AGRONOMIC EVALUATION OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES IN CONTRASTING AGRO-ECOLOGICAL REGIONS OF LIMPOPO AND MPUMALANGA PROVINCES

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DECLARATION

I, the undersigned, Siphiwe Kim Shilenge, (student no.: 11565175) hereby declare that this dissertation for the MSc degree at the University of Venda has not previously been submitted for a degree at this or any other University, and that it is my own work and that all reference material contained therein has been truly acknowledge.

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As the supervisor/co-supervisor of the candidate, we agree to the submission of this dissertation.

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DEDICATION

To my parents

ABSTRACT

Chickpea (*Cicer arietinum* L.) is an important grain legume in the world, ranking second after soybean (*Glycine max* L.). It accounts for a substantial proportion of human dietary nitrogen intake and plays a crucial role in food security in developing countries. Chickpea can grow in areas with low rainfall and poor soils, and thus may be an important food security crop for smallholder resource-poor farmers in the semi-arid tropics such as the dry environments of the Limpopo and Mpumalanga Provinces of South Africa. Preliminary studies showed the huge potential of chickpea production in these environments. However, no suitable genotypes have been identified and recommended for different agro-ecological zones of Limpopo and Mpumalanga Provinces. Therefore, the objective of this study was to evaluate the performance, and hence, identify the genotypes that are adapted/suitable to the contrasting agro-ecological conditions of Limpopo and Mpumalanga Provinces for production.

Field experiments were conducted in the winter cropping seasons of 2016 and 2017 at Thohoyandou (University of Venda experimental station), Syferkuil (University of Limpopo experimental station) and Nelspruit (University of Mpumalanga experimental station). Ten desi chickpea genotypes were sown in a completely randomized block design replicated three times on 10 May 2016 and 10 April 2017 (Thohoyandou), 13 May 2016 and 11 April 2017 (Syferkuil) and 03 May 2016 and 24 May 2017 (Nelspruit). Plant growth characteristics were assessed by determining plant height, crop phenology, number of primary and secondary branches, and canopy cover. Yield and yield components were assessed at harvest after physiological maturity. Carbon dioxide exchange rates (CER) was determined at different growth stages using the Infra-Red Gas Analyzer (IRGA). Chlorophyll content (CC) and intercepted radiation were determined weekly using the chlorophyll content meter (CCM-200 PLUS, Opti-Science, Tyngsboro, Massachusetts), and the AccuPAR, LP-80 ceptometer (Deacon Devices Ltd., Pullman, USA), respectively. Genotypes did not vary in CC at Thohoyandou in all seasons, but CC increased with stages of growth. Genotypes varied in the proportion of intercepted radiation (IR) at all measurement dates in Thohoyandou during the 2016 and 2017 growing seasons. The proportion of IR increased with growth stage, reached a peak and declined with plant age. Genotype affected photosynthesis and intercellular CO_2 concentration (C_i) but did not have any significant effect on stomatal conductance (gs), transpiration (T) and Leaf Vapour Pressure Deficit (VPDL) during the 2016 season in Thohoyandou. In contrast, genotype did not affect photosynthesis, C_i, gs, T and VPDL in the 2017 season in Thohoyandou. There was no variation among genotypes on number

of primary and secondary branches in Thohoyandou in both seasons. Genotypes showed no variation in plant height in the 2016 season in Thohoyandou agro-ecological condition. However, genotypes showed significant variation in plant height at 14, 70 and 84 days after emergence (DAE) in the 2017 cropping season. Moreover, genotypes showed significant variations in days to 50% flowering in Thohoyandou during the 2016 season, but showed no variations in days to 50% emergence and 75% physiological maturity. Genotypes showed no variations in days to 50% emergence, 50% flowering, 50% podding and 75% physiological maturity in the 2017 season in all locations. Genotypes showed significant variation in grain yield in Syferkuil agro-ecological condition, but showed no significant variations on all the other studied traits, while genotypes varied in 100 seed weight (SW) in Thohoyandou, but did not show any variations on the other studied traits during the 2016 season. Moreover, genotypes did not vary for all studied traits in Nelspruit during the 2016 season. The 2016 genotype and environment (G X E) interaction results showed no significant variations. However, results showed G X E interactions during the 2017 growing season suggesting that genotypes responded to environmental variation in a different way. Syferkuil had the greatest grain yield (2811 kg ha^{-1} and 3122 kg ha^{-1}) in both the 2016 and 2017 growing seasons respectively, as compared to Thohoyandou and Nelspruit.

These preliminary findings show that the studied genotypes responded differently in contrasting agro-ecological regions of Limpopo and Mpumalanga Provinces and that Syferkuil might be the best environment for chickpea production in this region due to its cooler temperatures. Of the genotypes evaluated the most promising genotypes are ICCV8101, ICCV3203 and ICCV4110 in these regions in terms of grain yield.

Key words: Agro-ecological, environment, genotypes, semi-arid, yield components

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CHAPTER 1

1. INTRODUCTION

1.1. BACKGROUND INFORMATION

Chickpea (*Cicer arietinum* L) is a legume in the family Fabaceae, subfamily Faboideae. It is also known as gram, Bengal gram, garbanzo (USDA, 2014), Egyptian pea, ceci, cece or chana, or Kabuli Chana (particularly in Northern India). It can grow in areas of low rainfall and poor soils (Neumann et al., 2011). It is one of the earliest cultivated legumes, 7,500-year-old remains have been found in the Middle East (Philologos, 2005). The plant grows between 20 to100cm high and has small feathery leaves on either side of the stem. Chickpeas are a type of pulse, with one pod containing 1-4 seeds (Herbst, 2001).

Chickpea is an important grain legume in the world ranking second after soybean (*Glycine max* L.) and common bean (*Phaseolus vulgaris*) ranking third (FAOSTAT, 2018). It accounts for a substantial proportion of human dietary protein intake and plays a crucial role in food security in developing countries (Varshney et al., 2013), and being a rich and cheap source of protein can help people improve the quality of their diets. Chickpea is grown in over 50 countries throughout the tropical, subtropical and temperate regions in South, West and East Asia, Australia, East and North Africa, North and South America and southern Europe (FAOSTAT, 2018). Asia accounts for 84.9% of the world chickpea production while Africa (4.7%), Oceania (4.4%), Americas (4.4%) and Europe (1.5%) are among chickpea producers (FAOSTAT, 2018). The top five chickpea producing countries are Ethiopia, Mexico, Canada, USA and Myanmar (FAOSTAT, 2018). In Africa, chickpea production is 731 thousand tones with an average yield of 1425.7 kg ha^{-1} (FAOSTAT, 2018). In Sub- Saharan Africa, Ethiopia is the largest producer, followed by Sudan (FAOSTAT, 2018). Currently there is hardly any chickpea production in South Africa and the rest of Southern Africa despite the high and increasing domestic demand (FAOSTAT, 2018; Thangwana and Ogola, 2012).

Chickpea is a good source of protein, complex carbohydrates, fibre and minerals; its protein quality is better than that of other legumes such as pigeon pea, black gram and green gram (Singh et al., 2005). Chickpea has significant amounts of all the essential amino acids except sulphur-containing amino acids, which can be complemented by adding cereals to the daily diet. It

contains 31% protein, 60% carbohydrate, 9% fat, and is a source of calcium, magnesium, iron, phosphorus, potassium and zinc (Yadav et al., 2007). Chickpea is a good source of important vitamins such as niacin, riboflavin, thiamin and folate (Jukanti et al., 2012; Singh et al., 2005). Also, chickpea is a significant contributor to agricultural sustainability through nitrogen fixation and as a rotation crop allowing the diversification of agricultural production systems (FAO, 2004). Moreover, chickpea is well adapted to environmental stresses such as drought, high temperatures and poor soils (Siddique et al., 1999) and may thus be an important food security crop for smallholder resource-poor farmers in the semi-arid tropics.

The Limpopo and Mpumalanga Provinces are characterized by low rainfall and poor soils. The regions receive an average annual rainfall of 500mm and 667mm, respectively (Masereka et al., 2018; Tadross et al., 2005), often receiving little or no rain during the winter season. Therefore, chickpea may be an important food security crop for smallholder resource-poor farmers in the dry environments of the Limpopo and Mpumalanga Provinces of South Africa, and serve as an important winter rotational crop for commercial cereal farmers in this region (Thangwana and Ogola, 2012). Previous studies have reported a significant genotypic variation in and across environments. Preliminary studies showed the huge potential of chickpea in these environments (Matthews et al., 2009; Matthews et al., 2011, Thangwana and Ogola, 2012). Thangwana and Ogola (2012) reported that grain yield was greater in the winter (3308.3 kg ha^{-1}) compared with the summer (1483.7 kg ha^{-1}). Similarly, Matthews et al. (2009) reported that grain yield was greater in May (877 kg ha^{-1}) plantings compared with the March (625 kg ha^{-1}) and April (711 kg ha^{-1}) plantings. In contrast, in 2007 grain yield was significantly greater in the May planting (662 kg ha^{-1}) compared with the March (310 kg ha^{-1}), February (435 kg ha^{-1}) and June/July (377 kg ha^{-1}) plantings.

The University of Venda in the Limpopo Province and the Department of Agriculture, Rural Development and Land Administration (DARDLA) in Mpumalanga Province, initiated research into chickpea production in the North-Eastern part of South Africa over 10 years ago. Over 200 chickpea genotypes have been evaluated so far, out of which 20 lines (hereafter referred to as “elite”) have been identified for further evaluation. However, there have not been suitable genotypes identified, recommended and released for the different agro-ecological zones of Limpopo and Mpumalanga Provinces for cultivation. The hypothesis tested was that chickpea genotypes are adapted to the different agro-ecological conditions of Limpopo and Mpumalanga

Provinces. Therefore, the aim of this study was to identify genotypes that are adapted/suitable to the contrasting agro-ecological conditions of Limpopo and Mpumalanga Provinces for cultivation.

1.2. OBJECTIVES

The main objective of this study was to identify genotypes that are adapted/suitable to the agro-ecological conditions of Limpopo and Mpumalanga Provinces.

The specific objectives of this study were to:

- To evaluate the genotypic effects on some physiological traits of chickpea across diverse environments.
- To evaluate the growth and yield of chickpea genotypes in diverse environments in Limpopo and Mpumalanga Provinces.

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CHAPTER 2

2. LITERATURE REVIEW

2.1. CHICKPEA TYPES

There are two distinct types of chickpea, namely Desi (microsperma) and Kabuli (macrosperma). Both are generally distinguished by their size, flower and seed coloration. Desi has small, dark (light to dark brown) seeds and a rough thick seed coat. Flower colour of Desi type are usually pink, purple, or blue (Muehlbauer and Rajesh, 2008). It is mostly grown in India, and other parts of the Indian subcontinent, as well as in Ethiopia, Mexico, and Iran (Mohammadi, 2015). The ecological adaptation of each type is related to their respective origins. Desi chickpeas are best suited to semi-arid areas of the tropics (Malhotra et al., 1987; Muehlbauer and Singh, 1987). Desi means 'country' or 'local' in Hindustani; its other names include Bengal gram or kala chana ("black chickpea" in both Hindi and Urdu) or chhola boot (Mohammadi, 2015). Desi is probably the earliest variety because it closely resembles seeds found both on archaeological sites and the wild plant ancestor (*Cicer reticulatum)* of domesticated chickpea, which only grows in southeast Turkey, where it is believed to have originated (Mohammadi, 2015). Desi chickpeas have markedly higher fibre content than Kabuli, and hence a very low glycemic index, which may make them suitable for people with blood sugar problems (Singh et al., 1994). The Desi type is used to make chana dal, which is a split chickpea with the skin removed, and flour (besan).

Kabuli has large, light-coloured seeds with a smooth seed coat, and is mainly grown in the Mediterranean, Southern Europe, Northern Africa, South America and Indian subcontinent (Mohammadi, 2015). Flower colour of Kabuli type is usually white (Muehlbauer and Rajesh, 2008). Plant height typically ranges from 20.4cm to 100cm, with Kabuli types often slightly taller than Desi types (McKay et al., 2002). Kabuli chickpeas are best grown in temperate areas (Malhotra et al., 1987; Muehlbauer and Singh, 1987). The name Kabuli means "from Kabul" in Hindi and Urdu, and this type was thought to come from Kabul, Afghanistan when it was introduced to India in the 18th century (Mohammadi, 2015). It is called Kabuli chana in Marathi and safed chana in India. Therefore, it is likely that the adaptation of both Kabuli and Desi genotypes may vary across environments and seasons in North Eastern South Africa. Thus, evaluation of different accessions of each of the two types across environment and seasons is important in identifying stable genotypes across environments and seasons.

2.2. CONSTRAINTS TO CHICKPEA PRODUCTION

2.2.1. Introduction

A number of factors have been shown to negatively affect chickpea productivity in diverse environments. These factors are divided into biotic and abiotic factors. The yield potential of chickpea is seldom achieved due to unsuitable cultivars to cope with these stresses. Major biotic stresses include diseases and insect pests, while major abiotic stresses include extremes of soil moisture (drought and waterlogging), temperature extremes (heat stress or cold temperature/frost), imbalance in soil fertility (nutrient deficiencies or toxicity including salinity). Despite its high yield potential, reportedly more than 6 t ha^{1} (Singh, 1987), low and unstable yields are generally due to the adverse effects of biotic and abiotic stresses.

2.2.2. Abiotic Stresses

Abiotic stress is the negative impacts of non-living organisms, for example high temperatures and drought, in a specific environment, on crop productivity (Biology Online, 2008). It is the most inimical factor concerning the growth and productivity of crops worldwide (Gao et al., 2007). Research has shown that abiotic stresses are at their most adverse when they occur in combination (Mittler, 2006). For example, in drought-stricken areas, many crops may encounter a combination of drought and other stresses, such as heat or salinity. Seed yield of chickpea is generally low, unstable and less than its potential as it is most often grown on marginal lands with minimum inputs. The most common abiotic stresses affecting chickpea production, in order of importance, are drought, heat, cold and salinity (Singh et al., 1994). Other abiotic stresses specific to some regions are waterlogging, soil alkalinity and acidity, and nutrient deficiencies and toxicities (Toker et al., 2007).

Drought which limits production in different parts of the world has remained the most recalcitrant to breeders' efforts (Toker et al., 2007; Tuberosa and Salvi 2006). Terminal drought is a major problem in chickpea production as 90% is grown under rainfed conditions (Kumar and Abbo, 2001) where terminal drought limits its productivity (Toker et al., 2007). The crop often experiences increasing drought stress during the reproductive growth stage, resulting in senescence and reduction in pod and seed development. Two strategies that are employed in chickpea for drought management are escape and tolerance. Developing early maturing cultivars to escape terminal drought is the most effective strategy as it enables the crop to complete its life

cycle before the onset of severe drought (Yadav et al., 2007). Breeding strategies for improving drought tolerance are already underway. Molecular markers and candidate genes associated with root traits are being targeted to introgress the quantitative trait loci for root traits from drought tolerant to drought sensitive genotypes following marker-assisted breeding strategies (Varshney et al., 2010). It is clear that new genotypes are continuously being developed, hence there is always a need to test these new genotypes for adaptation to target production environments.

Concerning heat stress, Wahid et al. (2007) reported that the rise in temperature beyond certain optimum levels is detrimental to crop growth causing severe injuries that are collectively termed as 'heat stress'. Significant progress has not been achieved regarding the effect of heat on different morphological and physiological stages of chickpea (Wang et al., 2006). Being a cool season crop, chickpea is susceptible to high temperature (30–35°) for a few days at flowering stage, which can cause substantial yield loss (Saxena et al., 1988; Summerfield and Wein, 1980). High temperature hampers photosynthesis by damaging both structural and functional activity of chlorophyll and lowers the chlorophyll content (Xu et al., 1995). Temperature beyond 40°C causes disruption in photosystem I and II (Baker, 1991; Sharkey, 2005) and affects respiration (Kurets and Popov, 1988), membrane composition and its stability, nitrogen fixation (Jha et al., 2014) and plant water relations (McDonald and Paulsen, 1997). High temperature stress also causes reduction in number of flowers, pollen production, pods /plant and most importantly, the filled pods/ plant (Devasirvatham et al., 2012; Makonya et al., 2019; Wang et al., 2006). This is due to the fact that chickpea has small flowers and the stamens are diadelphous (stamens are fused together into two sets by the filaments). Self-pollination takes place before the flower opens and pods form within 5 to 6 days (Singh, 1997). Heat stress during this reproductive phase is generally allied with lack of pollination, and abscission of flower buds, flowers and pods with substantial yield loss (Nakano et al., 1997, 1998). Temperature has an effect on the growing season of chickpea as it is the main factor in deciding the maturity of the plant and also controls plant growth and development. There is a wide variation in temperature across environments, hence three sites were selected for this study.

Cold temperature stress represents a major limiting factor in chickpea production especially in North India, Canada and some parts of Australia. Based on the severity of cold, low temperature injury can be classified into two types: (i) chilling injury when temperature remains above freezing point (>0 °C); and (ii) freezing injury at temperature below freezing point (0 °C). The chilling and

freezing injury cause serious damages to plants, including disruption of membrane (McKersie and Bowley, 1997; Steponkus et al., 1993), hampered pollen formation or pollen germination. The chilling and freezing injury also affects photosynthesis (Jha et al., 2014). Since this study was conducted across three diverse environments, the effect of cold temperatures was expected more especially in high altitude areas during the winter months. For example, in Syferkuil there are cases where temperatures may fall very low; this can help in identifying genotypes that are tolerant to cold temperatures. Therefore, it is important to test the different genotypes across these different environments.

Chickpea production is adversely affected by soil salinity in arid and semi-arid regions (Ali and Ahsan, 2012). Salt stress reduces water potential (Benlloch-Gonzalez et al., 2005; Hayashi and Murata, 1998; Munns, 2002), creates imbalance in ion (Hassanein, 2000), imposes osmotic stress and ion toxicity (Munns, 2005), and leads to nutrient deficiency (Tejera et al., 2006) in plants. In addition to inhibiting growth, photosynthesis, energy and lipid metabolism (Parida and Das, 2005; Ramoliya et al., 2004), salinity also restrains flower and pod formation (Katerji et al., 2001; Vadez et al., 2007). Samineni et al. (2011) declared that vegetative and reproductive stages are equally sensitive to salinity.

