Breeding for Durable Resistance to Cercospora Leaf Spot Diseases in Groundnuts (*Arachis hypogaea* L.) in Tanzania

By

Eliud Francis Kongola

BSc (Agronomy), MSc Crop Science (Crop Protection) Sokoine University of Agriculture, Tanzania.

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African Centre for Crop Improvement (ACCI)
School of Agricultural, Earth and Environmental Sciences
College of Agriculture, Engineering and Science
University of KwaZulu-Natal
Republic of South Africa

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THESIS SUMMARY

Groundnut (*Arachis hypogaea* L.) is one of the most important legume crops in Tanzania. However, production among smallholder farmers has declined in recent years. One of the constraints affecting groundnut production are the Cercospora leaf spot diseases (CLD). Therefore, the main objective of this study was to develop appropriate groundnut cultivars with resistance to CLD, combined with other traits preferred by farmers, traders and processors, in order to improve food security, income and livelihood of groundnut smallholder farmers in semi-arid parts of Tanzania.

The study had the following specific objectives: 1) to establish groundnut production constraints and identify traits preferred by smallholder farmers' and other stakeholders in the groundnut value chain in Tanzania; 2) to evaluate the performance of Tanzanian germplasm and introduced groundnut lines for yield and yield-related traits, and resistance to Cercospora leaf spot diseases in order to select promising parents for breeding; 3) to determine the association between yield and yield-related traits, and resistance to Cercospora leaf spot diseases through correlation coefficient, path and cluster analyses to guide future groundnut breeding, 4) to determine gene action and heritability of yield and resistance to Cercospora leaf spot diseases and to select promising parents and crosses with enhanced yield and durable resistance to Cercospora leaf spot diseases in groundnut, and 5) to determine performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials.

A participatory rural appraisal (PRA) study was conducted in six villages of three selected groundnut growing districts in the Dodoma region of Tanzania. The study identified several constraints facing groundnut farmers such as drought, poor soil fertility, plant diseases, insect pests, availability of seeds of improved varieties, unavailability of reliable market and a low market price. Constraints facing groundnut traders included poor grain quality of mixed sizes and colour. On the other hand, processors were constrained with low market price of their finished products (like peanut butter and cooking oil), high cost of packaging materials, lack of investment capital, bureaucratic procedure in business and brand registration, and the availability of other cheap sources of oil. The study identified farmers' trait preferences of groundnut varieties such as: an erect growth habit, high yielding ability, a high oil content, tolerance to diseases and other environmental stresses, early maturing, and with a large seed size, good taste, brown coloured seed and easy threshability. Traders preferred groundnut varieties with a medium to large seed size with a brown seed colour. Processors preferred groundnut varieties with a medium to large seed size, little pod constriction, a sharp beak and a brown seed colour. A breeding programme aimed at improving groundnut varieties for Cercospora leaf spot diseases resistance, and which specifically includes farmers'

preference traits, may be the best option for developing new groundnut varieties that will be adopted by the farmers.

To achieve the second objective, 84 groundnut genotypes from ICRISAT – Malawi, The Tanzania National plant genetic resource centre, smallholder farmers and local market were evaluated in field trials. The CLD was induced by inoculation of the fungi, which was cultured in the laboratory following its isolation from infected leaves of groundnut. Genotypes evaluated revealed significant variations in the CLD score and yield. Twenty one genotypes were identified with a significant tolerance to CLD disease, a high number of pods per plant, relatively early maturity, and a high number of mature pods per plant, pod yield, hundred seed weight and overall seed yield. In addition, these genotypes had farmers' preferred traits. The following groundnut genotypes; ICGV SM 96714, ICGV 6057, TZA 2426, Local Makulu, ICG 6022, ICGV SM 07539, TZA 254, TZA 4280, KAKOMA, ICGV SM 07508, TZA 2270, TZA 121, TZA 667, TZA 157, TZA 2498, TZA 3786, TZA 4390, TZA 4261, TZA 2444, TZA 534 and TZA 2518 were selected based on the above mentioned merits for the inclusion in further breeding programmes.

The third objective of the study was to determine the association between yield and yield-related traits, and resistance to Cercospora leaf spot diseases through correlation coefficient, path and cluster analyses, in order to guide future groundnut breeding. Days to 50% flowering (DFL) was positively correlated with days to maturity (DM) and Cercospora leaf spot diseases severity (CLDS). The DFL was negatively correlated with the number of pods per plant (NPP), hundred seed weight (HSW), number of seeds per pod (SPP) and seed yield (SY). The DM was positively correlated with CLDS. The DM was negatively correlated with HSW, SPP and SY. The length of reproductive branch (LRB) had no correlation with any of the traits studied. The CLDS was negatively correlated with NPP, HSW, SPP and SY. The HSW was positively correlated with NPP, SPP and SY. The SPP was positively correlated with SY. A positive direct effect on SY was depicted by SPP, CLDS, LRB and DFL. A negative direct effect on SY was depicted by DM, NPP and HSW. An indirect effect on SY via SPP was exhibited by HSW and NPP. Indirect effect on seed yield via CLDS was exhibited by DFL, DM and LRB. An indirect effect on seed yield via DM was exhibited by NPP and HSW. Five phenotypically diverse clusters were derived from the 84 groundnut genotypes sourced from ICRISAT–Malawi, Tanzania National plant genetic resource centre, local market and smallholder farmers. The five clusters had relatively different magnitude of means of yield and its related traits ranging from low to high yielding. The five clusters had different reaction to Cercospora leaf spot diseases ranging from tolerant to susceptible.

The fourth objective of this study was to determine the gene action and heritability of yield and resistance to Cercospora leaf spot diseases, and to select promising parents and crosses with

enhanced yield and resistance to Cercospora leaf spot diseases in groundnut. In this study it was found that there were significant variations among genotypes for both yield and its components, and Cercospora leaf spot disease severity (CLDS) in all three groundnut botanical groups (i.e. Valencia, Virginia and Spanish). Good general combiners in the Valencia botanical group were Local Makulu, TZA 121 and ICGV SM 96714; in the Virginia botanical group TZA 4280, TZA 4390 and ICGV 6022 and TZA 2518, while TZA 254 and ICGV SM 07508 were good general combiners in the Spanish botanical group. The study identified crosses Local Makulu x ICGV SM 96714, TZA 121 x Kakoma, TZA 3786 x Kakoma, TZA 157 x Kakoma, TZA 2498 x ICGV SM 96714 in the Valencia botanical group; TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022 and TZA 4261 x ICGV 6057 for Virginia botanical group; and TZA 2444 x ICGV SM 07539, TZA 2518 x ICGV SM 07508, TZA 254 x ICGV SM 07508, TZA 2426 x ICGV SM 07539, TZA 2270 x ICGV SM 07539 and TZA 2270 x ICGV SM 07508 in the Spanish botanical group with superior per se performance for CLD resistance and yield. Both additive and non-additive gene effects were important in the inheritance of CLD resistance and yield in all groundnut botanical groups. The dominance genetic variance was larger than the additive genetic variance; therefore, inheritance of CLD resistance can be transmitted to offspring by double cross mating design. Broad sense heritability was higher in magnitude than narrow sense heritability indicating that these traits can be transmitted to progenies through hybridization and selection can be conducted at later stages.

The last objective of this study was to determine performance of single cross parents versus double cross hybrids and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials. The study found out that, there were significant differences among evaluated genotypes across environments and significant genotype x environment interaction for the studied traits. In addition, there were significant G, E and GXE multiplicative terms for the studied traits. The genotypes accounted for 61.67% of the treatment sum of squares, the environments and the interaction between genotypes and the environment accounted for 18.95% and 19.38% of the treatment sum of squares, respectively. The first and second IPCAs captured 41.33% and 25.96% of the interaction sum of square and degree of freedom, respectively. The two IPCA axes jointly accounted for 67.29% of the interaction sum of squares, leaving 32.71% of the variation due to G xE interaction in the residual. The IPCA scores were both negative and positive for genotypes and environments, whereby three environments were most discriminating, while the other three had high correlation.

DECLARATION

I, Eliud Francis Kongola, declare that:

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

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

3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

4. This thesis does not contain other persons' writing, unless specifically acknowledged as being sourced from other researchers. Where other written sources have been quoted, then:

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

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Signed:…..……Date: ..……

Eliud Francis Kongola

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

Signed:……Date:……..……

Prof. Rob Melis (Main supervisor)

Signed:……Date:..……

Dr. Julia Sibiya (Co-supervisor)

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DEDICATION

This thesis is dedicated to my parents Francis Moses Kongola and Mary Zephania Massi who took action to send me to school, my wife Upendo, my children Festus and Ruth-Divine Eliud Kongola for their enduring love and patience during the whole period of my study.

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Introduction to the Thesis

1. Background

Groundnut is cultivated in more than 100 countries in the world. It is cultivated primarily in the semi-arid tropical regions of Africa and Asia, which together account for over 96% of world groundnut area and 92% of total global groundnut production. In 2014, groundnut was grown on 26.5 million ha with a production of 43.9 million tons globally, 14.4 million ha with a production of 13.8 million tons in Africa, and 1.6 million ha with a production of 1.6 tons in Tanzania (FAOSTAT, 2017). The average pod yield of groundnut in the world is 1.7 t ha^{-1}, Africa 1.0 t ha^{-1} and Tanzania 1.0 t ha^{-1} respectively.

1.1 Importance of groundnut

Groundnut is an important crop, both in subsistence and commercial agriculture in arid and semi-arid regions of the world (Upadhyaya et al., 2006). It is ranked the fourth largest oilseed crop in the world (FAOSTAT, 2012) and second most important food legume crop worldwide after soybean in production (CIAT, 2001). Groundnut is both an excellent cash and subsistence crop, with multipurpose uses of each plant part in direct consumption, confectionary preparations, cooking oil and a rich source of protein feed for animals (Pandey et al., 2012). The kernels are highly nutritious, containing fat (40–50%), protein (20–30%), carbohydrate (10–20%) and several other micronutrients and minerals (vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium). Therefore, groundnut is a very important crop economically and nutritionally for both farmers and livestock keepers.

1.2 Cercospora leaf spot disease and its control measures

Early leaf spot disease caused by *Cercospora arachidicola* Hori and late leaf spot disease caused by *Cercospora personatum* [(Berk. and Curt) Deighton], are among the major foliar diseases of groundnut in the world and Tanzania in particular. The diseases are reported to cause severe damage to the groundnut crop in different parts of the world (Haciwa and Kannaian, 1990). In most areas, both diseases occur together, but the incidence and severity of each disease varies with environment and cultivar (Naidu et al., 1999). Control measures for the diseases include chemical control using fungicides, crop rotation, deep ploughing, removal of debris, planting on time and disease resistant cultivars to suppress the two leaf spot diseases (Holbrook and Stalker, 2003).

1.3 Constraints to groundnut production

Despite the importance of the crop, pod yield of groundnut in developing countries averages only between 0.9 to 1.0 t ha^{-1} which is low compared to the average of 1.6 t ha^{-1} of the global yield (FAOSTAT, 2017). These low crop yields are attributed to both biotic and abiotic stresses in the cultivation of the crop, including unreliable rains, pest and disease occurrence (especially foliar diseases), poor technology available to smallholder farmers, poor seed variety, and increased cultivation on marginal land (ICRISAT, 2012).

1.4 Research justification

Early and late leaf spot diseases are among the major foliar diseases of groundnut around the world and Tanzania in particular. When cercospora leaf spot (CLD) diseases occur, farmers lose a very important source of protein, a valuable source of income and a substantial part of seed for next planting season, leading to food insecurity, and in addition rural economies that depend on groundnuts are completely disrupted since smallholder farmers in sub-Saharan Africa grow groundnut for both subsistence and as a cash crop (Naidu et al., 1999).

The CLD cause yield losses of 50 to 70% (Monfort et al., 2004) and reduce the photosynthetic surface through leaf abscission and low efficiency of the infected leaves if susceptible cultivars are not protected with chemicals (Subrahmanyam et al.,1984), and affect adversely the quality of its produce (Waliyar,1991). Although chemical control measures are available, they increase production costs, they are not always accessible, expensive and not affordable by small and marginal farmers with poor resources, who are the major producers of this crop (Coffelt and Porter, 1986; Ambang et al., 2011). Moreover, there is possible existence of fungicide-tolerant strains of the pathogens (Smith and Littrell, 1980). In addition, chemical pesticides can cause harmful effects to the environment. Disease-resistant cultivars are, therefore, the best way to control these diseases (McDonald et al., 1985; Holbrook and Stalker, 2003).

Despite the release of several new groundnut varieties, most farmers are still growing only landraces or old released varieties, which are susceptible to diseases and are low yielding (Minde et al., 2008). In Tanzania from 1983 to 2009 a total of 12 varieties were released (Mponda et al., 2012), but farmers are still growing local landraces and old released varieties, for instance, Mamboleo, Mambunga and Kongwa. Consequently, smallholder groundnut producers are faced with food insecurity and low income. Although breeding efforts of groundnut have led to the development of varieties with moderate levels of resistance to the diseases, farmers have not

adopted them because they lack farmers' and market preferred traits. This study therefore, focused on determining the reaction of different groundnut germplasm to CLD in order to create a basis for a resistance breeding programme for CLD in Tanzania

2. Overall objective

The overall goal of this study is to improve groundnut productivity in order to improve food security, income and livelihood of groundnut growers in Central Tanzania.

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3. Specific objectives

The study had the following specific objectives:

i. To establish groundnut production constraints and identify traits preferred by smallholder farmers and other stakeholders in the groundnut value chain in Central Tanzania.
ii. To evaluate the performance of Tanzanian germplasm and introduced groundnut lines for yield and yield-related traits, and the resistance to *Cercospora* leaf spot diseases, in order to select promising parents for breeding.
iii. To determine the associations between yield and yield-related traits, and resistance to *Cercospora* leaf spot diseases through correlation, cluster and path analysis in order to guide future groundnut breeding.
iv. To determine gene action and heritability of yield and resistance to *Cercospora* leaf spot diseases, and to select promising parents and crosses with enhanced yield and durable resistance to *Cercospora* leaf spot diseases in groundnut.
v. To determine the performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials.

4. Thesis outline

This thesis consists of seven distinct chapters in accordance with a number of activities related to the above mentioned objectives. Chapters 2-7 are written as discrete research papers, each following the format of a stand-alone research paper (whether or not the chapter has already been published). This is the dominant thesis format adopted by the University of KwaZulu-Natal. As such, there is some unavoidable repetition of references and some introductory information between chapters. The structure of the thesis is as indicated below:

Chapter	
	Thesis introduction
1	Literature review
2	To establish groundnut production constraints and identify traits preferred by smallholder farmers' and other stakeholders in the groundnut value chain in Central Tanzania.
3	To evaluate the performance of Tanzanian germplasm and introduced groundnut lines for yield and yield-related traits and resistance to *Cercospora* leaf spot diseases in order to select promising parents for breeding.
4	To determine the association between yield and yield-related traits, and resistance to *Cercospora* leaf spot diseases through correlation, cluster and path analysis in order to guide future groundnut breeding.
5	To determine gene action and heritability of yield and resistance to *Cercospora* leaf spot diseases, and to select promising parents and crosses with enhanced yield and durable resistance to *Cercospora* leaf spot diseases in groundnut.
6	To determine the performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials.
7	An overview of research findings and breeding implication

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Chapter 1: Literature Review

1.1 Introduction

In this chapter the literature on groundnut is reviewed to cover information relevant to the research focus in order to provide the theoretical basis for the research, and provide an insight into the following topics: botany, origin and taxonomy, importance, historical background; production, research and breeding of groundnut in Tanzania, and the productivity and importance of groundnut. In addition, literature on Cercospora leaf spot diseases (CLD), components of CLD disease resistance, breeding for durable resistance to CLD diseases, mating designs, combining ability study in groundnuts and factors influencing adoption of new varieties are reviewed.

1.2 Origin, botany and taxonomy of groundnut

1.2.1 Origin of groundnuts

The study on the origin of groundnuts (*Arachis hypogaea L.*) by Isleib and Wynne (1983) grouped lines using principal component analyses and found that most morphological differences are observed between subspecies. Six centres of diversity evolved in South America, including the geographic regions of (1) Guarani (Paraguay-Paraná), (2) upper Amazon and the west coast of Peru, (3) Goiás and the Minas Gerais region of Brazil, (4) Rondonia and the north west Mato Grosso regions of Brazil, (5) south west Amazon region in Bolivia, and (6) north eastern Brazil.

Although *A. hypogaea* is believed to have originated east of the Andes mountains, the oldest archaeological findings are in Peru, dated ca. 1500 BCE (Banks et al., 1993) where groundnut predates the remains of maize (*Zea mays* L.) in the region of the Casma valley. This Peruvian site may be the oldest simply because of good preservation conditions of pods in the dry climate, or there could have been a secondary domestication event; although recent molecular data indicates a single origin of *A. hypogaea* (Kochert et al., 1996).

1.2.2 Botany and taxonomy

Groundnut is an annual leguminous crop. It is an allotetraploid (AABB, 2n = 4x = 40 chromosomes) with ‘A’ and ‘B’ genomes, contributed by diploid progenitors, *Arachis duranensis* and *Arachis ipaensis*, respectively. The botanical name of groundnut is *Arachis hypogaea* derived from the Greek word *Arachis* meaning ‘legume’ and *hypogaea* meaning ‘below ground’, referring to the

formation of pods in the soil (Pattee and Stalker, 1995). Groundnut is a member of the family Leguminosae, tribe Aeschynomeneae, sub-tribe Stylosanthinae of genus *Arachis*.

Arachis hypogaea is an annual herb of indeterminate growth habit, and can be divided into two sub-species, *hypogaea* and *fastigiata*, each with several botanical cultivars (Holbrook and Stalker, 2003). Sub-specific and varietal classifications are mostly based on the location of flowers on the plant, patterns of reproductive nodes on branches, number of trichomes and pod morphology (Krapovickas and Gregory, 1994). The *hypogaea* sub-species do not flower on the main stem and, in general terms, mature later, have a high water requirement, have alternate branching patterns, and produce large seed. The *fastigiata* sub-species produce flowers on the main stem, have sequential branching, and, relative to the other sub-species, mature earlier, have a lower water requirement and produce smaller seed. These sub-species are further sub-divided into four types: Virginia, runner, Spanish, and Valencia. Virginia and runner types are in the *hypogaea* sub-species, while Spanish and Valencia are in the *fastigiata* sub-species (Krapovickas and Gregory, 1994).

The groundnut plant produces flowers within four to six weeks after emergence and continues to flower until late in the growing season, depending on the genotype and the environment (Stalker, 1997). Although flowering occurs above ground, seeds are produced underneath the soil surface. Flower colour varies from light yellow to deep orange and sometimes white. Flowers are borne in the axil of leaves, usually with three flowers per inflorescence, but only one of these flowers opens at a given time (Stalker, 1997). The groundnut plant produces more flowers than its photosynthetic capacity to fill the pods, and even under ideal conditions less than 20% produce mature pods (Rao and Murty, 1994).

The flowers are self-pollinated. However, at locations where insect activities are high, some cross-pollination may occur (Nigam et al., 1983). After fertilization of the ovule, an intercalary meristem becomes active and a pointed carpophore or gynophore, commonly known as a peg, is formed. The peg exhibits positive geotropism and grows downward into the soil where it becomes diageotropic and ceases to elongate, and develops into a pod (Shokes and Melouk, 1995). The pods are elongated spheres with various amount of reticulation on the surface and/or constriction between seeds. Although pods usually develop below ground aerial pods can occur (Holbrook and Stalker, 2003). The pods may grow up to 80 mm x 27 mm and normally contain two to five seeds. Although the number of seeds per pod depends on the cultivar, it can also be influenced by season and other factors (Stalker, 1997).

Seeds are either round or elliptical with pointed or flattened ends and range in their colours from off white to deep purple. Each seed consists of two large cotyledons, an epicotyl, and a primary root. The cotyledons comprise nearly 96% of the seed weight and are the major storage tissue for the developing seedling (Holbrook and Stalker, 2003).

1.3 Historical background of groundnut production, research and breeding in Tanzania

The history of groundnuts in Tanzania dates back to 1946. At that time, mainland Tanzania, the then Tanganyika, was a colony under British rule. Frank Samuel, the then head of the United Africa Company, a subsidiary of Unilever, came up with an idea for the colony to cultivate groundnuts, so as to produce vegetable oils. Both the idea and priority to introduce the groundnut production scheme in the colony were exclusively based on the interests of colonial government. Largely, the need was to have an exclusive large scale commercial production sector that would be state managed for export; although a smallholder production of the crop, which could be expanded and/or improved for household food and income earning, was already present

The first sites for cultivation were in Kongwa (Dodoma), Urambo (Tabora) and Nachingwea (Mtwara) where local people had already been cultivating groundnuts before (Ramadhan et al., 2002). The groundnut scheme failed in late 1950s and after independence in 1961 and up to 1970s research on groundnuts lacked cohesion. In 1978, the Oilseeds Research Project was started which included groundnuts, sesame and sunflower. Twelve varieties of groundnuts have been released to date, of which three varieties, namely Mangaka 09, Mnanje 09 and Masasi 09, are tolerant to early leaf spot but susceptible to late leaf spot, while Nachingwea 09 and Naliendele 09 are susceptible to both CLD (Mponda et al., 2012). Table 1.1 below summarizes the released varieties.

Today, smallholder farmers do the groundnut production in Tanzania. Major groundnut producing regions in Tanzania are Dodoma, Mtwara, Shinyanga, Tabora and Mbeya (NBS, 2012). It is the chief crop rotation component in many Sub-Saharan countries, Tanzania inclusive (Gbèhounou and Adango, 2003). It is one of several oilseed crops produced in the country, even though, edible oil production in the country is dominated by sunflower and cotton seed.

Groundnuts are a nutritional source of vitamin E and several minerals for human health including niacin, falacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium. Groundnut is useful in the treatment of haemophilia, and can cure stomatitis, prevent diarrhoea and is beneficial for growing children, and for both pregnant and nursing mothers (Akobundu, 1998). Kernels are consumed directly as raw, roasted or boiled nuts and vines are used as fodder for cattle (Pompeu, 1980; Hong et al., 1994). The crop is used as industrial materials for producing oil-cakes

and fertilizer. Extracted oil from kernel is used as culinary oil and other crop-extracts are used as animal feeds. Almost each part of the crop is used in some way. These multiple uses of groundnuts plant make it important for both food and cash-crop for the available domestic, or worldwide external markets in several developing and developed countries. Globally, 50% of the produce is used for oil extraction, 37% for confectionery use and 12% for seed purpose (Taru et al., 2010).

Table 1.1. Released groundnut varieties in Tanzania.

S/No.	Name of Variety	Group	Year of release
1	Nyota	Spanish	1983
2	Johari	Virginia	1985
3	Sawia	Virginia	1998
4	Pendo	Spanish	1998
5	Mnanje	Virginia	2009
6	Masasi	Virginia	2009
7	Mangaka	Spanish	2009
8	Nachingwea	Virginia	2009
9	Naliendele	Spanish	2009
10	Kuchele	Virginia	2015
11	Narinut	Virginia	2015
12	Nachi	Virginia	2015

Source: Naliendele Agricultural Research Institute (NARI)

1.4 Groundnut production and productivity

Groundnuts are grown in nearly 100 countries worldwide. China, India, Nigeria, USA, Indonesia Senegal and Sudan are major producers, growing an estimated total area of 21.8 million ha (Taru et al., 2010). Developing countries account for 96% of the global groundnuts area and 92% of the global production. Asia accounts for 58% of the global groundnuts area and 67% of the groundnuts production with an annual growth rate of 1.28% for area, 2.00% for production and 0.71% of productivity. Twenty-five countries in Asia produce 71.7% of the crop while 46 countries in Africa produce 18.6% of the total produce. North-Central America produces 7.5% from a small area of 3.7% of the overall estimated global area of producers. These countries produce about 28.5 million tons of shelled-nuts (ICRISAT, 2009). Global groundnut production with shells has not increased much, namely from 35.9 million tons in 2001 to 38.6 million tons in 2011 (FAOSTAT, 2011). Groundnuts in African countries such as Tanzania are grown on a small-scale level and with less application of modern inputs (Taru et al., 2010). For example, during the previous decade, production has not exceeded 8% of the world output (ITC, 2011). According to FAOSTAT (2011) groundnuts production in Africa in 2011 was 9.4 million tons, while Tanzania produced 0.7 million tons. Moreover, Tanzania produces fewer groundnuts compared with some other African countries. For instance, in 2011 groundnuts yield in the country was 0.96 t ha^{-1} while Nigeria recorded a yield of 1.26 t ha^{-1} and Guinea-Bissau had 1.72 t ha^{-1} of unshelled groundnut (FAOSTAT, 2011).

From the year 2010 to 2014 groundnut production in the world has been fluctuating from 43.4 to 43.9 million tons of unshelled groundnuts with the area under production increasing from 26.1 million ha in 2010 to 26.8 million ha in 2013 and then dropped to 26.5 million in 2014 (Table 1.2). Africa's production also kept fluctuating from 12.6 million tons in 2010, it dropped in 2011 and 2012, then it started to peak up in 2013 and in 2014 production reached 13.8 million tons of unshelled groundnuts while the area under production increased from 12.6 million ha in 2010 to 14.4 million ha in 2014 (Table 1.3). In Tanzania, production has been increasing steadily from 0.47 million tons in 2010 to 1.60 million tons of unshelled groundnuts in 2014 and the area under groundnut production has increased dramatically from 0.05 ha in 2010 to 1.60 million ha in 2014 (Table 1.4). In Tanzania groundnut production is mostly done by smallholder farmers (Adinya et al., 2010; Taru et al., 2010).

Table 1.2: World groundnut production (unshelled) 2010 to 2014.

Year	Groundnut production (tons)	Area harvested (ha)	Productivity (t ha^{-1})
2010	43421648	26142267	1.6610
2011	40860028	25105921	1.6275
2012	41311240	25194119	1.6397
2013	45836231	26880761	1.7052
2014	43915365	26541660	16546

Source: FAOSTAT database 2017

Table 1.3: Groundnut production (unshelled) in Africa from 2010 to 2014

Year	Groundnut production (tons)	Area harvested (ha)	Productivity (t ha^{-1})
2010	12670458	12673605	0.9998
2011	11348272	12185205	0.9313
2012	12490028	12839895	0.9728
2013	12923699	13997725	0.9233
2014	13895037	14402343	0.9648

Source: FAOSTAT database 2017

Table 1.4: Groundnut productions (unshelled) in Tanzania from 2010 to 2014

Year	Groundnut production (tons)	Area harvested (ha)	Productivity (t ha^{-1})
2010	465290	48230	0.9647
2011	651397	675226	0.9647
2012	810000	839631	0.9647
2013	1425000	943676	1.5101
2014	1635335	1619500	1.0098

Source: FAOSTAT database 2017

1.5 Importance and uses of groundnut

The crop is mainly grown for oilseed, food, and animal feed (Pande et al., 2003; Upadhyaya et al., 2006). It is the world's 13th most important food crop, 4th most important source of edible oil and 3rd most important source of vegetable protein (Taru et al., 2010). Since groundnut is one of the key sources of ingredients of household nutritional foods, women are mostly involved in producing the crop. In many developing countries, Tanzania inclusive, groundnut is the principal source of digestible protein and vitamins (25-34%) such as thiamine, riboflavin, and niacin (Naidu et al., 1999), 40-50% fats, 20-50% protein and 10-20 % carbohydrates (Sorrensen et al., 2004).

Groundnut seeds are consumed fresh, as roasted kernels or as boiled pods, and can be processed by grinding into powder for use as ingredients in vegetable, other food stuffs and confectionary products, and can also be ground to produce peanut butter (Sibuga et al., 1992). Generally, oil is the most important product of the crop and more than half of all groundnuts grown in the world are used to produce oil (Stalker, 1997). The groundnut oil content and quality varies depending on the cultivar, geographical location, season and growing conditions (Asibuo et al., 2008). The oil pressings, seeds and straw are also used in many countries as fuel and animal feed in the form of groundnut cakes and haulms (Wesche-Ebeling et al., 2002).

Groundnut is also a source of income to smallholder farmers in the developing countries of Asia and Sub-Saharan Africa, and therefore significantly contributes to food security and improvement of household livelihood (Naidu et al., 1999). In many sub-Saharan African countries, women predominantly grow and manage the crop; hence its production has a direct bearing on the overall economic and nutritional status of the household (Naidu et al., 1999).

According to Cox and Sholar (1995), groundnut is a legume crop with root nodules that can fix nitrogen in the soil, improving soil fertility, hence benefitting the productivity of the crop companion crops and subsequent crops in rotations. Studies show a range from 25 to 64% of plant N which can be derived from fixation by groundnuts (Sprent, 1994). Groundnut is also a relatively drought tolerant crop (Stalker, 1997) and grows well despite minimal inputs, making it suitable for low input agriculture practiced by smallholder farmers in the sub-Saharan Africa (Naidu et al., 1999).

1.6 Constraints to groundnut production

Groundnut production is constrained by several biotic and abiotic factors such as disease and pests (especially foliar diseases and aflatoxin contamination), nematodes and drought (Maiti, 2002). In the sub-Saharan region of Africa, diseases are generally regarded as a major constraint to groundnut production (Chiteka et al., 1992). The common diseases of groundnut are foliar and include rust, and early and late leaf spot. In addition to these, groundnut rosette disease (GRD), which occurs only in Africa, is also a major production constraint (Nigam, 2008).

Diseases such as early and late leaf spot, rust and GRD are widespread and reduce yields whenever they occur (Minde et al., 2008). It is estimated that early and late leaf spot diseases cause up to 70% yield loss (Monfort et al., 2004), while losses due to rust exceed 50% worldwide (Hagan et al., 2006). According to Monyo et al. (2008) Africa is the only place where GRD and leaf spot diseases regularly combine to cause devastating yield losses in groundnut crop. It has been reported that in Tanzania, the reasons for low yields in the country include the use of unimproved varieties with low yields, unreliable rainfall, pest and diseases, as well as lack of institutional support (BACAS, 2000).

