GENETIC ANALYSIS OF AGRONOMIC TRAITS AND TOLERANCE TO LATE LEAF SPOT IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)

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Declaration

I declare that the work in this dissertation entitled "GENETIC ANALYSIS OF AGRONOMIC TRAITS AND TOLERANCE TO LATE LEAF SPOT IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)" has been carried out by me in the Department of Plant Science, Ahamdu Bello University, Zaria. The information derived from the literature has been duly acknowledged in the text and the list of references provided. No part of this dissertation was previously presented for another degree or diploma at this or any other institution.

TAKYUN, AKOLO DANIEL	……..…	….……
Student	Signature	Date

Certification

The dissertation entitled "GENETIC ANALYSIS OF AGRONOMIC TRAITS AND TOLERANCE TO LATE LEAF SPOT IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)" by TAKYUN, Akolo Daniel meets the regulations governing the award of the degree of Masters of Science in Plant Breeding of Ahmadu Bello University, Zaria and is approved for its contribution to knowledge and literary presentation.

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Dedication

I dedicate this work to God Almighty the giver of knowledge.

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ABSTRACT

Late leaf spot (LLS) *Phaeoisariopsis personata* (Berk. and Curtis) Deighton is one of the most important foliar diseases of groundnut worldwide including Nigeria. Repeated application of fungicide could contribute to greater production cost and environmental pollution. The deployment of resistant cultivars offers a better option for the management of the disease in groundnut. Information on the genetic control of resistant to LLS will aid in the development of appropriate breeding methodology that will result in the development of resistant genotypes with high yielding potentials. The objectives of this study were to determine the mode of gene action controlling LLS in some groundnut genotypes, estimate heritability and to determine the degree of association between yield components and LLS resistance. Nine parental groundnut genotypes comprising of five LLS resistant (ICGV 12991, ICGV 7878, FDR-F7 82, FDR-F7 67 and FDR-F7 61) and four LLS susceptible (SAMNUT 23, SAMNUT 24, SAMNUT 25 and SAMNUT 26) genotypes obtained from IAR were used to generate F_1 hybrids using 4 x 5 North Carolina design II mating design. The $20F_1$s and the parental genotypes were evaluated for LLS in a randomized complete block design with three replications at the screen house of the Department of Plant Science under artificial inoculation. High relative humidity was maintained by covering the plants with polyethylene bags for 24 hours before and after inoculation. Data were collected on pod yield, disease severity, disease incidence and other agronomic traits. The results of the analysis of variance indicated highly significant ($P \leq 0.01$) differences for the traits of the genotypes evaluated which suggest that progress could be made through selection. High heritability coupled with low GAM for LLS tolerance traits, suggesting large environmental influence on the traits and predominant role of additive gene effect. Both narrow and broad sense heritability were high for the LLS tolerance traits, suggesting the role of additive gene action, hence mass selection could be effective to exploit any additive gene action. Highly

significant negative GCA effects were recorded for disease incidence in SAMNUT 25 (-0.05), indicating the genotype is a good general combiner for LLS disease incidence and SAMNUT 26 (-5.90) is a good general combiner for LLS disease severity. ICGV 12991 (-12.00), FDR-F7 67 (-.68) and FDR-F7 61 (-2.23) are good general combiner for LLS disease tolerance (disease incidence and severity) Among the crosses, significant and negative SCA effects were obtained for most of the crosses SAMNUT 24 x FDR-F7 67 and SAMNUT 24 x FDR-F7 61 for LLS tolerance (disease incidence and severity), indicating that they are good specific combiners for LLS tolerance. The ratio of the GCA and SCA variances indicated the preponderance of SCA variance over GCA variance for disease incidence and severity, indicating the role of non-additive gene effect and it may be due to difference in genotypes used as parents. The female parents contributed more than the male parents, suggesting the maternal effects and that when developing breeding population to LLS tolerance, the choice of maternal parent is very important. Significant negative correlation was observed between diseases (incidence and severity) and number of seed per pod as well as 100-seed weight which implies the selection for low disease incidence and severity would increase the number of seed per pod and 100-seed weight.

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List of Abbreviations

ANOVA	Analysis of Variance
AUDPC	Area under Disease Progress Curve
COV	Coefficient of Variation
DAS	Days after Sowing
DAPI	Diamidino-Phenylindole
Df	Degree of Freedom
EMS	Error Means Square
FAO	Food and Agricultural Organization
FDR	Folia Disease Resistant
F.S	Full Sib
F_1	First Filial Generation
GCV	Genotypic Coefficient of Variation
GISH	Genomic In Situ Hybridization
GA	Genetic Advance
GAM	Genetic Advance as Percent of Mean
GCA	General Combining Ability
GLM	Generalised Linear Model
H.S	Half Sib
H_b	Broad Sense Heritability
h_n	Narrow Sense Heritability
IAR	Institute for Agricultural Research
ICRISAT	International Crop Research Institute for Semi-Arid Tropics
ICGV	ICRISAT Groundnut Variety

LAD	Leaf Damage Area
LLS	Late Leaf Spot
LSD	Least Significant Difference
PDI	Percent Disease Incidence
PCR	Polymerase Chain Reaction
PCV	Phenotypic Coefficient of Variation
PDA	Potato Dextrose Agar
RCBD	Randomized Complete Block Design
SAMNUT	Samaru Groundnut
SAS	Statistical Analysis Software
SE	Standard Error
SCA	Specific Combining Ability

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CHAPTER ONE

1.0. INTRODUCTION

The cultivated groundnut (*Arachis hypogaea*) is an important food legume highly adapted to tropical and subtropical climates of the world. It is a key crop for small scale farmers especially in Africa and Asia where the crop serves as a valuable source of dietary protein, oil, and fodder for livestock. It is grown primarily as an oil crop, and largely grown in over 100 countries, with a world total production of 43.98 million tons on 21.8 million hectares (FAO, 2016). The global annual increase in production is 0.4% between 2009 and 2012 was attributed to both, an annual increase in yield by 0.1% and in area by 0.3% (Janila *et al*., 2013a). In West Africa, Nigeria is the largest producer of groundnuts with production of 3.0 million tons on about 2.4 million hectares (FAO, 2016). Nigeria and Senegal are the largest producers in West and Central Africa with 45% Africa total production (ICRISAT 2015).

Groundnut is used for preparation of peanut butter and confectionery products, the groundnut haulms are very nutritious fodder for animals and compost making (Janila *et al*., 2013b). The shells of groundnut are used in the manufacture of wallboard, abrasives, fuel and cellulose. Groundnut is valued as a rich source of energy whose oil content stood at 48–50% and protein 25–28% in the kernels (Janila *et al*., 2013b). The cake obtained after extraction of oil is used in animal feed industry, infant feed preparation and as soil amendment as it resist Pb absorption (Liu and Nie, 2013).

Despite the socio-economic and cultural importance of groundnut, its productivity in Nigeria is considered to be low (below 1 ton/ha) because of number of constraints like abiotic (droughts) and biotic (especially due to pests and diseases) stresses (Reddy *et al.*, 2003). Drought is the major abiotic constraints affecting groundnut productivity and quality worldwide (Reddy *et al.*,

2003). Two thirds of the global production occurs in rain-fed regions of the semi-arid tropics where rainfall is generally erratic and insufficient, causing unpredictable drought stress (Reddy *et al.,* 2003). Furthermore, groundnut yield and quality are severely constrained by a wide variety of fungal, bacterial, viral, and nematode pathogens. Late leaf spot is the most devastating fungal disease accounting for yield loss of over 60% (Okello *et al*., 2010). The disease is caused by *Phaeoisariopsis personata* with symptoms that are seen as small necrotic flecks that enlarge and become light to dark brown.

Previous studies have shown that efforts have been made to control late leaf spot disease using a combination of cultural and chemical measures with limited success (Page *et al*., 2002). Use of fungicides to control leaf spots usually increases production costs by 10% (Coffelt and Porter, 1986). Effective chemical control is heavily reliant upon multiple fungicide applications (Jordan *et al*., 2012), which are costly for resource poor farmers in Nigeria, and as well raises environmental and health concerns with significant decrease in crude protein and fiber contents with increasing disease severity (Coffelt and Porter, 1986). These factors coupled with health hazards associated with the use of insecticides suggested the use of host plant resistance as the most effective and environmentally friendly control measure for the management of LLS. In the last decades, groundnut varieties with resistance to late leaf spot have been developed including; 'York,' 'Georgia-07W', 'Georgia-03L' Southern Runner, Florida MDR98 and 'Georgia Green' which are commercially grown in Southeastern part of USA (Culbreath *et al*., 2009). Their uses in IAR, Nigeria is only limited to as sources of resistance to LLS because of genotype x environment interaction. The use of resistant genotypes and genetic information on inheritance of LLS will help in the development and utilization of LLS resistant cultivars which will reduce

production costs; and boost groundnut production in Nigeria. In view of the above; the research was carried out to achieve the following objectives:

i. To determine the mode of gene action controlling late leaf spot resistance in groundnut genotypes.
ii. To estimate heritability of resistance to late leaf spot and expected genetic gain from selection
iii. To determine the degree of association between yield components and late leaf spot resistance.

CHAPTER TWO

2.0. LITERATURE REVIEW

2.1. Groundnut (*Arachis hypogaea* L.)

Groundnut (*Arachis hypogaea* L.) is an annual plant that is distinguished from most other species by producing aerial flowers, but fruiting below the soil level. *Arachis* belongs to the family Fabaceae, tribe Aeschynnomeneae, sub-tribe Stylanthinae. *Arachis hypogaea* is the only domesticated species in the genus (Tillman and Stalker, 2009). Krapovickas (1969) reported that *A. hypogaea* var. *hypogaea* is likely the most ancient type because it has similar branching patterns as wild species, no compound florets, and a prostrate growth habit. The centre of origin for the genus *Arachis* is the Mato Grosso area of Brazil, but species evolved over a wide range of habitats in South America (Gregory *et al*., 1980). Molecular data indicate that the centre of genetic variation is also the Mato Grosso area of Brazil to eastern Bolivia (Stalker *et al*., 1994). Eighty species have been described (Krapovickas and Gregory, 1994; Valls and Simpson, 2005) which have been divided into nine sections based on morphology and cross-compatibility relationships. Smartt and Stalker (1982) proposed that the A and B genomes of section *Arachis* may be an A1 and A2 rather than being truly different based on chromosome pairing relationships. The species of different sections have overlapping distributions in many areas. Hybrids between species in different sections are difficult to produce and are usually sterile, while intrasectional hybrids can be fertile if they have similar genomic make-up (Stalker *et al.,* 1991). The species *A. hypogaea* has two subspecies *hypogaea* and *fastigiata* which are further divided into six botanical types *hypogaea, hirsuta, fastigiata, vulgaris, equatoriana* and *peruviana* botanical varieties. The subspecies are separated morphologically based on presence or absence of flowers on the main stem and regularly alternating vegetative and reproductive nodes on branches. The characteristics of these botanical varieties shows that *hypogaea* has no

floral axes or branches on main stem; alternating pairs of vegetative and reproductive axes on branches (alternate branching); inflorescence simple; vegetative branches moderate to profuse; primary branches longer than main stem; growth habit spreading, intermediate, or erect; usually two seeds per pod; pod beak not very prominent; seed size medium (runner market type) to large (Virginia market type); testa color generally tan (red, white, purple, or variegated also exist); cured seed dormancy moderate; maturity medium to late (Ntare *et al*., 2007). The *fastigiata* has floral axes on main stem; irregular pattern of vegetative and productive branches with reproductive branches predominating on branches (sequential branching); inflorescence usually simple; vegetative branches sparse; primary branches shorter than main stem; growth habit upright; two to four seeds per pod; pod beak absent, slight, or prominent; seed size small to medium; testa color tan, red, white, yellow, purple, or variegated; cured seed dormancy little (Ntare *et al.,* 2007).