The specific abiotic stresses characterizing the Limpopo and Mpumalanga Provinces are drought, heat stress and cold temperature stress. Some progress has been made in breeding for resistance to drought and heat. Recently, Makonya et al. (2019) reported that some genotypes were heat tolerant in the same study area and that stress in the field generally leads to reduced photosynthesis, as well as carbohydrate concentrations in leaves of heat sensitive genotypes. Therefore, identifying genotypes that can resist, tolerate or avoid these stresses is of importance for cultivation in such adverse environments.

2.2.3. Biotic stresses

Biotic stress is a general term for the adverse effects on plants caused by other living organisms such as insects, fungi, bacteria and viruses (Flynn, 2003). The types of biotic stresses imposed on a plant depend on both environment and the host plant and its ability to resist particular stresses (Carris et al., 2012). Major diseases of chickpea are divided into foliar and root diseases. Foliar diseases include Ascochyta blight (the fungus *Ascochyta rabiei* causes lesions to occur on

all above ground parts of the chickpea), Bacterial blight (the bacterium *Pseudomonas syringae* causes small water soaked lesions on leaves, pods and stems), Fusarium wilt (the fungus *Fusarium oxysporum* causes leaves to yellow and plants to become stunted), and Sclerotinia stem rot (the fungus *Sclerotinia sclerotiorum* causes white fungal growth on older individual plants) and Phoma blight (the fungus *Phoma Medicaginis*) causes root rot and black stem lesions, often below the soil surface (Gurjar et al., 2010). Also, there are viruses that infect green pea which may infect the chickpea and viruses that cause distinct symptoms on the green pea. The most important viral diseases in chickpea are stunt (bean leaf roll virus) and yellowing (pea enation mosaic virus) (Nene et al., 2012).

There are also a number of diseases that affect the roots. Soil-borne fungal pathogens generally act together to cause complex diseases rather than a single disease. Two to five pathogens commonly are identified in the chickpea root-rot complex. Each pathogen may cause seed rot, seedling damping-off, or root rot. Components of the complex may include the following pathogens and diseases: *Aphanomyces euteiches* (Aphanomyces root rot), *Fusarium solani* (black root rot), *Rhizoctoria solani* (wet root rot), *Pythium* species (Pythium damping-off and root rot), and *Thielaviopsis basicola* (black streak root rot) (Gurjar et al., 2010; Matthews et al., 2015). High incidences of root rot on chickpea caused by *Pythium* species have been reported in the study region (Matthews et al., 2015). Screening of resistant genotypes to the *Pythium* species is necessary as resistance is widely recognized as the safest and most effective method for protecting crops from diseases.

Cutworms, cabbage loppers, and army worms can cause damage to the chickpea plants (FAO, 2004). Pod borers such as *Helicoverpa armigera* also cause losses in the production of chickpea. Young larvae feed on foliage initially; young chickpea plants may be completely destroyed; older larvae bore into seed pods and consume seeds (Ogola, 2015; Nene et al., 2012). Birds and rodents also feed on chickpea seeds causing substantial yield losses (Castillo et al., 2008; Thangwana and Ogola, 2012).

Many species of plant-parasitic nematodes have been reported in the roots and rhizosphere of chickpea in the major growing regions of the world. However, only certain nematode species are considered constraints to chickpea production, causing an estimated 14% in annual yields losses

(Sasser and Freckman 1987; Sharma et al. 1992). The most important nematode pathogens of chickpea include root-knot nematodes (*Meloidogyne* spp.), root-lesions nematodes (*Pratylenchus* spp.), cyst-forming nematodes (*Heterodera* spp.), and the reniform nematode (*Rotylenchulus reniformis*).

Most of the breeding efforts made in chickpea have been focused on improving yield, resistance to diseases like Ascochyta blight and Fusarium wilt (Varshney et al., 2014a), and on resistance to various abiotic stresses (Varshney et al., 2013, 2014b). Since the type of biotic stresses imposed on a plant depend on both geography and climate, it is important to understand the biotic stresses in the diverse environments of Limpopo and Mpumalanga Provinces in order to identify genotypes with multiple-stress resistance. Identifying genotypes that are tolerant to such conditions will be used in improving varieties as well as benefit end users, mostly farmers with limited resources. This project will also build on the limited information on agronomic and yield traits of chickpea on contrasting agro-ecological conditions of both Limpopo and Mpumalanga Provinces.

2.3. GENOTYPIC VARIATION IN GROWTH AND YIELD OF CHICKPEA

Variation is the occurrence of differences among individuals due to their genetic makeup and the environment in which they are raised. A number of studies show that there is genotypic variation in growth and yield of chickpea under different environments. For example, a substantial variation among genotypes in number of pods per plant, number of seeds per plant, grain yield, days to flowering, plant height, number of primary and secondary branches per plant, 100-SW and yield per plant were reported (Hussain et al., 2015; Moucheshi et al., 2011). Mubvuma et al. (2015) reported that the effect of genotype on crop biomass, seed weight, number of pods per plant, pod weight, harvest index and grain yield was significant under well-watered and water stress conditions. In contrast, crop biomass varied with planting date but not genotype in both conditions. Similarly, significant variation for days to flowering, days to maturity, number of pods per plant and seed yield among chickpea genotypes were reported in Bakhsh et al. (2003). Bazvand et al. (2015) reported that there are genotypic variations in yield and some of the yield components in chickpea genotypes. Thangwana and Ogola (2012) reported that the effect of genotype on number of seeds per pod and 100-SW was significant in the summer and winter seasons. Similarly, Madzivhandila et al. (2012) reported that the effect of genotype on grain yield was

significant in both summer and winter sowings. Moreover, Makonya et al. (2019) also observed genotypic differences for grain yield and pod number across environments. It is clear from the foregoing that there is a wide genotypic variation in growth and yield of chickpea across environments, therefore there is a need to identify genotypes that are adapted to diverse environments.

2.4. YIELD STABILITY AND EFFECT OF ENVIRONMENT ON GROWTH AND YIELD OF CHICKPEA

The measured grain yield of a cultivar in an environment is due to the effect of genotype (G), environment (E) and G X E interaction (Yan and Kang, 2003). Preliminary studies show the huge potential of chickpea in these environments (Thangwana and Ogola, 2012; Matthews et al., 2009). However, no suitable genotypes have been identified and recommended for different agro-ecological zones of Limpopo and Mpumalanga Provinces. The variability in environment has been long recognized as an important factor influencing the performance of genotypes. Multi-environment trials (METs) are typically used in plant breeding programmes to evaluate material across a range of sites representing target environments for the crop (Berger et al., 2007). G x E interaction should be investigated so that the breeder can decide to restructure the programme to minimize the interaction effect, or exploit it to produce varieties with specific adaptation to particular environments. A key concept in G x E analysis is genotype stability and by definition, genotypes exhibiting a high degree of G x E interaction are unstable across sites (Berger et al., 2007).

The effect of G X E interaction on grain yield has been reported in wheat, chickpea, maize, sorghum and other crops (Dehghani et al., 2006). Therefore, this approach can be used for the identification of stable genotypes across environments. Mohamed et al. (2015) reported that environment contributed the highest proportion of the variation (42.5%), followed by genotype x environment interaction (33.4%), whereas genotype contributed 24.1% of total variation. Similarly, Mallu et al. (2014) reported that genotypes and genotype by environment interaction showed highly significant variations for all studied traits. Bakhsh et al. (2007) reported that the interaction of G X E was non-significant for number of primary and secondary branches. Genotypes show stable performances for days to flowering, number of pods per plant, grain yield per plant and 100-SW (Bakhsh et al., 2007). However, some studies also show that genotypes tend to have unstable performances across environments. For example, Shafi et al. (2012) reported that the

performance of genotypes were uneven across environments. More recently, Tilahun et al. (2015) reported that grain yield displayed significant effects of locations, genotypes and genotype by environment interaction. This indicates differences in environments and the presence of genetic variability among genotypes. Similarly, Thangwana and Ogola (2012) reported that grain yield was greater in the winter (3308.4 kg ha^{-1}) compared with the summer (1483.7 kg ha^{-1}). Moreover, Makonya et al. (2019) reported no interaction between genotypes and environment on yield and yield components of plants grown in either 2016 or 2017 cropping season and that environmental effects showed that the cooler site recorded higher grain yield than warmer sites. It is clear that some genotypes show a stable performance while other genotypes show variation in agronomic performance across environments and growing seasons, so it is important to assess the agronomic performance of genotypes across diverse environments.

2.5. THE VARIABILITY AMONG GENOTYPES IN RELATION TO PHYSIOLOGICAL TRAITS

Genotypic variation in physiological traits such as chlorophyll content, net-photosynthesis, stomatal conductance and transpiration rate have been reported in chickpea and other crops. For example, Dalvi et al. (2016) reported variations in chlorophyll content, stomatal conductance, transpiration rate and photosynthesis rate in tested chickpea genotypes during different growth stages. Moreover, Talebi et al. (2013) observed variations among chickpea genotypes in chlorophyll content in both irrigated and non-irrigated conditions. Koul et al. (2014) observed that chickpea genotype P362 showed maximum photosynthesis rate, stomatal conductance and chlorophyll content in both irrigated and non-irrigated conditions as compared to genotype P1103 and SBD377. Makonya et al. (2019) observed significant genotypic differences on Pn where genotype Acc#7 was similar to Acc#RR-3, but higher than the two similar Acc#RR-2 and Acc#8 genotypes. It is clear that there are variations in the physiological traits of chickpea, therefore identifying genotypes with better photosynthetic activity (which controls plant growth) and transpiration rate as well as low leaf conductance will help in obtaining genotypes with high yield and can be used for further evaluation.

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CHAPTER 3

3. MATERIALS AND METHODS

3.1. STUDY SITE

The study was conducted at the University of Venda, the University of Mpumalanga and the University of Limpopo experimental farms. The sites were selected because of variations in soil type, temperature, rainfall received per annum and soil pH levels and hence contrasting growth environments. The University of Venda is situated in Thohoyandou, Vhembe District in the Limpopo Province, South Africa. Thohoyandou is situated at a height of 595m above sea level, latitude of 22.97556ºS and longitude of 30.44444ºE (Tadross et al., 2005). The area receives an average of about 500mm of rainfall per annum. The average minimum and maximum temperatures are 18ºC and 31ºC (Tadross et al., 2005). The site is characterized by deep, well-drained clay soils, classified as Rhodic Ferralsols with a soil pH of 6.06 (Lusiba et al., 2016).

The University of Mpumalanga is situated in Nelspruit, Mbombela Municipality in the Mpumalanga Province, South Africa. Nelspruit is situated at a height of 677m above sea level, latitude of 25.4658ºS and longitude of 30.9853ºE (Masereka et al., 2018). The area normally receives about 667mm of rain per annum, with most rains occurring during summer (Climate data for Nelspruit, 2010). The average minimum and maximum temperatures are 21.4 ºC and 27.9 ºC respectively (Masereka et al., 2018). The soils in the study area have a generally light texture (loamy to sandy loam) (Paterson, 2013) and the soil pH ranges from 4.53 to 5.54 (this is according to soil sample and analysis done by one student at the same study area).

The University of Limpopo's experimental farm (Syferkuil) is situated near Ga-Mothapo, Capricon District Municipality in Limpopo Province, South Africa. Syferkuil is situated at a height of 1230m above sea level, latitude of 23.8888ºS and longitude of 29.7386ºE (Thabang et al., 2012). The area receives an average of about 451mm of rainfall per annum. The average minimum and maximum temperatures are 10 ºC and 25 ºC respectively (Thabang et al., 2012). The study site is characterized by sandy loam soil type, with a soil pH of 5.18 (Makonya et al., 2019).

3.2. EXPERIMENTAL DESIGN

Ten Desi genotypes (with genotype and environment as treatment factors) were each planted in experimental unit measuring 1.2 m x 12 m in a randomized complete block design replicated (RCBD) three times in each site. These genotypes were selected out of over 200 chickpea genotypes that were preliminarily evaluated, out of which 20 lines that performed better were identified for further evaluation. Plantings was done in winter 2016 and 2017 cropping seasons as previous studies reported that grain yield was greater in winter compared with summer (Madzivhandila et al., 2012; Thangwana and Ogola, 2012). Field sowing was done manually in 1.2 m long rows (0.4 m apart), with four rows per plot at seeds rates, which provided crop stands denser than the target density. The plants were thinned into target plant density (25 plants m^{-2}) at 14 days after emergence. There are no planting densities recommendations currently available for chickpea in these regions, South Africa. Therefore, the planting density that was used in this study was based on earlier studies at the same site showing that grain yield was greater at 25 plants m^{-2} compared to 20 and 33 plants m^{-2} in winter sowing (Thangwana and Ogola, 2012).

3.3. CULTURAL PRACTICES

The seedbed was prepared to a suitable tilth. The seeds were planted on 10 May 2016 and 10 April 2017 (Thohoyandou), 13 May 2016 and 11 April 2017 (Syferkuil) and 03 May 2016 and 24 May 2017 (Nelspruit). Chickpea seeds were planted 2 to 3.5 cm deep. The experimental plots were kept weed free throughout the cropping season. Fertilizer was applied during planting and was based on soil test recommendations and previous crop history. The plots were fertilized by super phosphate fertilizer (14.08% P with 50 kg P ha^{-1}) and nitrogen (N) as limestone ammonium nitrate (LAN 28% N with 20 kg N ha^{-1}). Chickpea seeds were inoculated at seeding stage with a *Bradyrhizobium* strain for *Cicer* species to ensure effective nodulation and nitrogen fixing. Irrigation was done immediately after sowing to promote germination, emergence and crop establishment, as well as during crop growth, whenever necessary.

3.4. MEASUREMENTS

3.4.1. Chlorophyll content

Chlorophyll content was measured from three selected plants from the middle rows in each plot. Young fully expanded leaves were measured using the chlorophyll content meter (CCM-200

PLUS, Opti-Sciences, Tyngsboro, Massachusetts). Measurements were taken on a weekly basis between 21 days after emergence (DAE) and physiological maturity (PM). The meter was calibrated before the readings were taken.

3.4.2. Plant growth

Plant growth was assessed by determining plant height, crop phenology, and number of primary and secondary branches, leaf area development and leaf area index. Plant height was measured from the base of the plant to the apical bud of the plant and expressed in centimetres (cm) using a 5 m measuring tape. The plants to be measured were the plants on the innermost row and 3 plants were measured per plot. Crop phenology was determined by the number of days to 50% flowering and the number of days to 75% physiological maturity. The number of primary and secondary branches were counted from three selected and tagged plants in each plot on a weekly basis. The proportion of intercepted radiation and canopy cover was measured using the AccuPAR, LP-80 ceptometer (Decagon Devices Ltd., Pullman, USA). The ceptometer uses the photosynthetic active radiation (PAR) inversion technique to measure leaf area index (LAI). The LP-80 calculates LAI by means of measuring the difference between light levels above the canopy and at ground level. The measurements were taken between 11:00 and 13:00 h on clear, cloudless days on a weekly basis. On each occasion, the ceptometer was positioned between the rows in such a manner that it ran perpendicular to the rows. Equation 1 was used to calculate the proportion of intercepted radiation:

$$\alpha = 1 - (P_a / P_-) \quad (1)$$

Where:

P_a is the photosynthetically active radiation (PAR) above the canopy

P_- is the photosynthetically active radiation (PAR) below the canopy

α is the proportion of the intercepted radiation

3.4.3. Carbon dioxide exchange rate (CER)

Carbon dioxide exchange rate (CER), transpiration rate, respiration rate and stomatal conductance were measured using the Infra-Red Gas Analyzer (IRGA). Three plants were selected and tagged per plot and young fully expanded leaves were selected for measurements on each occasion on different plant growth stages. To obtain a measurement, leaves were

allowed to equilibrate to 20°C cuvette conditions and at PPFD of ca 1000 µmol $m^{-2}s^{-1}$ for three minutes. After the three minutes, a button was pressed and readings taken.

3.4.4. Biomass, grain yield and yield components

Biomass, grain yield and yield components were assessed at harvest when the plants were matured. Plants were cut at ground level from the three innermost rows at an area of 2.4 m^2. All the plant samples (minus the pods) were oven-dried at 65 °C for 48 hours and the dry matter content determined. Grain yield and yield components were determined from the same plants that were used for biomass at harvest. The pods were manually removed from all the harvested plants and number of pods per plant were counted. All the pods were threshed by hand, and number of seeds per pod were counted. The seeds were air-dried, cleaned and weighed to determine grain yield (kg ha^{-1}). Sub-samples of the seeds were used to determine 100 seed weight (100-SW).

3.4.5. Yield stability

Yield stability was assessed by evaluating the genotype (G) x environment (E) interaction effects on grain yield in order to identify genotypes that are stable across environments. Combined analysis of variance (ANOVA) was performed to determine the effects of G, E, and GE interaction effects.

3.5. DATA ANALYSIS

Analysis of variance was performed using the GenStat (2014) statistical package 17th edition. Mean separation was done using the standard error of the difference of the means (SED). A significance level of 0.05 was used to test the probability level. An initial analysis of variance was performed for each environment to verify the existence of differences between genotypes. Principal Component Analysis (PCA) was used to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G X E interaction, with a minimum number of degrees of freedom.

