GENETICS OF APHID (*APHIS CRACCIVORA* KOCH.) AND ROSETTE RESISTANCE IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)

BY

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DECLARATION

I declare that the work in this dissertation entitled GENETICS OF APHID (*APHIS CRACCIVORA* KOCH.) AND ROSETTE RESISTANCE IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) has been carried out by me in the Department of Plant Science. The information derived from the literature has been duly acknowledged in the text and a list of references provided. No part of this dissertation was previously presented for another degree or diploma at this or any other Institution.

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CERTIFICATION

This dissertation entitled GENETICS OF APHID (*APHIS CRACCIVORA KOCH*.) AND ROSETTE RESISTANCE IN GROUNDNUT (*ARACHIS HYPOGAEA L*.) by VICTOR HASSAN MUSA meets the regulations governing the award of the degree of Masters of Science in Plant breeding of the 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 the service of humanity in general and students of plant breeding specifically.

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ABSTRACT

Groundnut production is largely constrained by biotic stresses with groundnut rosette virus disease seriously contributing to losses in yield in Nigeria and sub Saharan Africa and thus the need to study the mode of inheritance of aphid and rosette resistance in groundnut with these objectives; to investigate the gene action controlling the inheritance of aphid resistance, rosette resistance and other quantitative characters, to determine the relationship between aphid resistance, rosette resistance and other quantitative characters, to estimate the number of effective factors controlling the inheritance of aphid infestation, rosette disease and other quantitative characters and to determine genetic advance arising from selection against aphid resistance, rosette resistance and other quantitative characters. For this, two aphid resistance (ICGX-SM00020/5/9, P_1 and ICGX-SM0020/5/P4/P1, P_2), one rosette resistance, ICVIS07899 (P_3) and one aphid susceptible, ICGX-SM0027/5/P10/P1 (P_4), one rosette susceptible, Manipenta (P_5) lines were used as parents to develop F_1s. The F_1s were advanced to F_2s and backcrosses made to the reciprocal recurrent parents. The seventeen generations obtained were evaluated along with three checks (Samnut 24, Samnut 25 and Samnut 26) in three replications using randomized complete block design at Institute of Agricultural Research Samaru, Zaria during 2014 growing season. Significant differences in mean performance among the parents and the F_1s studied suggests sufficient variability across the generations for the characters studied. The three parameter model was adequate to explain variations observed in the inheritance of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage. It was inadequate to explain the variations observed in the inheritance of aphid infestation index, rosette disease incidence, rosette severity index, days to maturity, number of matured pods per plant, pod yield per plant and hundred seed weight hence, six parameter model was fitted. Non allelic

gene interactions were significant for number of matured pods per plant, pod yield per plant, rosette disease severity and rosette disease incidence. Dominance genes and epistasis bias the number of effective factors for days to fifty percent flowering, plant height, number of seeds per plant, shelling percentage, rosette disease incidence, rosette severity index, number of matured pods per plant and pod yield per plant hence, rendering the estimates less reliable. Wide ranges of narrow (33 to 95%) and broad (0 to 93%) sense heritability as well as genetic advance (0 to 32.3) were obtained for the characters studied. The genotypic correlation coefficients exceeded those of the corresponding phenotypic correlation coefficients for most of the character pairs indicating that the correlations were more genetic than environmental in the three sets of crosses. In conclusion, the set of groundnut crosses where non allelic interaction was significant with high narrow-sense heritability as obtained for rosette disease incidence, rosette severity index, number of matured pods per plant and pod yield per plant, it is possible to expect advance for these characters in further segregating generations. Broad sense and narrow sense heritability as well as genetic advance were moderate to high for most of the characters studied for the three sets of groundnut crosses. Genotypic coefficients of correlation were higher than phenotypic coefficients of correlation.

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List of Abbreviations

BC	Before Christ
FAO	Food and Agricultural Organization
ICRISAT	International Crop Research Institute for the Semi-Arid Tropics
IAR	Institute for Agricultural Research
GRVD	Groundnut rosette virus disease
GRV	Groundnut rosette virus
CIE	Commission Internationale de I'Ecaiage
GRAV	Groundnut rosette assistor virus
satRNA	Satellite ribonucleic acid
P_1	Parent one
P_2	Parent two
F_1	First filial generation
F_2	Second filial generation
BC_1	Backcross to parent one
BC_2	Backcross to parent two
RCBD	Randomized Complete Block Design
EF	Effective factor
C1	Cross 1
C2	Cross 2
C3	Cross 3

CHAPTER ONE

1. 0 INTRODUCTION

Groundnut originated from South America in the coastal regions of Peru where evidence of its cultivation between 300 and 2500 BC is supported by archaeological reports (Stalker, 1997; Maiti, 2002). The crop is believed to have been distributed to other parts of the world by the Spanish and Portuguese explorers in the sixteenth and seventeenth centuries (Hammons, 1994). Groundnut (also known as peanut) belongs to the family Fabaceae, tribe Aeschymanomeneae and sub tribe Stylosanthineae. The genus and species names *Arachis hypogaea* were derived from Greek words *arachos*, meaning weed, and *hypogea*, meaning underground chamber (Holbrook and Stalker 2003). The species is classified into two subspecies: *hypogaea* and *fastigiata* based on the presence or absence of flowers on the main axis (Moretzsohn *et al*., 2004).

Groundnut is the fifth largest oil crop cultivated in more than 100 countries around the globe between lat 40^{o} North and South of the equator (especially in Africa, Asia, North and South America) (Waliyar *et al*., 2007). In 2015, groundnut was grown on a total area of 21.8 million hectare worldwide with an estimated production of 38.6 million tonnes (unshelled) at an average yield of 1.58 tonnes per hectare (FAO 2015). China, India, USA, Nigeria and Myanmar are the major producers of Groundnut. Developing countries in Asia, Africa and South America account for over 97% of the world groundnut area and 95% of total production. Nigeria and Senegal are the largest producers in West and Central Africa with 45% Africa total production (ICRISAT 2015). Groundnut is one of the most popular commercial crops in Nigeria. Nigeria produces 41% of the total production in West Africa (Echekwu and Emeka 2005).

Groundnut seeds contain 40-60 % oil, 20-40% protein and 10-20 % carbohydrate. The crop has high nutritional value, possessing vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium. It is mainly used for direct consumption, in the confectionary industry, for vegetable oil in cooking and also as a source for protein feed in the animal industry. These multiple uses of peanut makes it an excellent cash crop for domestic as well as international trade (Manish *et al*., 2012). In West and Central Africa, it is an important food and cash crop: a major source of dietary oil and cash income for both urban and subsistence dwellers (Olorunju and Ntare 2001). As a legume, groundnuts improve soil fertility by fixing nitrogen and thereby increasing productivity of other crops in the semi-arid cereal cropping systems (Waliyar *et al.,* 2007), and other ecological zones.

Groundnut production in Nigeria is constrained by several abiotic and biotic stresses among which is the groundnut rosette virus disease. Groundnut rosette virus disease (GRVD) has been recognized in all groundnut growing countries on the African continent, including its offshore islands such as Madagascar, but not anywhere outside Africa (Nigam, 2008). GRVD is responsible for an annual groundnut loss of worth US$ 150 million (Waliyar *et al*.,2007). Nigeria alone lost about 0.7 million hectares of land to groundnut rosette virus epidemic which amounted to US$ 250million in 1975 (Yayock *et al*., 1976). The disease results from the synergistic interaction of three viral components; groundnut rosette virus (GRV), its satellite RNA (Sat-RNA), and groundnut rosette assistor virus (GRAV) (Taliansky *et al.,* 2000). The disease is spread by groundnut aphid.

Groundnut aphids, *Aphis craccivora* Koch, (Hemiptera: Aphididae) are an important group of insects with worldwide distribution. They are herbivorous insects that can affect plants directly or indirectly by feeding on the plant's sap. Most aphid species comprise a set of closely related populations which may have diverged genetically so that they could be considered as host races, incipient or sibling species (or subspecies) (Blackman and Eastop 2007). Groundnut aphid is the major pest of groundnut causing yield losses by feeding on phloem sap and through transmission of virus diseases (Padgham *et al*., 1990).

Viruses are the most difficult of all groundnut pathogens to control because no chemical substances (viricides) are available yet for eradicating viruses from plants (Olorunju and Ntare 2001). Insecticides for controlling virus vectors (groundnut aphids) are expensive and hardly available to farmers. Their application also poses detrimental effect to human health and environment. Improved cultural practices are not effective because farmers are reluctant to accept and adopt those practices (Waliyar *et al*., 2007). Host-plant resistance to *A. craccivora* in groundnut is recognized as the most effective, economic and sustainable method of limiting both the spread of the aphid and rosette viruses (Feakin 1973; Padgham *et al*., 1990).

This research work focussed on the studies of inheritance of aphid resistance and rosette resistance in groundnut based on host-plant resistance mechanism with these objectives;

1. To determine the gene action controlling the inheritance of aphid resistance, rosette resistance and other quantitative characters.
2. To determine the relationship between aphid resistance, rosette resistance and other quantitative characters.

3. To estimate the number of effective factors controlling the inheritance of aphid infestation, rosette disease and other quantitative characters.
4. To determine genetic advance arising from selection against aphid, rosette and other quantitative characters.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and Distribution

The origin of the *Arachis hypogaea* L. remains a subject of scientific inquiry, groundnut is believed to have been extensively cultivated in both Mesoamerica and South America. The remnant pericap (full hull) tissue recovered from archeological sites in Peru dates approximately 3900-3750 years before the present where it was used for agricultural purpose. No one can precisely say the exact time the domestication occurred but it probably first took place in the valleys of the Panamá and Paraguay River systems in the Gran Chaco area of South America (Hammons, 1994).

Groundnut is genetically a tetraploid that behaves as diploid (Stalker *et al*., 1991). The cultivated species, *A. hypogaea,* might have been derived from a unique hybridization between the wild diploid species *A. duranensis* (A-genome) and *A. ipaënsis* (B-genome) resulting in a hybrid followed by spontaneous chromosome duplication (Kochert *et al*., 1996; Seijo *et al*., 2004). It has been concluded that the A- and B-genomes contributed nearly equal amounts of DNA to the domesticated peanut (Singh *et al*., 1999).

The cultivated groundnut or peanut (*Arachis hypogaea* L.) were widely dispersed through South and Central America by the time the Europeans reached the continent probably by the Arawak Indians. After European contact, groundnuts were dispersed world-wide. The Peruvian runner type was taken to the Western Pacific, China, Southeast Asia and Madagascar. The Spanish

probably introduced the Virginia type to Mexico via the Philippines in the sixteenth century (Prasad *et al*., 2008). The Portuguese then took it to Africa and later to India via Brazil after they have established regular communication with the Indian subcontinent. The African continent can in fact be regarded as a secondary centre of variation of groundnut. Some of the most widely grown varieties of United States are believed to have come to North America from Africa; they are not found in South America except as introductions. Virginia types apparently reached the Southeast US with the slave trade (Gibbons *et al.*, 1972).

2.2 Botany and Classification of Groundnut

The groundnut is an annual herbaceous plant that grows to a maximum height of 60 cm. It is characterized by bearing of fruits that develop and mature underground. Fertilization of the ovary results in the development of an elongated stalk (peg) which grows downwards and carries the ovary into the soil to a depth of 2-7 cm. Pegs can attain a length of 15-30 cm. Once penetration of the soil surface has occurred, fruit enlargement proceeds at the peg tip with eventual formation of the peanut pod. Pods can contain 1-6 seeds.

Groundnut with indeterminate growth habit belongs to the family; Fabaceae, Genus; *Arachis* L. Species; *Arachis hypogaea* L. (Acquaah, 2007). The genus *Arachis* in subtribe *Stylosanthinae* of tribe *Aeschynomeneae* of family *Fabaceae* is made up of two subspecies, *hypogaea* and *fastigiata* which are distinguished based on branching pattern and distribution of vegetative and reproductive nodes along the main stem and lateral branches, the presence or absence of flowers on the main axis, numbers of trichomes and pod morphology (Moretzsohn *et al*., 2004).

2.3 Economic Importance of Groundnut in Nigeria

Groundnut is an important component of diet in Nigeria. It contributes about 5 percent of the estimated 58.9g of crude protein available per head per day (Abulu, 1978). Its flour is used as an ingredient in soup, confectionaries and pudding. Groundnut cake is deep fried to make a snack called *Kuli-kuli* (Hamidu *et al*. 2006). Its haulms are excellent source of hay for livestock.