Cultivated groundnut has an allotetraploid genome (AABB, 2n=4x=40). The low level of genetic variation within the cultivated gene pool and its polyploid nature limit the utilization of molecular markers to explore genome structure and facilitate genetic improvement. Nevertheless, a wealth of genetic diversity exists in diploid *Arachis* species (2n=2x=20), which represent a valuable gene pool for cultivated peanut improvement (Guo *et al.*, 2012). *Arachis hypogaea* is an allotetraploid (David *et al.,* 2012), most probably resulting from the hybridization of two wild species followed by natural chromosome duplication (Halward *et al.,* 1991; Young *et al*., 1996; Seijo *et al.,* 2007). The genome of *A. hypogaea* is large, being estimated at 2·8 Gb (Grilhuber, 2005) with a large repetitive fraction of approximately 64 % determined by DNA renaturation kinetics (Dhillon *et al*., 1980)

Cytogenetic analyses in *A. hypogaea* have revealed two types of chromosomes: ten pairs of A-type chromosomes, with strongly 4', 6-diamidino-2-phenylindole (DAPI)-stained (and hence AT-rich) heterochromatin at the centromeres, including the smallest pair of all chromosomes (Robledo *et al.,* 2010), and another ten pairs of chromosomes with more weakly staining centromeric heterochromatin bands, designated B chromosomes (Seijo *et al.,* 2004; Robledo *et al.,* 2010). Studies comparing the chromosomal heterochromatic banding patterns together with evidence from positions of rDNA clusters (Robledo, *et al*., 2010) and genomic in situ hybridization (GISH) (Seijo *et al.,* 2007) suggest that *A. hypogaea* A chromosomes are similar to those in the wild diploid *A. duranensis*, whilst the peanut B chromosomes are similar to those in the wild diploid *A. ipaënsis.* Other evidence such as species geographic distribution (Robledo *et al.,* 2010) and molecular phylogenies (Kochert *et al.,* 1996; Burow *et al.,* 2009; Moretzsohn *et al.,* 2013) corroborates that the most probable A and B genome donors to *A. hypogaea* are *A. duranensis* and *A. ipaënsis*.

Loss in crop yield due to diseases is one of the major constraints in meeting the demand of the world's ever increasing population. Though, crop losses due to diseases are being managed by use of chemicals and resistant cultivars, they are associated with limitations such as cost factor, health hazards and environmental pollution in the former, and time consuming laborious procedures and difficulty in ferrying the disease resistance genes in the latter. Nonetheless, Plant breeders have introgressed disease resistance genes from wild and cultivated plants to produce resistant varieties. In the recent years, integration of molecular techniques in to conventional breeding program has facilitated marker-assisted selection, as an attractive strategy for simultaneously improving a multitude of complex agronomic traits. The importance of rust and

late leaf spot in groundnut production has made researchers to increasingly concentrate on these diseases.

2.2. Importance of Late Leaf Spot Disease in Groundnut

Late leaf spot (LLS) is a foliar disease of groundnut in Africa and other parts of the world. Late leaf spot diseases symptoms are influenced by host genotype and environmental factors. For both diseases, small chlorotic spots appear on leaflets 10 days after infection. Late leaf spots pathogens are soil-borne and attack is most severe when groundnut follows groundnut in the rotation. LLS infection reduces the photosynthetic area by causing intense lesions on leaves, petioles, and stems that often lead to premature defoliation, loss of integrity of the peg, and hence yield loss. Photosynthesis of diseased canopies was reduced by defoliation and inefficient fixation of carbondioxide by diseased leaves. Pattee and Young (1982) reported reduction of leaf area index by 80 percent, carbon dioxide uptake by 85 percent and canopy carbon exchange rate by 93 per cent due to severe leaf spot damage. Reports have indicated over 50% yield losses from LLS (Kucharek, 2000; Grichar *et al*., 1998; Waliyar, 1991; McDonald *et al*., 1985). Subrahmanyam *et al.* (1992) reported yield reductions of 20 to 100% in South Africa and other parts of the world. Yussif (2010) reported 40-60% yield loss due to leaf spot in Ghana and late leaf spot was reported as the most predominant form in all locations of Northern Ghana. Leaf spots in Uganda has been reported to cause over 60% yield losses (Mugisha *et al*., 2004), mostly from LLS. Also, the control of this disease through application of plant protection measures does not only increases the cost of cultivation but also lead to environmental and health hazards. Hence, use of resistant cultivars is the best means of reducing crop losses ((Jordan *et al*., 2012; Shew *et al*., 2010; Page *et al*., 2002).

2.3. Late Leaf Spot Pathogen

Late leaf spot (LLS) disease is caused by a fungal pathogen (*Phaeoisariopsis personata*) (Berk. and Curt) (Shokes and Culbreath, 1997). The perfect state (*Mycosphaerella berkeleyii* W.A. Jenkins) is classified under the asogeneous fungi and both asci and spermatogonia occur on debris (Pattee and Young, 1982). Ijaz (2011) described the imperfect state as follows: Conidiophores are fasciculate, one to three geniculate with conspicuous conidial scars, mostly arranged in concentric rings on lower surface and darker in color. Conidia are olivaceous, obclavate, cylindrical and with one or more septa. Variation between isolates of leaf spot pathogens has been reported but the races have not been clearly characterized (Ijaz, 2011; Upadhyay *et al*., 2009; Holbrook and Stalker, 2003). Hossain and Ilag (1999) reported variability in virulence among eight *Phaeoisariopsis personata* isolates. Symptoms in plants inoculated with the least virulent isolate appeared later than in those inoculated with the most virulent isolate by an average of 1.25 days in both resistant and susceptible genotypes.

2.4. Inheritance of Late Leaf Spot Disease in Groundnuts

The genetic studies on late leaf spot (LLS) suggested that resistance is complex and polygenic in nature and probably controlled by several recessive genes (Khedikar *et al*., 2010; Upadhyay *et al*., 2009; Dwivedi *et al*., 2002; Motagi, 2001; Vasanthi and Reddy, 1997; Nevill, 1982). Resistance to LLS has been reported to be determined by two genes (Tiwari *et al*., 1984) and five-locus recessive genes in the crosses involving cultivated groundnut and wild *Arachis* species (Sharief *et al.,* 1978). Motagi (2001) reported duplicate recessive genes controlling resistance to LLS with favorable resistance alleles coming from inter-specific derivative CS 16 (ICGV 86855). Luo *et al*. (2005) identified 56 genes in response to late leaf spot resistance using microarray and real-time PCR. However, gene action of LLS resistance has been reported by

many workers but the genetics of a particular trait may vary with variation in plant material and environment in which the materials were evaluated from (Wambi, 2014).

Heritability estimates provides information about the correspondence between the phenotypic and genotypic variances. Thus heritability estimates provide information on which to base a breeding procedure (Dabholkar, 1992). Heritability estimates and genetic parameters are useful when comparing the expected genetic gain from selection based on alternative selection strategies. Hence heritability estimates can be used to predict gain from selection (Falconer and Mackay, 1996; Kearsey and Pooni, 1996). Effective selection in early generation of segregating materials can be achieved only when additive genetic effects are substantial and heritability is high (Kearsey and Pooni, 1996). Heritability (h_n^2) estimates from variance components were found to be low for most components of resistances to late leaf spot except for lesion size (mm) in Lampang × RLRS 15 (98%) and KhonKaen 60-1 × RLRS 15(91%) crosses and sporulation in Lampang × RLRS 15 (99%) cross in groundnut, suggesting that selection in early generation based on phenotype of individual plants would be ineffective (Kormsa-art *et al.*, 2002). According to Anderson *et al*. (1991) estimates of narrow sense heritability have ranged from low to high (0.18 to 0.74) for all components of resistance from parent-offspring regression estimates. Khedikar *et al*. (2010) however, reported high to very high (40.87 to 82.81%) heritability (broad sense) of LLS resistance in groundnut. Higher estimate of heritability do not necessarily provide high values of genetic advance Vishnuvardhan *et al*. (2012) and heritability alone provides no indication for the amount of genetic progress in the trait that can be achieved through selection. The effectiveness of selection depends upon genetic advance of the character selected along with heritability **(**Manju and Sreelathakumary, 2002). The information on genetic advance help in understanding the type of gene action involved in the expression of various

polygenic characters (Singh and Narayanan, 1993). Many studies have reported quantitative nature of inheritance of LLS resistance suggesting that the inheritance of LLS resistance is rather complicated and this could contribute to limited progress realized towards developing LLS resistant cultivars in groundnut breeding programs for LLS resistance. Information on heritability and gene effects of LLS resistance has been reported by many workers; however, it should be noted that the genetics of a particular trait may vary with variation in plant material and environment in which the materials are evaluated from. Therefore, it is important to understand the genetics of LLS resistance using the available IAR breeding materials before starting any breeding progress. The knowledge about heritability and nature of genetic effects prevailing in the breeding material is necessary to decide on a breeding procedure to be chosen.

Janila *et al*. (2013a) reported that resistance to LLS was controlled by a combination of both, nuclear and maternal gene effects in addition to epistatic effects (additive x additive, additive x dominance and dominance x dominance). While variation due to dominance effects and their interactions cannot be exploited effectively in groundnut, additive x additive epistatic variation is potentially useful, as it can be fixed in homozygous cultivars (Singh and Oswalt, 1991). The exploitation of the additive x dominance and dominance x dominance types of interactions require the maintenance of heterozygosity. Also, Shoba *et al*. (2010) suggested that epistasis may also be involved in the inheritance of many quantitative characters in groundnut including LLS resistance. Kaczamarek *et al*. (2002) reported that heterozygote populations are more adaptable than homozygote populations to varied environmental conditions; therefore, it is necessary to study gene action of quantitative traits before starting any breeding program. Resistance to leaf spot pathogens has been attributed to various morphological and anatomical characters of the host plant and to different chemical constituents of leaves and seeds (Wambi, 2014). It operates

by prolonging incubation and latent periods, and by reducing the number of lesions per unit area of leaf surface, defoliation, and sporulation. Resistance to leaf spots is recessive and independently inherited (Wambi, 2014). Nevill (1982) showed that late leaf spot resistance was determined by recessive alleles at five loci.