Major groundnut diseases in Tanzania include cercospora leaf spot, rust and the groundnut rosette disease (Mansoor, 2012). Furthermore, aflatoxin contamination forms a major problem, which reduces the price received for groundnut on the world market (ICRISAT, 2011). Moreover, many farmers stopped growing groundnuts as cash crop due to lack of reliable markets and low return per capital invested (NARI, 2008; Bucheyeki et al., 2010). Table 1.5 summarizes the constraints of groundnut production in Tanzania.

Table 1.5: Constraints of groundnut production in Tanzania.

Constraints	Descriptions
Diseases	Leaf spots (early and late leaf spot), rust, rosette virus and aflatoxin contamination
Drought	Intermittent and terminal drought
Seed availability	Inadequate production, Inadequate linkage in the seed value chain Low seed multiplication Low awareness and varietal promotion
Market access	Aflatoxin contamination, availability of cheap oil substitutes such as sunflower oil
Inadequate value addition utilization	Low focus on prepared nuts, peanut butter, groundnut oil production
Soils	Poor soil fertility in marginal areas where groundnuts are cultivated

1.7 Cercospora leaf spot diseases

As indicated in section 1.6 above, the cercospora leaf spot diseases are very destructive and can lower crop yield up to 70%. This section elaborates on the causative agents, disease symptoms and management options.

1.7.1 Causative agent and symptoms of Cercospora leaf spot disease

Among the foliar diseases, cercospora leaf spots (CLD), caused by *Cercospora arachidicola* Hori, causing early leaf spot, and *Cercospora personatum* [(Berk. and Curt) Deighton] causing late leaf spot are the most common, widespread, destructive and consistent in occurrence. The two pathogens are similar; they often form necrotic lesions on leaves and petioles and less frequently on stems, stipules and pegs. Symptoms of late leaf spot (LLS) are similar to those of early leaf spot (ELS), but yellow halos are not usually produced in LLS. Under field conditions, however, yellow halos may be altered by the genetic or nutritional status of the host or weather conditions, therefore under field conditions, both the diseases are generally considered as one (Holiday, 1980).

The CLD occur wide spread wherever groundnut is cultivated. The host range of *C. arachidicola* and *C. personatum* is confined to the genus *Arachis* (Stalker and Simpson, 1995). Conidia of CLD of groundnut produced on crop residues in the soil are the main cause of initial inoculum. Mycelia in spots on stems, petioles, and pegs are more likely to survive between seasons than those on leaflets and, therefore, initiate disease epidemics in the subsequent seasons (Shokes and Culbreath, 1997). Epidemics of CLD have frequently led to yield losses of 50% on unsprayed peanuts (Shokes and Melouk, 1995). The diseases cause damage to the plant by reducing the available photosynthetic area, by lesion formation and by stimulating leaflet abscission. In areas where rust disease is also present, a combined attack of the foliar diseases can cause yield losses of up to 70% (McDonald et al., 1985). Symptoms of the CLD are summarized in Table 1.6 below.

Table 1.6: Comparisons of symptoms of early and late leaf spot of groundnut

Character	Early leaf spot	Late leaf spot
Stage of occurrence	Early infection	Usually late infection
Shape of spot	Circular to irregular	Usually circular
Leaf surface on which most Spores are produced and arrangement	Upper surface, random	Lower surface, in concentric rings
Colour of spot on upper leaf surface	Light brown to black, tending towards brown with some yellow halo	Brown to black, tending towards black
Colour of spot on lower leaf surface	Brown	Black

1.7.2 Components of Cercospora leaf spot disease resistance

Sporulation, lesion size, and latent period are the important components of resistance to CLD and are highly correlated with each other and with the percentage of leaf necrotic area (Nevill, 1981; Chiteka et al., 1988). Lesion diameter, defoliation, and sporulation in glasshouse study are positively correlated with field disease score (Subrahmanyam et al., 1982). Previous studies show that wild *Arachis* species resistant to LLS in sections *Erectoides*, *Triseminalae*, *Extranervosae*, *Rhizomatosae*, and *Caulorhize* have small and non-sporulating lesions, whereas species in section *Arachis* have accessions either with non-sporulating lesions or with variably sporulating lesions. Frequency of infection and defoliation vary greatly within each section and species (Subrahmanyam et al., 1985).

Although, several interspecific derivatives resistant to late leaf spot and rust have been developed at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), the genetic variability for components of resistance to LLS have not been investigated. New sources of resistance to ELS in eastern and southern Africa include ICG 6022, ICG 405, ICG 14466, ICG 6057, ICG 9449 and ICG 12509 (Mponda et al., 2012).

1.8 Breeding for durable resistance against Cercospora leaf spot diseases in groundnut

According to Johnson (1981) durable resistance is defined as a resistance that remains effective while being extensively used in agriculture for a long period in an environment conducive to the disease. However, the length of time the resistance will last cannot be determined during the breeding process. Choice of the best genotypes for different resistance components are guided by the desirable direction of components of resistance.

The best genotypes for different resistance components should be intercrossed to generate progenies with higher resistance. Selection in the segregating generations, however, should be based on percentage defoliation in the field (Dwivedi et al., 2002). Monogenic or major gene resistance (vertical resistance) has been widely used by breeders, but the high selection pressure has led to rapid emergence of new virulent strains (McDonald and Linde, 2002). The use of extensive monoculture and other practices that favour pathogen proliferation increase the evolution of virulent strains that cause significant yield losses and devastating epidemics (Boyd et al., 2012).
Hence, there is need for durable resistance in crops. The use of minor genes of resistance (polygenic) has been recommended for durable resistance breeding programmes (Van der Plank, 1968; Robinson, 1980). However, it is difficult to differentiate the expression of resistance

conditioned by major and minor genes (Parlevliet and van Ommeren, 1988). The presence of the major genes confounds selection for the minor genes during breeding (Parlevliet, 1983). Therefore, there is a need to separate the two types of resistance to be able to accumulate the minor genes in the absence of the major genes.

In a breeding programme for minor gene resistance, selection against major genes can be done by removing the resistant or immune plants and selecting genotypes with intermediate resistance (Parlevliet and van Ommeren, 1988). Motagi (2001) and Dwivedi et al. (2002) in their genetic studies on CLD resistance suggested that resistance is complex and polygenic in nature and probably controlled by several recessive genes. Furthermore, Hamid et al. (1981) and Jogloy et al. (1987) reported that, additive genetic variance seems to contribute predominantly to the resistance.

According to Reddy et al. (2000) and Varman (2000), many sources of CLD resistance within cultivated species have been reported. However, complete resistance to CLD has not been found in the cultivated groundnut. Although a high level of resistance is present in some wild species of *Arachis*, the incorporation of these genes for resistance into improved cultivars is difficult (Company et al., 1982, Gardner et al., 1983). The development of high-yielding foliar disease resistant genotypes requires identification of resistant sources with good breeding potential. Information on genetic control of resistance and yield helps to plan appropriate breeding methodologies to identify resistant lines with high yield potential.

1.9 Mating designs use in breeding programs

Mating designs are used to generate genetic segregating populations that can be used in breeding programs and to generate genetic information such as gene effects (Dabholkar, 1992). The choice of mating design depends on the objectives and the overall breeding strategy of the particular breeding program. The most common objectives of mating designs are: a) to provide information for evaluating parents, b) to estimate genetic parameters, c) to produce a base population for advanced generation selection, and d) to estimate realized gain directly (McKinley, 1983).

In groundnut, pedigree and bulk-pedigree methods of breeding are most frequently used to handle segregating populations derived from hybridization. The pedigree method allows breeders to practice selection of traits with high heritability, such as plant type, pod and seed size, and the shape and testa colour of the seed, in early generations. Selections of quantitative traits such as seed yield and seed composition are made in later generations. The bulk-pedigree method is a modified method aimed at improving traits with low heritability traits (Wynne and Gregory, 1981). Single seed decent method is becoming popular as it has the advantage to save space and

resources (Isleib et al., 1994). Nevertheless, multiple crossing systems, such as the double or convergent cross are also used to create adequate genotypic variability before selection (Wynne and Gregory, 1981). To that effect, a double cross mating design was used in this study to breed for durable resistance against CLD in groundnuts.

1.10 Combining ability studies in groundnut

Several scientists have conducted genetic studies in groundnut. According to Hariprasanna et al. (2008), who used full diallel to examine the combining ability in order to understand the type of gene action governing shelling percentage, 100-pod weight, 100-seed weight, and number and proportion of mature seeds in groundnut. They found that additive gene action predominantly controlled the expression of the majority of the traits and non-additive gene action was important for on seed size. Anderson et al. (1992) complemented these results on F_1 and F_2 populations for pod and seed sizes. Mothilal and Ezhil (2010) found the magnitude of specific combining ability variances much greater than those of general combining ability for plant height, number of mature pods plant^{-1}, pod yield, seeds yield plant^{-1} and shelling percentage. Further findings by Layrisse et al. (1980), who studied the combining ability from F_2 generation of ten groundnut lines from South American centres of diversity for seed yield, pod mass, seed protein and oil content, show that, both general combining ability (GCA) and specific combining ability (SCA) were significant for all traits, except for the SCA estimates for protein content, and that the GCA component was larger than the SCA for all traits.

Additive and non-additive gene action was reported by Sangha and Labana (1982) for the number of pods and seed yield. Using a half diallel F_1 population, Jayalakshmi et al. (2002) studied the gene action of morphological and physiological attributes (specific leaf area, secondary nodes plant-^{1}, diseased and immature pods plant^{-1}, pod yield, root dry mass, shoot biomass and seed yield) influencing groundnut yield. They found that both additive and non-additive gene actions were important in the expression of most traits.

Redona and Lantican (1985) examined the GCA and SCA effects for seed and pod yield plant^{-1}, weight seed$^{-1,}$ weight pod^{-1}, number of pods and seeds plant^{-1}, and height of main axis. They reported that both GCA and SCA mean squares were significant, and estimates of GCA effects were greater than the SCA estimates for all traits, indicating that additive gene action was important in the expression of all traits.

1.11 Participatory plant breeding

The main breeding goals should meet the requirements of growers, processors and consumers. A grower requires high yield, disease resistance and tolerance to environmental stresses, and yield stability. A processor requires uniform maturity and processing characteristics. The consumer requires good quality oil and groundnut seeds with acceptable shape, size, colour and taste for confectionery purposes (Wynne and Gregory, 1981). Consequently, a participatory rural appraisal was conducted in the study area to obtain the views of farmers, traders and consumers on the variety preferences, and opportunities and challenges in groundnut production, marketing and processing.

1.12 Factors influencing variety adoption

Different factors determine the adoption of agricultural innovations and technologies. Much empirical adoption literature focuses on farm size as the first and probably the most important determinant (Doss and Morris, 2001; Daku, 2002). This is because farm size can affect, and in turn be affected by, the other factors influencing adoption. With small farms, it has been argued that large fixed costs become a constraint to technology adoption (Abara and Singh, 1993), especially if the technology requires a substantial amount of initial set-up cost.

Education is thought to create a favourable mental attitude for the acceptance of new practices, especially information-intensive and management-intensive practices (Caswell et al., 2001). According to Rogers (1995) and Ehler and Bottrell (2000), technology complexity has a negative effect on the adoption and this could only be dealt with through education. According to Weir (1999) education produces non-cognitive changes in attitudes, beliefs and habits which in turn may lead to a greater willingness to accept risk, adopt innovations, save for investment, and generally to embrace productive practices in a modernizing or rapidly changing environment. Further, findings by Mugisha et al. (2004), in their study on the adoption of IPM groundnut production technologies in Eastern Uganda, revealed that adoption was significantly influenced by education, family size, membership of associations, extension visits, access to credit, and household income.

Gender issues in agricultural production and technology adoption have been investigated for a long time. Most of such studies show mixed evidence regarding the different roles men and women play in technology adoption. Studies by Doss and Morris (2001) on factors influencing improved maize technology adoption in Ghana, and Overfield and Fleming (2001) studying coffee production in Papua New Guinea, there were insignificant effects of gender on adoption. A study by Kimmins et al. (1999) proved that in many Sub-Sahara African countries, women were predominantly growing

and managing groundnut crops. Therefore, cultivation of the crop has a direct bearing on the overall economic, financial and nutritional status of women and children in the household.

Age is an important factor that influences the probability of adoption of new technologies because it is said to be a primary latent characteristic in adoption decisions. However, there is contention on the direction of the effect of age on adoption. Age was found to positively influence adoption of sorghum in Burkina Faso (Adesiina and Baidu-Forson, 1995), IPM on groundnuts in Georgia (McNamara et al., 1991) and chemical control of rice stinkbug in Texas (Harper et al., 1990). In contrast, age has been found to be either negatively correlated with adoption, or not significant in farmers' adoption decisions. In studies on adoption of land conservation practices in Niger (Baidu-Forson, 1999), rice in Guinea (Adesiina and Baidu-Forson, 1995), fertilizer in Malawi (Green and Ng'ong'ola, 1993), IPM sweep nets in Texas (Harper et al., 1990), hybrid cocoa in Ghana (Boahene et al., 1999), age was either not significant or was negatively related to adoption.

Furthermore, access to funds including credit is expected to increase the probability of adoption. For instance, it has been reported that most small scale farmers in Tanzania are unable to afford basic production technologies such as fertilizers and other agrochemicals resulting in low crop yields due to poverty and limited access to credit (MAFC, 2010). From the above, it is concluded that though a number of studies have been conducted across the world on technology adoption, there is dearth of literature on the specific factors that influence the adoption of modern agricultural production technologies, especially among small scale farmers in Tanzania. This serious gap must be bridged if the problem of low technology adoption among farmers is to be addressed and agricultural productivity improved.

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Chapter 2: Groundnut production constraints and traits preferred by stakeholders in the groundnut value chain in semi- arid areas of Tanzania

Abstract

Groundnut (*Arachis hypogaea* L.), a self-pollinating legume, is an important crop cultivated on 24 million ha across the world for the extraction of edible oil and food uses. However, yields have remained low in most sub-Saharan Africa countries, Tanzania inclusive, regardless of the availability of improved varieties. The objectives of this study were to investigate the major crops grown, farmers' groundnut variety selection criteria, cropping systems, groundnut production constraints, and farmers' awareness of Cercospora leaf spot disease. Furthermore, the study intended to investigate preferences and challenges facing groundnut traders and processors. The study was conducted in Bahi, Dodoma municipal and Kongwa districts in the Dodoma region in the central zone of Tanzania. Semi-structured questionnaires were administered to obtain detailed information on groundnut production in the region. The study established that the main crops grown in the region were maize, groundnut, sunflower and sorghum. Groundnut was the most commonly grown crop, followed by maize, sunflower and sorghum, respectively. The major constraints for groundnut production were drought, diseases, insect pests, lack of suitable improved cultivars and reliable markets. About 85% of the farmers were growing local landraces, and 15% were growing improved varieties. Further findings identified four seed sources for the varieties used by the farmers, namely; farmer saved seed, seed purchase from fellow farmers, from the local market, or obtained from the government through researchers or extension workers. Farmers in this region preferred erect, brown seeded groundnut cultivars that have medium to large seed size, are early maturing, have a high yielding potential, high oil content, and are tolerant to drought, diseases and insect pests. While Cercospora leaf spot diseases infected over 70% of the fields evaluated in the region, farmers were not taking any action, thinking that leaf defoliation was a sign of maturity. There is, thus, a need to develop groundnut cultivars that are tolerant to biotic and abiotic stresses, and with characteristics preferred by the farmers and other stakeholders in the groundnut value chain.

Keywords: Cercospora leaf spot disease, groundnut (*Arachis hypogaea* L.), participatory rural appraisal, stakeholders, Tanzania, value chain.

2.1 Introduction

Agriculture is Tanzania's economic mainstay and contributed USD 13.9 billion to its gross domestic product (GDP) (nearly 30%) and 62.1% to the total employment during 2014. Agricultural land in Tanzania was last estimated at 396,500 km^2 in 2013 (45% of total area) versus 369,744 km^2 in 2008, representing an increase of 7% over the preceding five year period. During the same period, crop production rose by 44%, beating the sub- Saharan Africa's average crop production growth rate of 18% (NBS, 2015). Agriculture in Tanzania is dominated by smallholder farmers who grow different kinds of crops for both domestic consumption and cash earning. Food crops are commonly cultivated on relatively small areas averaging from 0.9 up to 3.0 ha per household (MAFSC, 2011).

Food legume crops represent an important component of the agricultural food crops consumed in developing countries and are considered a vital crop for achieving food and nutritional security for both producers and consumers. In dietary terms, food legumes complement cereal crops as a source of protein and minerals, while agronomically they serve as a rotation crop with cereals, reducing soil pathogens and supplying nitrogen to the cereal crop upon intercropping. Legumes, broadly defined by their unusual flower structure, podded fruit, and the ability of 88% of the species examined to date to form nodules with rhizobia (de Faria et al., 1989) are second only to the cereals in their importance to humans. Food legumes fetch higher prices compared to cereals and are increasingly grown to supplement farmers' income (Gowda et al., 2000). The important and diverse role played by food legumes in the farming systems and in diets of poor people, makes them ideal crops for achieving the millennium developmental goal of "reducing poverty and hunger, improving human health and nutrition, and enhancing ecosystem resilience'' (Akibode, 2011).

Conventional plant breeding has proved to be more beneficial to farmers in high potential environments or to those who can profitably modify their environment to suit new cultivars, than to the smallholder farmers who cannot afford to modify their environment through the application of additional inputs, and cannot face the risk due to the replacement of their traditional well known and reliable varieties. Consequently, low yields, crop failures and eventually poverty still affect a large proportion of humanity. Farmer's Participatory Varietal Selection is a way to overcome the limitations of conventional breeding by offering farmers the possibility to choose,

in their own environment, the varieties that suit better their needs and conditions (Ceccarelli and Grando, 2007).

Groundnut in Tanzania is grown by smallholder farmers, providing both food and income for households. Nearly 1 million smallholder farmers grow groundnut. Most groundnut farmers have less than 1.0 ha that is allocated to groundnuts on their farm. Since groundnut is one of the key sources of household nutrients, it is mostly women that contribute labour to the production of the crop (NARI, 2008). Groundnut is usually intercropped with cereals or cassava.

The low crop yields are attributed to both biotic and abiotic stresses in the cultivation of the crop, which include; unreliable rains, pest and diseases occurrence (especially foliar diseases), poor technology available to small-holder farmers, poor seed varieties, and increased cultivation on marginal land (ICRISAT, 2012). As a result, smallholder farmers growing groundnuts are faced with food insecurity, low income and poor livelihood.

Although efforts towards groundnut breeding have led to the development of varieties with moderate levels of resistance to cercospora leaf spot diseases, farmers have not widely adopted these varieties because they either lack farmers' and /or market preferred traits. According to Wynne and Gregory (1981), the main breeding goals should meet the requirements of growers, traders, processors, and consumers. This study therefore, intends to develop high yielding lines with durable resistance to cercospora leaf spot diseases and traits preferred by farmers and the market. In lieu of that, a participatory rural appraisal (PRA) was conducted in the study area so as to obtain views from the farmers, traders, processors and consumers on the preferred traits for groundnut, and opportunities and challenges in groundnut production, marketing and processing.

2.2 Material and methods

2.2.1 Description of the study area and sampling method

The PRA was conducted in six villages of three districts in the Dodoma region of central Tanzania, namely; Kigwe and Ilindi in Bahi district, Hombolo Makulu and Zepisa in Dodoma municipal district, and Ndulugumi and Laikala in Kongwa district. The three districts were selected because they are located in the groundnut growing areas.

In addition, a survey for groundnut leaf spot diseases was conducted in the villages in the growing season between January and May 2015, through direct visits to farmers' fields, during which leaf samples were taken for laboratory confirmation of the pathogen(s) involved. Thirty fields (i.e. five representative fields per village) were surveyed in the six villages (Figure 2.2 B). The CLD prevalence was determined by dividing the number of samples with disease symptoms over the total number of samples collected in each field and district (Waliyar et al., 2007).

Furthermore, interviews were conducted with traders who buy and sell groundnuts on the markets. In addition, processors were interviewed during agricultural shows/exhibitions conducted every year on 08th day of August, and commonly known as "Nane nane agricultural shows" (Figure 2.1).

Figure 2.1 Interview with groundnut processors during Nane nane Agricultural show at Dodoma region

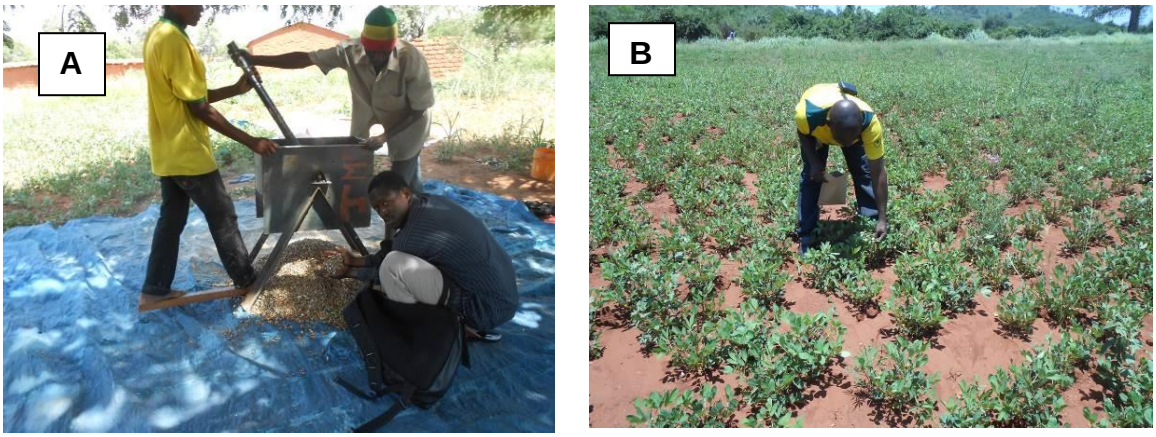

Figure 2.2: **A**=Groundnut shelling at Kigwe village, Bahi district; **B** = Cercospora leaf spot disease survey in the field at Hombolo Makulu village, Dodoma municipal district

2.2.2 Data collection

Tools used to gather information included interviews using a semi-structured questionnaire (Figure 2.3), whereby a total of 120 farmers (20 per village in six villages mentioned above) were interviewed, transect walk in all six villages, interviews with traders (buyers and sellers) and processors. Data gathered were used to supplement information obtained from the semi-structured questionnaire. Other supporting information was obtained from reports and other sources such as Ministry of Agriculture Food Security and Cooperatives, agricultural department of district councils, National Bureau of Statistics. The village/community leaders and village extension officers were contacted in the process to validate the information.

Figure 2.3: Interview with farmers during PRA

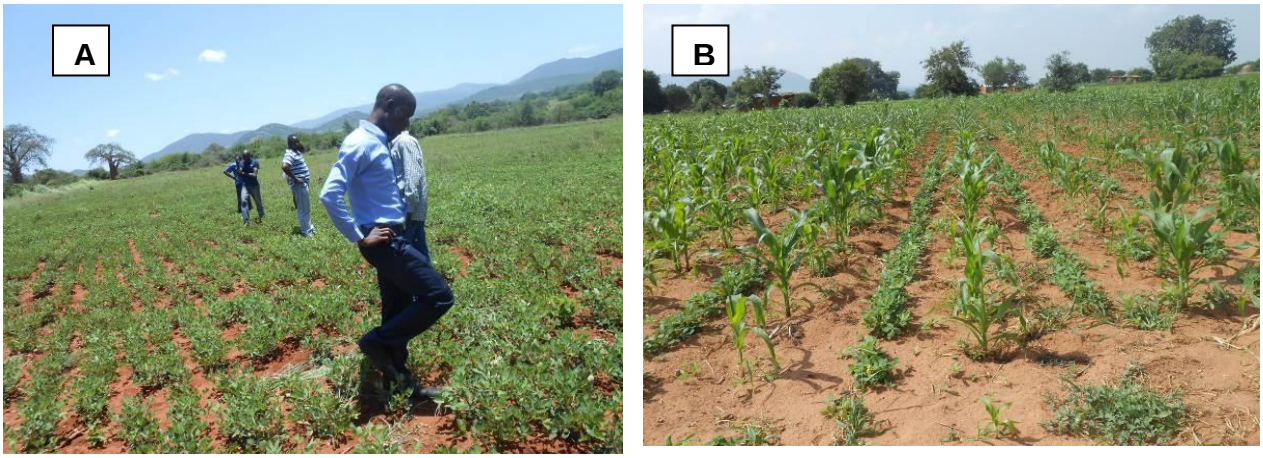

Figure 2.4: **A**= Groundnut in monoculture and **B**= Intercropped with maize

2.3 Data analysis

Statistical analyses for both quantitative and qualitative data were performed using the Statistical Package for Social Sciences (SPSS) (Release 21) computer package. Data were classified as nominal or ordinal when entered into the SPSS spreadsheet. For exploring relationships, frequencies, descriptive statistics and cross tabulation were computed; Charts were drawn in Microsoft Office Excel 2010 version.

2.4 Results

2.4.1 Socio-economic characteristics of the households

The majority (83.9%) of the household heads who engaged themselves in groundnuts production were aged between 21 to 60 years old, while very few (16.1%) were over 60 years old (Table 2.1). The data also revealed that, to a large extent groundnuts production in the study area was dominated by the male individuals (72.6%). The majority (96.8 %) of farmers had attended primary and secondary school education and were literate.

Table 2.1: Household socio-economic characteristics district wise

Age group of farmers		Bahi	Kongwa	Dodoma Municipal	Total	Percentage
21-30 years old		5	4	4	13	10.5
31-40 years old		13	13	13	39	31.4
41-50 years old		10	9	8	27	21.8
51-60 years old		8	10	7	25	20.2
above 60 years old		5	4	11	20	16.1
Total		**41**	**40**	**43**	**124**	**100**
Gender category of famers	Male	33	24	33	90	72.6
	Female	8	16	10	34	27.4
	Total	**41**	**40**	**43**	**124**	**100**
Education level	Primary	34	30	39	103	83.1
	Secondary	7	6	4	17	13.7
	Illiterate	0	4	0	4	3.2
	Total	**41**	**40**	**43**	**124**	**100**

Source: Household survey data.

2.4.2 Crops grown in the 2012/13 to 2014/15 production seasons

Table 2.2 presents the various crops grown by smallholder farmers in the study area in the three consecutive production seasons, namely 2012/13, 2013/14 and 2014/15. The findings revealed

that of all the crops grown, groundnut was the most frequently grown crop. For example, in the 2012/13 production season, 99.2% of the farmers interviewed reported to have grown groundnuts, while in 2013/14 and 2014/15 production seasons all the farmers interviewed (100.0%) grew groundnuts. Other crops grown were maize (79.0-79.8%), sorghum (40.3-40.9%) and sunflower (35.5%-36.5%). Minor crops grown were pearl millet, cowpea, Bambara groundnut, sesame and pigeon pea.

Table 2.2: Crops grown in the study area in three seasons across districts.

Production season	**Crop**	**Area (ha)**	**Multiple responses**		**Percentage of cases**
			Frequency	Percentage	
2012/2013 season	Groundnuts	24.8	123	29.3	99.2
	Maize	78.4	98	23.3	79.0
	Sorghum	20.5	50	11.9	40.3
	Sunflower	5.3	45	10.7	36.3
	Pearl millet	14.0	23	5.5	18.5
	Simsim	3.3	22	5.2	17.7
	Bambara groundnut	3.5	28	6.7	22.6
	Cowpea	2.3	19	4.5	15.3
	Cassava	2.5	10	2.4	8.1
	Pigeon pea	0.5	2	0.5	1.6
	Total	**154.9**	**-**	**100**	-
2013/14 season	Groundnut	27.9	124	29.4	100.0
	Maize	79.3	99	23.5	79.8
	Sorghum	15.6	52	12.3	41.9
	Sunflower	5.4	44	10.4	35.5
	Bambara groundnut	1.5	28	6.6	22.6
	Pearl millet	13.2	22	5.2	17.7
	Simsim	3.5	22	5.2	17.7
	Cowpea	2.0	20	4.7	16.1
	Cassava	1.8	9	2.1	7.3
	Pigeon pea	0.5	2	0.5	1.6
	Total	**150.6**	**-**	**100**	-
2014/15 season	Groundnut	22.4	124	29.2	100.0
	Maize	75.3	99	23.3	79.8
	Sorghum	20.8	52	12.3	41.9
	Sunflower	8.8	44	10.4	35.5
	Bambara groundnut	3.3	28	6.6	22.6
	Pearl millet	13.5	23	5.4	18.5
	Simsim	3.0	22	5.2	17.7
	Cowpea	2.0	21	5.0	16.9
	Cassava	2.0	9	2.1	7.3
	Pigeon pea	0.5	2	0.5	1.6
	Total	**151.5**	**-**	**100**	-

Source: Household survey data.

2.4.3 Groundnut varieties and seed sources

The results (Table 2.3) revealed that there were significant ($p<0.001$) differences in the varieties grown between different locations (Chi-square χ^2 =138.9; p=0.000). For instance, in the 2012/2013 cropping season most of the farmers in Kongwa district (100%), Dodoma municipal (97.1%) and Bahi (56.3%) grew landraces, while improved groundnut varieties were grown in Bahi (43.8%) and Dodoma municipal (2.9%), respectively.

There were significant ($p<0.001$) differences in the frequency of varieties grown in different locations (Chi-square i.e. χ^2 =137.9; p=0.000). For instance in the 2013/2014 cropping season most of the farmers in Kongwa district (97.5%), Dodoma municipal (97.7%) and Bahi (61.0%) grew landraces, while improved groundnut varieties were grown in Bahi (38.9%), Kongwa (2.4%) and Dodoma municipal (2.3%), respectively.