According to Echekwu and Emeka (2005), groundnut contains 25% protein and more than 40% oil. Groundnut oil has traditionally been a significant dietary component in several West African countries. Oil extraction from groundnut at the village level is quite common in Nigeria although industrial processing is available too. Over half of the groundnut and its oil are sold in the domestic market serving as a source of income to poor rural farmers.

2.4 Groundnut Production Trend and Constraints in Nigeria

Nigeria was among the leading exporters of groundnut in the fifties and between 1962 and 1972, export of groundnut accounted for 22% of the national annual export value (Ambang *et al*. 2008). Nigeria reached a peak production of 1.6 million metric tons in 1973. Production fell by almost half the 1973 figure, in less than a decade due to a combination of two important factors, drought and aphid infestation. The drought of 1974/75 growing season brought with it aphid infestation and rosette which wiped more than 750,000 hectares of groundnut fields (Yayock, 1976). Production declined from 1975 to 1985 and was lowest in 1982. Another rosette epidemic occurred again in 1985, with near total loss of yield in some regions of the country (Misari *et al*.

1988, Schilling *et al*. 1992). Production however, showed a constant increase since 1986 starting from 0.7 million tonnes in 1986 to 2.9 million tonnes in 1997. In 1995, rosette disease reappeared in an area of about one million ha in Nigeria leading to an overall loss in yield of groundnut estimated at over 0.57million tonnes (Olorunju and Joshua 1999, Robinson *et al*. 1999a). Annual growth in production has been estimated at 8.12% per annum from 1984 to 2008 largely due to both growth in area cultivated (6.23%) and yield (1.88%) (Ndjeunga *et al*., 2010). Groundnut is grown in thirty-one out of the thirty-six states and FCT. Kano, Niger, Kaduna, Benue, Zamfara, Taraba, Bauchi, Borno, Kastina and Nassarawa are the top ten producing states in Nigeria accounting for nearly 80% of the total production.

Despite the economic importance of groundnut, production of groundnut in Nigeria is limited by biotic and abiotic factors. The biotic factors affecting the production of groundnut are insect pests, diseases and weeds. The important diseases of groundnut are cercospora leaf spots, early leaf spot, late leaf spot, rust, collar or crown rot, root rot, groundnut bud necrosis disease and rosette disease.

The major abiotic factors affecting the production of groundnut are erratic or insufficient rainfall, early or mid-season drought and low moisture regimes (Stalker, 1997, Holbrook and Stalker, 2003, Madhava *et al*., 2003, Minde *et al*., 2008). Other factors are declining soil fertility due to poor management, inadequate extension services, demand for labour and inaccessibility to sufficient quantities of improved seeds (Minde *et al*., 2008, Simtowe *et al*., 2009).

2.5 Aphids and Virus Transmission

Aphis craccivora Koch (Hemiptera:Aphididae) is one of the major pests of groundnut in the tropics. It is the vector of viral components (groundnut rosette virus, its satellite and groundnut rosette assistor virus) that transmit groundnut rosette virus during nutrition (Dogimont *et al.*, 2010). The insect has been called by many English names, among which includes bean aphid, black legume aphid, black lucerne aphid, cowpea aphid, lucerne aphid, oriental pea aphid and several scientific names such as *A. leguminosae* Theobald, *Doralina craccivora* (Koch), *Doralina salsolae* but the most preferred is *A. craccivora* as described by Kock in 1854. It belongs to the domain; Eukaryota, Kingdom; Metazoa, Phylum; Arthropoda, Subphylum; Uniramia, Class; Insecta, Order; Hemiptera, Suborder; Sternorrhyncha, Super family; Aphidoidea, Family; Aphididae, Genus; *Aphis*, Species; *Aphis craccivora*.

Apart from serving as vector to viral components causing groundnut rosette virus disease (GRVD), it is also a vector to many other viruses that attacks other crops like cowpea, pigeon pea, chick pea, and quinoa (Waliyar *et al.*, 2007). Aphids are associated with many host plants in the Fabaceae and also in many other plant families so that it attacks about 50 crops in 19 different plant families (Blackman and Eastop, 2007). They are widely distributed across the tropical regions of the world even though some cases have been reported in temperate areas like Siberia (Russia) and Alberta (Canada). CIE (Commission Internationale de I'Elcairage known in English as International Commission on Illumination), 1983 reported Nigeria among the geographical areas were the insect is predominant in Africa.

Virus acquisition of all three GRD virus agents does not necessarily result in their transmission (Naidu *et al*., 1999). Separate infections with GRAV or with GRV+satRNA following aphid

transmissions from plants infected with all three agents have been consistently observed in the laboratory and field (Murant, 1990; Naidu *et al*., 1998, 1999). Aphids fail to transmit the disease in the absence of GRAV and plants lacking GRV and its satellite (satRNA) do not show disease symptom. GRV and satRNA must be packaged within the coat protein of luteovirus, which is the GRAV to be aphid transmissible.

GRAV is characterized and identified as Luteovirus belonging to the family Luteoviridae by Casper *et al*., (1983) and Reddy *et al*., (1985). The genome of Luteovirus is known to be non-segmented, single molecule of linear positive-sense, single-stranded RNA of c. 6900 nucleotides that encodes for structural and non-structural proteins (Murant *et al*., 1989). It shows no symptom or temporary mottle yet can cause great yield loss in infected groundnut plant (Olorunju *et al*., 1992).

Like GRAV, GRV is transmitted in a persistent way into the cytoplasm of an infected plant where it replicates itself (Robinson *et al*., 1999). Temporary symptoms may occur when a groundnut plant is infected with GRV but its association with satRNA results in rosette disease symptom. It has no protein and conventional particle structure. The genome is a non segmented single stranded linear molecule with positive sense RNA of size c. 4019 nucleotides that encodes four open reading frames. GRV was isolated and characterized to belong to the genus umbravirus (Reddy *et al.*, 1985; Taliansky and Robinson, 2003).

SatRNA is a sub-viral RNA of GRV. It is a non segmented single stranded linear RNA of 895 to 908 nucleotides (Taliansky *et al.,* 2000). It is dependent on GRV for its multiplication, movement and encapsulation among plants. It was found to be responsible for chlorotic, green or mottle rosette (Murant and Kumar, 1990; Taliansky and Robinson, 1997). It can only be contacted along with GRV and combines with both GRV and GRAV to cause rosette disease.

2.6 Groundnut Rosette Virus Disease (GRVD)

Groundnut rosette virus disease was first reported in Tanganyika (presently Tanzania). It is the major virus disease of groundnut in sub-Saharan Africa (Zimmerman, 1907, Reddy, 1991, Waliyar *et al*., 2007). A rosette epidemic was seen in Central Malawi from 1994 to 1996 where total area of land given to cultivation of groundnut fell from 89,000 ha to 69,000 ha. It has been estimated that yield loss of about US$156 million has been observed annually due to GRVD in Africa (Willekens, 2003). GRVD has been reported in Angola, Burkina Faso, Ivory Coast, Gambia, Ghana, Kenya, Madagascar, Malawi, Niger, Nigeria, Senegal, South Africa, Sudan, Swaziland, Tanzania, Uganda and Zaire (Gibbon, 1977, Naidu *et al*., 1999).

As earlier stated, it is transmitted by *A. craccivora* by the combined interaction between GRAV, GRV and SatRNA. In the groundnut field its presence could be visibly identified by chlorotic rosette, green rosette and mosaic rosette. The chlorotic rosette manifests on the leaves as bright yellow with few green colourations and the leaf lamina becomes coiled. This type of symptom occurs throughout the sub-Saharan Africa. The green rosette is usually mosaic in nature and could be found in Angola, Kenya, Malawi, Swaziland, Uganda and West Africa (Naidu *et al*.

1999). For the mosaic rosette, a mixture of chlorotic variant and mottle variant is observed as a result of mixed infection by satRNA. It occurs in East Africa (Storey and Ryland, 1957). These variations in symptom are caused by satRNA.

When infection affects the young plants a 100% yield loss can be realized. But infection at later growth stages (between flowering and pod setting) may show symptoms only in some branches or parts of branches and yield loss depends strongly on the severity of infection (Olorunju *et al*., 1991).

Studies have shown that two independent genes control resistance to GRVD. This resistance was targeted towards GRV and its satRNA and is ineffective against GRAV (Nigam and Bock, 1990; Bock *et al.*, 1990; Olurunju *et al.*, 1992).

2.7 Scaling Tests and Generation Mean Analysis in Groundnut

Scaling tests are tools used to determine the adequacy of the additive-dominance model. The scaling test can be solved individually using Mather A, B and C scaling test or jointly using Cavalli's joint scaling test. The individual scaling tests are based on generation mean values of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2). According to Mathers' A, B and C scaling tests, the heritable effects must on the average be additive. This criterion must be met before applying the statistical test to a set of data (Mather, 1949). Cavalli's joint scaling test has the advantage of

testing goodness of fit once, instead of in three separate instances and making clear at once if the fit is significant or insignificant in a set of data (Cavalli, 1952).

Generation mean analysis is a tool used to estimate gene effects for polygenic traits. It is vital in discriminating additive, dominant and epistatic gene effects due to allelic and non allelic genic interactions from the mean genotypic values of families and generations (Viana, 2000). Different models have been postulated for the estimation of gene effect. Initially, models were developed to estimate additive and dominant gene actions precluding epistasis (Comstock and Robinson, 1948; Mather, 1949; Jinks, 1954). This was based on the assumption that epistatic gene effects were negligible. As research progressed, studies ascertained that epistasis also affects the inheritance of quantitative traits due to fixation of genes in plants. Brim and Cockerham (1961) observed epistasis in soybean and Gamble (1962) in maize. Cavalli's (1952) model considers mean effect (m), additive gene effect (d) and dominant gene effect (h) as statistic for measuring gene effect. When the additive and dominant effects or estimates are significantly different from zero this model is considered not adequate to explain the gene action at work in a population. The six-parameter models by Hayman (1958) or Gamble (1962) is a more elaborate technique for explaining the inadequacy of the additive-dominance model. This model partitions gene effect into mean effect (m), additive gene effect (d), dominant gene effect (h) and epistatic gene effects such as additive x additive (i), dominant x dominant (j) and additive x dominant (l).

In groundnut, Sangha *et al.* (1990) reported additive x additive gene effect as the predominant gene effect for plant height. Shoba *et al*. (2010) also observed that plant height and hundred seed weight were under the control of additive gene effect or additive x additive gene effect.

Contrasting reports were obtained for maturity by Mohammed *et al.* (1978) and Rachmaler (1988) indicating that additive and additive x dominance effects were important, while Naazar *et al*. (1999) observed that dominance effects could also be responsible for the expression of maturity.

Number of matured pods per plant was found to be governed by additive and non additive gene effects with preponderance of dominant gene effect (Jivani *et al.,* 2009). Shoba *et al*. (2010) found epistasis at work in addition to additive and dominant gene effects in the expression of number of matured pods per plant. This confirms the report of Isleib and Wynne (1983) who suggested that epistasis could also be important for number of matured pods per plant and number of seeds per plant.

Sangha *et al*. (1990); Vindhiyavarman and Paramasivam (1992) and Ali *et al*. (1995) found that additive gene effect governs the expression of net pod weight, while Shoba *et al.* (2010) observed that additive, dominant, additive x additive and additive x dominant gene effects control the expression of this character. Hundred seed weight was observed to be governed by additive, dominant and additive x additive gene effect with preponderance of dominant gene

effect (Jivani *et al*., 2009; Shoba *et al*., 2010). For shelling percentage additive, dominant, additive x additive, additive x dominance with preponderance of dominance control the expression of the trait (Vindihiyavarman and Paramasivam, 1992; Manoharam and Thangavelu, 2009; Jivani *et al*., 2009; and Shoba *et al*., 2010).

2.8 Effective Factors Controlling Aphid and Rosette Resistance in Groundnut

This is the estimated minimum number of genes controlling the expression of a character. According to Wright (1968) and Lande (1981) there are under lying assumptions for the reliability of the estimates of minimum number of genes. These include: the segregating genes of interest should be located in one parent, the genes of interest must not be linked, the genes of interest should have equal effects in terms of expression. Dominance and epistatis should be absent and genotype x environment effects should be absent. When there is dominance and epistatic gene effects, they bias the estimate of the minimum number(s) of genes and thus rendering it unreliable. Reports on minimum number of gene controlling various characters in groundnut are scarce.