3.6. REFERENCES

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CHAPTER 4

ASSESSING VARIATION IN PHYSIOLOGICAL TRAITS AMONG CHICKPEA (*CICER ARIETINUM)* GENOTYPES

ABSTRACT

The North-Eastern parts of South Africa are characterized by high temperatures and receive very little rainfall per annum. In these areas, chickpea is continuously exposed to increasing drought and high temperatures during flowering and maturity stages due to insufficient rainfall. This study evaluated the genotypic effects on some physiological traits among chickpea genotypes that were sown in a completely randomized block design replicated three times in 2016 and 2017 cropping seasons in Thohoyandou. Chlorophyll content (CC), proportion of intercepted radiation (IR), stomatal conductance (gs), photosynthesis (Pn), transpiration (E), intercellular CO_2 concentration (Ci) and Leaf Vapour Pressure Deficit (VPDL) were determined at vegetative and reproductive (podding) stages. Pn, gs, E, Ci and VPDL were determined using the Infra-Red Gas Analyzer (IRGA), CC was measured using the chlorophyll content meter (CCM-200 PLUS, Opti-Sciences, Tyngsboro, Massachusetts) and proportion of IR was measured using the AccuPAR, LP-80 ceptometer (Decagon Devices Ltd., Pullman, USA). There was no variation in CC among genotypes at all measurement dates in both seasons, but CC increased with stage of growth from 1.15 (25 DAE) to 1.49 $mmolm^{-2}\ s^{-1}$ (117 DAE) and 1.04 (14 DAE) to 1.75$mmolm^{-2}\ s^{-1}$ (84 DAE) in 2016 and 2017, respectively. There was significant variation in the proportion of IR at all measurements dates in both seasons, except at 63 DAE during the 2017 season. The proportion of IR increased with growth stage from 26.45% (25 DAE), reached a peak at 82.41% (84 DAE) to 88.08% (101 DAE) and declined with plant age to 72.35% (108 DAE) and 63.85% (115 DAE) during the 2016 season. A similar trend was observed during the 2017 season. The proportion of IR increased with growth stage 35.77% (28 DAE), reached a peak at 90.57% (56 DAE) to 96.29% (77 DAE). Genotypes showed significant variation on Pn but showed no significant variation on gs, E and VPDL in 2016. Ci varied from 157.2 µmol $CO_2\ mol^{-1}$ (ICCV3110) to 417.4 µmol $CO_2\ mol^{-1}$ (ICCV8101). This variation may be attributed this to the relatively lower temperatures (22.6 °C) on the day of data collection. There were no variations on Pn, gs, E, Ci and VPDL among the genotypes during the 2017 season. These findings show that there are genotypic variations in some physiological traits among chickpea genotypes, which may be useful in crop improvement programmes.

Key words: Gaseous exchange, genotypic effect, genotypic variation, physiological traits, total intercepted radiation

4.1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is grown across a wide range of environments, from the subtropics (India and North-eastern Australia) to arid and semi-arid Mediterranean climatic regions (Mediterranean basin and Southern Australia) (Dhima et al., 2015). In subtropical areas it is sown after the summer monsoonal rains and grows on stored soil moisture. In Mediterranean-climatic regions it is sown in autumn or spring and grows during the cool wet months of winter and spring. In both environments chickpea crops are exposed to drought during pod set and seed filling (terminal drought). Additionally, the crops can be exposed to low temperatures at flowering that inhibit pod set and high temperatures during seed filling that limit yields (Lawlor et al., 1998; Srinivasan et al., 1999) . Several researchers (Siddique et al., 1999; Singh, 1993; Thangwana and Ogola, 2012) have reported that this crop can grow under environmental stress conditions such as drought, high temperatures and poor soils. Environmental stresses are responsible for reducing crop productivity as it affects growth and development through various physiological processes of the plant. Light is one of the most important factors, which plays a major role in development and yield of crop. The biochemical processes leading to growth of plant and chlorophyll formation depends upon the amount of radiation received. The yield or dry matter production of a crop is partly the reflection of efficiency of the conversion of light energy into chemical energy through photosynthesis (Murchie et al., 2009). The conversion efficiency is affected by the amount and intensity of photosynthetically active radiation (PAR) intercepted and the photosynthetic efficiency of the leaves of the crop. The North-Eastern parts of South Africa are characterized by high temperatures and receive very little rainfall per annum. In these areas, chickpea is continuously exposed to increasing drought and high temperatures during flowering and maturity stages (Talebi et al., 2013) due to insufficient rainfall. Studies have shown that there are variations in the physiological traits of chickpea genotypes across environments (Dalvi et al., 2016; Koul et al., 2014; Talebi et al., 2013). Makonya et al. (2019) observed significant genotypic differences in Pn among chickpea genotypes, where genotype Acc#7 was similar to Acc#RR-3, but higher Acc#RR-2 and Acc#8 genotypes. This shows that chickpea genotypes varies in terms of physiological traits. Thus, this study evaluated the genotypic variations in some physiological traits of chickpea genotypes under normal conditions.

4.2. MATERIALS AND METHODS

The detailed description of materials and methods is described in chapter 3, but a summary is outlined here. The study was conducted at the University of Venda experimental farm, Thohoyandou in winter 2016 and 2017 cropping season. Ten Desi genotypes (with genotype as treatment factor) were planted in a randomized complete block design replicated three times. Carbon dioxide exchange rate (CER), transpiration rate (E) and stomatal conductance (gs) were determined at flowering (77 DAE, 2016 season) and podding (93 DAE, 2017 season) using the Infra-Red Gas Analyzer (IRGA). Three plants were selected and tagged per plot and young fully expanded leaves were selected for measurements. To obtain a measurement, leaves were allowed to equilibrate to 20°C cuvette conditions and at PPFD of ca 1000 µmol $m^{-2}s^{-1}$ for three minutes. After the three minutes, a button was pressed and readings taken. Chlorophyll content was determined weekly, using the chlorophyll content meter (CCM-200 PLUS, Opti-Science, Tyngsboro, Massachusetts), from young fully expanded leaves of three selected plants from the middle rows in each plot between 21 DAE and physiological maturity (PM). The readings were taken between 11:00 and 13:00 h on clear cloudless days. The proportion of IR was measured weekly using the AccuPAR, LP-80 ceptometer (Decagon Devices Ltd., Pullman, USA). The ceptometer was positioned between the rows in such a manner that it runs perpendicular to the rows and readings recorded. Analysis of variance was performed using the GenStat (2014) statistical package 17th edition. Mean separation was done using the standard error of the difference of the means (SED). A significance level of 0.05 probability was used to test the probability level.

4.3. RESULTS AND DISCUSSIONS

4.3.1. Response of genotypes on chlorophyll content

The results showed no variation in chlorophyll content among the genotypes at all measurement dates in both seasons (Figure 4.1). However, the chlorophyll content of the 10 genotypes increased with crop growth stage from 1.15 mmol cm^{-2} s^{-1} at 25 DAE to 1.49 mmol cm^{-2} s^{-1} at 117 DAE in the 2016 season (Figure 4.1a). Most genotypes had peak CC at 84 DAE to 101 DAE. A similar trend was observed in the 2017 season. There was an increase in chlorophyll content from 1.04 mmol cm^{-2} s^{-1} at 14 DAE to 1.75 mmol cm^{-2} s^{-1} at 84 DAE (Figure 4.1b). This increase in CC with plant age may be attributed to change in season as growing conditions like temperature, precipitation and sunlight also changes. These results are comparable with those of Macil et al. (2017) who reported that chlorophyll content increased with crop growth. The high values in

chlorophyll content for Macil et al. (2017) were partly attributed to the effect of biochar on plant nutrient status. However, these results are not in agreement with that of Dalvi et al. (2016), who reported a decrease in chlorophyll content with crop stage. Moreover, Talebi et al. (2013) observed that genotypes with high yield in well-watered conditions also had high chlorophyll content, these results are not comparable with the results in this study. Ghiabi et al., 2013 reported that total chlorophyll content decreased in Kabuli chickpea accessions grown under rainfed conditions while chlorophyll content increased under irrigated conditions. The presence of nitrogen in the soil and chlorophyll in plants are closely related. Estimated remobilization of nitrogen is greater than that of carbon in all grain legumes (Masclaux-Daubresse et al., 2010). Therefore, remobilized nitrogen is predominantly derived from the breakdown of photosynthetic proteins including chlorophyll. Nitrogen is a component of the chlorophyll and if there is a deficiency it is reflected as chlorosis in the leaf. When unfavorable growing conditions cause physiological stress in a plant, the chlorophyll content of its leaves typically begins to decrease. However, this was not the case in this study as chlorophyll content increased with crop stage.

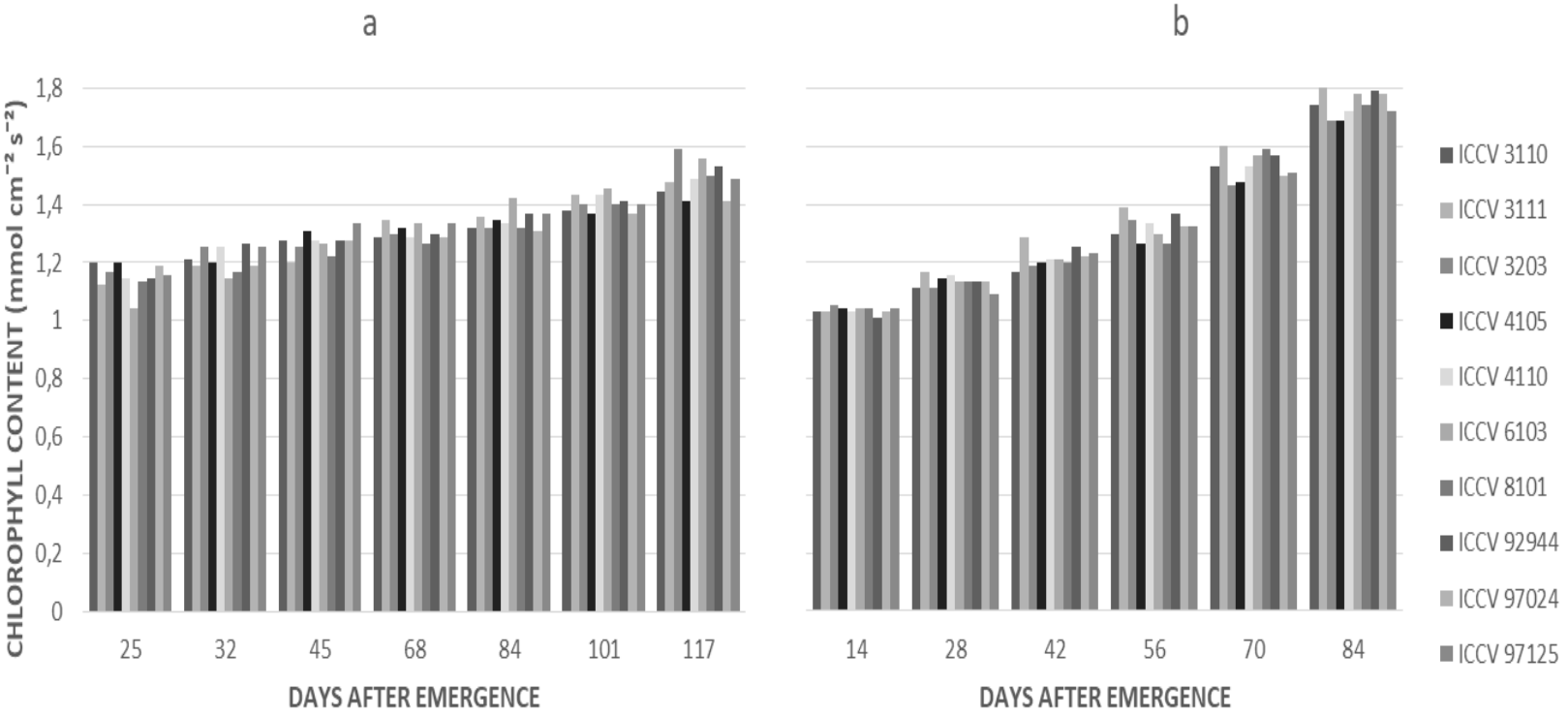

Figure 4.1 Chlorophyll content (mmol cm^{-2} s^{-1}) in the vegetative and reproductive stages of 10 desi chickpea genotypes during the 2016 (a) and 2017 (b) season in Thohoyandou

4.3.2. Response of genotypes on intercepted radiation

Genotypes showed a significant variation in the proportion of intercepted radiation at all measurement dates, in both seasons, except 63 DAE in 2017 (Figure4.2a and 4.3b). During the 2016 season, the proportion of IR increased with crop growth from 25 DAE, reached a peak at 84 to 101 DAE and then declined (Figure 4.2a). Genotype ICCV4105 had the highest peak proportion of IR at 115 DAE (73%), while genotype ICCV3203 (52.84%) had lowest peak proportion of IR during the 2016 season. Genotype ICCV4105 had the highest peak proportion of IR at 77 DAE (97.52%), while genotype ICCV92944 (94.56%) had lowest peak proportion of IR during the 2016 season. Genotypes attained a peak PAR interception (≈89%) at 101 DAE. All genotypes had dense canopies and were all approaching 90% canopy cover during the 2016 season. A similar trend was observed in 2017. The proportion of IR increased from 28 DAE, reached a peak at 63 DAE to 77 DAE (Figure 4.3b). All genotypes had dense canopies and were approaching 100% canopy cover. Genotypes attained a peak PAR interception (≈96%) at 70 DAE. These findings are comparable to results from previous studies in the same study area. For example, Macil et al. (2017) observed that an increased in the proportion of IR attributed to a larger leaf canopy. It is likely that the increase in the proportion of IR may be due to a larger leaf canopy (increase in leaf number and total leaf area), and the decline was due to leaf loss (senescence) as the crop reached maturity. As the plant grows, the amount of leaf material in the canopy increases, there is a proportional increase in the amount of light absorbed and a decreasing proportion of light will be transmitted to the ground surface increases LAI thereby, increasing the photosynthetic rate and evapotranspiration, thus increasing crop growth.

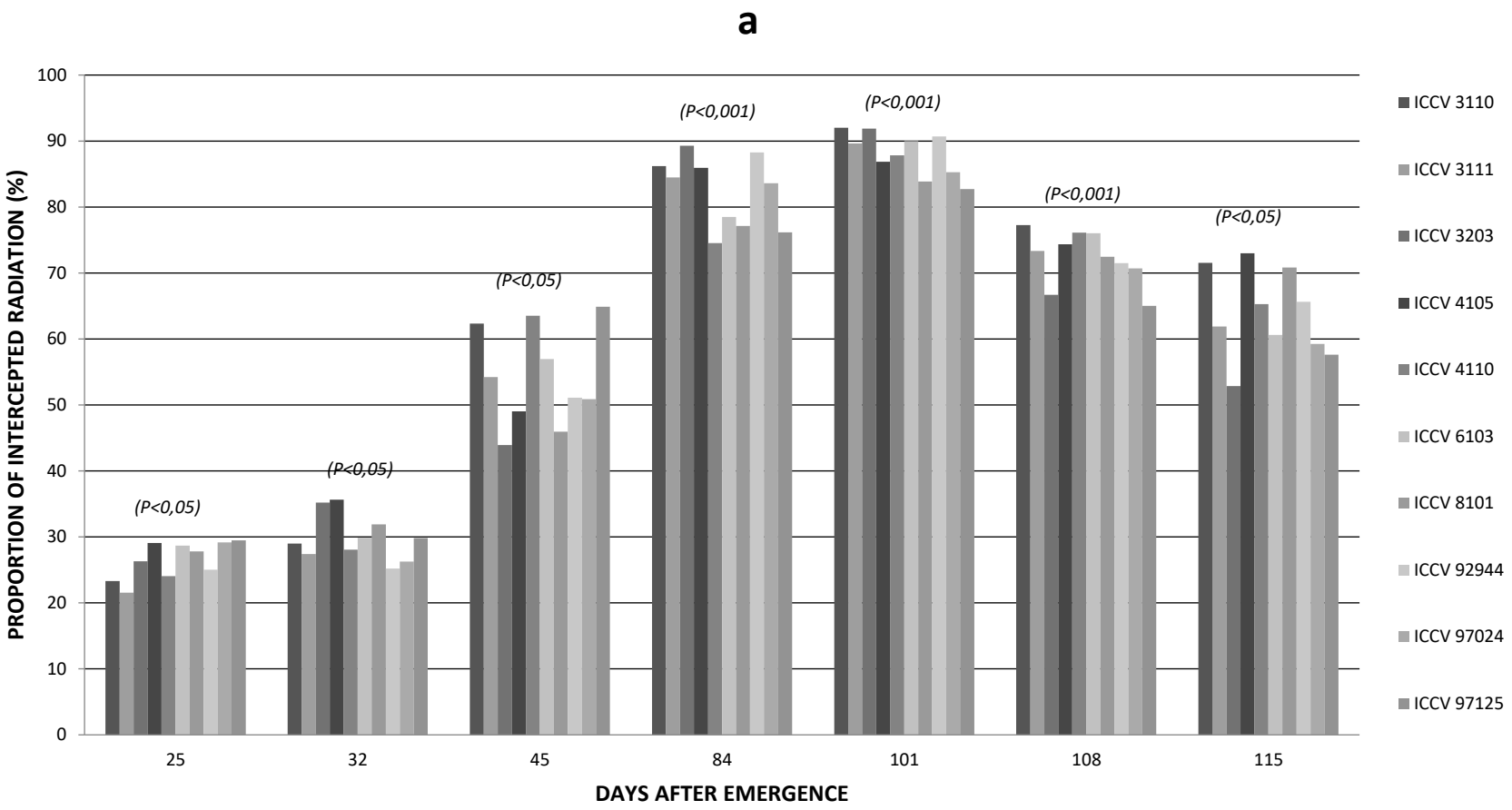

Figure 4.2 Proportion of intercepted radiation (%) in chickpea genotypes during the 2016 (a) season in Thohoyandou