2.5. Combining Ability and Gene Action

Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its crosses. The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942). According to them, the general combining ability (GCA) is the comparative ability of the line to combine with other lines. It is deviation of the mean performance of all the crosses involving a parent from overall mean. Specific combining ability (SCA) was defined as the deviation in the performance of specific cross from the performance expected on the basis of general combining ability effects of parents involved in the crosses. A positive general combining ability (GCA) indicates a parent that produces above average progeny, whereas parent with negative GCA produces progeny that performs below average of the population. Specific combining ability (SCA) can be either negative or positive and SCA always refers to specific cross and never to particular parent itself. In statistical terms, the general combining abilities are the main effects and the specific combining abilities is an interaction (Olfati *et al*., 2012).

The most commonly used designs for combining ability studies are line x tester (L x T) and diallel analysis. Combining ability analysis following line x tester given by Kempthorne (1957) and Arunachalam (1974) is frequently used for testing the performance of lines in hybrid combinations. It is also useful in characterizing the nature and magnitude of gene action involved in controlling the quantitative traits. The general and specific combining ability effects and

variances obtained from a set of F_1s would enable a breeder to select desirable parents and crosses for each of the quantitative components separately. From their results Spargue and Tatum (1942) concluded that the general combining ability was mainly the results of additive gene action while the specific combining ability due to dominance, epistasis and genotypic environment interaction.

Baker's ratio close to unity indicates additive genetic effect, whereas Baker's ratio less than unity indicate non-additive or dominant genetic effect. The predominance of SCA variance denotes that non-additive genetic effects were largely influencing the expression of any traits under study hence; heterosis and use of hybrid vigor could be applied for improving those traits (Alam *et al*., 2008).

Heritability in associated with genetic gain over mean (GAM%) is more effective and reliable in predicting the resultant effect of selection of best genotypes for yield and its attributing traits. It helps in determining the influence of environment on the expression traits on the genotype and reliability of character (Patil *et al.,* 1996 and Ramanjinappa *et al.,* 2011).

2.6. Management of Late Leaf Spot Disease

Losses in groundnut yield due to leaf spots vary from place to place and among seasons. In the southern USA, where fungicide application is a normal practice, pod yield losses are estimated at around 10%. But for much of the semi-arid tropics, where fungicides are rarely used, losses in excess of 50% are common. Haulm losses from leaf spots normally exceed kernel losses. It is important that effective management of leaf spot diseases be developed and applied.

Depending upon length of the growing season and cultivars grown, the time of sowing may be adjusted to avoid infection of the crop from outside sources and to avoid environmental conditions conducive for the disease build-up. Weeds should be kept under control because their

heavy growth may encourage disease development through modification of the crop microclimate.

Watson (1988) found that fungicide application reduced the rate of disease progress in Florunner, Southern Runner and UF 81206. Chlorothalonil applied on a 21-days schedule provided control of late leaf spot that was sufficient to prevent yield losses in Southern Runner, a cultivar with moderate resistance (Culbreath *et al.,* 1992). Fungicides are first applied before or just after the appearance of symptoms, and further applications are made at intervals of 10-14 days until 2-3 weeks before harvest. This normally means that 6-8 applications are made through the season. Intervals between applications may have to be shortened under environmental conditions highly favorable to the disease development. Fungicidal control of leaf spots has been tried in a number of developing countries of the semiarid tropics and large increases in yield of both kernels and haulms have been obtained.

2.7. Coefficient of Variability of Late Leaf Spot Study

Wynne and Gregory (1981) stated that improving traits in groundnuts requires sufficient variability and understanding of genetic control, techniques for assuring desired traits, and a breeding strategy for effective use of variability. Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) have been reported moderate for late leaf spot in 28 F2 populations involving eight parents Vishnuvardhan *et al*. (2012). Kumari, (2008) reported high PCV (29.96-36.070) and GCV (27.71-32.96) in a population involving mutant lines that were evaluated in the field for LLS severity under natural condition. However, Khedikar, (2008) observed high PCV (33.5) and moderate (14.6) GCV for late leaf spot.

2.8. Components of Resistance to Late Leaf Spot in Groundnut

Several components contribute to resistance, including initial infection, lesion size, lesion number, sporulation, and defoliation (Anderson *et al.,* 1993; Aquino *et al*., 1995; Dwivedi *et al.,* 2002). Resistance to Leaf Spot in groundnut has generally been associated with late maturity (Miller *et al.,* 1990; Singh *et al*., 1997). Sporulation, lesion size, lesion number and latent period are important components of resistance to LLS and are highly correlated to each other and with percentage of necrotic area on leaf (Anderson *et al.,* 1990). Dwivedi *et al.* (2002) observed longer incubation period, longer latent period, lesser lesions per leaf, smaller lesion diameter, lower sporulation index, lesser percentage leaf area damaged, and lower disease scores in the resistant genotype as compared to susceptible genotypes and also reported high correlation among components of resistance. Motagi (2001) reported incubation period, lesion size and lesion on main-stem as the most important components of resistance, having strong association with field disease score, defoliation and remaining green leaf area. Percent defoliation had a highly significant positive association with field disease score (Dwivedi *et al.,* 2002).

2.9. Sources of Resistance and Breeding Progress for Resistance to Late Leaf Spot in Groundnut

The knowledge of the sources of resistance as well as components and screening methods for resistance are the backbone for the success of disease resistance breeding program. With increased emphasis in screening groundnuts for disease resistance, several sources of resistance to late leaf spot have been identified in *A. hypogaea* in different parts of the world (Holbrook and Isleib, 2001; Holbrook and Anderson, 1995; Anderson *et al*., 1993; Singh *et al*., 1997), and have been used to develop breeding lines with LLS resistance (Holbrook and Stalker, 2003). Holbrook

and Isleib (2001) observed that *A. hypogaea* accessions originating from Bolivia were more frequently found with resistance to LLS.

Majority of the resistant sources belong to subspecies *fastigiata* var. *fastigiata* and are land races from South America (Subrahmanyam*et al*.,1989), which were reported to be moderately resistant to LLS but with so many undesirable pods and seed characteristics, not commercially accepted. Wild *Arachis* species in contrast have shown variation ranging from immune to highly resistant reaction to LLS (Subrahmanyam *et al.,* 1985; Abdou *et al.,* 1974). Despite the progress to develop LLS resistant groundnut cultivars; however, combining high levels of resistance into with acceptable market traits continues to be a challenge to groundnut breeders. The cross compatibility barriers, linkage drag associated with resistance, crop duration, the complex nature of resistance to this disease, and the long period required for cultivar development contribute to limited progress realized so far towards developing LLS resistant cultivars with acceptable pod/seed characteristics (Holbrook and Stalker, 2003; Nigam and Dwivedi, 2000).

Despite these obstacles, in some part of the world, efforts have been made to breed for resistance to LLS in groundnut, which resulted in release and cultivation of moderately LLS resistant cultivars such as 'York,' 'Georgia-07W', 'Georgia-03L', Southern Runner, Florida MDR98 and 'Georgia Green' in the Southeastern part of USA (Culbreath *et al*., 2009); Bailey, Sugg and Florida fancy in USA (Jordan *et al*., 2012; Shew *et al*., 2010); ICGV-SM 86715 in Mauritius (Moss *et al.,* 1998), and Yue You 223 in China (Liang *et al.,* 1999). A few interspecific derivatives; ICGV 87165, GPNCW 1, GPNCW 2, GPNCW 3, GPNCW 4, ICGV 86699, and ICGV 87167 possessing high levels of resistance to foliar diseases have also been reported (Moss *et al.,* 1997; Reddy *et al.,* 1996; Nigam *et al.,* 1992). However, these elite germplasms have not been released for cultivation due to undesirable agronomical traits such as late maturity

and inferior pod and seed characteristics in comparison with commercially grown cultivars (Khedikar, 2008).

2.10. Correlation Coefficient

Correlation is the proportion of variance that two traits share due to genetic causes. Genotypic and phenotypic correlations are important in determining the degree to which various yield contributing characters are associated. Phenotypic correlation reflects the observed relationship, while genotypic correlation underline the true relationship among characters. Correlation measures the degree of association, genetic or non-genetic between two or more characters (Echekwu, 1991). According to Anderson *et al.* (1990, 1991), moderate to high correlation (0.41 to 0.86) existed between early and late leaf spot disease components. Hemingway (1957) observed a positive correlation between the color of foliage and resistance to late leaf spot in groundnut and indicated that varieties with light-green foliage were more susceptible than those with dark foliage.

CHAPTER THREE

3.0. MATERIALS AND METHODS

3.1. Description of Experimental site

The research was conducted at the Institute for Agricultural Research (IAR), Samaru, Ahmadu Bello University, Zaria ($11^0$11'N, $07^0$38'E), 600m above sea level in the Northern guinea Savannah. The research was carried out during the 2015/2016 raining season.

3.2. Experimental Materials

The experimental materials for this study comprised of nine early maturing groundnut genotypes representing a range of resistance levels to Late Leaf Spot (LLS) obtained from IAR Samaru. The resistant genotypes were validated in the 2013/2014 growing season IAR at the farm, Samaru. Five of the groundnut genotypes are tolerant to the Late Leaf Spot (LLS), these are ICGV 12991, ICGV 7878, FDR-F7 82, FDR-F7 67 and FDR-F7 61. The other four genotypes are the improved and released material by IAR, which are all susceptible to the Late Leaf Spot. These are SAMNUT 23, SAMNUT 24, SAMNUT 25 and SAMNUT 26.

3.3. Population Development

Two seeds from each of the groundnut genotypes were sown in plastic pots measuring 50.91m^3 in June 2015. The susceptible genotypes were used as female parents while the resistant genotypes as male parents. The parental lines were crossed in a 4 x 5 North Carolina mating design II as described by Comstock and Robinson (1948) to generate 20 F_1 progenies.

Table 3.1: Hybridization Scheme, using North Carolina Design II.

♀ \ ♂	PARENT (MALES)			
PARENT(FEMALES)	1	2	3	4
6	X_{16}	X_{26}	X_{36}	X_{46}
7	X_{17}	X_{27}	X_{37}	X_{47}
8	X_{18}	X_{28}	X_{38}	X_{48}
9	X_{19}	X_{29}	X_{39}	X_{49}

3.4. Hybridization Activities

Hybridization exercise began in August, 2015 and lasted for three weeks. During the process of hybridization, proper care was taken to avoid contamination of genotypes as well as injury to the selected buds. Emasculation exercise was carried out between 1630hrs – 1830hrs depending on the prevailing environment (Nigam *et al.,* 2009). Pollination was done in the morning (0600hrs – 0730hrs). In both activities, different colored nylon threads were used to mark the emasculated and pollinated buds.