Table 2.3: Groundnut varieties grown in two seasons by district

Cropping season	Variety grown	District where groundnut varieties was grown (% of total)			Chi-square
2012/13		Bahi	Dodoma municipal	Kongwa	X^2=138.9
	Landraces	56.3	97.1	100.0	
	Pendo	31.3	0.0	0.0	P= 0.001
	Mamboleo	12.5	2.9	0.0	
	Total	**100**	**100**	**100**	
2013/14	Landraces	61.0	97.7	97.5	
	Pendo	29.3	0.0	0.0	X^2=
	Mamboleo	9.7	2.3	0.0	137.9
	Red seeded	0.0	0.0	2.5	P=0.001
	Total	**100**	**100**	**100**	

Source: Household survey data

2.4.4 Seed sources of groundnut varieties

The results presented in Table 2.4 show that the majority of the farmers in Dodoma municipal (93.0%) and those in Bahi (46.4%) plant groundnut seed saved (stored) from the previous seasons' crop, while (50.0%) of the farmers in Kongwa district buy seeds from their fellow farmers. The Chi square test results show that access to reliable seed sources among small-holder farmers significantly differed among the farmers by location (Chi square=190.1; p=0.001), and that only in the Bahi district farmers accessed seeds from extension workers (24.4%) and researchers (4.9%) in the 2012/13 production season. In the 2013/14 production

season most farmers in Bahi (46.2%) and Dodoma municipal (89.6%) used farmer saved seed, and in Kongwa (55.0%) farmers used seeds bought from fellow farmers as their main seed source. The Chi square test results show that access to reliable seed sources among small-holder farmers significantly differed among the farmers by location (Chi square=194.9; p=0.001), and that only in the Bahi district farmers accessed seeds from extension workers (24.4%) and researchers (4.8%), while in all districts farmers relied on their own farm saved seeds and farmer to farmer seed sources.

Across the district, most farmers used own saved seed (51.8%), followed by seed purchased from other farmers (19.9%), purchased from local market (10.4%), or acquired from relatives (4.5%) and fellow farmers (3.6%). The Chi square test results show that access to reliable seed sources among smallholder farmers significantly differed among the farmers by location (Chi square=194.9; p=0.001), whereby only farmers in Bahi district obtained seeds from the government extension staff (8.1%) and researchers (1.6%).

Table 2.4: Sources of groundnut seed (percentage) in two seasons in three districts

Source of groundnut cultivar	2012/13 cropping season			2013/14 cropping season			Average (%)
Districts	Bahi	Municipal	Kongwa	Bahi	Municipal	Kongwa	
Acquired from parents, relatives	4.9	2.3	10.0	0.0	0.0	10.0	4.5
Bought from other farmer	4.8	0.0	50.0	9.6	0.0	55.0	19.9
Bought from the market	9.8	4.7	17.5	12.2	5.7	12.5	10.4
Extension officer	24.4	0.0	0.0	24.4	0.0	0.0	8.1
Farmer own saved seeds	46.4	93.0	17.5	46.2	89.6	18.3	51.8
From fellow farmers (free)	4.8	0.0	5.0	2.8	4.7	4.2	3.6
Research institute	4.9	0.0	0.0	4.8	0.0	0.0	1.6
Total	**100**	**100**	**100**	**100**	**100**	**100**	**100**
Chi square value	X^2= 190.1; P= 0.000			X^2= 194.9; P= 0.000			

Source: Household survey data.

2.4.5 Groundnut production, consumption and marketing

The results presented in Table 2.5 show the production, consumption and sales for each household interviewed according to district. The results revealed that, farmers in Dodoma municipal had the highest (305.4 kg), mean production as compared to farmers in Bahi (250.5 kg) and Kongwa (156.6 kg) districts, respectively. Households in Kongwa, Bahi and Dodoma

municipal districts, consumed 42.8%, 26.5% and 76.3% of their production, respectively and marketed the remainder. The productivity was highest in Bahi (1141.2 kg ha^{-1}) followed by Dodoma municipal (1059 kg ha^{-1}) and Kongwa was the least (963.7 kg ha^{-1}).

Table 2.5: Mean production, consumption and sales district wise in 2013/14 season.

District	Production				Consumption		Sales	
	Total quantity (kg)	Average per farmer (kg)	Area cultivated (ha)	Productivity (kg ha^{-1})	Quantity kg)	Percentage of production	Quantity (kg)	Percentage of production
Bahi	10270.5	250.5	9.0	1141.2	66.4	26.5	184.1	73.5
Kongwa	6264.0	156.6	6.5	963.7	67.0	42.7	89.6	57.2
Dodoma Municipal	13132.2	305.4	12.4	1059.0	72.4	23.7	233.0	76.3
Total	29666.7	239.2	27.9	1063.3	205.8	28.9	506.7	71.1

Source: Household survey data.

2.4.6 Constraints experienced by groundnut smallholder farmers, traders and processors

The major constraints in groundnut production (Figure 2.5) as reported by the farmers were; drought in Bahi (97.6%), Dodoma municipal (96.0%) and Kongwa (92.7%); poor soil fertility in Bahi (45.2%), Dodoma municipal (49.2%) and Kongwa (40.3%); groundnut diseases in Bahi (41.9%); Dodoma municipal (44.4%) and Kongwa (46.8%); insect pest attack in Bahi (30.7%), Dodoma municipal (24.2%) and Kongwa (33.9%); and the availability of improved seeds of groundnut varieties in Bahi (28.2%), Dodoma municipal (20.2%) and Kongwa (30.7%). Other groundnut production constraint identified included poor varieties in Bahi (24.2%), Dodoma municipal (18.6%) and Kongwa (25.8%) and lack of market availability in Bahi (22.6%), Dodoma municipal (16.9%) and Kongwa (21.0%).

The traders faced constraints such as poor quality groundnut grains as the result of mixed colour (6.0%) and poor grain size (10.0%), a lack of a reliable markets (56.7%) and an unreliable quantity supplied by farmers (26.7%). Marketing was further constrained by a lack of uniformity of groundnut grains (i.e. colour and size), a limited market for their finished products, costly packaging materials and a lack of capital.

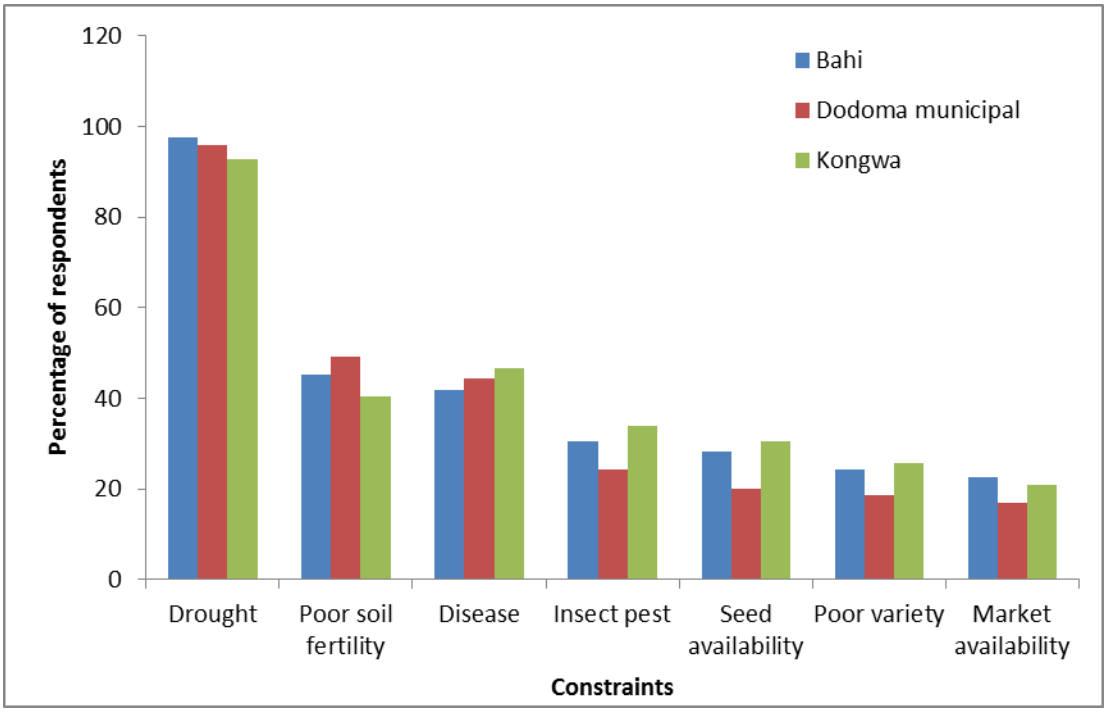

Figure 2.5: Constraints facing groundnut farmers in the different districts.

2.4.7 Groundnut variety characteristics preferred by small-holder farmers, traders and processors

The farmers prefer groundnut varieties with an erect growth type, that are high yielding, early maturing, have a high oil content, are highly tolerant to diseases and drought, have large seed size, seed with a good taste and the plants must be easy to thresh (Table 2.6). These were among the main groundnut varieties' good characteristics, which were reported by the farmers. On the other hand, some farmers mentioned late maturity and a runner growth habit as their preference. The majority (80.0%) of traders preferred medium to large groundnut seed size, while only a few (20.0%) of them preferred small sized groundnut seed (Table 2.6). The majority (66.7%) of processors (shelling and peanut butter makers) preferred medium to large seed size, less pod constriction and sharp beaked groundnut, while 33.3% of the respondents preferred small sized seed groundnut.

Table 2.6: Groundnut characteristics preferred by smallholder farmers, traders and processors in the study area.

Stakeholders in value chain	Good characteristics of cultivar	Bahi	Dodoma Municipal	Kongwa	Total frequency	Percentage of frequency
Farmers (producers)	high yield	27	30	32	89	71.8
	high oil content	27	30	32	89	71.8
	disease resistance	27	30	32	89	71.8
	erect growth habit	27	30	32	89	71.8
	drought tolerance	27	30	32	89	71.8
	early maturity	12	10	4	26	21.0
	large grain size	12	10	4	26	21.0
	good taste	12	10	4	26	21.0
	many seeds per pod	12	10	4	26	21.0
	good threshability	12	10	4	26	21.0
	late maturity	12	10	4	26	21.0
	runner growth habit	12	10	4	26	21.0
	good market	0	0	1	1	0.8
	easily available	2	3	3	8	6.4
	easy to weed and uproot	2	3	3	8	6.4
	Total	**41**	**43**	**40**	**124**	**100.0**
Traders	medium to large seed size, brown colour	5	12	7	24	80
	small seed size and brown colour	0	2	4	6	20
	Total	**5**	**14**	**11**	**30**	**100**
Processors	medium to large seed size, less pod constriction, sharp beak and brown colour	2	2	0	4	66.7
	small seed size, brown colour	0	0	2	2	33.3
	Total	**2**	**2**	**2**	**6**	**100**

Source: Household survey data

2.4.8 Awareness on Cercospora leaf spot disease and adoption of varieties by farmers

All the farmers interviewed experienced CLD in their fields. However, farmers generally were not aware that the symptoms were caused by a disease, but considered the symptoms as a sign of maturity. The majority (94.4%) of the farmers interviewed reported that they took no action to control the disease, while a few farmers reported that they uprooted the infected plants at the early stage and/or sometimes applied wood ashes or dried ground neem leaves. Most farmers (99.2%) interviewed were ready to adopt new varieties.

Table 2.7: Farmers' awareness and control measures of Cercospora leaf spot diseases.

Variable	Bahi	Dodoma municipal	Kongwa	Total	Percentage
Have you ever seen CLD					
Yes	41	43	40	124	100.0
No	0	0	0	0	0.0
Total	41	43	40	124	100.0
Action taken					
No action	39	42	36	117	94.4
Uprooting infected plant at early disease stage	0	0	4	4	3.2
Dried ground neem leaves application	0	1	0	1	0.8
Wood ashes application	2	0	0	2	1.6
Total	**41**	**43**	**40**	124	**100.0**
Willingness to adopt new varieties					
Yes	41	43	39	123	99.2
No	0	0	1	1	0.8
Total	**41**	**43**	**40**	124	**100.0**

Source: Household survey data.

Table 2.8: Cercospora leaf spot disease survey in the study area.

S/No	District	Village name	Fields surveyed	Percentage CLD_1	Percentage CLD_2	Overall incidence
1	Bahi	Ilindi	1	0	0	0
2	Bahi	Ilindi	2	40	60	50
3	Bahi	Ilindi	3	25	25	25
4	Bahi	Ilindi	4	0	0	0
5	Bahi	Ilindi	5	37.5	62.5	50
6	Bahi	Kigwe	1	45	55	50
7	Bahi	Kigwe	2	40	60	50
8	Bahi	Kigwe	3	0	0	0
9	Bahi	Kigwe	4	10	20	15
10	Bahi	Kigwe	5	30	70	50
11	Dodoma municipal	Hombolo makulu	1	0	0	0
12	Dodoma municipal	Hombolo makulu	2	12.5	17.5	15
13	Dodoma municipal	Hombolo makulu	3	0	0	0
14	Dodoma municipal	Hombolo makulu	4	0	0	0
15	Dodoma municipal	Hombolo makulu	5	0	0	0
16	Dodoma municipal	Zepisa	1	10	25	17.5
17	Dodoma municipal	Zepisa	2	0	0	0
18	Dodoma municipal	Zepisa	3	0	0	0
19	Dodoma municipal	Zepisa	4	0	0	0
20	Dodoma municipal	Zepisa	5	20	30	25
21	Kongwa	Ndulugumi	1	20	25	22.5
22	Kongwa	Ndulugumi	2	17.5	17.5	17.5
23	Kongwa	Ndulugumi	3	0	0	0
24	Kongwa	Ndulugumi	4	0	0	0
25	Kongwa	Ndulugumi	5	47.5	52.5	50
26	Kongwa	Laikala	1	0	0	0
27	Kongwa	Laikala	2	0	0	0
28	Kongwa	Laikala	3	22.5	27.5	25
29	Kongwa	Laikala	4	0	0	0
30	Kongwa	Laikala	5	15	35	25

Source: Field survey for Cercospora leaf spot disease incidence.

CLD1%= percentage of the samples infected with CLD during the first survey, CLD2%= percentage of the samples infected with CLD during the second survey

2.5 Discussion

The majority (83.8%) of the respondents engaged in groundnuts production were aged between 21- 60 years old, while very few were above 60 years old (Table 2.1). These findings are similar to what was reported by Akudugu et al. (2012). The majority (72.6%) of the groundnut farmers were males. Furthermore, results show that, most of the respondents (96.8%) had attended school. This implies that, the level of education of these farmers allows the extension service providers to communicate new technology both orally and in written documents. Generally, education is thought to create a favourable mental attitude for the acceptance of new practices, especially information and management-intensive practices (Caswell et al., 2001; Ehler and Bottrell, 2000). Groundnut was the leading crop among other crops grown by farmers in the study area for three consecutive production seasons from 2012 to 2015 (Table 2.2). Other crops grown were maize and sorghum. The current study findings are in accordance with a study by Upadhyaya et al. (2006) which found that groundnut is one of the important crops for both subsistence and commercial agriculture in semi-arid areas such as the Dodoma region.

The majority of the farmers in the study area grow primarily landraces from seeds, which they saved from previous seasons. Only a few farmers from Bahi, Dodoma municipal and Kongwa districts respectively, were growing improved cultivars of groundnuts for two consecutive production seasons from 2012 to 2014 (Table 2.3). The high rate of use of landraces can probably be attributed to the unavailability of improved groundnut cultivars with farmers' preferred traits. The low level of adoption of improved groundnut cultivars could also be attributed to lack of an efficient extension service. The seed sources commonly used by farmers in the study area were farmers' own saved seed, seed purchased from other farmers, seed purchased from local market, acquired free from relatives or fellow farmers, or from research institutions (Table 2.4). The results indicate that an informal seed system dominates the area. Only farmers in the Bahi district accessed seeds from extension staff and researchers, while in other districts farmers relied entirely on informal community seed system. This could have been due to lack of extension and the absence of a good seed multiplication system for the improved cultivars. FAOSTAT (2011) reported that seed recycling leads to a decline in groundnut production. Mangasini et al. (2014) reported that, most of the groundnut farmers have limited access to extension services and high yielding groundnut varieties.

Drought was the major constraint in groundnut production as was reported by most (95.4%) of the smallholder farmers. This finding agrees with a study by Kimmins et al. (1999), which found that drought and climatic variability contributing to declining groundnut productivity. Poor soil fertility was the second major constraint in groundnut production reported.

Diseases were mentioned by many farmers as one of the main constraints. Diseases of groundnut reduce yield and quality of grains and increase the cost of production in many groundnut growing areas (Wynne et al., 1992). A high disease pressure accounts for large yield losses, food insecurity and a reduction of the farm households' income. Additional constraints reported included seed availability (26.4%) and poor cultivars (22.9%). The limited availability of improved seeds to the farmers results in low productivity levels and emphasizes the need for a strong crop improvement program and a well-managed groundnut seed system.

Farmers mentioned the lack of good markets for their groundnut as one of their constraints and mentioned that they are often forced to use middlemen, resulting in lower prices for their product The traders, on the other hand, faced constraints such as poor quality groundnut grains, lack of a reliable market and the fluctuation in the quantity supplied by farmers. The processors were often constrained by the lack of seeds (i.e. colour and size), the low quantity supplied by farmers, the small and unreliable market for their finished products the cost of packaging and the lack of capital.

Farmers mentioned high yield, high oil content, tolerance to diseases and drought as important variety traits. In addition, characteristics such as early maturity, good taste, large seed size, threshability and high number of seeds per pod were also mentioned. Birru et al. (2005) reported that farmers' variety selection criteria largely depend on the importance of the crop in the farming system and their uses. Bucheyeki et al. (2008) reported that, in Tabora, Tanzania, farmers prefer groundnut varieties with high yield, large seed size and resistance to diseases. Furthermore, Ndjeunga et al. (2010) reported in their study on farmer preferences for groundnut traits in West Africa, that yield related traits were very important in varieties preferred by farmers.

All farmers interviewed had seen Cercospora leaf spot disease (CLD) in their fields. This implies that the disease was very common and rampant in the study area. A similar observation was made by Brandenburg (2003) who stated that, CLD incidence was 100% in all groundnut

growing regions in northern Ghana. A high disease pressure accounts for great losses in crop production, food insecurity and lowering of farming households' income.

The majority of the farmers reported that they took no action even if they observed CLD in their farms, though a few reported that they uprooted the infected plants at an early stage, or applied wood ashes to infected plants. However, it seems that the farmers have no efficient ways of controlling the disease within the study area. These findings are similar to earlier report by Nutsugah et al. (2007.) in their study on control measures of CLD in northern Ghana.

The majority of the farmers were ready to adopt new varieties if developed. This implies that, many farmers are aware of the problems and effects of not using improved technologies in solving the groundnut production problems, which have been the cause of low outputs and income. The study findings are in accordance to what was reported by Bucheyeki et al. (2008) namely that, farmers are receptive to new technologies that have an added advantage over their current existing technologies.

2.6 Conclusion

The study found out that, smallholder famers in the study area prefers groundnut varieties with erect growth habit because of the easiness of harvesting as compared to runner type of groundnut varieties which needs a lot of digging during harvesting. The farmers prefer brown coloured seeds because they do not stain the food in which it is used as an ingredient as opposed to red coloured seeds which if not removed the testa it will stain the food red and make it unattractive. Farmers prefer groundnut varieties with high oil content because the higher the oil content the softer the groundnut and vice versa. In addition, the farmers prefer groundnut varieties, which are high yielding, resistant to diseases and tolerant to drought and other abiotic. On the other hand traders and processors prefer groundnut varieties with medium to big sized seeds, resistant to disease, pests and tolerant to drought to have good market and processing quality and thereby, fetch a high.

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Chapter 3: Evaluation of Tanzanian and introduced groundnut germplasm for yield and its component traits, and reaction to Cercospora leaf spot diseases

Abstract

Groundnuts cultivated in the semi-arid tropics are often exposed to both biotic and abiotic stresses such as diseases, low rainfall and high temperatures during the critical stages of flowering and pod development. These harsh growing conditions affect the productivity of the crop. This study evaluated 84 groundnut genotypes from the Tanzania gene bank, ICRISAT-Malawi, smallholder farmers and the local market for yield and Cercospora leaf spot disease resistance in order to select promising parents for further breeding. The experiment was conducted in two growing seasons, namely 2014/2015 and 2015/16, at three sites *viz*. the Hombolo and Makutupora agricultural research stations, and the Bihawana farmers training centre, in Dodoma, Tanzania. The groundnut genotypes were planted in an alpha lattice design (12x7) with two replications. Inoculation to induce Cercospora leaf spot diseases was done at 10 and 45 days after emergence. The study revealed significant seasonal differences among groundnut genotypes for days to 50% flowering (DFL), number of mature pods per plant (NPP) and hundred seed weight (HSW). Genotypes differed significantly across sites for DFL and seed yield (SY). The significant season by site interactions were observed for NPP. Further, Cercospora leaf spot disease severity among genotypes was significantly different across sites and seasons. Furthermore, the results from broad sense heritability and genetic advance studies showed the preponderance of additive genes effect, and thus selection in early generations can be used in improving groundnut SY and CLD tolerance. Therefore, the current study recommended genotypes ICGV SM 96714, ICGV 6022, ICGV 6057, TZA 2426, Local Makulu, ICGV SM 07539, TZA 245, TZA 4280, KAKOMA, ICGV SM 07508, TZA 534, TZA 2444, TZA 2270, TZA 121, TZA 157, TZA 2498, TZA 3786, TZA 4390, TZA 4261, TZA 667 and TZA 2518 for use in further breeding programme due to their early days to flowering, high number of mature pods per plant, pod yield, hundred seed weight, seed yield and low Cercospora leaf spot disease score.

Key words: Cercospora leaf spot**,** broad sense heritability, genetic advance, groundnut (*Arachis hypogea* L.), yield, yield components.

3.1 Introduction

Yields of groundnut (*Arachis hypogaea L.*) are generally low in developing countries compared to developed countries due to biotic and abiotic factors, including diseases (Janila et al., 2013). Thakur et al. (2012) indicated that Cercospora leaf spot diseases (CLD) are the major diseases of groundnut and cause yield reduction of 50% or more. Macedo-Nobile et al. (2008) indicated that early leaf spot disease caused by *Cercospora arachidicola* Hori and late leaf spot disease caused by *Cercospora personatum* [(Berk. and Curt) Deighton] are the most destructive diseases in groundnut, and most commercial groundnut varieties are not resistant to the fungi. According to Walls and Wynne (1985), CLD were reported to be the major constraint to groundnut production causing yield loss of up to 70% worldwide where fungicides are not applied to control the disease. Fungicides can be applied to control leaf spot and reduce yield loss, but fungicide utilization at recurrent periods is expensive. A 10% reduction in yield was reported to be attributed to leaf spot epidemics irrespective of the use of six to eight chemical applications per crop cycle by most farmers (Alderman and Nutter, 1994).

In Tanzania groundnut cultivation dates back to 1946 when the United Africa Company, came up with an idea for the country to cultivate groundnut, so as to produce vegetable oils. Largely, the need was to have an exclusive large-scale commercial production sector that would be state managed for export, although household smallholder production of the crop, which could be expanded and/or improved for household food and income earning, was in existence. The first sites for cultivation were in Kongwa (Dodoma), Urambo (Tabora) and Nachingwea (Mtwara), where local people were already cultivating groundnuts (Ramadhan et al., 2002). The groundnut scheme failed in late 1950s, and after independence in 1961 up to 1970s, research on groundnuts lacked cohesion.

In 1978, the Oilseeds Research Project was started and included groundnuts, sesame and sunflower. Twelve varieties of groundnuts have been released to date of which three varieties, namely Mangaka 09, Mnanje 09 and Masasi 09, are tolerant to early leaf spot but susceptible to late leaf spot, while Nachingwea 09 and Naliendele 09 are susceptible to both CLD diseases (Mponda et al., 2012). However, these varieties have not been widely adopted by smallholder farmers, probably because they lack key traits; hence, CLD susceptible landraces are still commonly grown. There is a wide range of landraces currently grown by farmers in the country. Some of these landraces may already carry genes for resistance to CLD. There is a need for breeders to develop groundnut varieties that combine

resistance to CLD with agronomic traits preferred by stakeholders in the groundnut value chain, such as erect growth habit, high yield, medium to large seed size, early maturity and high oil content, in addition to other traits. Because most groundnut smallholder farmers in Tanzania are relatively poorly resourced, they do not use any form of fungicide to control leaf spot diseases. Host plant resistance has been preferred to other methods in leaf spots management due to its cost effectiveness and environmental friendliness (Jordan et al., 2013). However, reports indicate that disease resistance in groundnut is mostly associated with low yield, poor pod formation, poor kernel characteristics and late maturity, making breeding for leaf spot resistance difficult (Singh et al., 1997; Subrahmanyam et al., 1995). Groundnut genotypes, which combine tolerance to the diseases, with a high yield potential are beneficial to growers and can be used by breeders for further improvement through breeding (Gaikpa et al., 2015). Consequently, the identification of good sources of resistance to CLD and high yield is of paramount importance for groundnut breeding programmes. Therefore, this study evaluated a large germplasm collection for yield and yield related traits under Cercospora leaf spot disease infection (both early and late combined).

3.2 Material and methods

3.2.1 Plant materials

The study included 84 groundnut genotypes comprising of local and introduced varieties. The genotypes were collected from various sources, namely, farmers' fields in Tanzania, local markets, the Tanzania National Plant and Genetic Resource Centre (NPGRC), and the International Crop Research Institute for Semi-arid Tropics (ICRISAT-Malawi) as shown in Table 3.1. The germplasm acquired from ICRISAT was reported to be CLD resistant. The Nachingwea groundnut variety, which is widely grown in Tanzania, was used as a susceptible control. Local varieties were included because of their wide adaptability to various growing environments, and because they have agronomic and other traits preferred by farmers.

Table 3.1: List and sources of eighty-four groundnut genotypes used in the study.

Entry number	Accession number	Botanical group	source	Entry number	Accession number	Botanical group	Source
1	BAKA	Spanish	ICRISAT-Malawi	43	TZA 2270	Spanish	NPGRC
2	CG 7	Virginia	ICRISAT-Malawi	44	TZA 230	Spanish	NPGRC
3	CHITALA	Spanish	ICRISAT-Malawi	45	TZA 241	Spanish	NPGRC
4	ICG 405	Valencia	ICRISAT-Malawi	46	TZA 2417	Spanish	NPGRC
5	ICG 6022	Virginia	ICRISAT-Malawi	47	TZA 2421	Valencia	NPGRC
6	ICGV 07533	Spanish	ICRISAT-Malawi	48	TZA 2426	Spanish	NPGRC
7	ICGV 07544	Spanish	ICRISAT-Malawi	49	TZA 2444	Spanish	NPGRC
8	ICGV 6057	Virginia	ICRISAT-Malawi	50	TZA 2471	Spanish	NPGRC
9	ICGV SM 01706	Virginia	ICRISAT-Malawi	51	TZA 248	Spanish	NPGRC
10	ICGV SM 03557	Virginia	ICRISAT-Malawi	52	TZA 2485	Spanish	NPGRC
11	ICGV SM 03560	Virginia	ICRISAT-Malawi	53	TZA 2488	Valencia	NPGRC
12	ICGV SM 05521	Valencia	ICRISAT-Malawi	54	TZA 2497	Valencia	NPGRC
13	ICGV SM 07504	Valencia	ICRISAT-Malawi	55	TZA 2498	Valencia	NPGRC
14	ICGV SM 07508	Valencia	ICRISAT-Malawi	56	TZA 2518	Spanish	NPGRC
15	ICGV SM 07510	Valencia	ICRISAT-Malawi	57	TZA 254	Spanish	NPGRC
16	ICGV SM 07512	Valencia	ICRISAT-Malawi	58	TZA 2737	Spanish	NPGRC
17	ICGV SM 07518	Valencia	ICRISAT-Malawi	59	TZA 285	Spanish	NPGRC
18	ICGV SM 07536	Valencia	ICRISAT-Malawi	60	TZA 3222	Spanish	NPGRC
19	ICGV SM 07539	Valencia	ICRISAT-Malawi	61	TZA 3406	Spanish	NPGRC
20	ICGV SM 07556	Valencia	ICRISAT-Malawi	62	TZA 3783	Valencia	NPGRC
21	ICGV SM 07558	Valencia	ICRISAT-Malawi	63	TZA 3786	Valencia	NPGRC
22	ICGV SM 09511	Valencia	ICRISAT-Malawi	64	TZA 3806	Spanish	NPGRC
23	ICGV SM 95714	Spanish	ICRISAT-Malawi	65	TZA 3817	Spanish	NPGRC

Entry number	Accession number	Botanical group	source	Entry number	Accession number	Botanical group	Source
24	ICGV SM 96714	Spanish	ICRISAT-Malawi	66	TZA 3836	Spanish	NPGRC
25	JL-24	Spanish	ICRISAT-Malawi	67	TZA 4188	Spanish	NPGRC
26	KAKOMA	Spanish	ICRISAT-Malawi	68	TZA 4228	Virginia	NPGRC
27	Local (77)	Spanish	Saba saba Market	69	TZA 4237	Virginia	NPGRC
28	Local (Makulu)	Valencia	Hombolo village	70	TZA 4261	Virginia	NPGRC
29	Local (Miembeni)	Spanish	Miembeni Market	71	TZA 4280	Virginia	NPGRC
30	MANGAKA	Spanish	ICRISAT-Malawi	72	TZA 4291	Virginia	NPGRC
31	MNANJE	Virginia	ICRISAT-Malawi	73	TZA 4340	Virginia	NPGRC
32	Nachingwea	Virginia	ICRISAT-Malawi	74	TZA 4370	Virginia	NPGRC
33	PENDO	Spanish	ICRISAT-Malawi	75	TZA 4390	Virginia	NPGRC
34	NSINJIRO	Virginia	ICRISAT-Malawi	76	TZA 4391	Virginia	NPGRC
35	TZA 121	Valencia	NPGRC	77	TZA 4635	Spanish	NPGRC
36	TZA 142	Spanish	NPGRC	78	TZA 5212	Spanish	NPGRC
37	TZA 157	Valencia	NPGRC	79	TZA 534	Virginia	NPGRC
38	TZA 165	Spanish	NPGRC	80	TZA 549	Spanish	NPGRC
39	TZA 182	Spanish	NPGRC	81	TZA 597	Spanish	NPGRC
40	TZA 185	Spanish	NPGRC	82	TZA 613	Virginia	NPGRC
41	TZA 214	Spanish	NPGRC	83	TZA 664	Virginia	NPGRC
42	TZA 227	Spanish	NPGRC	84	TZA 667	Virginia	NPGRC

ICRISAT = International Crop Research Institute for Semi-Arid Tropics; NPGRC =National Plant Genetic Resource Centre of Tanzania

3.2.2 Inoculum preparation

Inocula (conidia) of *C. arachidicola* and *C. personatum* were collected from infected fields at Hombolo, Kigwe, Zepisa, and Laikala villages of the Dodoma region. The villages are main groundnut growing areas in which productivity is mostly constrained by the CLD disease. During the survey, infected plants were identified (Figure 3.1), uprooted and then sent to the pathological laboratory of the African Seed Health Centre at Sokoine University of Agriculture for fungal isolation. Infected leaves were suspended in sterile distilled water, and infected lesions were subsequently cut into small pieces and incubated in petri dishes

containing V8 juice as the growth media for *Cercospora spp* under aseptic condition on a laminar flow bench. The petri dishes were then incubated in a growth chamber for seven days, thereafter inocula (conidia) were collected from the petri dishes by washing the conidia with sterile distilled water, after which a few drops of a wetting agent (Tween 80) were added to the culture to improve its sticking capacity when inoculating.