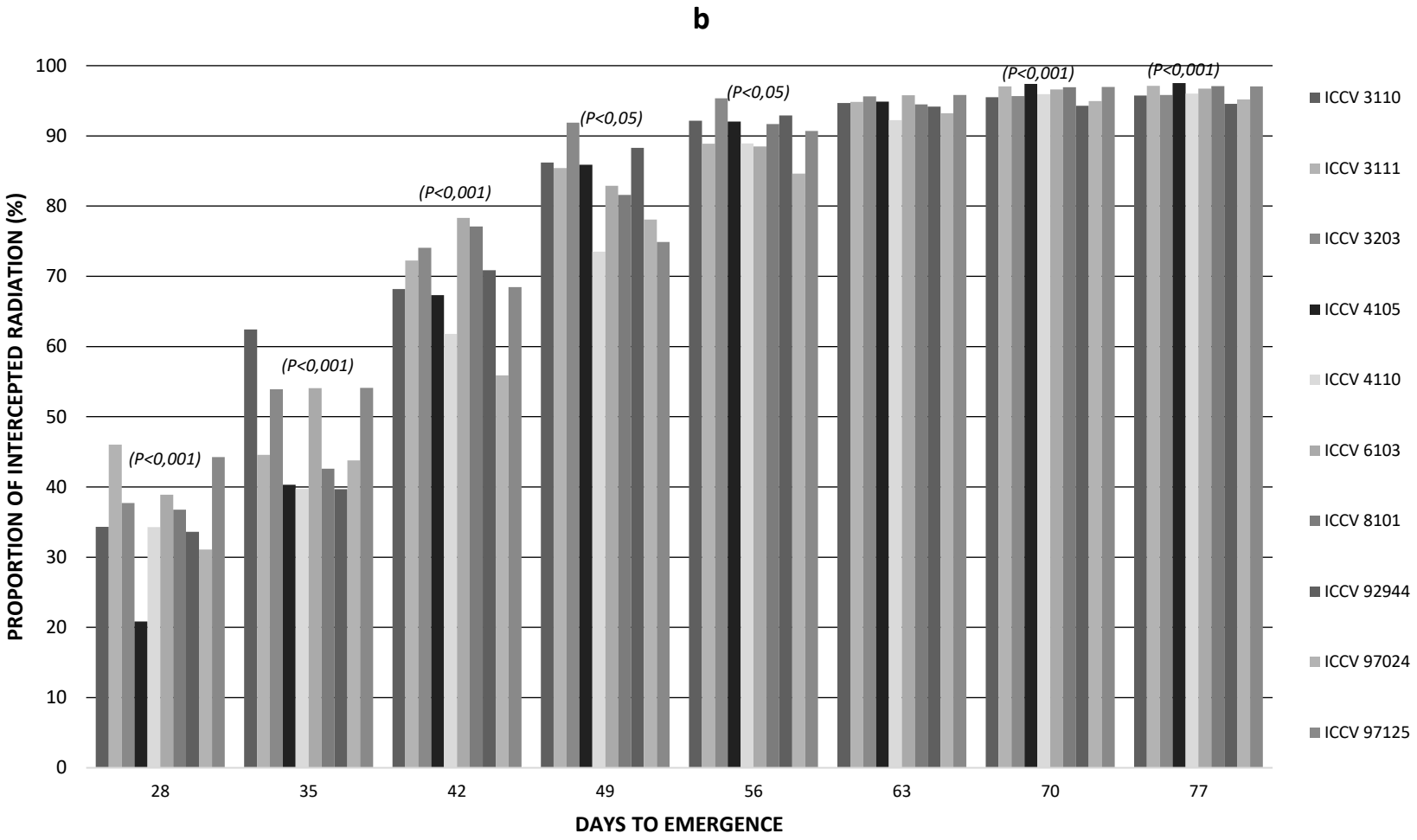

Figure 4.3 Proportion of intercepted radiation (%) in chickpea genotypes during the 2017 (b) season in Thohoyandou

4.3.3. Response of genotypes on carbon dioxide exchange rate (CER)

The results showed significant variation in Pn and Ci among genotypes but there was no variation on gs, T and VPDL at 71 DAE in the 2016 season among genotypes (Table 4.1). In contrast, there was no variation among genotypes in terms of Pn, gs, Ci, T and VPDL at 92 DAE during the 2017 season (Table 4.1). Genotype ICCV97125 had the highest photosynthetic rate during the 2016, while genotype ICCV3111 had the lowest photosynthetic rate. Genotype ICCV8101 had the highest Ci and genotype ICCV3110 had the lowest Ci in 2016. The current results are not comparable with that of Macil et al. (2017) who observed no significant variations in photosynthetic rate among genotypes. Moreover, Mythili and Nair (1996) obtained significant genotypic variabilities in CER in chickpea genotypes. The photosynthetic rates ranged from 12.5 in HG 1765B to 18.4 µmol CO_2 m^{-2} s^{-1}. Dalvi et al. (2016), also reported that mean photosynthesis rate of wilt resistant and susceptible chickpea genotypes with checks decreased from 16.89 µmol CO_2 m^{-2} s^{-1} (control) to 13.42 µmol CO_2 m^{-2} s^{-1} (water stress) at preflowering stage. Better water supply resulted in significantly higher stomatal conductance, net photosynthesis and transpiration rate. Kawale (2011), reported that physiological processes like photosynthesis, stomatal conductance, absorbed photosynthetically active radiation were found at highest rate in some genotypes which resulted in higher yield. Makonya et al. (2019) observed significant genotypic differences in Pn among chickpea genotypes, where genotype Acc#7 was similar to Acc#RR-3, but higher Acc#RR-2 and Acc#8 genotypes. This shows that chickpea genotypes varies in terms of physiological traits.

Table 4.1 The response of genotype on gaseous exchange parameters at 71 DAE (2016) and 92 DAE (2017) of 10 desi chickpea genotypes in Thohoyandou

Genotype	Leaf photosynthetic rate (µmol CO_2 m^{-2} s^{-1})	Stomatal conductance (mol H_2O m^{-2} s^{-1})	Intercellular CO_2 concentration (µmol CO_2 mol^{-1})	Transpiration (mmol H_2O m^{-2} s^{-1})	Leaf vapour pressure deficit (kPa)
2016					
ICCV 3110	10.65^{ab}	0.075	157.2^{a}	1.02	1.246
ICCV 3111	7.61^{a}	0.057	164.0^{ab}	0.79	1.257
ICCV 3203	10.41^{ab}	0.170	321.2^{cd}	1.88	1.133
ICCV 4105	9.31^{ab}	0.075	185.8^{ab}	1.05	1.211
ICCV 4110	10.08^{ab}	0.176	375.4^{cd}	2.04	1.209
ICCV 6103	11.36^{ab}	0.101	271.9^{bc}	1.09	1.116
ICCV 8101	10.51^{ab}	0.032	417.4^{d}	0.43	1.217
ICCV 92944	11.18^{ab}	0.135	270.9^{abc}	1.57	1.169
ICCV 97024	8.88^{ab}	0.091	275.6^{bc}	1.05	1.131
ICCV 97125	12.33^{b}	0.060	264.4^{abc}	0.70	1.116
Mean	10.23	0.097	270.4	1.16	1.180
SED	1.176	0.0541	29.42	0.553	0.1369
P value	*	ns	***	ns	ns
CV%	2.8	7.1	2.2	6.4	3.6
2017					
ICCV 3110	10.05	0.1331	202.3	1.54	1.539
ICCV 3111	12.15	0.1561	252.9	1.43	1.428
ICCV 3203	12.44	0.2025	266.4	2.09	1.378
ICCV 4105	13.81	0.1503	174.0	1.63	1.378
ICCV 4110	12.72	0.2060	254.0	2.32	1.419
ICCV 6103	14.01	0.2083	245.0	2.57	1.412
ICCV 8101	15.76	0.2335	235.4	2.30	1.390
ICCV 92944	12.71	0.1633	237.0	1.95	1.455
ICCV 97024	14.18	0.1739	215.9	1.87	1.427
ICCV 97125	13.42	0.2238	224.3	2.32	1.344
Mean	13.12	0.1851	230.7	2.00	1.417
SED	2.856	0.03893	30.40	0.564	0.1035
P value	ns	ns	ns	ns	ns
CV%	4.5	7.8	10.6	7.4	7.2

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Pn= Leaf photosynthetic rate, gs= Stomatal conductance, Ci= Intercellular CO_2 concentration, T= Transpiration, VPDL= Leaf vapour pressure deficit

4.4. CONCLUSION

Chickpea genotypes varied from each other in most of the physiological traits studied, which underlines the genotypic variation among the tested genotypes. Based on the analysis of 10 chickpea genotypes, it was concluded that there was a substantial variation in some of the physiological traits within chickpea genotypes. Genotypes ICCV97125 and ICCV8101 with the highest photosynthetic rates can be used for further evaluation. Nonetheless, the study recommends involving more sites, before definite conclusions can be drawn.

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CHAPTER 5

THE RESPONSE OF GENOTYPE ON GROWTH PARAMETERS OF TEN DESI CHICKPEAS

ABSTRACT

Chickpea (*Cicer arietinum*) is adapted to environmental stresses such as drought, high temperatures and poor soils and may thus be an important food security crop for smallholder farmers in the semi-arid tropics. This study assessed the variation in growth of ten desi chickpea genotypes. Field experiments were conducted in winter 2016 and 2017 seasons in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga). The sites were selected because of variations in soil type, temperature, rainfall received per annum and soil pH levels and hence contrasting growth environments. Crop phenology was determined by the number of days to 50% emergence, 50% flowering, 50% podding and 75% physiological maturity. Plant height and number of primary and secondary branches were determined at vegetative and reproductive stages in Thohoyandou. There was a significant variation in days to 50% flowering among genotypes but there was no variation to days to 50% emergence, 75% physiological maturity, and number of primary and secondary branches in 2016 in Thohoyandou among the genotypes. Moreover, results showed no variation in days to 50% emergence, 50% flowering, 50% podding, number of primary and secondary branches among genotypes in 2017 in Thohoyandou. There was no variation in days to 50% emergence, 50% flowering, 50% podding and 75% physiological maturity among chickpea genotypes in Syferkuil and Nelspruit in winter 2017. The results classified 6 genotypes as early (< 50 days), 1 as moderate (50- 55 days) and 3 as late (55- 60 days) in days to flowering in the 2016 season in Thohoyandou. However, all genotypes were classified as early (<50 days) in days to flowering in Thohoyandou, winter 2017. Moreover, in Syferkuil, 5 genotypes were classified as moderate and 5 genotypes classified as late during the 2017 season. In Nelspruit, all genotypes were classified as late (>55 days) in days to flowering. Crop phenology contributes a key role in increasing seed yield of chickpea. Genotypes flowered earlier in Thohoyandou (47.47 days), while days to 50% flowering was moderate in Syferkuil (54.27 days) and Nelspruit had very late flowering genotypes (76.37 days). There were no variations in case of number of primary and secondary branches among genotypes in Thohoyandou in both seasons. Genotypes ICCV8101 and ICCV3203 produced the tallest plants when compared to the other genotypes in the 2016 and 2017 seasons, respectively. Early phenology in Thohoyandou may be due to high temperatures which is known to shorten developmental stages, or it may be a way of the crop to escape some biotic and abiotic

stresses that occur in the growing season and to utilize the available soil moisture and nutrients. The early genotypes along with those medium reproductive duration and high yield traits can be used for potential breeding material in future improvement of chickpea in these regions.

Key words: Crop phenology, developmental stages, flowering, physiological maturity, reproductive duration,

5.1 INTRODUCTION

Chickpea (*Cicer arietinum* L.) is currently grown in over 50 countries representing a wide range of environments and cropping systems (FAOSTAT, 2018). Phenology is an important component of crop adaptation in these environments. Crop maturity ranges from 80 to 180 days depending on genotype, soil moisture (Saxena, 1990), time of sowing, latitude and altitude (Siddique and Sedgley, 1986; Singh and Dhaliwal, 1972) and depth of sowing (Saxena, 1987). After emergence, temperature and photoperiod (Sandhu and Hodges, 1971; Summerfield et al., 1980, 1984) coupled with the availability of soil moisture (Khanna-Chopra and Sinha, 1987; Piara, 1991) control the rate of progress towards any phenological stage. Lower temperatures, shorter photoperiods and optimal soil moisture, individually or in combinations, help in extending growth period, while higher temperatures, longer photoperiods and moisture stress conditions are known to shorten all developmental phases thereby reducing the crop duration (Summerfield et al., 1990). Winter sown chickpea in the dry environments of Limpopo Province may experience low temperature at flowering and podding leading to substantial reduction in grain yield, while summer sown chickpea may encounter significant yield decrease due to terminal drought and/or high temperatures during flowering and podding (Thangwana and Ogola, 2012). In chickpeas, flowering is considered the critical stage, because environmental conditions that prevail at flowering and the duration of the reproductive phase determine, to a large extent, percentage of fruit set and final yield (Savithri et al., 1980; Saxena, 1984). Evaluation of crop genetic resources is a pre-requisite for future breeding programmes. The value of germplasm relies upon the genetic variability present in those accessions for agronomic and yield components and not only on the number of accessions it possesses (Reddy et al., 2012). Previous studies in chickpea have reported substantial variation in plant height, as well as number of primary and secondary branches per plant (Ali et al., 2008; Aslamshad et al., 2009). In addition to genetic variation, heritability of economically important characters is essential for effective breeding programme and selection of specific traits. High broad sense heritability has been reported in chickpea for number of secondary branches and seed yield (Malik et al., 2009), days to flowering and plant height (Khan et al., 2011). In South Africa there is hardly any chickpea production despite the high and increasing domestic demand (FAOSTAT, 2018; Thangwana and Ogola, 2012). Preliminary studies show the huge potential of chickpea in these environments (Thangwana and Ogola, 2012). However, no suitable genotypes have been identified and recommended for different agro-ecological zones of Limpopo and Mpumalanga Provinces. Crop phenology and growth parameters such as plant height and number of branches are important traits in any

germplasm evaluation trial. Therefore, this study assessed the growth of ten desi chickpea genotypes under diverse environments of the Limpopo and Mpumalanga Provinces.

5.2 MATERIALS AND METHODS

The detailed description of materials and methods is given in chapter 3. The summary is outlined here. The study was conducted in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga) experimental farms in winter 2016 and 2017 in a randomized completely block design replicated three times. Plant growth was assessed by determining plant height, crop phenology, and number of primary and secondary branches. Plant height was measured from the base of the plant to the apical bud of the plant and expressed in centimetres (cm) using a 5m measuring tape. The plants that were measured, were the plants on the innermost row and 3 plants were measured per plot on each occasion. Crop phenology was determined by days to 50% emergence, number of days to 50% flowering, number of days to 50% podding and the number of days to 75% physiological maturity. The number of primary and secondary branches were counted from three selected and tagged plants in each plot on a weekly basis. Analysis of variance was performed using the GenStat (2014) statistical package 17th edition. Mean separation was done using the standard error of the difference of the means (SED). A significance level of 0.05 was used to test the probability level.

5.3 RESULTS AND DISCUSSION

5.3.1 Crop phenology

There results showed variation among genotypes in days to 50% flowering but there were no variations on days to 75% physiological maturity in 2016 in Thohoyandou. Days to flowering varied from 42.00 DAE (ICCV4105) to 56.00 DAE (ICCV97125 and ICCV8101) (Table 5.1). In contrast, there was no variation to 50% emergence, flowering, podding and 75% physiological maturity in all locations in winter 2017 among genotypes (Tables 5.1 and 5.2). According to Mallu et al. (2014), genotypes were grouped as late (> 120 days) in days to physiological maturity in both seasons and locations. The long growth duration was mainly due to the lower average temperature during the winter season. The results classified 6 genotypes as early (< 50 days), 1 as moderate (50- 55 days) and 3 as late (55- 60 days) in days to flowering in the 2016 season in Thohoyandou. However, all genotypes were classified as early (<50 days) in days to flowering in

Thohoyandou in 2017 (Table 5.1). Moreover, in Syferkuil, 5 genotypes were classified as moderate and 5 genotypes classified as late during the 2017 season (Figure 5.2). In Nelspruit, all genotypes were classified as late in days to flowering of >55 days (Figure 5.2). This variation across environments may be partly because flowering time in chickpea depends on season, sowing date, latitude and longitude (Summerfield and Roberts, 1998). Syferkuil had moderate (54.27 days) days to flowering and had higher yields (Chapter 6). This may be due to the crop having more time for biomass accumulation hence the higher yields. The longer growth duration in Syferkuil may be due to the lower minimum temperatures in the winter (10^{o}C) compared with Thohoyandou and Nelspruit. Thangwana and Ogola (2012) observed that the crop in the winter sowing reached physiological maturity (PM) 69 days later than the summer crop.

Crop phenology (flowering and maturity) contributes a key role in increasing seed yield of chickpea. Genotypes flowered earlier in Thohoyandou (47.47 days), while days to 50% flowering was moderate in Syferkuil (54.27 days) and Nelspruit recorded late flowering (76.37 days). Early flowering trait is useful in crops with indeterminate growth habit such as chickpea, in which vegetative growth, flowering, podding and pod filling period occur concurrently as long as conditions for growth are favourable. Early phenology in Thohoyandou may be due to high temperatures which is known to shorten developmental stages. The minimum and maximum temperatures during the growing season were 12/24 ºC (Thohoyandou) and 4/20 ºC (Syferkuil). Thus early genotypes along with those medium reproductive duration and reasonable yield traits can be used for potential breeding material in future improvement of chickpea in these regions. Earlier studies have reported significant genotypic variability for days to 50% flowering in chickpea (Gul et al., 2013) and other legumes (Imani et al., 2013; Oladejo et al., 2011). These findings are not in agreement with those of Mallu et al (2014), who reported highly significant variations for 75% maturity in chickpea. Overall, the reasons for these variations in days to flowering, podding and physiological maturity may be due to the genetic make-up, the environmental factors and the environment in which the experiments were conducted.

5.3.2 Number of branches

The number of primary and secondary branches were not influenced by genotypes in Thohoyandou in both seasons (Table 5.3). The genotype ICCV8101, albeit not significant recorded greater number of branches, greater number of pods per plant and greater grain yield compared to the other genotypes during the 2016 season (Chapter 6). A similar trend was seen during the 2017 winter season in Thohoyandou, genotype ICCV8101 and ICCV4105 recorded

greater number of secondary branches (Table 5.3) and were among genotypes that produced greater yields. Therefore, this trait may be used in future chickpea breeding programs for further exploitation of the genetic variability in the Limpopo and Mpumalanga Provinces. The current results are in agreement with those of Ahmad et al. (2003) who reported a high variability in the number of secondary branches. Genetic variation and heritability of economically important characters is essential for effective breeding programme and selection of specific traits. High broad sense heritability has been reported in chickpea for number of secondary branches, days to flowering and plant height (Khan et al., 2011).