2.9 Genetic Variability in Groundnut

Genetic variability is created through hybridization. It is the basic requirement for crop improvement as this provides wider scope for selection. Thus effectiveness of selection is dependent on the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable (Vishnuvardhan *et al.*, 2012). Mean performance, analysis of

variance, components of variance (phenotypic, genotypic and environmental), coefficients of variation (phenotypic and genotypic) and heritability (broad and narrow sense) have been used to understand the magnitude and inheritance of the available genotypic variation for different characters in groundnut.

Analysis of variance has shown that genotypes perform differently despite passing through the same conditions during an experiment. Although experimental error could be estimated as one of the sources of variation, most of the variations in the genotypes are genetic in nature indicating genetic variability. Highly significant, significant and non significant differences have been reported for different characters.

Kumar *et al*. (2014) reported highly significant differences in mean squares for days to fifty percent flowering, plant height, days to maturity, number of pods per plants, net pod yield, number of seed yield per plant and shelling percentage. These results were in line with those of Korat *et al*. (2009) and Savaliya *et al*. (2009). John *et al*. (2013) also obtained similar result with most of these characters hundred seed weight inclusive.

Variance components have been partitioned into phenotypic, genotypic and environmental components in order to appreciate the extent of heritability of a character as it varies within genotypes. The magnitude of the phenotypic component relative to genotypic component indicates if the observed variation is genetic or merely due to environment. In other words, the

phenotypic expression of the plant character is mainly controlled by the genetic makeup of the plant and the environment in which it is growing. Genotypic component is further divided into heritable and non heritable components. These components can be deduced from phenotypic and genotypic coefficients of variation (Ashish *et al*., 2014). In most cases, the phenotypic coefficient of variation is higher than the genotypic coefficient of variation indicating that the variation of a character is affected by environment. At times equal magnitude of both can be obtained indicating that the variation of the character could be attributed to genetic causes than to environment. In a situation where the variation is partitioned into three viz: additive, dominance and environmental variances, the extent to which the variation is genetic (additive or dominance) could be ascertained.

Phenotypic coefficient of variation was found to be greater than genotypic coefficient of variation in days to fifty percent flowering, days to maturity, plant height, number of matured pods per plant, sound kernel percentage, shelling out turn and pod yield per plant by Vishnuvardhan *et al*. (2012). This finding was corroborated by Korat *et al*. (2009) and Savaliya *et al*. (2009). Rao *et al*. (2014) showed that phenotypic coefficient of variation was higher than genotypic coefficient of variation in days to fifty percent flowering, days to maturity, plant height, shelling percentage, number of pods per plant and hundred kernel weight among others.

Moderate genotypic coefficient of variation was obtained for pod yield, seed yield and low for plant height, days to fifty percent flowering, shelling percentage and days to maturity by Maurya *et al*. (2014). The same report was given by Venkataramana *et al*. (2001) and Nath and Alam

(2002). Similarly, moderate genotypic coefficient of variation was observed for days to fifty percent flowering and low for shelling percentage and days to maturity (Kumar *et al.* 2014). This finding is at par with that of Venkataramana *et al*. (2001). Injeti (2008) and Nath and Alam (2002) had the same result for days to maturity.

On the other hand, moderate phenotypic coefficient of variation was observed for pod yield and low for plant height, days to fifty percent flowering, shelling percentage and days to maturity (Maurya *et al.*, 2014). Similar findings were observed for days to maturity by John *et al*. (2008), Sangram *et al.* (2013) and Shukla and Rai (2014).

2.10 Heritability and Genetic Advance in Groundnut

Heritability is a measure of the extent of phenotype caused by the action of gene. A good estimate of heritability is a useful tool that helps the breeder to determine traits that can serve as criteria for selection of parental lines for breeding program (Vange and Maga, 2014; Kumar *et al*., 2014). The magnitude of possible improvement in mean from the previous generation to the next could be obtained from genetic advance. When the heritability and the genetic advance are high further improvement through plant selection could be considered (Nath and Alam, 2002).

In days to fifty percent flowering, Nath and Alam (2002) reported high narrow sense heritability and low genetic advance. This was corroborated by Vange and Maga (2014). For heritability in broad sense, Kumar *et al*. (2014) observed high heritability and genetic advance estimates. This is in contrast with the result of Rao *et al*. (2014) where both heritability and genetic advance were found to be low. Reports from Vishnuvardhan *et al.* (2012), John *et al.* (2013), Vange and

Maga (2014), Rao *et al.* (2014), Kumar *et al*. (2014) and Maurya *et al*. (2014) indicated consistent high broad sense heritability and low to high genetic advance.

Results for plant height were found to have high broad sense heritability and genetic advance (John *et al*., 2013). Kumar *et al*. (2014), Maurya *et al.* (2014) and Rao *et al*. (2014) recorded high and low broad sense heritability, while John and Rhaghava (2014) observed low values for broad sense heritability and genetic advance. High narrow sense heritability with low genetic advance was reported by Nath and Alam (2002).

Low broad sense heritability and genetic advance was revealed in days to maturity (Rao *et al*., 2014; Kumar *et al*., 2014) and in narrow sense heritability (Naazar *et al*., 1999). Vishnuvardhan *et al.* (2012) and John and Rhaghava (2014) reported high and low, while Maurya *et al.* (2014) discovered moderate and low for broad sense heritability and genetic advance.

Number of matured pods per plant showed high to moderate broad sense heritability but high narrow sense heritability while genetic advance remained low (Nath and Alam, 2002; John *et al.,* (2013), Rao et al., 2014; Kumar *et al*., 2014,). Maurya *et al.,* (2014) obtained low broad sense heritability and genetic advance.

High heritability both in narrow and broad sense and low genetic advance were discovered for net pod yield (Nath and Alam, 2002; John *et al*., 2013; Rao *et al*., 2014; Kumar *et al*., 2014 and

Maurya *et al.,* 2014) and number of seeds per plant (Nath and Alam, 2002). Low broad sense heritability and genetic advance were reported by John and Rhaghava (2014) and Vishnuvardhan *et al.* (2012).

Shelling percentage was found to have high broad sense heritability and low genetic advance (Nath and Alam 2002; John *et al*., 2013; Rao *et al.,* 2014; Kumar *et al.,* 2014). However, low broad sense heritability and low genetic advance were observed by Vishnuvardhan *et al.* (2012) and Maurya *et al*. (2014).

High broad sense heritability and low genetic advance were reported for hundred seed weight (Vange and Maga, 2014; Rao *et al.,* 2014 and Maurya *et al.,* 2014). On the contrary, John and Rhaghava (2014) and Vishnuvardhan *et al.* (2012) reported moderate to low broad sense heritability and low genetic advance.

2.11 Phenotypic and Genotypic Correlations in Groundnut

A plant breeder's choice of a breeding and selection procedure may be influenced by his understanding of genetic correlations as well as heterotic phenomenon. Genetic correlation is the correlation of the breeding values of character pair and may be due to pleiotrophy or linkage (Falconer, 1960). It provides the measure of the genotypic associations between traits, gives an indication of the characters that may be useful as indices of the more important characters under consideration, and may also identify traits that have little or no importance in the selection

program. Phenotypic correlation is an association between characters that can be directly observed as they appear on the individuals, while genotypic correlation is the association of the breeding values of a pair of characters (Redona and Lantican, 1986).

Existence of genetic association means that selection for one trait will cause changes in the other trait, this is called correlation response. Genotypic and phenotypic correlation coefficients can be at par with each other suggesting less influence of the environment (Rao *et. al*., 2014). However, in most cases genotypic correlation coefficients exceed the corresponding phenotypic coefficient of variation indicating the presence of strong inherited association between character pairs (Ibrahim, 2001). Weber and Moorthy (1952) explained that low phenotypic correlations could be attributed to the masking or modifying effect of the environment on the genetic characteristics.

Days to fifty percent flowering was found to have positive and highly significant genotypic correlation with days to maturity and simply correlated with plant height and shelling percentage but negatively correlated with number of pods per plant, hundred seed weight and net pod weight (Rao *et al.,* 2014).

According to Redona and Lantican (1986) plant height has positive genotypic and phenotypic correlation with number of matured pods per plant and number of seeds per plant where as Rao *et al*. (2014) observed positive genotypic association with shelling percentage but negatively with number of seeds per plant and hundred seed weight. Positive genotypic correlation was seen

between days to maturity with shelling percentage but negatively with plant height, number of matured pods per plant and hundred seed weight by Rao *et al.* (2014).

Narasinmhulu *et al.* (2012) reported that shelling percentage had highly positive genotypic correlation with mature kernel weight and highly negatively correlated with pod yield per plant in terms of phenotype. On the other hand, it was positively genotypically correlated with mature kernel weight but negatively with number of matured pods per plant (Rao *et al*., 2014). Number of pods per plant was found to be highly significantly correlated with hundred seed weight and seed yield per plant but not significantly correlated with number of seeds per plant and net pod yield in terms of genotype (Redona and Lantican, 1986; Rao *et al*., 2014). In the same vein, it is highly significantly correlated with number of seeds per plant and net pod yield (Redona and Lantican, 1986).

Significant and highly significant genotypic correlations between number of seeds per plant and net pod yield, number of seeds per plant and seed yield per plant. Similarly, significant and highly significant phenotypic associations were recorded between number of seeds per plant and net pod yield, and seed yield per plant (Redona and Lantican, 1986). Redona and Lantican (1986) and Rao *et al*. (2014) observed a good correlation between hundred kernel weight with seed yield per plant and pod yield per plant.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Description of Experimental Site

The field evaluations were conducted at the Institute of Agricultural Research (I.A.R) farm, Samaru with an altitude of 686m above sea level, lat $11^0$11□ N, long 07^{0}38□ E during the 2014 growing season in the Northern guinea savanna zone of Nigeria, with a mean annual rainfall of 1050 mm distributed within five months (June to October). The soil type is loamy.

3.2 Description of Plant Materials

The plant materials for this research consisted of four entries obtained from West and Central Africa groundnut improvement program, Mali (ICGX-SM00020/5/9, ICGVIS07899, ICGX-SM0017/5/P10/P1 and ICGX-SM0020/5/P4/P1), one local variety (MANIPENTA) and three checks (SAMNUT 22, SAMNUT 23, and SAMNUT 24). Lines ICGX-SM00020/5/9 and ICGX-SM0020/5/P4/P1 are resistant to groundnut aphid, line ICGVIS07899 is resistant to rosette, while line ICGX-SM0017/5/P10/P1 is susceptible to groundnut aphids and MANIPENTA is susceptible rosette. The genetic populations were developed through crossing of the resistant P_1s (paternal parents) to susceptible P_2s (maternal parents) to obtain the F_1s. The F_1s were advanced to obtain the F_2s. The F_1s were also crossed to the reciprocal recurrent parents to obtain BCP_1 and BCP_2. The resulting generations (P_1, P_2, F_1, F_2, BCP_1 and BCP_2) were evaluated with the three checks. Table 3.1 gives information about the genotypes.

Table 3. 1: Description and Source of Groundnut Genotypes used in the Study

Genotypes	Coding	Description	Source
Resistant lines			
ICGX-SM00020/5/9	P_1	Aphid Resistant, early maturing	ICRISAT
ICGX-SM0020/5/P4/P1	P_2	Aphid Resistant, early maturing	ICRISAT
ICGVIS07899	P_3	Rosette Resistant, early maturing	ICRISAT
Susceptible lines			
ICGX-SM0017/5/P10/P1	P_4	Aphid Susceptible, early maturing	ICRISAT
MANIPENTA	P_5	Rosette Susceptible, late maturing	Local variety
Checks			
SAMNUT26	P_6	Aphid Resistant, early maturing	IAR
SAMNUT23	P_7	Rosette Resistant, early maturing	IAR
SAMNUT24	P_8	Rosette Resistant, early maturing	IAR

ICRISAT-International Crops Research Institute for the Semi-Arid Tropics.
IAR-Institute for Agricultural Research.

3.3 Development of Genetic Population

Paired crosses were made using five parents through hand emasculation by biparental mating design at the screen house of Plant Science Department, Ahmadu Bello University Zaria as follows; ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 (P_1 x P_4), ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 (P_2 x P_4), ICGVIS07899 x Manipenta (P_3 x P_5), to obtain three F_1s between August and December 2013.

