INHERITANCE OF RESISTANCE TO APHID (*Aphis craccivora* Koch) IN GROUNDNUT (*Arachis hypogeae* L.)

By

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Declaration

I declare that the work in the thesis entitled '**INHERITANCE OF RESISTANCE TO APHID *(Aphis craccivora* Koch) IN GROUNDNUT (*Arachis hypogeae* L.)'** has been carried out by me in the Department of Plant Science under the supervision of Prof. C.A. Echekwu, Dr. M. Yusuf and Prof. J.D. Olarewaju. The information derived from literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or diploma at any other institution to the best of my knowledge.

Yusuf Rini Bashir _____ _____

Signature Date

Certification

The thesis entitled '**INHERITANCE OF RESISTANCE TO APHID *(Aphis craccivora Koch*) IN GROUNDNUT (*Arachis hypogeae* L.)'** by **Yusuf Rini Bashir** meets the regulation governing the award of the Degree of Master of Science (M.Sc.) of the Ahmadu Bello University, Zaria and is approved for its contribution to scientific knowledge and literary presentation.

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Dedication

This research is dedicated to my family, parents, brothers and sisters and to humanity.

Acknowledgement

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Abstract

Nine Groundnut genotypes, consisting of three male testers (ICGV-SM 00020/5/9, 1CGX-SM 00017/5/P10/P1, ICGX-SM 00020/5/P4/P1) and six female lines (ICGV IS 07890, 1CGV IS 07899, ICIAR-19BT IS 07899, SAMNUT 14, KWANKWASO, and MANIPENTA) were crossed in a line x tester mating design to develop 18 hybrids. The resultant hybrids and parents were evaluated in the screen house using a complete randomize design at Samaru (Northern Guinea savanna 11^0 11', 7^0 38' E, 686m above sea level) in 2012 to obtain information on genetic variation, combining ability, heritability and correlation for resistance aphid and several quantitative traits. The variances due to SCA and GCA showed that both additive and non-additive, possibly dominant gene actions are important. Highly significant differences were observed among all entries for aphid damage index (D.I) and days to maturity. Significant differences were recorded among hybrids for seed weight(g), number of pods, days to maturity and aphid damage index. Significant effects among female parents were observed in their GCA for pod yield, 100-seed weight, and number of pods per plant and among male parents for 100-seed weight and days to maturity. Specific combining ability (SCA) for ICGX – SM 00020/5/P4/P1 x ICGV IS 07890, ICGX – SM 00017/5/P10/P1 x KWANKWASO and ICGX – SM 00017/5/P10/P1 x SAMNUT 14 revealed maximum positive result for pod weight. Lower negative SCA was observed among most of the hybrids for the characters studied. It was observed that genotypic correlation coefficients were higher than phenotypic correlation, genetic advance as a percentage of mean was generally low for all the characters studied (0.22 -10.68) indicating less progress in selection. Narrow sense heritability ($h^{2)}$ was generally low as low as (1.80%) for days to maturity and seed weight and as high as (6.3 %) for pod yield indicating non- additive gene action.

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CHAPTER ONE

1.0 INTRODUCTION

1.1 Preamble

Groundnut (*Arachis hypogeae* L.) is an annual leguminous crop. It is a self-pollinated, allotetraploid (2n=4x=40), with a genome size of 2891 Mbp. The genus *Arachis* belongs to the family fabaceae and sub-family papilanoceae (Nigam and Bock, 1990). It has three sub-species Namely*; hypogeae var.hypogeael* (Virginia), *fastigiata var.fastigia* (Valencia), *fastigiata var.vulgaris* (Spanish). (Krapovickas and Gregory, 1994).

Groundnut is grown on nearly 23.95 million ha worldwide with the total production of 36.45 million tons and an average yield of 1520 kg/ha in 2009 (FAOSTAT, 2011). China, India, Nigeria, and USA are the major groundnut growing countries. Developing countries in Asia, Africa and South America account for over 97% of world groundnut area and 95% of total production. Production is concentrated in Asia (50% of global area and 64% of global production) and Africa (46% of global area and 28% of global production), where the crop is grown mostly by smallholder farmers under rain-fed conditions with limited inputs. Nigeria currently produces about two million MT representing 5% of world production. Groundnut constitutes a major source of foreign exchange as an export commodity as well as generating local income to Farmers. Groundnut is rich in protein (25-34%) and oils (44-56%); it is used in the manufacture of cooking oil as well as making a paste for the preparation of groundnut sauce in many African communities. It is also eaten boiled, fried or roasted, and its by-products can be used as animal feed. As a legume, groundnut improves soil fertility by fixing nitrogen and thereby increases productivity of

other crops in the semi-arid cereal cropping systems. Groundnut requires little in-put, making it appropriate for cultivation in low in put agriculture by smallholding farmers.