Table 5.1 Days to 50% emergence, days to 50% flowering and 75% days to physiological maturity of 10 desi chickpea genotypes during the 2016 and 2017 season in Thohoyandou

Genotype	Days to emergence (50%)	Days to flowering (50%)	Days to physiological maturity (75%)
2016			
ICCV 3110	10.00	48.00[a]	132.3
ICCV 3111	10.00	49.33[a]	128.0
ICCV 3203	10.00	54.33[a]	133.7
ICCV 4105	10.00	42.00[a]	131.0
ICCV 4110	10.00	55.33[a]	131.3
ICCV 6103	10.00	45.67[a]	128.7
ICCV 8101	10.00	56.00[b]	128.7
ICCV 92944	10.00	48.00[a]	129.7
ICCV 97024	10.00	43.33[a]	119.0
ICCV 97125	10.00	56.00[b]	131.7
Mean	10.00	49.80	129.4
SED	0.002	4.435	5.31
P value	ns	*	ns
CV%	1.0	1.1	2.0
2017			
ICCV 3110	10.67	49.33	78.00
ICCV 3111	10.67	44.00	79.33
ICCV 3203	10.67	46.67	78.33
ICCV 4105	10.67	49.33	76.00
ICCV 4110	10.67	48.33	78.00
ICCV 6103	10.67	47.67	78.33
ICCV 8101	10.67	46.67	78.33
ICCV 92944	10.67	49.33	77.00
ICCV 97024	10.67	44.00	78.33
ICCV 97125	10.67	49.33	80.67
Mean	10.67	47.47	78.23
SED	1.568	2.517	2.779
P value	ns	ns	ns
CV %	5.4	2.7	4.9

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Table 5.2 Days to 50% emergence, 50% flowering, 50% podding and days to 75% physiological maturity of 10 desi chickpea genotypes during the 2017 season in Syferkuil and Nelspruit

Genotype	Days to emergence (50%)	Days to flowering (50%)	Days to podding (50%)	Days to physiological maturity (75%)
SYFERKUIL				
ICCV 3110	10.00	53.33	100.00	156.33
ICCV 3111	10.00	53.33	97.67	154.00
ICCV 3203	10.00	58.00	100.00	156.33
ICCV 4105	10.00	53.33	100.00	156.33
ICCV 4110	10.00	55.67	100.00	154.00
ICCV 6103	10.00	55.67	97.67	156.33
ICCV 8101	10.00	55.67	95.33	156.33
ICCV 92944	10.00	55.67	97.67	154.00
ICCV 97024	10.00	51.00	97.67	156.33
ICCV 97125	10.00	51.00	97.67	156.33
Mean	10.00	54.27	98.37	155.63
SED	2.182	2.761	2.931	2.172
P value	ns	ns	ns	ns
CV %	7.1	2.0	1.8	1.7
NELSPRUIT				
ICCV 3110	13.00	77.33	98.67	132.00
ICCV 3111	12.00	74.00	96.33	133.00
ICCV 3203	12.00	78.33	98.33	133.00
ICCV 4105	12.00	74.67	100.00	132.00
ICCV 4110	12.00	75.00	97.33	133.00
ICCV 6103	11.00	77.33	96.33	132.00
ICCV 8101	12.00	80.00	98.67	132.00
ICCV 92944	11.00	73.00	95.00	132.00
ICCV 97024	12.00	73.67	95.00	133.00
ICCV 97125	12.00	80.33	98.67	132.00
Mean	11.90	76.37	97.43	132.40
SED	1.498	2.663	1.635	0.856
P value	ns	ns	ns	ns
CV %	5.2	1.6	2.1	0.8

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Table 5.3 Number of primary and secondary branches of 10 desi chickpea genotypes during the 2016 and 2017 season in Thohoyandou

	Number of branches at 84 DAE	
Genotype	**Primary branches**	**Secondary branches**
2016		
ICCV 3110	2.00	5.89
ICCV 3111	2.56	4.44
ICCV 3203	2.78	7.33
ICCV 4105	2.11	9.56
ICCV 4110	2.33	8.56
ICCV 6103	2.33	5.67
ICCV 8101	3.00	9.78
ICCV 92944	2.56	6.33
ICCV 97024	2.67	8.33
ICCV 97125	2.67	6.56
Mean	2.50	7.24
SED	0.523	2.025
P value	ns	ns
CV%	6.1	9.3
2017		
ICCV 3110	2.44	8.89
ICCV 3111	2.78	11.11
ICCV 3203	2.89	10.11
ICCV 4105	2.78	11.22
ICCV 4110	2.56	11.11
ICCV 6103	2.33	8.00
ICCV 8101	3.11	11.22
ICCV 92944	2.89	8.89
ICCV 97024	2.78	8.67
ICCV 97125	2.67	8.00
Mean	2.72	9.74
SED	0.468	1.399
P value	ns	ns
CV %	5.5	9.4

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

5.3.3 Plant height

There was no variation among genotypes in terms of plant height at all measurement dates in 2016 (Figure 5.1a), but there was a significant variation among genotypes at 14, 70 and 84 DAE in season 2 (Figure 5.1b). The average plant height for all the genotypes was 11.92cm (14 DAE), 60.57cm (70 DAE) and 69.14cm (84 DAE) with genotype ICCV3203 producing the tallest plants. Plant height is one of the desirable characters in chickpea which enhance ultimate seed yield. For example, genotype ICCV8101 which produced the tallest plants, albeit non-significant, during the 2016 season (Figure 5.1a), had greater yield when compared to the rest of the genotypes in Thohoyandou (Chapter 6). However, genotype ICCV3203 produced the tallest plants but did not produce greater yield (Chapter 6), while genotype ICCV3111 produced the shortest plants during the 2017 season in Thohoyandou (Figure 5.1b). According to Mallu et al., 2015 all the genotypes studied in both seasons can be classified as tall (> 55 cm). Non-significant variations in plant height were reported in other legumes, for example, Roy et al. (2013) reported non-significant variations for plant height in lentil germplasm. Ogola (2015) observed differences in plant height of two desi chickpea genotypes in Thohoyandou. The results indicated the potential of the evaluated germplasm in obtaining genotypes with modest plant height along with other yield traits. Hence genotypes with modest plant height and reasonable yield traits could be used for genetic programmes of chickpea varieties in this region.

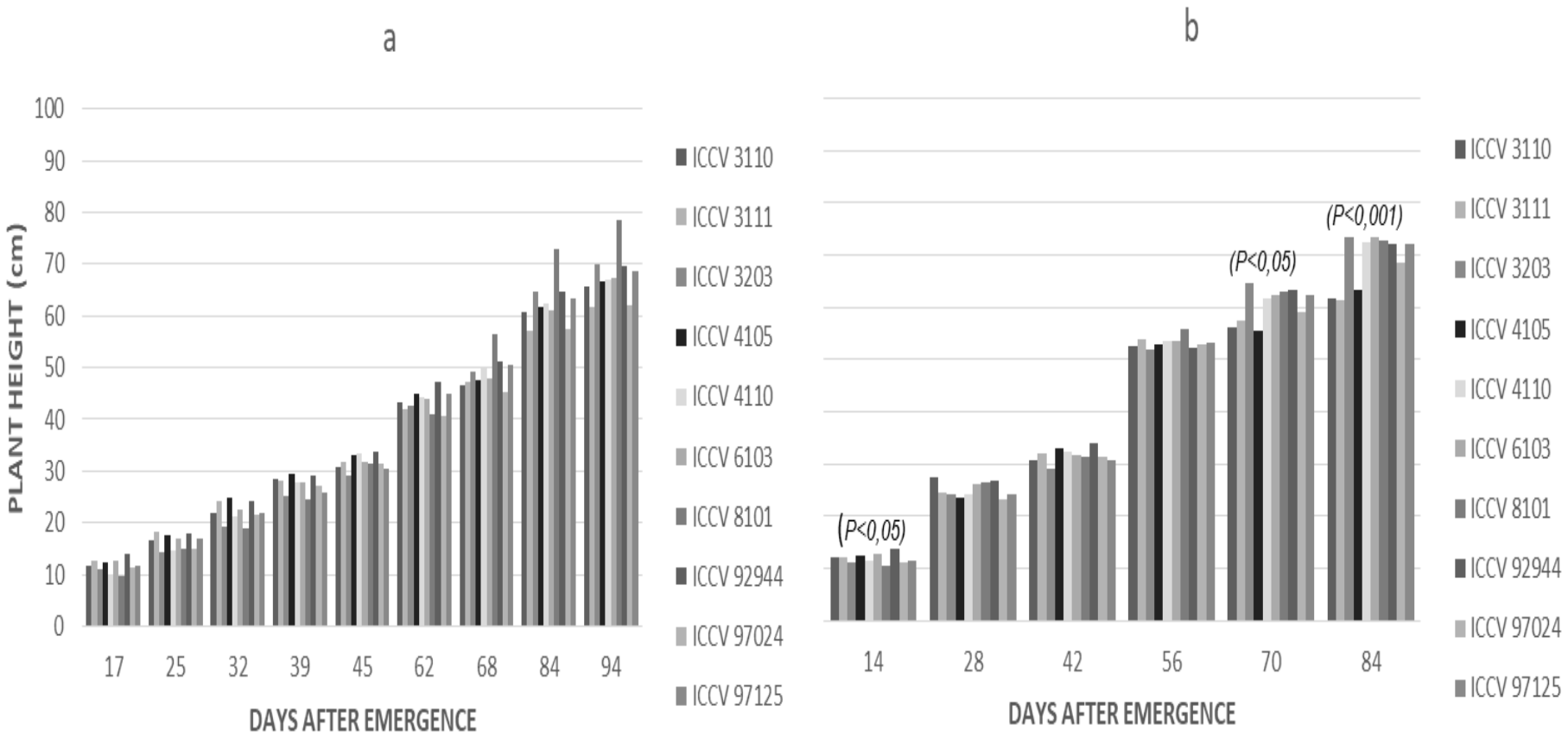

Figure 5.1 Plant height (cm) of 10 desi chickpea genotypes during the 2016 (a) and 2017 (b) season in Thohoyandou

5.4 CONCLUSION

Genotypes in this study were classified as early, moderate and late on the basis of their flowering and maturity across environments. The genotypes varied with respect to days to flowering. Early genotypes along with those medium reproductive duration and reasonable yield traits can be used for potential breeding material in future improvement of chickpea in these regions. These preliminary findings show that are variations in the growth of chickpea genotypes. Nonetheless, more studies are recommended before a definite conclusion can be drawn.

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CHAPTER 6

THE RESPONSE OF GENOTYPE ON YIELD AND YIELD COMPONENTS OF TEN DESI CHICKPEAS IN DIVERSE ENVIRONMENTS OF LIMPOPO AND MPUMALANGA PROVINCES

ABSTRACT

Currently there is hardly any chickpea production in South Africa and the rest of Southern Africa despite the high and increasing domestic demand. This study evaluated yields of ten chickpea genotypes across diverse environments of Limpopo and Mpumalanga Provinces. Field experiments were sown in winter 2016 and 2017 seasons in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga). Grain yield and yield components were determined at harvest maturity. There was a significant variation in grain yield among the studied genotypes but there was no variation on number of pods per plant, seeds per plant, seeds per pod, 100SW and above ground biomass in Syferkuil during the 2016 season among genotypes. However, during the 2016 season in Thohoyandou, the results showed a significant variation among genotypes on 100SW but showed no variations on the other yield components. Moreover, there were no variations on all studied traits in Nelspruit during the 2016 season. Syferkuil produced the highest number of pods per plant (37.4), seeds per plant (45.1), 100SW (24.38g), greater grain yield (2811 kg ha^{-1}) and above ground biomass (6391 kg ha^{-1}) during the 2016 season when compared to the other two sites. Genotype, site and G X E interactions varied significantly in all studied traits during the 2017 season. The highest number of pods per plant (40.68), seeds per plant (51.28), 100SW (25.14g), grain yield (3122 kg ha^{-1}) and above ground biomass (6775 kg ha^{-1}) were recorded in Syferkuil. The ANOVA indicated that the response of genotypes were unstable and fluctuated in their trait expression with environment change. These results clearly show that the environments treated the genotypes differently which may be due to genetic variability and the environments in which they were raised. Genotypes ICCV4110, ICCV8101 and ICCV3203 with high yield from this study could be utilized in future chickpea breeding in the region and identifying genotypes with best performance for the different agro-ecological zones. These preliminary findings show that, there are variations in grain yield of chickpea genotypes across diverse environments and that Syferkuil may be the best environment for chickpea production in this region probably because of its high altitude. Nonetheless, more studies are recommended before a definite conclusion can be drawn.

Key words: Altitude, environment, GXE interaction, grain yield, site

6.1 INTRODUCTION

Chickpea is an important grain legume in the world ranking second after soybean (*Glycine max* L.) (FAOSTAT, 2018). It accounts for a substantial proportion of human dietary nitrogen intake and plays a crucial role in food security in developing countries, and being a rich and cheap source of protein can help people improve the quality of their diets (Varshney et al., 2013). Asia accounts for 84.9% of the world chickpea production while Africa (4.7%), Oceania (4.4%), Americas (4.4%) and Europe (1.5%) are among chickpea producers (FAOSTAT, 2018). In Africa, chickpea produces a total of 731 thousand tones with an average yield of 1425.7 kg ha^{-1}. In Sub- Saharan Africa, Ethiopia is the largest producer, followed by Sudan (FAOSTAT, 2018). There is hardly any chickpea production in South Africa and the rest of Southern Africa. With the objective to increase the flexibility of South African farmers to the impacts of drought and climate change, the crop is being introduced to South Africa. In South Africa, chickpea is becoming one of the most consumed pulses but its demand is currently met through imports. Local industries in South Africa import the crop mainly from Canada and East Africa (Univen, 2018). In general, the imported chickpea is costly with a relatively lower nutritional value as is largely the case with most imported food products (Mpai and Maseko, 2018). Studies conducted in South Africa have assessed the crop's suitable planting season and where planted in winter, irrigation has sustained its growth (Mpai and Maseko, 2018).

Grain yield is the main consideration and the most complex trait from breeder's point of view as it depends on the interaction of genetic makeup of plant and environment. Apart from direct selections for grain yield, the objective of enhanced yield may, in most situations, be more effectively fulfilled on the basis of performance of yield and its components. These components may contribute directly or indirectly to the overall yield (Zeeshan et al., 2013). Climate change forecasts have shown that temperatures in North-Eastern parts of South Africa, will increase by 3-4 °C, whilst rainfall will decrease by 15-20% by the year 2100 (Webber et al., 2014). Therefore, management practices such as choice of crop genotypes may be an important strategy for improving the effects of climate change on crop productivity especially in the dry environments such as the NE parts of SA. There are growing fears that the predicted climate change may lead to worsening drought conditions and moisture stress, especially in the dry environments, and hence decrease in crop productivity (Mubvuma et al., 2015). Therefore, there is a need for continuous development of crop species genotypes for the ever changing environment. Although

preliminary studies have shown a huge potential of chickpea in these dry environments, no suitable genotypes have been identified and recommended for the different agro-ecological zones. The hypothesis tested was that there is variation in yield of chickpea genotypes across diverse environments of Limpopo and Mpumalanga Provinces.

6.2 MATERIAL AND METHODS

The detailed description of materials and methods is described in chapter 3. The summary is outlined here. Field experiments were conducted in winter 2016 and 2017 seasons in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga). Ten desi chickpea genotypes were sown in a completely randomized block design replicated three times on 10 May 2016 and 10 April 2017 (Thohoyandou), 13 May 2016 and 11 April 2017 (Syferkuil) and 03 May 2016 and 24 May 2017 (Nelspruit), respectively. The experimental plots were kept weed free throughout the cropping season by weeding manually. Biomass, grain yield and yield components were determined at harvest maturity. Plants were cut at ground level from the three innermost rows at an area of 2.4 m^2. All the plant samples (minus the pods) were oven-dried at 65°C for 48 hours and the dry matter content determined. Grain yield and yield components were determined from the same plants that were used for biomass at harvest maturity. The pods were manually removed from all the harvested plants and number of pods per plant determined. All the pods were threshed by hand, and number of seeds per pod determined. The seeds were air-dried, cleaned and weighed to determine grain yield (kg ha^{-1}). Sub-samples of the seeds were used to determine 100 seed weight (100-SW). Combined analysis of variance (ANOVA) was performed to determine the effects of G, E, and GE interaction effects. Mean separation was done using the standard error of the difference of the means (SED). A significance level of 0.05 was used to test the probability level. The 2016 season results showed no GXE interaction, therefore, each environment was analyzed separately. There was total crop damage in 2017 in Thohoyandou, therefore, there was no harvest.

6.3 RESULTS AND DISCUSSION

Genotypes varied in grain yield but did not have any significant variations on yield components in Syferkuil during the 2016 season (Table 6.1). Genotype ICCV3203 produced the greatest grain yield while genotype ICCV6103 had the lowest grain yield. However, during the 2016 season in

Thohoyandou, genotype varied in 100SW but did not have any significant variations on grain yield and other yield components (Table 6.2). Moreover, genotype did not have any significant variation on yield and yield components in Nelspruit during the 2016 season (Table 6.3). These preliminary results clearly show that the environments treated the genotypes differently. Genotype ICCV4110 had high grain yield of 2267 kg ha^{-1} in Nelspruit, while genotype ICCV8101 had high grain yield of 3040 kg ha^{-1} in Thohoyandou and genotype ICCV3203 had high grain yield of 4037 kg ha^{-1} in Syferkuil (Tables 6.1, 6.2 and 6.3). The current findings are not comparable to earlier studies at the same site (Madzivhandila et al., 2012; Makonya et al., 2019; Thangwana and Ogola, 2012), which reported variation in grain yield with genotypes. Moreover, Madzivhandila et al. (2012) and Thangwana and Ogola (2012) reported significant variations in cultivar on number of pods per plant, seeds per pod and 100SW among genotypes in the same study location which are not in agreement with the results in this study.

Genotype, site and GXE interactions varied in all yield components during the 2017 season (Table 6.4). There was a high level of variability for all yield components across environments. The ANOVA revealed that the environments on which the experiments were conducted were different from one another in treating the genotypes. Moreover, it also indicates that the response of genotypes were unstable and fluctuated in their trait expression with environment change. This clearly confirms the existence of GEI in this study. The highest number of pods per plant (40.68), seeds per plant (51.28), 100SW (25.14g), grain yield (3122 kg ha^{-1}) and above ground biomass (6775 kg ha^{-1}) were recorded in Syferkuil while Nelspruit had the highest HI (51.4%). Genotype ICCV4110 had greater grain yield (2476 kg ha^{-1}), number of pods per plant (30.13) and number of seeds per plant (35.47) as compared to the other genotypes across environments. The findings exhibited significant differences for all studied traits among studied genotypes, which indicated considerable diversity. These results are comparable with those of Madzivhandila et al. (2012), Makonya et al. (2019) and Thangwana and Ogola (2012) who obtained significant differences in number of pods per plant, seeds per pod, 100SW and grain yield among genotypes in the same study area. Moreover, these results are consistent with those of Win (2011) who obtained significant GXE interactions for yield components except for 100SW. Similarly, Mallu et al. (2014) reported that genotypes and GXE interactions showed highly significant variations for all studied traits.

