06	40.75	236.50
38	54	Cross	Pan 148	Ly4-4-4-B (D)	42.75	42.85	9.65	4.50	31.75	233.25
39	20	Cross	Chambeshi	SER 124	44.75	37.25	8.65	5.00	46.50	231.50
40	46	Cross	Kalungu	ZM 4497 (H)	48.00	30.90	6.40	3.81	38.25	219.00
41	47	Cross	Kapisha	Ly4-4-4-B (D)	40.33	34.33	11.60	4.17	51.33	215.33
42	36	Cross	Kapisha	SER 124	35.00	28.30	13.33	13.69	24.75	214.00
43	62	Cross	Kalungu	SEN 39	45.00	27.85	5.10	4.69	38.00	212.00
44	63	Cross	SCCI-2	ZM 4497 (H)	44.75	35.20	17.05	4.56	45.75	208.50
45	16	Cross	Chambeshi	SEN 39	48.25	33.20	17.25	5.13	42.25	204.75
46	9	Male parent	SER 124	SER 124	36.00	31.70	11.60	18.50	31.50	199.50
47	15	Cross	Lyambai	Ly4-4-4-B (D)	42.00	23.95	8.70	4.44	37.00	195.25
48	30	Cross	Kabulangeti	Ly4-4-4-B (D)	48.00	39.33	13.80	5.17	38.33	191.67
49	37	Cross	Kabulangeti	ZM 4143 (H)	44.75	44.40	5.80	4.63	42.50	189.00
50	21	Cross	Kalungu	ZM 4143 (H)	46.67	39.47	14.73	5.42	44.00	186.00
51	26	Cross	Kapisha	ZM 3831 (D)	40.67	27.33	7.93	5.25	42.33	175.00
52	13	Cross	SCCI-2	ZM 3831 (D)	46.75	31.80	11.25	4.19	38.25	165.75
53	43	Cross	Lyambai	ZM 4143 (H)	47.75	33.65	9.50	4.50	33.50	164.50
54	57	Female parent	Kapisha	Kapisha	47.50	31.55	23.95	4.56	36.25	161.25
55	52	Cross	Kabulangeti	ZM 3831 (D)	49.50	27.55	8.75	5.56	30.75	154.25
56	53	Cross	Kapisha	SEN 39	48.67	18.47	9.60	6.50	31.67	146.67
57	38	Cross	SCCI-2	SEN 39	48.75	27.20	10.80	4.25	44.25	141.00
58	10	Cross	Kalungu	SER 124	49.75	36.35	7.80	3.75	37.25	131.00
59	19	Cross	Kabulangeti	SEN 39	40.00	36.24	7.05	3.31	32.50	128.75
60	7	Male parent	ZM 4482-2	ZM 4482-2	49.00	28.80	7.87	3.50	22.33	114.67
61	64	Cross	Kapisha	ZM 4143 (H)	48.25	28.65	6.10	3.88	35.00	100.25
62	51	Cross	Kalungu	ZM 3831 (D)	45.50	34.00	8.60	3.81	39.50	97.50
63	28	Female parent	Kabulangeti	Kabulangeti	44.75	30.10	12.75	4.25	39.25	94.50
64	60	Cross	Kalungu	Ly4-4-4-B (D)	47.50	18.35	6.30	4.38	20.25	83.25
<b>Mean</b>					<b>44.97</b>	<b>33.18</b>	<b>15.41</b>	<b>6.29</b>	<b>41.28</b>	<b>273.58</b>
<b>CV</b>					<b>11.97</b>	<b>14.43</b>	<b>16.34</b>	<b>10.31</b>	<b>16.01</b>	<b>15.70</b>
<b>LSD</b>					<b>14.87</b>	<b>45.30</b>	<b>139.62</b>	<b>16.56</b>	<b>29.16</b>	<b>52.59</b>
<b>MSE</b>					<b>44.75</b>	<b>225.97</b>	<b>31823.92</b>	<b>1.09</b>	<b>144.90</b>	<b>31823.92</b>

Note: NSP-number of seeds per pod; D50F – days to 50% flowering; FA – flower abortion; NPPI – number of pods per plant; HSW – hundred seed mass

## CHAPTER SIX

### General overview and conclusion

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Drought and high temperature stress are the most serious threats to common bean production in the low altitude areas and are likely to impact negatively on the productivity, farm incomes and household food security in general. In Zambia the frequently occurring droughts and high temperatures during the growing seasons coincide with flowering stage of common bean in the low altitude areas and causes damage to bean crops annually leading to loss in yields. These yield losses have been partially blamed on lack of cultivars that can withstand the two stresses.

In this study, genetic factors for drought and heat tolerance in common bean were evaluated in order to contribute to the genetic improvement for improved adaptation of common bean to the low altitude regions. Farmers' preferences were also explored for preferred common bean traits.

Key criteria used by farmers to adopt varieties were bush type growth habit, red speckled bean color, large bean size and shape, taste, early maturity and high number of pods per plant for crop related characteristics. Taking the research findings of the participatory rural appraisal and survey, into account the results further showed that the farmers chose the variety Lyambai, an elite and released variety in Zambia which had most of the preferred characteristics. This implies that new varieties with the background of Lyambai were more likely to be adopted. The other factors included some social economic factors; source of income, education level, and the use of common bean in crop rotations, and demographic characteristics; gender which was inherent in the population.