The three F_1 hybrids were advanced to obtain three F_2 generations through selfing. Six BCs were also obtained through reciprocal crosses to recurrent parents between February and June 2014 at Institute for Agricultural Research farm Samaru. The table below show the set of crosses organized.

Table 3. 2**:** Crosses, F_1, F_2 and backcrosses developed

Female parent	Male parent	F_1	F_2	BCP_1	BCP_2
P_1	P_4	$P_1 \times P_4$	$(P_1 \times P_4) \times (P_1 \times P_4)$	$P_1 \times (P_1 \times P_4)$	$P_4 \times (P_1 \times P_4)$
P_2	P_4	$P_2 \times P_4$	$(P_2 \times P_4) \times (P_2 \times P_4)$	$P_2 \times (P_2 \times P_4)$	$P_4 \times (P_2 \times P_4)$
P_3	P_5	$P_3 \times P_5$	$(P_3 \times P_5) \times (P_3 \times P_5)$	$P_3 \times (P_3 \times P_5)$	$P_5 \times (P_3 \times P_5)$

3.4 Field Evaluation

The five parents, three F_1s, three F_2s, six backcrosses along with the three checks making a total of twenty entries were evaluated at the Institute for Agricultural Research farm Samaru. The experiment was laid out in a Randomized Complete Block Design (RCBD) in three replications with one row plot each of 5m in length and an inter row and intra row spacing of 0.75m by 0.25m. The rows containing the genotypes under test were flanked by two infector rows of MANIPENTA a highly susceptible cultivar. This technique, called infector-row technique was described by Olorunju *et al*. (2001). An alley of 1m separated one block from the other. MANIPENTA was sown two weeks earlier to allow build up of infestation. *Aphis cracccivora* were collected from infested groundnut *Arachis hypogaea* and cowpea *Vigna unguiculata* plants in fields within Zaria and environs. These colonies were maintained on susceptible local groundnut genotype MANIPENTA. Three wingless (apterae) aphids were introduced on the tender leaves of 14 day-old seedlings of each of the twenty genotypes under trial. Each genotype was observed for the presence or absence of the aphids. Plants with no aphid were re-infested 7days after the first infestation. It is rare to find plants without aphids in choice test because the aphids were free to roam to find suitable plants within the field. No measure was taken to confine the aphids within the field. Data were collected from 40 plants for non-segregating populations (P_1, P_2, F_1) while 100 plants and 80 plants were considered for F_2 and BC_1 P_1 and BC_2 P_2 segregating populations respectively.

3.5 Data collection

Data were collected on the following characters.

3.5.1 Plant height (centimeter): the distance from ground to the top of the main axis was measured using meter rule shortly before harvest.

3.5.2 Days to 50% flowering: the days after sowing when 50% of the plants had at least one flower was recorded.

3.5.3 Days to maturity: the number of days after sowing when the pods were fully matured was recorded.

3.5.4 Number of mature pods per plant: mature pods were counted during harvest to calculate the mean number of pods per plant.

3.5.5 Number of seeds per pod: the average number of seeds obtained from mature pods per plant were counted and recorded.

3.5.6 Pod yield per plant (gram): mature pods were stripped, dried and cleaned, and then weighed using a weighing balance and recorded.

3.5.7 Hundred seed weight (gram): a random sample of hundred seeds were taken from the harvested bulk of each genotype and weighed using Mottler PM16-N weighing balance of model ISC07501.

3.5.8 Shelling percentage: the ratio of the weight of seed to the weight of pod expressed as a percentage.

3.5.9 Rosette severity index: The disease severity was recorded as the amount of plant tissue that was diseased with green or chlorotic rosette. Reaction to rosette were scored based on the scale developed by groundnut germplasm programme the year 2000 below

1 = No apparent rosette symptoms
3 = 10% -20% rosette symptoms
5 = 20% - 60% rosette symptoms
7 = 60 -80% rosette symptoms

9 = 100% rosette symptoms

Disease severity index were then obtained using the formula described by Sherwood and Hagedron, 1958

$DSI = \sum \left(\frac{s \times n}{t \times 3} \right) \times 100$, where

$DSI =$ Disease Severity Index

$s =$ score (class)

$n =$ number of plants in class

$t =$ total number of plants

3.5.10 Rosette disease incidence: The ratio of number of plants that showed green or chlorotic conditions to the total number of plants in the row expressed in percentage. The percent disease incidence was scored based on the scale below as recommended by ICRISAT (Waliyar *et al*. 2007).

Table 3.3 Percent disease incidence PDI scale for groundnut rosette disease virus

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

3.5.11 Aphid infestation index: Aphid infestation index for each line was calculated by the formula and scale developed by Mensah *et al.* (2005, 2008).

$$DI = \sum \left(\frac{SV \times NA}{4 \times NP} \right) \times 100$$,where

$DI =$ Aphid damage index

$SV =$ Scale value

$NA =$ Total number of aphids in the category

$NP =$ Total number of plants

Table 3. 4: Aphid damage index (D.I) based on four point scale

Score	Symptoms description	No. of aphids
0	No aphid.	< 1
0.5	Fewer than 10 aphids per plant, no colony formed.	< 10
1.0	Plant appears healthy.	11- 100
1.5	Plant appears healthy	101 – 150
2.0	Aphids mostly on young leaves, or tender stem, plant appear healthy.	151 – 300
2.5	Plants appear healthy.	301 – 500
3.0	Plants appear healthy, young leaves and tender stems are covered with aphids, leaves appear slightly curly and shiny.	501 – 800
3.5	Plants appear stunted, leaves appear curled and slightly yellow, no sooty mould and few cast skin.	>800
4.0	Plants appear stunted, leaves appear severely curled and yellow and are covered with soothy mould and cast skin.	>800

Developed by Mensah *et al*. (2005, 2008)

3.6 Statistical Analysis

Data collected from different genetic populations were subjected to appropriate statistical analyses using the following statistical tools. Mean separation was undertaken using Duncan's Multiple Range Test. Means with the same letter are not significantly different at 5% probability level. The Least significant difference was noted.

3.6.1 Scaling Tests

Joint scaling test of Cavalli (1952) was performed to estimate the three-parameter model consisting of mid-parental value (m), dominance (h) and additive (d) gene effects following the weighted least square method proposed by Mather and Jinks, 1971. Adequacy of three-parameter model was tested using chi-square test for goodness of fit at degrees of freedom, where n is the number of generation from which the three parameters were estimated. The information on gene action controlling the inheritance of the characters under study was obtained from six parameters model suggested by Hayman (1958) using the means of the generations (P_1, P_2, F_1, F_2, BC_1P_1, BC_1P_2) as shown below:

Mean effect=m

Additive=d

Dominance=h

Additive x Additive=i

Additive x Dominance=j

Dominance x Dominance=l

$$m = \overline{F_2}$$

$$d = \overline{BCP_1} - \overline{BCP_2}$$

$$h = 2\overline{BCP_1} + 2\overline{BCP_2} + \overline{F_1} - 4\overline{F_2} - \tfrac{1}{2}\overline{P_1} - \tfrac{1}{2}\overline{P_2}$$

$$i = 2\overline{BCP_1} + 2\overline{BCP_2} - \tfrac{1}{2}\overline{P_1} + \tfrac{1}{2}\overline{P_2}$$

$$j = \overline{BCP_1} - \overline{BCP_2} - \tfrac{1}{2}\overline{P_1} + \tfrac{1}{2}\overline{P_2}$$

$$l = \overline{P_1} - \overline{P_2} + \tfrac{1}{2}\overline{F_1} + 4\overline{F_2} - 4\overline{BCP_1} - 4\overline{BCP_2}$$

The variances of the estimates of gene effects were obtained as follows:

$$V_m = V(F_2)$$

$$V_d = V(BCP_1) + V(BCP_2)$$

$$V_h = 4V(BCP_1) + 4V(BCP_2) + V(F_1) + 16V(F_2) + \tfrac{1}{2}V(P_1) + \tfrac{1}{2}V(P_2)$$

$$V_i = 4V(BCP_1) + 4V(BCP_2) + 16V(F_2)$$

$$V_j = V(BCP_1) + V(BCP_2) + \tfrac{1}{2}V(P_1) + \tfrac{1}{2}V(P_2)$$

$$V_l = V(P_1) + V(P_2) + 4V(F_1) + 16V(F_2) + 16V(BCP_1) + 16V(BCP_2)$$

Standard error was obtained by taking the square root of the respective variances and significant departure of the estimate of the parameters from zero was tested applying ‘t’ test with the tabular

t value at n-1 degrees of freedom, where n is the number of plants used in deriving the variances of all the generations involved.

3.6.2 Heritability

Broad sense heritability and narrow sense heritability were estimated following the formula suggested by Wright (1968) using the following relation:

$$H_b^2 = \frac{\sigma_{F2}^2 - \sigma_E^2}{\sigma_{F2}^2} \times 100$$

Where, H_b^2 = broad sense heritability

$\sigma^2 F_2$ = variance of F_2 population of a set

σ_E^2 = environmental variance

The narrow sense heritability were computed using the formula

$$H_{(N)} = \frac{\sigma_A^2}{\sigma_{F2}^2} \times 100$$

Where, σ_A^2 =additive variance as a component of genetic effect,

σ_{F2}^2 =variance of the F_2 population of a cross

Additive variance (σ_A^2) as a component of genetic effect was computed using the formula

$$\sigma_A^2 = 2\sigma_F^2 - \left(\sigma_{B1}^2 + \sigma_{B2}^2\right)$$

Where, σ_F^2 = variance of the F_2 population of a cross

σ_{B1}^2 = variance of backcross to parent 1 population

σ_{B2}^2 = variance of backcross to parent 2 population

3.6.3 Genetic Advance

Expected gain in selection from selecting desirable F_2 plants to generate F_3 populations or from the segregating population to the next generation was computed as per cent of means based on the formula and procedure suggested by Allard (1960) as:

$$G_s = k * \sigma^2{}_F * h^2$$

Where: G_s = expectation of genetic advance under selection

k = Standardized selection differential, at 10% selection intensity=1.755

$\sigma^2{}_F$ = variance of the F_2 population of a cross

h^2 = narrow sense heritability

3.6.4 Correlations

Genotypic and phenotypic correlations were used to investigate the association among characters studied. Correlation coefficients were calculated from component of variance and covariance according to Shivaji and Gritton (1975) the genotypic components were computed by equating the genotypic variances and covariance to the expected mean square and set products, and hence genotypic correlations were computed by this formula:

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

r_g = genotypic correlation coefficient

COV_{g12} = estimate of the genotypic variance of character 1 and 2

σ^2_{g1} = estimate of the genotypic variance of character 1

σ^2_{g2} = estimate of the genotype variance of character 2

Phenotypic correlation were computed using the following formula:

$$r_p = \frac{COV_{ph12}}{\sqrt{\left(\sigma^2_{ph1}\right)\left(\sigma^2_{ph2}\right)}}$$ where

r_p = phenotypic correlation coefficient

COV_{ph12} = estimate of phenotypic covariance for characters 1 and 2

σ^2_{ph1} = estimate of phenotypic variance for character 1

σ^2_{ph2} = estimate of phenotypic variance for character 2

Decision for significance was made using error degree of freedom at 5% and 1% probability levels from pearson's correlation table.

3.6.5 Number of Effective Factors

This is the estimated minimum number of genes controlling the expression of a character. Effective factors (EF) were estimated using five methods. Method 1 (EF_1) was proposed by Wright (1968), method 2 (EF_2) was proposed by Mather and Jinks (1982), methods 3 to 5 were proposed by Lande (1981).

$$EF_1=\frac{(P_2-P_1)^2[.5-2h(1-h)]}{8[\sigma_{F2}^2-0.25(\sigma_{P1}^2+\sigma 2\sigma_{F1}^2)]}, \text{ where } h=\frac{F_1-P_1}{P_2-P_1}$$

$$EF_2=\frac{[.5(P_2-P_1)^2]}{[2\sigma_{F2}^2-(\sigma_{B1}^2+\sigma_{B2}^2)]}$$

$$EF_3=\frac{(P_2-P_1)^2}{8[\sigma_{F2}^2-0.25(\sigma_{P1}^2+\sigma_{P2}^2+2\sigma_{F1}^2)]}$$

$$EF_4=\frac{(P_2-P_1)^2}{8[2\sigma_{F2}^2-(\sigma_{B1}^2+\sigma_{B2}^2)]}$$

$$EF_5=\frac{(P_2-P_1)^2}{8[\sigma_{B1}^2+\sigma_{B2}^2-(\sigma_{F1}^2+0.5\sigma_{P1}^2+0.5\sigma_{P2}^2)]}$$

Where P_1=mean of parent 1 population,

P_2=mean of parent 2 population,

F_1=mean of first filial generation population,

σ_{P1}^2 = variance of parent 1 population,

σ_{P2}^2 = variance of parent 2 population,

σ^2_{F1} = variance of first filial generation population,

σ^2_{F2} = variance of second filial generation population,

σ^2_{B1} = variance of backcross to parent 1 population,

σ^2_{B2} = variance of backcross to parent 2 population.