These results clearly show that the environments treated the genotypes differently, which may be due to variability in genotypes and the environments in which they were grown, that can produce a wide range of phenotypic expressions for the traits evaluated. The wide variation in grain yield could be attributed to similar variation in plant height, number of secondary branches, number of pods per plant and seed weight. In Syferkuil, genotype ICCV3203 had greater grain yield as compared to the other genotypes in 2016 (Table 6.1). However, genotype ICCV8101 which recorded greater number of branches and produced tall plants (Chapter 5), albeit non-significant, recorded greater number of pods per plant and greater grain yield compared to the other genotypes during the 2016 season in Thohoyandou (Table 6.2). Moreover, genotype ICCV4110 had greater grain yields as compared to the other genotypes in Nelspruit in 2016 (Table 6.3). Syferkuil had high grain yield as compared to the other two sites. The combined ANOVA for grain yield during the 2017 season, showed that genotype ICCV4110 had greater grain yield as compared to the other genotypes and that Syferkuil had the highest grain yield relative to Nelspruit (Table 6.4).

Grain yield is directly determined by seed weight, pod number and seed number per pod and is also indirectly influenced by other yield-related traits, such as biomass, plant height and branch number. Yield is a quantitative character, the result of various physiological and biochemical processes. Yield and yield contributing traits could have dynamic correlation with environmental effects. The findings displayed wide genetic variability among studied genotypes for grain yield in chickpea germplasm, in line with other previous studies (Farshadfar and Farshadfar, 2008; Malik et al., 2010). In other legumes, Hegde and Mishra, 2009; Furat and Uzun, 2010 and Roy et al. (2013), have reported substantial variation for seed yield in lentil, cowpea and sesame germplasm respectively.

Table 6.1 The response of 10 desi chickpea genotypes on yield and yield components during the 2016 season in Syferkuil

Genotype	No. of pods per plant	No. of seeds per plant	No. of seeds per pod	100SW (g)	Grain yield (kg ha^{-1})	Above ground biomass (kg ha^{-1})	HI (%)
ICCV 3110	29.5	34.9	1.186	24.70	2858^{ab}	7312	39.00
ICCV 3111	32.7	37.8	1.172	27.80	2520^{ab}	5593	44.12
ICCV 3203	50.8	64.2	1.256	26.33	4037^{b}	7928	51.01
ICCV 4105	40.1	47.6	1.182	24.40	3240^{ab}	6695	48.31
ICCV 4110	45.2	53.5	1.183	25.17	3148^{ab}	6685	47.85
ICCV 6103	23.1	30.4	1.212	24.73	1760^{ab}	4482	41.16
ICCV 8101	41.9	52.8	1.252	23.70	3470^{ab}	7047	48.43
ICCV 92944	41.8	50.7	1.217	22.87	3203^{ab}	6922	46.24
ICCV 97024	35.3	41.3	1.165	22.47	1887^{a}	6862	36.52
ICCV 97125	33.1	37.7	1.169	21.67	1988^{ab}	4383	45.49
Mean	37.4	45.1	1.199	24.38	2811	6391	44.81
SED	8.02	10.60	0.1193	2.291	646.7	1333.7	4.187
P value	ns	ns	ns	ns	*	ns	ns
CV%	3.8	3.7	1.9	8.0	5.8	5.6	5.8

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Table 6.2 The response of 10 desi chickpea genotypes on yield and yield components during the 2016 season in Thohoyandou

Genotype	No. of pods per plant	No. of seeds per plant	No. of seeds per pod	100SW (g)	Grain yield (kg ha^{-1})	Above ground biomass (kg ha^{-1})	HI (%)
ICCV 3110	31.7	52.7	1.251	21.90^{ab}	2049	5140	54.2
ICCV 3111	31.6	40.7	1.270	24.40^{b}	2433	4678	49.6
ICCV 3203	21.3	31.2	1.392	24.30^{ab}	1774	4045	48.3
ICCV 4105	32.3	41.0	1.265	23.13^{ab}	2352	4695	51.6
ICCV 4110	27.0	36.4	1.303	21.53^{ab}	1829	5290	49.7
ICCV 6103	27.7	29.2	1.078	25.80^{ab}	1840	4812	38.3
ICCV 8101	43.1	65.5	1.511	21.23^{a}	3040	6083	49.3
ICCV 92944	36.3	30.4	1.165	24.27^{ab}	2388	3663	46.5
ICCV 97024	31.0	43.2	1.044	20.63^{ab}	2220	4253	51.6
ICCV 97125	32.4	42.4	1.302	23.57^{ab}	2458	4458	54.8
Mean	31.4	41.3	1.258	23.08	2238	4712	49.4
SED	8.47	12.59	0.1296	1.508	634.9	976.2	7.50
P value	ns	ns	ns	*	ns	ns	ns
CV%	8.0	9.9	2.0	2.9	7.9	7.7	6.2

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Table 6.3 The response of 10 desi chickpea genotypes on yield and yield components during the 2016 season in Nelspruit

Genotype	No. of pods per plant	No. of seeds per plant	No. of seeds per pod	100SW (g)	Grain yield (kg ha^{-1})	Above ground biomass (kg ha^{-1})	HI (%)
ICCV 3110	28.9	31.0	0.854	21.33	1656	4483	48.4
ICCV 3111	23.9	29.3	1.046	17.67	1267	3267	39.0
ICCV 3203	36.8	43.0	1.164	19.00	1983	5083	39.5
ICCV 4105	31.5	30.7	0.692	22.00	1667	4667	36.0
ICCV 4110	38.7	41.3	1.047	22.67	2267	4667	48.7
ICCV 6103	30.1	28.4	1.035	19.33	1433	2682	42.3
ICCV 8101	36.1	38.7	1.084	20.33	2017	4567	44.1
ICCV 92944	27.1	23.6	0.997	24.33	1567	3950	40.5
ICCV 97024	30.5	31.1	1.024	21.67	1700	3950	42.3
ICCV 97125	36.8	37.4	1.123	21.00	1850	308	45.9
Mean	32.0	33.5	1.007	20.93	1741	4062	42.7
SED	8.86	11.08	0.2043	3.433	401.9	713.2	8.88
P value	ns	ns	ns	ns	ns	ns	ns
CV%	6.6	3.8	5.7	4.6	7.1	9.2	3.6

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

Table 6.4 The response of genotypes on yield and yield components and GXE interaction across 3 diverse locations during the 2017 season

Treatment	No. of pods per plant	No. of seeds per plant	No. of seeds per pod	100SW (g)	Grain yield (kg ha^{-1})	Above ground biomass (kg ha^{-1})	HI (%)
SITE							
Thohoyandou	-	-	-	-	-	-	-
Syferkuil	40.68^{c}	51.28^{b}	1.271^{b}	25.14^{c}	3122^{c}	6775^{c}	47.64^{b}
Nelspruit	30.87^{b}	38.81^{c}	1.293^{c}	19.78^{b}	2132^{b}	4517^{b}	51.40^{c}
Genotype							
ICCV 3110	19.87^{a}	25.71^{a}	0.8775^{ab}	15.39^{ab}	1665^{a}	2928^{ab}	43.29^{d}
ICCV 3111	21.09^{ab}	27.36^{ab}	0.8778^{ab}	14.99^{ab}	1801^{ab}	3395^{abcd}	35.39^{abcd}
ICCV 3203	28.16^{cd}	32.67^{ab}	0.7675^{a}	15.28^{ab}	1716^{a}	4663^{d}	26.59^{ab}
ICCV 4105	21.96^{abc}	29.38^{ab}	0.9101^{b}	15.56^{ab}	1886^{ab}	3620^{abcd}	35.76^{abcd}
ICCV 4110	30.13^{d}	35.47^{b}	0.7924^{ab}	17.21^{b}	2476^{b}	4185^{bcd}	39.85^{bcd}
ICCV 6103	22.96^{abc}	31.16^{ab}	0.9101^{b}	15.58^{ab}	1619^{a}	4265^{cd}	25.74^{ab}
ICCV 8101	26.91^{bcd}	34.69^{b}	0.8643^{ab}	13.15^{a}	1578^{a}	4664^{d}	22.74^{a}
ICCV 92944	24.09^{abcd}	28.67^{ab}	0.8235^{ab}	15.61^{ab}	1912^{ab}	3989^{bcd}	32.59^{abcd}
ICCV 97024	20.87^{ab}	27.62^{ab}	0.9038^{b}	12.95^{a}	1538^{a}	2618^{a}	41.34^{cd}
ICCV 97125	22.49^{abc}	27.60^{ab}	0.8198^{ab}	14.01^{a}	1323^{a}	3310^{abc}	26.83^{abc}
Mean	23.85	30.03	0.8547	14.97	1751	3764	33.01
SED	1.899	2.376	0.03691	0.887	215.1	376.2	4.253
CV%	1.1	1.7	0.8	4.7	5.4	3.7	2.9
P value							
Site	***	***	***	***	***	***	***
Genotype	***	***	***	***	***	***	***
G X E	***	***	***	*	*	***	***

*** Highly significant (P<0.001), significant * (P<0.05) and ns (not significant)

6.4 CONCLUSION

Best performance and high seed yield is one of the basic criteria for identifying and selecting superior genotypes for different regions. Hence genotypes with high grain yield (ICCV8101, ICCV3203 and ICCV4110) from this study could be utilized in future chickpea breeding and evaluation in the region. These preliminary findings show that, there are variations in grain yield of chickpea genotypes across diverse environments and that, Syferkuil may be the best environment for chickpea production in this region because of its high altitude. Nonetheless, more studies are recommended before a definite conclusion can be drawn.

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CHAPTER 7

GENOTYPE X ENVIRONMENT INTERACTION AND YIELD STABILITY OF TEN DESI CHICKPEA GENOTYPES ACROSS THREE DIVERSE ENVIRONMENTS OF LIMPOPO AND MPUMALANGA PROVINCES

ABSTRACT

Multivariate analysis techniques are a series of methods to study genotypes diversity such as principal component analysis (PCA). These techniques can be utilized for identifying genotypes with traits for breeding and instructing the patterns of variation in genotype accession, to recognize relationships between genotypes. PCA summarizes the variability between original data. The study was undertaken to identify stable and high yielding genotypes across environments. Ten desi chickpea genotypes were evaluated and the experiment was laid out in a Randomized Complete Block Design with three replications in each site. The experiment was sown in winter 2016 and 2017 seasons in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga). For the 2016 season, the average grain yield of the genotypes was 2092 kg ha^{-1} with the outstanding genotypes being ICCV8101 (2842 kg ha^{-1}), ICCV4105 (2419 kg ha^{-1}) and ICCV3203 (2389 kg ha^{-1}) respectively, and the low yielding genotype was ICCV6103 (1499 kg ha^{-1}). For the 2017 season, the average grain yield of the genotypes was 1751 kg ha^{-1} with the outstanding genotypes being ICCV4110 (2476 kg ha^{-1}), ICCV92944 (1912 kg ha^{-1}) and ICCV4105 (1886 kg ha^{-1}) respectively, and the low yielding genotype was ICCV97125 (1323 kg ha^{-1}). The combined ANOVA for grain yield showed significant effects of the genotypes, environments and genotype x environment interaction in 2017. During the 2016 season, the additive main effect and multiplicative interaction bi-plot (AMMI bi-plot) and Genotype x Environment interaction bi-plot (GGE bi-plot) results showed that ICCV8101 was the most stable, and ICCV97024 and ICCV6103 were the unstable genotypes. Furthermore, the Genotype main effects and GGE bi-plot showed Nelspruit as the most discriminating and representative environment. The GGE bi-plot also identified two different growing environments, the first environment containing Syferkuil and Nelspruit with the winning genotype ICCV3203; and the second environment encompassing Thohoyandou with the winning genotype ICCV8101. The 2017 season indicated a different trend; genotype ICCV4110 was the most stable, and ICCV8101 and ICCV97125 were the unstable genotypes. Furthermore, the genotype main effects and GGE bi-plot showed Thohoyandou as the most discriminating and representative environment. The GGE bi-plot also identified two different growing environments,

the first environment containing Syferkuil and Nelspruit with the wining genotype ICCV4110; and the second environment encompassing Thohoyandou without winning genotypes. This indicates that particular genotypes tended to rank differently in grain yields at different locations.

Key words: AMMI bi-plot, environment, GEI, GGE bi-plot, stable

7.1 INTRODUCTION

Seed yield of chickpea is influenced by many factors including genotype and environment. Therefore identifying genotypes that perform consistently better across the environments of Limpopo and Mpumalanga Provinces is required. According to Ceccarelli (2012) the response of genotypes across environments may be with no interaction, quantitative interaction or qualitative interaction. No interaction means there is no genotype influence across environments. Quantitative interaction refers to the situation in which the direction of the main effects does change and qualitative interaction refers to a situation where both the magnitude and direction of each variable's effect can depend on the value of the other variable (GenStat, 2014). Genotype x environment interaction (GEI) occurs when different genotypes respond differently to different environments and it is familiar in agricultural research. Chickpea is a quantitative long day plant and sensitive to high and cold temperatures, drought, soil salinity, moisture stress, water logging and different management practices and its yield and yield attributes are not stable and vary widely over different environments (GenStat, 2014).

There are a number of ways that can be used to identify stable and high yielding genotypes. Multivariate (involves observation and analysis of more than one statistical outcome variable at a time) stability measures are used in the presence of significant GEI. Additive main effect and multiplicative interaction (AMMI) is important in analyzing multi-environment trials as it visualizes the GEI, identifies genotypes that are adapted to particular environments, identifies genotypes that are broadly adapted, classifies environments into groups and measures the stability of genotypes (GenStat, 2014). Another way to identify stable and high yielding genotypes is the Genotype main effects and Genotype X Environment interaction (GGE). GGE effects is also important to identify mega-environments, the "which-won-where" pattern, and to evaluate genotypes and test environments (Yan et al., 2007). Moreover the GGE (genotype plus genotype by environment interaction) analysis is an effective method which is based on principal component analysis (PCA) to fully explore multi-environment trials (METs). GGE analysis partitions G+GE into principal components through singular value decomposition of environmentally centered yield data (Vaezi et al., 2018; Yan, 2001).

This experiment was undertaken to identify stable and high yielding genotype(s) to recommend best performing genotype(s) for the different agro-ecological regions of Limpopo and

Mpumalanga Provinces for further evaluation so as to boost chickpea production and productivity in these study areas.

7.2 MATERIALS AND METHODS

The detailed description of materials and methods is presented in chapter 3, but a summary is outlined here. Field experiments were conducted in winter 2016 and 2017 seasons in Thohoyandou (University of Venda), Syferkuil (University of Limpopo) and Nelspruit (University of Mpumalanga). Ten desi chickpea genotypes were sown in a completely randomized block design replicated three times on 10 May 2016 and 10 April 2017 (Thohoyandou), 13 May 2016 and 11 April 2017 (Syferkuil) and 03 May 2016 and 24 May 2017 (Nelspruit), respectively. Grain yield and yield components were determined from the same plants that were used for biomass at harvest maturity. The pods were manually removed from all the harvested plants and number of pods per plant determined. All the pods were threshed by hand, and number of seeds per pod determined. The seeds were air-dried, cleaned and weighed to determine grain yield (kg ha^{-1}). Yield stability was assessed by evaluating the genotype (G) x environment (E) interaction effects on grain yield in order to identify genotypes that are stable across environments. Analysis of variance was performed using the GenStat (2014) statistical package 17th edition. Combined analysis of variance (ANOVA) was performed to determine the effects of G, E, and GE interaction effects. An initial analysis of variance was performed for each environment to verify the existence of differences between genotypes. Principal Component Analysis (PCA) was used to analyze the residual multiplicative interaction between genotypes and environments (Silveira et al., 2013) to determine the sum of squares of the G x E interaction, with a minimum number of degrees of freedom.

7.3 RESULTS AND DISCUSSION

7.3.1 Additive Main Effects and Multiplicative Interaction (AMMI) bi-plot analysis

The AMMI1 bi-plot, containing the genotype and environment means against interaction principal component analysis one (IPCA1) scores for the 2016 season is illustrated in Figure 7.1. The displacement along the cartesian coordinate reflected differences in the main effects, whereas the displacement along the ordinate reflected differences in interaction effects. According to Yan and Thinker (2006) and Farshadfar et al. (2013), genotypes and environments with IPCA1 greater

than zero are classified as high yielding genotypes and favourable environments whereas those with IPCA1 lower than zero are classified as low yielding genotypes and unfavourable environments. Accordingly genotypes such as ICCV3203, ICCV4105, ICCV4110, ICCV8101 and ICCV94944 were genotypes with above average mean grain yield as they were on the right side of the grand mean of the genotypes and environments. Conversely, genotypes ICCV3110, ICCV6103 and ICCV97024, had yield below grand mean as they were on the left side of the grand mean of the genotypes and environments. Genotypes ICCV3111 and ICCV97125 laid down almost close to the vertical line, indicating that the mean yield of these genotypes were highly similar over all environments and parallel to the grand mean of all the genotypes. ICCV8101 followed by ICCV4105 had higher mean yield in the favourable environments, whereas ICCV6103 had lower mean yield in the unfavourable environments. Regarding the environments, Syferkuil had above grand mean yield and was considered as favourable environment. Similarly, Makonya et al. (2019) concluded that Syferkuil (Polokwane) was more suitable for chickpea production compared to Thohoyandou. On the other hand, Nelspruit had below average grain yield and was considered as unfavourable environment. Thohoyandou laid close to the grand mean line indicating that genotypic yield in Thohoyandou represents the overall genotypic mean across all environments.

