PERFORMANCE OF ELITE COWPEA (*Vigna unguiculata*) GENOTYPES AT MANKWENG AND BELA-BELA, LIMPOPO PROVINCE

by

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DEDICATION

With gratitude to God, this study is dedicated to my parents (Masilo and Moshala), my siblings (Rosina, Mollale, Thekgi, Modibe, Johanna, Mapula and Mmoloro), my niece (Makoma), my nephews (Matome, Mmoloro, Masilo and Legobole) for putting their lives on hold to assist me financially and for taking care of my son while I was busy studying. This study is lastly dedicated to my beloved son (Thapelo Thekgi) and his father (Ken Phokane) for their unconditional love and support.

DECLARATION

I hereby declare that this research report is my own work. It is being submitted for the degree Masters of Science in Agriculture (Agronomy) at the University of Limpopo, Turfloop campus. It has not been submitted for any other degree or examination at any other university.

Sekgobela Molebjane

Date

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ABSTRACT

Cowpea (*Vigna unguiculata*) is a multi-purpose crop as it can be used for human consumption and livestock feeding. Cowpea serves as one of the cheapest sources of vegetable protein as the dry grain contains 25-30% protein. Its ability to tolerate drought and fix atmospheric nitrogen makes it suitable for marginal areas with low rainfall and poor soil fertility. However, low cowpea yields are common in Limpopo province due to shortage of improved varieties and lack of good seed for planting. The objectives of the present study were to determine growth, yield components and grain yield of elite cowpea genotypes across two locations and seasons, and to determine grain yield and yield components stability of the elite cowpea genotypes across the environments. The experiments were conducted at the University of Limpopo Experimental farm (Syferkuil) in Mankweng and Towoomba Research Station located in Bela-Bela, Limpopo Province during 2015/16 and 2016/17 growing seasons. The trials were carried out in a randomized complete block design (RCBD) consisting of three replications. Ten elite cowpea breeding lines (L1-L10) and a control check Bechuana White (BW) were planted at inter-row and intra-row spacings of 1 m and 0.3 m, respectively, in two rows of 6 m length. Round-up (isopropylamine salt of glyphosate) and Dual (S-metalachlor) at the rate of 3 L/ha and 0.5 L/ha, respectively, were used to control weeds at planting. Insecticide Karate (lambda-cyhalothrin) and Aphox (pirimicarb) at the rate of 1 L/ha and 500 g/ha were applied to control aphids, pod borers and other insects. Initial soil sampling was done at the depth of 0-20 cm to determine soil pH, organic matter, nitrate, ammonium, phosphorus and soil particle size. Agronomic data collected included number days to 50% flowering, number of days to 90% maturity, canopy width, plant height, peduncle length, number of pods per plant, pod length, hundred seed weight, fodder and grain yield. The collected data were subjected to analysis of variance using SAS software to determine the performance of the cowpea genotypes across the two locations and seasons. Means showing significant differences were separated using Duncan Multiple Range Test at the probability level of 5%. Data for number of days to 90% maturity, grain and fodder yields were further subjected to stability analysis through GGE biplot using Genstat software application. The results showed statistical differences for most of the studied traits as affected by genotype, location, seasonal effects and their interactions. Among the genotypes, average number of days to 50% flowering ranged from 53 to 60 days,

while number of days to 90% maturity ranged from 89 to 96 days, with line L9 being the earliest to flower and mature. Tall plants were given by Line L5 (48.94 cm), followed by L7 (48.72 cm) and L10 (48.35 cm). Breeding line L7 recorded long peduncles with a mean of 36.37 cm. Number of pods per plant had a range of 16.00 to 25.52, while pod length varied from 14.46 to 17.63 cm, with line L7 having the highest number of pods per plant with long pods. Line L3 produced least number of pods per plant and shorter pods. Local check BW produced more number of seeds per pod as compared to all the breeding lines with a mean of 12.89 seeds/pod. One hundred seed weight varied from 15.67 g to 22.70 g among the genotypes. Grain yield among the genotypes ranged from 1441.20 to 2595.20 kg/ha with the best yielder being line L7, which was followed by line L2 (1928.00 kg/ha), L10 (1891.70 kg/ha) and Local variety BW (1858.70 kg/ha). The least grain yield was observed for line L8. Among the locations, Towoomba had significantly higher grain yield than Syferkuil with mean values of 1604.20 and 1982.20 kg/ha respectively. Significantly higher grain yield was recorded in 2016/17 season with a mean value of 1854.80 kg/ha than 2015/16 season (1732.30 kg/ha). Fodder yield ranged from 1934.20 to 3611.00 kg/ha, with line L3 being the highest yielder and it was followed by line L10 with an average of 3022.00 kg/ha. Local check BW produced the least fodder yields. The GGE biplot showed that lines L2, L9 and L4 matured earlier than all other lines including local variety BW and were stable across locations and seasons in terms of maturity. The biplot identified breeding lines L7, L2, L10 and Local check BW as the highest grain yielders but only line L7 and L2 were stable across the two locations and seasons. Lines L4, L10, L3, and L2 were the highest fodder yielders but only line L2 was stable across locations and seasons. Therefore, breeding lines L7 and L2 are recommended for both grain and fodder yield in both locations.

Key words: cowpea, elite, breeding line, location, seasons, grain yield and stability.

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CHAPTER 1

INTRODUCTION

1.1. Background

Cowpea (*Vigna unguiculata*) is a leguminous crop belonging to the Fabaceae family and sub family Papillnoideae. Cowpea is the third most important grain legume crop in South Africa after groundnut and soybean. The largest production of this crop is in Sub-Saharan Africa where it is mostly used as an intercrop with cereal crops such as maize, sorghum and millet (Timko and Singh, 2008). Though it is also grown in other parts of the world, Nigeria remains the largest producer and consumer of cowpea (AATF, 2012). Cowpea plays a very important role as a source of livelihood for millions of people in West and Central Africa (Akibode and Maredia, 2011; Timko and Singh, 2008).

Cowpea is a versatile crop as it can be used as several dishes for human consumption. Almost every part of cowpea plant is consumed. The green leaves are used as vegetables, the green pods, green seeds and dried seeds are used to make relish that is served with pap (Agbogidi and Egho, 2012; Moalafi *et al*., 2010; Timko and Singh, 2008). Tarawali *et al*. (1997) reported that the stem and leaves of cowpea plants are used to make high quality hay, which is fed to livestock. Cowpea serves as the cheapest source of protein to poor resource farmers in cowpea growing areas as the dry grain contains 25 - 30% protein (Asiwe, 2017; Hall *et al*., 2003), whereas the leaves contain about 9.3 - 12.4% protein (Sebetha *et al*., 2010). The high protein content of this crop can assist in alleviating protein malnutrition. According to FAO (2010), Sub-Saharan Africa is home to some of the most nutritionally insecure people in the world. Sub-Saharan Africa holds the second highest burden of those who suffer from hunger with 239 million people as food insecure after Asia and the pacific (578 million people) (FAO, 2010). The overall number of African children who are stunted as a result of protein malnutrition increased from an estimated 43 million in 1990 to 52 million in 2008 (UNICEF, 2009).

Biradar *et al*. (2010) indicated that cowpea can assist in the conservation of soil and moisture due to its rapid growth and improved ground cover. The cowpea crop in association with rhizobia bacteria can fix atmospheric nitrogen into plant available

forms making it a suitable crop to use in rotations (Belane *et al*., 2011; Carsky *et al.,* 2002 as cited by Ekpo *et al*., 2012). Olayiwola *et al*. (2015) reported that soils on which cowpea have previously been grown have enough residual nitrogen that can support the growth of the succeeding crop in rotation which tends to be a cereal most of the time.

Nevertheless, Asiwe (2009) reported that cultivation and research on cowpea have been neglected in the last thirty years in South Africa due to unavailability of funds from the government and lack of researchers interested in the improvement of the crop. Lack of knowledge on good agronomic practices, absence of good seeds for planting and discouraging poor marginal returns to farmers were also reported to contribute to the negligence. Smallholder farmers in Limpopo, Mpumalanga and Kwa-Zulu Natal provinces are the main growers of cowpea in South Africa (Asiwe, 2009; DAFF, 2011). Asiwe (2009) also indicated that the land area planted by local farmers ranges between 0.25 and 2.0 hectare per farmer and the yields obtained from these lands are very low. These assessments confirmed that cowpea production in South Africa is still at subsistence level and necessitates detailed research on breeding and evaluation of new varieties for adaptability and stability in order to improve the yields and cowpea production in South Africa.

1.2. Problem statement

Cowpea is an important grain legume crop as it contains 25-30% protein (Asiwe, 2009; Belane *et al*., 2011; Hall *et al*., 2003). Cowpea production in Limpopo Province is constrained by shortage of improved varieties and unavailability of good seed for planting (Asiwe, 2009; Moalafi *et al*., 2010). These problems are causing farmers to have less interest in cultivating this crop, therefore resulting in low cowpea productivity. However, the breeding programme at the University of Limpopo has led to the development of high yielding and resource efficient genotypes. These genotypes have not been tested in more than one location for adaptation. There is therefore a need to screen these improved cowpea genotypes in multi-locations to test their stability and adaptation.

1.3. Motivation of the study

Food security may not be fully realised if food crops that constitute people's dietary needs are not produced in large quantities (Kalanda, 2014). Cowpea is an important grain legume crop and has the potential of improving food security, as it is widely adapted, drought tolerant (Timko and Singh, 2008) and high in protein (Asiwe, 2009; 2017). Cowpea can fix atmospheric nitrogen through its symbiotic relationship with the rhizobia bacteria (Belane *et al*., 2011). Zahran (1999) reported that the amount of nitrogen fixed by the cowpea crop ranges between 65 to 335 kg N/ha, thereby reducing its fertiliser demand and cost of production. This study selected cowpea varieties that are stable and high yielding. This was meant to increase the availability and range of varieties that farmers can grow and invariably result in increased cultivation of the crop by farmers, which will in the long term improve the protein consumption by smallholder farmer communities in Limpopo Province. Increased cowpea production will also maintain the productivity of the low input cropping systems of the smallholder farming sector.

1.4. Purpose of the study

1.4.1. Aim

The study was aimed at assessing the performance of the elite cowpea genotypes in two distinct locations

1.4.2. Objectives

The specific objectives of the study were to:

i. Determine growth, yield components and grain yield of the cowpea genotypes across two locations and seasons
ii. Determine grain yield and yield components' stability of the cowpea genotypes across the environments

1.4.3. Hypotheses

i. The cowpea genotypes do not differ in growth, yield components and grain yield in two locations and seasons
ii. Grain yield and yield components of the cowpea genotypes are not stable across the environments

CHAPTER 2

LITERATURE REVIEW

2.1. Origin, domestication and distribution

A report by DAFF (2011) indicated that there are contradicting views about the origin of cowpea because of lack of archaeological evidence. The centre of origin of cowpea is believed to be West Africa and Southern Africa because both wild and cultivated species exist in large numbers in these regions. The production of cowpea has spread to East and central Africa, India, Asia, South and Central America. The highest genetic diversity of primitive wild species of cowpea are found in the southern region of the African continent currently encompassed by Namibia, Botswana, Zambia, Zimbabwe, Mozambique, Swaziland, and South Africa (DAFF, 2011). Padulosi (1993), cited by Ademeyi (2011) indicated that the most primitive species of cowpea were observed in the Transvaal (consists of Gauteng, Limpopo and Mpumalanga Provinces), Western Cape and Swaziland.

2.2. Description of cowpea

Cowpea (*Vigna unguiculata* (L.) Walp) is a self-pollinating and climbing annual crop in the family Fabaceae grown for its edible seeds and pods. The cowpea plant is usually erect and possesses ribbed stems and smooth trifoliate leaves arranged alternately on the stems (DAFF, 2011; Timko and Singh, 2008). The plant produces cluster of flowers at the end of a peduncle and 2 to 3 pods per peduncle. The pods are smooth, cylindrical curved and straight, reaching up to 35 cm in length, with distinctive coloration, usually green, purple or yellow. The pods may contain seed ranging from 8 to 18 per pod, as the seeds reach maturity the pod changes colour to tan or brown (Timko and Singh, 2008).

A report by DAFF (2011) indicated that cowpea seeds might be white, cream, green, red brown or black in colour or be a mottled combination. The seed may also possess an ‘eye’ where a darker colour is surrounded by a lighter colour (Timko and Singh, 2008). Cowpea can reach 80 cm in height and as an annual plant, survive for only one growing season before harvest. Cowpea is also regarded as black-eyed pea, southern pea, field pea (Timko and Singh, 2008).

2.3. World cowpea production

According to DAFF (2011) World annual cowpea grain production is 3 million tons that is produced on 12.5 million hectares but only a small proportion enters the international trade. West and Central Africa is the leading cowpea producing regions in the world producing 64% of the estimated 3 million tons of cowpea seed produced annually. Nigeria is the world's leading cowpea producing country, followed by Brazil, other countries in Africa, e.g. West Africa, Senegal, Ghana, Mali and Burkina Faso. Ghana, Niger and Cameroon are significant producers (Akibode and Maredia, 2011). The major production areas elsewhere in the world are Asia (India, Myanmar) and the Americans (USA, Brazil, West Indies) (Akibode and Maredia, 2011). Conservative estimates suggest that greater than 12.5 million ha are planted annually to cowpea around the world. Of this area, about 9.8 million ha are planted in West Africa, making it the region with the largest production and consumption of cowpea in the world (DAFF, 2011).

2.4. Production levels of cowpea in South Africa

DAFF (2011) reported that small-scale farmers achieve cowpea production in South Africa under rain-fed farming conditions but there are no records regarding the size of area under production and yields produced. However, Asiwe (2009) reported that land area that farmers produce cowpea ranges between 0.5 to 2.0 hectares per farmer. The major cowpea producing areas in South Africa are Limpopo, Mpumalanga, North-West and KwaZulu-Natal (DAFF, 2011). A study by Asiwe (2009) showed that farmers in Limpopo and KwaZulu-Natal grow cowpea for consumption and as a source of income.

It was also indicated by Asiwe (2009) that in Limpopo province most farmers plant cowpea under mixed planting while in KwaZulu-Natal the most cowpea cropping system used is row cropping. Farmers prefer important traits such as seed colour, seed size, growth habit and maturity periods. Maturity periods were reported to be mostly preferred by Limpopo farmers based on the duration of rainfall. In Limpopo Province, some farmers choose early maturing varieties in order to escape moisture deficits and frost damage. Farmers who choose late maturing types were more interested on the fodder for livestock feeding. On the other hand, KwaZulu-Natal farmers preferred cowpea varieties based on growth habit (Asiwe, 2009).

2.5. Nutritional importance of cowpea

Cowpea plays a very important role as a source of livelihood for millions of people in the developing world (Akibode and Maredia, 2011; Timko and Singh, 2008). Cowpea provides nutritious grain and an inexpensive source of plant protein for rural dwellers as the grain contains protein content that ranges from 23 to 32% (Asiwe, 2017; Hall *et al*., 2003; Nielson *et al*., 1993) and 64% carbohydrate (Bressani, 1985). Cowpea has the same nutritional profile with other pulses as they have a low fat content, a protein content that is two to four times higher than cereals and tuber crops (Lambot, 2002).

The proteins in cowpea seeds are rich in amino acids lysine and tryptophan when compared to cereal grains, but low in methionine and cysteine when compared to animal proteins (Timko and Singh, 2008). Cowpea seeds are also a rich source of minerals and vitamins (Hall *et al*., 2003) and among plants have one of the highest contents of folic acid and vitamin B necessary during pregnancy to prevent birth defects in the brain and spine of the child (Timko and Singh, 2008). Cowpea leaves contain protein content ranging from 27 to 34% (Tarawali *et al*., 1997).

2.6. Economic and agronomic importance of cowpea

Almost every part of the cowpea plant is consumed as the green leaves of cowpea are used as vegetables, the green pods, green seeds and dried seeds (Singh *et al.*, 2002). Timko and Singh (2008) indicated that the most important part of cowpea plant is the grain, which is consumed by humans. The dry seed can be cooked whole and be used as a dish to compliment the low protein cereals and tuber crop staples or milled, fresh seeds and green pods can also be cooked (Nielsen *et al.,* 1993). In some areas, fresh or dried cowpea leaves are also consumed as a side dish therefore providing significant nutritional value. Tarawali *et al*. (1997) reported that cowpea leaves and stems are important sources of livestock feed as they can produce high quality hay for animals to feed on during the dry season.

The cowpea value chain involves many people contributing to the development of the commodity in many countries. This chain includes producers (farmers), transporters, traders of the commodity and those working in the local value addition enterprises (AATF, 2012). A report by AATF (2012) indicated that many farmers where only surviving on cowpea farming as a business and selling their cowpea harvests enable

them to not only buy supplementary cereal grains such as maize meal or rice but also inputs for the next season.

Cowpea is also a valuable component of farming systems in regions where soil fertility is low, especially nitrogen (AATF, 2012) This is due to its unique ability to fix atmospheric nitrogen at a higher rate when it is in a symbiotic relationship with the beneficial bacteria (Belane *et al*., 2011; Singh *et al*., 2003). Cowpea can withstand extensive range of soil pH better than other leguminous plants (Fery, 1990 as cited by Ademeyi, 2011). Its ability to fix high amounts of nitrogen makes it an efficient main component in crop rotation systems as it replenishes soil fertility for succeeding cereal crops (Belane *et al*., 2011). Cowpea can withstand extreme temperatures (AATF, 2012) and tolerate moisture stress (Magloire, 2005) better than many legumes, which makes it even suitable in marginal rainfall areas.

2.7. Cowpea production constraints in South Africa

According to Asiwe (2009), cowpea research and commercial production in South Africa have been abandoned for the last thirty years. Cowpea production is further limited by shortage of improved varieties or cultivation of low yielding unimproved varieties by the farmers (Asiwe, 2009; Moalafi *et al*., 2010), lack of knowledge of good agronomic practices, unavailability of good seeds and low returns farmers are getting (Asiwe, 2009). A study by Asiwe (2009) indicated that pest damage, diseases and weeds are among constraints to cowpea production in South Africa. It was further noted that drought, lack of large markets for farmer's produce, poor pricing and shortage of storage facilities serve as barriers to the increased production of this crop.

Cowpea is susceptible to a wide range of bacterial, fungal and viral diseases and different types of insect pests (Timko *et al*., 2007). The major insect pests that affect cowpea are aphids (*Aphis craccivora*), thrips (*Megaluro thripssjostedti*) and Maruca pod borer (*Maruca vitrata*). Parasitic weeds such as *Striga gesnerioides* and *Alectra vogeliii* also constitute some of the limitations to cowpea production in Africa (Timko *et al.,* 2007). Asiwe (2009) also reported aphids, thrips, pod-sucking bugs and cowpea weevil as major insect pests in cowpea. Among the diseases, virus diseases seemed to be affecting cowpea the most than fungal and bacterial diseases in South Africa.

Some of the devastaiting cowpea diseases are Bacterial blight, Cowpea yellow mosaic virus and Brown blotch. Bacterial blight is caused by bacterium *Xanthomonas,* this disease can reduce yield up to 90% and emergence in infected seeds by 67% (Asiwe, 2009). Cowpea yellow mosaic virus is caused by yellow mosaic virus. This diseases is destrictive and can cause yield reduction up to 80-100% (Williams, 1977 as cited by Kumar *et al*., 2017). Brown blotch is caused by *Colletotrichum capsica,* this disease was reported by Mark and Channya (2016) to be destructive, causing up to 85% damage. Seed-borne diseases are especially problematic as smallholder farmers use home-grown seed in the production of the crop.

2.8. Environmental requirements for cowpea production

According to Bull *et al.* (1992) and Kang (2005), the yielding ability of a genotype is due to favourable interaction between the environment and genotype. The environmental factors such as soil characteristics and soil fertility, soil moisture, relative humidity, air temperature and photoperiod length differ across seasons and locations and they significantly affect crop growth and development.

2.8.1. Soil

DAFF (2008, 2011) reported that cowpeas can be grown under a wide range of soil types varying from sandy to clay soil and it is more tolerant to infertile and acidic soil than other leguminous crops. There are different views regarding suitable soil pH for cowpea production. Dugje *et al.* (2009) reported that cowpeas give a reasonable yield when grown in well-drained soil with a pH ranging from 5.6 to 6.5. This is because the rhizobia bacteria that is responsible for biological nitrogen fixation in association with the crop does not survive under waterlogging conditions as well as under highly acidic soils, while DAFF (2011) and Zahran (1999) reported that cowpea yield well in soils with a pH ranging from 5.6 to 6.0. On the other hand, Ekpo *et al*. (2012) reported that cowpeas grow best on loamy soil with a soil pH ranging from 6.0 to 7.0.

2.8.2. Fertilisation

Nkaa *et al*. (2014) indicated that phosphorus is important for cowpea production as phosphorus fertilisers significantly improved growth and yield characters of the three cowpea genotypes they studied and they recommended phosphorus application rate of 40 kg/ha for cowpea production. Haruna and Usman (2013) also reported that

phosphorus is important as it stimulates growth, initiates nodule formation and influences the efficiency of the rhizobium-legume symbiosis resulting in improved biological nitrogen fixation. For cowpea to nodulate and fix the atmospheric nitrogen into available forms, it requires phosphorus more than nitrogen and about 30 kg/ha of phosphorus in the form of SUPA is recommended (FAO, 2005). FAO (2005) indicated that cowpea does not require nitrogen fertilization as this will result in luxurious growth with poor grain yields but starter nitrogen of about 15 kg/ha is sometimes required for good cowpea growth.

2.8.3. Moisture

Water is very important for plant growth, development and productivity. Permanent or temporary water stress limits the growth and the performance of cultivated plants more than any other environmental factor (Lobato *et al*., 2008). Cowpea can grow well under rainfall ranging from 400 to 700 per annum which is well distributed (DAFF, 2011). AATF (2012) and Timko and Singh (2008) have reported that cowpea can tolerate moisture stress more than other leguminous crops such as soybean, mung bean and others. as it has a deep tap root system which allows the crop to extract moisture deep in the soil profile. Though cowpea is drought tolerant, moisture stress during reproductive stage causes a sharp decline in flowering and grain filling leading to poor yields (Ahmed and Suliman, 2010; Shiringani, 2007). Abayomi and Abidoye (2009) reported that days to onset of flowering increase with increased moisture stress, that is, cowpea genotypes flowered earlier when moisture stress was mild and flowered late when moisture stress was severe.