Harvesting of the crosses started 90 days after the last pollination. All the matured pods originating from the nodes that had nylon threads on their upper internodes were picked as hybrid pods. All selfed pods from the female plants were discarded. The hybrid pods removed were immediately dried for 15 days. The pods were then shelled and caution was taken to prevent any damage of the seed component (testa, cotyledons and embryo).

3.5. Evaluation of F1 for response to LLS

The 20 F_1 progenies and the 9 parents were evaluated for LLS in the screen house using randomized complete block design (RCBD) with three replications. Two pots were allocated for each genotype and two seed were sown per pot. Agronomic practices were carried out for groundnut production according to IAR recommendations were adhered to (weeding; was carried

out three times, fumigating; was done once, watering; was carried out three times a week, to ensure proper growth and development of the groundnut genotypes).

3.6. Inoculation

Inoculum was obtained from groundnut leaves infected with LLS collected from IAR field. Fungal isolation was done using scheduled isolation trials at the IAR groundnut farm as described by (Riker and Riker, 1936; Khan *et al.,* 2013). The diseased portion of leaves was cut into small pieces of 1-2 mm and surface sterilized with 0.1% mercuric chloride solution for 1-2 minutes. The small pieces were rinsed twice in sterilized water and transferred to sterilized paper in petri dishes for drying. Plating of these dried pieces was done on Petri plates containing potato dextrose agar (PDA) medium in a laminar hood. The petri plates were then incubated at $27^{o}C \pm 2^{o}C$ for 57 days to allow the fungi to grow. After five days the margins of the developed mycelium were sub-cultured on PDA at $25^{o}C$ for seven days to get the pure culture of LLS. Single spore method was used for the identification of the LLS on the basis of morphological characters. Mycelial growth of the LLS in petri plates was blended with sterilized distilled water in a blender. Numbers of spores were diluted with sterile distilled water to reach 3.3×105 CFU ml^{-1}. The spores were used as inoculum which was sprayed on all the treatments except control. To provide favorable environment for disease development, watering was carried out regularly (Ijaz, 2011).

Thirty-five days old plants were inoculated with LLS at 106 conidia/ml inoculum concentrations. Hand held sprayer was used for the inoculation; 0.1 ml spore suspension was dropped on the leaves. High relative humidity around the plants was maintained by covering the plants with wet polythene bags 24 hours before inoculation. Inoculated plants were covered for another 24 hours to maintain high humidity. Plants were observed weekly for development of disease after

inoculation and disease score was recorded using 1-9 scale describes by Subrahmanyam *et al*., (1995) as presented in Table 3.2 below.

3.7. Data collection

Data on the following characters were recorded from four selected plants used for analysis.

Plant height (cm): The plant height was measured in centimetre at maturity using a thread and meter rule. The measurement was taken from the groundnut level (base) to the tip of the plant.

Days to 50% flowering: The days after sowing when two of the plants in each pod have flowered were recorded.

Days to maturity: The number of days that the plants took to attain maturity was recorded from the day of sowing.

Number of mature pods per plant: Number of mature pods was counted at harvest to calculate the mean number of pods per plant.

Number of seeds per pod: The average number of seeds obtained from ten randomly selected mature pods per plant were counted and recorded.

100 seed weight (gram): One hundred (100) seed weight were counted from the threshed pods weighed and measured in grams.

LLS disease severity: The disease severity was scored at 65 and 90 days after sowing (DAS) as described by Wambi (2014) using a modified nine-point scale as described by Subrahmanyam *et al*., (1995) as showed in Table 3.2.

LLS disease incidence: The per-cent disease incidence was scored using the scale recommended by ICRISAT (Waliyar *et al*., 2007) as showed in Table 3.3.

Table 3.2: Description of Leaf Spot scale (1-9)

Leaf spot score	Description	Disease Severity (%)
1	No disease	0
2	Lesion larger on lower leaves, no defoliation	1 – 5
3	Lesion larger on lower leaves, very few lesion on middle leaves, defoliation of some leaflets evident	6 – 10
4	Lesion on the lower middle leaves, but severe on lower leaves, defoliation of some leaflets evident on lower leaves	11 – 20
5	Lesion on all lower and middle leaves, over 50% defoliation of lower leaves	21 – 30
6	Lesion severe on lower and middle leaves, defoliation of some leaflets evident on middle leaves	31 – 40
7	Lesion on all leaves but less severe on top leaves, defoliation of all lower and some middle leaves	41 – 60
8	Defoliation of almost all middle leaves, lesion severe on top leaves and some defoliation of top leaves evident	61 – 80
9	Defoliation of almost all leaves having bare stems, some leaflets may be present, but with severe leaf spot	81– 100

Subrahmanyam *et al*. (1995) discussed the procedure for the screening for leaf spot disease in the green house.

Table 3.3: Percent Disease Incidence PDI scale for Groundnut LLS

PDI	Inference
Less than 10%	Highly resistant
11-30%	Resistant
31-50%	Moderately resistant
More than 50%	Susceptible

3.8. Data Analysis

3.8.1. Analysis of Variance (ANOVA)

Data collected on disease severity and incidences were transformed using log10 and were all subjected to analysis of variance using General Linear Model procedure of Statistical Analysis System (SAS) package (SAS, 2002). The ANOVA were based on the linear mathematical model:

$Y_{ijk} = \mu + r_i + g_j + e_{ijk}$;

Where Y_{ijk} = observed effect for $_i th$ replication and $_j th$ genotype,

μ = grand mean of the experiment,

r_i = effect of the $_i th$ replication,

g_j = effect of the $_j th$ genotype,

e_{ijk} = residual effect.

Significant difference between treatment means were compared using the Least Significant Difference (LSD) at 5% level of probability (Payne *et al*. 2010).

Form of ANOVA and Expected Means Square

Table 3.4: Form of ANOVA and Expected Mean Squares

Sources of variation	Df	Mean Squares	Expected Mean Squares
Replication	(r - 1)		
Genotype	(g - 1)	MS_2	$\sigma_e^2 + r\sigma_g^2$
Error	(g -1)(r -1)	MS_1	σ_e^2

Where g = number of genotypes, σ_g^2 = genotypic variance, r = number of replication, replication, $\sigma^2{}_e$ = error variance, df= degree of freedom, MS= observed mean squares, EMS = expected mean squares

3.8.2. Estimates of Coefficient of Variation

The phenotypic and genotypic coefficients of variation were computed using the formulae given by Singh and Chaudhary (1985).

(a) Phenotypic coefficient of variation (PCV %) $= \frac{\sqrt{\sigma_{ph}^2}}{\overline{X}} \times 100$

(b) Genotypic coefficient of variation (GCV %) $= \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$

GCV and PCV values were classified as low (<10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Menon (1973).

Table 3.5: Form of ANOVA for North Carolina mating design for model 1 (Comstock and Robinson, 1948)

Sources of Variation	Degree of Freedom	Mean Squares	Expected Means Square
Replications	$(r-1)$		
Males	$(m-1)$	MS_m	$\sigma^2{}_e + r\sigma^2{}_{fm} + rf\sigma_m^2$
Females	$(f-1)$	MS_f	$\sigma^2{}_e + r\sigma^2{}_{fm} + rm\sigma_f^2$
Males x Females	$(m-1)(f-1)$	MS_{fm}	$\sigma^2{}_e + r\sigma^2{}_{fm}$
Error	$(r-1)(mf-1)$	MS_e	$\sigma^2{}_e$

From the ANOVA, component of variance of the following would be estimated

$$\sigma^2{}_f = \frac{MS_f - MS_e}{rm} \qquad \sigma^2{}_m = \frac{MS_m - MS_e}{rf} \qquad \sigma^2{}_{fm} = \frac{MS_{fm} - MS_e}{r}$$

The linear model for analysis of variance for one location is given as:

$$Y_{ijk} = \mu + m_i + f_j + (m \times f)_{ij} + e_{ijk}$$

Where; Y_{ijk} = is the response of k^{th} observation in the i^{th} environment of the plant

μ = general mean; m_i = effect of the i^{th} male;

f_j = effect of the j^{th} female; $(m \times f)_{ij}$ = interaction effect;

e_{ijk} = error associated with each observation. i = number of males and j = number of females

2.8.3. Proportional Contributions of Males, Females and Crosses

The proportional contributions of males, females and their crosses to the total variance were calculated in accordance with Singh and Chaudhary (1985).

Contribution of males = $\frac{SS(Males)}{SS(Crosses)} \times 100$

Contribution of females = $\frac{SS(Females)}{SS(Crosses)} \times 100$

Where $SS(Males), SS(Females)$ and $SS(Crosses)$ were the sum of squares of Males, Females, and crosses respectively.

3.8.4. Estimation of General Combining Ability (GCA) and Specific Combining Ability (SCA) Variances

σ_f^2 = COV (H.S) females = $\frac{MS_f - MS_{fm}}{rm}$ σ_m^2 = COV (H.S) males = $\frac{MS_m - MS_{fm}}{rf}$

σ_{mf}^2 = COV (F.S) females = $\frac{MS_{fm} - MS_{lfm}}{r}$

Average estimates of the COV (H.S) were also estimated as follows:

$$\frac{MS_m + MS_f - 2MS_{fm}}{rl(m+f)}$$

The estimates of COV (H.S) and COV (F.S) were used to estimate GCA (σ^2_{GCA}) and SCA (σ^2_{SCA}) variances as described by Hallauer and Miranda (1988):

σ^2_{GCA} = 2COV (H.S) average

σ^2_{SCA} = COV (F.S) – COV (H.S) males – COV (H.S) females.

After estimating the GCA and SCA variances as mentioned above, the $\sigma^2_{GCA}/\sigma^2_{SCA}$ ratios was computed to predict the type of gene action involved.

$\sigma^2_{GCAm} = GCA_m - COV(H.S)m \quad \sigma^2_{GCAf} = GCA_f - COV(H.S)f$

$\sigma^2_{SCA} = SCA_{mf} - COV(F.S)mf$

3.8.5. Estimation of General Combining Ability (GCA) and Specific Combining Ability (SCA) Effects

Data for the genotypes were subjected to line x tester analysis (Singh and Chaudhury 1977) to estimate general combining ability (GCA) and specific combining ability (SCA) effects.

3.8.5.1. Estimation of GCA effect

(a) Females:

GCA (females) = $gi = \frac{x_i..}{tr} - \frac{x...}{ltr}$

(b) Males:

GCA (males) = $gi = \frac{x._j.}{lr} - \frac{x...}{ltr}$

3.8.5.1.2. Estimation of SCA effect

(a) Male x females

$s_{ij} = \frac{x_{ij.}}{r} - \frac{x_{i.}}{tr} - \frac{x_{.j}}{lr} - \frac{x...}{ltr}$

Where; s_{ij} = Specific combining ability, l = number of females, t = number of males

r = number of replications, $x_{i.}$ = total of all the hybrids containing an i^{th} female,

$x._j$ = total of all the hybrids containing an j^{th} male,

x_{ij} = total of all the hybrids containing an i^{th} (female) x j^{th} (male),

$x...$ = Ground total of crosses

The significance of the GCA (male), GCA (female) and SCA effects were estimated based on the procedure described by Singh and Chaudhary (1985).