All of the formulae assume segregating genes are not linked, all the genes have equal effects on characters studied, epistatic effects are absent, dominance effects are absent, and genotype x environment effects are absent (Wright, 1968).

CHAPTER FOUR

4.0 RESULT

4.1 Mean Performance

The mean performance of the parents, F_1s and the segregating generations (F_2, BC_1P_1, BC_1P_2) for days to fifty percent flowering, aphid infestation index, rosette disease incidence, rosette severity index, plant height, days to maturity, mature pods per plant, pod yield per plant, number of seeds per plant, shelling percentage and hundred seed weight are presented in table 4.1.

There were significant differences between the parents for all the traits measured in the three sets of crosses. Among the parents, ICGVIS07899 was the best performer in terms of days to fifty percent flowering (36.67days), aphid infestation index (2.16%), rosette disease incidence (2.78%) and rosette severity (0.93%) followed by ICGX-SM0020/5/P4/P1. The tallest (43.78cm) and the shortest (31.56cm) plants were ICGX-SM0020/5/P4/P1 and Manipenta. The earliest maturing (98.67days) was Manipenta followed by ICGX-SM0017/5/P10/P1. The latest was ICGX-SM0020/5/9. ICGVIS07899 exhibited superiority in terms of number of matured pods per plant (35pods) and pod yield per plant (27.78pods) with ICGX-SM0017/5/P10/P1 ranking second. Considering number of seeds per plant (18.56seeds) and shelling percentage (74.69%), Manipeta was also the highest. The heaviest in terms of hundred seed weight (59.07g) was recorded in ICGX-SM00020/5/9 and ICGX-SM0017/5/P10.

Among the F_1 hybrids, ICGX-SM0020/5/9 x ICGX-SM0017/P10/P1 ranked best in the characters studied except in plant height (37.33cm) where it ranked last. ICGX-SM0017/5/P10/P1x ICGX-SM0020/5/P4/P1 ranked second in most of the characters performing best in plant height (43.33cm) and last in days to maturity (104.33days) and shelling percentage (63.33%). ICGVIS07899 x Manipenta was the least in performance but ranked second in plant height (41.44cm), days to maturity (104.33days) and shelling percentage (65.25%).

Table 4.1 Mean performance for aphid infestation index, rosette disease incidence, rosette severity index and other quantitative characters in the three sets of groundnut crosses evaluated at Samaru in 2014

Character	Generation	ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1	ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1	ICGVIS07899 x Manipenta
Days to fifty percent flowering	P_1(R)	45.67a	41.00a	36.67cde
	P_2(S)	38.67bc	38.00abcd	39.00b
	F_1	32.00f	36.67cd	38.00bc
	F_2	41.00b	40.33ab	42.33a
	BCP_1	35.33de	39.33abc	36.00cdef
	BCP_2	37.67cd	40.00abc	34.33f
	LSD	2.44	3.40	2.23
	Range	32.00-45.67	36.67-41.00	34.33-42.33
Aphid infestation index (%)	P_1(R)	5.13ab	5.13	2.16b
	P_2(S)	5.27ab	2.19	57.50a
	F_1	1.76b	2.31	4.55b
	F_2	2.28ab	2.87	1.92b
	BCP_1	2.63ab	3.82	2.08b
	BCP_2	10.88a	2.03	4.05b
	LSD	8.85	3.25	28.49
	Range	1.78-10.88	2.03-5.13	1.92-57.50
Rosette disease incidence (%)	P_1(R)	20.36cd	20.36bc	2.78bc
	P_2(S)	32.54ab	11.48cd	42.50a
	F_1	13.39d	16.98c	18.73abc
	F_2	37.06a	31.11a	30.16ab
	BCP_1	31.31ab	26.76ab	36.15a
	BCP_2	26.48bc	31.11a	32.84a
	LSD	9.90	9.07	28.12
	Range	13.39-37.06	11.48-31.11	2.78-42.50
Rosette severity index (%)	P_1(R)	26.71bc	26.71	0.93c
	P_2(S)	38.89ab	10.31	50.83ab
	F_1	11.81cd	16.99cd	25.08bc
	F_2	45.95ab	51.85a	45.50ab
	BCP_1	52.19a	40.44ab	60.25a
	BCP_2	39.69ab	49.77a	54.73ab
	LSD	21.67	17.61	34.35
	Range	11.81-52.19	10.31-51.85	0.93-60.25
Plant height (cm)	P_1(R)	37.22ab	37.22	34.56cd
	P_2(S)	36.00ab	43.78	31.56d
	F_1	37.33ab	43.33	41.44a
	F_2	37.56ab	36.56	38.11abc
	BCP_1	32.67b	38.78	37.33bc
	BCP_2	31.11b	37.57	35.33cd
	LSD	8.11	7.71	5.60
	Range	31.11-37.56	37.22-43.78	31.56-41.44
Days to maturity	P_1(R)	115.67a	115.67a	108.33a
	P_2(S)	102.00c	108.33ab	98.67bc
	F_1	99.00cde	107.00abc	104.33ab
	F_2	109.00b	104.33bc	103.00abc
	BCP_1	101.67cd	110.33ab	100.33abc
	BCP_2	96.67de	115.00a	94.00c
	LSD	5.18	9.07	9.59
	Range	96.67-115.67	104.33-115.67	94.00-108.33

Table 4.1 Continues

Character	Generation	ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1	ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1	ICGVIS07899 x Manipenta
Number of matured pods per plant	P_1(R)	8.56d	8.56c	35.00a
	P_2(S)	33.44a	22.56ab	22.56abcd
	F_1	32.11a	23.33ab	11.11d
	F_2	17.89c	18.33b	16.44cd
	BCP_1	28.44ab	24.56ab	33.78ab
	BCP_2	22.44bc	23.00ab	33.67ab
	LSD	7.96	9.06	12.63
	Range	8.56-33.44	8.56-24.56	11.11-35.00
Pod yield per plant	P_1(R)	10.44e	10.44c	27.78a
	P_2(S)	18.52cd	18.32b	17.59bcd
	F_1	25.64ab	23.02ab	8.52d
	F_2	20.10bcd	21.93ab	13.01cd
	BCP_1	25.00abc	23.36ab	26.14ab
	BCP_2	15.00de	21.00ab	20.07abc
	LSD	6.93	7.84	9.93
	Range	10.44-25.00	10.44-23.36	8.52-27.78
Number of seeds per plant	P_1(R)	15.67ab	15.67c	15.44b
	P_2(S)	15.33b	18.00ab	18.56a
	F_1	18.22a	17.44abc	16.67ab
	F_2	15.00b	15.67c	16.67ab
	BCP_1	16.78ab	16.00c	17.33ab
	BCP_2	16.89ab	15.44c	17.11ab
	LSD	2.87	2.25	2.18
	Range	15.00-18.22	15.44-18.00	15.44-18.56
Shelling percentage	P_1(R)	66.94cd	66.94ab	69.05ab
	P_2(S)	71.95abc	70.71ab	74.69a
	F_1	71.85abc	63.33b	65.25bc
	F_2	64.50d	68.93ab	61.08c
	BCP_1	72.44ab	71.13ab	73.77a
	BCP_2	71.79abc	65.24ab	70.17ab
	LSD	5.14	10.33	6.52
	Range	64.50-71.95	63.33-71.13	61.08-74.69
Hundred seed weight (g)	P_1(R)	59.07ab	59.07ab	39.27cde
	P_2(S)	30.73f	45.17cd	44.90bc
	F_1	46.13cde	44.60cd	30.13g
	F_2	59.87a	70.57a	32.10fg
	BCP_1	44.40de	47.53bcd	41.80cd
	BCP_2	31.60f	45.17cd	33.20efg
	LSD	8.36	13.06	6.70
	Range	31.60-59.87	45.17-70.57	30.13-44.90

P_2=Parent 2, P_1=Parent 1, F_1=First filial generation, F_2=Second Filial generation, BC_1=Backcross to parent 1, BC_2=Backcross to parent 2. R=resistance, S=susceptible. LSD= Least significant difference. Means with the same letter are not significantly different at 0.05 probability level.

The mean performances of the segregating generations for the characters studied showed that among the F_2s, ICGVIS07899 x Manpenta was outstanding in performance for aphid infestation index (1.92%), rosette disease incidence (30.16%), rosette disease severity (45.50%), plant height (38.11cm), days to maturity (103days) and number of seeds per plant (16.67seeds) with ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 ranking second. However, ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 ranked first in performance for days to fifty percent flowering (42.33days), number of matured pods per plant (18.33pods), pod yield per plant (21.93g) and hundred seed weight (70.57g). ICGX-SM0020/5/9 x ICGX-SM0017/P10/P1 performed least among the sets of crosses although ranking second for number of matured pods per plant (17.89pods), shelling percentage (64.50%) and hundred seed weight (70.57g).

Among the backcross generations, BC_1P_2 of ICGVIS07899 x Manpenta performed best for days to fifty percent flowering (34.33days) and days to maturity (94days). BC_1P_1 of ICGVIS07899 x Manpenta performed best for number of matured pods per plant (33.78 pods), pod yield per plant (26.14g) and number of seeds per plant (17.33seeds), while BC_1P_2 of ICGVIS07899 x Manpenta and BC_1P_1 of ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 ranked second for number of matured pods and pod yield per plant respectively. BC_1P_2 of ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 was outstanding for aphid infestation index. BC_1P_2 of ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 ranked first for rosette disease incidence (26.48%) and BC_1P_1 of ICGVIS07899 x Manpenta for shelling percentage (73.77%). BC_1P_1 of ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 took the lead for plant height (38.78cm) and hundred seed weight (47.53g). For rosette severity index, BC_1P_2 of ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 is the best performer with a severity of 39.69%.

4.2 Gene Effects and Heritability

In the present study, determination of mode of inheritance according to generation mean is based, according to Fisher *et al*. (1932) and Mather (1949), on parameters, which reflect mutual relationships between homozygous parents and their progenies for a particular quantitative characteristic. The method is in fact based on the existence of connections among mean generation values, which are dependent solely on additive and dominant gene effects. There are several ways to test these relationships as well as the verity of the hypothesis that these relationships depend solely on additive and dominant genes. One of them is Cavalli's 1952 joint scaling test. The joint scaling test is considered more appropriate than Mather's scaling test for checking the adequacy of the additive-dominance model. The test estimates, the parameters $|m|$, $|d|$ and $|h|$ were obtained from means of the six generations followed by a comparison of the observed generation means with expected values derived from the estimates of the three parameters.

The results of the joint scaling test are shown in table 4.2. The sum contributions of the six generations for all the eleven characteristics in the three sets of crosses representing chi-square values for three degrees of freedom were significantly different from zero. This implies the inadequacy of the additive-dominance model and indicates that additive and dominant genes do not exclusively control the expression of the studied characteristics but non-allelic interactions were also present.