The 120 genotypes screened under drought stress showed variation between them. Ly4-4-4-B was identified as the most drought tolerant genotype followed by LY1-2-B, ZM 3831, KAL-ZA, SCCI 13, ZM 4512-5 and LYA-ZA. The selected genotypes comprised three landraces, two genotypes from mutagenesis and two market class cultivars, one of which was still under official variety testing for release. These genotypes were also found to be stable in both drought stressed and non-drought stressed environments. This study also established that seed mass was not useful in explaining the performance of

genotypes in both stressed and non-stressed conditions. The genotypes reduced their number of days to flowering probably exhibiting an escape mechanism.

In the results of an evaluation of the 120 genotypes and the  $F_2$  populations under high temperature field conditions and explain the genetic inheritance for heat stress tolerance in the Zambian germplasm. The results showed that ZM 4143, ZM 4497, SCCI 4, KE 1, ZM 07, SZ4BB, ZM 4512-3, LY-2-3-B, ZM 4520, KE3, ZM 4489 and Ly -2 -8-B had the highest yield under high temperatures in Lusitu. ZM 4497 and ZM 4143 were found to be the highest yielding male parents under high temperatures. The GCA mean squares for yield, number of seeds per pod and number of pods per plant indicated the presence of additive gene action for heat stress tolerance. The SCA effects for yield were also significant even though these are not important results in bean since its self-pollinating.

The results of the genetic study for drought tolerance (Chapter 5) genotypes ZM 4143 and ZM 3831 recorded positive GCA effects for yield and high yielding under drought stressed conditions and therefore identified as drought tolerant genotypes. The  $F_2$  populations; 4 (Chambeshi X ZM 4143), 35(Pan 148 X ZM 4143), 61 (Lyambai X SER 124), 14 (Chambeshi X ZM 3831), 5 (SCCI 2 X Ly 4 -4-4-B), 48 (ZM 05 X SER 124) and 45 (Lyambai and ZM 3831) recorded high yields under drought conditions which could imply that further selections may give rise to high yielding segregants. The heritability estimate for yield of 60% was found for drought stress and this was adequate for making quick progress during selection based on yield.

Based on the combination of the results obtained in this study, it can be concluded that ZM 4143 could possess both high temperature tolerance genes and drought tolerance genes worth exploring further for use in breeding for both drought and heat tolerance. Lyambai, a red speckled bean which was highly preferred by the farmers, as revealed by the participatory research and survey, would be the most suitable parent for drought and heat tolerant genotypes with the selected drought and heat tolerant genotypes that may not possess desirable characteristics through backcrossing. In both cases the positive GCA effects for drought and heat stresses exhibited in the selected genotypes implies quick progress in breeding for the two stresses.

Though not tested, it is generally agreed that improved remobilization of photosynthates to grain under drought condition for this category of genotypes is an important mechanism to enhance yield formation, it may also suggest that pyramiding of various

tolerance mechanisms might be needed for breeders to improve drought adaptation in common bean. This could be achieved through pyramiding traits for early maturity, improved photosynthetic ability by maximising possible leaf area, and efficiency in the photosynthates accumulation along with better remobilization to grain under drought stress.

The hybridization generated showed transgressive segregation for traits such as yield, number of pods per plant and number of seeds per pod. These traits would therefore be useful in selecting for drought tolerance.

## **7.0 Implications and recommendations for breeding**

Based on the results of this study the following recommendations are made for breeding drought and heat tolerant genotypes for low altitudes:

- i. The study on farmers' preference revealed that the breeding objectives should take into account the farmers preferences in the target environments, a concept well supported by Ceccarelli et al. (2003). In this study, high yielding red speckled large type of bean with desirable traits such as early maturity, and dwarf type would be the preferred bean types to breed. Ideally the process of variety evaluation should be set to be conducted in the target and similar environments where the varieties will be grown as alluded to by (Odendo et al., 2002).
- ii. The screening of landraces provided an opportunity for selecting genotypes with drought and heat tolerant genes. This implies that when considering to breed for drought and heat tolerance, the landraces are a useful genetic resource hence the importance to conserve it. The performance of landraces studied varied but in some cases, they were as good as the improved varieties. One problem of the landraces was the poor resistance to some biotic stresses. This would therefore imply that one develops a variety that could be drought tolerant but highly susceptible to diseases. This would imply a very long process to get the genotypes.
- iii. Most of the drought and heat tolerant genotypes had dark colours such as black, brown and goldish and are less desirable by the consumers. Breeding should therefore target to introgress the genes from these genotypes into popular and adaptable genotypes. However, seed size did not genetically affect selection gains suggesting that selection for drought and heat tolerance will not affect seed acceptance.
- iv. The high susceptibility levels of all the improved varieties imply that breeders did not consider evaluating the genotypes under drought and heat stress conditions. It is necessary for breeders to screen all potential bean lines for drought and heat tolerance at the same time screening for a trait of interest.

- v. The parental genotypes used in the development of  $F_2$  genotypes had high and positive GCAs implying they would facilitate quick transfer of desirable genes for drought and heat tolerance.
- vi. The  $F_2$  populations derived forms a base for further selections while performing necessary back crosses to retain the background of the most preferred genotypes of common bean.