(a) General combining ability effect:

$$t = \frac{GCA}{SE_{gca}(male)} \quad \text{where, } S.E_{gca(male)} = \left(\frac{Me}{r \times f}\right)^{1/2}$$

$$t = \frac{GCA}{SE_{gca}(female)} \quad \text{where, } S.E_{gca(female)} = \left(\frac{Me}{r \times m}\right)^{1/2}$$

Where: Me = error means square, r = number of replications, f = number of females, m = number of males, $S.E$ = Standard error

(b) Similarly, significance of SCA effect:

$$t = \frac{SCA}{SE_{sca}(males. \times females)} \text{ where, } S.E_{(sca)} = \left(\frac{Me}{r}\right)^{1/2}$$

Where: Me = error mean square,

r = Number of replications

3.8.6. Heritability

Variance components (environmental, genotypic, additive and dominance) obtained above were used to determine broad sense (H^2) and narrow sense (h^2) heritability (Kearsey and Pooni, 1996).

The heritability values were categorised as low, moderate and high as suggested by Robinson *et al.* (1949). Where 0-30% (Low), 30-60% (Moderate) and >60% (High).

Broad-sense (H^2) = $$\frac{\sigma^2_{GCA_m} + \sigma^2_{GCA_f} + \sigma^2_{SCA}}{\sigma^2_{GCA_m} + \sigma^2_{GCA_f} + \sigma^2_{SCA} + \sigma^2_e}$$

Narrow-sense heritability (h^2) = $$\frac{\sigma^2_{GCA_m} + \sigma^2_{GCA_f}}{\sigma^2_{GCA_m} + \sigma^2_{GCA_f} + \sigma^2_e}$$

3.8.7. Genetic advance (GA)

Genetic advance was estimated following Singh and Chaudhury (1985) method.

Genetic advance (GA) = $h \times i \times \sigma_p$

Where, h = Narrow sense heritability estimate, σ_p = Phenotypic standard deviation and i = Selection intensity at 5% is equal to 2.06

3.8.8. Genetic advance as percent of mean (GAM)

GAM% = (GA/ $\overline{X}$)*100. Where $\overline{X}$ = Grand mean of the trait, GA = Genetic advance

3.8.9. Correlations

Genotypic and phenotypic correlations were used to investigate the association among traits studied. Correlation coefficients were calculated from component of variance and covariance according to Singh and Chaudhury (1985).

$$r_g = \frac{COV_{g12}}{\sqrt{\left(\sigma^2_{g1}\right) \times \left(\sigma^2_{g2}\right)}}$$ Where

r_g = genotypic correlation coefficient, COV_{g12} = estimate of the genotypic variance of traits 1 and 2, σ^2_{g1} = estimate of the genotypic variance of trait 1, σ^2_{g2} = estimate of the genotype variance of trait 2

Phenotypic correlations were computed using the following formula:

$$r_p = \frac{COV_{ph12}}{\sqrt{\left(\sigma^2_{p1}\right) \times \left(\sigma^2_{p2}\right)}}$$ Where

r_p = phenotypic correlation coefficient, COV_{ph12} = estimate of phenotypic covariance for traits 1 and 2, σ^2_{ph1} = estimate of phenotypic variance for trait 1, σ^2_{ph2} = estimate of phenotypic variance for trait 2.

CHAPTER FOUR

4.0. RESULTS

4.1 Analysis of Variance for Late Leaf Spot and other Agronomic Traits.

The mean squares from analysis of variance of groundnut genotypes for Agronomic traits and Late Leaf Spot are presented in Tables 4.1. The result showed highly significant ($P \leq 0.01$) differences among the genotypes for all traits except, plant height and days to 50% flowering ($P > 0.05$). A highly significant difference was observed in the replication ($P \leq 0.01$) on days to maturity, disease incidence and disease severity. These indicate the heterogeneity in the screen house.

Table 4.1: Mean Squares from ANOVA of Groundnut Genotypes for Agronomic Traits and Late Leaf Spot Evaluated at Samaru in 2016

Source	Df	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
Replication	2	8.35	13.20	16.10**	0.33	0.01	22.94	0.06**	0.08**
Genotype	28	24.97	3.71	11.72**	29.25**	0.18**	227.31**	0.03**	0.03**
Error	56	15.68	5.80	3.99	0.81	0.01	22.22	0.00	0.00

** = significant at 0.01 probability levels respectively. PLHT (cm)= plant height, 50%F=days to flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT(g)= 100 seed weight, DS (%)=disease severity in percentage, DI (%)=disease incidence in percentage

4.2. Mean Performance of the Genotypes

The mean performance of groundnut genotypes studied for late leaf spot and other agronomic traits are presented in Table 4.2. Plant height had a mean of 18.68 cm and ranged between 12.92cm (SAMNUT 24 x FDR-F7 61) and 26.68cm (SAMNUT 25 x ICGV12991). Days to 50% flowering varied from 30.67 (SAMNUT 25 x ICGV 7878 and SAMNUT 23 x ICGV 7878) and 35.45 (SAMNUT 24 x FDR-F7 82) with a mean of 33.19. All the genotypes matured were early and varied from 97.10 days (SAMNUT 25 x FDR-F7 61) and 105.94 (SAMNUT 26 x FDR-F7 67) with a mean of 100.97. Number of matured pods per plant had a mean of 10.89 and ranged between 6.74 for (SAMNUT 24 x FDR-F7 67) and 17.90 for (SAMNUT 24 x ICGV 7878). Disease incident among the parents were categorized as; susceptible (SAMNUT 23 and SAMNUT 24), tolerance (SAMNUT 25, SAMNUT 26, ICGV12991, ICGV7878, FDR-F7 82 and FDR-F7 67) and resistant (FDR-F7 61), and among the crosses were; susceptible (SAMNUT 23 x FDR-F7 61, SAMNUT 24 x ICGV 12991, SAMNUT 24 x ICGV 7878, SAMNUT 25 x ICGV 7878, SAMNUT 25 x FDR-F7 61, SAMNUT 26 x ICGV 12991 and SAMNUT 26 x FDR-F7 67), tolerance (SAMNUT 23 x ICGV 12991, SAMNUT 23 x ICGV 7878, SAMNUT 23 x FDR-F7 82, SAMNUT 23 x FDR-F7 67, SAMNUT 23 x FDR-F7 61, SAMNUT 24 x FDR-F7 82, SAMNUT 24 x FDR-F7 67, SAMNUT 24 x FDR-F7 61, SAMNUT 25 x FDR-F7 82, SAMNUT 25 x FDR-F7 67, SAMNUT 26 x ICGV 7878, SAMNUT 26 x FDR-F7 82 and SAMNUT 26 x FDR-F7 61). Disease severity among the parents; FDR-F7 61 with 19% on a score of 4 (lesion on the lower middle leaves, but severe on lower leaves, defoliation of some leaflets evident on lower leaves), SAMNUT 26, ICGV 12991, ICGV 7878, FDR-F7 82, FDR-F7 67 with 21- 30% on a score of 5 (lesion on lower and middle leaves, over 50% defoliation of lower leaves), SAMNUT 25 with 40% on a score of 6 (lesion severe on lower and middle leaves,

defoliation of some leaflet evident on middle leaves), SAMNUT 23 with 42.7% on a score of 7 (lesion on all leaves but less severe on top leaves, defoliation of all lower and some middle leaves). Among the crosses, SAMNUT 24 x FDRF7 82, SAMNUT 24 x FDRF7 61,SAMNUT 25 x FDR-F7 82, SAMNUT 26 x ICGV 12991, SAMNUT 26 x FDR-F7 82 and SAMNUT 26 X FDR-F7 61 with 21-30% on a score of 5 (lesion on lower and middle leaves, over 50% defoliation of lower leaves), SAMNUT 23 x ICGV 12991, SAMNUT 23 x ICGV 7878, SAMNUT 23 x FDR-F7 82, SAMNUT 23 x FDR-F7 67, SAMNUT 23 x FDR-F7 61, SAMNUT 24 x ICGV 7878, SAMNUT 24 x FDR-F7 67, SAMNUT 25 x ICGV 12991, SAMNUT 25 x ICGV 7878, SAMNUT 25 x FDR-F7 67, SAMNUT 26 x ICGV 12991 and SAMNUT 26 x FDR-F7 67 with 31-40% on a score of 6 (lesion severe on lower and middle leaves, defoliation of some leaflet evident on middle leaves) and SAMNUT 24 x ICGV12991 and SAMNUT 25 x FDR-F7 61 with 41- 60% on a score of 7 (lesion on all leaves but less severe on top leaves, defoliation of all lower and some middle leaves). Generally, there were wide variations owing to the high CVs for all the traits studied except days to maturity, disease incidence and disease severity.

Table 4.2: Mean Performance of 29 Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016.

GENOTYPE	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
Parents								
SAMNUT 23	13.33	33.45	97.33	8.33	1.37	62.67	61.7(1.79)	42.7(1.63)
SAMNUT 24	19.00	32.65	99.67	18.67	2.10	54.67	55.0(1.74)	35.3(1.54)
SAMNUT 25	19.33	35.55	98.33	7.67	1.77	54.33	48.3(1.68)	40.0(1.52)
SAMNUT 26	22.67	31.23	101.33	12.00	1.83	45.00	35.0(1.52)	25.2(1.38)
ICGV12991	16.00	33.23	101.67	12.33	1.87	48.33	33.3(1.51)	24.9(1.39)
ICGV7878	19.67	32.11	98.00	8.33	1.80	61.67	40.0(1.60)	27.7(1.44)
FDR-F7 82	21.67	35.24	99.67	8.67	1.80	73.33	33.3(1.52)	23.4(1.37)
FDR-F7 67	13.67	35.11	102.00	13.67	2.17	62.33	31.7(1.50)	21.5(1.33)
FDR-F7 61	18.00	33.11	101.00	9.67	2.17	52.33	26.7(1.42)	19.0(1.28)
Crosses								
SAMNUT 23 x ICGV12991	17.10	35.23	100.57	8.06	1.79	51.78	50.0(1.74)	38.9(1.63)
SAMNUT 23 x ICGV7878	17.98	30.67	97.37	12.88	1.74	59.71	45.0(1.64)	31.8(1.48)
SAMNUT 23 x FDR-782	21.61	31.56	102.74	9.37	1.88	69.66	50.0(1.73)	32.8(1.55)
SAMNUT 23 x FDR-F767	19.88	32.67	102.29	12.70	1.91	58.42	46.7(1.66)	33.6(1.54)
SAMNUT 23 x FDR-F761	13.58	31.55	101.19	7.23	1.84	64.73	51.7(1.72)	36.5(1.56)
SAMNUT 24 x ICGV12991	22.82	31.22	100.32	15.91	1.77	48.10	60.0(1.74)	42.4(1.57)
SAMNUT 24 x ICGV7878	14.95	34.22	102.51	17.90	1.90	55.96	51.7(1.69)	37.7(1.56)
SAMNUT 24 x FDR-F782	19.90	35.45	102.16	9.22	1.50	39.66	40.0(1.61)	27.7(1.42)
SAMNUT 24 x FDR-F767	23.12	34.56	105.38	6.74	1.71	53.19	45.0(1.66)	31.8(1.52)
SAMNUT 24 x FDR-F761	12.92	34.87	98.53	10.00	1.35	41.62	35.0(1.54)	25.2(1.38)
SAMNUT 25 x ICGV12991	26.68	31.23	101.89	13.17	1.93	64.70	56.7(1.77)	40.2(1.61)
SAMNUT 25 x ICGV7878	16.55	30.67	100.95	11.16	1.61	46.39	60.0(1.79)	40.6(1.61)
SAMNUT 25 x FDR-F782	20.37	30.77	102.51	7.56	1.90	44.80	41.7(1.60)	28.1(1.44)
SAMNUT 25 x FDR-F767	16.77	32.22	100.15	8.27	1.15	43.91	41.7(1.64)	31.1(1.49)
SAMNUT 25 x FDR-F761	15.13	32.34	97.10	8.71	0.97	44.32	63.3(1.80)	42.7(1.63)