Ahmed and Suliman (2010) reported that subjecting cowpea genotypes to moisture stress during vegetative stages has no effect on seed yield as growth resumes when moisture becomes available. However, they also reported that subjecting cowpea to moisture stress during reproductive stages results in abscission of flowers, poor pod set and poor grain filling thereby leading to reduced grain yield. This suggests that cowpea should be planted in such a way that the critical stages coincide with the period when moisture is available or there should be supplementary irrigation to avoid moisture stress during flowering and grain filling stages to achieve high yields.

2.8.4. Temperature

Hall (1992) reported that high temperature adversely affects productivity of many crops and these adverse effects are the result of planting date. Cowpeas grow and yield well at a mean temperature of 27 ^{o}C (Ekpo *et al.,* 2012). Ehlers and Hall (1996), cited by Ekpo *et al*. (2012), reported that many cowpea varieties have heat induced suppression of floral bud development. Such genotypes will flower two weeks later than flowering usually occurs if they are grown in very hot field conditions under long days. Ahmed *et al*. (1992) reported that the first four weeks after cowpea have germinated are most critical because if the seedlings are exposed to very hot nights for two consecutive weeks or more, complete suppression of the development of the first five floral buds on the main stem of the sensitive varieties is always the end result. This suppression can reduce pod set, number of seeds per pod and consequently reduce grain yield.

2.9. Variety selection

According to Patel and Hall (1986), variety selection is an important decision that plant breeders and growers have to make year after year. Variety selection is the foundation for effective and successful crop management plan. Becker and Leon (1988), Misra and Panda (1990) and Patel and Hall (1986) indicated that although weather conditions cannot be predicted during the growing season, selection of the right variety could assist in minimising weather related risks. The performance of a variety may vary from season to season even within the same field; these differences are due to differences in the climatic and soil factors in the field (Hussain *et al*., 2011). When varieties are tested over a range of locations and years their performance changes, indicating that some varieties are better adapted to specific environments than others (Yan and Tinker, 2006). Becker and Leon (1988) indicated that to minimise risks, variety selection should be based on the variety information obtained from performance trials that have been replicated in different locations and years. This will enable selection of varieties that have high and stable yield within a region and across years.

2.10. Genotype by environment interaction (GEI)

Multi-environment trials (MET) are a set of experiments repeated in number of locations or over several years. Multi-environment trials result in the phenomena known as genotype by environment interaction (Yan and Tinker, 2006). Multiple environment trials are important in plant breeding as they assist in selecting the best performing genotypes at different locations or over a number of years by providing essential information before its commercial release (Yan and Tinker, 2006). Sabaghnia (2015) defined genotype by environment interaction as the failure of two or more genotypes to have the same response to a test environment.

According to Dixon *et al*. (1991), genotype by environment interaction occurs in two ways. Firstly, the difference between genotypes varies without alteration in their rank i.e. genotype by environment interaction is present as one genotype yields more than another genotype in all the environments. Secondly, the ranking between the genotypes changes across environments, while the other genotype is more productive in another environment. The inconsistent yield performance of genotypes in different environments may be a contributing factor to productivity due to large genotype by environment interaction (Misra and Panda, 1990).

This genotype by environment interaction poses a serious problem in breeding programmes as it can have an influence at any stage of the breeding programmes from identifying appropriate sources or parent materials to selecting the best genotype but it can also play a pivotal role in expressing the quantitative traits (Yan and Hunt, 2001). Yan and Tinker (2006) also indicated that the studying and understating of the genotype by environment interaction is important to plant breeders in the sense that these interactions can limit the progress in the selection process and it is the basic cause of differences between genotypes for yield stability. Yan (2001) explained that understanding the cause of genotype by environment interaction can assist in the selection of genotypes with best adaptability and that give stable yields. Breeders and farmers desire genotypes that show low genotype by environment interaction and have high stable yields as this indicates that the environment has less effect on them and their high yields are largely because of their genetic composition.

Beyene *et al*. (2012) indicated that when genotype by environment interaction is present, the best thing the breeder can do is to use stability analysis in order to identify

the highest yielding and stable genotypes. Yan (2001) suggested the sites regression model as the appropriate model for analysing multi-environment trials when large yield variation is as a result of differences in the environments. The sites regression model uses a graphical display known as the genotype plus genotype by environment (GGE) biplot. This biplot identifies genotypes that are superior in different environments and therefore, the estimation of stability performance becomes important to identify consistent and high yielding genotypes.

2.11. Importance of genotype by environment interaction

Yan and Hunt (2001) indicated that understanding of environmental and genotypic causes and their interaction is important at all the stages of breeding. This includes ideo-type design, parental line selection, selection based on traits and selection based on yields. Yan and Kang (2003) opined that knowledge and understanding of genotype by environment interaction is necessary to establish breeding objectives, identify ideal test conditions and recommend environments for optimal cultivar adaptations. Evaluation of newly developed cowpea genotypes in several locations is necessary so that their performance and adaptability can be determined before commercial release.

2.12. Types of genotype by environment interactions

Yan and Kang (2003) classified genotype by environment interaction into three different types viz: no interaction, non-crossover and crossover interaction, where crossover interaction is further sub-dived into three categories.

2.12.1. No interaction genotype by environment interaction

A no genotype by environment interaction occurs when one genotype performs better than the other genotype across all the test environments (Simmonds, 1979: Yan and Kang, 2003). A no genotype by environment is indicated in Figure 2.1(a) which shows that genotype A and B responses are parallel in the two test environments.

2.12.2. Non-crossover genotype by environment interaction

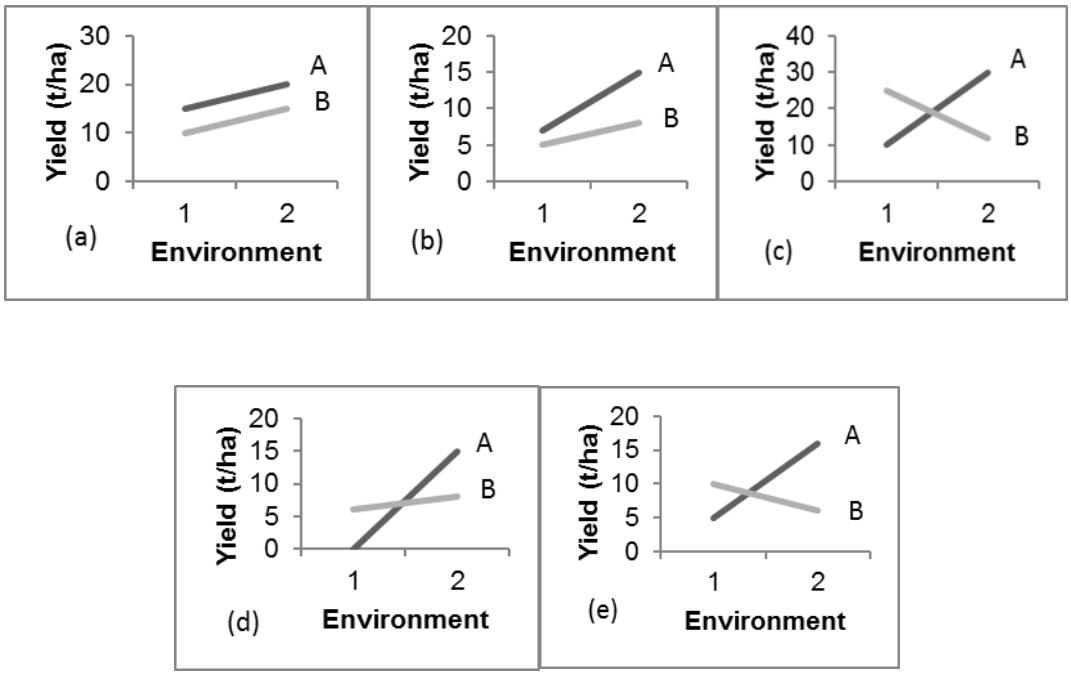
Kang (2005) reported that non-crossover genotype by environment interaction occurs when one genotype consistently outperforms the other genotype across all the test environments. In non-crossover genotype by environment interaction, both genotype

A and B increase but unequal intergenotypic difference in the two test environments (Yan and Kang, 2003) (Figure 2.1(b).

2.12.3. Cross-over genotype by environment interaction

According to Acquaah (2007) crossover genotype by environment interaction is mostly important to plant breeders. Crossover genotype by environment interaction occurs when genotype A is more productive in one environment and genotype B is more productive than genotype A in the other location. Yan and Kang (2003) divided crossover genotype by environment interaction into three categories based on intergenotypic differences.

i. Crossover interaction – genotypic modification by the environment in opposite direction but intergenotypic differences remains the same (Figure 2.2(c).
ii. Crossover interaction – unequal intergenotypic difference but both genotype A and B increase (Figure 2.2(d).
iii. Crossover interaction – unequal intergenotypic difference in the two test environments, genotype A shows an increase whereas genotype B shows a decrease in the test environment 2 (Figure 2.2(e).



Adapted from Yan and Kang (2003)

Figure 2.1: Types of genotype by environment interactions

2.13. Concepts of genotypic stability

Becker and Leon (1988) indicated that in order for plant breeders to recommend new varieties, the varieties have to exhibit high performance for yield and other important agronomic traits and in addition to that, the variety must be stable over a wide range of environmental conditions. A stable genotype is the one that has a constant performance regardless of the environmental changes (Becker and Leon, 1988). Aliyu and Makinde (2016) reported that twenty-one cowpea genotypes were evaluated in the southern guinea savanna agro-ecology of Nigeria where six genotypes among them were selected based on their phenotypic stability for immediate farmer use and future crop improvements. Olayiwola *et al*. (2015) also reported that seven cowpea genotypes were evaluated for stability over four years in Abeokuta South-western Nigeria and only one genotype was selected as best combiner of high yield and stability across four seasons.

Becker and Leon (1988) differentiated concepts of stability into static and dynamic. With the static or biological concept of stability, a genotype has a consistent performance even if the environmental conditions change. This means that differences between the tests environments is zero and the stable genotypes exhibit minimal variance in contrasting environments. On the other hand, with the dynamic or agronomic concept of stability, the performance of a stable genotype in each environment corresponds to the estimated level. Hussain *et al*. (2011) indicated that the most stable genotype might not be the highest yielder, so this necessitates the use of yield performance and stability to enable selection of superior genotypes or high yield stability. High yield stability is the ability of a genotype to have a consistent performance over a wide range of environments with high performance. Becker and Leon (1988) and Lin *et al*. (1986) classified stability statistics into four distinctive groups:

i. Group A – based on deviation from average genotype effect; represents sums of squares
ii. Group B – based on genotype by environment interaction; represents sums of squares

iii. Groups C and D – based on either deviation from average genotype effect or genotype by environment interaction; represent regression coefficient or deviations from regression.

Lin *et al*. (1986) further allocated these stability statistics groups to three classes of stability:

i. Group A – Type 1 stability

This type of stability is equal to biological stability; a genotype is stable if it has minimal variance in contrasting environments

ii. Group B and C – Type 2 stability

The type 2 stability is equal to agronomic stability; a genotype in this type of stability is stable if its response to test environments is parallel to response of all genotypes in a test.

iii. Group D – Type 3 stability

In type 3 stability, a genotype is stable if the residual mean square following regression of genotype performance on environmental index is small.

2.14. Methods used to measure stability

Stability measures can be characterised into univariate and multivariate analysis. Several statistical procedures have been developed to improve the understanding of genotype by environment interaction and its relationship to stability.

2.14.1. Univariate stability analysis

Freeman (1973) termed the main type of stability analysis, joint regression analysis or joint linear regression. Joint regression analysis involves the regression of the genotypic means on an environmental index. This stability measure provides a means of testing whether the genotypes have characteristic linear responses to changes in environments. The joint regression analysis was first proposed by Yates and Cochran (1938) and was widely used and reviewed by numerous authors (Becker and Leon, 1988; Crossa, 1990; Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Freeman, 1973; Lin *et al*., 1986).

i. Regression analysis (b_i)

Joint linear regression is a model used for analysing and interpreting non-additive genotype x environment interaction of two-way classification data. The genotype x environment interaction is partitioned into a component due to the linear regression (b_i) of the i^{th} genotype on environmental mean, and a deviation (d_{ij})

$$(GxE)_{ij} = b_i E_j + d_{ij} \quad \text{... (1)}$$

and therefore

$$Y_{ij} = \mu + G_i + E_j + (b_i E_j + d_{ij}) + e_{ij} \text{ ... (2)}$$

Where: E_j is the environmental index, b_i is the regression coefficient that measures the response of the genotype on varying environments, d_{ij} stands for the deviation from regression of the i^{th} genotype at j^{th} environment. Y_{ij} is the observed mean of the i^{th} genotype at the j^{th} environment, for i = 1, 2.....,n, and j= 1, 2,.....,n; μ is the overall mean of the i^{th} genotype; G_i is the effect of the i^{th} genotype, E_j represents the effect of the j^{th} environment and e_{ij} is the mean error related to the observed Y_{ij}.

The regression coefficient was introduced by Finlay and Wilkinson (1963) as the regression of the mean of i^{th} genotype in j^{th} environment on the mean performance of all genotypes in that environment and is expressed as:

$$bi = 1 + \left[\frac{\Sigma_i (X_{ij} - X_i - X_j + X)(X_j - X)}{\Sigma_j (X_j - X)^2}\right] \text{ ... (3)}$$

Where: X_{ij} is the performance of the i^{th} genotype in j^{th} environment. X_i is the mean performance of the i^{th} genotype and X_j is the mean performance on the j^{th} environment. X is the overall mean.

Finlay and Wilkinson (1963) indicated that a genotype is considered to have adaptation to a specific environment if its regression line crosses that for overall mean performance. A genotype is regarded to have low performance adaptability across environments if its regression line is placed below that for the overall mean performance. The regression coefficient (b_i) mainly indicates the adaptation of a genotype to several environments and describes linear response between environments (Finlay and Wilkinson, 1963). However, Eberhart and Russel (1966) and Yue *et al*. (1997) have opined that regression coefficient does not reflect stability and

crop performance. Altay (2012) also suggested that the regression coefficient is a preferable method for the assessment of specific or wide adaptation of genotypes. Therefore, it is not advisable to use regression coefficient in determining genotype stability.

ii. Deviation mean square (S^2d_i)

Eberhart and Russell (1966) suggested using the mean of squared deviations from regression (S^2d_i) (Equation 4) for measuring stability. The authors defined a stable genotype as the one that has a small deviation from regression mean squares.

$$S^2d_i = \frac{1}{E-2}[\sum_i(X_y - X_i - X_j + X)^2 - (b_i - 1)^2\sum_i(X_j - X)^2] \quad \text{... (4)}$$

All the components in this formula have their usual meanings, which are indicated in equations 1, 2 and 3.

According to Eberhart and Russell (1966), genotypes are grouped based on their variance of the regression deviation (either equal or not to zero). A genotype with variance in regression deviation equal to zero is highly predictable, whilst a genotype with regression deviation more than zero has less predictable response. Although, regression models have been displayed to be the most useful approach for determining genotype stability. Becker and Leon (1988), Crossa (1990) and Westcott (1986) have found a number restrictions and criticisms. One of the problems of this analysis is that the mean of all genotypes in each environment is considered as a measure of the environmental index and is used as an independent variable in the regression. According to the regression analysis assumptions, no independence can be among the variables, particularly when the numbers of genotypes are less than 15 (Becker and Leon, 1988 and Crossa, 1990). Furthermore, the authors indicated that the variation in regression coefficient result is most often so small making it difficult to rank the genotypes for stability and adaptability. Westcott (1986) reported that regression analysis should be used with caution when the data set includes results from only a few low or high performance sites; since the genotype fit may be determined greatly by its performance in a few extreme environments, leading to the generation of misleading results.

iii. Cultivar superiority measure (P_i)

Lin and Binns (1988) proposed the superiority measure (P_i) of the i^{th} genotype as the performance difference comparison among a set of genotypes compared with a reference genotype with the maximum performance within each environment. The model is as follows:

$$P_i = \frac{\sum_{j=1}^{n}(X_{ij}-M_j)^2}{2E} \quad \text{... (5)}$$

.

Where X_{ij} is the average performance of the i^{th} genotype in the j^{th} environment, M_j is the genotype with maximum performance among all genotypes in the j^{th} environment and E is the number of environments.

According to Lin and Binns (1988) small P_i values indicate less distance between the i^{th} genotype and the genotype with maximum performance and the stable genotypes. Although this measure does not have restrictions of the regression model, it has however been reported to extremely measure genotype performance rather than stability (Fasahat *et al*., 2015). This is because this method is based on both the average genotype and genotype x environment interaction effects and each genotype is compared only with the genotype that has maximum performance at each environment (Fasahat *et al*., 2015).

2.14.2. Multivariate approaches for stability analysis

There are different multivariate models that are more commonly used for measuring genotype stability, which are AMMI and GGE biplot.

i. The additive main effects and multiplicative interaction (AMMI)

The additive main effects and multiplicative interaction (AMMI) gives information on the main and multiplicative interaction effects in addition to a biplot. AMMI model intergrates analysis of variance and principal component anlysis into a unified approach that can be used to analyse multi-location trials (Gauch and Zobel, 1996) AMMI has been reported by Annicchiarico (1997a) and Fasahat *et al*. (2014) to be specifically efficient for illustrating adaptive genotype responses and is recently suggested as a replacement to the joint regression analysis for most of the breeding

programmes (Annicchiarico, 1997b). However, AMMI have been reported by Carbonell (2004) and Fasahat *et al*. (2015) to need greater number of genotypes, small number of replications, and also several years of evaluation in comparison with other models. Furthermore, AMMI results are difficult to interpret as compared to other stability methods and the method is incapable of finding close relationship between high performance and stability (Annicchiarico, 1997a; Fasahat *et al*., 2015).

ii. Genotype plus genotype by environment (GGE) biplot

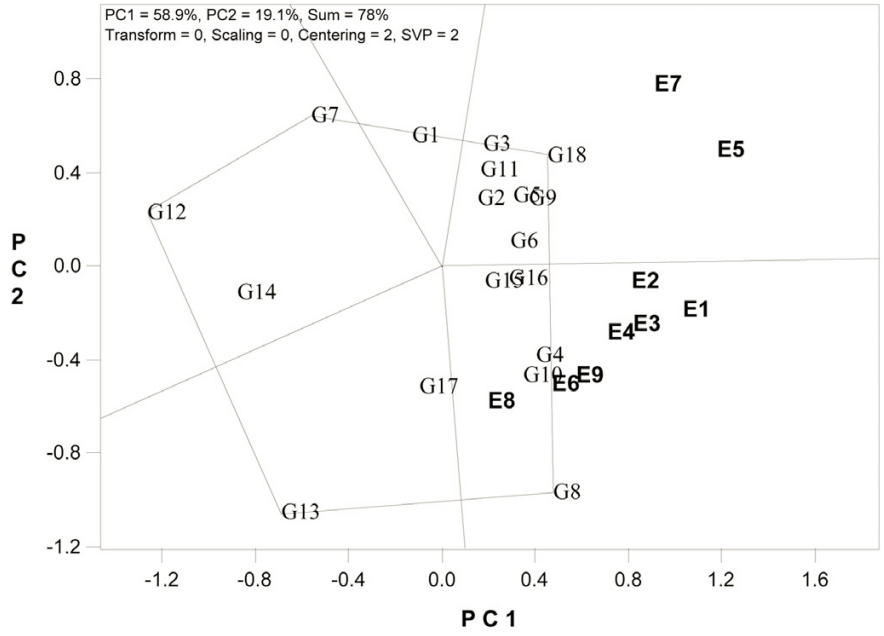
The GGE biplot technique was developed by Yan *et al*. (2000) to represent genotype main effects and genotype by environment interaction graphically. Although biplot analysis is not sensitive to the number of genotypes, it is the best predictor of genotype stability for a small number of genotypes (Rose *et al*., 2008). Although AMMI and GGE are equivalent in achieving predictive accuracy, the GGE biplot analysis considers both the genotype (G) and genotype by environmnet (GE) interaction effects and graphically displays genotype by environment interaction in a two-way table (Yan *et al*., 2000). GGE biplot is an effective method based on principal component analysis (PCA) to fully explore multiple environment trial data. GGE biplot allows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions (Yan *et al*., 2000).

GGE biplot is an effective tool for:

- Mega-environment analysis (e.g. “which-won-where” pattern),

The “which won where” pattern of the GGE biplot assists in recommending specific genotypes to specific mega-environments (Ezeaku *et al*., 2015; Olayiwola *et al*., 2015; Yan and Kang, 2003; Yan and Tinker, 2006). To construct the “which-won-where” patterns from the biplot, lines that connect the furthest genotypes in the biplot in such a way that the lines form a polygon where all other genotypes are contained inside. Then perpendicular lines to each side of the polygon are drawn starting from the origin of the biplot where the lines subdivide the polygon into sectors involving different environments and genotypes (Yan and Tinker, 2006; Yan *et al*., 2007). Dehghani *et al*. (2006) and Yan and Tinker (2006) stated that the genotype that is located at the corner of one polygon is the best performer in that environment included in that sector. The environment that is situated far away from the origin discriminates the genotypes

more than those near the origin (Figure 2.2). For example, the nine environments fell into two sectors with different genotypes being the highest performers in those two sectors. G18 was the highest yielding genotype in E5 and E7 while G8 was the highest yielding genotype in all other environments (Figure 2.2).