3.2.3 Inoculation of Cercospora leaf spot diseases in groundnut genotypes

Before inoculation, the inoculum concentration was adjusted to approximately 50 000 conidia per ml^{-1} of solution. Inoculations (Figure 3.2) were carried out at 10 days and 45 days after emergence to capture both early and late Cercospora leaf spot disease infestation.

Figure 3.1: Field identification of symptoms of Cercospora leaf spot diseases

Figure 3.2: *Cercospora* fungi inoculation in the field trial

3.3 Study site, experimental design and trial management

Trials were established at three sites in the Dodoma region, central Tanzania, namely the Hombolo (5^0 54' S, 35^0 57' E) and the Makutupora (5^0 58' S, 35^0 46.033' E) research stations, and the Bihawana (6^0 2' 717'' S, 35^0 6' 397'' E) farmers training centre (Figure 3.3). The experiments were laid out in an alpha lattice design (12 x 7) with two replications in two consecutive growing seasons of 2014/15 and 2015/16. The groundnuts were grown in plots of 1.5 x 1 m long with inter-row and intra-row spacing of 0.5 and 0.1 m, respectively. Conventional tillage was done before planting, and this was followed by regular hand weeding. During prolonged dry spells, watering was done to supplement moisture, no fertilizer was used. Ridging, harvesting and post-harvest practices were done as recommended.

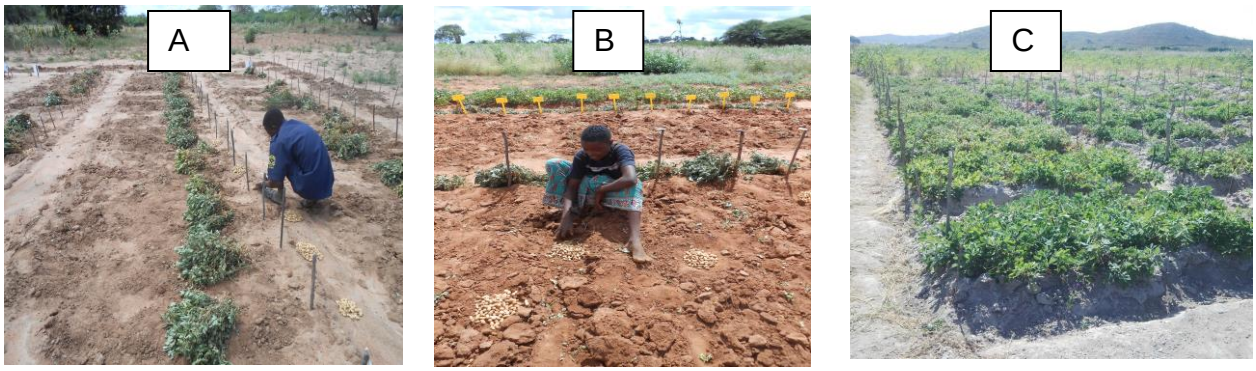

Figure 3.3**:** Screening plots: A is Makutupora research station; B is Hombolo research station; C is Bihawana farmers' training centre

3.4 Data collection

Data on Cercospora leaf spot disease score (CLD score) were recorded from the symptoms (Figure 3.4) on individual plants grown in the middle rows of each plot at 28, 35 and 42 days after first inoculation. The ratings for both early and late leaf spot were carried out using 1 - 9 visual canopy rating scale, where 1 represent highly resistant (green and healthy leaves without leaf spot) and 9 highly susceptible (dead and defoliated plants) and CLD severity (CLDS) was rated at 42 days after first inoculation (Table 3.2) as suggested by Subrahmanyam et al. (1995).

Yield and yield- related data collected included days to emergence (DTE), days to 50% flowering (DFL), length of reproductive branches (LRB) (cm), number of pods per plant (NPP), number of seeds per pod (SPP), 100 seed weight (HSW) and seed yield (SY)(g) as suggested by IBPGR; ICRISAT (1985).

Figure 3.4: **A**= Early leaf spot; **B**= Late leaf spot disease symptoms

Table 3.2: Cercospora leaf spot disease scale.

Score	Description of the disease	Disease severity (%)
1	No disease	0
2	Lesions largely on lower leaves; no defoliation	1-5
3	Lesions largely on lower leaves; very few lesions on middle leaves; defoliation of some leaflets evident on lower leaves.	6-10
4	Lesions on lower and middle leaves, but severe on lower leaves; defoliation of some leaflets evident on lower leaves	11-20
5	Lesions on all lower and middle leaves, over 50% of the lower leaves defoliated	21-30
6	Lesions severe on lower and middle leaves; lesions on top leaves but less severe; extensive defoliation of lower leaves; defoliation of some leaflets evident on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and some middle leaves.	41-60
8	Defoliation of all lower and middle leaves; lesions severe on top leaves and some defoliation of top leaves evident.	61-80
9	Defoliation of almost all leaves leaving bare stems; some leaflets may be present, but with severe leaf spots.	81-100

Source: Subrahmanyam et al. (1995)

3.5 Data analysis

The data on CLD score were used to calculate the area under disease progress curve (AUDPC) as suggested by Campbell and Madden (1990). Thereafter, all data were assembled in Microsoft Excel and subjected to the analysis of variance (ANOVA) using procedure of GENSTAT 14th Edition (Payne et al., 2011). The alpha-lattice design was applied to evaluate the main and interaction effects of the disease on the groundnut genotypes. Treatment means ($P < 0.05$) were separated using the Fisher's Least Significant difference procedure. The linear statistical model used was:-

$$Y_{ijk} = \mu + \tau_i + \beta_j + \tau\beta_{ij} + \gamma_k + \tau\gamma_{ik} + \beta\gamma_{jk} + \tau\beta\gamma_{ijk} + \varepsilon_{ijk}$$

Where: μ =grand mean, τ_i = effect due to i^{th} genotype, β_j = effect due to j^{th} environment γ_k = effect due to k^{th} season and ε_{ijk} = uncontrolled variation associated with i^{th} genotype j^{th} environment and k^{th} season

Further analysis was done to calculate the area under disease progress curve (AUDPC) as suggested by Campbell and Madden. (1990):

$$A_k = \sum_{i=1}^{N_i-1} \frac{(y_i + y_{i+1})}{2}(t_{i+1} - t_i)$$

Where: t_i = the time interval between two recording time points; y_i = associated measures of the disease level.

The analysis of variance components were performed using SAS 9.4 software (SAS, 2012) and thereafter, variance components were used to calculate the phenotypic coefficient of variations (GCV) and genotypic coefficient of variations (GCV) as suggested by Singh and Chaudhury (1985). The genetic advance (GA) was calculated according to Johnson et al. (1955). The genetic advance as percentage of mean (GAM) was calculated as suggested by Shukla et al. (2006). The formulae used were as follows;-

PCV% = [Phenotypic variance/x] x 100

GCV% = [Genotypic variance/x] x 100

GA = [Genotypic variance/Phenotypic variance] x K

GAM% = [GA /x] x 100

Where: GCV% = Genotypic Coefficient of variation; PCV % = Phenotypic Coefficient of variation; GA=Genetic Advance; GAM= Genetic Advance as percentage of Mean, x = the pooled mean from general analysis of variance, K = selection differential, a constant (z/p) at 5% which is a value of 2.06.

3.6 Results

3.6.1 Analysis of variance for Cercospora leaf spot disease score, yield and yield related traits

The analysis of variance for Cercospora leaf spot disease severity and agronomic performance of groundnut genotypes are presented in Table 3.3. Groundnut genotypes differed significantly ($p< 0.001$) in days to 50% flowering (DFL), number of mature pods per plant (NPP), hundred seed weight (HSW), seed yield (SY), CLD severity (CLDS) and area under disease progress curve (AUDPC). The sites only differed significantly for HSW ($P<0.05$). Season and site interacted significantly for SY ($p<0.05$) and AUDPC ($p<0.01$). The genotype x season interaction was significant ($P<0.001$) for DFL, NPP, HSW and AUDPC. Genotypes interacted significantly with site for DFL ($p<0.05$) and SY ($p<0.001$). The genotypes, sites and season interacted significantly for NPP ($p<0.001$).

Table 3.3: Analysis of variance for Cercospora leaf spot disease severity, yield and selected yield related traits across sites and seasons.

Source of variation	DF	DFL	NPP	CLD S	HSW	SY	AUDPC
Replication	1	48.9	36.6	111.3	49.7	124	10.9
Season	1	9.2^{ns}	817.0^{ns}	2558.5^{ns}	248.9^{ns}	113774^{ns}	21.4^{ns}
Error	1	59.3	89.7	265.6	473.6	245085	447.0
Site	2	102.9^{ns}	143.3^{ns}	708.4^{ns}	18439.8*	780502^{ns}	400.5^{ns}
Season x site	2	1.0^{ns}	919.7^{ns}	2950.6^{ns}	602.9^{ns}	48338*	131.7**
Error	4	17.4	108.3	393.5	549.1	27408	49.1
Genotypes	83	52.0***	106.8***	350.4***	1019.5***	382790***	514.2***
Season x genotype	83	13.7***	10.2***	38.5^{ns}	81.9***	8251^{ns}	39.9***
Site x genotypes	166	9.7*	6.2^{ns}	27.7^{ns}	15.8^{ns}	12262***	44.0^{ns}
Season x site x genotype	166	8.7^{ns}	9.5***	32.2^{ns}	18.6^{ns}	9647^{ns}	18.6^{ns}
Error	498	7.3	6.1	29.9	18.2	9190	22.2
Total	1007						

*, **, *** = significantly different at 0.05; 0.01 and 0.001 probability levels; ns = non-significant; DF = degrees of freedom; DFL= days to 50% flowering; NPP = number mature of pods per plant; CLDS = Cercospora leaf spot disease severity; SY= seed yield; HSW = hundred seed weight and AUDPC=area under disease progress curve.

Means for CLD severity, and yield and yield related traits of the 84 groundnut genotypes evaluated across three sites and two seasons are presented in Table 3.4. The DFL ranged from 37 to 48 days with a mean of 42 days after emergence. The LRB ranged from 19.4 to 36.8 with a mean of 27.9 cm. The NPP ranged from 16.8 to 30.5 with a mean of 21.5 pods per plant. The SPP ranged from 1.0 to 3.7 with a mean of 2.3 SPP. The HSW ranged from 25.4 to 56.6 g with a mean of 37.6 g. The SY ranged from 204.3 g to 1138.3 with a mean of 563.5 g. The CLDS ranged from 16 to 39% with a mean of 31%. The AUDPC ranged from 35.9 to 63.9 with a mean of 53.6.

Table 3.4: Means of agro-morphological characters and Cercospora leaf spot disease severity for groundnut genotypes evaluated across sites and seasons.

Genotypes	DFL	LRB	CLDS	NPP	HSW	SPP	SY	AUDPC
BAKA	40	28.2	32.5	20.4	28.2	2.00	454.7	51.0
CG 7	41	22.8	33.3	20.0	26.1	2.33	521.8	50.8
CHITALA	42	23.0	34.2	19.4	29.9	2.00	432.0	55.4
ICG 405	40	32.0	32.5	21.3	53.3	2.83	665.2	51.3
ICG 6022	42	22.7	18.3	21.4	52.7	3.00	714.2	39.7
ICGV 07533	41	32.3	31.7	21.0	38.6	2.83	660.4	53.1
ICGV 07544	41	26.2	31.7	21.5	38.3	2.00	479.2	54.3
ICGV 6057	40	28.8	19.6	21.0	53.3	3.00	701.4	41.1
ICGV SM 01706	40	26.8	30.8	21.2	40.8	2.00	471.6	56.0
ICGV SM 03557	40	25.5	33.3	20.3	37.9	2.42	546.0	57.5
ICGV SM 03560	42	28.7	32.5	20.3	38.4	2.50	546.9	56.0
ICGV SM 05521	39	23.5	31.7	20.8	38.1	2.75	635.3	54.5

Genotypes	DFL	LRB	CLDS	NPP	HSW	SPP	SY	AUDPC
ICGV SM 07504	39	20.0	32.5	25.8	52.6	3.00	859.2	46.7
ICGV SM 07508	41	24.5	17.9	28.3	53.8	3.00	945.8	35.9
ICGV SM 07510	43	20.6	22.9	26.0	40.2	2.58	752.1	51.6
ICGV SM 07512	42	31.9	30.0	22.3	42.0	2.42	601.1	54.0
ICGV SM 07518	41	32.3	31.7	21.0	38.8	2.83	661.5	56.6
ICGV SM 07536	39	26.4	27.1	23.8	40.3	2.75	723.5	51.6
ICGV SM 07539	41	25.1	23.8	25.5	54.8	3.00	850.5	41.1
ICGV SM 07556	41	25.7	28.8	22.9	38.7	2.00	509.7	56.0
ICGV SM 07558	43	25.5	31.7	21.7	39.3	2.75	655.7	56.6
ICGV SM 09511	41	19.4	18.8	29.1	53.6	3.00	869.8	43.5
ICGV SM 95714	39	22.6	25.8	24.2	42.0	2.42	649.4	50.8
ICGV SM 96714	37	25.5	16.3	29.8	53.2	3.00	994.6	37.3
JL-24	40	28.1	35.8	18.9	29.8	2.17	451.5	51.0
Kakoma	41	23.1	18.6	20.6	51.4	3.00	686.3	40.0
Local 77	43	20.3	35.8	18.3	35.4	2.00	408.7	63.0
Local Makulu	39	31.5	18.8	27.8	53.8	3.67	1138.3	46.4
Local Miembeni	45	28.5	33.3	20.2	38.7	2.50	560.0	56.6
Mangaka	41	28.7	33.8	20.6	30.8	2.00	457.4	60.1
Mnanje	40	27.5	34.2	19.8	30.6	2.00	439.0	53.1
Nachingwea	39	25.5	33.3	19.9	29.5	2.67	589.9	63.3
Pendo	40	36.8	24.2	25.3	54.8	2.00	433.7	46.4
Nsinjiro	40	26.1	33.3	19.7	26.0	2.50	705.0	54.0
TZA 121	45	28.8	37.5	17.8	25.7	3.00	894.8	49.9
TZA 142	42	32.3	36.7	18.8	25.4	2.00	417.4	61.3
TZA 157	48	26.7	35.8	18.8	27.0	3.00	828.1	50.5
TZA 165	44	32.9	35.0	19.2	28.4	2.00	426.2	60.7
TZA 182	43	27.8	35.0	19.0	32.0	2.00	423.3	59.5
TZA 185	41	33.5	34.2	19.9	43.0	2.00	443.6	57.2
TZA 214	44	27.0	34.2	20.1	31.5	2.00	447.1	60.4
TZA 227	44	24.7	37.5	18.2	29.4	1.00	204.3	62.1
TZA 2270	44	26.8	35.0	19.5	30.7	3.00	851.7	49.3
TZA 230	44	30.5	32.5	20.6	29.8	2.00	459.0	61.8
TZA 241	44	26.7	34.2	19.6	29.7	1.50	324.7	58.6
TZA 2417	45	27.8	33.3	19.2	37.0	1.33	279.6	58.3
TZA 2421	38	29.0	24.2	25.0	52.9	1.83	501.1	47.3
TZA 2426	42	33.7	19.6	26.8	40.7	3.00	895.6	46.1
TZA 2444	41	35.8	27.1	23.5	42.5	2.50	848.2	46.4
TZA 2471	43	32.0	32.1	20.7	38.6	2.00	460.7	58.0
TZA 248	45	27.9	32.5	20.5	34.2	2.00	457.0	61.0
TZA 2485	43	27.6	32.5	20.3	35.8	2.00	419.9	58.9
TZA 2488	42	30.0	30.8	21.4	35.2	2.17	515.5	56.9

Genotypes	DFL	LRB	CLDS	NPP	HSW	SPP	SY	AUDPC
TZA 2497	43	32.9	30.8	21.1	34.4	2.00	469.6	61.5
TZA 2498	41	29.8	35.8	19.6	35.2	2.83	820.0	58.3
TZA 2518	37	25.8	22.3	28.9	56.6	3.00	964.6	44.3
TZA 254	41	31.5	23.6	27.7	52.7	3.00	923.2	44.6
TZA 2737	43	25.3	29.2	21.8	31.8	1.67	404.5	55.7
TZA 285	43	26.4	31.7	20.8	30.9	2.00	461.7	55.7
TZA 3222	43	30.6	35.0	19.1	27.8	2.00	425.7	59.8
TZA 3406	43	27.5	35.8	18.9	27.5	2.00	421.6	60.1
TZA 3783	42	28.0	35.0	19.3	29.0	2.17	460.5	58.0
TZA 3786	43	28.3	33.3	19.9	30.1	2.67	795.4	51.0
TZA 3806	45	32.3	34.2	19.8	28.9	2.00	441.6	59.8
TZA 3817	44	32.6	34.2	19.9	28.9	1.50	341.4	57.8
TZA 3836	43	29.5	31.7	20.3	30.2	2.00	452.5	47.8
TZA 4188	43	30.8	32.5	20.8	36.2	2.00	463.4	58.3
TZA 4228	44	25.1	32.5	19.7	35.0	2.00	437.5	58.0
TZA 4237	46	27.5	33.3	20.4	36.7	2.00	455.1	60.7
TZA 4261	40	27.1	23.8	24.4	53.0	2.50	879.1	46.7
TZA 4280	38	33.1	22.3	30.5	55.2	2.50	943.3	45.5
TZA 4291	42	29.9	27.9	23.2	38.6	2.00	515.7	55.1
TZA 4340	42	26.0	29.6	22.0	37.6	2.00	489.8	56.9
TZA 4370	43	31.5	29.2	21.6	37.4	2.00	447.0	60.1
TZA 4390	43	30.7	28.8	22.6	37.9	3.00	753.5	47.0
TZA 4391	45	26.9	30.0	21.7	38.5	2.00	483.4	53.4
TZA 4635	45	21.2	30.0	21.8	35.2	2.00	492.9	56.3
TZA 5212	44	27.4	37.5	18.8	27.0	2.00	417.8	60.1
TZA 534	40	30.8	26.7	22.9	51.6	2.00	534.5	47.8
TZA 549	42	27.2	33.3	19.7	29.0	2.00	437.8	54.5
TZA 597	43	20.7	37.5	18.7	30.1	2.00	416.1	53.1
TZA 613	44	27.0	39.2	16.8	27.9	2.00	374.4	63.9
TZA 664	45	34.2	37.5	18.5	28.8	2.00	412.6	60.7
TZA 667	45	30.6	35.8	18.8	27.8	3.00	726.5	51.3
LSD	2.2	2.4	4.4	2.0	3.4	0.2	76.9	5.6
CV %	4.4	10.7	17.8	11.5	11.4	12.7	17.0	8.8
Grand mean	42.0	27.9	30.8	21.5	37.6	2.3	563.5	53.6
Minimum	37.0	19.4	16.3	16.8	25.4	1.0	204.3	35.9
Maximum	48.0	36.8	39.2	30.5	56.6	3.7	1138.3	63.9

*** = highly significant different at 0.001 probability level; ns= non-significant; DFL= days to fifty per cent flowering; LRB= length of reproductive branch; NPP = number of mature pods per plant; CLDS= Cercospora leaf spot disease severity; HSW= hundred seed weight; SY= seed yield; AUDPC= area under disease progress curve; CV= coefficient of variation; LSD= least significant difference.

3.6.2 Genetic variability among groundnut genotypes

Results of the phenotypic and genotypic coefficient of variations and genetic advance are presented in Table 3.5. The coefficient of variation of groundnut genotypes evaluated at three sites for two seasons at the phenotypic levels was relatively higher than at the genotypic level for the AUDPC (12.2 and 11.6), SY (34.1 and 33.7), HSW (24.4 and 23.5), SPP (21.3 and 21.1), NPP (13.6 and 13.1), LRB (10.2 and 8.0), DM (0.59 and 0.58) and DFL (4.3 and 3.7).

The highest heritability in the broad sense was recorded for DM (99.4%), SY (98.9%), SPP (98.8%), NPP (96.4%), AUDPC (95.0%), DFL (86.1%) and LRB (78.7%), respectively. In the present study the DM had the highest potential for genetic advance (2.05) followed by SY (2.04), SPP (2.04), HSW (1.99), NPP (1.99), AUDPC (1.96), DFL (1.77) and LRB (1.62), respectively.

Table 3.5: Genetic variability, heritability and genetic advance among groundnut genotypes.

TRAIT	PCV	GCV	GA	GAM	BSH
AUDPC	12.2	11.6	1.96	3.65	0.950
SY	34.1	33.7	2.04	0.36	0.989
HSW	24.4	23.5	1.99	5.29	0.965
SPP	21.3	21.1	2.04	88.48	0.988
NPP	13.6	13.1	1.99	9.24	0.964
LRB	10.2	8.0	1.62	4.40	0.787
DM	0.59	0.58	2.05	1.67	0.994
DFL	4.287512	3.693179	1.774444	3.727823	0.861381

AUDPC=area under disease progress curve; DFL=days to 50% flowering; DM= days to maturity; LRB=length of reproductive branch; NPP= number of mature pods per plant; SPP=number of seeds per pod; HSW=hundred seed weight; SY= seed yield; PCV=phenotypic coefficient of variation; GCV=genotypic coefficient of variation; GA= genetic advance; GAM= genetic advance as percentage of mean and BSH= broad sense heritability.

3.7 Discussion

Significant differences were observed among groundnut genotypes for CLDS and AUDPC. The response of groundnut genotypes to environmental adaptability and utilization of the available resources have been reported to vary significantly among genotypes (Weiss, 2000). The significance of the seasonal effect for AUDPC and CLDS could be attributed to the variation in the amount and distribution of rainfall, and temperature differences between

the seasons. The variation in AUDPC and CLDS among the genotypes could be attributed to the virulence of the pathogen, environmental conditions and the variation in the ability of the genotype to resist the infection. The significant interaction of groundnut genotypes with season for DFL, NPP and HSW and between genotypes with site for DFL and SY could be attributed to the combination effect of the differences in soil types, rainfall and temperatures across the sites.

Variation in DFL, NPP, DFL, HSW and SY among groundnut genotypes across sites has been reported in earlier studies (Janamatti et al., 1986; Prasad et al., 2000; Weiss, 2000; Chandrika et al., 2008; Patel et al., 2010; Bapuji et al., 2011; Narh et al., 2014; Zhao et al., 2015). Their results reported a synergistic effect of the amount and distribution of rainfall, and variations of temperature and soil types on groundnut yield and yield related components. They further reported variations in influence of these factors among groundnut genotypes. These variations suggest the possibility of selecting groundnut genotypes based on their performance across the environment or in a specific environment.

The selection criteria was based on the farmers' preference of groundnut variety which indicated brown coloured seed coat, erect growth habit, tolerance to diseases and drought, high yielding ability and early maturity as their major preferred traits (Chapter 2). From the study, the following genotypes; local Makulu, TZA 2518, TZA 4280, TZA 254, TZA 2426, TZA 121, TZA 4261, TZA 2270, TZA 2444, TZA 534, TZA 157, TZA 2498, TZA 3786, TZA 4390 and TZA 667 were selected for further breeding due to their early DFL, larger number of SPP and higher SY. Genotypes ICGV SM 07508, ICGV SM 96714, ICGV SM 09511, ICGV 6022, ICGV 6057, Kakoma and ICGV SM 07539 were selected for their tolerance to CLD and CLDS and used as the male parents (Chapter 5).

Comparison of seed yield and CLD resistance levels among Valencia, Virginia and Spanish showed significant variation. This indicated a variation in the genetic constitution for CLD resistance and SY performance. Comparison of the best ten CLD tolerant and high yielding genotypes found out that several Valencia (Local Makulu, ICGV SM 07508, TZA 121, ICGV SM 09511) and Spanish (ICGV SM 96714, TZA 2518, TZA 254 and TZA 2426) varieties combine a good tolerance to CLD and a high SY. Virginia varieties ICG 6022 and TZA 4261 had good CLD resistance and a high SY (Table 3.4).

The phenotypic coefficient of variation was relatively higher than the genotypic coefficient of variation for AUDPC, SY, HSW, SPP, NPP, LRB, DM and DFL. This was probably attributed to the dominant influence of the environmental condition on the expression of these traits. The influence of environments on expression of similar traits was also reported on chickpea (Joshi, 1972; Chandra, 1968) and in bambara groundnut (Makanda et al., 2009).

The high broad sense heritability and genetic advance for DM, SY, SPP, NPP, AUDPC, DFL, HSW and LRB indicated the predominance high genetic control. This indicated the possibility of improving these traits through selection in early generations. The traits may be used as the selection criteria for yield and CLD resistance improvement. The need of associating heritability and genetic advance in selection has been suggested by Katiyar et al. (1974) and Johnson et al. (1955).

3.8 Conclusion

The present study found significant variation in CLD tolerance, yield and yield related components among groundnut genotypes evaluated across the environments. Groundnut genotypes; ICGV SM 96714, ICGV 6057, TZA 2426, TZA 2444, TZA 121, TZA 157, TZA 2270, TZA 667, Local Makulu, ICG 6022, ICGV SM 07539, TZA 254, TZA 4280, TZA 4390, TZA 4261, Kakoma, ICGV SM 07508, TZA 534, TZA 2498, TZA 3786 and TZA 2518 were selected for their good performances on DFL, low CLDS, larger NPP, heavy HSW, small AUDPC and high SY. These are recommended as parents in future breeding programme. The outcome from broad sense heritability and genetic advance studies showed the preponderance of additive genes effect, and thus selection in early generations can be used in improving groundnut SY and CLD tolerance. Furthermore, evaluation of these genotypes in other agro-ecologies infected with CLD is required in developing lines with durable resistance to CLD and high yield.

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Chapter 4: Correlation, path-coefficient and cluster analyses of yield and yield-related traits and resistance to Cercospora leaf spot diseases in groundnut

Abstract

Groundnut (*Arachis hypogaea* L.) is one of the most important oilseed crops in Tanzania for food security and income generation. Despite its importance, the productivity of the crop is low. Information on the nature and magnitude of trait association between yield contributing characters and overall yield is a pre-requisite for crop improvement programmes. Hence, the present study was conducted to investigate correlation, path-coefficient and cluster analyses of yield, its related traits and the resistance to Cercospora leaf spot diseases. Eighty-four groundnut genotypes were planted in three locations for two seasons in Dodoma, Tanzania, to evaluate yield potential and reaction to Cercospora leaf spot diseases (CLD). Data on yield, yield contributing traits and CLD severity (CLDS) were collected and subjected to IBM SPSS to compute correlation coefficients, while MS Excel was used to calculate the direct and indirect effects of yield contributing characters via yield (path analysis). A cluster analysis to group genotypes according to their genetic similarities was performed by IBM SPSS following the Ward Linkage and Squared Euclidean Distance methods. The results showed a positive and significant association between days to 50% flowering (DFL) and days to maturity (DM). Furthermore, there was a positive association between days to maturity (DM) and CLDS and between CLDS with DFL. The number of mature pods per plant (NPP) was positively associated with seed yield (SY). The SY was positively correlated with DFL, DM, CLDS, length of reproductive branch (LRB), NPP and number of seeds per pod (SPP). The cluster analysis provided five different clusters, suggesting a high phenotypic diversity among groundnut genotypes, showing its usefulness in future hybridization and selection programmes for various agronomic traits and CLD resistance. Several genotypes from Cluster I (five genotypes), II (eight genotypes), III (seven genotypes) and IV (one genotype), with the lowest DFL, highest NPP and SY and lowest CLDS were selected for use in future breeding programmes.

Key words: Cercospora leaf spot disease, cluster analysis, correlation coefficient, groundnut, path coefficient.

4.1 Introduction

Yield is complex, quantitative character with low heritability and greatly influenced by environmental conditions. Various yield related components contribute to yield. As a result, indirect selection for yield using the yield related secondary traits could assist the breeder in improving productivity of the crop. Knowledge of the degree of association existing between yield and the yield components is very important during selection of genotypes for further breeding (Gomes and Lopes, 2005). In groundnuts, the pods are formed underground and unless association between external plant characteristics and yield are established, it may not be possible to effect proper selection of plants prior to harvest (Gomes et al., 2007).

The correlations can be better understood using a path analysis, which allows the partitioning of the correlations into direct and indirect effects, and is therefore a valuable tool in breeding programs of various crops (Vieira et al., 2007). Several studies have demonstrated the utility of a correlation analysis in groundnut selection (Santos et al., 2000). Furthermore, genetic diversity is the pre-requisite for a hybridization programme to obtain desirable genotypes. An understanding of the genetic diversity is essential to meet the diverse goals in plant breeding such as increased yield (Joshi and Dhawan, 1966), wider adoption, desirable quality and pest resistance (Nevo et al., 1982). According to Tomooka (1991), the evaluation of diversity is important in order to identify the sources of genes for particular traits within the available germplasm. Therefore, it is essential to know the genetic diversity of the existing genotypes before undertaking any crop improvement programme by grouping them according to genetic similarities. A cluster analysis is an appropriate method to be used in this study. The present study undertook correlation, path-coefficient and cluster analyses of yield, yield-related traits and resistance to Cercospora leaf spot diseases in groundnut.