Table 4.1 continue

Genotype	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
SAMNUT 26 x ICGV12991	21.11	32.35	100.39	13.62	1.87	50.47	53.3(1.72)	38.0(1.58)
SAMNUT 26 x ICGV7878	16.83	32.34	101.81	10.21	1.80	39.36	41.7(1.60)	28.1(1.44)
SAMNUT 26 x FDR-F782	14.95	33.66	102.77	9.60	1.54	41.67	38.3(1.59)	27.4(1.44)
SAMNUT 26 x FDR-F767	19.56	31.55	105.94	12.94	1.40	42.12	51.7(1.73)	38.0(1.59)
SAMNUT 26 x FDR-F761	18.90	31.34	98.48	13.90	1.81	67.31	40.0(1.57)	26.2(1.41)
MEAN	18.68	33.19	100.97	10.89	1.72	53.81	45.8(1.65)	32.2(1.50)
LSD	6.47	3.93	3.26	1.47	0.16	7.70	10.4(0.10)	7.0(0.09)
CV	21.20	14.19	1.98	8.27	5.87	10.34	3.55	3.83

PLHT (cm) = plant height, 50%F=days to flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT (g),= 100 seed weight, DS (%)=disease severity in percentage, DI (%)=disease incidence in percentage. The values in parenthesis () are the transformed value

4.3. Estimates of Coefficients of Variation and Heritability

The estimates of coefficient of variation for the 29 groundnut genotypes evaluated at Samaru screen house are presented in Table 4.3. The total variation of Phenotypic Coefficients of variations (PCV) and Genotypic Coefficients of variations (GCV) showed that, PCV were higher than or equal to the Genotypic GCV for all the traits measured. High broad sense heritability estimates were recorded for all the traits studied except days to 50% flowering, which recorded a moderate value. Moderate to high values of narrow sense heritability were recorded for number of mature pod per plant (0.71), number of seed per pod (0.78), 100 seed weight (0.94), disease severity (0.60) and disease incidence (0.67). The genetic gain as a percent mean in this study was high for plant height (27.59), number of mature pod per plant (58.43%), number of seed per pod (29.01%), low genetic gain in percentage mean was observed on and 100-seed weight (0.14%), disease severity (0.34%) and disease incidence (0.51%).

Table 4.3: Estimates of Variance Components and Heritability of Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016

Traits	σ_g^2	σ_e^2	σ_{ph}^2	PCV (%)	GCV (%)	H^2	h^2	GA	GAM%
Plant height(cm)	3.10	15.68	8.32	15.4	9.4	0.87	0.73	5.15	27.59
Days to 50% flowering	0.70	5.80	2.63	9.6	4.9	0.56	0.26	1.29	7.58
Days to maturity	2.58	3.99	3.91	2.0	1.6	0.90	0.81	3.65	3.61
Mature pods per plant	9.48	0.81	9.75	28.7	28.3	0.99	0.71	6.36	58.43
Seed per pod	0.06	0.01	0.06	14.3	13.9	0.98	0.78	0.50	29.01
100-seed weight	1.23	0.13	1.28	2.1	2.1	0.99	0.94	0.07	0.14
Disease Severity (%)	0.08	0.03	0.09	0.7	0.6	0.80	0.60	0.16	0.34
Disease Incidence (%)	0.08	0.03	0.09	0.9	0.9	0.83	0.67	0.17	0.51

σ_g^2 =Genotypic variance, σ_e^2 = Environmental variance, σ_{ph}^2 = phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H^2= Broad sense heritability, h^2= Narrow sense heritability, GA=Genetic Advance, GAM%= Genetic advance as percent of mean.

4.4. Combining Ability Effects

4.4.1. General Combining Ability (GCA) effects

The estimates of GCA effects of male and female parents for some agronomic traits and groundnut genotypes are presented in Table 4.4.1. Among the male parents, ICGV 12991 showed negative significant GCA effect for plant height (-3.18), days to maturity (-20.87) and disease severity (-12.00), and positive significant GCA effect for 100-seed weight (3.28). ICGV 7878 had the highest significant positive GCA effect on 100 seed weight (6.72). FDR-F7 82 had a positive and significant GCA effect on days to maturity (27.05) and number of mature pods per plant (1.22). FDR-F7 67 and FDR-F7 61 had negative and significant GCA effect for disease severity (-0.68 and -2.23 respectively). FDR-F7 67 had a negative and significant GCA effect on number of mature pod per plant (-1.15) and number of seed per pod (-0.19). FDR-F7 61 had positive significant GCA effect on number of mature pods per plant (1.15) and number of seed per pod (0.08). Among the female parents, SAMNUT 23 had a positive and significant GCA effect on plant height (2.40), number of seed per pod (0.13), disease incidence (0.06) and disease severity (11.93) and a negative and significant GCA effect on days to maturity (-20.80). SAMNUT 24 had a positive and significant GCA effect on number of mature pod per plant (2.25), number of seed per pod (0.13) and disease severity (6.00). SAMNUT 25 had negative significant GCA effects on days to maturity (-20.40), number of mature pod per plant (-1.75) and disease incidence (-0.05). SAMNUT 26 also showed negative significant GCA effect on days to maturity (-19.07), number of seed per pod (-0.12) and disease severity (-5.90).

Table 4.4.1: Estimates of General Combining Ability effects of Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016.

GENOTYPE	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
Males								
ICGV12991	-3.18**	0.37	-20.87**	-0.50	-0.13**	3.28**	-0.01	-12.00**
ICGV 7878	-0.93	-0.35	23.72**	-1.12**	0.10**	6.72**	0.01	2.08**
FDR-F7 82	0.07	0.45	27.05**	1.22**	0.02	-3.02**	-0.02	0.83**
FDR-F7 67	1.07	0.12	23.63**	-1.25**	-0.19**	-2.02**	0.04*	-0.68**
FDR-F7 61	-0.20	-0.22	26.80**	1.15**	0.08**	-1.68	-0.03	-2.23**
SE±	0.92	0.68	0.61	0.25	0.02	1.85	0.02	0.02
Females								
SAMNUT 23	2.40**	-0.63	-20.80**	0.33	0.13**	1.03	0.06**	11.93**
SAMNUT 24	-0.85	0.45	-20.07**	2.25**	0.13**	0.53	0.01	6.00**
SAMNUT 25	1.82*	-0.13	-20.40**	-1.75**	-0.02	-1.80	-0.05**	-0.02
SAMNUT 26	-0.18	-0.05	-19.07**	-0.33	-0.12*	-3.05	-0.01	-5.90**
SE±	1.03	0.76	0.69	0.28	0.03	2.07	0.02	0.02

* and ** = significant at 0.05 and 0.01 probability levels respectively. PLHT (cm)= plant height, 50%F=days to 50% flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT(g),= 100 seed weight, DS (%)=disease severity in percentage, DI (%)=disease incidence in percentage.

4.4.2. Specific Combining Ability (SCA) effects

The specific combining ability (SCA) effects for some agronomic traits and Late Leaf Spot of groundnut genotypes are presented in Table 4.4.2. No significant SCA effects were observed for plant height, days to 50% flowering and days to maturity. Nearly 50% of the crosses showed positive and negative SCA effects for these parameters. For number of mature pods per plant, SAMNUT 23 x FDR-F7 67 (3.53), SAMNUT 24 x ICGV 12991 (3.62), SAMNUT 23 x ICGV 12991 (1.33), SAMNUT 23 x FDR-F7 67 (1.60) and SAMNUT 23 x FDR-F7 61 exhibited a positive and significant SCA effects. SAMNUT 23 x FDR-F7 67 (0.16), SAMNUT 24 x FDR-F7 67 (0.14), SAMNUT 25 x ICGV 12991 (0.23), SAMNUT 25 x FDR-F7 82 (0.28) and SAMNUT 26 x FDR-F7 67 (0.20) showed a significant positive SCA effect for number of seed per pod. For 100 seed weight, SAMNUT 25 X ICVG 12991 (11.77) and SAMNUT 26 x FDR-F7 61 (12.52) had significant and positive SCA effect while other crosses showed a negative and significant SCA effects for disease incidence were exhibited by SAMNUT 25 x FDR-F7 67 (-0.08) and SAMNUT 24 x FDR-F7 61 (-0.10). SAMNUT 23 x ICGV 12991 (-0.74), SAMNUT 24 x FDR-F7 82 (-0.12), SAMNUT 24 x FDR-F7 67 (-0.09), SAMNUT 24 x FDR-F7 61 (0.11), SAMNUT 25 x ICGV 7878, SAMNUT 25 x FDR-F7 67, SAMNUT 26 x FDR-F7 67 (-0.08) and SAMNUT 26 x ICGV 7878 (-0.13) showed a negative significant SCA effects for disease severity.

Table 4.4.2: Estimates of Specific Combining Ability effects of Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016.