Adapted from Yan *et al*. (2007)

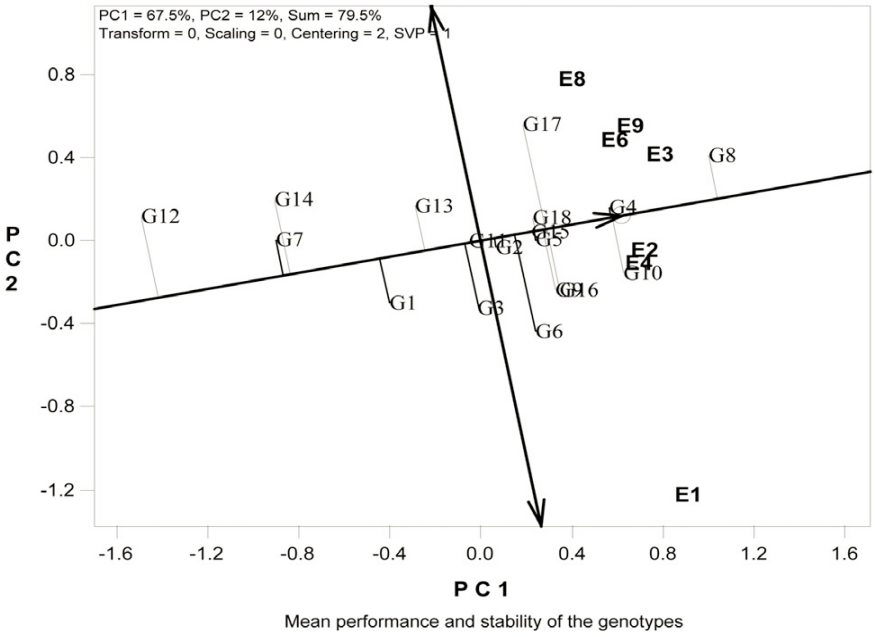
Figure 2.2: GGE biplot: "which won where" polygon. G = genotype, E = environment

- Genotype evaluation (the mean performance and stability)

Genotype evaluation is meaningful only for a specific mega-environment, and an ideal genotype should have both high mean performance and high stability within a mega-environment (Yan *et al*., 2007). The abscissa (single-arrowed) and the ordinate (double arrowed and is perpendicular to the AEC abscissa) of the Average Environment Coordinate (AEC) are the two lines passing through the origin of the biplot (Figure 2.3). The small circle on the abscissa delineates the AEC which is the environment PC1 and PC2 mean scores (Yan and Kang, 2003). This AEC view is based on genotype-focused singular value partitioning (SVP), that is, the singular values are entirely partitioned into the genotype scores (SVP = 1) (Yan, 2001). This AEC view with SVP = 1 is also referred to as the "Mean vs. Stability" view as it facilitates genotype comparisons based on mean performance and stability across environments within a mega-environment (Yan *et al*., 2007). The arrow shown on the axis of the AEC abscissa points in the direction of higher mean performance of the genotypes and, consequently ranks the genotypes with respect to mean performance

(Yan, 2001; Yan and Kang, 2003). The genotypes are therefore ranked as follows: G8 > G4 = G10 > G5 = G9 = G15= G16 = G17 = G18 > G6 > G2 > Mean = G11 > G3 >G13 > G1 > G14 > G7 > G12 (Figure 2.3).

Yan and Kang (2003); Yan *et al*. (2007) indicated that the projection on the abscissa towards the ordinate of the Average Environment Coordinate (AEC) irrespective of direction is a measure of stability. Therefore, G4 was the most stable genotype, as it was located almost on the AEC abscissa and had a near zero projection onto the AEC ordinate. In contrast, G17 and G6 were two of the least stable genotypes with above average mean performance (Figure 2.3).



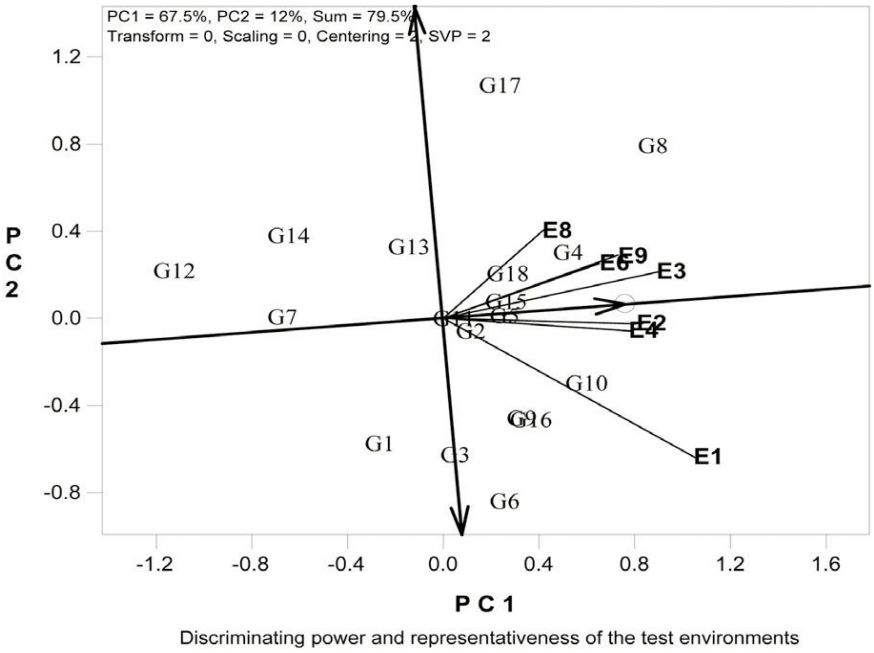
Adapted from Yan *et al*. (2007)

Figure 2.3: GGE biplot: Mean vs stability. G = genotype, E = environment

- Environmental evaluation (the power to discriminate among genotypes in target environments)

Yan (2001); Yan *et al*. (2007) reported that the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis. Yan and Kang (2003); Yan *et al*. (2007) reported that the purpose of test-environment evaluation is to identify test environments that effectively identify superior genotypes for a mega-environment. The authors indicated that an “ideal” test environment should be both discriminating of the genotypes and representative of the mega-environment. Figure 2.3 is the same GGE

biplot as Figure 2.4 except that it is based on environment-focused scaling (Yan, 2001), that is, the singular values were entirely partitioned into the environment scores (SVP = 2) so that it is appropriate for studying the relationships among test environments (Yan *et al*., 2007). Yan *et al*. (2007) reported that the test environments with longer vectors (like E1) are more discriminating of the genotypes. If a test environment marker falls close to the biplot origin, that is, if the test environment has a very short vector, it means that all genotypes performed similarly in that environment (Yan *et al*., 2007). The environment evaluation also indicates the test-environments' representativeness of the mega-environment. Yan *et al*. (2007) reported that the test environments that have small angles with it (e.g., E2, E3, E4, E6, and E9 are more representative of the mega-environment than those that have larger angles with it, e.g., E1 and E8) (Figure 2.4).



Adapted from Yan *et al*. (2007)

Figure 2.4: GGE biplot: Representativeness and discriminatory power. G = genotype, E = environment

Farshadfar *et al*. (2012) and Yan and Kang (2003) have proposed that GGE biplot analysis is a useful method for the analysis of genotype by environment interactions and stability. The GGE biplot had been exploited in the variety evaluation of several crops such as wheat (Yan and Hunt 2001; Yan *et al*., 2000), maize (De Oliveira *et al*., 2016), okra (Olayiwola and Ariyo, 2013) and cowpea (Ezeaku *et al*., 2015; Olayiwola *et al*., 2015).

2.15. Farmers' preferences in cowpea varieties

Recommendation of cowpea varieties for release should also meet farmer preference, as this will ensure that farmers adopt these newly released genotypes. The results of survey study conducted by Asiwe (2009) indicated that farmers in Limpopo Province preferred among others, maturity periods (77.8%), seed colour (70.4%) and seed size (25.9%). The seed colours identified by farmers varied from red (from light red to dark red), cream, white with varying eye colours (back, brown and grey), black and mottled colours (brown, white, grey or red). Asiwe (2009) reported that farmer preference for maturity periods were based on the length of rainfall and occurrence of frost. Asiwe (2009) further indicated that Limpopo farmers preferred both early, for escaping drought and frost and late maturing varieties for higher fodder production. Seed size preferred where between medium and large seed. The recommended genotypes must therefore meet the specified traits required by Limpopo Province farmers to ensure greater adoption of these genotypes.

CHAPTER 3

MATERIALS AND METHODS

3.1. Study sites

The experiments were conducted at the University of Limpopo experimental farm (Syferkuil) in Mankweng and Towoomba research station located in Bela-Bela, Limpopo Province during 2015/16 and 2016/17 growing seasons. The soil at Syferkuil is sandy loam in texture and belongs to Hutton form. Mean average summer day temperature at Syferkuil varies from 28° C to 30° C while the area receives mean annual rainfall ranging from 400 to 600 mm. At Towoomba, the average annual rainfall is 630 mm with the rainy season usually extending from October to March. The average summer temperature ranges from 17.6° C to 30.2° C. The soil is sandy loam in texture and belongs to the hutton form. The coordinates of the two locations are given in Table 3.1.

Table 3.1: Description of the two study sites

Location	Coordinates	Altitude (m above sea level)
Syferkuil	23°51'S, 29°42'E	1250
Towoomba	24°25’S, 28°21’E	1184

3.2. Plant materials

Planting materials included ten elite cowpea breeding lines (L1-L10) and a control check Bechuana White (BW) (Table 3.2). The breeding lines were developed in South Africa. The parental lines of the ten breeding lines were sourced from International Institute of Tropical Agriculture, Ibadan, Nigeria and Bechuana White is a South African cultivar.

Table 3.2: Seed characteristics of cowpea genotypes that were used in the study

Identification	Coat colour	Coat texture	Growth habit
L1	White	Wrinkled	Upright
L2	White	Wrinkled	Spreading
L3	White	Wrinkled	Spreading
L4	White	Rough	Upright
L5	Cream	Smooth	Upright
L6	Brown	Smooth	Spreading
L7	White	Smooth	Upright
L8	Brown	Rough	Upright
L9	White	Rough	Upright
L10	White	Wrinkled	Spreading
BW (Local check)	White	Smooth	Spreading

3.3. Research design and procedures

The land was prepared using harrow and disc plough to enhance good seedbed. The trial was laid out in a Randomized Complete Block Design consisting of three replications.. The genotypes were planted at an inter-row and intra-row spacing of 1 m and 0.3 m respectively, in two rows of 6 m length. The trials were planted when rainfall was consistent in each location as the trials were under dry land conditions without any supplementary irrigation. The first season planting was done on 11 and 18 January 2016 in Syferkuil and Towoomba, respectively and the second planting was done on 13 and 14 December 2016 in Syferkuil and Towoomba, respectively. Round-up (isopropylamine salt of glyphosate) and Dual (S-metalachlor) at a rate of 3 L/ha and 0.5 L/ha, respectively were used to control weeds before emergence. Selective post-emergence herbicides Fusilade (fluazifop-p-butyl) and Bentazone (bentazon) both at the rate of 3 L/ha were applied 3 weeks after emergence of the crops to control weeds in the field. Manual weeding was carried out on growing weeds in the field when necessary. Insecticide Karate (lambda-cyhalothrin) and Aphox (pirimicarb) at the rate of 1 L/ha and 500 g/ha, respectively were applied to control aphids, pod borers and other insects from seedling stage until pod maturity. Vine separation was done before flowering to avoid intertwining of genotypes and to ease harvesting.

3.4. Data collection

3.4.1. Soil sampling and laboratory analysis

Representative soil samples were taken from the experimental plots during the two seasons at the two locations using soil auger at the depth of 0-20 cm. Laboratory analyses were done on the soil samples to determine soil pH, nitrate, ammonium, available phosphorus and percentage organic carbon. Soil pH was measured in soil: water ratio of 1:2.5 as described by Eckert (1988) while Ammonium and Nitrate nitrogen were determined by colorimetric determination. Available P was extracted using Bray1 extractable P as described by Kuo (1996). Organic carbon was determined by Walkley-Black method as described by Jackson (1967).

3.4.2. Agronomic data

The following agronomic parameters were collected virtually the same way in the two locations and seasons.

Table 3.3: Agronomic parameters recorded

Number of days to 50 percent flowering	This was calculated as days from planting to when 50 percent of the plants in each plot have flowered.
Number of days to 90 percent to maturity	This was calculated as days from planting to the day when 90 percent of the pods within the plot have dried.
Plant height	This was measured from the ground surface to the tip of the growing point using meter rule on five randomly selected plants at maturity and recorded in centimetres.
Canopy width	This was measured from the outer edges of each row (swath) using meter rule and recorded in centimetres.
Peduncle length	This was measured from the base of the peduncle to its tip using meter rule averaged over five randomly selected plants and recorded in centimetres.
Number of pods per plant	All the pods per plant were harvested, counted and averaged over five plants.
Pod length	The length of five randomly selected pods per plot were measured using a rule and average length per pod expressed in centimetres.

Number of seeds per pod	The total number of seeds in each pod were counted and averaged over five pods.
Hundred seed weight	Two samples of hundred good seeds were randomly counted and weighed in grams using digital scale. Their average was computed.
Seed weight	After threshing the dried pods from each net plot, the seeds were weighed using digital weighing scale and expressed in kilograms. Seed weights were then converted to kilograms per hectare.
Dry fodder weight	The fresh fodder was sun-dried and weighed using top loading scale to determine dry fodder weight in kilograms. Fodder weights were then converted to kilograms per hectare.
Harvest index	Harvest index was determined by using the following formula:- HI = Grain yield/fodder weight

3.4.3. Weather data

Monthly averages of rainfall and temperature for the two locations and seasons were obtained from University of Limpopo Experimental Farm weather records and Agricultural Research Council - Institute for Soil, Climate and Water.

3.5. Data analysis

Data for agronomic characteristics of the two locations and seasons were subjected to analysis of variance using SAS software to determine the performance of different genotypes across locations and seasons as well as to establish genotype by environment interaction. Means that showed significance were separated using Duncan Multiple Range Test at the probability level of 5%. GGE biplot analysis was performed using Genstat to determine the effect of genotype by environment interaction on cowpea genotypes and to determine stability of the tested genotypes.

CHAPTER 4

RESULTS AND DISCUSSION

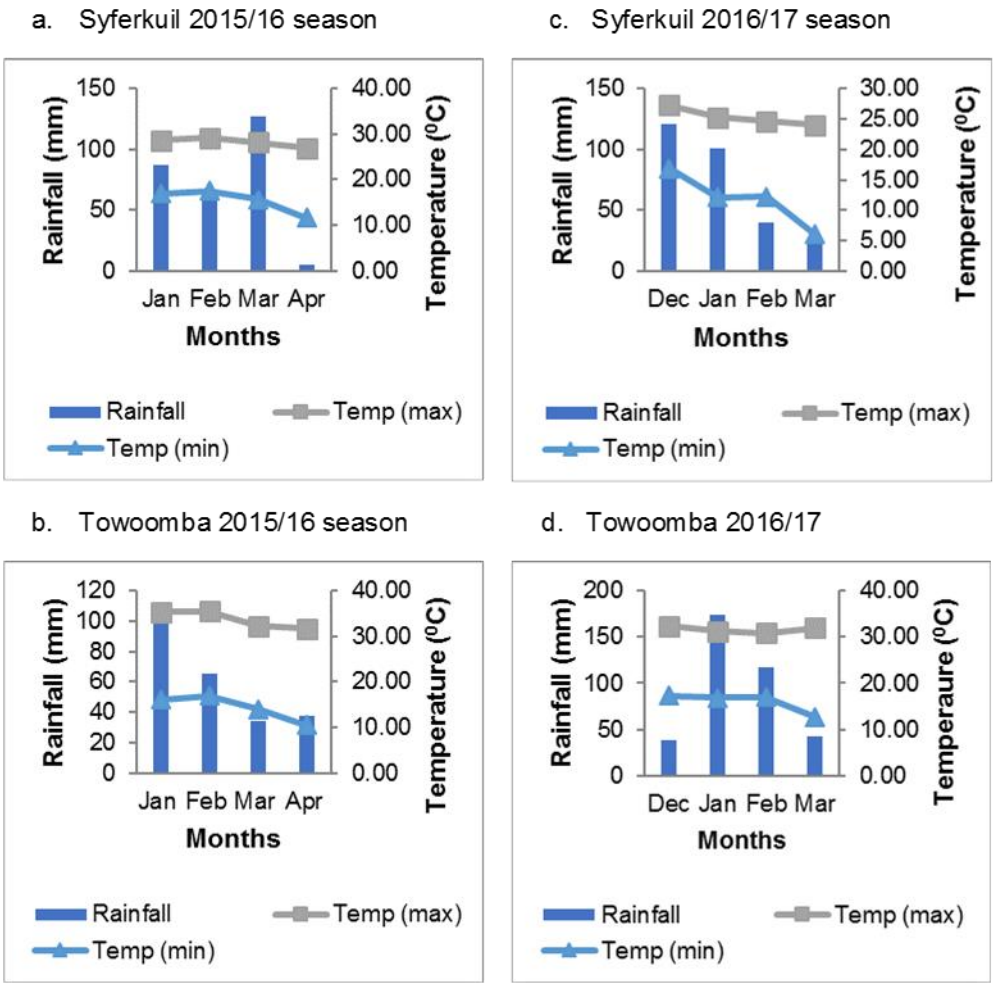
4.1. Soil analysis and weather results

Physio-chemical characteristics of the experimental areas during the two seasons are shown in Table 4.1. The Particle size analysis showed that the soil type of the experimental areas in both seasons were sandy loam with a very high proportion of sand, less silt and much less clay. The results from the chemical analysis showed that the soil was slightly alkaline in Syferkuil in the 2015/16 season and moderately alkaline in the 2016/17 season whereas in Towoomba the soil was moderately acidic in both seasons. Organic carbon content was adequate only in Syferkuil in 2015/16 season (1.84%), whereas the levels were very low at Syferkuil in 2016/17 (0.58%) and Towoomba with 0.24% in 2015/16 and 0.65% in 2016/17 (Table 4.1). This is based on the organic carbon critical level of 1% as established by Kyei-Boahen *et al*., (2017). Available P was high but not adequate at Towoomba in the 2016/17 season and Syferkuil in the 2015/16 season with an average of 2.22 and 2.05 mg/kg, respectively which are lower than 7.0 mg/kg established by Aune and Lai (1995) as the critical soil available P level required for proper growth and development of cowpea. Available P was low at Towoomba in the 2015/16 season and Syferkuil in the 2016/17 season. Ammonium was 0.95, 0.79, 0.77, and 0.88 mg/kg whereas nitrate was 0.19, 0.16, 0.14 and 0.15 mg/kg at Syferkuil 2015/16, Syferkuil 2016/17, Towoomba 2015/16 and Towoomba 2016/17, respectively (Table 4.1).

Table 4.1: Physio-chemical properties of the soil in the two experimental sites during the two seasons

Soil composition	Syferkuil		Towoomba	
	2015/16 season	2016/17 season	2015/16 season	2016/17 season
Physical properties				
Clay	3	2	11	8
Silt	13	14	16	16
Sand	84	84	73	76
Textural class	Sandy loam	Sandy loam	Sandy loam	Sandy loam
Chemical compositions				
pH in H_2O (1:2.5)	7.4	8.2	5.9	5.8
Organic carbon (%)	1.84	0.58	0.24	0.65
Organic matter (%)	3.17	1.00	0.41	1.12
Available P (mg/kg)	2.05	1.49	1.35	2.22
Ammonium (mg/kg)	0.95	0.79	0.77	0.88
Nitrate (mg/kg)	0.19	0.16	0.14	0.15

The total rainfall during the growing period at Syferkuil was 277 and 285 mm for 2015/16 and 2016/2017 cropping seasons, respectively (Figure 4.1 a & c), whereas in Towoomba the total rainfall was 239 and 373 mm, respectively (Figure 4.1 b & d). During 2015/16 season, most of the rainfall occurred in March at Syferkuil but the peak of the rain at Towoomba was in January. During 2016/17 season, peak rainfall occurred in December and January at Syferkuil, while at Towoomba most rainfall occurred in January and February (Figure 4.1 a-d). Temperatures at the locations during the two cropping seasons were slightly different. Towoomba was generally hotter than Syferkuil in both cropping seasons and 2015/16 season was hotter than 2016/17 season which was cooler (Figure 4.1 a-d).



Source: Agricultural Research Council - Institute for Soil, Climate and Water and University of Limpopo weather station records

Figure 4.1: Mean monthly rainfall, minimum and maximum temperatures during the growing seasons at the two locations

4.2. Growth and reproductive components of elite cowpea genotypes

4.2.1. Number of days to 50% flowering

4.2.1.1. Effects of cowpea genotypes, locations and seasons

The analysis indicated significant differences (P≤0.05) among the locations (L), genotypes (G), seasons (S), genotype x location (GxL), genotype x season (GxS), season x location (SxL) and genotype x season x location (GxSxL) interactions (Table 4.2). Kamai *et al*. (2014) also reported that number of days to 50% flowering varied significantly between the cowpea genotypes, locations and seasons. Akande (2007) reported significant variation between cowpea genotypes (G), season x location (SxL), genotype x season (GxS) and genotype x season x location (GxSxL), but reported

non-significant variation between locations (L) and genotype x location (GxL) interaction effects; this is in partial agreement with the findings of the study.

Cowpea genotypes attained 50% flowering early when planted at Towoomba and took longer at Syferkuil with mean values of 55 and 56 days, respectively (Table 4.5). These may be attributed to high day and night temperatures that were prevalent at Towoomba during both seasons. Similarly, cowpea genotypes reached 50% flowering earlier in 2015/16 season than in 2016/17 season with mean values of 54 and 56 days, respectively (Table 4.5). These might be ascribed by the fact that 2015/16 season was generally hotter than 2016/17 season in both locations. Averaged across the two locations and seasons, early flowering was observed in line L9 with a mean of 53 days and L7 took longer to attain 50% flowering with a mean value of 60 days. The control check BW also attained 50% flowering late with a mean of 57 days ranking second after L7 (Table 4.5). The difference between the genotypes shows that they differ genetically with respect to 50% flowering. This corroborates with the findings of Kamai *et al.* (2014) who reported that cowpea genotypes vary in terms of flowering duration.

4.2.1.2. Interactive effect of cowpea genotype x season x location on number of days to 50% flowering

At Syferkuil during 2015/16 growing season, line L2 displayed minimum days to flowering (52 days) followed by lines L10 and L8 both with 53 days. Line L9 took maximum days to reach 50% flowering with average of 57 days, followed by line L3 and local check BW both with 55 days. In 2016/17 growing season, line L9 flowered early with 51 days. During this season breeding lines that delayed to reach 50% flowering were lines L7, L3 and local check BW with mean values of 64, 63 and 60 days, respectively (Figure 4.2).

At Towoomba during 2015/16 growing season, cowpea line L2 reached 50% flowering early with mean value of 52 days, which was followed by lines L1 and L5 both with mean values of 54 days. Breeding line that attained 50% flowering late was L10 (57 days) followed by local check BW and line L7 both with 56 days. In 2016/17 growing season, cowpea line that flowered early was L9 (51 days) followed by lines L10 and L3 both with mean values of 52 days, respectively. Late flowering was recorded in line

L7 (65 days) which was followed by local check BW with an average of 60 days (Figure 4.2). The presence of the three-way interaction (GxSxL) indicated that genotypes responded differently to the seasonal and climatic factors, especially temperature which was reported by Summerfield (1980) to be the dominant factor that affects duration to flowering in cowpea. Jadhav *et al*. (1991) reported that higher day and night temperatures along with moderate humidity favours early flowering in cowpea. In their study, Jadhav *et al*. (1991) reported that night temperature and humidity plays a major role in flowering than day length and indicated that flowering was delayed as the night temperatures became cooler and relative humidity reduced below 68%. Nevertheless, Summerfield (1980) mentioned in their study that warmer temperature hastens the initiation of flowering in day-length sensitive breeding lines.