4.2 Material and methods

4.2.1 Study site, experimental design and trial establishment

Trials were established at three sites namely the Hombolo (5^0 54' S, 35^0 57' E) and Makutupora (5^0 58' S, 35^0 46.033' E) research stations, and the Bihawana (4^0 12' S, 35^0 24' E) farmers training centre situated in Dodoma, central Tanzania. The experiment was laid out in an alpha lattice design (12 x 7) with two replications in two consecutive seasons of 2014/15 and 2015/16. The groundnuts were grown in the field plots of 1.5 x 1 m size with inter-row and intra-row spacing of 0.5 and 0.1 m respectively. Each plot had three rows each with 10 plants. Conventional tillage was done before planting; this was followed by regular

hand weeding. During prolonged dry spells, watering was done to supplement moisture, no fertilizer was applied. Ridging, harvesting and post-harvest practices were done as recommended. Inocula (conidia) of *Cercospora arachidicola* and *Cercospora personatum* were collected from the infected fields, whereby the infected leaves were detached and incubated in the pathological laboratory of African Seed Health Centre at Sokoine University of Agriculture in Morogoro, Tanzania, for fungi isolation and culture. Before inoculation, the inoculum concentration was adjusted to approximately 50 000 conidia ml^{-1} of solution. Thereafter inoculations were carried out with a hand sprayer at 10 and 45 days after groundnut emergence to capture both early and late Cercospora leaf spot diseases infection (Subrahmanyam et al., 1995).

4.2.2 Data collection

Data on Cercospora leaf spot diseases were scored from the individual plants grown in the middle rows of each plot at 28, 35 and 42 days after first inoculation. The ratings for both early and late leaf spot were carried out using 1 - 9 visual canopy rating scale, where 1 represent highly resistant (green and healthy leaves without leaf spot) and 9 highly susceptible (dead and defoliated plants), and CLD severity (CLDS) was rated at 42 days after first inoculation (Table 3.2) as suggested by Subrahmanyam et al. (1995). Yield and yield- related data collected included days to emergence (DTE), days to 50% flowering (DFL), length of reproductive branches (LRB) (cm), number of mature pods per plant (NPP), number of seeds per pod (SPP),100 seed weight (HSW) and seed yield (SY)(g) as suggested by IBPGR; ICRISAT, (1985).

Table 4.1: Description of Cercospora leaf spot disease rating scale (1-9).

Score	Description of the disease	Disease severity (%)
1	No disease	0
2	Lesions largely on lower leaves; no defoliation	1-5
3	Lesions largely on lower leaves; very few lesions on middle leaves; defoliation of some leaflets evident on lower leaves.	6-10
4	Lesions on lower and middle leaves, but severe on lower leaves; defoliation of some leaflets evident on lower leaves	11-20
5	Lesions on all lower and middle leaves, over 50% of the lower leaves defoliated	21-30
6	Lesions severe on lower and middle leaves; lesions on top leaves but less severe; extensive defoliation of lower leaves; defoliation of some leaflets evident on middle leaves	31-40
7	Lesions on all leaves but less severe on top leaves; defoliation of all lower and some middle leaves.	41-60
8	Defoliation of all lower and middle leaves; lesions severe on top leaves and some defoliation of top leaves evident.	61-80
9	Defoliation of almost all leaves leaving bare stems; some leaflets may be present, but with severe leaf spots.	81-100

Source: Subrahmanyam et al. (1995)

4.3 Data analysis

The data were analysed following the biometrical techniques developed by Mather (1949), using the IBM SPSS statistics 21 and MS excel software. Path coefficient analysis was done as suggested by Wright, (1921) and extended by Dewey and Lu (1959). The mean data of yield, yield related traits, and Cercospora leaf spot disease severity shown in Table 4.1 were used for correlation coefficient analysis to compute phenotypic correlation to measure the association between the traits among the groundnut genotypes. Microsoft excel was used to calculate the matrix inverse of correlations to obtain direct path values and to calculate indirect path values, whereby seed yield and Cercospora leaf spot disease severity were considered the main trait, and the others as independent or explanatory variables. The cluster analysis was performed in IBM SPSS 21 version to group genotypes according to their similarities following the Ward Linkage and Squared Euclidean distance methods.

Table 4.2 : Means of yield related traits and Cercospora leaf spot disease severity of eighty-four genotypes.

SNo.	Genotypes	DFL (day)	DM (day)	LRB (cm)	CLDS (%)	HSW (g)	NPP (No.)	SPP (No.)	SY (g)
1	BAKA	40.0	123.0	28.2	32.5	28.2	20.4	2.0	454.7
2	CG 7	41.0	122.0	22.8	33.3	26.1	20.0	2.3	521.8
3	CHITALA	42.0	119.0	23.0	34.2	29.9	19.4	2.0	432.0
4	ICG 405	40.0	121.0	32.0	32.5	53.3	21.3	2.8	665.2
5	ICG 6022	42.0	122.0	22.7	18.3	52.7	21.4	3.0	714.2
6	ICGV 07533	41.0	120.0	32.3	31.7	38.6	21.0	2.8	660.4
7	ICGV 07544	41.0	120.0	26.2	31.7	38.3	21.5	2.0	479.2
8	ICGV 6057	40.0	119.0	28.8	19.6	53.3	21.0	3.0	701.4
9	ICGV SM 01706	40.0	118.0	26.8	30.8	40.8	21.2	2.0	471.6
10	ICGV SM 03557	40.0	118.0	25.5	33.3	37.9	20.3	2.4	546.0
11	ICGV SM 03560	42.0	122.0	28.7	32.5	38.4	20.3	2.5	546.9
12	ICGV SM 05521	39.0	120.0	23.5	31.7	38.1	20.8	2.8	635.3
13	ICGV SM 07504	39.0	121.0	20.0	32.5	52.6	25.8	3.0	859.2
14	ICGV SM 07508	41.0	124.0	24.5	17.9	53.8	28.3	3.0	945.8
15	ICGV SM 07510	43.0	122.0	20.6	22.9	40.2	26.0	2.6	752.1
16	ICGV SM 07512	42.0	120.0	31.9	30.0	41.9	22.3	2.4	601.1
17	ICGV SM 07518	41.0	120.0	32.3	31.7	38.8	21.0	2.8	661.5
18	ICGV SM 07536	39.0	120.0	26.4	27.1	40.3	23.8	2.8	723.5
19	ICGV SM 07539	41.0	119.0	25.1	23.8	54.8	25.5	3.0	850.5
20	ICGV SM 07556	41.0	120.0	25.7	28.8	38.7	22.9	2.0	509.7
21	ICGV SM 07558	43.0	120.0	25.5	31.7	39.3	21.7	2.8	655.7
22	ICGV SM 09511	41.0	118.0	19.4	18.8	53.6	29.1	3.0	869.8
23	ICGV SM 95714	39.0	120.0	22.6	25.8	42.0	24.2	2.4	649.4
24	ICGV SM 96714	37.0	118.0	25.5	16.3	53.2	29.8	3.0	994.6
25	JL-24	40.0	120.0	28.1	35.8	29.8	18.9	2.2	451.5
26	KAKOMA	41.0	119.0	23.1	18.6	51.4	20.6	3.0	686.3
27	Local (77)	43.0	120.0	20.3	35.8	35.4	18.3	2.0	408.7
28	Local (Makulu)	39.0	120.0	31.5	18.8	53.8	27.8	3.7	1138.3
29	Local (Miembeni)	45.0	125.0	28.5	33.3	38.7	20.2	2.5	560.0
30	MANGAKA	41.0	125.0	28.7	33.8	30.8	20.6	2.0	457.4
31	MNANJE	40.0	122.0	27.5	34.2	30.6	19.8	2.0	439.0
32	Nachingwea	39.0	120.0	25.5	33.3	29.5	19.9	2.7	589.9
33	PENDO	40.0	125.0	36.8	24.2	54.8	25.3	2.0	433.7

SNo.	Genotypes	DFL (day)	DM (day)	LRB (cm)	CLDS (%)	HSW (g)	NPP (No.)	SPP (No.)	SY (g)
34	NSINJIRO	40.0	125.0	26.1	33.3	26.0	19.7	2.5	705.0
35	TZA 121	45.0	120.0	28.8	37.5	25.7	17.8	3.0	894.8
36	TZA 142	42.0	120.0	32.3	36.7	25.4	18.8	2.0	417.4
37	TZA 157	48.0	125.0	26.7	35.8	27.0	18.8	3.0	828.1
38	TZA 165	44.0	125.0	32.9	35.0	28.4	19.2	2.0	426.2
39	TZA 182	43.0	125.0	27.8	35.0	32.0	19.0	2.0	423.3
40	TZA 185	41.0	125.0	33.5	34.2	43.0	19.9	2.0	443.6
41	TZA 214	44.0	125.0	27.0	34.2	31.5	20.1	2.0	447.1
42	TZA 227	44.0	125.0	24.7	37.5	29.4	18.2	1.0	204.3
43	TZA 2270	44.0	125.0	26.8	35.0	30.7	19.5	3.0	851.7
44	TZA 230	44.0	120.0	30.5	32.5	29.8	20.6	2.0	459.0
45	TZA 241	44.0	125.0	26.7	34.2	29.7	19.6	1.5	324.7
46	TZA 2417	45.0	125.0	27.8	33.3	37.0	19.2	1.3	279.6
47	TZA 2421	38.0	118.0	29.0	24.2	52.9	25.0	1.8	501.1
48	TZA 2426	42.0	120.0	33.7	19.6	40.7	26.8	3.0	895.6
49	TZA 2444	41.0	122.0	35.8	27.1	42.5	23.5	2.5	848.2
50	TZA 2471	43.0	125.0	32.0	32.1	38.6	20.7	2.0	460.7
51	TZA 248	45.0	125.0	27.9	32.5	34.2	20.5	2.0	457.0
52	TZA 2485	43.0	125.0	27.6	32.5	35.8	20.3	2.0	419.9
53	TZA 2488	42.0	125.0	30.0	30.8	35.2	21.4	2.2	515.5
54	TZA 2497	43.0	125.0	32.9	30.8	34.4	21.1	2.0	469.6
55	TZA 2498	41.0	125.0	29.8	35.8	35.2	19.6	2.8	820.0
56	TZA 2518	37.0	118.0	25.8	22.3	56.6	28.9	3.0	964.6
57	TZA 254	41.0	120.0	31.5	23.6	52.7	27.7	3.0	923.2
58	TZA 2737	43.0	125.0	25.3	29.2	31.8	21.8	1.7	404.5
59	TZA 285	43.0	125.0	26.4	31.7	30.9	20.8	2.0	461.7
60	TZA 3222	43.0	125.0	30.6	35.0	27.8	19.1	2.0	425.7
61	TZA 3406	43.0	125.0	27.5	35.8	27.5	18.9	2.0	421.6
62	TZA 3783	42.0	125.0	28.0	35.0	29.0	19.3	2.2	460.5
63	TZA 3786	43.0	125.0	28.3	33.3	30.1	19.9	2.7	795.4
64	TZA 3806	45.0	125.0	32.3	34.2	28.9	19.8	2.0	441.6
65	TZA 3817	44.0	125.0	32.6	34.2	28.9	28.9	1.5	341.4
66	TZA 3836	43.0	125.0	29.5	31.7	30.2	30.2	2.0	452.5
67	TZA 4188	43.0	125.0	30.8	32.5	36.2	36.2	2.0	463.4
68	TZA 4228	44.0	125.0	25.1	32.5	35.0	35.0	2.0	437.5
69	TZA 4237	46.0	125.0	27.5	33.3	36.7	36.7	2.0	455.1
70	TZA 4261	40.0	122.0	27.1	23.8	53.0	53.0	2.5	879.1
71	TZA 4280	38.0	119.0	33.1	22.3	55.2	55.2	2.5	943.3
72	TZA 4291	42.0	124.0	29.9	27.9	38.6	38.6	2.0	515.7
73	TZA 4340	42.0	125.0	26.0	29.6	37.6	37.6	2.0	489.8
74	TZA 4370	43.0	125.0	31.5	29.2	37.4	37.4	2.0	447.0
75	TZA 4390	43.0	125.0	30.7	28.8	37.9	37.9	3.0	753.5
76	TZA 4391	45.0	125.0	26.9	30.0	38.5	38.5	2.0	483.4
77	TZA 4635	45.0	125.0	21.2	30.0	35.2	35.2	2.0	492.9
78	TZA 5212	44.0	125.0	27.4	37.5	27.0	27.0	2.0	417.8
79	TZA 534	40.0	118.0	30.8	26.7	51.6	51.6	2.0	534.5
80	TZA 549	42.0	125.0	27.2	33.3	29.0	29.0	2.0	437.8
81	TZA 597	43.0	125.0	20.7	37.5	30.1	30.1	2.0	416.1
82	TZA 613	44.0	125.0	27.0	39.2	27.9	27.9	2.0	374.4
83	TZA 664	45.0	125.0	34.2	37.5	28.8	28.8	2.0	412.6
84	TZA 667	45.0	125.0	30.6	35.8	27.8	27.8	3.0	726.5

DFL= days to 50% flowering, DM= days to maturity, LRB= length of reproductive branch, NPP = number of mature pods per plant, HSW= hundred seed weight, SPP= number of seeds per pod, CLDS = Cercospora leaf spot disease severity and SY= seed yield.

4.4 Results

4.4.1 Correlation analysis

The correlation analysis results are presented in Table 4.3. Several significant positive (P≤0.01) correlations were detected. The DFL had a significant positive correlation with DM (r=0.66) and CLDS (r=0.53), and was significant and negatively correlated with the HSW (r=-0.59), SPP (r=-0.35) and SY (r=-0.42). The DM was positively correlated with CLDS (r=0.47), but negatively correlated with HSW (r=-0.54), SPP (r=-0.45) and SY (r=-0.45). The CLDS was negatively correlated with NPP (r=-0.36), HSW (r=-0.83), SPP (r=-0.50) and SY (-0.62). The HSW was positively correlated with NPP (r=0.39), SPP (r=0.49) and SY (r=0.58). The SPP was positively correlated with SY (r=0.91).

Table 4.3: Phenotypic correlation coefficients among selected yield characters and Cercospora leaf spot disease severity.

Traits	DFL	DM	LRB	CLDS	HSW	NPP	SPP	SY
DFL	**1.00**							
DM	0.66**	**1.00**						
LRB	0.06	0.18	**1.00**					
CLDS	0.53**	0.47**	0.06	**1.00**				
HSW	-0.59**	-0.54**	-0.02	-0.83**	**1.00**			
NPP	-0.17	-0.03	0.07	-0.36**	0.39**	**1.00**		
SPP	-0.35**	-0.45**	-0.08	-0.50**	0.49**	0.02	**1.00**	
SY	-0.42**	-0.45**	-0.04	-0.62**	0.58**	0.21	0.91**	**1.00**

** Correlation is significant at the 0.01 level (2-tailed).

DFL= days to 50% flowering, DM= days to maturity, LRB= length of reproductive branch, CLDS= Cercospora leaf spot disease severity, NPP= number of mature pods per plant, HSW= hundred seed weight, SPP=number of seeds per pod and SY= seed yield.

4.4.2 Path analysis for seed yield

The results of the direct and indirect effects of yield components contributing to seed yield are presented in Table 4.4. The results showed that a positive direct effect on SY was exhibited by the following characters; SPP (0.7736), CLDS (0.0859), NPP (0.0505), LRB (0.0440), DFL (0.0414) and DM (0.0132). However, HSW (-0.0251) had a negative direct effect on SY. Indirect effect on seed yield via DFL was exhibited by DM (0.0274), CLDS (0.0219) and LRB (0.0024). Indirect effect on SY via DM was exhibited by DFL (0.0088), LRB (0.0023) and CLDS (0.0062). Indirect effect on SY via LRB was exhibited by DFL (0.0025), DM (0.0077), CLDS (0.0025) and NPP (0.0033). Indirect effect on SY via CLDS was exhibited by DFL (0.0454), DM (0.0405) and LRB (0.0049). Indirect effect on SY via

HSW was exhibited by DFL (0.0149), DM (0.0136), LRB (0.0006) and CLDS (0.0209). Indirect effect on SY via NPP was exhibited by LRB (0.0037), HSW (0.0196) and SPP (0.0012). Indirect effect on SY via SPP was exhibited by HWS (0.3767), NPP and (0.0181).

Table 4.4: Direct (diagonal) and indirect (non-diagonal) effects of selected yield contributing characters on seed yield among 84 groundnut genotypes.

TRAIT	DFL	DM	LRB	CLDS	HSW	NPP	SPP
DFL	**0.0414**	0.0088	0.0025	0.0454	0.0149	-0.0059	-0.2708
DM	0.0274	**0.0132**	0.0077	0.0405	0.0136	-0.0014	-0.3450
LRB	0.0024	0.0023	**0.0440**	0.0049	0.0006	0.0037	-0.0584
CLDS	0.0219	0.0062	0.0025	**0.0859**	0.0209	-0.0180	-0.3860
HSW	-0.0246	-0.0072	-0.0010	-0.0716	**-0.0251**	0.0196	0.3767
NPP	-0.0048	-0.0004	0.0033	-0.0307	-0.0097	**0.0505**	0.0181
SPP	-0.0145	-0.0059	-0.0033	-0.0429	-0.0122	0.0012	**0.7736**

Diagonal values (bolded) indicate direct effects of respective characters and indirect effects for above and below bolded values.

DFL= days to 50% flowering, DM= days to maturity, LRB= length of reproductive branch, CLDS= Cercospora leaf spot disease severity, HSW=hundred seed weight, NPP= number of mature pods per plant, SPP= number of seeds per pod.

4.4.3 Path analysis for Cercospora leaf spot diseases

The results of the direct and indirect effects of Cercospora leaf spot disease on yield contributing characters and seed yield are presented in Table 4.5. Positive direct effect of CLDS on SY and its related traits was exhibited in NPP (0.0356) and SY (0.2524). However, CLDS had a negative direct effect on SY and its related traits through DFL (-0.0680), DM (-0.0271), LRB (-0.0116), HSW (-0.5165) and SPP (-0.2283). The indirect effect of CLDS through DFL was exhibited by HSW (0.0403), SY (0.0283) and SPP (0.0238). The indirect effect through DM was exhibited by HSW (0.0147), SY (0.0123) and SPP (0.0121). The indirect effect through LRB was exhibited by SY (0.0005) and SPP (0.0009). The indirect effect through HSW was exhibited by DFL (0.3063), DM (0.2799) and LRB (0.0118). The indirect effect through NPP was exhibited by HSW (0.0138). The indirect effect through SPP was exhibited by DM (0.1018), DFL (0.0799) and LRB (0.0172), while the indirect effect through SY was exhibited by SPP (0.2300) and HSW (0.1472).

Table 4.5: Direct (diagonal) and indirect (non-diagonal) effects of Cercospora leaf spot disease severity on selected yield contributing characters among 84 groundnut genotypes.

TRAIT	DFL	DM	LRB	HSW	NPP	SPP	SY
DFL	**-0.0680**	-0.0180	-0.0007	0.3063	-0.0041	0.0799	-0.1053
DM	-0.0450	**-0.0271**	-0.0020	0.2799	-0.0010	0.1018	-0.1143
LRB	-0.0039	-0.0048	**-0.0116**	0.0118	0.0026	0.0172	-0.0108
HSW	0.0403	0.0147	0.0003	**-0.5165**	0.0138	-0.1112	0.1472
NPP	0.0079	0.0008	-0.0009	-0.1999	**0.0356**	-0.0054	0.0538
SPP	0.0238	0.0121	0.0009	-0.2515	0.0008	**-0.2283**	0.2300
SY	0.0283	0.0123	0.0005	-0.3011	0.0076	-0.2079	**0.2524**

Diagonal values (bolded) indicate direct effects of respective characters and indirect effects for above and below bolded values.

DFL= days to 50% flowering, DM= days to maturity, LRB= length of reproductive branch, HSW=hundred seed weight, NPP= number of mature pods per plant, SPP= number of seeds per pod.

4.4.4 Cluster analysis based on agro-morphological traits in groundnut

The results of the cluster analysis among groundnut genotypes based on DFL, DM, LRB, CLDS, HSW, NPP, SPP and SY characters are presented in Table 4.6. At five units of distance of similarity the groundnut genotypes were grouped into five clusters (Figure 4.1).

Cluster I consisted of 12 groundnut genotypes, with a DFL that ranged from 39.0 to 45.0 with a mean of 41.3 days. Their DM ranged from 119.0 to 125.0, with a mean of 120.9 days. The LRB ranged from 22.6 to 32.3, with an average of 28.0 cm. The CLDS ranged from 18.3 to 35.8, with a mean of 28.0%. The HSW ranged from 27.8 to 53.3, with a mean of 42.9 g. The NPP ranged from 20.6 to 37.9, with a mean of 23.4 pods per plant. The number of seeds per pod ranged from 2.4 to 3.0, with a mean of 2.8 seeds per pod and the SY ranged from 601.1 to 753.5, with an average of 675.9 g.

Cluster II consisted of 12 groundnut genotypes with a DFL ranging from 39.0 to 48.0, with a mean of 42.0 days. The DM ranged from 119.0 to 125.0, with a mean of 122.6 days. The LRB ranged from 20.0 to 35.8, with a mean of 26.8 cm. The CLDS ranged from 22.9 to 35.8 with a mean of 30.7%. The HSW ranged from 26.0 to 54.8, with a mean of 38.2 g. The NPP ranged from 18.8 to 53.0, with a mean of 24.4 pods per plant. The SPP ranged from 2.5 to 3.0, with a mean of 2.8 seeds per pod, while the SY ranged from 705.0 to 879.1, with a mean value of 817.3 g.

Cluster III consisted of eight genotypes with a DFL ranging from 37.0 to 42.0, with a mean of 39.5 days. The DM ranged from 118.0 to 120.0, with a mean of 119.6 days. The LRB ranged from 19.4 to 33.7, with a mean of 28.1 cm. The CLDS ranged from 16.3 to 23.6, with a mean of 19.9%. The HSW ranged from 40.7 to 56.6, with a mean of 52.4 g. The NPP ranged from 26.8 to 55.2, with a mean of 31.7 pods per plant. The SPP ranged from 2.5 to 3.7, with a mean of 3.0 seeds per pod and the SY ranged from 869.8 to 1138.3, with a mean of 959.4 g.

Cluster IV consisted of 17 genotypes with a DFL ranging from 38.0 to 45.0, with a mean of 41.7 days. The DM ranged from 118.0 to 125.0, with a mean of 122.0 days. The LRB and the CLDS ranged from 21.2 to 32.9 and 22.1 to 33.3, with mean values of 27.5 cm and 30.4%, respectively. The HSW ranged from 26.1 to 52.9, with a mean of 38.2 g and NPP ranged from 19.9 to 51.6 with a mean of 27.8 pods per plant. The SPP ranged from 1.8 to 2.7, with a mean of 2.1 seeds per pod and the SY ranged from 447.0 to 589.9, with a mean of 510.3 g.

Cluster V consisted of 35 genotypes with a DFL that ranged from 40.0 to 46.0, with a mean of 43.0 days. The DM ranged from 119.0 to 125.0, with a mean of 124.1. The LRB ranged from 20.7 to 36.8, with a mean of 28.4 cm. The CLDS ranged from 24.2 to 39.2, with a mean of 34.0%. The HSW ranged from 25.4 to 54.8, with a mean of 32.0 g. The NPP ranged from 18.2 to 36.7, with a mean of 23.1 pods per plant. The SPP ranged from 1.0 to 2.2, with a mean of 1.9 seeds per pod and the SY ranged from 204.3 to 463.4, with a mean of 419.0 g.

Table 4.6: Cluster means and ranges for seed yield and its component traits, and reaction to Cercospora leaf spot disease among 84 groundnut genotypes.

Cluster (number of genotypes in the cluster)	Days to 50 % flowering		Days to maturity		Length of reproductive branches (cm)		*Cercospora* leaf spot disease severity (%)		Hundred seed weight (g)		Number of pods per plant		Number of seeds per pod		Seed yield (kg ha^{-1})	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range	Mean	Range
I (12)	41.3	39.0-45.0	120.9	119.0-125.0	22.6	28.0-32.3	28.0	18.3-35.8	42.9	27.8-53.3	23.4	20.6-37.9	2.8	2.4-3.0	675.9	601.1-753.5
II (12)	42.0	39.0-48.0	122.6	119.0-125.0	26.8	20.0-35.8	30.7	22.9-35.8	38.2	26.0-54.8	24.4	18.8-53.0	2.8	2.5-3.0	817.3	705.0-879.1
III (8)	39.5	37.0-42.0	119.6	118.0-120.0	28.1	19.4-33.7	19.9	16.3-23.6	52.4	40.7-56.6	31.7	26.8-55.2	3.0	2.5-3.7	959.4	869.8-1138.3
IV (17)	41.7	38.0-45.0	122.1	118.0-125.0	27.5	21.2-32.9	30.4	22.1-33.3	38.2	26.1-52.9	27.8	19.9-51.6	2.1	1.8-2.7	510.3	447.0-589.9
V (35)	43.0	40.0-46.0	124.1	119.0-125.0	28.4	20.7-36.8	34.0	24.2-39.2	32.0	25.4-54.8	23.1	18.2-36.7	1.9	1.0-2.2	419.0	204.3-463.4

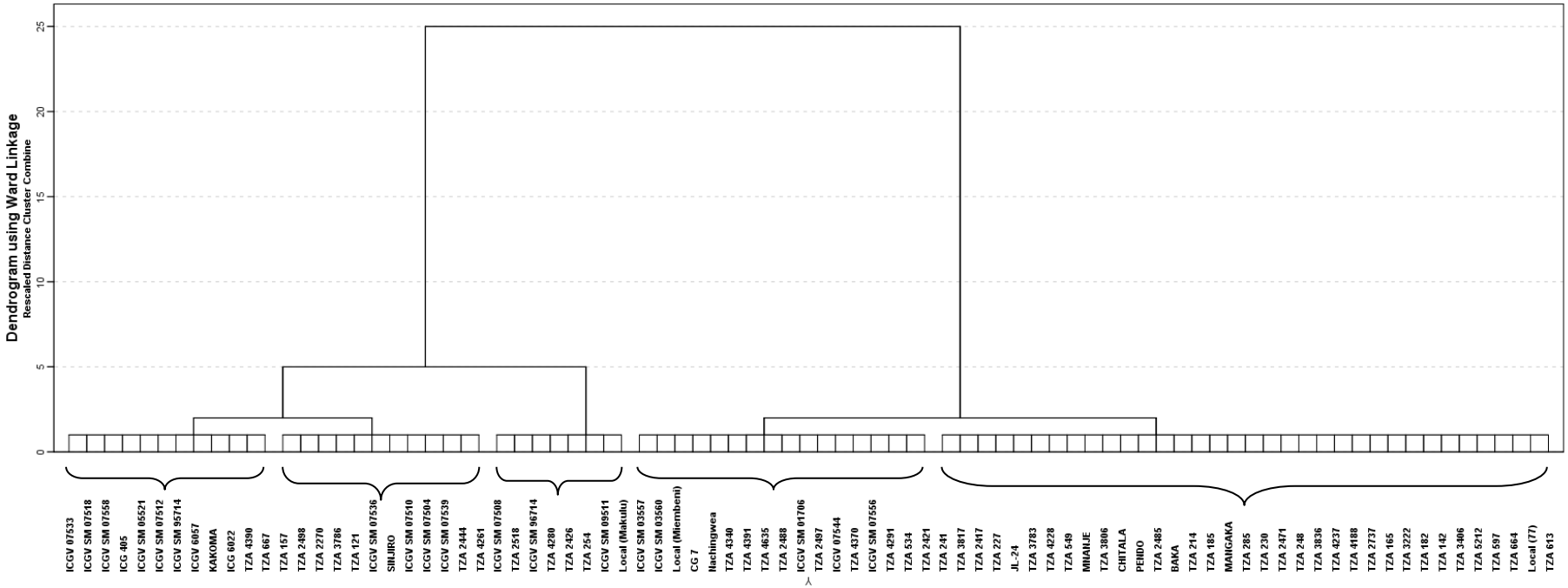

Figure 4.1: Dendrogram of 84 genotypes based on hierarchical cluster analysis using Ward Linkage Methods and Squared Euclidean Distance Measure as distance measure.

4.5 Discussion

Correlation coefficient for Cercospora leaf spot disease and yield related traits among groundnut genotypes

The significant (P≤0.01) negative correlation of CLDS with SY was attributed to the negative effect of the disease on NPP, HSW and SPP, which are yield related traits. Groundnut genotypes severely infected by CLD usually suffer excessive leaf abscission, which lowers photosynthetic efficiency, and ultimately reduces dry matter production thus lowering SY. The CLD causes damage to the plant by reducing the available photosynthetic area, due to leaf lesion formation and abscission as reported by McDonald et al. (1985). Yield losses of 50% in groundnut due to leaf defoliation caused by CLD has been reported by Melouk and Shokes (1995).

The significant (P≤0.01) positive correlation of NPP with HSW was expected since vigorous plants often produce many pods containing heavy seeds and hence high SY. The significant (P≤0.01) positive correlation of SPP with SY was probably attributed to the large SPP, which increases SY. Furthermore, SY was positively correlated with HSW and SPP, indicating that the higher the SPP and HSW the higher the SY. The significant correlation between these traits in groundnut yield was also reported by Jogloy et al. (2011). Yield improvement in groundnut, therefore, may be achieved through selection of genotypes with early DFL and DM, as they will escape the dry spell that occurs during the growing season especially in the study area, which is characterized by semi-arid climate, high NPP, low CLDS, large SPP and HSW, and high SY.

Path analysis for seed yield

The positive direct effect on SY was depicted by DFL, LRB, CLDS and SPP (Table 4.4). Early flowering genotypes with long LRB, many SPP and low CLDS tend to have a higher SY. In order to directly improve yield of groundnuts these characters can be taken into consideration during selection of parents for further breeding in addition to CLD resistance. Pavankumar et al. (2014) and Thirumala et al. (2014) reported that the highest direct positive effect of seed yield, days to maturity, number of pods per plant and hundred seed weight was revealed on pod yield which is similar to findings in this study. Indirect effect on SY via SPP was exhibited by NPP and HSW. This is because the higher the NPP, the higher the PY and HSW and therefore, the

overall SY. The SY was indirectly influenced by DM via HSW and NPP; this is because genotypes with high NPP have high HSW.