CROSSES	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI(%)	DS (%)
SAMNUT 23 x ICGV12991	-4.07	-1.23	-0.23	-3.80**	-0.25**	-11.30*	-0.04	-0.74**
SAMNUT 23 x ICGV7878	2.85	2.35	-0.48	0.95	-0.02	1.87	-0.05	0.22**
SAMNUT 23 x FDR F782	0.85	-0.40	0.27	1.28*	0.00	6.20	0.06	0.13**
SAMNUT 23 x FDR F767	-0.15	-0.82	-1.40	3.53**	0.16**	-0.88	0.00	0.19**
SAMNUT 23 x FDR F761	0.52	0.10	1.85	-1.97**	0.11*	4.12	0.04	0.20**
SAMNUT 24 x ICGV12991	0.93	-0.03	0.10	2.53**	0.02	-1.57	0.06	0.34**
SAMNUT 24 x ICGV7878	-0.15	-0.78	0.85	3.62**	0.05	6.27	0.04	-0.01
SAMNUT 24 x FDR F782	0.52	-0.20	-0.40	-0.72	-0.10*	-3.40	0.00	-0.12**
SAMNUT 24 x FDR F767	0.52	1.05	0.93	-4.47**	0.14*	6.52	0.00	-0.09*
SAMNUT 24 x FDRF761	-1.82	-0.03	-1.48	-0.97	-0.11*	-7.82	-0.10*	-0.11*
SAMNUT 25 x ICGV12991	1.60	0.63	1.50	1.33*	0.23**	11.77*	-0.03	0.22**
SAMNUT25 x ICGV7878	-2.15	-1.78	-0.42	-0.92	-0.10*	-1.40	0.06	-0.08*
SAMNUT 25 x FDR F782	0.52	1.47	-1.00	-0.25	0.28**	0.60	-0.04	-0.06
SAMNUT 25 x FDR F767	0.85	-0.95	-0.33	-0.67	-0.22**	-2.15	-0.08*	-0.08*
SAMNUT 25 x FDR F761	-0.82	0.63	0.25	0.50	-0.20**	-8.82*	0.09*	-0.01
SAMNUT 26 x ICGV12991	1.53	0.63	-1.37	-0.07	0.00	1.10	0.01	0.18**
SAMNUT 26 x ICGV7878	-0.55	0.22	0.05	-3.65**	0.07	-6.73	-0.04	-0.13**
SAMNUT 26 x FDR F782	-1.88	-0.87	1.13	-0.32	-0.18**	-3.40	-0.01	0.05
SAMNUT 26 x FDR F767	-1.22	0.72	0.80	1.60*	-0.08	-3.48	0.08	-0.02
SAMNUT 26 x FDR F761	2.12	-0.70	-0.62	2.43**	0.20**	12.52**	-0.03	-0.08*
SE±	2.06	1.52	1.37	0.57	0.05	4.13	0.04	0.04

* and ** = significant at 0.05 and 0.01 probability levels respectively. PLHT (cm)= plant height, 50%F=days to 50% flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT(g),= 100 seed weight, DS (%)=disease severity in percentage, DI (%)=disease incidence in percentage.

4.5. Combining Ability Estimate

The mean squares from analysis of variance for NCII mating design for some agronomic traits and Late Leaf Spot in groundnut genotypes are presented in Tablet 4.5. The mean squares obtained for the male genotypes showed highly significant differences ($p \leq 0.01$) for all traits except, days to 50% flowering and days to maturity. There were highly significant differences ($p \leq 0.01$) among the female genotypes for all traits except, plant height, days to 50% flowering, disease severity and disease incidence. The female x male interaction showed highly significant differences ($p \leq 0.01$) for all traits except, plant height, days to 50 % flowering and days to maturity.

Table 4.5: Mean Squares for some Agronomic Traits and Late Leaf Spot of Groundnut Genotypes Generated using North Carolina Design II Evaluated at Samaru in 2016.

Sources of variation	Df	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
Rep	2	16.65	19.72	18.15	0.82	0.02	0.16	0.05	0.07
Male	4	59.85**	2.28	10.03	35.79**	0.20**	1.63**	0.02**	0.03**
Female	3	10.27	1.93	33.91**	28.06**	0.26**	65.38**	0.01	0.01
Female x Male	12	12.85	4.72	4.37	24.88**	0.12**	4.44**	0.01**	0.01**
Error	38	12.70	6.97	5.63	0.97	0.01	0.14	0.01	0.01

** = 0.01 probability levels respectively. PLHT (cm) = plant height, 50%F=days to 50% flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT (g), = 100 seed weight, DS (%) =disease severity in percentage, DI (%) =disease incidence in percentage.

4.6. Proportional Contributions of Males and Females

The proportional contribution of male parents and female parents to the variations in total sums of squares of progenies for late leaf spot and agronomic traits is presented in Table 4.6. As shown, the male parents contributed significantly to the variances observed on days to maturity (52.37%) and 100-seed weight (24.70%). The female parents contributed more variations in plant height (56.41%), days to 50% flowering (12.72%), number of mature pod per plant (27.22%), number of seed per pod (27.08%), disease severity (40.41%) and disease incidence (29.18%). The sum contribution of both male and female parents were greater than the contributions of the progenies in the variations observed for plant height (63.67%), days to maturity (73.01%), number of seed per pod (53.19%) and disease severity (51.31%).

Table 4.6: Percentage Contributions of Males and Females to Progeny Variation of Groundnut Genotypes for Agronomic traits Late Leaf Spot at Samaru in 2016

Contribution due to	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
Male	7.26	8.09	52.37	16.01	26.11	24.70	12.73	10.90
Female	56.41	12.72	20.64	27.22	27.08	8.21	29.18	40.41
F x M	36.33	79.19	26.99	56.77	46.81	67.09	58.08	48.68

PLHT (cm)= plant height, 50%F=days to 50% flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT(g)= 100 seed weight, LLS65=late leaf spot 65 days after sowing, LLS90=late leaf spot 90 days after sowing, DS (%)=disease severity in percentage, DI (%)=disease incident in percentage.

4.7. Component of General Combining Ability Variance (σ^2_{GCA}) and Specific Combining Ability Variance (σ^2_{SCA})

The general combining ability (σ^2_{GCA}) and specific combining ability variances (σ^2_{SCA}) for some agronomic traits and Late Leaf Spot in groundnut genotypes are presented in Table 4.7. The specific combining ability variance was greater than general combining ability variance for all the traits except days to 50% flowering (-9.59). The ratios of general combining ability variance to specific combining ability variance for all the traits were less than unity (one).

Table 4.7: Component GCA and SCA Variance of Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016.

Estimates	PLHT(cm)	50%F	DM	MPPP	SPP	SWGT(g)	DI (%)	DS (%)
σ^2_{GCA}	8.57	3.15	2.91	16.59	0.08	2.96	0.01	0.01
σ^2_{SCA}	40.99	-9.59	30.09	63.46	0.44	63.38	0.02	0.03
$\frac{\sigma^2_{GCA}}{\sigma^2_{SCA}}$	0.21	-0.33	0.10	0.26	0.18	0.05	0.40	0.27

PLHT(cm)= plant height, 50%F=days to 50% flowering, DM=days to maturity, MPPP= number of mature pod per plant, SPP= number of seed per pod, SWGT(g)= 100 seed weight, DS (%)=disease severity in percentage, DI (%)=disease incidence in percentage.

4.8. Correlation

The estimate of Pearson correlation coefficient of some agronomic traits and Late Leaf Spot incidence and severity in groundnut genotypes are presented in Table 4.9. Number of seed per pod exhibited significant negative correlation with disease incidence (-0.31) and disease severity (-0.34). 100 seed weight and number of seed per pod showed significant negative correlation with disease incidence (-0.20) and disease severity (-0.24).

Table 4.8: Correlation Coefficients of Groundnut Genotypes Evaluated for some Agronomic Traits and Late Leaf Spot at Samaru in 2016.

Traits	DI (%)	DS (%)
Plant height	0.09	0.11
Days to50% Flowering	0.10	0.10
Days to Maturity	-0.04	-0.03
Mature Pod Per Plant	0.09	0.07
Seed Per Pod	-0.31**	-0.34**
100-seed weight	-0.20*	-0.24**
Disease Incident	1.00	0.96
Disease Severity		1.00

* and ** = significant at 0.05 and 0.01 probability levels, respectively. DS (%) Disease severity in percentage, DI (%)=Disease incidence in percentage.



Plate 1: An F1 hybrid derived from a cross between SAMNUT 23 x FDR-F7 61 (Tolerance to LLS)



Plate 2: An F1 hybrid derived from a cross between SAMNUT 25 x FDR-F7 82(Tolerance to LLS)



Plate 3: An F1 hybrid derived from a cross between SAMNUT 26 x ICGV12991 (Susceptible to LLS)



Plate 4: An F1 hybrid derived from a cross between SAMNUT 24 x ICGV 7878 (Susceptible to LLS)

CHAPTER FIVE

5.0. DISCUSSION

Plant breeding research with self-pollinated crops has been traditionally performed with single crosses between any two parents. This method generally results in reasonable amount of genetic variability needed for selection. In this study, 4 x 5 North Carolina design II model I was used to develop an F_1 population and evaluated using RCBD with three replications. Significant differences among the groundnut genotypes used in the study indicated the presence of sufficient variability in the material used and provide opportunity for improving groundnut for LLS resistance. The amount of improvement that can be achieved by selection among a number of crosses is dependent on the amount of variation between the crosses and the intensity of selection, since selection is ultimately applied to the crosses. The parental lines: SAMNUT 25, SAMNUT 26, ICGV12991, ICGV 7878, FDR-F7 67 and FDR-F7 61 that showed tolerance to LLS disease incidence with low severity could be used to develop crosses that can be used as genetic materials for improvement of LLS and other agronomic traits of groundnut. AMONG The crosses between SAMNUT 23 x ICGV 7878, SAMNUT x FDR-F7 67, SAMNUT 24 x FDR-F7 82, SAMNUT 24 x FDR-F7 67, SAMNUT 24 x FDR-F7 61, SAMNUT 25 x FDR-F7 82, SAMNUT 25 x FDR-F7 67, SAMNUT 26 x ICGV 7878, SAMNUT 26 x FDR-F7 82 and SAMNUT 26 X FDR-F7 61 all showed tolerance to LLS disease incidence with low severity. This result corroborated with the findings of John *et al*. (2008) who reported moderate incidence of LLS in F2 population of the Kadiri-3 × ICGV-88083. 100-seed weight recorded for the crosses SAMNUT 23 x FDR-F7 82, SAMNUT 23 x FDR-F7 61, SAMNUT 25 x ICGV 12991 and SAMNUT 26 x FDR-F7 61 gave a mean weight of 60g and above which indicated that for targeting confectionary traits (large seeded) groundnut, such crosses are good hybrids. These

findings corroborate with the work of Milton (2013), Ramanatha and Murty (1994) who reported that 100-seed weight higher than 60g were for confectionary varieties.

In the present study, the estimate of PCV were in accordance with those of GCV for number of mature pods per plant, number of seed per pod, 100-seed weight, disease severity and disease incidence. This finding corroborate with the work of Nath and Alam (2002) who reported close or corresponding PCV and GCV estimates100-seed weight, number of seed per pod and number of mature pods per plant. The low PCV (0.9) and GCV (0.9) in this study, it contradicts the findings of Kumari (2008) who reported high values of PCV and GCV. High heritability coupled with high genetic advance as percent of mean exhibited by number of mature pods per plant and number of seed per pod; indicate environmental influence on the traits and a predominant role of additive gene actions. Thus, these traits could be amenable for phenotypic selection in early generation. Choudhary *et al.* (2013) who reported high heritability and genetic advance as per cent mean on number of mature per plant. High heritability estimate was accompanied with low genetic advance as per cent of mean for 100-seed weight, disease incidence and disease severity revealing preponderance of non-additive gene effect activity, presence of large environmental effects or a relatively small population that was used. In such a case, simple selection methods may be rewarding, suggesting maintenance of heterozygosity in the population. Wambi (2014) and Dashora and Nagda (2002) reported high heritability couple with low genetic advance as per cent mean on 100-seed weight and LLS.