Table 4.2: Analysis of variance for number of days to 50% flowering

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	1.89	0.95	0.28	0.7556^{ns}
Location (L)	1	56.03	56.03	16.72	0.0002*
LxR	2	3.94	1.97	0.59	0.5601^{ns}
Genotype (G)	10	451.31	45.13	13.47	<.0001*
GxL	10	106.89	10.69	3.19	0.0037*
GxLxR	40	161.26	4.03	1.20	0.2740^{ns}
Season (S)	1	144.27	144.27	43.06	<.0001*
SxL	1	88.36	88.36	26.37	<.0001*
GxS	10	340.64	34.06	10.17	<.0001*
GxSxL	10	83.55	8.36	2.49	0.0182*
Error	44	147.42	3.35		
Total	131	1585.56			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

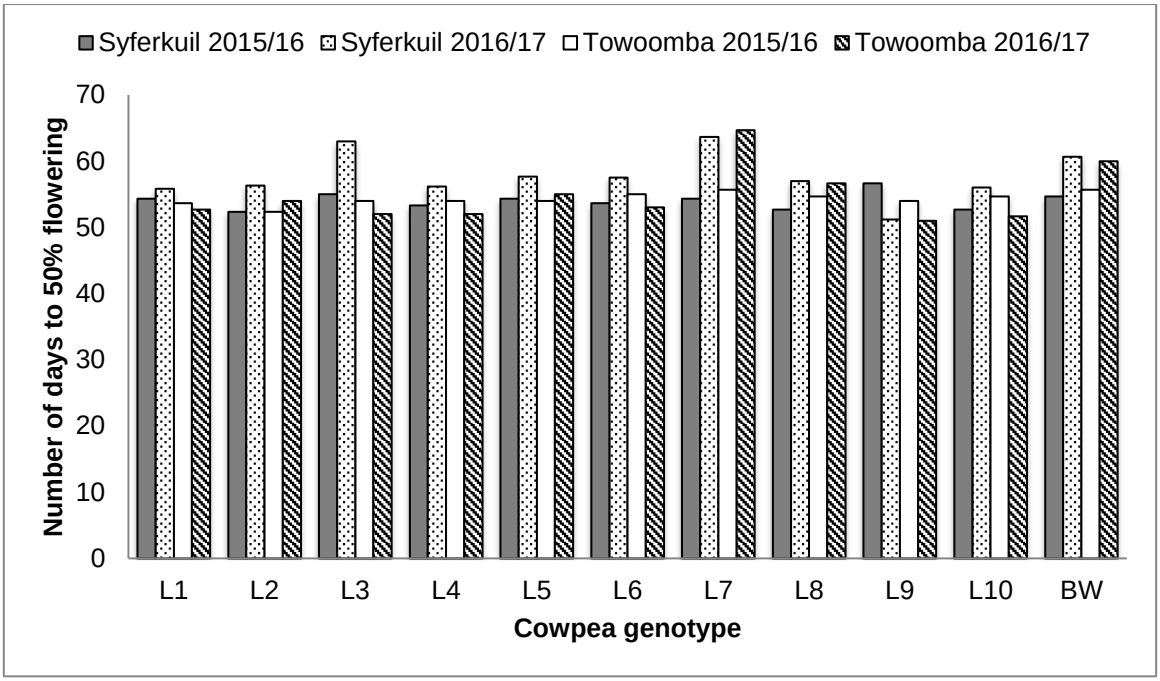


Figure 4.2: Interactive effect of cowpea genotype x season x location on number of days to 50% flowering

4.2.2. Number of days to 90% maturity

4.2.2.1. Effects of cowpea genotypes, locations and seasons

Highly significant differences (P≤0.05) were observed for the effect of genotypes (G), seasons (S), genotype x location (GxL) and genotype x season (GxS) (Table 4.3). This suggests that some genotypes matured earlier in one location and season but were relatively late in the other location and season. The results of Kamai *et al*. (2014) are in agreement with the results of the current study, as they reported significant variation among year and genotypic effects. The cowpea genotypes matured early in 2015/16 season (91 days) as compared to 2016/17 season (96 days) (Table 4.5). This may be due to high temperatures that were observed in 2015/16 season than in 2016/17 season. Averaged across the two locations and seasons, almost all the breeding lines including the local check BW matured late with mean range of 94 days in line L10 to 96 days in line L7. The breeding lines that matured early were L9 (89 days) and L2 (90 days) (Table 4.5). This indicates that the genotypes used in this study are predominantly early to medium maturing.

4.2.2.2. Interactive effect of cowpea genotype x location on number of days to 90% maturity

At Syferkuil, cowpea line L9 matured early with an average of 88 days. The breeding line that took longer to mature was L3 with an average of 98 days. At Towoomba, breeding lines that matured early were L9 (90 days) and L2 (91 days). The local check BW and L7 matured late than any other breeding lines with average of 98 and 97 days, respectively (Figure 4.3). Figure 4.3 shows that almost all the breeding lines in Towoomba matured earlier than when they were grown in Syferkuil. This may be ascribed to high temperatures that were prevalent in Towoomba during pod ripening. These results are in accordance with the results of Ishiyaku *et al*. (2017) who reported highly significant differences for maturity periods because of the interaction of cowpea genotype x location (GxL).

4.2.2.3. Interactive effect of cowpea genotype x season on number of days to 90% maturity

During 2015/16 season, the cowpea line that matured early was L9 (85 days). The breeding line that took longer to attain maturity late was L7 (98 days). During 2016/17 season, early maturity was attained by lines L9 and L2 both with 93 days. The breeding lines that took longer to reach maturity were L3, L1, L8 and L6 all with an average of 99 days (Figure 4.4). Warmer temperatures were observed in 2015/16 season as compared to 2016/17 season which had cooler temperatures, thus most of the cowpea breeding lines matured earlier when grown in 2015/16 season due to high temperatures which were reported. Craufurd *et al*. (1996) reported that in day neutral cowpeas, temperature is the determinant for rate of reproductive development. Their statement was supported by Ehlers and Hall (1996) who also indicated that temperature does have an influence on maturity of cowpea. In their study Craufurd *et al*. (1996) also indicated that the optimum average temperature for reproductive development of cowpea to be around 28^{o}C.

Table 4.3: Analysis of variance for number of days to 90% maturity

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	4.55	2.27	0.19	0.8249^{ns}
Location (L)	1	10.09	10.09	0.86	0.3594^{ns}
LxR	2	17.73	8.87	0.75	0.4766^{ns}
Genotype (G)	10	561.72	56.17	4.78	0.0001*
GxL	10	334.72	33.47	2.85	0.0081*
GxLxR	40	417.97	10.45	0.89	0.6464^{ns}
Season (S)	1	807.59	807.59	68.65	<.0001*
SxL	1	12.43	12.43	1.06	0.3097^{ns}
GxS	10	446.72	44.67	3.80	0.0010*
GxSxL	10	99.05	9.91	0.84	0.5917^{ns}
Error	44	517.58	11.76		
Total	131	3230.16			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

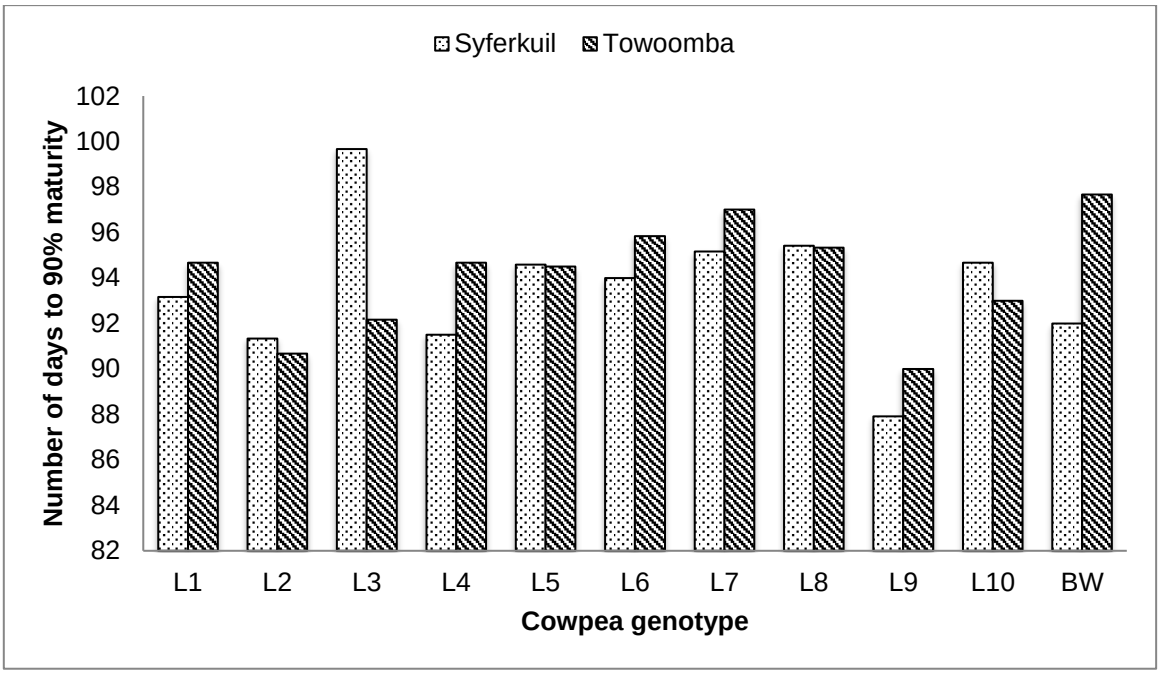


Figure 4.3: Interactive effect of cowpea genotype x location on number of days to 90% maturity

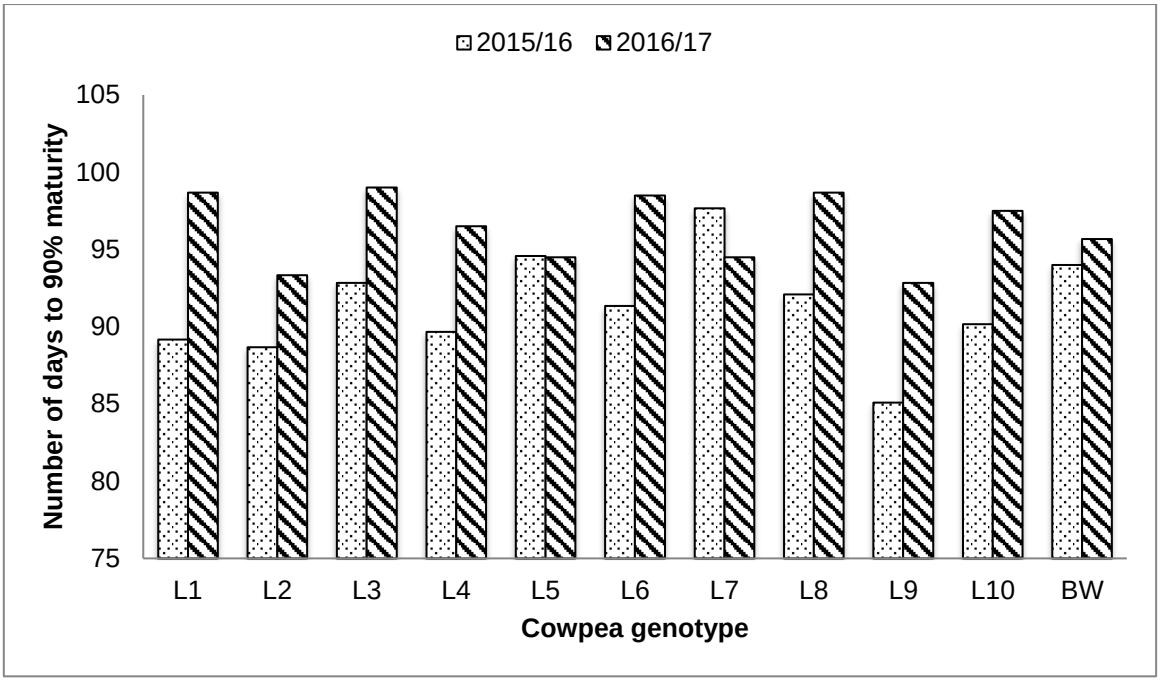


Figure 4.4: Interactive effect of cowpea genotype x season on number of days to 90% maturity

4.2.3. Canopy width

4.2.3.1. Effects of cowpea genotypes, locations and seasons

Highly significant differences (P≤0.05) were observed among the locations (L) and a significant season x location (SxL) and genotype x season x location (GxSxL) interactions were observed; however, the effect of genotypes (G), seasons (S) and genotype x location (GxL) and genotype x season (GxS) interactions were not significantly different (Table 4.4). The absence of significant variation in cowpea genotypes shows that the genotypes had almost the same width of the canopy cover across the locations and seasons. The widest canopy cover was observed when the lines were tested at Towoomba (65.14 cm) than when planted at Syferkuil (57.38 cm) (Table 4.5). This may be due to high moisture regime that was observed at Towoomba, especially in 2016/17 season. Most of the genotypes that had wider canopy cover were the spreading types.

4.2.3.2. Interactive effect of cowpea genotype x season x location on canopy width

At Syferkuil during 2015/16 season, local check BW gave the widest canopy cover with an average of 76.67 cm, followed by L6 (70.00 cm). Line L3 recorded the narrowest canopy cover with a mean of 50.00 cm, followed by L4 and L9 with mean

values of 51.67 and 52.33 cm, respectively. In 2016/17 growing season the breeding lines which had the widest canopy cover was L3 (69.75 cm) followed by L7 and L6 with mean values of 65.42 and 61.08 cm, respectively. L4 had a narrow canopy cover with an average of 44.92 cm (Figure 4.5). Most of the breeding lines in 2016/17 season had the narrowest canopy cover than other breeding lines in any other environment except for L7 which showed to be most tolerant to moderately alkaline soils in the area. The narrowest canopy in Syferkuil was mainly because plant growth was negatively affected by moderately alkaline soil in the area in 2016/17 season.

At Towoomba during 2015/16 season, line L4 had the broadest canopy cover with a mean of 70.33 cm. The narrowest canopy cover was attained by L5 (56.33 cm) followed by L8 (59.33 cm). During 2016/17 season, Local check BW had the broader canopy cover of 75.00 cm, followed by breeding lines L3 and L5 both with a mean of 72.08 cm. Line L2 recorded the narrowest canopy cover with a mean of 55.83 cm (Figure 4.5). Biradar *et al*. (2010) reported that canopy cover is important as it assist in the conservation of soil moisture by reducing evaporation due to reduced soil temperatures in the canopies. The widest canopy cover was also reported by Ndiso *et al*. (2017) to suppress weed growth, thus reducing competition that might be exerted by the weeds on growth and yields. In their study, Ndiso *et al*. (2017) however mentioned that the genotypes that produce the widest canopy and high biomass tend to have low seed yield, therefore farmers need to know which cowpea genotype is best suited for their production i.e. grain or fodder.

Table 4.4: Analysis of variance for canopy width

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R	2	589.85	294.93	3.86	0.0286*
Location (L)	1	1985.94	1985.94	25.97	<.0001*
LxR	2	677.19	338.59	4.43	0.0177*
Genotype (G)	10	1455.54	145.55	1.90	0.0704^{ns}
GxL	10	1266.36	126.64	1.66	0.1224^{ns}
GxLxR	40	3350.48	83.76	1.10	0.3828^{ns}
Season (S)	1	30.55	30.55	0.40	0.5306^{ns}
SxL	1	334.09	334.09	4.37	0.0424*
GxS	10	1213.75	121.38	1.59	0.1423^{ns}
GxSxL	10	1617.29	161.73	2.11	0.0435*
Error	44	3364.69	76.47		
Total	131	15885.73			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

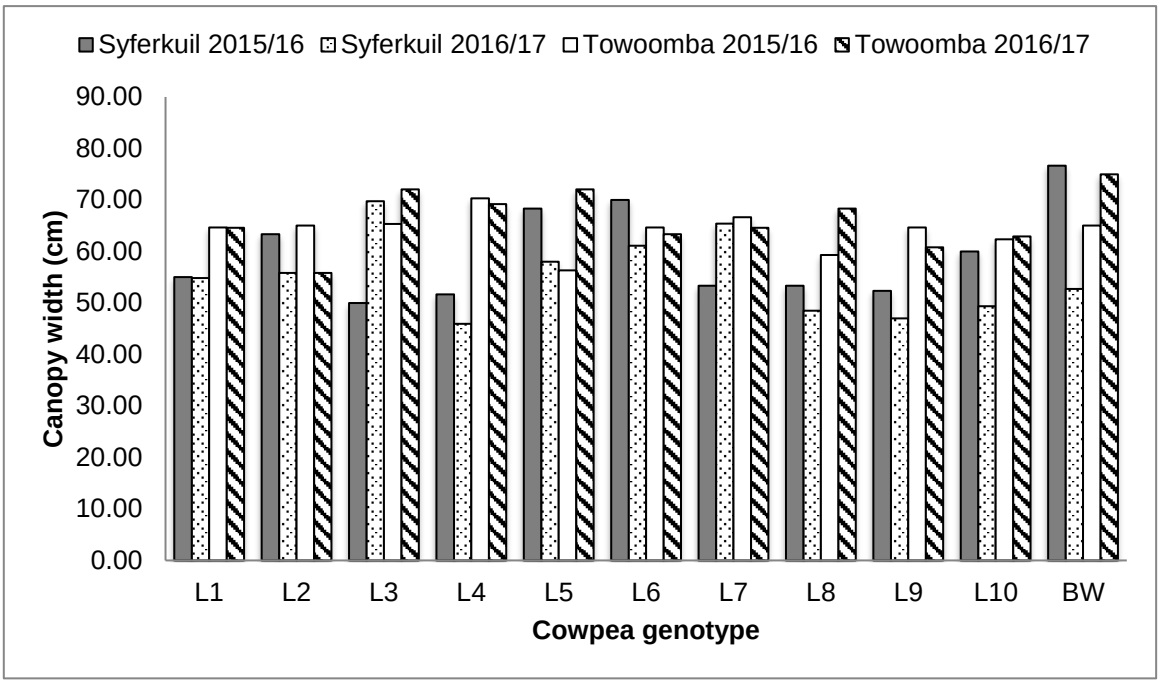


Figure 4.5: Interactive effect of cowpea genotype x season x location on canopy width

Table 4.5: The effects of location, genotype and season on number of days to 50% flowering, number of days to 90% maturity and canopy width of eleven cowpea genotypes

VARIABLE	Days to 50% flowering	Days to 90% maturity	Canopy width (cm)
LOCATION (L)			
SYFERKUIL	56[a]	94[a]	57.38[b]
TOWOOMBA	55[b]	94[a]	65.14[a]
SEM	**0.17**	**0.35**	**1.19**
GENOTYPE (G)			
L1	54[de]	94[a]	59.77[a]
L2	54[de]	90[c]	60.00[a]
L3	56[c]	96[a]	64.29[a]
L4	54[de]	93[ab]	59.27[a]
L5	55[cd]	95[a]	63.69[a]
L6	55[cd]	95[a]	64.77[a]
L7	60[a]	96[a]	62.50[a]
L8	55[cd]	95[a]	57.38[a]
L9	53[e]	89[c]	56.21[a]
L10	54[de]	94[a]	58.65[a]
BW (Local check)	58[b]	95[a]	67.35[a]
GRAND MEAN	**55**	**94**	**61.26**
SEM	**0.58**	**0.37**	**2.26**
SEASON (S)			
2015/16	54[b]	91[b]	61.74[a]
2016/17	56[a]	96[a]	60.78[a]
SEM	**0.23**	**0.42**	**1.08**

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

4.2.4. Plant height

4.2.4.1. Effects of genotypes, locations and seasons

Significant differences (P≤0.05) were observed for the effect of locations (L), genotypes (G), seasons (S), genotype x location (GxL), genotype x season (GxS), location x season and genotype x season x location (GxSxL) (Table 4.6). The effect of location showed that genotypes were significantly taller at Syferkuil (46.10 cm) than at Towoomba (43.33 cm) (Table 4.8). This may be due high organic matter and good nutrient status that led to the production of taller plants that were observed in Syferkuil in the 2015/16 season. Similarly, the tallest plants were observed in 2015/16 season (48.05 cm) than in 2016/17 season (41.38 cm) (Table 4.8). Averaged across both locations and seasons, the tallest plants were observed in breeding lines L5, L7, L10,

L8 and L9 with mean values of 48.94, 48.72, 48.35, 46.72 and 46.52 cm, respectively however, these breeding lines were statistically not different from each other. The shortest plants were observed in local check BW (28.63) (Table 4.8). The presence of all the interactions (GxL, GxS, LxS and GxSxL) serves as an indication that the environment especially weather factors had a huge influence on plant height of the breeding lines. This agrees with the results of Ichi *et al*. (2013) who reported that the environmental and genotypic effects played a significant role in their effects on cowpea plant height. Most of the lines that have smaller plants are the spreading types for example, line L3 and Local check BW.

4.2.4.2. Interactive effect of cowpea genotype x season x location on plant height

At Syferkuil in 2015/16 season, plant height ranged from 48.80 to 63.92 cm. The breeding lines that had taller plants were L5, local check BW, L8, L6 and L10 with mean values of 63.92, 63.91, 63.58, 63.40 and 62.83 cm, respectively. The shortest plants were observed in line L1 (47.80 cm). In 2016/17 season as shown by Figure 4.6, plant height was greatly reduced in all breeding lines except for L7. This reduction may be due to moderately alkaline soils and low rainfall during vegetative growth stage that was observed during 2016/17 season at Syferkuil. This is in accordance with the findings of Goenaga *et al*. (2013) who reported that cowpea is sensitive to alkaline soils leading to stunted plant growth. The tallest plants were recorded in line L7 (50.9 cm) with the shortest plants obtained by line L3 (20.90 cm) (Figure 4.6).