Path analysis for Cercospora leaf spot disease

The positive direct effect of CLDS on seed yield and its contributing traits was exhibited in NPP and SY (Table 4.5). This shows the effect of Cercospora leaf spot disease on the pod production, which is a very important yield determinant and, therefore, yield of the groundnut genotypes infected with the disease will have low seed yield. This is because CLD is associated with leaf defoliation which causes low dry matter production and therefore low pod production. However, CLDS had no direct influence on DFL, DM, LRB, HSW and SPP. Therefore, selection of genotypes for resistance breeding may be done considering NPP and SY of the genotypes.

The indirect effect of CLD through DFL exhibited by HSW, SY and SPP can be attributed to excessive defoliation inflicted by the diseases which cause poor photosynthesis, poor pod formation, poor pod filling leading to shrivelled seeds with less weight. The indirect effect of CLD through DM exhibited by HSW, SY and SPP might have been attributed to late maturity, which coincides with harsh growing conditions leading to poor pod and seed yield, increased number of immature pods causing low weight seeds per pod. The indirect effect of CLD through LRB exhibited by SY and SPP could have been caused by a reduced length of reproductive branches, which leads to a reduction in NPP, SY and damaged seeds, which reduces SPP. The indirect effect of CLD through HSW and SPP exhibited by DFL, DM and LRB was probably due to shrivelled infected seeds due to late flowering, maturity and reduced length of reproductive branches**.** The indirect effect of CLD through SY exhibited by SPP and HSW can be due to unfilled pods with a low number of seeds per pod and low seed weight.

Cluster analysis for selected yield components and CLD in groundnut genotypes.

The five clusters derived from the cluster analysis of the 84 groundnut genotypes suggest the availability of a high-level phenotypic diversity among the groundnut genotypes. The selection and hybridization can be effective for CLD resistance because the genotypes ranged from susceptible to tolerant, and for yield because genotypes ranged from low to high yielding. These findings are in accordance with an earlier report by Swamya et al. (2003). From the present study, several genotypes from clusters I (ICGV 6057, Kakoma, ICGV 6022, TZA 4390 and TZA 667), II(TZA 157, TZA 2498, TZA 2270, TZA 3786, TZA 121, ICGV SM 07539, TZA 2444 and

TZA 4261), III(ICGV SM 07508, TZA 2518, ICGV SM 96714, TZA 4280, TZA 2426, TZA 254 and Local Makulu) and IV(TZA 534) were selected for further breeding programme due to their low CLDS, large NPP, HSW and overall high SY. Therefore, simultaneous selection of genotypes for high yield contributing characters and low CLDS can be achieved in groundnut improvement breeding programmes (Venkataravana et al., 2000).

4.6 Conclusion

The current study has revealed that, there were significant and positive associations between yield and its yield components. The CLDS was negatively associated with yield contributing characters. The study also observed the direct and positive effects of yield contributing characters on yield. Furthermore, the study grouped the genotypes into five clusters according to their genetic similarities, which will be of value to the breeding programme aimed at improving Cercospora leaf spot disease resistance and enhanced yield in groundnuts. Furthermore, the study has shown the importance of establishing the associations between Cercospora leaf spot disease, yield and its contributing characters, and their direct and indirect effect on the overall seed yield as a prerequisite for parental selection.

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Chapter 5: Gene action and heritability of groundnut seed yield and resistance to Cercospora leaf spot diseases

Abstract

Groundnut (*Arachis hypogaea* L.) is a highly self-pollinated crop grown in tropical and subtropical areas. The crop has a narrow genetic base, and therefore, it is essential to create more variability in the segregating materials. The effectiveness of selection is dependent upon the magnitude of genetic variability present in the material, nature of gene action and the extent to which it is heritable. This study was conducted, to determine the gene action and heritability of resistance to Cercospora leaf spot diseases (CLD) and seed yield (SY) in groundnuts, and to select promising parents and crosses with durable resistance to CLD and enhanced yield. The study involved three groundnut botanical groups, (Valencia, Virginia and Spanish) crossed in a line x tester mating design and evaluated at three sites (the Hombolo and Makutupora agricultural research stations, and the Bihawana farmers' training centre), in Tanzania. The results revealed that, parents Local Makulu, TZA 121 and ICGV SM 96714 in the Valencia botanical group; TZA 4280, TZA 4390 and ICGV 6022 in the Virginia botanical group and TZA 2518, TZA 254 and ICGV SM 07508 in the Spanish botanical group had good general combining ability (GCA) for CLD resistance and SY and contributed to significant specific combining ability (SCA) in the crosses they were involved. The F1 crosses; Local Makulu x ICGV SM 96714, TZA 121 x Kakoma, TZA 3786 x Kakoma, TZA 157 x Kakoma, TZA 2498 x ICGV SM 96714 in the Valencia group; TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022 and TZA 4261 x ICGV 6057 in the Virginia group, and TZA 2444 x ICGV SM 07539, TZA 2518 x ICGV SM 07508, TZA 254 x ICGV SM 07508, TZA 2426 x ICGV SM 07539, TZA 2270 x ICGV SM 07539 and TZA 2270 x ICGV SM 07508 in the Spanish group had significant negative SCA for CLD resistance and positive for SY which is desirable for individual selection. Further, the study revealed, both additive and non-additive gene effects were important in the inheritance of CLD resistance and SY. In addition, additive genetic variance (GV_A) was larger than dominance genetic variance (GV_D) in Valencia group however, in Virginia and Spanish group, GV_D was larger than GV_A thus, selection of genotypes from initial generations for resistance to CLD may be difficult due to high influence of dominance effects in the expression of the total phenotypic variance. Furthermore, broad sense heritability was

higher than narrow sense heritability on the studied traits for all the three botanical groups implying that these traits can be transmitted from parents to progenies through hybridization.

Key words: additive genetic variance, broad sense heritability, dominance genetic variance, gene action, general combining ability, groundnuts, narrow sense heritability, specific combining ability.

5.1 Introduction

Cultivated groundnut (*Arachis hypogaea* L.) belongs to the family Fabaceae. Botanically, cultivated groundnut is classified into two sub-species, which differ in their branching patterns (sub-species *hypogaea* with alternate branching habit and sub-species *fastigiata* with sequential branching habit). Each sub-species is divided into two botanical varieties, sub-species *hypogaea* into var. *hypogaea* (Virginia) and var. *hirsuta*; and sub-species *fastigiata* into var. *fastigiata* (Valencia) and var. *vulgaris* (Spanish). The Virginia bunch seeds are richest in oil and chemical contents, followed by Spanish bunch type. The protein content and oil quality is highest in the Valencia types, while soluble sugars are highest in *hirsuta*. Groundnut is an important oilseed crop. The groundnut kernel is a rich source of energy because of its high oil (44-50%) and protein content (25-33%). It contains 18% carbohydrates, and is rich in minerals (calcium, magnesium and iron) and vitamins (B1, B2 and Niacin) (Naidu et al., 1999). The crop is grown for food security and cash in most of the semi-arid tropics including Tanzania (Upadhyaya et al., 2006).

The low productivity of the crop in Tanzania and several other African countries is ascribed to many biotic and abiotic stresses. Among the biotic factors, Cercospora leaf spot diseases (CLD) is one of the most economically important foliar diseases of groundnut, which can cause yield losses of up to 80% (Grichar et al., 1998). The development of resistant or tolerant cultivars to these diseases could be effective in decreasing the production costs associated with chemical application, in improving the production in terms of quantity and quality, and in reducing the detrimental effects of chemicals on our ecosystem. The development of high-yielding CLD resistant genotypes requires the identification of resistant sources with good breeding potential (Bhailalbhai, 2012). The partitioning of genetic effects into general combining ability (GCA) and specific combining ability (SCA) is essential for understanding the types of gene action governing the important quantitative traits. Estimates of combining ability effects are essential in

identifying superior parents as this indicates the ability of pure line to transmit desirable performance to its hybrid progenies. The GCA is associated with the genes which are additive in effects and are fixable, while the SCA is more dependent on genes with dominance and epistasis and is non-fixable (Rojas and Sprague, 1952; Sprague and Federer, 1952). Several mating designs including complete diallel, half diallel, line x tester, one way and three way crosses are used to partition genetic variability into portions due to GCA and SCA effects.

The success of crop improvement programmes depends on the choice of parents for improvement of any plant character through hybridization. It is therefore, necessary to understand the nature of gene action and the genetic architecture of the donor parents for a particular character. Information on the combining ability status of the genotypes will give an indication of how well they combine with a given genotype to produce potential and productive populations, and on the nature of gene action involved. This helps the breeder to decide upon the choice of parents for hybridization. Therefore, this study was undertaken (i) to estimate the general combining ability (GCA) and specific combining ability (SCA) effects for CLD resistance, and seed yield and its component traits in groundnut, (ii) to study the nature and magnitude of gene action for quantitative characters in groundnuts and (iii) to estimate the heritability for CLD resistance and yield.

5.2 Material and methods

5.2.1 Study site and parental selection

The selection of parents was done based on the results of the screening experiments conducted at the Hombolo and Makutupora agricultural research stations, and the Bihawana farmers training centre in the Dodoma region (Chapter three). Twenty-one genotypes were selected from the genotype evaluation experiments (Table 3.1). The parents included three sets of seven entries each from the Valencia, Virginia and Spanish types with either tolerance to CLD disease or high yield potential and farmers' preferred traits. The 21 selected parents were planted in a screen house for crossing. The parents in each set were crossed in a line x tester mating design involving five lines and two testers to produce ten single cross hybrids for each botanical group. The single cross lines were evaluated for combining ability, heritability and gene action governing the inheritance of yield and CLD resistance. The crossing scheme of single crosses for CLD resistance and parental material are summarized in Table 5.1.

Table 5.1: List of parental material used in the Line x Tester mating design to develop single crosses.

SNo.	Genotype	Source	Botanical group	Parental type	Characteristics
1	Local Makulu	Landrace	Valencia	Female	Farmers' preference, high yield
2	TZA 3786	NPGRC	Valencia	Female	Farmers' preference, high yield
3	TZA 2498	NPGRC	Valencia	Female	Farmers' preference, high yield
4	TZA 157	NPGRC	Valencia	Female	Farmers' preference, high yield
5	TZA 121	NPGRC	Valencia	Female	Farmers' preference, high yield
6	ICGV SM 96714	ICRISAT-Malawi	Valencia	Male	Tolerance to CLD, high yield
7	Kakoma	ICRISAT-Malawi	Valencia	Male	Tolerance to CLD, high yield
8	TZA 4280	NPGRC	Virginia	Female	Farmers' preference, high yield
9	TZA 4390	NPGRC	Virginia	Female	Farmers' preference, high yield
10	TZA 534	NPGRC	Virginia	Female	Farmers' preference, high yield
11	TZA 667	NPGRC	Virginia	Female	Farmers' preference, high yield
12	TZA 4261	NPGRC	Virginia	Female	Farmers' preference, high yield
13	ICGV 6022	ICRISAT- Malawi	Virginia	Male	Tolerance to CLD, high yield
14	ICGV 6057	ICRISAT- Malawi	Virginia	Male	Tolerance to CLD, high yield
15	TZA 2444	NPGRC	Spanish	Female	Farmers' preference, high yield
16	TZA 2518	NPGRC	Spanish	Female	Farmers' preference, high yield
17	TZA 254	NPGRC	Spanish	Female	Farmers' preference, high yield
18	TZA 2426	NPGRC	Spanish	Female	Farmers' preference, high yield
19	TZA 2270	NPGRC	Spanish	Female	Farmers' preference, high yield
20	ICGV SM 07539	ICRISAT- Malawi	Spanish	Male	Tolerance to CLD, high yield
21	ICGV SM 07508	ICRISAT- Malawi	Spanish	Male	Tolerance to CLD, high yield

5.2.2 Hybridization procedure

Hybridization was done by hand emasculation followed by hand pollination (Patel et al., 1936). The well-developed flowers, about to open the next morning, were selected and emasculated in the evening (between 3.00 and 6.00 pm). These flowers were pollinated in the next day (between 6.00 and 9.00 am) by collecting the pollen grains from flowers of male parent. The pollen grains were applied on receptive stigma with a sharp pointed needle. The pegs were tagged to identify the crosses at the time of harvesting. The flowers, which were not used in the crossing programme were removed every morning to maintain purity. The seeds of each cross were harvested separately, cleaned and stored properly for next stage of the breeding programme.

5.2.3 Experimental design and field establishment

The thirty single crosses developed were planted in three locations, namely, the Hombolo and Makutupora agricultural research stations and the Bihawana farmers' training centre in Dodoma, Tanzania. The experiment was laid out in an alpha lattice design (6 x 5) with two replications for one season. The single crosses were planted in the field plots of 1.5 x 1 m size with inter-row

and intra-row spacing of 0.5 and 0.1 m respectively. Each plot had three rows each with 10 plants. Other cultural practices were done as recommended.

5.3 Data collection

5.3.1 Yield and related parameters

Data on days to emergence (DTE), days to 50% flowering (DFL), length of reproductive branches (LRB) (cm), number of mature pods per plant (NPP), number of seeds per pod (SPP), seed colour (SC), 100 seed weight (HSW) and seed yield (SY) (g) were collected as described in section 3.4.

5.3.2 Cercospora leaf spot disease resistance

The CLD severity among the genotypes were recorded on individual plots towards the end of growing season. The early and late leaf spot diseases were evaluated together on a 1-9 visual canopy rating scale, where 1 = highly resistant (green and healthy leaves without leaf spot) and 9 = highly susceptible (dead and defoliated plants) as shown in (Table 4.1) (Subrahmanyam et al., 1995).

5.4 Statistical analyses

5.4.1 Analysis of variance and estimation of combining ability

The collected data were assembled in excel and subjected to analysis of variance (ANOVA to test for the significance of genotypes across environments for all the characters measured. The botanical groups were considered as sets and the analysis was done separately for each set. Estimation of combining ability effects (GCA) effects of the lines and testers, the specific combining ability (SCA) effect of crosses, and their interactions with the environment were determined following the procedure of Hallauer and Miranda (1988). The statistical model used was as follows:

$Y_{ijk} = \mu + g_i + g_j + S_{ij} + e_k + (ge)_{ik} + (ge)_{jk} + (se)_{ijk}$, where Y_{ijk} = the performance of the hybrid developed with i^{th} *male* and j^{th} *female*, in the k^{th} location, μ = the overall mean; g_i = the effect of the i^{th} male; g_j = the effect of the j^{th} female; s_{ij} = the interaction of the i^{th} male with the j^{th} female;

e_k = the effect of the k^{th} environment; $(ge)_{ik}$ = the interaction of the g_i and e_k; $(ge)_{jk}$ = the interaction of the g_j and e_k; $(se)_{ijk}$ = the interaction of s_{ij} and e_k.

The GCA and SCA effects were calculated using the relationships: $g_i = \acute{Y}_{i.} - \acute{Y}..$, $g_j = \acute{Y}_{j.} - \acute{Y}..$, and $s_{ij} = \acute{Y}_{ij} - \acute{Y}_{i.} - \acute{Y}_{.j} + \acute{Y}..$

Where, g_i = GCA of i^{th} female, g_j = GCA of j^{th} male, s_{ij} = SCA of j^{th} male parent with all females in hybrid combinations, $\acute{Y}_{ij}$ = mean performance of hybrid combination with i^{th} female and j^{th} male, $\acute{Y}_{i.}$ = mean performance of i^{th} female parent with all males in hybrid combinations, $\acute{Y}_{.j}$ = mean performance of j^{th} male parent with all females in hybrid combinations, and $\acute{Y}..$ = overall mean performance of hybrids.

5.4.2 Estimation of heritability

The broad sense and narrow sense heritability were determined following (Burton, 1952) using the relationships: $V_P = V_G + V_E$, $V_P = V_A + V_D + V_E$, $H^2 = V_G/V_P$, and $h^2 = V_A/V_P$

Where: V_P = phenotypic variance, V_A =additive variance, V_D = dominance variance, and V_E =environmental variance, H^2=broad sense heritability, and h^2= narrow sense heritability.

5.5 Results

In the Valencia botanical group, the environments and females were significant for all the evaluated traits at different levels; males were significant for all the measured traits except CLDS. The environment x female were significant for CLDS and SY at $p<0.05$ and $p<0.001$ respectively. The interaction between environment x female x male was significant ($p<0.05$) for SY. The percentage contributions of SS_F were found to be the highest for all measured traits followed by SS_M and the lowest contribution was by the SS_{FM} (Table 5.2).

Table 5.2: Mean squares and significance tests for yield, selected yield related traits and Cercospora leaf spot disease severity of parents and crosses derived from the **Valencia** groundnut botanical group evaluated in three sites in Tanzania.

Source	DF	DFL	CLDS	NPP	HSW	SY
Env	2	10.62**	12.80***	11.47*	45.32**	41963.22***
Rep / Env	3	4.28*	6.53**	44.72***	43.43**	43484.62***
Female	4	169.19***	172.53***	616.65***	2257.23***	1483950.14***
Male	1	10.42**	3.27^{ns}	50.42***	209.07***	60738.02***
Female x Male	4	0.54^{ns}	0.48^{ns}	0.83ns	1.69^{ns}	1791.06^{ns}
Env x Female	8	2.49^{ns}	2.49*	3.74ns	11.71^{ns}	4038.28***
Env x Male	2	0.42^{ns}	0.87^{ns}	0.87ns	1.52^{ns}	1177.52^{ns}
Env x Female x Male	8	0.54^{ns}	0.51^{ns}	0.47ns	1.33^{ns}	3811.12**
$\%SS_F$		98.17	97.88	92.33	97.67	98.87
$\%SS_M$		1.51	1.85	7.55	2.26	1.01
$\%SS_{FM}$		0.31	0.27	0.12	0.07	0.12
Grand Mean		60.22	19.80	30.12	54.57	887.18
R^2		0.97	0.97	0.97	0.98	1.00
CV (%)		1.85	4.90	5.55	5.11	3.23

*=significant at 0.05 probability level; ***= significant at 0.001; ns= non-significant; DF= degree of freedom; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; Env = environment; Rep / Env = replication within environment; $SS_F\%$= percentage contribution of the sum of square of female; $SS_M\%$= percentage contribution of sum of square of male and $SS_{FM}\%$= percentage contribution of the sum of square of interaction between female and male; CV= coefficient of variation and R^2=coefficient of determination.

The findings from this study in the Virginia botanical group showed that, environments were significant ($p<0.001$) for all the measured traits except DFL. Female, male and the environment x female interaction were significant for all the measured traits at different levels. The percentage contribution of SS_F was the highest followed by SS_M and the least was SS_{FM} (Table 5.3).

Table 5.3 : Mean squares, significant tests of yield, selected yield related traits and Cercospora disease severity of crosses derived from the **Virginia** groundnut botanical group evaluated in three sites in Tanzania.

Source	DF	DFL	CLDS	NPP	HSW	SY
Env	2	0.60^{ns}	28.82***	202.82***	51.47***	1616640.35***
Rep / Env	3	0.45^{ns}	7.35**	9.88*	19.60**	10620.30***
Female	4	1044.02***	646.78***	5954.36***	2168.73***	835349.48***
Male	1	43.35***	12.15**	88.82***	64.07***	6448.08**
Female x Male	4	1.77^{ns}	1.28^{ns}	2.78^{ns}	1.53^{ns}	465.19^{ns}
Env x Female	8	5.14**	3.90*	29.36***	18.36**	82138.91***
Env x Male	2	0.20^{ns}	0.35^{ns}	1.22^{ns}	0.87^{ns}	45.42^{ns}
Env x Female x Male	8	0.49^{ns}	1.10^{ns}	1.55^{ns}	1.14^{ns}	66.60^{ns}
$\%SS_F$		95.86	99.34	99.58	99.2	99.75
$\%SS_M$		3.98	0.47	0.37	0.73	0.19
$\%SS_{FM}$		0.16	0.20	0.05	0.07	0.06
Grand Mean		55.85	15.62	44.12	55.57	1077.90
R^2		0.99	0.99	1.00	0.99	1.00
CV (%)		2.04	7.13	3.70	3.64	2.30

*=significant at 0.05 probability level; ***= significant at 0.001; ns= non-significant; DF= degree of freedom; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; Env = environment; Rep / Env = replication within environment; $SS_F\%$= percentage contribution of the sum of square of female; $SS_M\%$= percentage contribution of sum of square of male and $SS_{FM}\%$= percentage contribution of the sum of square of interaction between female and male; CV= coefficient of variation and R^2=coefficient of determination.

The mean squares and significant tests for yield and its related components, and CLDS for the Spanish botanical group are presented in Table 5.4. The environments, females, males and the female x male interaction were significant ($p<0.001$) for all the measured traits. Among the measured traits, only DFL was significant ($p<0.05$) for environment x female, environment x male and environment x female x male interactions. The percentage contributions of SS_F were found to be the highest followed by SS_M and the lowest contribution was by the SS_{FM} for all measured traits (Table 5.4).

Table 5.4: Mean squares and significant tests of yield, yield related traits and Cercospora leaf spot disease severity of crosses derived from the **Spanish** groundnut botanical group evaluated in three sites in Tanzania.

Source	DF	DFL	CLDS	NPP	HSW	SY
Env	2	21.80***	5.22***	15.20***	31.52***	14842.717***
Rep / Env	3	3.33^{ns}	0.15^{ns}	2.73^{ns}	4.57^{ns}	1526.35^{ns}
Female	4	171.07***	98.11***	234.96***	732.02***	315058.64***
Male	1	308.27***	170.02***	308.27***	1382.40***	593418.15***
Female x Male	4	71.93***	23.48***	45.56***	169.73***	66404.69***
Env x Female	8	6.97*	0.45^{ns}	2.28^{ns}	4.20^{ns}	2414.53^{ns}
Env x Male	2	8.87*	0.42^{ns}	3.47^{ns}	4.85^{ns}	3683.15^{ns}
Env x Female x Male	8	5.53*	1.06^{ns}	1.13^{ns}	2.75^{ns}	816.63^{ns}
$\%SS_F$		53.45	59.79	65.71	58.69	59.47
$\%SS_M$		24.08	25.9	21.55	27.71	28.00
$\%SS_{FM}$		22.47	14.31	12.74	13.61	12.53
Grand Mean		57.80	22.22	26.50	40.27	610.98
R^2		0.96	0.98	0.97	0.98	0.99
CV (%)		2.54	3.25	4.81	4.28	5.64

*=significant at 0.05 probability level; ***= significant at 0.001; ns= non-significant; DF= degree of freedom; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; Env = environment; Rep / Env = replication within environment; $SS_F\%$= percentage contribution of the sum of square of female; $SS_M\%$= percentage contribution of sum of square of male and $SS_{FM}\%$= percentage contribution of the sum of square of interaction between female and male; CV= coefficient of variation and R^2=coefficient of determination.

The GCA_F effects for Valencia parents (Table 5.5) Local Makulu and TZA 121 were significant ($p<0.01$) and negative for DFL, CLDS, NPP, HSW and SY. The parent TZA 3786 had significant ($p<0.01$) and positive GCA for HSW and SY. The parents TZA 157 and TZA 2498 had significant ($p<0.01$) and positive GCA for DFL and CLDS, and significant ($p<0.01$) and negative GCA for NPP, HSW and SY. The GCA_M was significant ($p<0.01$) and positive for NPP, HSW and SY for parent ICGV SM 96714 and negative for parent Kakoma for NPP, HSW and SY.

Table 5.5: Estimates of the General Combining Ability effects of **Valencia** groundnut genotypes used as parents for yield, yield related traits and resistance to Cercospora leaf spot disease.

Females (GCA_F)	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
Local Makulu	-5.10**	-2.72**	5.43**	8.87**	173.28**
TZA 121	-1.93**	-1.22**	1.85**	4.78**	151.53**
TZA 3786	0.57^{ns}	0.45^{ns}	-0.15^{ns}	0.87**	65.28**
TZA 157	2.48**	1.20**	-1.57**	-5.38**	-89.13**
TZA 2498	3.98**	2.28**	-5.57**	-9.13**	-300.97**
Males (GCA_M)					
ICGV SM 96714	-0.22^{ns}	-0.27^{ns}	1.18**	1.08**	18.35**
Kakoma	0.22^{ns}	0.27^{ns}	-1.18**	-1.08**	-18.35**

**= significant at 0.01; ns= non-significant; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; GCA_F general combining ability of female parents and GCA_M= general combining ability of male parents.

The GCA effects of Virginia parents are presented in Table 5.6. The results showed a significant ($p<0.01$) and positive GCA_F for DFL of parents TZA 534, TZA 4261 and TZA 667. A significant ($p<0.01$) and positive GCA for CLDS was exhibited by parents TZA 667, TZA 4390, TZA 4261, while parent TZA 534 had a significant ($p<0.05$) and positive GCA for CLDS. For NPP, HSW and SY a significant ($p<0.01$) and positive GCA was exhibited by TZA 4280. A significant ($p<0.01$) and negative GCA for DFL was observed by parents TZA 4280 and TZA 4390, for CLDS by TZA 4280, for NPP by TZA 432, TZA 4390, TZA 4261 and TZA 667, for HSW by TZA 4390, TZA 4261 and TZA 667 and for SY by parents TZA 534, TZA 4390, TZA 4261 and TZA 667. Parent ICGV 6057 had the significant ($p<0.01$) and positive GCA for DFL and CLDS, while it had a significant ($p<0.01$) and negative GCA for NPP, HSW and SY. Parent ICGV 6022 had a significant ($p<0.01$) and positive GCA for NPP, HSW and SY, while it had a high negative GCA for DFL and CLDS.

Table 5.6 : Estimates of the General Combining Ability effects of **Virginia** groundnut genotypes used as parents for yield, yield related traits and resistance to Cercospora leaf spot disease.

GCA_F	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
TZA 534	2.98**	0.30*	-2.88**	-0.40^{ns}	-64.52**
TZA 4280	-4.43**	-5.30**	6.37**	3.77**	161.40**
TZA 4390	-2.10**	2.62**	-0.55^{ns}	-2.15**	-12.10**
TZA 4261	0.98**	1.62**	-1.47**	-0.98**	-47.35**
TZA 667	2.57**	1.37**	-1.47**	-0.23^{ns}	-37.43**
GCA_M					
ICGV 6057	1.07**	0.97**	-2.92**	-4.30**	-83.73**
ICGV 6022	-1.07**	-0.97**	2.92**	4.30**	83.73**

***= significant at 0.001; ns= non-significant; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; GCA_F general combining ability of female parents and GCA_M= general combining ability of male parents.

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The GCAs of the Spanish parents are presented in Table 5.7. Significant ($p<0.05$) and positive GCA_F effects for DFL were exhibited by parents TZA 2444 and TZA 2426, a significant ($p<0.01$) positive GCA effect for DFL was exhibited by genotype TZA 2270, a significant ($P<0.01$) and negative GCA for DFL was exhibited by TZA 2518 and significant ($P<0.05$) and negative GCA for DFL was exhibited by TZA 254. A significant ($p<0.01$) and positive GCA for CLDS was observed in genotype TZA 254 and TZA 2518, a significant ($p<0.01$) and negative GCA for CLDS was shown by TZA 2518 and TZA 254. A significant ($p<0.01$) and positive GCA for NPP was shown by TZA 2518 and TZA 254, a significant ($p<0.01$) and negative GCA for NPP was exhibited by TZA 2444, TZA 2426 and TZA 2270. A significant ($p<0.01$) and positive GCA for HSW was observed in genotypes TZA 2444, TZA 2518 and TZA 254. A significant ($p<0.01$) and negative GCA for HSW was exhibited by TZA 2518, TZA 254TZA 2426 and TZA 2270 and, a significant ($p<0.01$) and positive GCA for SY was exhibited by genotypes TZA 2518 and TZA 254, a significant ($p<0.01$) and negative GCA for SY was exhibited by TZA 2444, TZA 2426 and TZA 2270. Male parent ICGV SM 07539 had a significant ($p< 0.05$) and positive GCA for DFL and CLDS, and had a significant ($p<0.01$) and negative GCA for NPP, HSW and SY. Male parent ICGV SM 07508 had significant ($p< 0.05$) and negative GCA for DFL and CLDS, and a significant ($p<0.01$) and positive GCA for NPP, HSW and SY.

Table 5.7: Estimates of the General Combining Ability effects of **Spanish** groundnut genotypes used as parents for yield, yield related traits and resistance to Cercospora leaf spot disease.

GCA_F	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
TZA 2444	0.83*	0.87**	-2.43**	0.53**	-74.95**
TZA 2518	-2.33**	-2.13**	4.23**	8.47**	122.38**
TZA 254	-0.83*	-0.80**	1.48**	3.55**	86.88**
TZA 2426	0.83*	1.03**	-1.60**	-8.12**	-68.28**
TZA 2270	1.50**	1.03**	-1.68**	-3.37**	-66.03**
GCA_M					
ICGV SM 07539	0.68*	0.37*	-0.95**	-3.77**	-58.13**
ICGV SM 07508	-0.68*	-0.37*	0.95**	3.77**	58.13**

***= significant at 0.001; ns= non-significant; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield; GCA_F general combining ability of female parents and GCA_M= general combining ability of male parents.

Estimates of the SCA effects of the crosses derived from Valencia botanical group are presented in Table 5.8. The results showed that the SCA for all the crosses were non-significant for DFL, except TZA 157 x Kakoma and TZA 2498 x Kakoma, which had a significantly ($p<0.01$) negative SCA and TZA 2498 X ICGV SM 96714 with a significant ($p<0.01$) and positive SCA. The crosses Local Makulu x ICGV SM 96714, TZA 121 x Kakoma, TZA 3786 x Kakoma, TZA 157 x Kakoma and TZA 2498 x ICGV SM 96714 had a negative non-significant SCA for the CLDS. All crosses were non–significant for NPP, except TZA 2498X ICGV SM 96714 which had significant ($p<0.01$) positive SCA and TZA 2498 x Kakoma with significant ($p<0.01$) negative SCA. The SCA for all crosses were non-significant for HSW. The SCA for SY was significant ($p<0.01$) and positive for Local Makulu x ICGV SM 96714 and TZA 121 x Kakoma, while it was significant ($p<0.01$) and negative Local Makulu x Kakoma and TZA 121 x ICGV SM 96714.