Table 4. 2: The estimates of gene effects, heritability and genetic advance for aphid infestation index, rosette disease incidence, rosette severity index and other quantitative characters from the three sets of crosses evaluated at Samaru in 2014

Character	Days to fifty percent flowering			Aphid infestation index (%)			Rosette disease incidence (%)		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	4.20±2.8**	39.6±1.7**	34.8±1.6**	7.2±3.9	2.9±1.1	17.3±17.1	25.4±6.1**	13.5±4.7**	43.6±15.8**
D	-2.7±1.4	-1.3±0.8	0.9±0.8	0.8±1.9	-1.5±0.6**	25.8±8.4**	5.1±3.0	-3.5±2.3	17.2±7.7
H	-6.9±3.1	-0.4±1.8	1.6±1.8	-2.2±4.3	-1.5±1.2	-40.1±19.0*	2.0±7.1	15.4±5.2**	7.7±17.9
χ^2	1.7	0.6	1.9	12.7**	0.01	186.9**	26.1**	29.2**	44.5**
Gene effects estimated from six parameter model									
M	-	-	-	-14.2±16.5	0.2±5.1	24.8±77.6	-35.7±19.2	-31.4±16.1	-199±76.9
D	-	-	-	-0.1±1.9	-1.5±0.6	28.3±9.4**	5.9±2.1	-4.4±2.1	19.9±8.6
H	-	-	-	53.3±41.8	3.4±13.0	-92.3±196.4	122.6±46.8	124.2±43.9	164.0±187.0
I	-	-	-	21.3±16.0	2.8±4.9	-5.8±75.0	62.0±18.7**	45.0±17.6	62.4±74.8
J	-	-	-	18.2±12.2	-0.7±3.8	-52.8±57.5	-20.4±12.8	14.8±12.0	-46.4±50.9
L	-	-	-	-34.9±27.6	-1.5±8.6	57.8±129.6	-49.7±30.3	-64.3±28.2	-94.4±120.5
H%	60	55	57	0.0[x]	65	65	62	57	60
h%	53	40	46	0.0[x]	51	48	74	65	69
GA	21.5	15.8	18.6	0.0[x]	6.3	5.6	32.3	26.6	29.5

Cross1=ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1, Cross 2=ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1, Cross 3=ICGVIS07899 x Manipenta. Estimate of gene effects were significantly different from zero at 0.05(*) and 0.01(**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, χ^2 =chi square, H=broad sense heritability, h=narrow sense heritability, GA=genetic advance, (x) value assumed to be zero due to negative estimate.

Table 4.2 Continues

Character	Rosette severity index (%)			Plant height (cm)			Days to maturity		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	38.2±13.2**	15.5±11.1	42.7±19.5*	35.3±3.5**	38.2±3.1**	32.0±3.0**	105.4±4.1**	110.7±4.2**	101.8±4.7**
D	3.7±6.3	-6.7±5.2	21.9±9.3	-0.8±1.8	2.7±1.6	-1.6±1.5	-6.7±2.0*	-2.6±2.1	3.4±2.3
H	-0.7±15.3	27.7±12.6*	22.3±22.4	-0.8±3.9	-2.5±3.4	7.3±3.3	-7.0±4.4	-6.4±4.5	-2.3±5.0
χ^2	342.6**	480.7**	554.2**	3.2	3.3	0.1	4.1	4.5	9.2**
Gene effects estimated from six parameter model									
M	-100.6±40.5	-95.3±34.7**	-94.3±78.3	-	-	-	106.8±11.5**	86.6±17.2**	130.7±17.9**
D	5.1±4.8	-8.9±4.2	25.1±9.4	-	-	-	-6.8±1.4**	-3.7±2.1	4.8±2.2*
H	316.8±102.8**	291.7±87.7**	376.9±197.7	-	-	-	-37.4±28.8	57.4±42.4	-81.0±44.5
I	139.5±39.1**	111.0±33.4**	134.7±75.5	-	-	-	0.7±11.2	23.6±16.6	-28.2±17.4
J	-33.8±30.0	35.2±25.6	-60.7±57.6	-	-	-	3.6±8.3	16.9±12.1	-22.4±12.7
L	-1634.0±69.4	-148.0±59.1	-223.9±133.0	-	-	-	38.2±18.7	-41.5±27.4	52.5±28.8
H%	76	75	75	52	53	52	54	52	53
h%	94	95	93	52	47	49	29	33	31
GA	14.3	15.3	14.8	20.7	20.1	20.4	10.1	12.2	11.2

Cross1=ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1, Cross 2=ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1, Cross 3=ICGVIS07899 x Manipenta. Estimate of gene effects were significantly different from zero at 0.05(*) and 0.01(**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, χ^2 =chi square, H=broad sense heritability, h=narrow sense heritability, GA=genetic advance, (x) value assumed to be zero due to negative estimate.

Table 4.2 Continues

Character	Number of mature pods per plant			Pod yield per plant			Number of seeds per plant		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from joint scaling test									
M	14.6±5.4	150±4.4**	24.5±7.4*	7.6±4.2	14.1±3.8**	16.1±1.4**	14.6±1.4**	16.5±1.1**	17.1±1.0**
D	111.0±2.6**	6.3±2.1**	-5.8±3.6	1.9±2.2	3.03±1.90	-5.4±3.0	-0.1±0.7	0.9±0.6	-1.3±0.5**
H	5.7±6.0	8.7±5.0	-12.8±8.3	10.3±4.9*	11.0±4.3	-9.9±6.4	1.4±1.6	-1.1±1.2	-0.4±1.2
χ^2	14.9**	5.1	24.9**	18.4**	8.7*	15.6**	0.3	0.8	0.2
Gene effects estimated from six parameter model									
M	40.0±16.2	11.9±19.1	-65.6±26.2	30.2±12.1	17.7±15.5	-42.5±20.2	-	-	-
D	12.4±1.7**	7.0±3.4**	-6.2±2.9*	4.0±1.6	4.1±2.0	-5.2±2.7	-	-	-
H	-32.0±41.2	33.9±48.4	212.2±66.5**	-30.1±29.6	14.0±37.7	128.7±48.6	-	-	-
I	-26.8±15.8	1.9±18.6	90.0±25.5**	-23.5±11.7	-4.4±15.0	58.6±19.5**	-	-	-
J	-36.8±12.0**	-17.3±14.0	12.5±19.3	-28.00±8.2**	-12.9±10.4	-1.6±13.3	-	-	-
L	2.1±27.1	-29.1±31.8	-134.5±43.6*	12.2±19.3	-11.1±24.5	-79.7±31.2	-	-	-
H%	0.0(x)	65	64	62	60	51	57	55	65
h%	0.0(x)	35	33	89	87	74	75	71	85
GA	0.0(x)	12.1	11.0	15.3	16.1	15.7	17.5	17.5	17.5

Cross1=ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1, Cross 2=ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1, Cross 3=ICGVIS07899 x Manipenta. Estimate of gene effects were significantly different from zero at 0.05(*) and 0.01(**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, χ^2 =chi square, H=broad sense heritability, h=narrow sense heritability, GA=genetic advance, (x) value assumed to be zero due to negative estimate.

Table 4.2 Continues

Character	Shelling percentage (%)			Hundred seed weight (g)		
Cross	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Gene effects estimated from three parameter model						
M	72.6±2.4**	70.8±3.4**	73.9±3.4**	40.8±4.5**	56.6±5.3**	39.1±2.2**
D	2.2±1.2	0.9±2.1	-2.9±1.6	-14.3±2.0**	-6.5±2.5	-3.1±1.0**
H	-1.1±2.6	-2.8±4.8	-8.9±3.7	4.2±6.0	-1.5±7.0	-18.1±3.2**
χ^2	1.8	1.9	3.4	18.8**	24.5**	2.5
Gene effects estimated from six parameter model						
M	-	-	-	79.6±23.7**	52.3±23.6*	9.8±11.4
D	-	-	-	-14.4±1.9**	-7.2±2.0**	-3.0±0.8**
H	-	-	-	-113.7±64.2	-31.3±63.6	50.8±32.1
I	-	-	-	-35.3±23.4	5.6±23.3	29.6±11.3
J	-	-	-	3.3±19.5	11.0±19.3	-11.4±10.1
L	-	-	-	93.3±43.9	54.9±43.5	-31.2±22.5
H%	55	56	59	86	85	93
h%	51	47	53	62	68	72
GA	25.3	23.0	24.0	21.6	25.5	23.5

Cross1=ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1, Cross 2=ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1, Cross 3=ICGVIS07899 x Manipenta. Estimate of gene effects were significantly different from zero at 0.05(*) and 0.01(**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, χ^2 =chi square, H=broad sense heritability, h=narrow sense heritability, GA=genetic advance, (x) value assumed to be zero due to negative estimate.

The six-parameter model (Hayman, 1958) was fitted to establish the presence of effects of the non-allelic interaction on the expression of the studied characteristics. The six parameters were evaluated based on the mean values of the parents, F_1, F_2 and reciprocal backcrosses to recurrent parents.

The joint scaling test showed that the estimate of three parameter model was adequate to explain the gene effects controlling days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage in the three sets of groundnut crosses confirming significant additive and dominance gene effects. However, it was inadequate to confirm the gene effects controlling aphid infestation index, rosette disease incidence, rosette severity index, plant height, days to maturity, number of matured pod per plant, pod yield per plant and hundred seed weight in the three groundnut sets of crosses. Therefore, six parameter model was fitted to estimate gene effects that govern the expression of these characters.

In the six parameter model, additive x additive gene effect was significant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for rosette disease incidence and rosette severity index. It was significant in ICGX-SM0017/5/P10/P1 x ICGX-SM0020/5/P4/P1 for rosette severity index and in ICGVIS07899 x Manipenta for matured pods per plant and pod yield per plant. Additive x dominant gene effect was significant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for number of matured pods per plant and pod yield per plant.

The six parameter model was inadequate to elucidate the type of gene effects governing the expression of aphid infestation index, days to maturity and hundred seed weight in three sets of

groundnut crosses. This suggests the presence of complex genes controlling the manifestation of the characters.

4.3 Heritability and genetic advance

The estimates of heritability and genetic advance for the eleven characters in the three sets of crosses are presented in table 4.2. Estimates of heritability were categorized based on three level scale with <20% regarded as low, 20 to 40% moderate and >40% high as reported by Robinson *et al.* (1949). Similarly, an estimate of genetic advance that was less than 10% was considered low, 11 to 20% moderate and above 20% high.

High broad sense heritability estimates were recorded in the three sets of groundnut crosses studied for days to fifty percent flowering (55 to 60%), rosette disease incidence (57 to 62%), rosette severity index (75 to 76%), plant height (52 to 53%), days to maturity (52 to 54%), pod yield per plant (51 to 62%), number of seeds per plant (55 to 65%), shelling percentage (55 to 59%) and hundred seed weight (85 to 93%). It was also high in two sets of crosses for aphid infestation index (65%) and number of mature pods per plant (64 to 65%). Negative broad sense heritability estimates were recorded in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for aphid infestation index and number of matured per plant.

High estimates of narrow sense heritability were recorded for the three sets of groundnut crosses studied for days to fifty percent flowering (40 to 53%), rosette disease incidence (65 to 74%), rosette severity index (93 to 95%), plant height (47 to 52%), pod yield per plant (74 to 89%),

number of seeds per plant (71 to 85%), shelling percentage (47 to 53%) and hundred seed weight (62 to 72%). Moderate estimates were obtained for days to maturity. Narrow sense heritability was high in two sets of crosses for aphid infestation index and moderate for number of matured pods per plant. Negative narrow sense heritability which was equated to zero was recorded in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 for aphid infestation index and number of matured pods per plant.

Non allelic interaction was significant with high narrow-sense heritability for rosette disease incidence (i=62.0±18.7**, h=74% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1), rosette severity index (i=139.5±39.1**, h=94% and 111.0±33.4**, h=95% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1 and ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1), number of matured pods per plant (i=90.0±25.5** and j=-36.8±12.0** with h=33% in ICGVIS07899xManipenta) and pod yield per plant (i=58.6±19.5**, h=74% in ICGVIS07899xManipenta, j=-28.00±8.2**, h=89% in ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1).

High genetic advance (20.1 to 32.3) was obtained in the three sets of groundnut crosses for rosette disease incidence, plant height, shelling percentage, and hundred seed weight. Moderate to low (15,8 to 21.5) estimate was recorded in days to fifty percent flowering. Moderate values were obtained for rosette severity index, days to maturity, number of matured pods per plant, pod yield per plant and number of seeds per plant. Aphid infestation index recorded low genetic advance.

4.4 Genotypic and Phenotypic Correlations

The phenotypic and genotypic correlation coefficients at 5% and 1% levels of significance among the characters in the three sets of groundnut crosses are given in table 4.3, 4.4 and 4.5. The coefficients indicated that genotypic correlations were larger than the phenotypic correlations for most of the character pairs. There were differences in magnitude and signs in genotypic and phenotypic correlation coefficients.