At Towoomba in 2015/16 season, plant height ranged from 33.74 to 47.59 cm. This was due low rainfall during vegetative stage. The tallest plants were observed for line L10 (47.59 cm) while line L6 recorded the shortest plants with an average of 33.74 cm. In 2016/17 season, plant height was greater than the previous season. This may be attributed to higher moisture availability during vegetative stage and better nutrient status observed in the 2016/17 season. The tallest plants were recorded in lines L5 and L7 with mean values of 58.33 and 58.23 cm, respectively. The shortest plants were obtained in lines L6 (38.17 cm) and L2 (39.12 cm) (Figure 4.6). The results of the current study are in accordance with the findings of Abayomi and Abidoye (2009) who reported that cowpea height ranges from 20 to 65 cm; however, this contradicts the findings of Basaran *et al*. (2011) who reported higher range (101 to 123 cm). In their study, Basaran *et al*. (2011) indicated that cowpea grows best at day

temperatures range of 25 to 35 ^{o}C, with night temperatures above 15 ^{o}C and its growth is retarded at altitudes above 700 meters above sea level. This confirms the findings of this study since the altitudes in the two locations are above 700 meter above sea level as indicated in Table 3.1.

Table 4.6: Analysis of variance for plant height

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R	2	73.71	36.86	1.01	0.3719^{ns}
Location (L)	1	253.04	253.04	6.95	0.0116*
LxR	2	94.24	47.12	1.29	0.2845^{ns}
Genotype (G)	10	1486.62	148.66	4.08	0.0005*
GxL	10	1185.00	118.50	3.25	0.0032*
GxLxR	40	2347.75	58.69	1.61	0.0620^{ns}
Season (S)	1	1468.13	1468.13	40.30	<.0001*
SxL	1	6903.78	6903.78	189.52	<.0001*
GxS	10	1608.14	160.81	4.41	0.0003*
GxSxL	10	817.44	81.74	2.24	0.0323*
Error	44	1602.85	36.43		
Total	131	17840.69			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

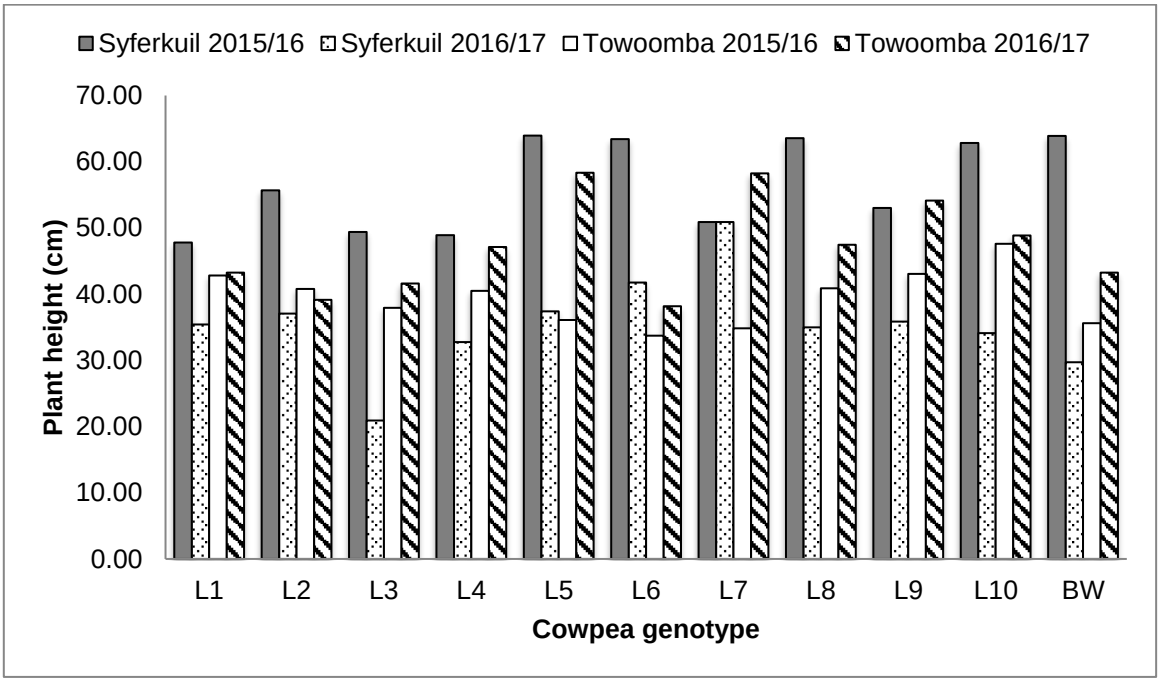


Figure 4.6: Interactive effect of cowpea genotype x season x location on plant height

4.2.5. Peduncle length

4.2.5.1. Effects of cowpea genotypes, locations and seasons

The analysis revealed non-significant differences (P≤0.05) among the locations (L), genotype x location (GxL) and genotype x season x location (GxSxL), nevertheless the effect of genotypes (G), seasons (S), genotype x season (GxS) and location x season (LxS) interactions were found to be statistically different (Table 4.7). The results agree with the findings of Kamai *et al*. (2014) who reported significant variations in peduncle length of cowpea varieties as influenced by genotypic effects. The genotypes produced the longest peduncles in 2015/16 season with a mean value of 35.52 cm as compared to when they were grown in 2016/17 season (Table 4.8). This is because in Syferkuil during 2016/17 season the plants recorded shorter peduncles because of very high soil pH that hampered plant growth and development. Averaged across both locations and seasons, the longest peduncles were recorded for cowpea line L7 (36.37 cm) whereas local check BW recorded the shortest peduncles with a mean value of 28.63 cm. All other breeding lines had longer peduncles as compared to the local check BW (Table 4.8). Ezeaku *et al*. (2015) also reported that improved cultivars always have longer peduncles as compared to local varieties.

4.2.5.2. Interactive effect of cowpea genotype x season on peduncle length

During 2015/16 season, peduncle length ranged from 30.60 to 39.53 cm. The longest peduncles were obtained by lines L5, L10 and L4 with mean values of 39.53, 38.38 and 38.23 cm, respectively. The shortest peduncles were observed for L2 (30.60 cm). During 2016/17 season, peduncle length ranged from 23.80 to 37.23 cm. The longest peduncles were recorded for line L7 (37.23 cm) whereas local check BW had the shortest peduncles with an average of 23.80 cm (Figure 4.7). This shows that the cowpea genotypes responded differently as influenced by the environmental conditions.

4.2.5.3. Interactive effect of location x season on cowpea peduncle length

The breeding lines recorded the longest peduncles when grown at Syferkuil during 2015/16 season with mean value of 39.05 cm while the shortest peduncles were recorded at Syferkuil during 2016/17 season with an average of 28.51 cm. The shortest peduncle reported at Syferkuil in 2016/17 season were mainly because of soil

alkalinity that was observed in the area that adversely affected the growth of the cowpea breeding lines. The breeding lines recorded intermediate peduncles when grown at Towoomba during both seasons with mean values of 32.01 cm during 2015/16 season and 34.41 cm during 2016/17 season (Figure 4.8). Hall *et al.* (1997) reported that the longest peduncle tends to display the pods above the canopy, this is important as this provides fewer oviposition sites for pests particularly pod borers. Kamai *et al*. (2014) indicated that when cowpea with long peduncles are grown under heavy rainfall conditions, they are less likely to be damaged by wet and dry pod rot organisms as pods dry out more evenly after heavy rains than genotypes with short peduncles that retain pods within the canopy. The longest peduncles have also been reported to make manual harvesting easier as pods will be picked up with less difficulty (Kamai *et al*. 2014).

Table 4.7: Analysis of variance for peduncle length

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R	2	163.23	81.61	3.55	0.0371*
Location (L)	1	10.94	10.94	0.48	0.4937^{ns}
LxR	2	6.00	3.00	0.13	0.8779^{ns}
Genotype (G)	10	585.73	58.57	2.55	0.0159*
GxL	10	220.11	22.01	0.96	0.4918^{ns}
GxLxR	40	1147.37	28.68	1.25	0.2355^{ns}
Season (S)	1	544.12	544.12	23.69	<.0001*
SxL	1	1382.57	1382.57	60.20	<.0001*
GxS	10	471.53	47.15	2.05	0.0501*
GxSxL	10	165.81	16.58	0.72	0.6995^{ns}
Error	44	1010.46	22.96		
Total	131	5707.87			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

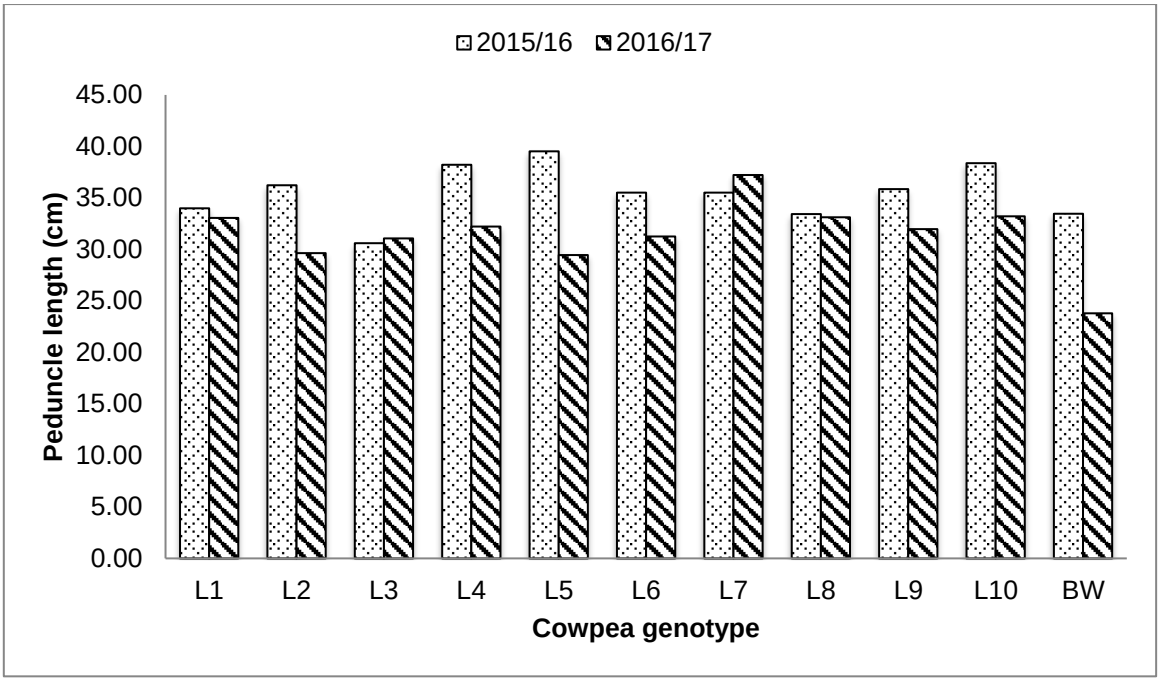


Figure 4.7: Interactive effect of cowpea genotype x season on peduncle length

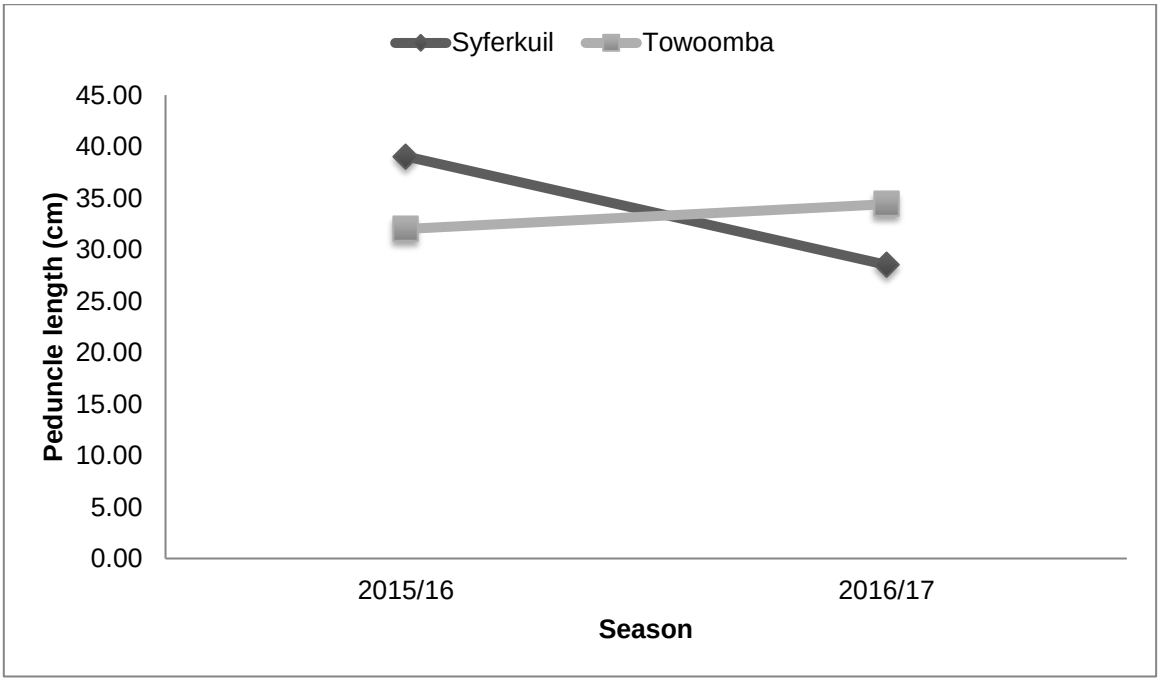


Figure 4.8: Interactive effect of season x location on cowpea peduncle length

Table 4.8: The effects of location, genotype and season on plant height and peduncle length of eleven cowpea genotypes

VARIABLE	Plant height (cm)	Peduncle length (cm)
	LOCATION (L)	
SYFERKUIL	46.10[a]	33.78[a]
TOWOOMBA	43.33[b]	33.20[a]
SEM	**0.92**	**0.42**
	GENOTYPE (G)	
L1	42.32[ab]	33.53[a-c]
L2	43.15[ab]	32.94[a-c]
L3	37.44[b]	30.83[bc]
L4	42.31[ab]	35.23[ab]
L5	48.94[a]	34.49[ab]
L6	44.27[ab]	33.38[a-c]
L7	48.72[a]	36.37[a]
L8	46.72[a]	33.28[a-c]
L9	46.52[a]	33.92[ab]
L10	48.35[a]	35.80[ab]
BW (Local check)	43.11[ab]	28.63[c]
GRAND MEAN	**44.71**	**33.49**
SEM	**0.84**	**0.21**
	SEASON (S)	
2015/16	48.05[a]	35.52[a]
2016/17	41.38[b]	31.46[b]
SEM	**0.74**	**0.59**

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

4.3. Yield and yield components of elite cowpea genotypes

4.3.1. Number of pods per plant

4.3.1.1. Effects of genotypes, locations and seasons

The effects of locations (L), seasons (S), genotype x location (GxL), genotype x season (GxS) were not significantly different (P≤0.05), however statistical differences were observed for the effect of genotypes (G), location x season (LxS) and genotype x season x location (GxSxL) interactions (Table 4.9). These results are in accordance with the results by Peksen (2007) who also reported significant differences for genotypic effect regarding number of pods per plant of cowpea. Averaged across the two locations and seasons, the highest number of pods per plant were observed for line L7 (25.52 pods/plant) with the lowest number of pods per plant recorded in L3 (16.00 pods/plant) (Table 4.11).

4.3.1.2. Interactive effect of cowpea genotype x season x location on number of pods per plant

During 2015/16 season at Syferkuil, cowpea line L8 produced the highest number of pods per plant with a mean of 33.07 pods/plant, followed by breeding lines L1, L4 and L5 with mean values of 29.27, 28.20 and 28.13 pods/plant, respectively. The lowest number of pods per plant were recorded in breeding lines L3 (11.00 pods/plant) and L9 (15.80 pods/plant). In 2016/17 season, the genotypes that exhibited the highest number of pods per plant were breeding lines L4, L7 and L6 with means of 24.27, 22.23 and 22.00 pods/plant, respectively. The lowest numbers of pods per plant were recorded in breeding lines L3, L5 and L8 with means of 9.03, 9.20 and 10.13 pods/plant, respectively (Figure 4.9).

During 2015/16 season at Towoomba, the highest number of pods per plant were given by line L2 (30.57 pods/plant), followed by line L7 and local check BW with average means of 28.17 and 27.33 pods/plant, respectively. The lowest number of pods per plant was recorded in breeding lines L5 (10.70 pods/plant) which was followed by L9 and L3 with mean values of 15.20 and 16.53 pods/plant, respectively. During 2016/17 season, line L7 produced the highest number of pods per plant with a mean value of 31.55 pods/plant, followed by L5, L10 and local check BW with mean values of 29.17, 29.11 and 28.06 pods/plant, respectively. The lowest number of pods

per plant were recorded for breeding lines L1 and L2 with averages of 20.00 and 20.56 pods/plant, respectively (Figure 4.9).

Figure 4.9 shows that most lines produced the highest number of pods per plant at Syferkuil in the 2015/16 season and Towoomba in 2016/17 season. This could be attributed to the favourable moisture regime and high phosphorus content that were observed in the areas. Hall and Patel (1985), cited by Addo-Quaye *et al*. (2011) observed that number of pods per plant were higher under high moisture conditions. The findings of Suliman (2007) also showed that number of pods per plant reduced with increasing moisture stress. Makwunyne and Batino (2002) and Singh *et al*. (2011) reported that phosphorus is an essential nutrient for photosynthesis, pod development and grain filling in leguminous crops. Hence more number of pods per plant were produced in Towoomba in the 2016/17 and Syferkuil in the 2015/16 as available P were high.

Table 4.9: Analysis of variance for number of pods per plant

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	42.10	21.05	0.48	0.6220^{ns}
Location (L)	1	13.63	13.63	0.31	0.0604^{ns}
LxR	2	75.95	37.97	0.87	0.4277^{ns}
Genotype (G)	10	787.72	78.77	1.80	0.0270*
GxL	10	582.03	58.20	1.33	0.0761^{ns}
GxLxR	40	2031.07	50.78	1.16	0.3168^{ns}
Season (S)	1	623.96	623.96	14.23	0.7265^{ns}
SxL	1	1008.12	1008.12	22.99	<.0001*
GxS	10	1057.58	105.76	2.41	0.2796^{ns}
GxSxL	10	1232.38	123.24	2.81	0.0118*
Error	44	1929.65	43.86		
Total	131	9384.18			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

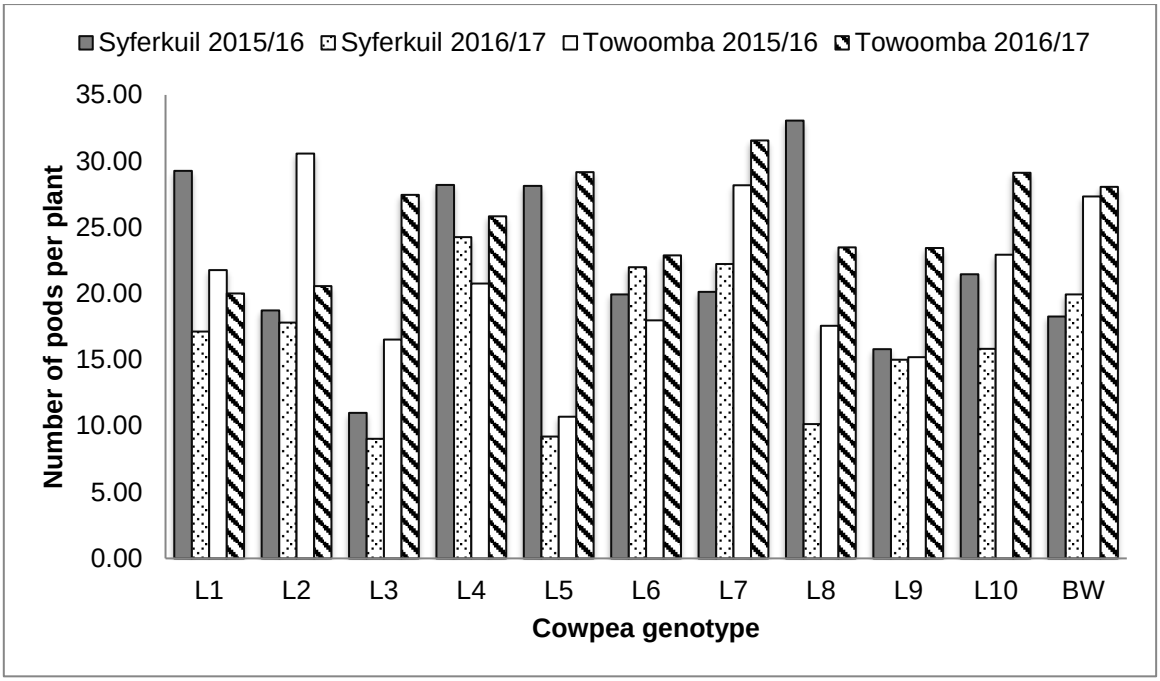


Figure 4.9: Interactive effect of cowpea genotype x season x location on number of pods per plant

4.3.2. Pod length

4.3.2.1. Effects of cowpea genotypes, locations and seasons

The results revealed highly significant differences (P≤0.05) between the locations, genotypes (G), genotype x location (GxL) and location x season (LxS) interactions; however, the effect of seasons (S), genotype x season (GxS) and genotype x season x location (GxSxL) interactions were not significantly different (Table 4.10). Basaran *et al*. (2011) also reported significant variation in pod length as influenced by locational and genotypic effects. The longest pods were recorded at Towoomba with an average of 16.54 cm as compared to Syferkuil that had the shortest pods (15.05 cm) (Table 4.11). This may be due to high moisture content and good soil nutrient status reported in Towoomba especially in 2016/17 season and moderate alkaline soil, which was reported in Syferkuil during the same season which resulted in production of shorter pods. Averaged across the two locations and seasons, the longest pods were observed for line L7 with an average of 17.63 cm, followed by lines L1 and L5 both with a mean value of 16.21 cm. The shortest pods were recorded for lines L3 (14.46 cm) and L8 (14.73 cm). All other breeding lines including local check BW recorded intermediate pods with means ranging from 15.18 to 16.09 cm (Table 4.11). This

shows that the genotypes used in this study differ genetically as others have longer pods, some are characterised with shorter pods.

4.3.2.2. Interactive effect of cowpea genotype x location on pod length

At Syferkuil, the longest pods were observed in line L7 (17.29 cm) which was followed by L5 (16.46 cm) whereas the shortest pods were obtained in line L10 with an average of 12.86 cm. At Towoomba, the longest pods were produced by cowpea line L10 (18.31 cm) followed by L7 (17.97 cm) and L4 (17.57 cm) (Figure 4.10). The presence of this interaction indicates the cowpea genotypes responded differently to varying moisture content and soil nutrient status observed in the two locations.