Table 5.8: Estimates of Specific Combining Ability effects of the hybrids of Valencia groundnut botanical group for days to flowering, Cercospora leaf spot disease severity number of mature pods per plant, hundred seed weight and seed yield evaluated in three sites.

Crosses (SCA)	DFL	CLDS	NPP	HSW	SY
Local Makulu x ICGV SM 96714	0.13^{ns}	-0.32^{ns}	-0.10^{ns}	0.17^{ns}	29.98**
Local Makulu x Kakoma	-0.13^{ns}	0.32^{ns}	0.10^{ns}	-0.17^{ns}	-29.98**
TZA 121 x ICGV SM 96714	-0.20^{ns}	0.02^{ns}	-1.35^{ns}	-0.25^{ns}	-16.43**
TZA 121 X Kakoma	0.20^{ns}	-0.02^{ns}	1.35^{ns}	0.25^{ns}	16.43**
TZA 3786 X ICGV SM 96714	-0.20^{ns}	0.35^{ns}	-1.02^{ns}	0.00^{ns}	-0.85^{ns}
TZA 3786 X Kakoma	0.20^{ns}	-0.35^{ns}	1.02^{ns}	0.00^{ns}	0.85^{ns}
TZA 157 x ICGV SM 96714	0.22^{ns}	0.27^{ns}	0.23^{ns}	0.08^{ns}	-2.60^{ns}
TZA 157 X Kakoma	-0.22**	-0.27^{ns}	-0.23^{ns}	-0.08^{ns}	2.60^{ns}
TZA 2498X ICGV SM 96714	0.05**	-0.32^{ns}	2.23**	0.00^{ns}	-10.10^{ns}
TZA 2498 X Kakoma	-0.05**	0.32^{ns}	-2.23**	0.00^{ns}	10.10^{ns}

***= significant at 0.001; ns= non-significant; DFL= days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield and SCA=specific combining ability.

Estimates of the SCA effects of crosses derived from Virginia botanical group are presented in Table 5.9. The results showed that the SCA effects for DFL of all crosses were significant ($p<0.01$) except TZA 534 x ICGV 6057, TZA 4280 x ICGV 6057, TZA 4390 x ICGV 6022 and TZA 4261 x ICGV 6022 which had significant negative SCA value, TZA 4280 x ICGV 6057 and TZA 4280 x ICG 6022 were significant ($p<0.05$) while, TZA 667 x ICGV 6057 and TZA 667 x ICG 6022 were non-significant. The SCA effects for CLDS were significant ($p<0.01$) for all crosses except TZA 4280 x ICGV 6057, TZA 4261 x ICGV 6022 and TZA 667 x ICGV 6057 which had non-significant and negative SCA, TZA 4280 x ICGV 6022, TZA 4261 x ICGV 6057, and TZA 667 x ICGV 6022 which had non-significant and positive SCA. The SCA effects for

NPP were non-significant for all crosses except TZA 4390 x ICGV 6057 and TZA 667 x ICGV 6057 which had significant ($p<0.01$) and positive SCA effects, and TZA 4390 x ICGV 6022 and TZA 667 x ICGV 6022, which had significant and negative SCA effects. The SCA effects for HSW were significant ($p<0.01$) for crosses TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022, TZA 4261 x ICGV 6057 and TZA 667 x ICGV 6057 which had positive SCA and TZA 534 x ICGV 6022, TZA 4280 x ICGV 6057, TZA 4390 x ICGV 6057 and TZA 667 x ICGV 6022 which had negative SCA values. The SCA for SY were significant for crosses; TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022, TZA 4261 x ICGV 6057 and TZA 667 x ICGV 6057 which had positive SCA values and TZA 534 x ICGV 6022, TZA 4280 x ICGV 6057, TZA 4390 x ICGV 6057, TZA 4261 x ICGV 6022 and TZA 667 x ICGV 6022 which had negative SCA values.

Table 5.9: Estimates of Specific Combining Ability effects of the hybrids of Virginia groundnut botanical group for days to flowering, Cercospora leaf spot disease severity, number of mature pods per plant, hundred seed weight and seed yield evaluated in three sites.

Crosses (SCA)	DFL	CLDS	NPP	HSW	SY
TZA 534 x ICGV 6057	-1.98**	-1.30**	0.58^{ns}	3.30**	89.32**
TZA 534 x ICGV 6022	1.98**	1.30**	-0.58^{ns}	-3.30**	-89.32**
TZA 4280 x ICGV 6057	-0.73*	-0.63^{ns}	-0.33^{ns}	-2.70**	-76.10**
TZA 4280 x ICGV 6022	0.73*	0.63^{ns}	0.33^{ns}	2.70**	76.10**
TZA 4390 x ICGV 6057	1.60**	1.95**	-5.08**	-5.62**	-183.60**
TZA 4390 x ICGV 6022	-1.60**	-1.95**	5.08**	5.62**	183.60**
TZA 4261 x ICGV 6057	1.18**	0.62^{ns}	-0.50^{ns}	2.22**	80.48**
TZA 4261 x ICGV 6022	-1.18**	-0.62^{ns}	0.50^{ns}	-2.22**	-80.48**
TZA 667 x ICGV 6057	-0.07^{ns}	-0.63^{ns}	5.33**	2.80**	89.90**
TZA 667 x ICGV 6022	0.07^{ns}	0.63^{ns}	-5.33**	-2.80**	-89.90**

***= significant at 0.001; ns= non-significant; DFL= days to 50% flowering; CLDS= Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield and SCA=specific combining ability.

Estimates of the SCA effect of crosses derived from Spanish groundnut botanical group are presented in Table 5.10. The results revealed that, the SCA for DFL were non-significant for all crosses however, TZA 2444 x ICGV SM 07539, TZA 2518 x ICGV SM 07508, TZA 254 x ICGV SM 07508, TZA 2426 x ICGV SM 07508 and TZA 2270 x ICGV SM 07539 had negative SCA and TZA 2444 x ICGV SM 07508, TZA 2518 x ICGV SM 07539, TZA 254 x ICGV SM 07539, TZA 2426 x ICGV SM 07539 and TZA 2270 x ICGV SM 07508 had positive SCA. The SCA for CLDS were significant ($p<0.01$) and positive for crosses TZA 2444 x ICGV SM 07508 and ($p<0.05$) for crosses TZA 254 x ICGV SM 07539 while cross TZA 2444 x ICGV SM 07539 had

significant (p< 0.01) and negative SCA and TZA 254 x ICGV SM 07508 had significant (p<0.05) and negative SCA, respectively. The SCA for NPP were significant (P< 0.01) and positive for crosses TZA 2444 x ICGV SM 07539, TZA 2518 x ICGV SM 07508 and (p<0.05) for crosses TZA 254 x ICGV SM 07508 and significant (p<0.01) negative for crosses TZA 2444 x ICGV SM 07508, TZA 2518 x ICGV SM 07539 and (p<0.05) for crosses TZA 254 x ICGV SM 07539. The SCA for HSW were significant (p<0.01) and positive for crosses TZA 2444 x ICGV SM 07539, TZA 254 x ICVG SM 07508 and TZA 2426 x ICGV SM 07508 and negative for crosses TZA 2444 x ICGV SM 07508, TZA 254 x ICGV SM 07539, TZA 2426 x ICGV SM 07539 and TZA 2270 x ICGV SM 07539. The SCA for SY were significant (p<0.01) and positive for crosses TZA 2444 x ICGV SM 07539, TZA 2518 x ICGV SM 07508, TZA 254 x ICGV SM 07508, TZA 2426 x ICGV SM 07539 and TZA 2270 x ICGV SM 07539 and negative for crosses TZA 2444 x ICGV SM 07508, TZA 2518 x ICGV SM 07539, TZA 254 x ICGV SM 07539, TZA 2426 x ICGV SM 07508 and TZA 2270 x ICGV SM 07508.

Table 5.10: Estimates of Specific Combining Ability effects of the hybrids of Spanish groundnut botanical group for days to flowering, Cercospora leaf spot disease severity, number of mature pods per plant, hundred seed weight and seed yield in three sites.

SCA	DFL	CLDS	NPP	HSW	SY
TZA 2444 x ICGV SM 07539	-0.77^{ns}	-1.20**	3.37**	7.60**	78.72**
TZA 2444 x ICGV SM 07508	0.77^{ns}	1.20**	-3.37**	-7.60**	-78.72**
TZA 2518 x ICGV SM 07539	0.73^{ns}	0.30^{ns}	-1.97**	-0.07^{ns}	-84.78**
TZA 2518 x ICGV SM 07508	-0.73^{ns}	-0.30^{ns}	1.97**	0.07^{ns}	84.78**
TZA 254 x ICGV SM 07539	0.57^{ns}	0.80*	-1.38*	-1.48**	-95.12**
TZA 254 x ICGV SM 07508	-0.57^{ns}	-0.80*	1.38*	1.48**	95.12**
TZA 2426 x ICGV SM 07539	0.07^{ns}	-0.20^{ns}	0.70^{ns}	-1.82**	52.05**
TZA 2426 x ICGV SM 07508	-0.07^{ns}	0.20^{ns}	-0.70^{ns}	1.82**	-52.05**
TZA 2270 x ICGV SM 07539	-0.60^{ns}	0.30^{ns}	-0.72^{ns}	-4.23**	49.13**
TZA 2270 x ICGV SM 07508	0.60^{ns}	-0.30^{ns}	0.72^{ns}	4.23**	-49.13**

***= significant at 0.001; ns= non-significant; DFL= days to 50% flowering; CLDS= Cercospora leaf spot disease severity; NPP= number of mature pods per plant; HSW= hundred seed weight; SY= seed yield and SCA=specific combining ability.

The estimates of the genetic variance components and heritability for the Valencia botanical group are presented in Table 5.11. The additive genetic variance was larger than the dominance genetic variance and the broad sense heritability was higher than the narrow sense heritability in CLDS, NPP and SY, while the narrow sense heritability was higher in DFL and HSW.

Table 5.11: Estimates of the variance components and heritability for yield and its related traits and Cercospora leaf spot disease score for the Valencia groundnut botanical group.

Parameter	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
Additive genetic variance	3.209	0.959	3.909	13.563	9591.534
Dominance genetic variance	0.375	0.016	3.419	-0.280	637.064
Phenotypic variance	5.6244	2.2707	9.556	15.0308	10233.1268
H^2	0.6372	0.4294	0.7668	0.8837	0.9996
h^2	0.5705	0.4223	0.4091	0.9023	0.9373

DFL=days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of pods per plant; HSW= hundred seed weight; SY= seed yield; Sed GCA_F=Standard error of difference of females' general combining ability; Sed GCA_M= Standard error of difference of males' general combining ability; Sed SCA= Standard error of difference of specific combining ability; H^2 = broad sense heritability and h^2 = narrow sense heritability.

The estimates of genetic variance components and heritability for the Virginia botanical group are presented in Table 5.12. The dominance genetic variance was larger than the additive genetic variance and the broad sense heritability was higher than the narrow sense heritability for all the traits.

Table 5.12: Estimates of the variance components and heritability for yield and its related traits and Cercospora leaf spot disease score for Virginia botanical group.

Parameter	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
Additive genetic variance	2.195	2.205	1.667	2.113	522.346
Dominance genetic variance	4.126	3.230	27.093	31.114	31016.942
Phenotypic variance	7.2472	6.4357	30.6862	34.3115	31543.2192
H^2	0.8722	0.8445	0.9372	0.9684	0.9998
h^2	0.3029	0.3426	0.0543	0.0616	0.01656

DFL=days to 50% flowering; CLDS= Cercospora leaf spot disease severity; NPP= number of pods per plant; HSW= hundred seed weight; SY= seed yield; Sed GCA_F=Standard error of difference of females' general combining ability; Sed GCA_M= Standard error of difference of males' general combining ability; Sed SCA= Standard error of difference of specific combining ability; H^2 = broad sense heritability and h^2 = narrow sense heritability.

The estimates of genetic variance components and heritability for the Spanish botanical group are presented in table 5.13. The dominance genetic variance was larger than the additive genetic variance, while the broad sense heritability was higher than the narrow sense heritability for all the traits.

Table 5.13: Estimates of the variance components and heritability for yield and its related traits and Cercospora leaf spot disease score for Spanish botanical group.

Parameter	**DFL**	**CLDS**	**NPP**	**HSW**	**SY**
Additive genetic variance	0.606	0.362	0.818	8.076	1207.421
Dominance genetic variance	0.626	1.031	8.729	40.306	13775.667
Phenotypic variance	2.8428	2.4438	11.3004	50.0150	14987.2092
H^2	0.4333	0.5700	0.8448	0.9673	0.9997
h^2	0.2132	0.1481	0.0724	0.1615	0.0806

DFL=days to 50% flowering; CLDS = Cercospora leaf spot disease severity; NPP= number of pods per plant; HSW= hundred seed weight; SY= seed yield; Sed GCA_F=Standard error of difference of females' general combining ability; Sed GCA_M= Standard error of difference of males' general combining ability; Sed SCA= Standard error of difference of specific combining ability; H^2 = broad sense heritability and h^2 = narrow sense heritability.

5.6 Discussion

5.6.1 Combined analysis of variance for the different botanical groups

The significant difference of mean squares of sites, genotypes and interaction (Table 5.2-5.4) for the studied traits of the Valencia, Virginia and Spanish botanical groups revealed the responses of the genotypes across the testing sites were different and there were existence of genetic variability among genotypes, which can be exploited in breeding programmes. The percentage contribution of sum of square of females were greater than that of males and of the interaction effects of females to males, for all traits studied, indicating that additive genetic variance played a preponderant role in the inheritance of traits studied viz DFL, CLDS, NPP, HSW and SY. Therefore, hybridization and or selection in early generation may be recommended for breeding. These findings conform with earlier reports by Ali et al. (1995) who observed that the magnitude of GCA was greater than SCA for all the traits recorded, indicating that additive genetic variance was more important than non-additive genetic variance.

5.6.2 General combining ability effects of parents for Valencia botanical group

The GCA effects for Valencia female parents (Table 5.5) revealed that, genotype Local Makulu and TZA 121 had significant negative GCA for DFL; the parents are good combiners for earliness because negative GCA value will reduce number of days to maturity of the cross derived from such parents. The parents are also good combiners for CLD resistance because the negative GCA value indicates high resistance to the disease. Female parent TZA 3786 had significant positive GCA for HSW and SY, which was in a desirable direction; therefore, the

parent is a good combiner in breeding for yield improvement. Genotypes TZA 157 and TZA 2498 had significant positive GCA for DFL and CLDS and significant negative GCA for NPP, HSW and SY, these parents are not good combiners because positive GCA for DFL and CLDS will lead to increased number of days to maturity and susceptibility to CLD. General combining ability for male parents was significant and positive for NPP, HSW and SY, and significant negative for DFL and CLD in parent ICGV SM 96714. The GCA values were in a desirable direction; therefore, this male parent is a good combiner. On the other hand, it was significantly negative in Kakoma for NPP, HSW and SY and positive for DFL and CLDS; therefore, Kakoma was not a good general combiner.

5.6.3 General combining ability effects of parents for Virginia botanical group

Genotypes TZA 4280 and TZA 4390 had the lowest GCA values for DFL in a desirable direction (Table 5.6). Therefore, these parents are good general combiners when breeding for early maturity. Early maturity is a desirable trait for groundnuts because they can easily escape harsh environmental conditions such as drought and diseases including CLD. All female parents had low significantly positive GCA effects for CLDS except genotype TZA 4280. Low and negative GCA effects are desirable for disease resistance breeding. Therefore, genotype TZA 4280 is a good combiner for CLD resistance. Positive GCA is desirable for breeding of high NPP; therefore, genotype TZA 4280, which had positive GCA is a good general combiner. Farmers in Tanzania prefer high yielding groundnut varieties for both food security and income earning. Genotypes TZA 4390 and TZA 4261 had negative GCA effects for HSW, implying that using these genotypes as parents in breeding for yield improvement reduce seed weight of the crosses derived from them and consequently lower the overall yield. On the other hand, the female parent TZA 4280, which had positive significant GCA effects for seed yield is a good general combiner for yield improvement breeding programmes. Significant and negative GCA values for CLDS and positive GCA for seed yield were observed in male parent ICGV 6022, which could be useful for resistance breeding or direct production.

5.6.4 General combining ability effects of Spanish parents

The significant positive GCA for Cercospora leaf spot disease score was shown by female parents TZA 2444, TZA 2426 and TZA 2270 (Table 5.7), which is undesirable because high GCA value means increasing in disease susceptibility; therefore, the parents were bad combiners. The significant negative GCA for CLDS was observed in female parents TZA 2518 and TZA 254; therefore, these parents were good combiners because they will pull down the GCA_M counterparts and in so doing increasing CLD résistance. The significant positive GCA for HSW was observed in female parents TZA 2444, TZA 2518 and TZA 254, which was in a desirable direction. Significant positive GCA for seed yield, which was portrayed by parents TZA 2518 and TZA 254 indicate that these were good general combiners because their GCA values were towards the desirable direction for yield improvement. The male parent ICGV SM 07508 had significantly negative GCA effects for DFL and CLD as well as highly positive GCA effects for NPP, HSW and SY. This genotype can be considered as a good general combiner for early maturity, disease resistance and yield improvement. According to Busa et al. (2008), good general combiners are effective in developing superior groundnut varieties.

5.6.5 Specific combining ability effects for Valencia botanical group

All crosses had non-significant SCA effects for CLD (Table 5.8), although Local Makulu x ICGV SM 96714, TZA 121 x Kakoma, TZA 3786 x Kakoma, TZA 157 x Kakoma and TZA 2498 x ICGV SM 96714 had negative SCA which is in a desirable direction because low SCA values will increase disease resistance, while the rest had positive SCA values which is in an undesirable direction. All crosses were non-significant for HSW;.However Local Makulu x ICGV SM 96714, TZA 121 x Kakoma and TZA 157 x ICGV SM 96714 had positive SCA, which is in a desirable direction. SCA for SY was significant positive in Local Makulu x ICGV SM 96714 and TZA 121 x Kakoma, which was in a desirable direction, while it was significant negative for Local Makulu x Kakoma and TZA 121 x ICGV SM 96714, which is in an undesirable direction, the rest of crosses were non-significant.

5.6.6 Specific combining ability effects for Virginia botanical group

The significant positive SCA effects for Cercospora leaf spot disease score was observed in crosses TZA 534 x ICGV 6022 and TZA 4390 x ICGV 6057, while it was significantly negative in crosses TZA 534 x ICGV 6057, TZA 4280 x ICGV 6057 and TZA 4390 x ICGV 6022, which is in the desirable direction (Table 5.9). The significant positive SCA effects for the number of mature pods per plant was exhibited by crosses TZA 4390 x ICGV 6022 and TZA 667 x ICGV 6057, therefore, were considered to be superior as they recorded positively significant SCA effect for number of pods per plant. A significant positive SCA effects for hundred seed weight was portrayed by crosses TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022, TZA 4261 x ICGV 6057 and TZA 667 x ICGV 6057, which were in a desirable direction. Significant positive SCA effects for seed yield were observed on crosses TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022, TZA 4261 x ICGV 6057 and TZA 667 x ICGV 6057, which were in a desirable direction.

5.6.7 Specific combining ability for Spanish groundnut botanical group

The significant negative SCA for Cercospora leaf spot disease score was portrayed by cross TZA 2444 x ICGV SM 07539 and significant negative by cross TZA 254 x ICGV SM 07508, which was in a desirable direction (Table 5.10). However, crosses TZA 2518 x ICGV SM 07508, TZA 2426 x ICGV SM 07539 and TZA 2270 x ICGV SM 07508 were non-significant but with negative SCA value for Cercospora leaf spot disease score which was in a desirable direction. The low and negative SCA value is desirable for disease resistance breeding because as it becomes low the level of disease resistance increases. The significant positive SCA for hundred seed weight was observed in crosses TZA 2444 x ICGV SM 07539, TZA 2270 x ICGV SM 07508, TZA 2426 x ICGV SM 07508 and TZA 254 x ICGV SM 07508; therefore, these crosses are potential high yielding genotypes. The cross TZA 2518 x ICGV SM 07508 was non-significant but with positive SCA, which is a desirable value for high yielding; therefore is a potential candidate for further breeding programme. Significant positive SCA for seed yield was exhibited by crosses TZA 254 x ICGV SM 07508, TZA 2518 x ICGV SM 07508, TZA 2444 x ICGV SM 07539, TZA 2426 x ICGV SM 07539 and TZA 2270 x ICGV SM 07539, which is a desirable trait to farmers and therefore can be useful in their fields because they can tolerate Cercospora leaf spot disease and yield high. These crosses can be advanced for further selection to obtain high yielding segregants in the segregating generation (Manivannan et al., 2008).

5.6.8 Heritability for yield, yield components and Cercospora leaf spot disease in different groundnut botanical groups

Significant estimates of genetic variance components and heritability presented in Tables 5.11, 5.12 and 5.13 for Valencia, Virginia and Spanish groundnut botanical groups respectively revealed that, additive genetic variance were larger than dominance genetic variance in Valencia group. However, in Virginia and Spanish group dominance genetic variance was larger than additive genetic variance. Broad sense heritability was higher than narrow sense heritability on DFL, CLDS, NPP, HSW and SY for all the three botanical groups. Implying that these traits can be transmitted from parents to progenies through hybridization. Low narrow sense heritability observed in all the crosses were due to larger dominance or environmental effects on the trait than the additive gene effects. The increase in magnitude of dominance component of the variance implies a decrease in narrow sense heritability (Kearsey and Pooni, 1996). Thus, selection of genotypes from initial generations for resistance to CLD may be difficult due to high influence of dominance effects in the expression of the total phenotypic variance (Kormsa-art et al., 2002). For this reason, selection based on individual plants for CLD resistance would be more effective when carried out on later generations. In this way, the occurrence of heterozygotes is reduced and the available additive variance for selection is increased, thereby providing higher possibilities of selection gains for the trait. Jinks and Pooni (1984) reported that if selection were delayed there would be an increase in narrow sense heritability and hence, increase in response to selection. However, if selection is based on early generations for characters with low narrow sense heritability estimates, Oeveren and Stam (1993) and Kearsey and Pooni (1996) recommended that bulk and single seed descent (SSD) breeding methods, followed by selection on family mean can ensure high genetic gain among the progenies.

5.7 Conclusion

The analysis of variance across sites revealed significant differences among genotypes for both yield and its components, and CLDS for all the three groundnut botanical groups (Valencia, Virginia and Spanish). Significant differences were detected among parents, crosses, parents x crosses interaction for CLD resistance, SY and its traits. These sources of variations had significant interactions with the testing sites for DFL, CLDS, NPP, HSW and SY. The significance of the mean squares of the GCA effects of females and males, and SCA effects of

female x male indicated the importance of both additive and non-additive gene effects for inheritance of CLD resistance and seed yield in all groundnut botanical groups respectively. Dominance genetic variance was larger than additive genetic variance, and broad sense was higher in magnitude than narrow sense heritability, respectively, in DFL, CLDS, NPP, HSW and SY; indicating that these traits can be transmitted to progenies through hybridization and selection.

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Chapter 6: Performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials

Abstract

Lack of high yielding groundnut cultivars tolerant to Cercospora leaf spot disease (CLD) and stable across different environments is one of the challenges to groundnut production by smallholder farmers in Tanzania. This makes selection of adaptable high yielding stable varieties under the different agro-ecological zones before release a very important part of the breeding program as this has an impact on the adoption and productivity of the cultivar. The objectives of this study were to evaluate and select genotypes that are tolerant to CLD, high yielding and identify environments that can be used for selection. A total of 24 groundnut genotypes comprising of six double cross population, twelve single cross parents and six checks from the three botanical groups (Valencia, Virginia and Spanish) were evaluated over six environments (viz Tumbi in Tabora region, Mlali, Ilindi and Hombolo in Dodoma region, Njoro in Manyara region and Ikhanoda in Singida region in Tanzania in the 2016/17 cropping season. The experiment was laid out in a 6x4 alpha lattice design replicated twice. Additive main effect and multiplicative interaction (AMMI) model was used in analysis. The study result revealed that, Tumbi (E1) was the most discriminating environment followed by Ilindi (E3), Mlali (E2), Hombolo (E4), Njoro (E5) and Ikhanoda (E6) respectively. The Hombolo (E4), Njoro (E5) and Ikhanoda (E6) environments showed a high correlation, therefore, indirect selection can be applied across the environments. The existence of such unique correlation among test environments has the advantage of reducing the number of sites used for evaluation and thus reducing cost of evaluating the genotypes. Using the first and second interaction principal component axis (IPCA1 and IPCA 2) genotype G2, G5, G11, G7, G3 and G8 was identified as the best performing genotypes however, G7 had relative stability and adaptability across the testing environments. These crosses will be advanced through selfing and selection of CLD tolerant progenies that are yielding high.

Key words: AMMI, Cercospora leaf spot disease, Environments, Groundnuts, IPCA1, IPCA2, Stability, Adaptability.

6.1 Introduction

The interaction between the performance of the genotype as determined by its genetic composition and the environment can greatly influence the performance of the genotype (Yan and Wu, 2008). Testing of genotypes across different locations over years and seasons has been used by many breeders to evaluate the stability of genotypes across different environments. This helps to develop breeding strategies that can assist in breeding superior cultivars for the target environments (Kang, 2002). Over the years, many terminologies have been used to refer to the genotype by environment interaction (GEI) analysis, for instance, specific adaptation, stability studies, and mega environments (Yan and Hunt, 2002). For each specific environment the mean genotype`s performance and stability over different environments have been used to evaluate the genotypes and mega environments were classified and identified (Casanoves et al., 2005).

The best varieties are those with good stability in terms of performance across a wide range of different environments, they exhibit small GEI effects as opposed to the unstable varieties with a large GEI effects. Such varieties make the breeder`s work of selecting the best varieties for the farmers very difficult (Yusuf, 2009). The performance of any cultivar is a combination of the cultivar and the environment in which it is grown over seasons (Bernardo, 2002), and the interaction that exists between the genotype and the environments GEI (Hallauer et al., 2010). Other factors that play part in the GEI and can be source of the variation observed includes temperature, duration of the growing season, lack of enough water, sub-soil pH, rainfall and social economic factors (Bänziger et al., 2006). Other factors include the biotic factors (Butron et al., 2004).

In this study, the stability and adaptability of the genotypes were analysed using additive main effects and multiplicative interaction (AMMI) model (Rad et al., 2013) in multi-environment (MET) two-way data matrices. The GEI has been the main area of focus in AMMI analysis, leaving out the component of the effect of the genotype. AMMI model are useful for understanding GEI (Kaya et al., 2002).

6.2 Materials and methods

6.2.1 Study site and parental selection

The selection of F_1 hybrids was done based on evaluation of single cross hybrids for their combining ability, heritability and gene action governing the inheritance of yield, yield related traits and CLD resistance conducted at three sites in the Dodoma region (Chapter five). The two best performing F_1 hybrids were selected from each botanical group based on CLD tolerance and farmers' preferred traits, and were inter-crossed to produce double cross populations. Thereafter, the six heterogametic double cross populations (i.e. with reciprocals), the twelve F_1 hybrids and six checks were evaluated in six locations viz Ilindi, Mlali and Hombolo in Dodoma region, Ikhanoda in Singida region, Njoro in Manyara region and Tumbi in Tabora region, to determine GEI of the double crosses compared with their single cross parents and checks and to select populations with improved CLD tolerance.

6.2.2 Experimental design and field establishment

The twelve F_1 hybrids, six standard checks and six double cross populations from the three groundnut botanical groups (i.e. Valencia, Virginia and Spanish) as shown in Table 6.1 were planted in six locations, viz Ilindi (6^0 1' 0'' S, 35^0 34' 0'' E) on 8th January, 2017, Mlali (6^0 17.791' S, 36^0 44.938' E) on 17th January, 2017 and Hombolo (5^0 54' S, 35^0 57' E) on 10th January, 2017 in the Dodoma region, Ikhanoda (6^0 37.10' S, 34^0 57. 5' E) on 23rd December, 2016 in Singida region, Njoro (5^0 15.237' S, 36^0 28.454' E) on 1st February, 2017 in the Manyara region and Tumbi (5^0 07.32' S, 32^0 6.913' E) on 30th November, 2016 in the Tabora region. The experiment was laid out in an alpha lattice design (6 x 4) with two replications in one cropping season namely, 2016/17. The double crosses were planted in the field plots of 1.5 x 1 m size with inter-row and intra-row spacing of 0.5 and 0.1 m respectively. Each plot had three rows each with 10 plants. Other cultural practices were done as recommended. The crossing schemes of single crosses to obtain double crosses and their reciprocals are summarized in table 6.2a and 6.2b.

Table 6.1: List of 24 groundnut genotypes evaluated for CLD tolerance and, yield and yield related traits across six sites in Tanzania.