Heritability is the heritable portion of phenotypic variance and it is a good index of transmission of a character from parents to their off springs. Its estimation is important because, it determines the expressivity of genes carried by a genotype. If the heritability of a character is high, the phenotypic value provides a fairly close measure of the genotypic value and thus, breeder can

base his selection on the phenotypic performance, thereby the knowledge of heritability helps the plant breeder in pre-assessing the results of selection for a particular character. However, for predicting the effect of selection, heritability estimates along with genetic advance are useful than the heritability estimates alone (Johnson *et al.*, 1955).

Breeders make rapid progress where heritability is high using selection methods that are dependent solely on phenotype (example, mass selection). However, where heritability is low, the method of selection based on families and progeny testing are more effective and efficient (Acquaah, 2007). Most of the characters were highly heritable as indicated by their high broad sense heritability estimates. Heritability estimate were generally high for all traits except days to 50% flowering, suggesting that mass selection could be effective to exploit any additive gene effect. Basu (1969) and Hamasselbe (2006) reported high heritability values for number of pods per plant and 100-seed weight.

Negative GCA effect observed for days to maturity is required for the development of early maturing genotype as reported by Vishnuvardhan, *et al.* (2012). The negative and significant GCA effect exhibited by SAMNUT 25 indicated that it is a good general combiner for disease incidence. SAMNUT 26 is a good general combiner with a negative and significant GCA effect for disease severity. ICGV 12991, FDR-F7 67 and FDR-F7 61 are good general combiners with negative GCA effects on LLS tolerance (disease severity and incidence).

The progenies with negative SCA effects for disease incidence and disease severity SAMNUT 24 x FDR-F7 61 and SAMNUT 25 x FDR-F7 67 were identified as the most promising genotypes in breeding programme for LLS tolerance traits. These progenies originated from parents with negative and positive GCA values. This suggest the difficulty in predicting the *P. personata* tolerance level of the progenies based on GCA alone and should necessitate testing of

specific male x female combinations. Arunga *et al.* (2010) reported that the SCA effect alone has limited value for parental choice in breeding programmes. They, therefore suggested that SCA effects should be used in combination with other parameters, such as hybrid means and the GCA of the respective parents such that hybrid combination with both high mean and favourable SCA estimates and involving at least one of the parents with high GCA, would tend to increase the concentration of favourable alleles; which is desired by any breeder. Furthermore, it was observed that crosses involving one good combiner and one average or poor combiner showed negative SCA effects. For instance, SAMNUT 25 and FDR-F7 67 have a poor GCA values for disease incidence and severity tolerance, while their cross shown a negative and desirable SCA effects. This manifestation of progenies having reactions not related to the parent's attributes introduced a different dimension in the inheritance of groundnuts to tolerance to LLS. John *et al.* (2012) and Ayo-Vaughan *et al.* (2013) observe similar phenomena in groundnuts and cowpeas, respectively and attributed it to genetic interaction between favourable alleles and between unfavourable alleles contributed by both parents. This suggests that inheritance of this trait is not simple and that inter-allelic interactions due to epistasis could be responsible. However, SCA effects are not very important for crops like groundnuts that are highly self-pollinated and difficult to produce commercial hybrids, a point advanced by Kimani and Derera (2008) while working on beans; self-pollinated counterpart of groundnut.

The results of the proportional contribution of the parents and their progenies to the total variation indicated that the male parents contributed more to variation only on days to maturity and the female contribution to variation on the remaining traits. This suggests the influence of maternal effects in the variation observed in the characters and indicates that when developing breeding populations for resistance to *P. personata* disease, the choice of a maternal parent is

very important. The proportional contribution of the parents was higher than their progenies for LLS tolerance, thus confirming the preponderance of additive gene action for the expression of this character. Janila *et al*. (2013a) reported that resistance to LLS was controlled by a combination of both, nuclear and maternal gene effects. Such variation in the results is probably due to genetic background of the parents and variation in environmental conditions in which the populations were evaluated.

The relative importance of GCA to SCA variance was judged from the ratio of the GCA to SCA variance which helps to indicate the predominance of either additive or non-additive action. The predominance of non-additive genetic variance over additive genetic variance indicated by the values with magnitude less than unity for all the traits measured, it may be due to differences in the genotypes used as parents as stated by Abul-Kalam, *et al.* (2014). Additionally, higher SCA than GCA variances can be due to one or all of the following: (i) negative associations between genes, (ii) previous selection that narrowed the genetic base of the lines tested and (iii) directional selection. This further implies that identifying good parents is essential when improvements are intended for number of mature pods per plant, number of seed per pod, 100-seed weight and LLS. This result corroborates with earlier work of Dwivedi *et al*., (1989) who reported variation in the inheritance of traits may be due to differences in the method of analysis (random or fixed model) and/or in the parental materials used in the study.

The significant positive and negative correlation was observed between disease severity and disease incidence with (number of seed per pod and 100-seed weight), it indicates that selection of plants with less disease incidence and severity of LLS will result in the production of more seeds per pod and heavier seeds (100-seed weight), that is higher yield. Therefore, selection for low disease incidence and severity will result in progress for number of seed per pod and 100-

seed weight but in a regress for negatively correlated characters (Gomez and Lopez, 2005). However, the significant and negative correlation observed between number of seed per pod as well as 100-seed weight will reduce disease severity and incidence, it implies that selection for low disease severity and incidence would increase number of seed per pod and 100-seed weight (yield). This result corroborates with the findings of Anderson *et al.* (1991) who reported resistance to LLS could be improved through selection for genotypes which had low disease severity scores and high pod yield at harvest.

CHAPTER SIX

6.0. Summary, Conclusion and Recommendation

6.1. Summary

This research work was conducted with the main objective of studying Genetic Analysis of late leaf spot of groundnut in Ahmadu Bello University Zaria. The parental materials used comprised of nine (9) parents of which four are male (4) and five are females (5) based on their resistant and susceptibility to LLS respectively. The parental lines were mated using a North Carolina mating design II in the screen house and 20 F_1 progenies were generated. The parent sand F_1 progenies were evaluated for LLS and some agronomic traits in the screen house during the 2015/2016 rainy season using a randomized complete block design (RCBD) with three replications. Thirty-five days old plants were inoculated with LLS at 106 conidia/ml inoculum concentrations. Data collected include: plant height, days to 50% flowering, days to maturity, number of mature pods per plant, number of seed per pod, 100-seed weight, LLS disease severity and disease incidence. Data collected were subjected to ANOVA using SAS package and estimate of variance components, GCA, SCA, GCA effect, SCA effect, heritability, genetic advance and correlation coefficient were estimated.

The crosses SAMNUT 23 x ICGV 7878, SAMNUT x FDR-F7 67, SAMNUT 24 x FDR-F7 82, SAMNUT 24 x FDR-F7 67, SAMNUT 24 x FDR-F7 61, SAMNUT 25 x FDR-F7 82, SAMNUT 25 x FDR-F7 67, SAMNUT 26 x ICGV 7878, SAMNUT 26 x 82 and SAMNUT 26 X FDR-F7 61 all showed tolerance to LLS disease incidence with low severity. A corresponding PCV and GCV values were observed for the LLS tolerance traits (diseases incidence and severity), number of mature pods per plant, number of seed per pod and 100-seed weight.

High broad and narrow sense heritability and low genetic gain as percent of mean [were] exhibited by 100-seed weight and LLS (disease incidence and disease severity). This gave an indication of

the importance of non-additive gene effects governing these characters which could be due to relatively small population that was used. A moderate to high heritability and genetic gain as percent of mean were recorded for seed per pod, plant height, and matured pod per plant which indicates the importance of additive gene effects, indicating the influence of environment.

General combining ability made significant and important contributions to hybrid variations for LLS tolerance. The analysis revealed that a non-additive gene action was important for the inheritance of tolerance to LLS. This was further confirmed by Baker's ration which was less than unity for the LLS resistance traits. However, parents that are good combiner do not always produce best hybrid combinations. General combining ability of parents showed that SAMNUT 25 is good general combiner for disease incidence. SAMNUT 26 is good general combiner for disease severity. ICGV 12991, FDR-F7 67 and FDR-F7 61 are good general combiners for LLS tolerance traits (disease severity and incidence). Eight of progenies showed a great deal for disease severity. SAMNUT 24 x FDR-F7 67 and SAMNUT 25 x FDR-F7 61 are good specific combiners for LLS tolerance traits (disease severity and incidence). SAMNUT 26 x FDR-F7 61 is a good specific combiner for disease severity and yield components.

The correlation coefficient showed that, selection of plants with less disease incidence and severity will result in the production of more seed per pod and heavier seeds (100-seed weight) which will in turn to produce higher yield.

6.2. Conclusions

The study revealed ample genetic variability for the agronomic traits in the parents used for the study. Both additive and non-additive gene actions were important in controlling the inheritance of LLS. There was however, the preponderance of non-additive gene action to the inheritance of LLS as indicated by Baker's ratio which was less than unity. Both Broad and narrow sense

heritability estimates were high (> 60%) for all the traits studied except days to 50% flowering (0.26%), indicates high heritability coupled with low genetic advance as percent of mean, due to relatively small population used in the study. However, the amount of variation and magnitude of gene effects depended on the genetic backgrounds of the materials used in the study. Significant and negative correlation was observed between LLS tolerance traits (disease severity and incidence) and number of seed per pod ($r = -0.34$) and 100-seed weight ($r = -0.24$). This implies that selection of plants with low incidence and severity will result in the production of more seeds per pod and 100-seed weight.

6.3. Recommendations

Based on the observed results, it can be recommended that there is need to advance the segregating population of the selected crosses to higher generation while selection is carried out for tolerance of LLS among SAMNUT 24 x FDR-F7 67, SAMNUT 25 x FDR-F7 61 and SAMNUT 26 x FDR-F7 61. The promising parents for late leaf spot tolerance are ICGV 12991, FDR-F7 67, FDR-F7 61 and SAMNUT 26.

High heritability estimate on LLS tolerance traits suggesting that mass selection could be effective to exploit any additive gene effect. A more detailed heritability study is recommended at advanced generations, other than F_1 to yield more accurate heritability estimates by backcrossing to recoup more genes in the following crosses.

It is recommended that selection for low LLS tolerance (disease severity and incidence) would result in the production of more seed per pod and heavier seeds (100 seed weight).

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