The AMMI2 bi-plot, containing the first interaction principal component (PC1 or IPC1) in the X-axis and the second interaction principal componemt (PC2 or IPC2) in the Y-axis for the 2016 season, is plotted in Figure 7.2. The PC1 explains 79.82% and the PC2 explains about 20.18% of the GXE sum of squares and the two interaction principal components cumulatively explained about 100% of the sum of squares of the genotype by environment interaction of the genotypes (Figure 7.2). Genotypes that cluster together behave similarly across the environments. Baraki et al. (2016) and Hagos and Abay (2013) stated that the closer the genotypes are to the origin, the more the stable and the furthest genotypes from the origin the more the unstable. In addition the closer the genotypes to the given vector of any environment is the more adaptive to that specific environment and the furthest the genotypes to the given vector of any environment is the less adaptive to that specific environment. Genotypes ICCV3203, ICCV4110 and ICCV97024 are far apart from the bi-plot origin suggesting that these genotypes were more responsive and contributed largely to the interation component. In contrast, genotype ICCV4105, ICCV92944, ICCV8101, ICCV3110 and ICCV3111 located near the bi-plot origin, were the genotypes with the least contribution to the interaction component, indicating their wider adaptability. Regarding the adaptability of genotypes to the environments; genotypes ICCV3110 and ICCV3203 were

adaptable to Syferkuil; genotypes ICCV6103, ICCV4110 and ICCV97125 were adaptable to Nespruit and genotypes ICCV3111 and ICCV97125 were adaptable to Thohoyandou.

The AMMI1 bi-plot, containing the genotype and environment means against IPCA1 scores for the 2017 season is illustrated in Figure 7.3. Genotypes ICCV4110 and ICCV92944 were the genotypes with above average mean grain yield as they were on the right side of the grand mean of the genotypes and environments. Conversely, genotypes ICCV97125 and ICCV97024, had yield below grand mean as they were on the left side of the grand mean of the genotypes and environments. Genotypes ICCV3203 and ICCV3111 lay almost close to the vertical line, indicating that the mean yield of these genotypes were highly similar over all environments and parallel to the grand mean of all the genotypes. ICCV8101 followed by ICCV4105 had higher mean yield in the favourable environments, whereas ICCV97125 had lower mean yield in the unfavourable environments. Genotypes ICCV3110, ICCV6103, ICCV34105 and ICCV92944 fall on the same vertical line, showing their similarity in their mean yield. Regarding the environments, Syferkuil had above grand mean yield and was considered as favourable environment while Nelspruit was the average environment. Similarly, Makonya et al. (2019) concluded that Syferkuil (Polokwane) was more suitable for chickpea production compared to Thohoyandou.

The AMMI2 bi-plot, containing the first interaction principal component (PC1 or IPC1) in the X-axis and the second interaction principal componemt (PC2 or IPC2) in the Y-axis for the 2017 season, is plotted in Figure 7.4. The PC1 explained 62.51% and the PC2 explained about 37.49% of the GXE sum of squares and the two interaction principal components cumulatively explained about 100% of the sum of squares of the genotype by environment interaction of the genotypes (Figure 7.4). Genotypes ICCV8101, ICCV4110, ICCV97125 and ICCV97024 are far apart from the bi-plot origin indicating that these genotypes were more responsive and contributed largely to the interaction component and considered as specifically adapted genotypes. On the other hand, genotypes ICCV3203, ICCV6103, ICCV3111, ICCV92944, ICCV3110 and ICCV4105 located near the bi-plot origin, were the genotypes with the least contribution to the interaction component, indicating their wider adaptability. Genotypes ICCV92944, ICCV3110 and ICCV4105 indicated a wider adaptability in both 2016 and 2017 seasons. Regarding the adaptability of genotypes to the environments; genotypes ICCV4105 and ICCV92944 were adaptable to Syferkuil and genotypes ICCV4110 was adaptable to Nespruit.

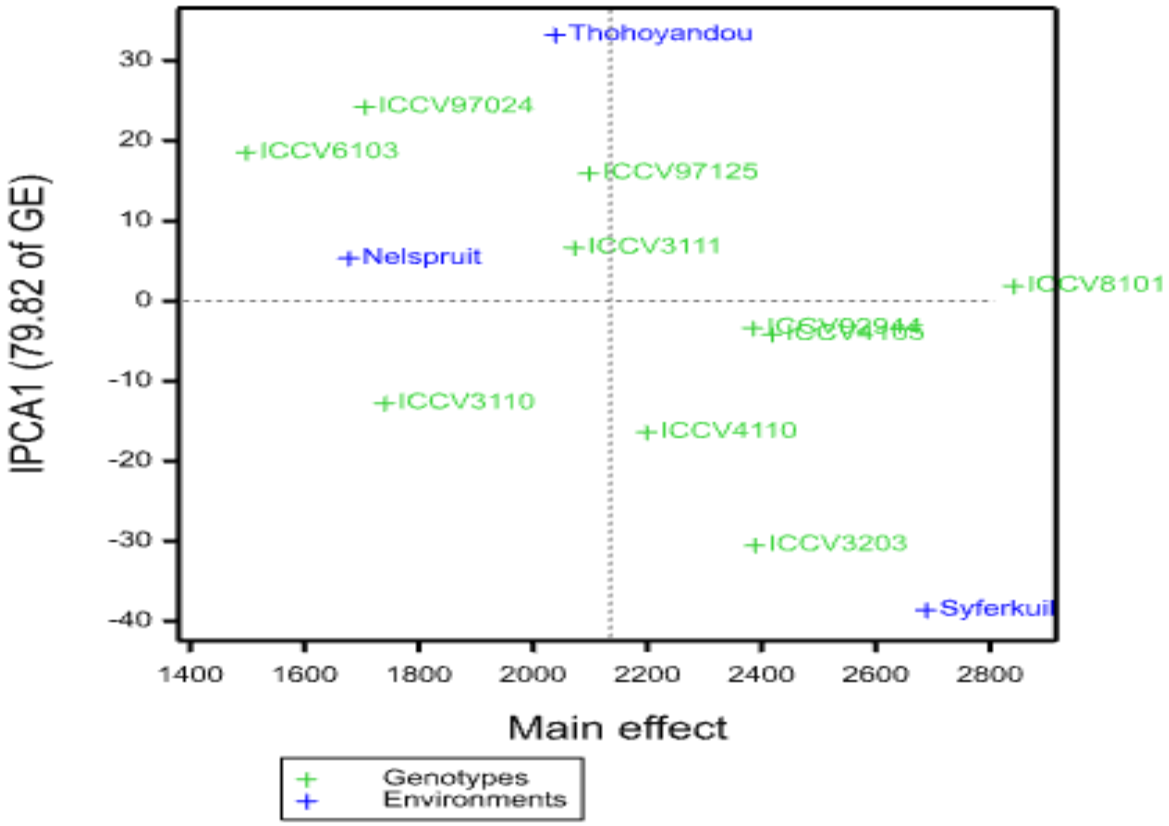

Figure 7.1. AMMI1 bi-plot showing Genotype and Environmental means against IPCA1 for the 2016 season

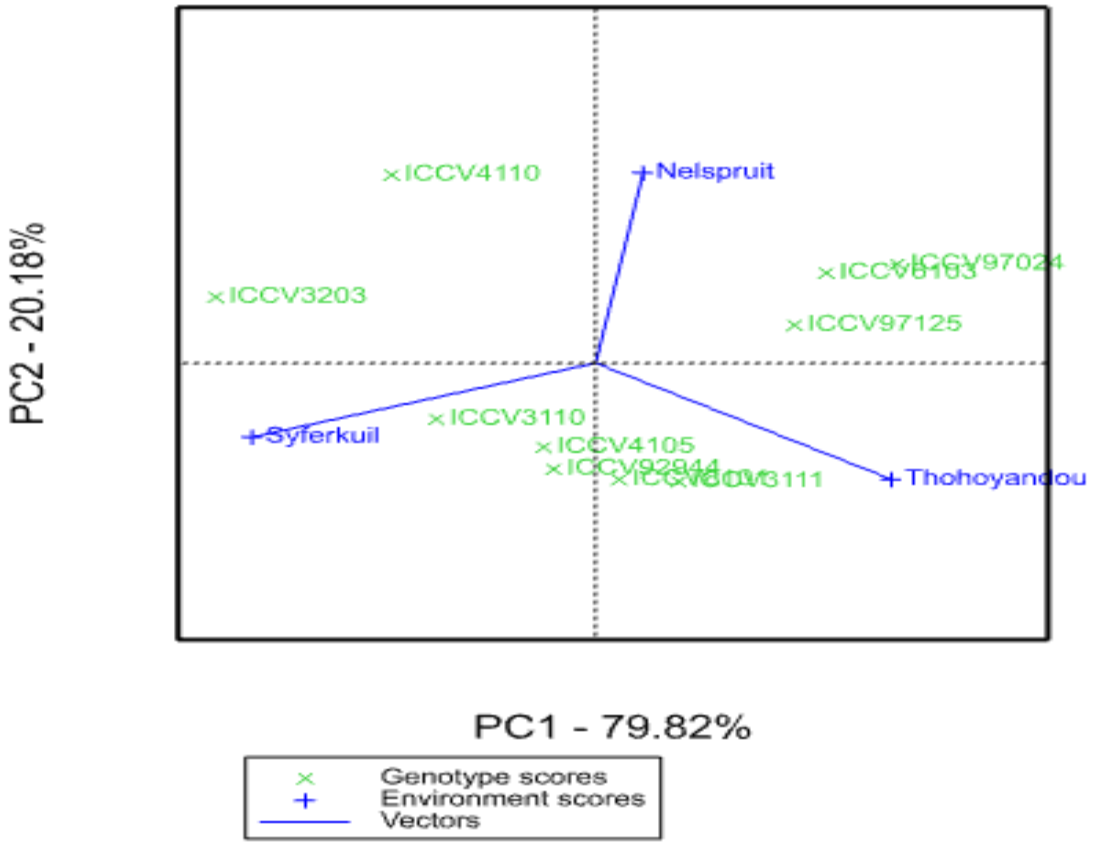

Figure 7.2. AMMI2 bi-plot showing PC1 versus PC2 indicating the stability of the Genotypes for the 2016 season

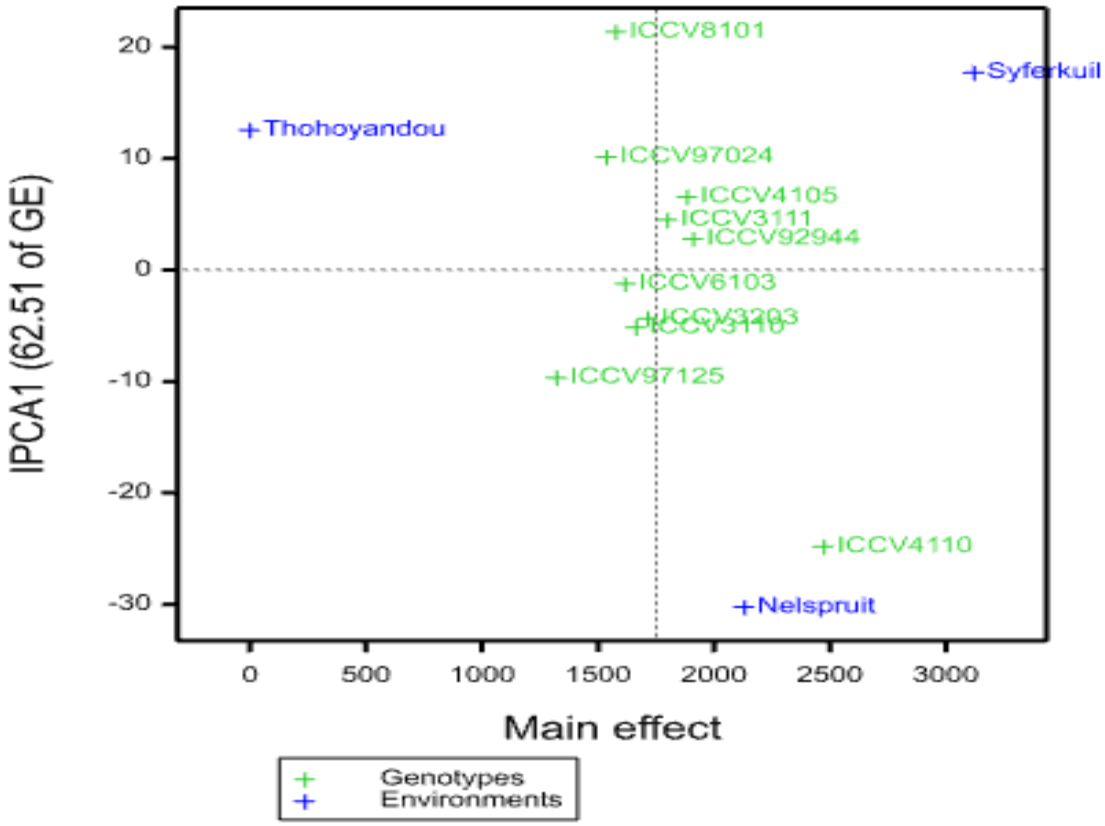

Figure 7.3. AMMI1 bi-plot showing Genotype and Environmental means against IPCA1 for the 2017 season

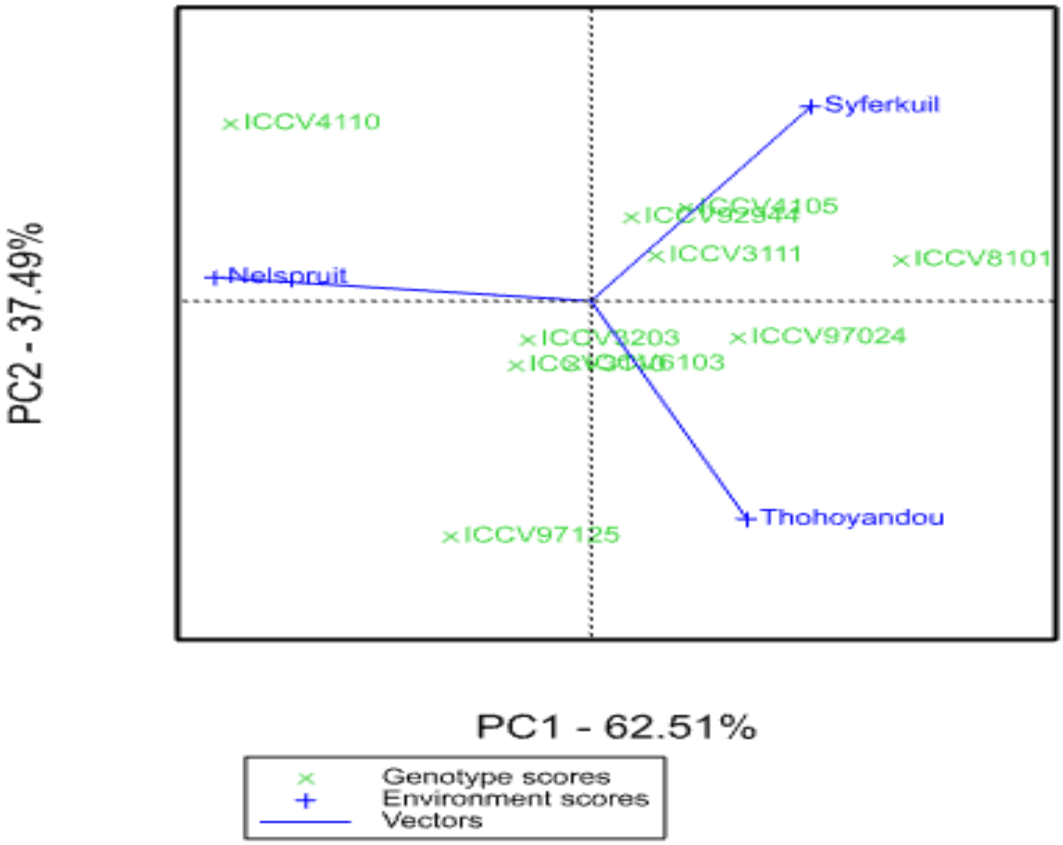

Figure 7.4. AMMI2 bi-plot showing PC1 versus PC2 indicating the stability of the Genotypes for the 2017 season

7.3.2 Genotype main effect plus Genotype by Environment Interaction (GGE bi-plot)

The GGE bi-plot used in this study constitutes a summed up of 91.67% total variance of the first two principal components during the 2016 season (Figure 7.5). The angle between environment vectors provide correlation between the environments. Nelspruit is less than 90º with Syferkuil, which indicates positive correlation.Thohoyandou is more than 90° with Syferkuil and Nelspruit indicating that it had a negative correlation with these environments and could produce less similar information about the tested genotypes. Syferkuil had the longest vector and considered as the ideal environment for generally adapted genotypes. To clearly display graphically, the 'which won-where' pattern of a polygon view of GGE bi-plot is exhibited in Figure 7.6. Genotype ICCV3111 which lies near the biplot origin was practically stable and had wide adaptability; and genotypes ICCV97125, ICCV92944 and ICCV4105 were located a little further from the origin and hence had medium stability across the 3 environments. On the other hand, genotypes ICCV3203, ICCV8101, ICCV97024, ICCV6103, ICCV3110 and ICCV4110 located far from the origin were more responsive to environment change and were considered specifically adapted (Erdemci, 2018; Wardofa et al., 2019; Yan et al., 2007).

A polygon was formed by connecting the vertex genotypes that were furthest away from the bi-plot origin such that all other genotypes were included in the polygon. From the polygon view of the bi-plot analysis (Figure 7.6), the bi-plot showed there were two different chickpea growing environments or mega environments (Yan et al., 2007). Ellipses were drawn around the environments within the same sector to form mega environments. One environment includes Syferkuil and Nelspruit and the other environment include Thohoyandou (Figure 7.6). Sectors were also added by drawing lines perpendicular to each side of the convex hull. As a general rule, genotypes that appear in the same sector as a particular environment are the best performers in that environment, and hence genotypes ICCV4110, ICCV3110 and ICCV3203 which were located in the same sector as Nelspruit and Syferkuil, were the best performers in these environments (Yan et al., 2007). Additionally, genotypes ICCV8101, ICCV92944, ICCV3111 and ICCV4105 which were located in the same sector as Thohoyandou may indicate that these genotypes perfomed best in this environment. The other vertex genotypes without any environment in their sectors were not the highest yielding genotypes at any environment, rather they were the poorest genotypes of all or some environments. For example, genotype ICCV6103 was poorest yielding genotype in Syferkuil and Nelspruit (Erdemci, 2018; Wardofa et al., 2019; Yan et al., 2007).