SNo.	Genotype code	Genotype name	Botanical group
1	G1	[(Local Makulu x ICGV SM 96714) x (TZA 121 x Kakoma)]	Valencia
2	G2	[(ICGV SM 96714 x Local makulu) x (Kakoma x TZA 121)]	Valencia
3	G3	(ICGV SM 96714 x Local Makulu)	Valencia
4	G4	(Local Makulu x ICGV SM 96714)	Valencia
5	G5	(Kakoma x TZA 121)	Valencia
6	G6	(TZA 121 x Kakoma)	Valencia
7	G7	ICGV SM 09511	Valencia
8	G8	TZA 2421	Valencia
9	G9	[(TZA534 x ICGV 6057) X (TZA 4390 x ICGV 6022)]	Virginia
10	G10	[(ICGV 6057 x TZA 534) x (ICGV 6022 x TZA 4390)]	Virginia
11	G11	(ICGV 6057 x TZA 534)	Virginia
12	G12	(TZA 4390 x ICGV 6022)	Virginia
13	G13	(ICGV 6022 x TZA 4390)	Virginia
14	G14	(TZA 534 x ICGV 6057)	Virginia
15	G15	CG 7	Virginia
16	G16	TZA 4291	Virginia
17	G17	[(TZA 2518 x ICGV SM 07508) X (TZA 254 x ICGV SM 07508)]	Spanish
18	G18	[(ICGV SM 07508 x TZA 2518) x (ICGV SM 07508 x TZA 254)]	Spanish
19	G19	(ICGV SM 07508 x TZA 2518)	Spanish
20	G20	(TZA 254 x ICGV SM 07508)	Spanish
21	G21	(ICGV SM 07508 x TZA 254)	Spanish
22	G22	(TZA 2518 x ICGV SM 07508)	Spanish
23	G23	JL 24	Spanish
24	G24	Pendo	Spanish

Table 6.2a: Crossing scheme of single crosses to obtain double crosses for Cercospora leaf spot disease resistance and yield in groundnuts.

Valencia type	Virginia type	Spanish type	Description
AB x CD	EF x GH	IJ x KL	Crossing between best performing single crosses to produce F_1 heterogametic double crosses.
↓	↓	↓	
F_1(ABCD)	F_1(EFGH)	F_1(IJKL)	

Table 6.2b: Crossing scheme of reciprocal single crosses to obtain double crosses for Cercospora leaf spot disease resistance and yield in groundnuts.

Valencia type	Virginia type	Spanish type	Description
BA x DC	FE x HG	JI x LK	Crossing between reciprocals of best performing single crosses to produce F_1 heterogametic double crosses.
↓	↓	↓	
F_1(BADC)	F_1(FEHG)	F_1(JILK)	

6.3 Data collection

Data on the CLD score were recorded from the symptoms on individual plants grown in middle rows of each plot at 28, 35 and 42 days after first inoculation. The ratings for both early and late leaf spot were carried out using 1 - 9 visual canopy rating scale expressed in percentage severity (refer to Table 4.1) as suggested by Subrahmanyam et al. (1995).

Yield and yield related data collected included days to emergence (DTE), days to 50% flowering (DFL), length of reproductive branches (LRB) (cm), number of pods per plant (NPP), pod yield (PY), number of seeds per pod (SPP), seed colour (SC), 100 seed weight (HSW) and seed yield (SY)(g), as suggested by IBPGR; ICRISAT (1985).

6.4 Statistical analysis

Collected data were analysed using Genstat version 14. The combined analysis of variance (ANOVA) model used was:

$$Y_{ijk} = \mu + \beta_{ij} + g_{ki} + e_{jk} + (ge)_{ij} + \varepsilon_{ijk}$$

Where Yij is the disease score of the genotype i in environment j, μ is overall disease mean score, gi and ej are genotypic and environmental effect, $(ge)ij$ is the effect of interaction between the i^{th} genotype and j^{th} environment, $\in ij$ is the mean random error of the i^{th} genotype and ej environment.

The dataset presented in the current study was from a replicated yield and disease trial, which were analysed as an alpha lattice design and therefore, the equation for the AMMI model used was as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum \lambda^2{}_n \gamma_{gn} + \Delta_{en} + \rho_{ge} + K_{r(e)} + \varepsilon_{ger}$$

where Y_{ger} is disease score of genotype *g* in environment *e* for replicate *r*, μ is the grand mean of disease score, α_g is the genotype deviation from the grand mean, β_e is the environment deviation, λ_n is the singular value for interaction principal component (IPC) *n* and correspondingly λ^2_n is its eigenvalue, γ_{gn} is the eigenvalue for genotype *g* and component *n*, Δ_{en} is the eigenvector value for environment *e* and component *n*, with both eigenvectors scaled as unit vectors, ρ_{ge} is the residual, $K_{r(e)}$ is the block effect for replication *r* within environment *e*, and ε_{ger} is the error.

6.5 Results

6.5.3 Combined analysis of variance

The combined AMMI analyses of variance (ANOVA) of the twenty-four genotypes evaluated across six environments are presented in Table 6.3. The result revealed highly significant differences (P<0.001) for environments in CLD, NPP, HSW and SY. CLD, DFL, DM, NPP, HSW and, SY differ significantly (p<0.001) among evaluated genotypes. The interaction between genotypes x environment was significant in CLDS, NPP, HSW, SY, DFL and DM.

Table 6.3: Combined analysis of variance for CLDS, SY and yield related traits over six environments.

Source of variation	DF	CLDS	DFL	DM	NPP	HSW	SY
Replication	1	3.337	0.056	62.35	8	0.23	2298
Environments	5	14.16***	5.18^{ns}	58.14^{ns}	513.70***	1923.19***	372041***
Genotypes	23	127.26***	128.72***	1027.06***	127.11***	525.12***	263217***
Gen x Env. Interaction	115	3.03***	6.68**	15.44*	8.57***	45.99***	16551***
Error	138	1.533	2.037	10.24	3.683	4.651	6825
Total	287						

*** = Significant at P<0.001, **= significant at p<0.01, *= significant at p<0.05, ns=non-significant, DF=Degrees of freedom, CLDS= Cercospora leaf spot disease severity, DFL=days to 50% flowering, DM= days to maturity, NPP= number of mature pods per plant, HSW= hundred seed weight, SY= seed yield

The mean performance of CLDS, SY and yield related traits for the twenty-four groundnut genotypes evaluated in six environments are presented in Table 6.4. Groundnut genotypes differed significantly (P<0.001) for all the evaluated traits. Groundnut genotype G21, G22, G14, G5 and G13 were the best five in CLD resistance and had disease score of 12.08 to 13.67 which was lower than the mean (i.e. 17.75), genotypes G6, G5, G4, G2 and G21 were the best five in yield and had seed yield of 848.10 to 1071.50 which was above the mean (i.e. 759.70).

Table 6.4: Mean performance of groundnut CLDS, seed yield and yield related traits across six environments.

SNo.	Genotype code	CLDS	DFL	DM	NPP	HSW	SY
1	G1	19.25	42.25	123.92	23.83	45.16	796.60
2	G2	18.08	39.92	121.00	27.92	50.05	898.70
3	G3	19.33	42.92	124.50	20.92	42.58	741.80
4	G4	17.58	40.42	122.42	22.67	46.92	1024.00
5	G5	13.58	37.83	113.08	28.25	43.35	1033.60
6	G6	13.75	42.92	123.92	28.17	39.12	1071.50
7	G7	24.00	41.25	121.75	24.00	45.67	561.00
8	G8	21.42	41.50	122.17	23.83	44.34	768.90
9	G9	19.00	44.58	104.25	24.42	37.50	676.50
10	G10	17.25	44.17	102.25	27.58	39.83	778.30
11	G11	18.67	43.83	106.67	24.08	36.58	667.70
12	G12	17.08	43.08	102.50	26.92	40.38	785.60
13	G13	13.67	36.08	96.83	33.08	45.50	814.30
14	G14	13.33	38.58	99.75	30.42	43.17	793.80
15	G15	22.08	48.08	114.42	21.75	32.27	532.00
16	G16	20.50	48.50	116.92	21.58	33.23	549.40
17	G17	19.33	40.17	115.92	23.42	30.89	729.90
18	G18	17.08	38.67	111.67	25.75	34.00	753.10
19	G19	19.33	40.33	115.25	23.25	29.57	693.40
20	G20	16.08	39.08	111.67	25.33	32.88	732.20
21	G21	12.08	36.17	99.42	29.75	39.98	848.10
22	G22	12.25	36.75	101.17	27.83	37.94	829.00
23	G23	21.25	41.75	121.00	22.08	27.30	572.80
24	G24	19.92	43.17	122.08	20.83	25.57	582.10
Grand Mean		17.75	41.33	113.10	25.32	38.49	759.70
F Test		***	***	***	***	***	***
LSD		1.00	1.15	2.58	1.55	1.74	66.69
CV (%)		7.00	3.50	2.80	7.60	1.74	10.90

***= significant at p< 0.001, CLDS=Cercospora leaf spot disease severity, DFL= days to 50% flowering, DM= days to maturity, NPP= number of mature pods per plant, HSW= hundred seed weight, SY= seed yield, LSD= least significant difference, CV= coefficient of variation.

Additive main effect and multiplicative interaction analysis of variance for CLD severity

The AMMI analysis of variance is presented in Table 6.5. The analysis revealed that G, E and GXE multiplicative terms were significant ($p<0.001$). The genotypes accounted for 61.67% of the treatment sum of squares. The environments and the interaction between genotypes and the environment however, contributed significantly lower to the variations and accounted for 18.95% and 19.38% of the treatment sum of squares, respectively. The mean square for the first IPCA axis was larger than the residual indicating that, the partitioning of the interaction sum of squares by AMMI was very effective. The first and second IPCAs captured 41.33% and 25.96% of the interaction sum of square and degree of freedom, respectively. The two IPCA axes jointly accounted for 67.29% of the interaction SS, leaving 32.71% of the variation due to G x E interaction in the residual.

Table 6.5: Analysis of variance based on the AMMI model for Cercospora leaf spot disease severity of 24 genotypes over six environments.

Source	DF	SS	MS	TVE	GEE (%)	Cumulative (%)
Block	6	45985	7664			
Treatments	143	9817519	68654***			
Genotypes	23	6053995	263217***	61.67		
Environments	5	1860206	372041***	18.95		
Interactions	115	1903318	16551***	19.38		
IPCA 1	27	1098024	40668***		41.33	41.33
IPCA 2	25	549057	21962***		25.96	67.29
Residuals	63	256237	4067			
Error	138	941857	6825			
Total	287	10805361	37649			

***, ** Significant at 0.001 and 0.05 probability levels respectively, DF=Degrees of freedom, SS=Sum of squares, MS=Mean Square, IPCA=Interaction Principal Component Axis, TVE = Total Variation explained, GEE = explained G x E interaction.

The AMMI analysis data with IPCA1 and IPCA2 scores for the groundnut genotypes and the test environments are shown in Tables 6.6 and 6.7, respectively. The IPCA scores were both negative and positive for genotypes and environments. The Tumbi (E1) was the most discriminating environment as it had the largest IPCA1 score and the longest vector, followed by Ilindi (E3), Mlali (E2), Hombolo (E4), Njoro (E5) and Ikhanoda (E6) respectively (Table 6.7). The environments Hombolo (E4), Njoro (E5) and Ikhanoda (E6) had high correlation (Figure 6.1)

Table 6.6: The IPCA1 and IPCA 2 scores for 24 groundnut genotypes evaluated in six evironments.

Genotype code	Genotype name	Botanical group	IPCAg1 score	IPCAg2 score
G1	[(Local Makulu x ICGV SM 96714) x (TZA 121 x Kakoma)]	Valencia	-7.23	-6.05
G2	[(ICGV SM 96714 x Local makulu) x (Kakoma x TZA 121)]	Valencia	-10.44	2.57
G3	(ICGV SM 96714 x Local Makulu)	Valencia	-8.26	-4.47
G4	(Local Makulu x ICGV SM 96714)	Valencia	-5.05	-8.65
G5	(Kakoma x TZA 121)	Valencia	3.67	-11.18
G6	(TZA 121 x Kakoma)	Valencia	-3.93	-2.54
G7	ICGV SM 09511	Valencia	-15.32	10.68
G8	TZA 2421	Valencia	-1.02	-7.54
G9	[(TZA534 x ICGV 6057) X (TZA 4390 x ICGV 6022)]	Virginia	0.27	-0.96
G10	[(ICGV 6057 x TZA 534) x (ICGV 6022 x TZA 4390)]	Virginia	4.18	0.56
G11	(ICGV 6057 x TZA 534)	Virginia	0.67	-0.85
G12	(TZA 4390 x ICGV 6022)	Virginia	4.92	2.09
G13	(ICGV 6022 x TZA 4390)	Virginia	6.25	1.95
G14	(TZA 534 x ICGV 6057)	Virginia	5.79	1.79
G15	CG 7	Virginia	4.82	1.77
G16	TZA 4291	Virginia	4.04	1.79
G17	[(TZA 2518 x ICGV SM 07508) X (TZA 254 x ICGV SM 07508)]	Spanish	-2.23	2.05
G18	[(ICGV SM 07508 x TZA 2518) x (ICGV SM 07508 x TZA 254)]	Spanish	2.09	-0.01
G19	(ICGV SM 07508 x TZA 2518)	Spanish	1.91	1.07
G20	(TZA 254 x ICGV SM 07508)	Spanish	2.47	1.80
G21	(ICGV SM 07508 x TZA 254)	Spanish	1.56	4.16
G22	(TZA 2518 x ICGV SM 07508)	Spanish	1.79	4.42
G23	JL 24	Spanish	3.76	4.08
G24	Pendo	Spanish	5.30	1.46

Table 6.7: The IPCA1, IPCA2 scores of six environments based on environmental mean CLD

Environment	Environment name	IPCAe1	IPCAe2
1	Tumbi	12.33	3.19
2	Mlali	5.49	-2.11
3	Ilindi	7.77	-5.91
4	Hombolo	5.01	6.77
5	Njoro	-16.86	13.64
6	Ikhanoda	-13.75	-15.58

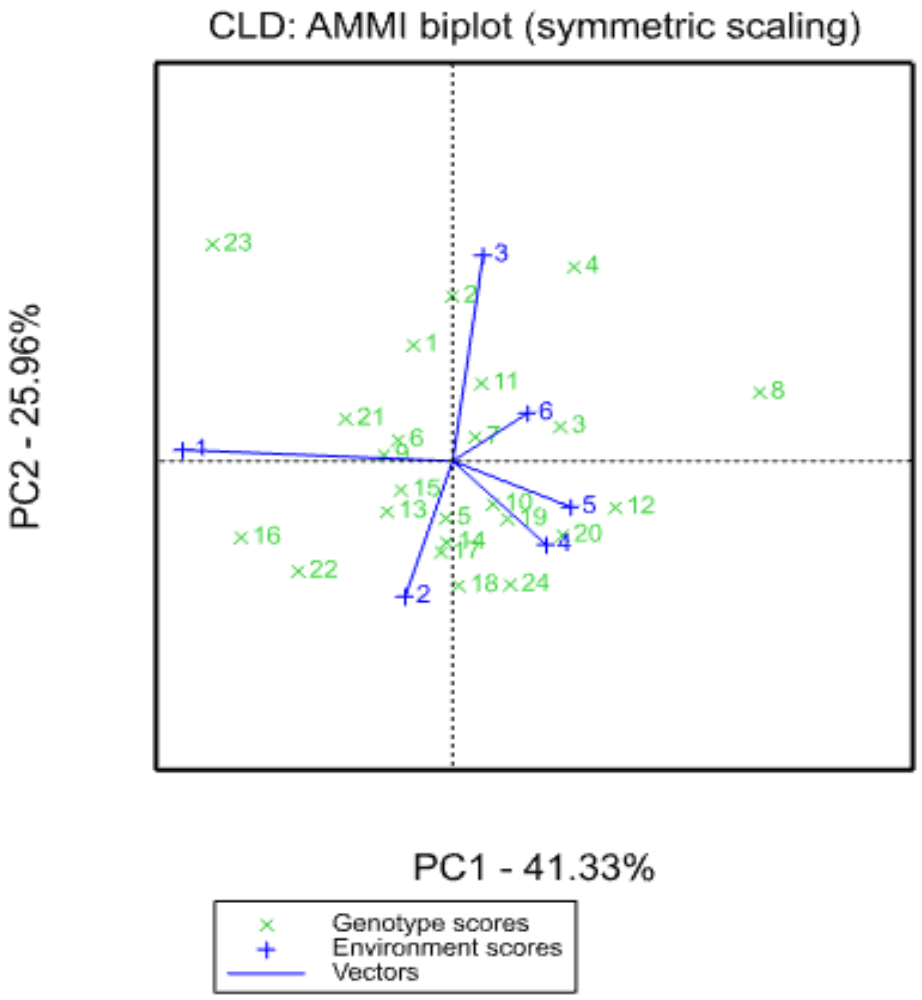

Figure 6.1: Cercospora leaf spot disease severity Bi-plot of GE based on AMMI2 for the first two interactions principal component scores.

6.6 Discussion

Significant differences in genotypes performances across environments and their interaction in all evaluated traits indicated their variation in genetic composition and ability to adapt to various environmental conditions. The G+E+GEI variation was explained in three proportions, which are genotype (G), the environment (E) and the genotype by environment interactions (GEI) (Table 6.5). The genotype had the biggest contribution to the variation with 61.67% of the total treatment sum of squares while GEI contributed 19.39% with environment contributing only 18.95%. Similarly, Sewagegne et al. (2013) and Negash et al. (2013) reported lower environmental contribution to the total variation than GEI contribution. The high genotype percentage contribution was a result of variation in genotypes performance across environments, referred to as crossover. The difference in contribution due to G, E and GEI from the AMMI analysis meant that the environments were diverse and caused a great variation in CLD tolerance. The variations amongst environments indicated the importance of multi-environment trials. The large differences in performance due to change in environment is applicable to genotype assessment and mega environment analysis (Gauch and Zobel, 1996).

The Tumbi (E1) was the most discriminating environment as it had the largest IPCA1 score and the longest vector, followed by Ilindi (E3), and Mlali (E2). They could be used for culling inferior genotypes and selection of specifically adapted genotypes (Yan and Tinker, 2006). Hombolo (E4), Njoro (E5) and Ikhanoda (E6) showed high correlation, indicating the possibility of using indirect selection. The existence of such correlation has the advantage of reducing the number of sites without affecting the results. The Njoro (E5), Hombolo (E4) and Ikhanoda (E6) were the most representative. They had smaller angle with the average environment axis and could be used for selecting generally adapted genotypes (Yan and Tinker, 2006).

Using the first and second interaction principal component axis (IPCA1 and IPCA2), genotypes G2, G11, G7, G3 and G8 were relative stable and adaptable across the testing environments. Therefore, can be advanced as transgressive segregants up to later generations and selected for CLD tolerance and seed yield before utilization in crop improvement or commercial cultivation. There were more genetic diversity in double crosses as compared to single crosses indicating the powerfulness of double crossing as compared to single crossing mating design.

6.7 Conclusion

The Tumbi, Mlali and Ilindi sites were most discriminating sites while Hombolo, Njoro and Ikhanoda were highly correlated therefore only one of the sites could be selected for further screening of the genotypes to reduce cost of running the experiment. The double cross hybrid G2 and single cross hybrids G4, G5, G6, G13, G14, G21 and G22 performed the best across environments in terms of CLD tolerance and seed yield therefore, are recommended for further segregation in the breeding programme. In order to develop high yielding CLD resistant varieties.

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Chapter 7: An overview of the research findings

7.1 Introduction and objectives of the study

Groundnut (*Arachis hypogaea* L.) belongs to genus *Arachis* in the subtribe Stylosanthinae of the tribe Aeschynomeneae of the family Leguminosae and originates from South America (Naidu et al., 2006). It is the most important summer season cash crop as well as oil seed crop in the world (Mensah and Obadoni, 2007). Various fungal diseases reduce groundnut yield but Cercospora leaf spot disease (CLD is the most detrimental one causing yield loss of up to 70% (Waliyar, 1990). Use of chemicals for the control of CLD has been practiced for a long time having varying degrees of success (Backman et al., 1977). In most countries, chemical control of CLD of groundnut is not widely practiced due to high costs of chemicals, the detrimental effect to the environment and farmers lack of knowledge on the use of these chemicals. The development of CLD resistant cultivars is the most appropriate strategy to reduce yield loss caused by the fungi. The current study identified promising genotypes that can be used by farmers either directly or by breeders to develop resistant varieties to improve productivity of groundnuts, especially under the smallholder farming system. This chapter presents the highlights of the objectives of the study and gives a concise summary of the core findings of each objective. Finally, the implications of the study findings to plant breeding against Cercospora leaf spot diseases are inferred.

The study had the following specific objectives:

i. To establish groundnut production constraints and identify traits preferred by smallholder farmers' and other stakeholders in the groundnut value chain in Central Tanzania.
ii. To evaluate the performance of Tanzanian germplasm and introduced groundnut lines for yield and yield-related traits and resistance to Cercospora leaf spot diseases to select promising parents for breeding.
iii. To determine association of yield and yield-related traits, and resistance to Cercospora leaf spot diseases through correlation and path analysis to guide future groundnut breeding.
iv. To determine gene action and heritability of yield and resistance to Cercospora leaf spot diseases and to select promising parents and crosses with enhanced yield and durable resistance to Cercospora leaf spot diseases in groundnut.

v. To determine the performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials.

7.2 Research findings in brief

7.2.1 Groundnut production constraints and traits preference by smallholder farmers' and other stakeholders in the groundnut value chain in Central Tanzania.

This study was conducted in three districts and six villages involving 124 farmers in Central Tanzania. Furthermore, interviews with groundnut traders and processors were conducted based on semi-structured questionnaire and observations following transect walk were used to gather data. The main findings of the study were:

- 83.9% of the groundnut growers were aged between 21 to 60 years old.
- 72.6% of the groundnut growers were males.
- 96.8% of the groundnut growers were able to read and write..
- Main crops grown were groundnuts, maize, sorghum and sunflower.
- 84.5% of groundnut growers planted landraces and had not adopted newly released varieties, and only 10.4 and 5.1% of the farmers from Bahi and Dodoma municipal respectively, grew improved varieties.
- 51.8% of the farmers used own saved seed, 19.9% purchased seed from fellow farmers, 10.4% purchased seed from the local market, and 9.8% purchased seed from government research and extension services.
- 71.1% of groundnut produced were sold, while 28.9% was for consumption and seed for the next season.
- Constraints facing farmers include drought, poor soil fertility, plant diseases, insect pest, availability of seeds of improved varieties and, unavailability of reliable and low market price.
- Constraints facing groundnut traders include poor grain quality with mixed size and colour.
- Constraints to processors include low market of finished products, high cost of packaging materials, lack of investment capital, bureaucratic procedure in business and brand registration, availability of other cheap sources of oil.

- Farmers preferred groundnut varieties with erect growth habit, high yield, a high oil content, tolerant to diseases and other environmental stresses, early maturing, with large seed size, good taste, brown coloured seed and easy threshability.
- Traders preferred groundnut varieties with medium to large seed size with brown colour.
- Processors preferred groundnut varieties with medium to large seed size, less pod constriction, sharp beak and brown colour.
- 94.4% of groundnut farmers do not apply any control measure against Cercospora leaf spot diseases thinking that the yellow and dark spots on leaves are signs of maturity.

7.2.2 Evaluation of Tanzanian germplasm and introduced groundnut lines for resistance to Cercospora leaf spot diseases, yield and yield-related traits and selection of promising parents for further breeding.

Eighty-four groundnut genotypes sourced from ICRISAT–Malawi, the Tanzanian National plant genetic resource centre, local market and smallholder farmers were evaluated across three sites for two seasons. Data on Cercospora leaf spot diseases score was collected using a 1-9 visual canopy scale. In addition, data on yield and yield components were. The main findings of the study were:

- There were significant variations among groundnut genotypes evaluated.
- Twenty-one genotypes were identified with significant tolerance to CLD disease, a high number of pods per plant, relatively early maturity, high number of mature pods per plant and pod yield, higher seed weight and seed yields, and with farmer preferred agronomic traits.
- The following groundnut genotypes; ICGV SM 96714, ICGV 6057, TZA 2426, Local Makulu, ICG 6022, ICGV SM 07539, TZA 254, TZA 4280, KAKOMA, ICGV SM 07508, TZA 2270, TZA 121, TZA 667, TZA 157, TZA 2498, TZA 3786, TZA 4390, TZA 4261, TZA 2444, TZA 534 and TZA 2518 were selected based on the above mentioned merits.
- The coefficient of variation at phenotypic levels was relatively higher than genotypic variation for Cercospora leaf spot disease resistance and seed yield.
- There were small differences between the genotypic and phenotypic coefficient of variations among the studied traits.
- The broad sense heritability was higher than the narrow sense heritability.
- The interaction between the performance of the genotype as determined by its genetic composition and the environment can greatly influence the performance of the genotype

- The present study demonstrated the significance of screening genotypes before selecting parental material for further breeding.

7.2.3 Association of yield and yield-related traits and resistance to Cercospora leaf spot diseases through correlation, path and cluster analysis to guide future groundnut breeding.

Eighty-four groundnut genotypes were evaluated in the field at three sites for two seasons in Central Tanzania. Data on Cercospora leaf spot disease score was collected using 1-9 visual canopy scale, also data on seed yield and yield related components were collected as per ICRISAT groundnut descriptors. The study was conducted to investigate correlation, path-coefficient and cluster analyses of yield and its related traits and CLDS in groundnut, in order to investigate the nature and magnitude of trait association between CLDS, seed yield and its contributing characters as the pre-requisite for selection of parental material for breeding for CLD resistance. The main findings were:

- Days to 50% flowering (DFL) was negatively correlated with days to maturity (DM) and Cercospora leaf spot diseases severity (CLDS).
- Number of mature pods per plant (NPP) was positively correlated with hundred seed weight (HSW).
- Number of seeds per pod was positively correlated with hundred seed weight (HSW) and seed yield (SY).
- Seed yield was positively correlated with hundred seed weight and number of seeds per pod
- Hundred seed weight was negatively correlated with days to maturity and Cercospora leaf spot diseases severity.
- Pod yield was negatively correlated with days to 50% flowering, days to maturity and Cercospora leaf spot diseases severity.
- Positive direct effect on seed yield was depicted by the number of seeds per pod, pod yield, Cercospora leaf spot diseases severity, length of reproductive branch and days to 50% flowering.
- Negative direct effect on seed yield was depicted by days to maturity, number of mature pods per plant and hundred seed weight.
- Indirect effect on seed yield via SPP was exhibited by HSW and NPP.
- Indirect effect on seed yield via CLD was exhibited by DFL, DM and LRB.

- Indirect effect on seed yield via DM was exhibited by NPP and HSW.
- Five phenotypically diverse clusters were derived from 84 groundnut genotypes sourced from ICRISAT–Malawi, the Tanzanian National plant genetic resource centre, local market and smallholder farmers.
- The five clusters had relatively different magnitude of means of yield and its related traits, ranging from low to high yielding.
- The five clusters had different reaction to Cercospora leaf spot diseases ranging from tolerant to susceptible.

7.2.4 To determine gene action and heritability of yield and resistance to Cercospora leaf spot diseases and to select promising parents and crosses with enhanced yield and durable resistance to Cercospora leaf spot diseases in groundnut.

Twenty-one parents were selected from screening experiment for yield potential and tolerance to Cercospora leaf spot disease. The parents included seven Valencia, Virginia and Spanish types with either tolerance to Cercospora leaf spot disease or a high yield potential. The 21 selected parents were planted in the screen house. The parents were crossed using (3x7) line x tester mating design each botanical group were crossed separately to produce single crosses. The single cross hybrids were evaluated for combining ability estimates and gene action governing inheritance of yield and CLD tolerance in three locations for one season. The main findings of the study were:

- There were variation among genotypes for both yield and its components, and Cercospora leaf spot disease severity (CLDS) for all three groundnut botanical groups (Valencia, Virginia and Spanish).
- Good general combiners for the Valencia botanical group were Local Makulu, TZA 121 (females) and ICGV SM 96714 (male); for the Virginia botanical group these were TZA 4280, TZA 4390 (females) and ICGV 6022 (male) and TZA 2518, TZA 254 (females) and ICGV SM 07508 (male) were good general combiners for the Spanish botanical group.
- The study identified crosses; Local Makulu x ICGV SM 96714, TZA 121 x Kakoma, TZA 3786 x Kakoma, TZA 157 x Kakoma, TZA 2498 x ICGV SM 96714 for Valencia group; TZA 534 x ICGV 6057, TZA 4280 x ICGV 6022, TZA 4390 x ICGV 6022 and TZA 4261 x ICGV 6057 for Virginia group, and TZA 2444

x ICGV SM 07539, TZA 2518 x ICGV SM 07508, TZA 254 x ICGV SM 07508, TZA 2426 x ICGV SM 07539, TZA 2270 x ICGV SM 07539 and TZA 2270 x ICGV SM 07508 for Spanish group with superior per se performance for CLD resistance and yield.

- Both additive and non-additive gene effects were predominantly important in the inheritance of CLD resistance and yield in all groundnut botanical groups.
- Dominance genetic variance was larger than additive genetic variance; therefore, inheritance of CLD and, yield and its components can be transmitted to offspring by hybridization and selection at later stages in the segregating populations.
- Broad sense heritability was higher in magnitude than narrow sense heritability, indicating that these traits can be transmitted to progenies through hybridization, and selection can be conducted at later stages in the segregating populations.

7.2.5 Performance of single cross parents versus double crosses and checks among groundnut (*Arachis hypogaea* L.) intra botanical groups in multi-location trials.

The two best performing F_1 single cross hybrids (section 6.5.4) were selected from each botanical group based on CLD tolerance and farmers' preferred traits, and were inter-crossed to produce double cross populations. Thereafter, the six double cross populations (i.e. with reciprocals), the twelve F_1 single cross hybrids and six checks were evaluated in six locations viz Ilindi, Mlali and Hombolo in the Dodoma region, Ikhanoda in the Singida region, Njoro in the Manyara region and Tumbi in the Tabora region, to determine GEI of the double crosses compared with their single cross parents and checks and to select populations with improved CLD tolerance. The experiment was laid out in an alpha lattice design (6 x 4) with two replications in one cropping season (2016/17). The main findings of the study were:

- There were significant differences among evaluated genotypes across environments for the studied traits.
- There were significant G, E and GXE multiplicative terms for the studied traits.
- The genotypes accounted for 61.67% of the treatment sum of squares, the environments and the interaction between genotypes and the environment accounted for 18.95% and 19.38% of the treatment sum of squares, respectively.
- The first and second IPCAs captured 41.33% and 25.96% of the interaction sum of square and degree of freedom, respectively.

- The two IPCA axes jointly accounted for 67.29% of the interaction sum of squares, leaving 32.71% of the variation due to G x E interaction in the residual.
- The IPCA scores were both negative and positive for genotypes and environments, and three environments were most discriminating while the other three had high correlation.