4.3.2.3. Interactive effect of season x location on cowpea pod length

The longest pods were observed at Towoomba in the 2016/17 season with an average of 17.12 cm (Figure 4.14). This is because of high moisture content, favourable soil pH and good soil nutrient status while the shortest pods were produced at Syferkuil in the 2016/17 season (Figure 4.11). This is because of high soil pH in the area which affected growth and development of cowpea genotypes.

Table 4.10: Analysis of variance for pod length

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	4.49	2.24	1.12	0.3340^{ns}
Location (L)	1	73.26	73.26	36.73	0.0227*
LxR	2	3.44	1.72	0.86	0.4287^{ns}
Genotype (G)	10	87.11	8.71	4.37	0.0002*
GxL	10	104.43	10.44	5.24	<.0001*
GxLxR	40	74.42	1.86	0.93	0.5866^{ns}
Season (S)	1	0.41	0.41	0.21	0.6523^{ns}
SxL	1	53.76	53.76	26.95	<.0001*
GxS	10	37.22	3.72	1.87	0.0766^{ns}
GxSxL	10	32.29	3.23	1.62	0.1328^{ns}
Error	44	87.76	1.99		
Total	131	558.59			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

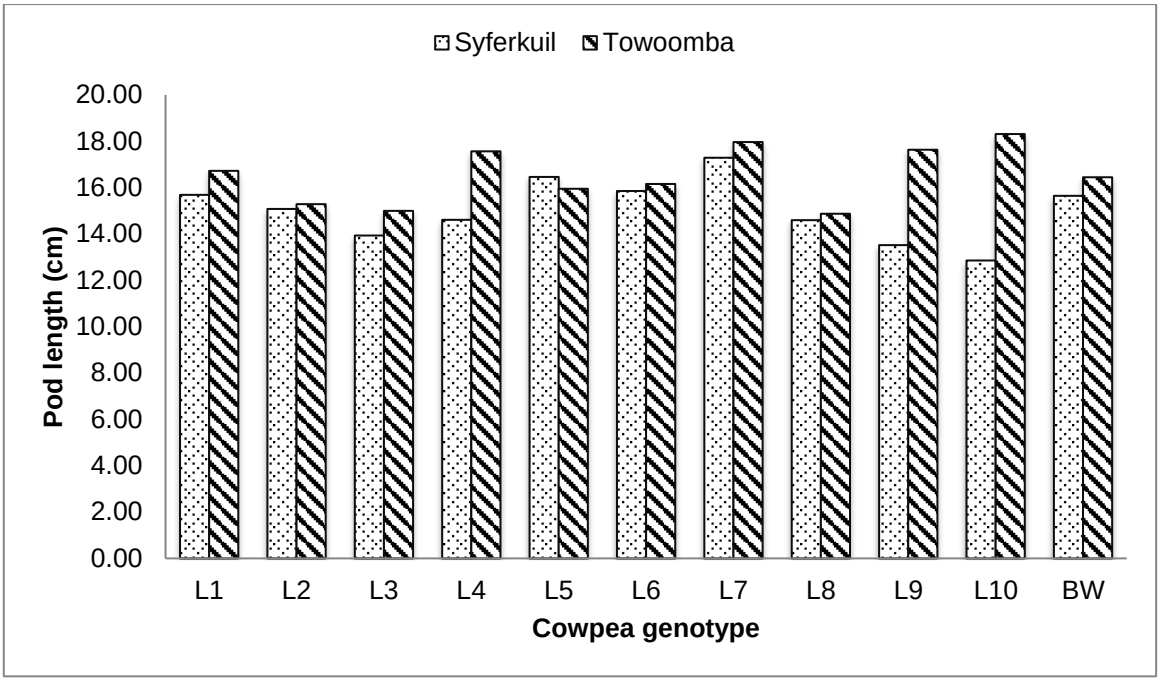


Figure 4.10: Interactive effect of cowpea genotype x location on pod length

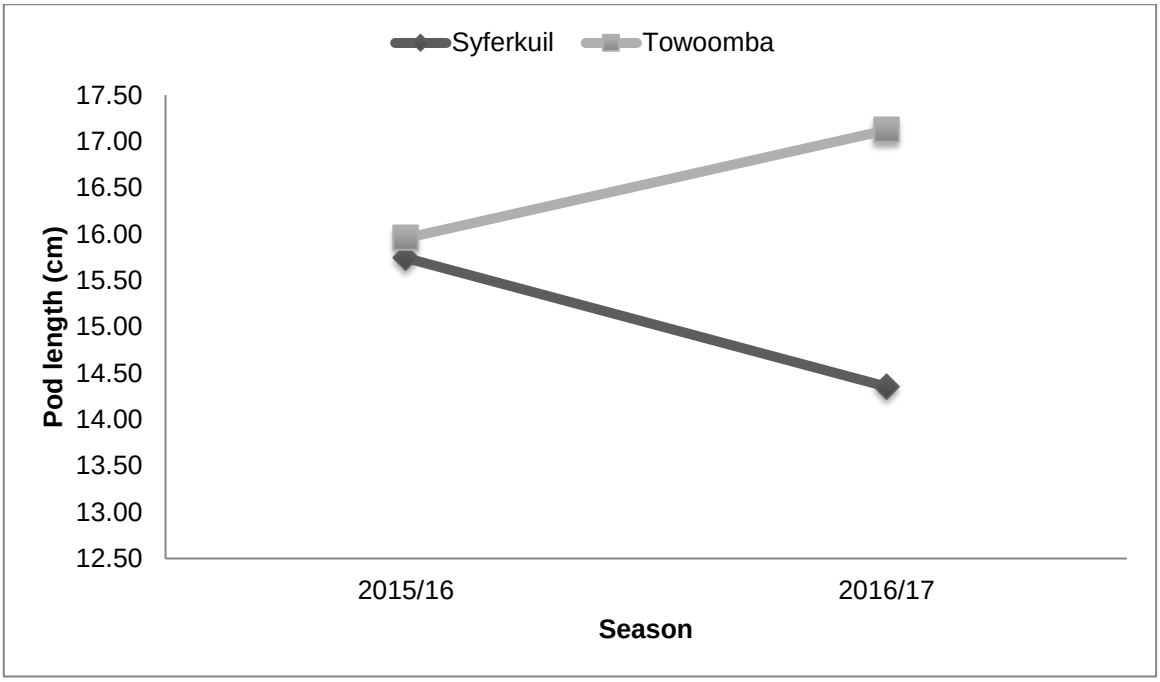


Figure 4.11: Interactive effect of location x season on cowpea pod length

Table 4.11: The effect of location, genotype and season on number of pods per plant and pod length of eleven cowpea genotypes

VARIABLE	Pods per plant	Pod length (cm)
LOCATION (L)		
SYFERKUIL	19.39[a]	15.05[b]
TOWOOMBA	23.23[a]	16.54[a]
SEM	**0.7**	**0.16**
GENOTYPE (G)		
L1	22.04[ab]	16.21[ab]
L2	21.91[ab]	15.18[b]
L3	16.00[b]	14.46[b]
L4	24.77[ab]	16.09[ab]
L5	19.30[ab]	16.21[ab]
L6	20.70[ab]	16.01[ab]
L7	25.52[a]	17.63[a]
L8	21.07[ab]	14.73[b]
L9	17.36[ab]	15.58[b]
L10	22.34[ab]	15.59[b]
BW (Local check)	23.40[ab]	16.05[ab]
GRAND MEAN	**21.31**	**15.79**
SEM	**1.90**	**0.39**
SEASON (S)		
2015/16	21.52[a]	15.74[a]
2016/17	21.09[a]	15.85[a]
SEM	**0.86**	**0.17**

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

4.3.3. Number of seeds per pod

4.3.3.1. Effects of genotypes, locations and seasons

The results revealed highly significant differences (P≤0.05) among the locations (L) genotypes (G), seasons (S) and location x season (LxS) interaction (Table 4.12). These findings are in accordance with the results of Basaran *et al*. (2011) who reported variations among the cowpea genotypes, seasons and locations for number of seeds per pod. The cowpea genotypes gave the highest number of seeds in a pod when grown in Towoomba than in Syferkuil with mean values of 12.12 seeds/pod at Towoomba, which is statistically different from 10.55, seeds/pod recorded in Syferkuil (Table 4.14). This may be due to shorter pods that were recorded in Syferkuil in 2016/17 season as compared to longer pods that were obtained in Towoomba in 2016/17 season. The highest number of seeds in a pod was obtained by the cowpea

genotypes in 2015/16 season and the lowest number of seeds in a pod was observed in 2016/17 season with mean values of 11.78 and 10.89 seeds/pod respectively (Table 4.14). This was affected by reduced pod length at Syferkuil in 2016/17 season leading to reduced number of seeds in a pod during that season. The highest number of seeds in a pod were recorded by Local check BW (12.89 seeds/pod) which was followed by L3, L1 and L7 each with 11.84, 11.51 and 11.35 seeds/pod, respectively. The lowest number of seeds in a pod was recorded in genotype L8 (10.18 seeds/pod) (Table 4.14).

4.3.3.2. Interactive effect of location x season on number of seeds in a pod of cowpea

The number of seeds in a pod were the highest when the cowpea genotypes were grown in Towoomba in 2016/17 season (12.30 seeds/pod). The lowest number of seeds in a pod were observed when the breeding lines were grown in Syferkuil in 2016/17 season (9.47 seeds/pod) (Figure 4.12). This may be due to higher moisture regime and good soil fertility status that was observed at Towoomba in 2016/17 season that resulted in more number of seeds per pod than at Syferkuil in 2016/17 season. The presence of these interactions contradics with the evidence by Singh *et al*. (2003) that number of seeds per pod is more influenced by genetic make-up than the environment.

Table 4.12: Analysis of variance for number of seeds per pod

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	6.55	3.27	1.63	0.2072^{ns}
Location (L)	1	81.31	81.31	40.54	<.0001*
LxR	2	0.28	0.14	0.07	0.9334^{ns}
Genotype (G)	10	76.12	7.61	3.79	0.0010*
GxL	10	28.77	2.88	1.43	0.1973^{ns}
GxLxR	40	66.33	1.66	0.83	0.7278^{ns}
Season (S)	1	26.37	26.37	13.15	0.0007*
SxL	1	52.44	52.44	26.14	<.0001*
GxS	10	18.14	1.81	0.90	0.5374^{ns}
GxSxL	10	18.62	1.86	0.93	0.5170^{ns}
Error	44	88.26	2.01		
Total	131	463.19			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

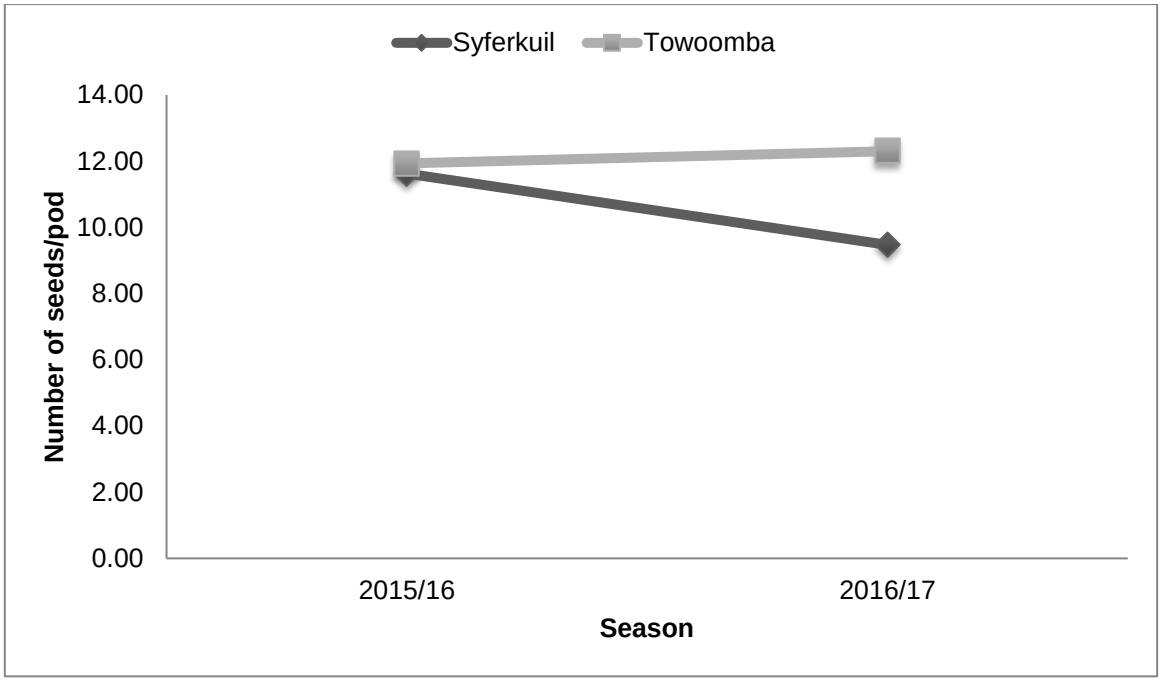


Figure 4.12: Interactive effect of location x season on number of seeds in a pod of cowpea

4.3.4. Hundred seed weight

4.3.4.1. Effects of genotypes, locations and seasons

There were highly significant differences (P≤0.05) among the genotypes (G), seasons (S) and genotypes x season x location (GxSxL) interactions (Table 4.13). The results of the current study are in accordance with the previous study by Kamai *et al*. (2014) who reported significant differences in hundred seed weight as affected by genotypic and seasonal effects. The heaviest hundred seed weight was observed in 2016/17 season with a mean of 20.41 g/100 seeds whereas the lowest weight was recorded in 2015/16 season (19.16 g/100 seeds) (Table 4.14). This may be due to increased moisture content during grain filling stage in the 2016/17 season than in the 2015/16 season. Averaged across both locations and seasons, breeding lines that had the heaviest weight were L4 (22.70 g/100 seeds), followed by L7 and L10 with mean values of 22.08 and 21.86 g/100 seeds, respectively. The lowest weight was obtained by local check BW with a weight of 15.73 g/100 seeds (Table 4.14).

4.3.4.2. Interactive effect of genotype x season x location on hundred seed weight of cowpea

At Syferkuil during 2015/16 season, hundred seed weight ranged from 16.61 to 20.85 g/100 seeds. The heaviest hundred seed weights were noted in lines L7, L1 and L4 with mean values 20.85, 20.69 and 20.10 g/100 seeds, respectively. The breeding lines that recorded the lowest hundred seed weight were L9 (16.61), local check BW (17.27), L3 (17.31) and L5 (17.36). During 2016/17 season the average hundred seed weight ranged from 15.05 to 22.98 g/100 seeds. Breeding lines L7, L4 and L10 had the highest hundred seed weight with an average of 22.98, 22.41 and 22.08 g/100 seeds. The lowest hundred seed weight was observed for local check BW (15.05) (Figure 4.13).

At Towoomba during 2015/16 season, mean hundred seed weight ranged from 15.23 to 23.30 g/100 seeds. The highest seed weights were obtained in L10 (23.30), L6 (21.90) and L7 (20.87). In 2016/17 season, average hundred seed weight ranged from 15.63 to 25.86 g/100 seeds. The heaviest weight was obtained from L4 (25.86) and L7 (23.55). The local check BW had the lowest hundred seed weight in both seasons with 15.23 g/100 seeds in 2015/16 season and 15.63 g/100 seeds in 2016/17 season (Figure 4.13).

The results of this study show that cowpea genotypes performed inconsistently across the environments. This indicates that the environment played a huge role in its influence on this trait. The elite cowpea breeding lines used in the study had large seeds (> 18 g) whereas the local check BW had medium sized seeds (12-18 g) based on the classification guide by Drabo *et al*. (1984). In their study, Drabo *et al*. (1984) concluded that seed size in cowpea is highly heritable but they also indicated that the environment could modify seed size; this is in conformity with the findings of the current study that shows that hundred seed weight varied across the four environments.

Table 4.13: Analysis of variance for hundred seed weight

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	29.39	14.69	4.73	0.0148*
Location (L)	1	6.84	6.84	2.20	0.1461^{ns}
LxR	2	20.17	10.09	3.25	0.0501*
Genotype (G)	10	420.40	42.04	13.54	<.0001*
GxL	10	27.20	2.72	0.88	0.5630^{ns}
GxLxR	40	171.21	4.28	1.38	0.1633^{ns}
Season (S)	1	44.37	44.37	14.29	0.0006*
SxL	1	0.00	0.00	0.00	0.9900^{ns}
GxS	10	44.05	4.41	1.42	0.2103^{ns}
GxSxL	10	73.47	7.35	2.37	0.0279*
Error	44	114.86	3.10		
Total	131	1022.77			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

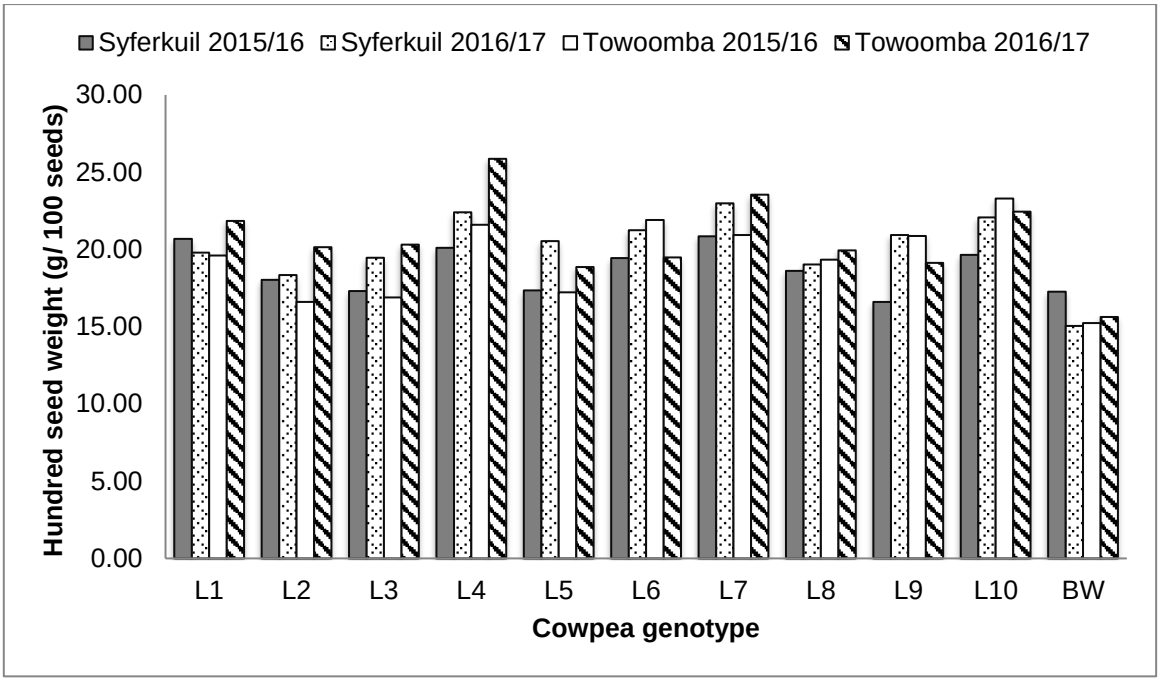


Figure 4.13: Interactive effect of cowpea genotype x season x location on hundred seed weight

Table 4.14: The effect of location, genotype and season on number of seeds in a pod and hundred seed weight of eleven cowpea genotypes

VARIABLE	Seeds per pod	100 Seed weight (g)
LOCATION (L)		
SYFERKUIL	10.55^{b}	19.56^{a}
TOWOOMBA	12.12^{a}	20.03^{a}
SEM	**0.15**	**0.26**
GENOTYPE (G)		
L1	11.51^{bc}	20.46^{bc}
L2	10.93^{cd}	18.30^{d}
L3	11.84^{a-c}	18.61^{cd}
L4	10.71^{cd}	22.70^{a}
L5	12.34^{ab}	18.60^{cd}
L6	10.77^{cd}	20.52^{bc}
L7	11.43^{bc}	22.08^{ab}
L8	10.18^{d}	19.28^{cd}
L9	11.35^{b-d}	19.39^{cd}
L10	10.72^{cd}	21.86^{ab}
BW (Local check)	12.89^{a}	15.67^{e}
GRAND MEAN	**11.33**	**19.78**
SEM	**0.05**	**0.67**
SEASON (S)		
2015/16	15.85^{a}	19.13^{b}
2016/17	15.74^{a}	20.41^{a}
SEM	**0.17**	**0.21**

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

4.3.5. Grain yield

4.3.5.1. Effects of cowpea genotypes, locations and seasons

The analysis revealed significant variations (P≤0.05) among the locations (L), genotypes (G), seasons (S) and location x season (LxS) interaction (Table 4.15). This is in conformity with the findings of Basaran *et al*. (2011) who reported significant variation on cowpea grain yield as influenced by the effects of genotypes, years and locations. The genotypes produced highest grain yield when grown in Towoomba (1982.90 kg/ha) than when grown in Syferkuil (1604.20 kg/ha). This may be due to reduced grain yield that was observed in Syferkuil in the 2016/17 season due to high soil pH which adversely affected growth, development and yields of cowpea. Similarly, the breeding lines gave the highest yield in 2015/16 season as compared to when grown in 2016/17 season with mean values of 1834.80 and 1732.30 kg/ha,

respectively. This is because at Syferkuil in the 2016/17 season, grain yield was reduced due to low rainfall and moderate alkalinity observed in the area. Averaged across the two locations and seasons, the highest grain yield was recorded by breeding line L7 (2595.20 kg/ha) which was followed by L2, L10 and local check BW with mean values 1928.50, 1891.70 and 1858.70 kg/ha, respectively (Table 4.17). Lines L7, L2 and L10 outperformed the local check BW having a percentage differences of 39.6, 3.8 and 1.8, respectively. Yield in cowpea is the result of many interacting components such as number of pods per plant, pod length, number of seeds per pod and mean seed weight (Bull *et al.,* 1992). This is supported by the fact that line L7 produced more pods per plant, long pods, higher number of seeds per pod and large seeds with mean values of 25.52 pods/plant, 17.63 cm, 11.43 seeds/pod and 22.08 g/100 seeds, respectively. The local check BW also gave more pods per plant (23.40 pods/plant) following L7, longer pods (16.05 cm) and higher number of seeds in a pod (12.89 seeds/pod) (Table 4.11). The lowest grain yield was obtained by line L8 with an average of 1441.20 kg/ha. Although, L8 had more pods per plant (21.07 pods/plant), it produced the shortest pods (14.73 cm) which had the lowest number of seeds per pod (10.18) and the lightest mean hundred seed weight (19.28 seeds/pod) these resulted in the line having the lowest mean grain yield (Table 4.11 and Table 4.17).