1.2 Research Problem

Aphis craccivora Koch is a major pest of groundnut (*Arachis hypogeae* L.) causing losses by feeding on phloem sap and through transmission of virus disease (Padgham *et al*., 1990, Feakin 1973). It is a vector of at least seven viruses that attack groundnut, the most important of which is groundnut rosette virus (GRV) in Africa. Rosette is the most destructive virus disease of groundnut in Africa. In 1975 rosette affected about 0.7 million ha of groundnut in Nigeria and caused yield losses estimated at over 0.5 million tonnes, with a value estimated at US$250 million (Yayock *et al*., 1976). Rosette disease is caused by a complex of groundnut rosette virus (GRV), together with an associated satellite RNA, and a helper virus, Groundnut Rosette Assistor Virus (GRAV; family Luteoviridae) , on which the other two components depend for transmission by the Aphid *Aphis craccivora.*

1.3 Justification

Aphids are the most prevalent insect vectors of virus disease with over 200 species known to transmit plant pathogenic viruses. They are responsible for the transmission of 50% of the insect vectored viruses (Ng and Perry, 2004). It is clear that the intense selection pressure placed on aphids through insecticide use is enough to result in the continued development of resistance. Hence, it is vital that alternative methods of control are developed for contingency before there is a significant build-up of neonicotinoid resistance in natural aphid populations. To achieve this, a greater understanding of natural plant resistance mechanisms is required with the goal of implementing this knowledge in protecting crop species from aphids and subsequent virus infection. Host-plant resistance to

Aphis craccivora in groundnut is recognised as the most effective, economic and sustainable method of limiting both the spread of the aphid and the viruses (Padgham *et al*.,1990). Screening germplasm for aphid resistance led to the discovery of resistant accession in several crop species against various aphid species. However, sources of aphid resistance are limited and usually scarce. More often, aphid resistance have been identified in unimproved landraces, in wild accessions or even in related species, thus requiring a long breeding process to introduce the resistance into cultivated varieties.

As a result of increased demands on food production from escalating population growth and environmental degradation, interest in improved breeding strategies for agricultural crops is growing. The main aim of any plant breeding programme is to develop special high yielding hybrids that are resistance to insect, pest and diseases. To accomplish this, the breeding programme can efficiently be planned with prior knowledge of the genetic makeup of complex quantitative characters like yield and its attributes. It is therefore, necessary to examine the genetic architecture of various quantitative characters in relation to breeding behavior of the genetic material available.

The knowledge of combining ability provides a useful clue for selection of desirable parents for the development of superior hybrids that are resistant to insect, pest and diseases. Thus, the information regarding combining ability and nature of gene action are the basis requirements for a thorough understanding of genetic architecture of aphid resistance, yield, and its components. The present study therefore, was undertaken to study the genetics of eight quantitative traits in six lines (females) and three testers (males) using line × tester analysis with the following objectives.

1.4 Objectives

The objectives of this research are as follows;

1. To determine the relative importance of general and specific combining abilities for resistance to *Aphis craccivora* using line x tester analysis.
2. To estimate genetic variability and heritability of some selected agronomic traits.
3. To assess the phenotypic and genotypic correlations among the traits for further selection.

CHAPTER TWO

LITERATURE REVIEW

2.1 Groundnut

Groundnut (*Arachis hypogeal L.)* is an annual important oil and forage crop cultivated in the semi- arid tropical and sub-tropical regions of 100 countries on six continents between 40^0 N and 40^0 S latitude of the equator. The genus *Arachis* belongs to the family Fabaceae and sub family papilonaceae (Nigam and Bock, 1990). Groundnut has three subspecies and they are: *hypogeae* var. *hypogea* (Virginia), *fastigiata* var. *fastigiata* (Valencia) and *fastigiata* var. *vulgaris* (Spanish).