The GGE bi-plot used in this study constitutes a summed up of 100% total variance of the first two principal components for the 2017 season (Figure 7.7). Syferkuil, Thohoyandou and Nelspruit were linked with less than 90° indicating that these environments were positively correlated with each other (Yan et al., 2007). Nelspriut had the longest vector and considered as the ideal environment for generally adapted genotypes. To clearly display graphically, the 'which won-where' pattern of a polygon view of GGE bi-plot is exhibited in Figure 7.8. Genotypes ICCV6103 and ICCV3203 which lay near the biplot origin were practically stable and had wide adaptability; and genotypes ICCV97024, ICCV92944, ICCV3110 and ICCV3111 were located a little further from the origin and hence had medium stability across the 3 environments. On the other hand, genotypes ICCV4105, ICCV8101, ICCV97125 and ICCV4110 located far from the origin were more responsive to environment change and were considered specifically adapted (Erdemci, 2018; Wardofa et al., 2019; Yan et al., 2007).

From the polygon view of bi-plot analysis (Figure 7.8), the bi-plot showed there were two different chickpea growing environments or mega environments. One environment includes Syferkuil and Nelspruit and the other environment include Thohoyandou. Genotype ICCV4110 was located in the same sector as Nelspruit and Syferkuil, therefore this genotype was the best performer in these environments (Yan et al., 2007). Genotype ICCV92944 had medium stabilty across the 3 environments, while genotypes ICCV8101 and ICCV4110 were more responsive to environmental and were considered specifically adapted in both the 2016 and 2017 seasons. ICCV4110 was the best performing genotype in Syferkuil and Nelspruit in both seasons (Erdemci, 2018; Wardofa et al., 2019; Yan et al., 2007).

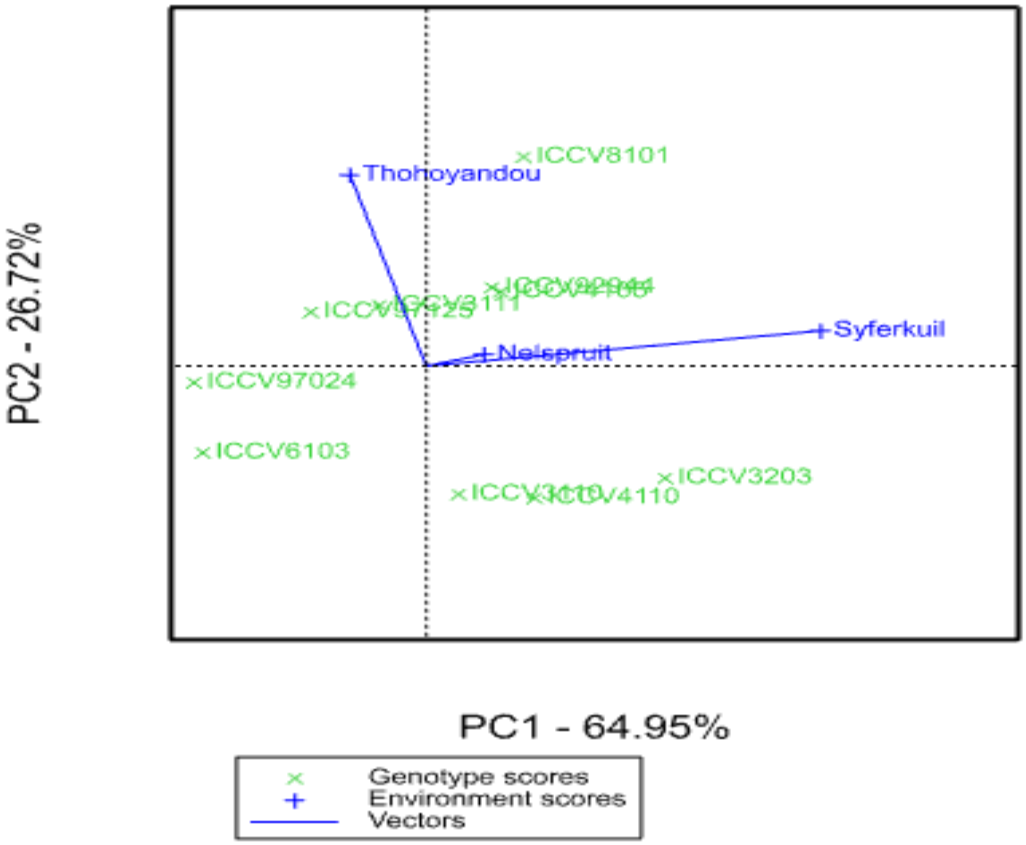

Figure 7.5. The environment view of the GGE bi-plot for the 2016 season

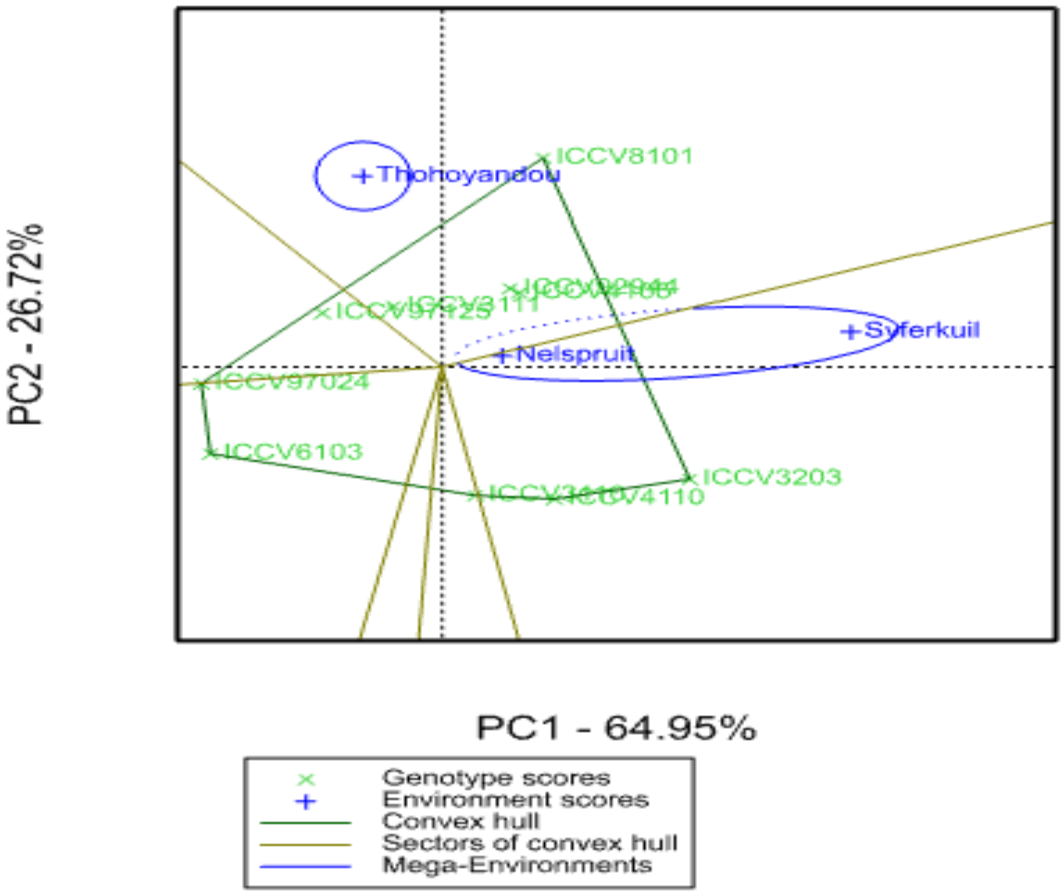

Figure 7.6. The which-won-where view of the GGE bi-plot for the 2016 season

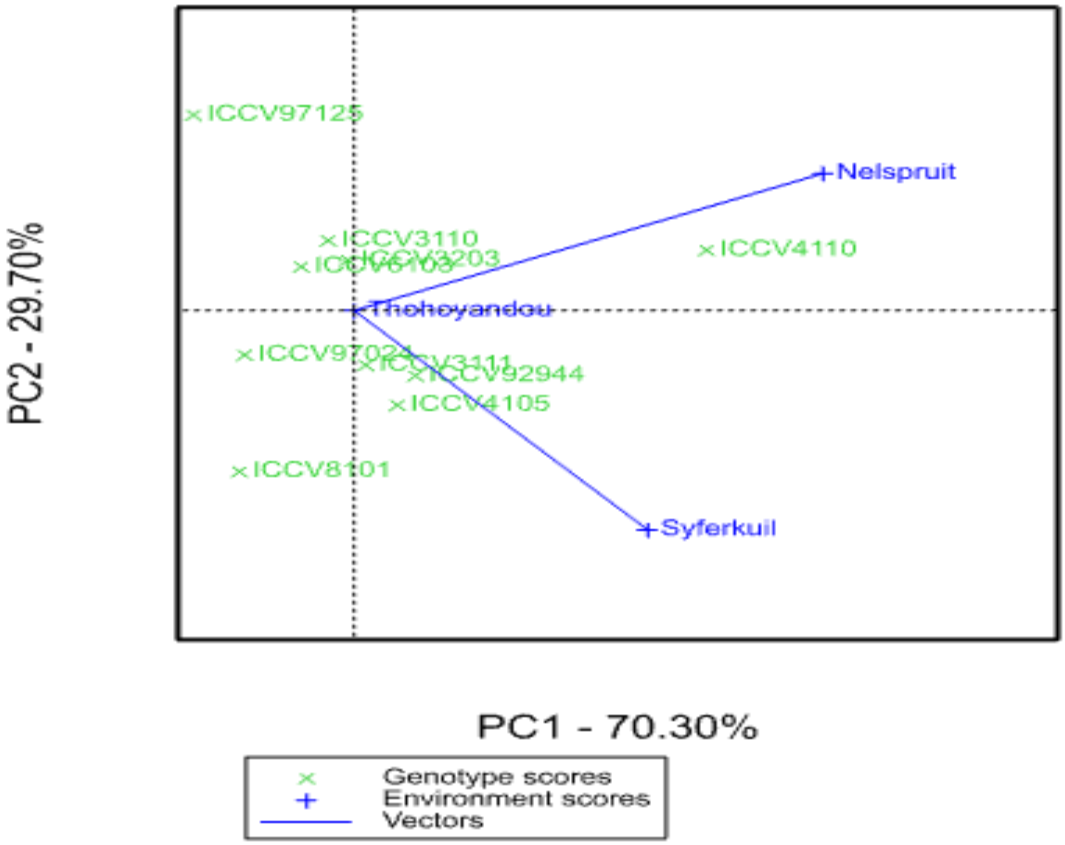

Figure 7.7. The environment view of the GGE bi-plot for the 2017 season

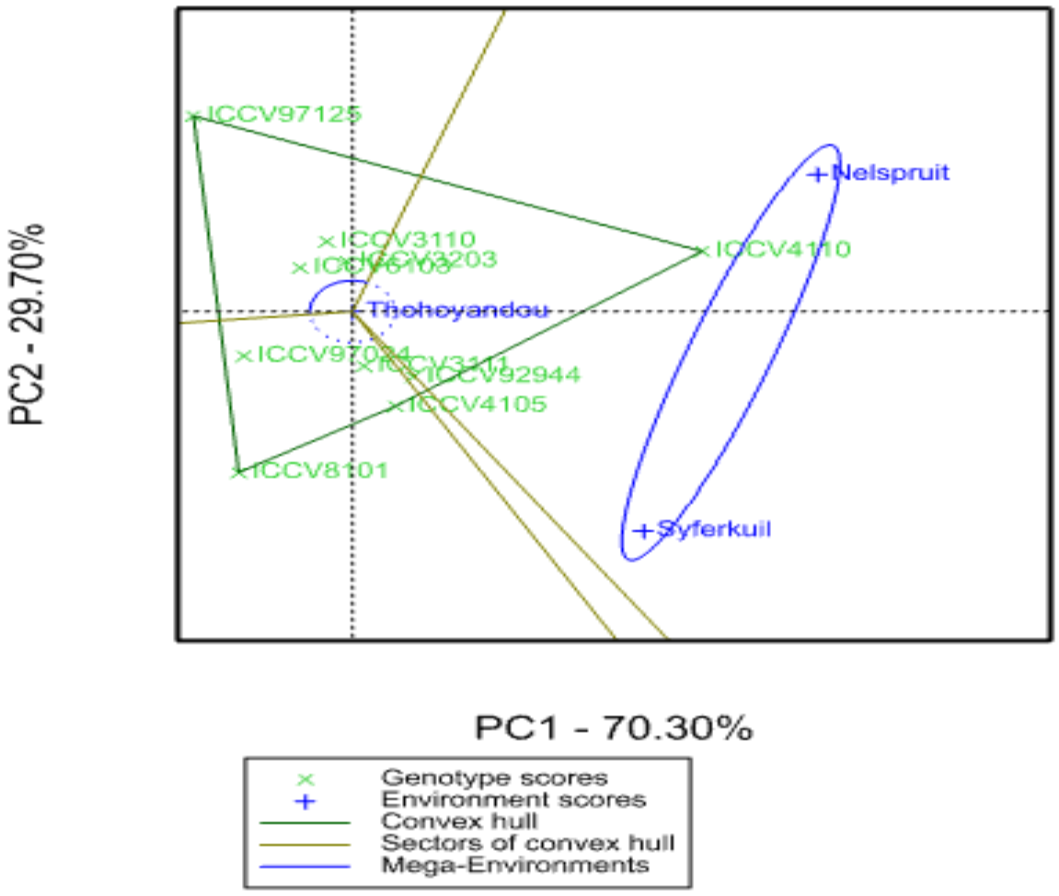

Figure 7.8. The which-won-where view of the bi-plot for the 2017 season

7.4 CONCLUSION

The presence of the genotype by location interaction for grain yield was indicated by the differential ranking of genotypes over the various locations, which shows variations among the chickpea genotypes. From this study it can be concluded that the significant GEI in grain yield among the genotypes revealed differential response of the genotypes across the testing sites which are exposed to variations in climate and edaphic factors. It is therefore, difficult to identify one superior genotype for all the locations which were included in the trial. This indicates that, particular genotypes tended to rank differently in grain yields at different locations due to the presence of either genetic diversity or variation in locations. Thus, further studies are recommended, involving more chickpea genotypes and sites, before definite conclusions may be drawn.

7.5 REFERENCES

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CHAPTER 8

8. GENERAL DISCUSSION, CONCLUSION AND RECOMMENDATIONS

8.1. GENERAL DISCUSSION

The University of Venda and the Department of Agriculture, Rural Development and Land Administration (DARDLA) Mpumalanga, initiated research into chickpea production in the North-Eastern part of South Africa about 10 years ago. Over 200 chickpea genotypes have been evaluated so far, out of which 20 lines (hereafter referred to as “elite”) have been identified for further evaluation. Chickpea can grow in areas with low rainfall and poor soils, and thus may be an important food security crop for smallholder resource-poor farmers in the semi-arid tropics such as the dry environments of the Limpopo and Mpumalanga Provinces of South Africa. Preliminary studies show the huge potential of chickpea in these environments. However, there have not been suitable genotypes identified, recommended and released for the different agro-ecological zones of Limpopo and Mpumalanga Provinces. The hypothesis tested in this study was that the 10 genotypes are adapted to the agro-ecological conditions of Limpopo and Mpumalanga Provinces. Therefore, the aim of this study was to identify genotypes that are adapted/suitable to the agro-ecological conditions of Limpopo and Mpumalanga Provinces.

Genotypes tended to rank differently in grain yields at different locations due to the presence of either genetic diversity or variation in locations. Genotype ICCV3203 had high grain yield in Syferkuil, had the highest number of pods per plant, seeds per plant and seeds per pod in 2016 (Table 6.1). Genotype ICCV8101 which had high grain yield in Thohoyandou, also had high number of pods per plant, number of seeds per plant, number of seeds per pod, high number of primary and secondary branches and produced tall plants in 2016 (Table 6.2). In Nelspruit, ICCV4110 had high grain yield as well as high pod number per plant in 2016 (Table 6.3). In 2017, genotype ICCV4110 had high yield across environments, the genotype also had high number of pods per plant and number of seeds per plant (Table 6.4). Therefore plant height, number of branches and number of pods per plant can be used in chickpea breeding programmes in these regions. Syferkuil had greater yields in both the 2016 and 2017 season when compared to the other sites and may be the best chickpea production in this region. Syferkuil had moderate days to flowering and late days to physiological maturity and had greater grain yield as compared to the other 2 sites. However more studies needs to be conducted before a definite conclusion can be drawn.

8.2. GENERAL CONCLUSION

Chickpea genotypes varied from each other in most of the physiological traits studied. Based on the analysis of 10 chickpea genotypes, it was concluded that there was a substantial variation in some of the physiological traits within chickpea genotypes. Genotypes in this study were classified as early, moderate and late on the basis of their flowering and maturity across environments. These preliminary findings show that there are variations in grain yield of chickpea genotypes across diverse environments, and that Syferkuil may be the best environment for chickpea production in this region because of its high altitude. From this study it can be concluded that the significant GEI in grain yield among the genotypes revealed differential response of the genotypes across the testing sites which are exposed to variations in climate and edaphic factors. It is therefore, difficult to identify one superior genotype for all the locations which were included in the trial.

8.3. RECOMMENDATIONS

- Early genotypes along with those medium reproductive duration and reasonable yield traits may be used for potential breeding material in future improvement of chickpea in these regions.
- Genotypes with high grain yield (ICCV8101, ICCV3203 and ICCV4110) from this study could be utilized in future chickpea breeding and evaluation in the region.
- Genotypes tended to rank differently in grain yields at different locations (ICCV4110 (Nelspruit), ICCV8101 (Thohoyandou), ICCV3203 (Syferkuil)) due to the presence of either genetic diversity or variation in locations. Thus, further studies are recommended, involving more chickpea genotypes and sites, as well as different moisture regimes before definite conclusions may be drawn.