4.3.5.2. Interactive effect of location x season on cowpea grain yield

The highest grain yield was achieved when the cowpea genotypes were grown at Towoomba in the 2016/17 season with an average of 2213.90 kg/ha (Figure 4.14). This may be due to high rainfall that was well distributed and high phosphorus content that was present in the area that resulted in higher number of pods per plant, longer pods; higher number of seeds per pod and higher mean seed weights that ultimately resulted in high grain yield. The lowest grain yield was obtained in Syferkuil in the 2016/17 season with an average of 1250.70 kg/ha (Figure 4.14). This may be due to high soil pH that has been reported by Goenaga *et al*. (2010; 2013) to cause nutrient deficiencies and toxicities that resulted in reduced number of pods per plant and shorter pods leading to actual yield reduction.

Table 4.15: Analysis of variance for grain yield

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	266393.00	133196.00	0.01	0.9877^{ns}
Location (L)	1	4731164.00	4731164.00	27.17	0.0349*
LxR	2	348310.00	174155.00	7.54	0.0016*
Genotype (G)	10	11282390.00	1128239.00	12.6	<.0001*
GxL	10	229357.00	22935.70	0.26	0.9872^{ns}
GxLxR	40	3580801.00	89520.00	0.25	1.0000^{ns}
Season (S)	1	495401.00	495401.00	5.97	0.0186*
SxL	1	1127058.32	1127058.32	135.96	<.0001*
GxS	10	549603.00	54960.30	0.66	0.7520^{ns}
GxSxL	10	912209.00	91220.90	1.1	0.3835^{ns}
Error	44	3649471.00	82942.50		
Total	131	37320617.22			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

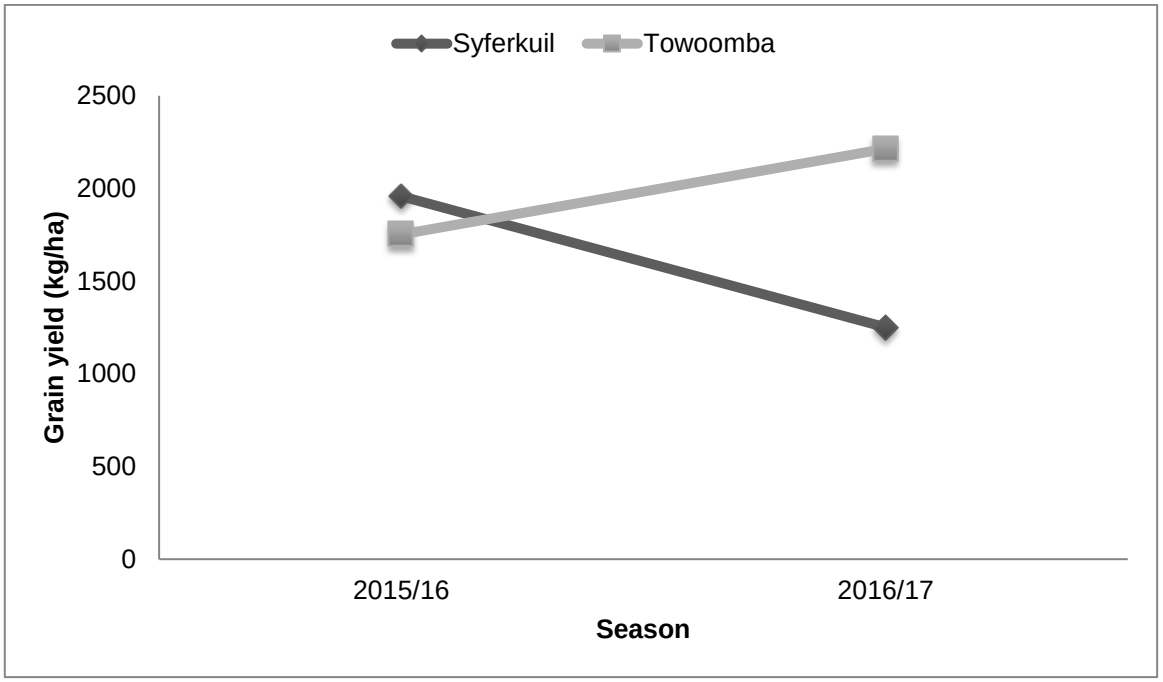


Figure 4.14: Interactive effect of location x season on cowpea grain yield

4.3.6. Fodder yield

4.3.6.1. Effects of cowpea genotypes, locations and seasons

The analysis revealed significant variations (P≤0.05) among the locations (L), genotypes (G), location x season (LxS) and genotype x season (GxS) interactions (Table 4.16). This is in conformity with the findings of Ayan *et al*. (2012) who reported significant variation in fodder yield as a result location and genotype effects. Cowpea fodder is an important attribute in cowpea production as it can be used to make high quality hay for feeding livestock during winter (Tarawali *et al*., 1997). The genotypes gave the highest fodder yield at Towoomba (2928.50 kg/ha) as compared to Syferkuil (2299.40 kg/ha). Similarly, the genotypes had the highest fodder yield during 2016/17 season as compared to 2015/16 season with mean values of 2740.70 and 2487.30 kg/ha, respectively (Table 4.17). This was due to high rainfall that was received in the 2016/17 season. Averaged across the two locations and seasons, the highest fodder yield was recorded by breeding line L3 (3611.00 kg/ha) which was closely followed by line L10 with mean value of 3022.00 kg/ha. The genotypes that produced low fodder yields were local check BW (1934.20 kg/ha) and line L1 (1987.70 kg/ha) (Table 4.17). Although all the lines had high percentage difference with local check BW, line L3 and L10 had the highest percentage difference of 86.7 and 56.2, respectively. Agyeman *et al*. (2014) reported that fodder yield in cowpea is the result of many interacting components such as number of branches, number of leaves and leaf area.

4.3.6.2. Interactive effect of location x season on cowpea fodder yield

The highest fodder yield was achieved when the cowpea genotypes were grown at Towoomba in the 2016/17 season with an average of 3628.50 kg/ha (Figure 4.15). This may be due to high rainfall which was well distributed which favoured high biomass production. The lowest fodder yield was obtained in Syferkuil in the 2016/17 season with an average of 1852.80 kg/ha (Figure 4.15).

4.3.6.3. Interactive effect of cowpea genotype x season on fodder yield

During 2015/16 season, high fodder yields were given by lines L4 (3489.30 kg/ha), L6 (3030.90 kg/ha) and L5 (3009.6 kg/ha) while low fodder yields were recorded in line L1 and local variety BW with averages of 1622.50 and 1951.60 kg/ha, respectively. During 2016/17 season, Lines L3, L10 and L7 had high fodder yields with averages of

4454.0, 3620.50 and 3004.60 kg/ha, respectively. Low fodder yields were recorded for local variety BW (1916.90 kg/ha) and L4 (2103.60 kg/ha) (Figure 4.16). Figures 4.15 and 4.16 showed that the genotypes produced high fodder yields at Towoomba in the 2016/17 season as compared to the first season. This may be due to high rainfall observed at Toowomba in the second season. Agyeman *et al*. (2014); Karungi *et al*. (2000) reported that heavy rainfall favours excessive vegetative growth while it causes lower seed yield.

Table 4.16: Analysis of variance for fodder yield

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	4493112	2246556	1.56	0.2228^{ns}
Location (L)	1	13064075.99	13064075.99	16.79	0.0547*
LxR	2	1556037	778018	0.75	0.4779^{ns}
Genotype (G)	10	26183167	2618316.7	2.58	0.0162*
GxL	10	5379296	537929.6	0.5	0.8582^{ns}
GxLxR	40	40594904.93	1014872.62	1.01	0.4878^{ns}
Season (S)	1	2118916	2118916	2.06	0.1578^{ns}
SxL	1	43384020.41	43384020.41	42.27	<.0001*
GxS	10	24922514.9	2492251.49	2.43	0.0211*
GxSxL	10	7535962	753596.2	0.73	0.6884^{ns}
Error	44	45155432	1026259.82		
Total	131	214419504.6			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

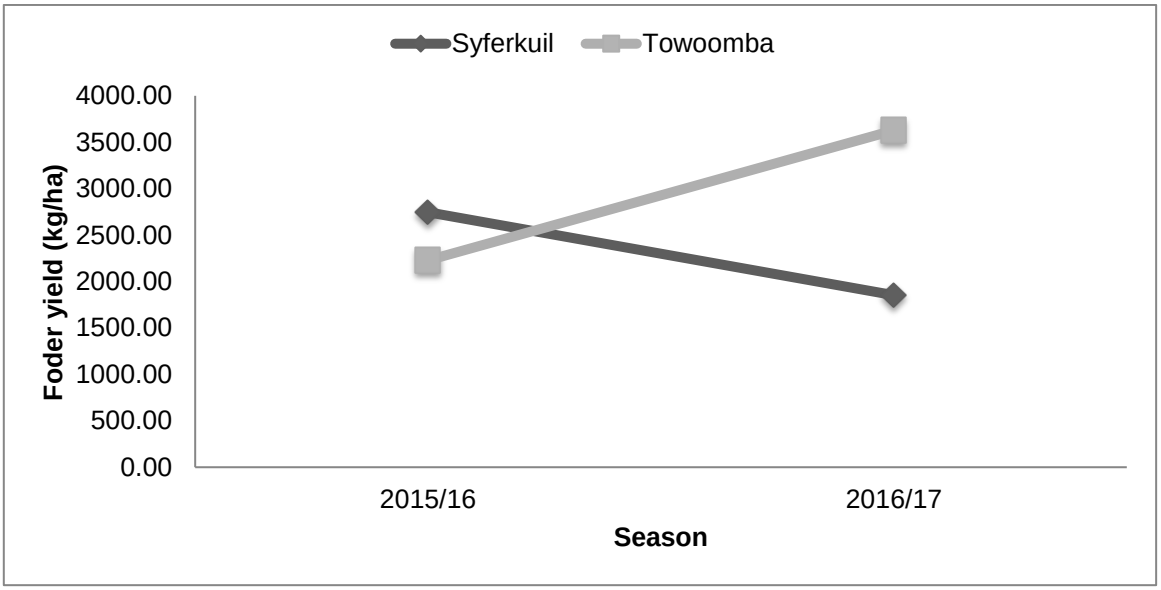


Figure 4.15: Interactive effect of location x season on cowpea fodder yield

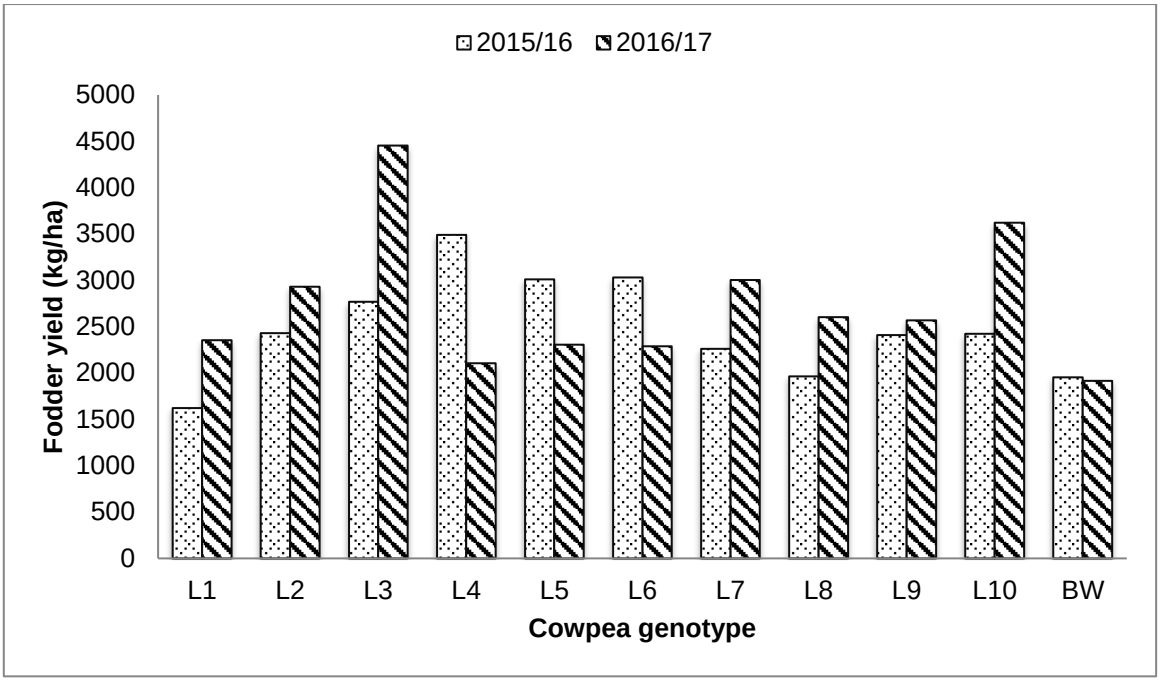


Figure 4.16: Interactive effect of cowpea genotype x season on fodder yield

Table 4.17: The effect of location, genotype and season on grain and fodder yields of eleven cowpea genotypes

VARIABLE	Grain yield (kg/ha)	% Grain yield differnce with BW	Fodder yield (kg/ha)	% Fodder yield difference with BW
		LOCATION (L)		
SYFERKUIL	1604.20^{b}	-	2299.40^{a}	-
TOWOOMBA	1982.20^{a}	-	2928.50^{b}	-
SEM	**51.37**	-	**108.57**	-
		GENOTYPE (G)		
L1	1740.50^{bc}	-6.4	1987.70^{cd}	2.8
L2	1928.50^{b}	3.8	2679.70^{b-d}	38.5
L3	1557.90^{cd}	-16.2	3611.00^{a}	86.7
L4	1670.60^{b-d}	-10.1	2796.50^{a-c}	44.6
L5	1561.70^{cd}	-16.0	2658.10^{b-d}	37.4
L6	1675.40^{b-d}	-9.9	2659.50^{b-d}	37.5
L7	2595.20^{a}	39.6	2633.10^{b-d}	36.1
L8	1441.20^{d}	-22.5	2283.10^{b-d}	18.0
L9	1807.50^{bc}	-2.8	2488.60^{b-d}	28.7
L10	1891.70^{b}	1.8	3022.00^{ab}	56.2
BW (Local check)	1858.70^{b}	0.0	1934.20^{d}	0.0
GRAND MEAN	**1793.5**	**-**	**2614**	**-**
SEM	**86.37**	**-**	**290.71**	-
		SEASON (S)		
2015/16	1834.80^{a}		2487.30^{a}	
2016/17	1732.30^{b}	-	2740.70^{a}	-
SEM	**35.45**	-	**124.7**	-

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

4.3.7. Harvest index

4.3.7.1. Effects of cowpea genotypes, locations and seasons

The analysis revealed significant variations (P≤0.05) among the genotypes (G) and location x season (LxS) interaction (Table 4.18). The genotype that had high harvest index were local check BW and line Line 7 with mean values of 1.21 and 1.19 (Table 4.19) which was not significantly different from each other. The lowest harvest index was obtained for lines L5 (0.67) and and L3 (0.61) (Table 4.19). Harvest index is an important aspect in variety evaluations as it allows the identification of genotypes as either the grain or fodder type. The high harvest index observed for local check BW and line L7 indicates that these genotypes are grain types. Line L5 and L3 can be

classified for fodder types due to their low harvest index. This indicates that the two lines had higher above ground biomass and less grain yield. The results of the study are however in disagreement with Suliman (2000) who repoted that introduced cultivars had greater harvest index than the local cultivars.

4.3.7.2. Interactive effect of location x season on cowpea harvest index

The highest harvest index of 1.28 was achieved when the cowpea genotypes were grown at Syferkuil in the 2016/17 season (Figure 4.16). this may be due to high grain yield than fodder yield observed in that environment. Low harvest index was obtained at Towoomba in the 2016/17 season with an average of 0.54 (Figure 4.16). This may be due to high rainfall which was well distributed which favoured high biomass production as compared to the grain. This results are in accordance to Ahmed *et al*. (2012) who reported that greater dry matter content lead to reduced harvest index in cowpea genotypes.

Table 4.18: Analysis of variance for harvest index

Source of variation	DF	Type III SS	MS	F Value	Pr > F
Replication (R)	2	0.1842	0.0921		
Location (L)	1	0.6609	0.6609	0.55	0.5355^{ns}
LxR	2	2.4018	1.2009		
Genotype (G)	10	5.2395	0.5239	2.09	0.0488*
GxL	10	2.7206	0.2721	1.08	0.3966^{ns}
GxLxR	40	10.0355	0.2509		
Season (S)	1	0.0585	0.0585	0.33	0.5684^{ns}
SxL	1	11.8678	11.8678	67.04	0.0000*
GxS	10	2.1791	0.2179	1.23	0.2987^{ns}
GxSxL	10	1.6043	0.1604	0.91	0.5357^{ns}
Error	44	7.7891	0.177		
Total	131	44.7411			

DF= degree of freedom, SS= sum of squares, MS= mean squares, Pr = Probability, ns= not significant and * significant at (P≤0.05)

Table 4.19: The effect of location, genotype and season on grain and fodder yields of eleven cowpea genotypes

VARIABLE	Harvest index
LOCATION (L)	
SYFERKUIL	0.96[a]
TOWOOMBA	0·82[a]
SEM	0.1349
GENOTYPE (G)	
L1	1.12[ab]
L2	0.92[a-c]
L3	0.61[c]
L4	0.72[bc]
L5	0.67[c]
L6	0.76[bc]
L7	1.19[a]
L8	0.90[a-c]
L9	0.86[a-c]
L10	0·77[bc]
BW (Local check)	1.21[a]
GRAND MEAN	0.89
SEM	0.14
SEASON (S)	
2015/16	0.87[a]
2016/17	0.91[a]
SEM	0.05

Means followed by the same letters in each column do not differ significantly at P≤ 0.05. SEM= Standard error of means

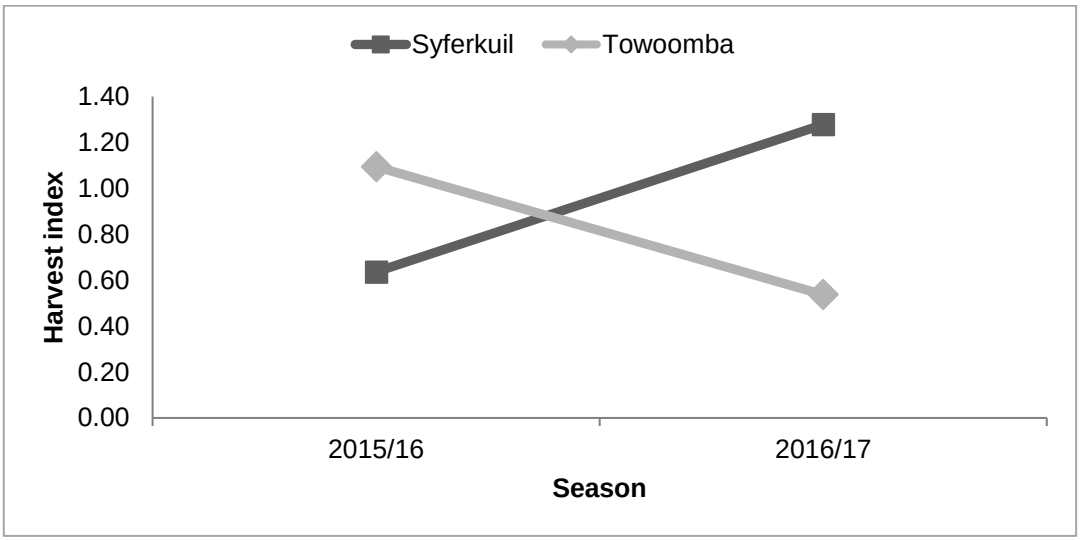


Figure 4.17: Interactive effect of location x season on cowpea harvest index

4.4. Grain yield and yield components stability

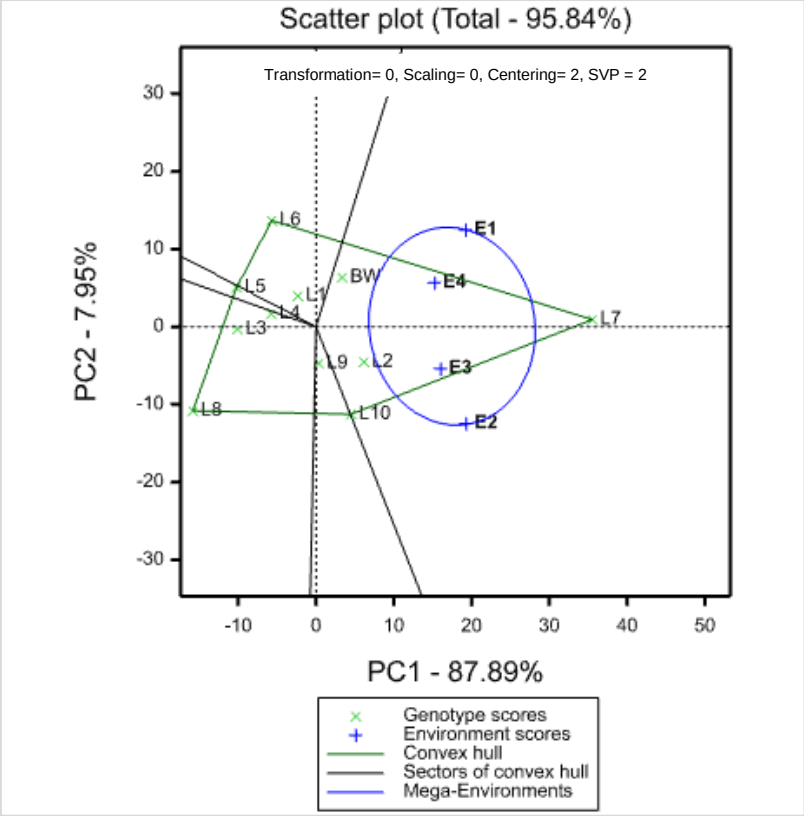
Stability analysis is most important in plant breeding as it allows for selection of superior genotypes that combine high yield and stability for variety release. Identification and release of superior varieties in any crop is hindered by the presence of genotype by environment interaction. Genotype by environment interaction refers to the differential response of genotypes in different environments (location, year, season, etc.) (Yan and Kang, 2003). Olayiwola and Ariyo (2013) reported that selection of genotypes based on yield alone is not sufficient, as high yielding genotypes may be unstable. Yan and Kang (2003) indicated that to statistically detect genotype by environment interaction, it is required that at least two genotypes are evaluated in at least two various locations. There are several techniques that can be employed in genotype by environment studies but GGE (Genotype + Genotype × Environment) biplot is the recent and was proven by several authors to be suitable and efficient (Ezeaku, 2015; Bhartiya *et al*., 2017; Olayiwola *et al*., 2015; Olayiwola and Ariyo, 2013; Yan, 2001; Yan and Kang, 2003; Yan *et al*., 2007). Becker and Leon (1988) identified an ideal cultivar as one that possesses high and consistent yield potential over a wide range of environmental conditions. This ideal genotype can therefore be recommended for release to farmers as it is high yielding and have consistent performance despite fluctuations in the environmental conditions.