4.4.1 Genotypic Correlations

For genotypic coefficient of correlations, negative and highly significant correlations were obtained between aphid infestation index and number of matured pods per plant, pod yield per plant and number of seeds per plant in the three sets. There was also negative and highly significant correlations between days to fifty percent flowering and number of matured pods per plant, pod yield per and shelling percentage in the three sets of crosses.

Positive and highly significant associations were obtained between rosette disease incidence and pod yield per plant and between number of matured pods per plant and number of seeds per plant in the three sets of crosses.

Table 4. 3: Genotypic and phenotypic correlations for aphid infestation index, rosette disease incidence, rosette disease severity and other quantitative characters in groundnut cross 1 (ICGX-SM00020/5/9 x ICGX- SM0017/5/P10/P1) evaluated at Samaru in 2014

Character(s)	Aphid infestation index(%)	Rosette disease incidence(%)	Rosette severity index(%)	Days to fifty % flowering	Plant height (cm)	Days to maturity	No of matured pods/ plant	Pod yield/plant (g)	No of seeds/ Plant	Shelling percentage	Hundred seed weight(g)
Aphid infestation index(%)		1.00**	-0.50*	1.00**	-0.70**	0.88**	-1.00**	-1.00**	-1.00**	-1.00**	1.00**
Rosette disease incidence(%)	-0.07		0.02	-1.00**	1.00**	-0.02	0.33	1.00**	-1.00**	-1.00**	0.04
Rosette severity index(%)	0.14	0.37		0.05	-0.63**	0.08	0.08	0.26	-0.10	-0.20	-0.33
Days to fifty percent flowering	-0.21	-0.19	0.25		0.38	0.82**	-0.90**	-1.00**	-1.00**	-0.82**	0.52*
Plant height(cm)	-0.21	0.09	-0.15	0.42		0.94**	-0.17	-0.44	-1.00**	-1.00**	0.17
Days to maturity	-0.04	-0.40	-0.03	0.18	0.35		-0.71**	-0.48*	-0.96**	-1.00**	0.86**
Number of mature pods per plant	0.10	0.47	-0.02	-0.23	0.38	-0.17		0.77**	0.65**	0.98**	-0.74**
Net pod yield(%)	0.01	0.54	0.04	-0.13	0.22	-0.11	0.72**		1.00**	0.64**	-0.15
Number of seeds per plant	0.49	0.19	0.33	-0.12	0.06	-0.20	-0.07	-0.16		0.11	-0.16
Shelling percentage	0.37	0.09	0.18	-0.09	0.39	0.15	-0.01	-0.18	0.79**		-1.00**
Hundred seed weight(g)	-0.36	-0.25	0.33	-0.24	-0.37	0.37	-0.26	-0.07	-0.48	-0.27	

The upper diagonal is genotypic correlation while the lower is phenotypic correlation. At p>or =0.05(*), r=0.468 and at p>or=0.01(**), r=0.590.

Table 4. 4: Genotypic and phenotypic correlations for aphid infestation index, rosette disease incidence, rosette disease severity and other quantitative characters in groundnut cross 2 (ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1) evaluated at Samaru in 2014

Character(s)	Aphid infestation index (%)	Rosette disease incidence (%)	Rosette severity index (%)	Days to 50% flowering	Plant height (cm)	Days to maturity	No of matured pods/plant	Pod yield/plant (g)	No of seeds/plant	Shelling percentage	Hundred seed weight(g)
Aphid infestation index(%)		0.02	-0.26	1.00**	-1.00**	1.00**	-1.00**	-1.00**	-1.00**	0.42	1.00**
Rosette disease incidence(%)	0.26		1.00**	0.87**	-1.00**	0.65**	0.20	0.56*	-1.00**	-1.00**	0.64**
Rosette severity index(g)	0.45	0.93**		1.00**	-1.00**	0.53*	0.11	0.45	-1.00**	-1.00**	0.64**
Days to fifty percent flowering	0.05	0.41	0.36		-1.00**	0.11	-0.85**	-0.54*	-1.00**	-1.00**	0.88**
Plant height(cm)	0.01	-0.08	-0.21	-0.15		-1.00**	1.00**	0.51*	1.00**	1.00**	-1.00**
Days to maturity	-0.20	0.65**	0.66**	0.58*	-0.23		0.70**	0.23	-1.00**	0.01	-1.00**
Number of matured pods per plant	0.33	-0.43	-0.24	-0.43	-0.12	-0.32		0.95**	0.52*	-1.00**	-0.85**
Net pod yield(g)	0.10	-0.29	-0.17	-0.49*	0.06	-0.11	0.79**		0.19	-1.00**	0.50**
Number of seeds per plant	0.77**	0.33	0.52*	-0.12	-0.08	-0.04	0.20	0.07		0.004	-0.54*
Shelling percentage	0.20	0.21	0.31	0.32	-0.93**	0.22	0.29	0.06	0.22		0.15
Hundred seed weight(g)	-0.32	-0.21	-0.17	0.45	-0.02	0.35	0.05	0.32	-0.49*	0.13	

The upper diagonal is genotypic correlation while the lower is phenotypic correlation. At p>or =0.05(*), r=0.468 and at p>or=0.01(**), r=0.590.

Table 4. 5: Genotypic and phenotypic correlations for aphid infestation index, rosette disease incidence, rosette disease severity and other quantitative characters in groundnut cross 3 (ICGVIS07899xManipenta) evaluated at Samaru in 2014

Character(s)	Aphid infestation index(%)	Rosette disease incidence(%)	Rosette severity index(%)	Days to 50% flowering	Plant height(cm)	Days to maturity	No of matured pods/plant	Pod yield/plant(g)	No of seeds/ plant	Shelling percentage	Hundred seed weight(g)
Aphid infestation index(%)		0.24	1.00**	-0.03	0.35	-0.18	-0.57*	-0.67**	-0.68**	-0.09	-0.41
Rosette disease incidence(%)	0.13		-0.005	0.18	-0.38	1.00**	1.00**	1.00**	-0.32	0.07	0.06
Rosette severity index(%)	0.16	0.81**		-1.00**	-0.42	-0.24	1.00**	0.01	-0.33	0.01	0.003
Days to fifty percent flowering	-0.08	-0.27	-0.45		0.27	1.00**	-0.89**	-0.90**	-0.28	-0.84**	-0.37
Plant height(cm)	-0.82**	0.16	0.20	-0.32		0.73**	-0.70**	-0.69**	0.22	-0.74**	-0.79**
Days to maturity	0.75**	0.28	0.24	-0.002	-0.58*		-0.76**	-0.42	-0.12	-0.46	-0.04
Number of matured pods per plant	-0.28	-0.26	-0.01	0.23	0.02	-0.48*		0.96**	0.51*	1.00**	0.86**
Net pod yield(%)	-0.32	-0.36	-0.18	0.30	0.05	-0.40	0.89**		0.69**	1.00**	1.00**
Number of seeds per plant	-0.84**	-0.04	0.06	-0.51*	0.81**	-0.58*	0.32	0.34		0.30	0.40
Shelling percentage	-0.63**	0.05	0.14	-0.47*	0.54*	-0.39	0.15	0.29	0.68**		0.94**
Hundred seed weight(g)	-0.64**	-0.39	-0.38	0.32	0.25	-0.14	0.13	0.33	0.48*	0.30	

The upper diagonal is genotypic correlation while the lower is phenotypic correlation. At p>or =0.05(*), r=0.468 and at p>or=0.01(**).

Positive and highly significant correlations were obtained between rosette disease incidence and days to maturity and between rosette severity index and hundred seed weight. Aphid infestation index had positive and highly significant correlation with days to fifty percent flowering, days to maturity and hundred seed weight. Days to fifty percent flowering had positive and highly significant correlations with days to maturity and hundred seed weight. Plant height had positive and highly significant correlations with days to maturity. There was positive and highly significant correlation between number of matured pods per plant and shelling percentage. Positive and highly significant correlations were obtained between pod yield per plant and number of seeds per plant, shelling percentage and hundred seed weight in two sets of crosses.

There were positive and highly significant associations between aphid infestation index and rosette disease incidence. Rosette disease incidence had positive and highly significant associations with rosette severity index, days to fifty percent flowering, plant height, number of matured pods per plant and hundred seed weight. Positive and highly significant associations were obtained between rosette severity index and days to fifty percent flowering, days to maturity, number of matured pods per plant and hundred seed weight. Similarly, positive and highly significant associations were obtained between plant height and number of matured pods per plant, pod yield per plant, number of seeds per plant, shelling percentage and hundred seed weight. Days to maturity had positive and highly significant associations with number of matured pod per plant and hundred seed weight. Number of matured pods per plant had positive and highly significant associations with hundred seed weight. Shelling percentage also had positive and highly significant associations with hundred seed weight in a single set.

In two of the three sets of crosses, negative and highly significant associations were obtained between aphid infestation index and plant height. Rosette disease incidence had negative and highly significant associations with number of seeds per plant and shelling percentage. There were negative and highly significant associations between rosette disease severity and plant height and between days to fifty percent flowering and number of seeds per plant. The same associations were obtained between plant height and shelling percentage and hundred seed weight. Days to maturity had negative and highly significant associations with number of matured pods per plant and number of seeds per plant. Negative and highly significant associations were obtained between number of matured pods per plant and hundred seed weight.

4.4.2 Phenotypic Correlations

For phenotypic coefficient of correlations, positive and highly significant associations were obtained between number of matured pods per plant and pod yield per plant in three sets of crosses. There was also positive and highly significant associations between rosette disease incidence and rosette severity index. There was positive and highly significant association between number of seeds per plant and shelling percentage in two sets of crosses.

Positive and highly significant correlations were obtained between aphid infestation index and days to maturity and shelling percentage. Rosette disease incidence was positive and significantly highly correlated with days to maturity. Rosette severity index had positive and highly significant correlations with days to maturity and number of seeds per plant. Days to fifty percent flowering were positive and highly significantly correlated with days to maturity. There

was positive and highly significant correlation between plant height and number of seeds per plant and shelling percentage and between number of seed per plant and hundred seed weight in a single set.

Negative and highly significant associations were obtained between number of seed per plant and shelling percentage in two sets of crosses. Also, negative and highly significant associations were obtained between aphid infestation index and number of seeds per plant and shelling percentage. There were negative and highly significant associations between days to fifty percent flowering and pod yield per plant, number of seeds per plant and shelling percentage. Negative and highly significant associations existed between plant height and days to maturity and shelling percentage and between days to maturity and number of matured pods per plant and number of seeds per plant. There was negative and highly significant association between number of seeds per plant and hundred seed weight.

4.5 Estimates of Number of Effective Factors

Estimates of the minimum number of genes (effective factors) controlling the eleven characters obtained using the five methods are presented in table 4.6. Estimates over all the three sets of crosses ranged from 0.05 to 2.30 for days to fifty percent flowering, from -2.47 to 2.97 for aphid infestation index, from 0.02 to 4.05 for rosette disease incidence and from 0.26 to 18.43 for rosette severity index. It ranges from 0.02 to 1.88 for plant height, from 0.62 to 16.22 for days to maturity and from -34.84 to 14.23 for number of matured pods per plant. The estimate for pod yield per plant ranged from 0.85 to 10.29, for number of seeds per plant it ranged from 0.00 to

0.49, for shelling percentage it ranged from 0.10 to 1.16 and for hundred seed weight it ranged from 0.23 to 32.77.

Mean estimates of the minimum number of genes for each set of cross ranged from 0.09 to 1.13 for days to fifty percent flowering, from -0.49 to 1.05 for aphid infestation index, from 0.83 to 2.34 for rosette disease incidence and from 4.09 to 7.51 for rosette severity index. The mean estimate for plant height ranges from 0.03 to 0.75, for days to maturity it ranged from 1.42 to 5.69, for number of matured pods per plant it ranged from -16.38 to 5.18 and for pod yield per plant it ranged from 2.38 to 4.71. It ranged from 0.05 to 0.23 for number of seeds per plant, from 0.30 to 0.58 for shelling percentage and from 0.84 to 11.49 for hundred seed weight.