2.2 Distribution of Groundnut

The genus *Arachis* probably originated in the Matto Grosso of Brazil. The wild species are limited in their distribution to an area bordered by the Amazon, the Andes and North Bank of La Plata River. Groundnut has spread throughout the tropics and sub-tropics from two secondary centers of diversification; West Africa and part of South East Asia (the Philippines, Indonesia and Malaysia). Groundnut was first introduced into Africa especially countries in West and East Africa by early traders and travellers. Groundnut was introduced into Nigeria in the 16^{th} Century and it is extensively grown in West Africa (Gibbons *et al*., 2002).

2.3 Production of Groundnut

Between 2000 and 2009, the annual global production increased marginally by 0.4%, the area by 0.3% and yield by 0.1% During the same period in Asia, groundnut area declined by 1.36 million ha, an annual decline of 1.1%. However, the annual decline in production

was only 0.1% due mainly to a 0.9% annual increase in productivity (1970 kg/ha in 2009) In Africa both groundnut area and production grew during the 2000-2009 period. The groundnut area grew by 2.17 million ha, an annual increase of 1.9%. The annual increase in production was 1.5%, crossing the 10 million ton level in the year 2009. However, grain yields declined by 0.4% annually and remained below 1000 kg/ha during the entire decade with the exception of 2006. In Nigeria and Ghana, groundnut yields were above 1000 kg/ha in 2009. Groundnut production in West and Central Africa averaged 7.3 million tons (78% of African production) from 72% of groundnut area in Africa. Nigeria and Senegal are the largest producers in West and Central Africa accounting together for about 45% of total African production (FAOSTAT, 2011).

2.4 Botany of Groundnut

Groundnut is an erect, semi-erect or trailing annual legume 30-70cm tall. Groundnut has 70 species in nature of which *Arachis hypogeae* L. is commonly cultivated. It is a frost tender plant. It has tap root; sometimes the root may be adventitious. The leaves are alternate, stipulate and quadrifoliate. The structure of the flower is unusual, sepals, petals and stamens are fused at their bases to form a tube or cup or cup-like structure. It produces two kinds of flowers; male (staminate) flowers which are bright yellow and quite pretty and female flowers (pistillate) which are inconspicuous. After the female flowers are fertilized, they turn face down and corkscrew themselves into the ground. Each corkscrew or peg grows 1-4 peanuts, 5-13cm underground. The peanut consists of 2-5 seeds, which are encased in a papery shell (Feakin, 1973)

2.5 Agronomy of Groundnut

Groundnut is grown throughout the world, but it predominates in seasonally arid areas. Groundnuts prefer light humus-rich well-drained soils in a warm sunny sheltered position, though it will tolerate heavier soils. The sequence of cultural operations involved in producing groundnut is the same with other crops. These practices include land preparation, sowing, weed control, harvesting and storage. Fertile loamy soils encourages pegging of groundnut. Ridging on heavy soils is useful for groundnut cultivation (Huxley, 1992; Duke 1983).

2.6 Uses of Groundnut

Groundnut (*Arachis hypogeae L.)* is an important food legume containing digestible protein (25-34%), oil (44-56%), amino acids and vitamins. In West and Central Africa (WCA), It is an important food and cash crop: it can be eaten boiled, fried and row. Also a major source of dietary oil and cash income for both urban and subsistence farmers and also use as fodder, it is a principal crop for exportation and important source of activities for agriculture (Housou, 1999). The seeds are commonly processed and used as peanut butter in sandwich e.t.c (Duke, 1983). They can also be cooked in a variety of dishes, and are also ground into powder where they can be used with cereal to greatly improve the protein content of bread, cakes, e.t.c. it is also a good source of minerals and vitamins especially B Complex(Huxley, 1992).

2.7 Viral Diseases of Groundnut

Several virus diseases occur on groundnuts that are considered as important constraints to production. These include mottle, caused by peanut mottle virus (PeMoV) genus *Polyvirus,* stripe caused by peanut stripe virus, stunt caused by peanut stunt virus (PSV) genus *Cucumovirus*. Tomato spotted wilt caused by tomato spotted wilt virus (TSWAV) genus *Tospovirus*, groundnut steak necrosis caused by sunflower yellow blotch virus (SuYBU) genus *Umbra* virus, cowpea mild mottle caused by peanut clump virus (PCV) genus *Furovirus* and groundnut rosette caused by complex of two viruses, groundnut rosette virus (GRV) genus *Umbra virus* and groundnut rosette assistor virus (GRAV) genus *Luteovirus* and a satellite RNA. The most important disease of the stem and twig of groundnut especially in Africa is the groundnut rosette disease caused by groundnut rosette virus (GRV) (Frohlich *et al*., 1970).