4.4.1. Grain yield stability

Figure 4.18 clearly showed the polygon view of the GGE biplot with the “Which-won-where” pattern. The first and second principal components (PC1 and PC2) accounted 87.89 and 7.95%, respectively, accounting for 95.84% of the total variation in grain yield per hectare (Figure 4.18). All the test environments fell into one of the five sectors outlined on the polygon view, thus, all the environments formed one mega-environment. Breeding line L7 was the vertex genotype in that one mega-environment, indicating that line L7 had high grain yield in Syferkuil and Towoomba in 2015/16 and 2016/17 seasons outperforming lines L2, L10 and local check BW that were associated with the mega-environment. Breeding lines L1, L3, L4, L5, L6 and L8 fell into sectors containing none of the test environments. This indicates that these genotypes were poor yielding in one or more test environments (Yan and Kang, 2003).

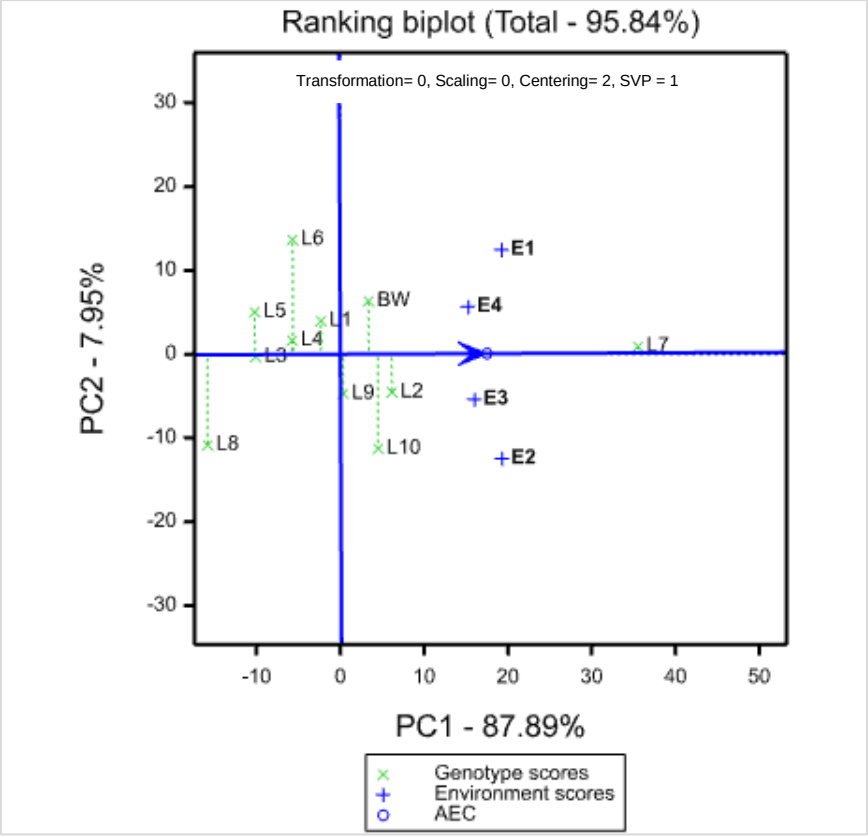
The mean vs. stability for grain yield of the evaluated genotypes is presented in Figure 4.19. The abscissa (single-arrowed) and the ordinate (double arrowed, which in this case is without arrows) of the Average Environment Coordinate (AEC) are the two lines passing through the origin of the biplot. The small circle on the abscissa delineates the AEC which is the environment PC1 and PC2 mean scores (Yan and Kang, 2003). The ordinate divides the genotypes into two; those that yielded above and below average (Yan, 2001; Yan and Kang, 2003). Entries on the right [L9, local check BW, L10, L2 and L7] in increasing order, yielded above average while those on the left [L1, L4, L6, L3, L5 and L8] in decreasing order, fell below average performance. The abscissa therefore points towards increased order of genotype performance based on yield. L7 was on the extreme right while L8 was on the extreme left.

Yan and Kang (2003) indicated that the projection on the abscissa towards the ordinate of the Average Environment Coordinate irrespective of direction is a measure of stability. Breeding line L7 and L3 had the shortest projection thereby being the most stable genotypes, which was followed by line L4, L1 and L2. Line L6 and L10 had the longest projection, followed by L8 and local check BW being the most unstable genotypes in terms of grain yield. The small circle (AEC) on the abscissa of the mean vs. stability biplot represents the “ideal genotype” (Yan, 2001). Becker and Leon (1988) identified an ideal cultivar as one that possesses high and consistent yield potential over a wide range of environmental conditions. However, Yan and Kang (2003) indicated that this “ideal” genotype rarely exists in nature, so the closest genotype to the Average Environment Coordinate is considered the “ideal” genotype. The biplot also showed that breeding line L2 and L7 were the closest to the small circle (AEC), thereby being the “ideal” genotypes as they are the best combiners of high and stable grain yield. Line L10 performed above average, however it was unstable, indicating that it had inconsistent performance across the four environments and therefore unpredictable. Line L3 on the other hand was stable but its performance was below average thereby becoming undesirable for selection.



E1= Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

Figure 4.18: GGE biplot displaying the mega-environments and the "Which-won-where" pattern for grain yield of cowpea genotype



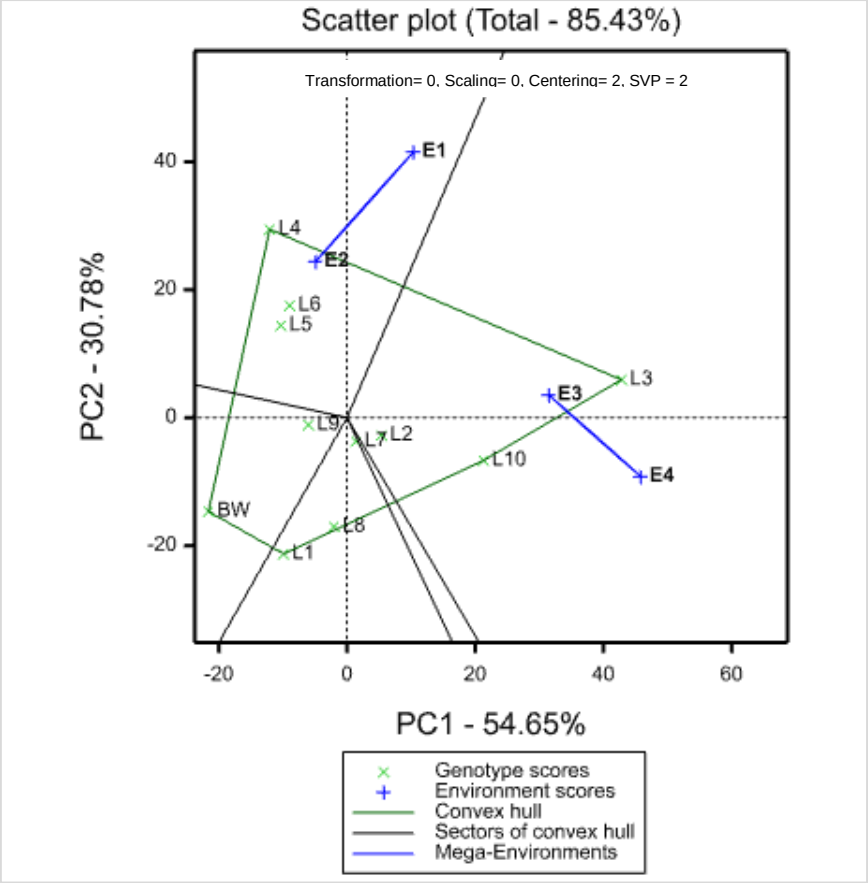
E1= Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

Figure 4.19: GGE biplot of mean yield performance and stability for grain yield of cowpea genotypes

4.4.2. Fodder yield stability

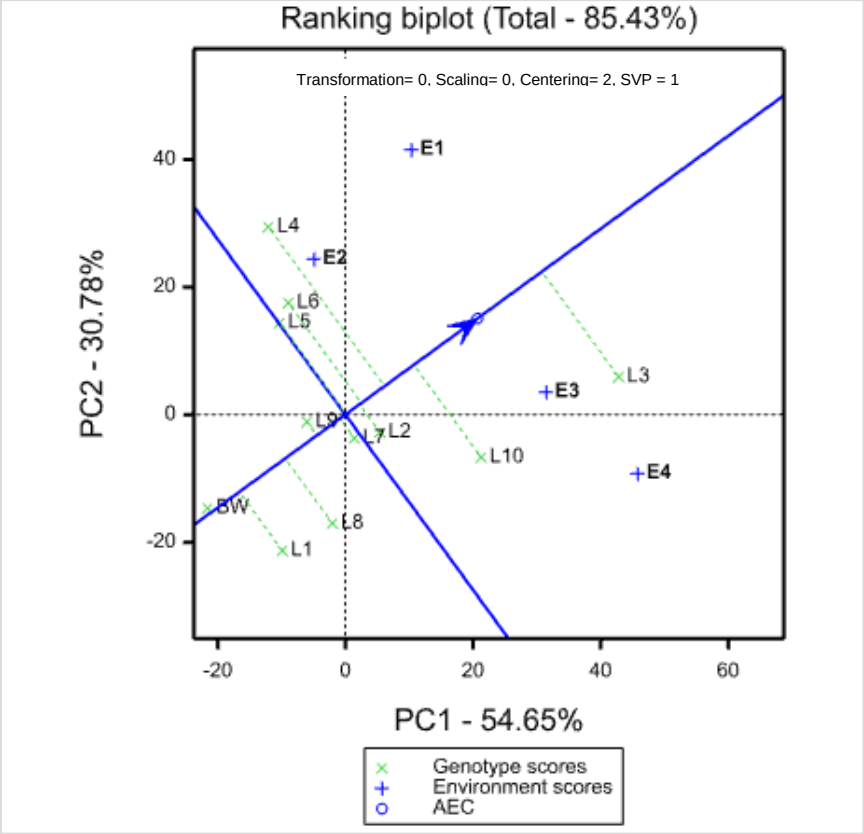
The biplot for dry fodder yield of genotypes across test environments explained 85.43% (PC1= 54.65% + PC2= 30.78%) of the GGE variation of the trait as showed in Figure 4.20. The test environments fell into two of the five sectors outlined on the polygon view, thus, two mega-environments were identified. E1 (Syferkuil 2015/16) and E2 (Towoomba 2015/16) were in the same sector to form mega-environment 1. E3 (Syferkuil 2016/17) and E4 (Towoomba 2016/17) occupied a sector to form mega-environment 2. Breeding line L4 was the vertex genotype, outperforming L6 and L5 in the mega-environment 1, while Line L3 was the vertex genotype in mega-environment 2 having higher fodder yield than lines L10 and L2 in the associated environment. Local variety BW, L1, L7, L8 and L9 however fell into sectors containing none of the test environments indicating that they had below average fodder yield in one or more environments (Ezeaku *et al*., 2015).

The mean vs. stability of the genotypes evaluated for fodder yield is showed in Figure 4.21. The abscissa (single-arrowed) and the ordinate (without arrows) of the Average Environment Coordinate (AEC) are the two lines passing through the origin of the biplot. The small circle on the abscissa delineates the AEC which is the environment PC1 and PC2 mean scores (Kang, 2005). Yan and Kang (2003) indicated that the right-hand side of the ordinate lies genotypes that yielded above average, whereas on the left-hand side lies genotypes that performed below average. The biplot placed lines L7, L2, L6, L4, L10, and L3 (in increasing order) on the right-hand side of the ordinate thereby indicating that these genotypes yielded above average. Breeding lines L5, L8, L9, L1 and local check BW (in decreasing order) fell below average performance as the biplot placed then on the left-hand side of the ordinate line. Yan and Kang (2003) reported that stability of the genotypes is measured by the projection on the abscissa towards the ordinate of the Average Environment Coordinate. The shorter the projection the more stable and the longer the projection the more unstable the genotype. The local check BW had the shortest projection thereby being the most stable which was followed closely by L9, L7 and L2. Breeding lines L4, L10 and L3 had the longest being the most unstable genotypes in terms of fodder yield. Breeding line L2 can be recommended for fodder yield production as it combines high fodder yield and stability as compared to local check BW that was most stable but performed below average.



E1= Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

Figure 4.20: GGE biplot displaying the mega-environments and the "Which-won-where" pattern for fodder yield of cowpea genotypes



E1=Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

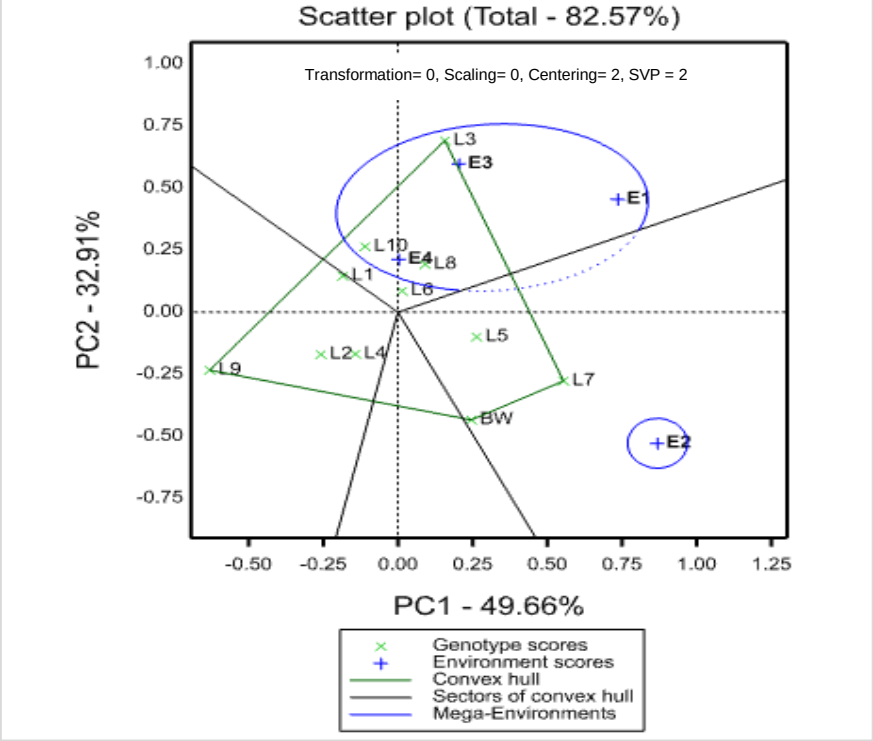
Figure 4.21: GGE biplot of mean yield performance and stability for fodder yield of cowpea genotypes

4.4.3. Stability in number of days to maturity

Number of days to maturity was choosen to be anaysed for stability to enable farmers to choose cultivars that are stable so that they can have one harvesting time rather than unstable geneotypes which will be harvested in varying times. Figure 4.22 presents the GGE biplot for number of days to 90% maturity across the genotypes and environments which captured 82.57% (PC1= 46.66% + PC2= 32.91%) of the variation of the number of days to maturity. The biplot showed that the test environments fell into two of the four sectors outlined in the polygon view. E1 (Syferkuil 2015/16), E3 (Syferkuil 2016/17) and E4 (Towoomba 2016/17) were grouped together to form mega-environment 1 with breeding line L3 being the vertex genotype wherein, showing that the line matured late in those three environments. Local check BW and Line L7 were the vertex genotypes in mega-environment 2 (E2 -Towoomba 2015/16) indicating late maturity. The vertex genotypes in each environment indicate that the genotypes matured late in those environments. Breeding lines L1, L2, L4 and L9 fell

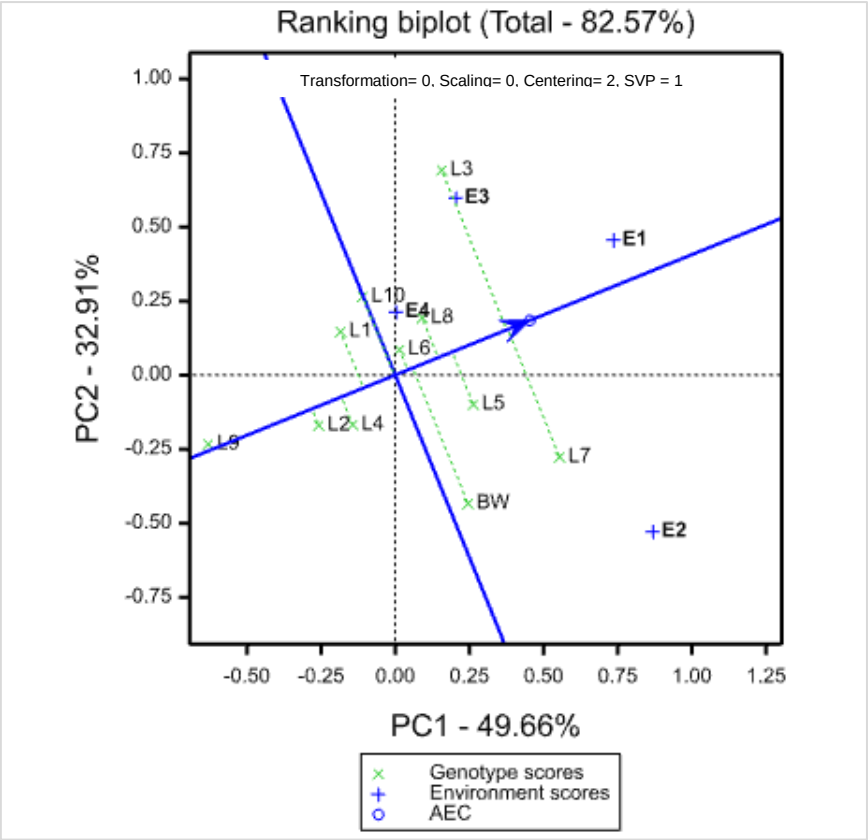
into sectors containing none of the test environments, indicating that the genotypes matured early in one or more environments.

Figure 4.23 shows the mean vs. stability of the genotypes evaluated. According to Yan and Kang (2003), the two lines passing through the biplot origin are (the abscissa (single-arrowed) and the ordinate (without arrows)) are the most important as the ordinate divides the genotypes into those that yielded above and below average. Entries on the left-hand side of the ordinate (L1, L4, L2 and L9) performed below average, which in this case indicates that the genotypes took minimum days to reach maturity. Entries on the right (L10, L6, local check BW, L8, L5, L3 and L7) performed above average, indicating that these genotypes matured late. The projection on the abscissa towards the ordinate of the Average Environment Coordinate is a measure of stability, the shorter the projection the most stable and the longer the projection, the more unstable the genotype (Kang, 2005; Yan and Kang, 2003). The most stable genotypes for maturity where L2, L9, L6 and L4 as they had the shortest projections, while Longest projections were observed for local check BW, lines L7 and L3 and making these genotypes most unstable genotypes in terms of maturity period.



E1= Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

Figure 4.22: GGE biplot displaying the mega-environments and the "Which-won-where" pattern for number of days to 90% maturity of cowpea genotype



E1= Syferkuil 2015/16 season, E2= Towoomba 2015/16 season, E3= Syferkuil 2016/17, E4= Towoomba 2016/17

Figure 4.23: GGE biplot of mean yield performance and stability for number of days to 90% maturity of cowpea genotypes

CHAPTER 5

SUMMARY, CONCLUSION AND RECOMMENDATIONS

The genotypes performed better at Towoomba as they flowered and matured early and they exhibited broader canopy cover as compared to when they were grown at Syferkuil. Grain, fodder yields and grain yield components were greater at Towoomba. The genotypes responded well in the 2015/16 season as compared to the 2016/17 season. Most of the lines performed better than control check BW. Breeding line L9 was the earliest to flower and mature. Tall plants were observed for line L5, which was followed by line L7 and L10. Line L7 produced longer peduncles as compared to all other breeding lines including local variety BW. The highest number of pods/plant were recorded for line L7, followed by local check BW, line L4. Line L7 produced long pods, which was followed by lines L5, L4 and local check BW. Local check BW gave more number of seeds per pod as compared to all the breeding lines; hence, its 100 seed weight was the least. Breeding line L7 produced the highest grain yield with an average of 2595.20 kg/ha which was followed by line L2 (1928.00 kg/ha), L10 (1891.70 kg/ha) and Local variety BW (1858.70 kg/ha). High dry fodder yields were observed for lines L3 and L10 with an average of 3611.00 kg/ha and 3022.00 kg/ha, respectively. The performances of these genotypes were indeed confirmed by the GGE biplot analysis as it placed these genotypes at the right-hand side of the biplot, indicating above average performance (Yan and Kang, 2003).

The biplot identified breeding line L7 and L2 as the best combiners of high and stable grain yield. Although local variety BW had high grain yield, its yields were inconsistent across the environments. Breeding lines L4, L10 and L3 were the highest yielders but most unstable genotypes in terms of fodder yield. Breeding line L2 can be recommended for fodder yield production as it combined high and stable fodder yield as compared to local check BW that was most stable but performed below average. The most stable genotypes for maturity where lines L2, L9, L6 and L4 and they also matured earlier except line L9 which was classified as medium maturing line. However Local variety BW and line L7 were also classified as late maturing genotypes which were also the most unstable genotypes in terms of maturity period. The methods for measuring stability were highly satisfactory as they enabled easier visualisation of high

yielding, and stable genotypes and identified ideal genotypes for the test environments.

Based on the above findings, it can be recommended that breeding line L7 be requested for a release as it combines stable and high grain yield for both locations. Line L4 can be released as the best genotype for fodder production. Line L2 can be classified as early maturing genotype and can be released as dual-purpose cowpea genotype as it is combines both stable high grain and fodder yields. When farmers plant this genotype, they will benefit from both the grain and fodder. These recommended genotypes will in a small way enhance the profit margins and earnings of farmers. The recommended lines meet the requirements of the preferred traits by Limpopo Province farmers. The recommended lines can be futher evaluated in other parts of Limpopo Province and around the country to increase the recommendation domain.

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