Table 4. 6: Estimates of effective factors (EF) for aphid, rosette and other quantitative characters from the three sets of groundnut crosses evaluated at Samaru in 2014

S/No.	Character(s)	Cross	EF1	EF2	EF3	EF4	EF5	Mean
1	Days to fifty percent flowering	C1	2.30	2.01	0.44	0.50	0.39	1.13
		C2	0.25	0.50	0.09	0.13	0.07	0.21
		C3	0.05	0.26	0.05	0.06	0.04	0.09
2	Aphid infestation index (%)	C1	-2.47	0.00	0.00	0.00	0.00	-0.49
		C2	0.34	1.22	0.24	0.30	0.20	0.46
		C3	0.56	2.97	0.55	0.74	0.44	1.05
3	Rosette disease incidence (%)	C1	3.97	4.05	1.20	1.01	1.48	2.34
		C2	0.76	2.61	0.74	0.65	0.85	1.12
		C3	4.04	0.07	0.02	0.02	0.02	0.83
4	Rosette severity index (%)	C1	19.59	9.15	2.82	2.29	3.69	7.51
		C2	4.96	15.47	4.88	3.87	6.60	7.15
		C3	18.43	1.02	0.32	0.26	0.42	4.09
5	Plant height (cm)	C1	0.03	0.06	0.02	0.02	0.02	0.03
		C2	0.58	1.88	0.42	0.47	0.38	0.75
		C3	1.52	0.39	0.09	0.10	0.09	0.44
6	Days to maturity	C1	4.46	16.22	2.19	4.06	1.50	5.69
		C2	1.19	3.88	0.62	0.97	0.45	1.42
		C3	1.10	7.36	1.08	1.84	0.77	2.43
7	No of matured pods/plant	C1	-12.50	-20.50	-8.93	-5.12	-34.84	-16.38
		C2	3.15	14.23	1.95	3.56	1.34	4.85
		C3	7.87	12.35	1.56	3.09	1.05	5.18
8	Pod yield/plant	C1	6.59	3.76	1.37	0.94	2.50	3.03
		C2	4.19	3.38	1.23	0.85	2.26	2.38
		C3	10.29	5.82	2.12	1.46	3.87	4.71
9	Number of seeds/plant	C1	0.24	0.01	0.00	0.00	0.00	0.05
		C2	0.10	0.27	0.09	0.07	0.12	0.13
		C3	0.16	0.49	0.16	0.12	0.22	0.23
10	Shelling percentage	C1	0.30	0.88	0.20	0.22	0.19	0.36
		C2	0.60	0.55	0.12	0.14	0.10	0.30
		C3	0.96	1.16	0.26	0.29	0.23	0.58
11	Hundred seed weight (g)	C1	5.94	32.77	5.91	8.19	4.63	11.49
		C2	2.12	6.67	1.34	1.67	1.11	2.58
		C3	2.31	1.19	0.23	0.30	0.19	0.84

EF1=Effective Factors (Wright,1968), EF2=Effective Factors (Mather and Jinks 1981), EF2 to EF3=Effective factors (Lande, 1981), C1=ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, C2=ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1, C3=ICGVIS07899xManipenta.

CHAPTER FIVE

5.0 DISCUSSION

In general, significant differences in performance among the parents, F_1s, F_2s and backcrosses studied suggest that there was sufficient variability across the generations for the characters studied. The F_1 generations had mean values higher than those of their parental lines suggesting the presence of heterosis. The mean values of the segregating generations were higher or lower than those of the parental lines suggesting the presence of transgressive segregation. Heterosis may result from over dominance of gene pair, depression of the dominant increasing alleles in the parental lines or both, while transgressive segregation may result from recombination of additive alleles and epistasis.

The results of joint scaling test indicated that the three parameter model was adequate to explain variations observed in the inheritance of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage in the three sets of groundnut crosses studied. The estimates of the gene effects revealed that both the additive and dominance gene effects contributed significantly to the inheritance of the characters studied. This finding is explicit from the chi-square analysis which showed insignificance in the three sets tested. However, the three parameter model was inadequate to explain the inheritance of rosette disease incidence, rosette severity index, pod yield per plant, rosette severity index and pod yield per plant and days to maturity in the three sets of groundnut crosses studied. To improve these characters, selection in the early generations will be desirable. Six parameter model was used to establish the presence of the effects of the non-allelic interaction on the expression of the studied characteristics. Non

allelic gene interactions were significant for number of matured pods per plant, pod yield per plant, rosette severity index and rosette disease incidence. Selection in the early generations will be ineffective and so must be delayed till later generations. Crosses where non allelic interaction was not significant to explain all variation in generation means along with low heritability imply more complex nature of inheritance and/or influence of the environment on the expression of these characters.

Heritability estimate gives information on transmissibility of the quantitative characters and are important for effective breeding strategy. The magnitude of the heritability is used to predict the behaviour of succeeding generations through the use of appropriate selection criteria to access the level of genetic improvement. Genetic advance on the other hand provides explicit information and precise view of segregating generations for selection. High heritability along with high genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics. Negative heritability estimates were equated to zero (Robinson *et al*.1955), as reported by (Dudley and Moll, 1969). Based on the variance estimates of the parent-offspring regression model, the error mean squares (expressed as error variance, σ^2) resulted in negative estimates for rosette disease incidence, rosette severity index, mature pods per plant and pod yield per plant.

The high broad sense heritability estimates obtained for the characters studied in the three sets of groundnut crosses except for aphid infestation index and number of matured pod per plant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 indicate that the genotypic variances were higher than the phenotypic variances. The genetic variation was large due to major genes

controlling the characters which can easily be inherited thus selection would be effective in the desired direction for each of the characters in the groundnut sets of crosses tested (Aba, 1998).

The moderate to high narrow sense heritability that was exhibited in the characters studied except for aphid infestation index and number of matured pods per plant in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 indicate the preponderance of additive gene effect in the three sets of groundnut crosses studied. The variation shown in the narrow sense heritability estimates may also be due to the fact that only one environment was used thus the genotype x environment estimates was not obtained. This had been reported to cause bias in the estimate of narrow sense heritability (Obilana and Fakorede, 1981). However, the high narrow sense heritability values indicated that the characters studied were highly transmissible and selection can be done to improve these characters.

Similarly, the characters studied showed moderate to high genetic advance except for aphid infestation index. According to Johnson *et al*. (1955), characters with high heritability accompanied with high genetic advance also result in better genetic gain through selection.

Wide ranges obtained for number of effective factors could be as a result of the failure to meet some of the under lying assumptions of the five methods. The presence of dominant genes as can be deduced from the adequacy of the three parameter model in the joint scaling test for days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage rendered the estimates of the number of effective factors less reliable. The presence of epistasis as can be deduced from the six parameter model for rosette disease incidence, rosette severity index,

number of matured pods per plant and pod yield per plant rendered the estimates of number of effective factors less reliable. Secondly, genes may be inherited in blocks of DNA segregates and may be estimated as though they are inherited as single strands of DNA. However, based on the present study mean estimates of number of effective factors showed that approximately one gene controls the expression of days to fifty percent flowering and plant height in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1, aphid infestation index and shelling percentage in ICGVIS07899 x Manipenta. An approximate of two genes controls the expression of rosette disease incidence in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1. These suggest that few genes are responsible for the manifestation of these characters hence, the evidence of monogenic and oligogenic inheritance. This result is in concordance with Van der Merwe (2001) who showed that resistance to aphid vectors is controlled by a single recessive gene while resistance to groundnut rosette virus is controlled by two recessive genes De Berchoux (1960). The expression of number of matured pods per plant and pod yield per plant in ICGVIS07899 x Manipenta are controlled by about five genes. Days to maturity, rosette severity index and hundred seed weight in ICGX-SM00020/5/9 x ICGX-SM0017/5/P10/P1 are controlled by about six, eight and eleven genes respectively. These suggest that many genes are responsible for the manifestation of these characters hence, the evidence of polygenic inheritance.

The genotypic correlation coefficients exceeded those of the corresponding phenotypic correlation coefficients for most of the character combinations in the three sets of crosses studied. These phenomena can be seen in correlations between aphid infestation index and number of matured pods per plant and net pod weight. Correlations between rosette disease incidence and plant height, pod yield per plant and number of seeds per plant and between

rosette disease severity and plant height indicating the correlations are genetic rather than environmental (Weber and Morthy, 1952). Similar result was obtained by Abdelmula *et al.* (1993) in faba bean, Brindha *et al.* (1997), Gasim and khidir (1998), Ibrahim (2001) in roselle and Ibrahim *et al.* (2013) in guar.

CHAPTER SIX

6.0 SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 Summary

Significant differences in mean performance were obtained in the three sets of crosses for the characters studied in the parents, F_1s, F_2s and backcrosses.

The joint scaling test revealed that three parameter model was adequate to explain the gene effects that govern the expression of days to fifty percent flowering, plant height, number of seeds per plant and shelling percentage with non allelic interactions manifested for number of matured pods per plant, pod yield per plant, shelling percentage, rosette severity index and rosette disease incidence when the six parameter model was fitted.

Dominance genes and epistasis bais the number of effective factors for days to fifty percent flowering, plant height, number of seeds per plant, shelling percentage, rosette disease incidence, rosette severity index, matured pods per plant and pod yield per plant hence, rendering the estimates less reliable.

High broad and narrow sense heritability was exhibited in the characters studied except for aphid infestation index, days to maturity and matured pods per plant in the three sets of groundnut

crosses studied. Moderate to high genetic advance estimates were also recorded in the three sets of groundnut crosses except for aphid infestation index.

Genotypic coefficients of correlation exceeded the corresponding phenotypic coefficients of correlations implying the correlations are genetic rather than environmental.

6.2 Conclusions

In conclusion, in the set of crosses where non allelic interaction was significant with high narrow-sense heritability as obtained for rosette disease incidence, rosette severity index, number of matured pods per plant and pod yield per plant, it is possible to expect advance for these characters in further segregating generations. Crosses where non allelic interaction was not significant to explain all variation in generation means along with low heritability imply more complex nature of inheritance and/or influence of the environment on the expression of these characters. Broad sense and narrow sense heritability as well as genetic advance were moderate to high for most of the characters studied for the three sets of groundnut crosses. Genotypic coefficients of correlation were higher than phenotypic coefficients of correlation.

6.3 Recommendations

This study revealed that the parents used had no complete resistance to aphid and rosette resistance. I recommend that the level of resistance can be improved further by pyramiding resistance genes from different and diverse sources. Efficient and more reliable screening

techniques should be readily available for revalidation of resistance in the genotypes. Genotypes reported to be resistant to aphid and rosette virus should be extensively screened across diverse growing environments to identify stable sources of resistance. The use of biotechnology to understand the mechanisms governing the resistance pathways should be harnessed and the information should be used in breeding programs for the control of aphids and rosette disease. It is necessary to study resistance of the sets of crosses using molecular marker to obtain more stable and reliable sources of resistance.

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Appendices

Appendix 1

Mean squares of set of groundnut crosses for characters studied at Samaru during 2014 growing season

Cross	SOV	FFL	ADI(%)	RDI(%)	RSI(%)	PLHT(cm)	DMAT	MPP	NPY(g)	SPP	SHP	HSWT(g)
C1	Mean square	47.3**	24.08	622.53**	1332.29**	38.42	131.58**	183.50**	87.58**	4.22	30.39**	15.45**
	Error	1.98	26.15	32.70	156.97	21.98	8.96	21.13	16.02	2.76	8.83	23.33
C2	Mean square	14.41	3.71	450.86**	1338.48**	27.56	158.98**	105.16**	64.31	3.57	38.54	279.93**
	Error	3.86	3.53	27.47	105.89	19.81	27.48	27.44	20.53	1.69	35.61	56.92
C3	Mean square	18.17**	991.45**	876.47	2088.32**	39.09**	65.95	206.26**	129.29**	2.64	62.92**	208.70**
	Error	1.65	270.95	263.94	393.89	10.45	30.66	53.24	32.91	1.59	14.20	14.94

At $p \leq 0.05$(*)=significant and at $p \leq 0.01$(**)=highly significant. SOV=Sources of Variation, C1=ICGX-SM00020/5/9xICGX-SM0017/5/P10/P1, C2=ICGX-SM0017/5/P10/P1xICGX-SM0020/5/P4/P1, C3=ICGVIS07899xManipenta, FFL=Days to fifty percent flowering, ADI=Aphid Infestation Index, RDI=Rosette Disease Incidence, RSI=Rosette Severity Index, PLHT=Plant height, DMAT=Days to maturity, MPP=Number of mature pods per plant, NPY=Net pod yield, SPP=Number of seeds per plant, Shelling%=Shelling percentage, HSWT=Hundred seed weight.