2.8 Aphid/Rosette

Aphids, also known as *plant lice* and in Britain and the Common wealth as greenflies, blackflies or whiteflies, (not to be confused with "jumping plant lice" or true whiteflies) are small sap-sucking insects, and members of the superfamily Aphidoidea. Aphids are among the most destructive insect pests on cultivated plants in temperate regions. The damage they do to plants has made them enemies of farmers and gardeners the world over, but from a zoological standpoint they are a very successful group of organisms. Their success is in part due to the asexual reproduction capability of some species. Compared to other insects, aphids cause relatively little mechanical damage to their host plant due to their specialized mode of feeding. They use stylets to target the vascular tissue of their host and probe plant tissue intercellularly, thus preventing extensive tissue damage. The impact of this

‘‘piercing-sucking’’ mode of feeding on their plant host is therefore mainly through the transmission of one of the approximately 300 viruses which are aphid transmissible, although the direct effects of assimilate withdrawal from the vasculature cannot be discounted completely. *Aphis craccivora* Koch is a major pest of groundnut (*Arachis hypogaea L.*) causing yield losses by feeding on phloem sap and through transmission of virus diseases (Padgham *et al*., 1990, Feakin 1973). It is a vector of at least seven viruses that attack groundnuts, the most important of which are groundnut rosette virus (GRV) in Africa and peanut stripe virus in Asia. Groundnut rosette virus disease has been given more attention in the laboratory and field studies than other groundnut viruses in Africa because of its most destructive nature. It was first observed and reported by Zimmerman in 1907. Groundnut rosette disease is the most destructive economically important virus disease of groundnut (Naidu *et al.,* 1999). Diseases symptoms were first reported by Hayes (1932) as chlorotic and green. Most prevalent in West Africa is green rosette but some areas show high incidence of chlorotic rosette. The virus are transmitted by *Aphis craccivora* Koch (Storey and Bottomley 1925; 1928) and have alternate host such as *Nicotiana* and *Chenopodium spp*, *Glycine max. Trifolium incarnatum* L.*(* Okusanya and Watson 1966; Reddy *et al.,* 1985).

2.9 Mechanism of Host Plant Resistance

2.9.1 Physical defences

Many plant species have a first line of nonspecific defence to aphid infestation that enables the plant to resist colonization to varying degrees. At the leaf surface, trichomes play an important role in basal defence and may confer both anti-xenotic and anti-biotic properties to the plant. Non glandular trichomes provide a barrier to aphid infestation in many plant

species. It was first reported by Johnson (1953) that the hooked nonglandular trichomes of the French bean *(Phaseolus vulgaris*) had a detrimental effect on populations of the cowpea aphid (*Aphis craccivora)*; Johnson, 1953). High densities of nonglandular trichomes in wheat and crosses of tomato with wild potato have also been demonstrated to deter feeding by the yellow sugarcane aphid (*Siphus flava*) and *Myzus persicae*, respectively (Simmons *et al*., 2005; Webster *et al*., 1994). However, not all plants with high trichome densities deter aphid colonization, as glabrous varieties of cotton are more resistant to colonization by *Aphis gossypii* than their pubescent counterparts (Weathersbee and Hardee, 1994; Weathers bee *et al*., 1994, 1995).Glandular trichomes are also an important basal defence system against aphid infestation. Poly phenolic fluids either contained in the tips of the hairs or encased in a spherical head have significant antibiotic effects against aphid infestation (Van Emden, 2007).

2.9.2 Chemical defence

Many recent studies have examined host plant transcriptomes before and after aphid feeding and identified defence responses common to both compatible and incompatible interactions (Delp *et al*., 2009; Gao *et al*., 2007; Moran and Thompson, 2001; Thompson and Goggin, 2006). Basal defences that are induced by aphid feeding include cell wall modification and up regulation of anti-insect compounds such as proteinase inhibitors, secondary metabolites, and volatiles. Transcriptomes changes induced by aphid feeding are often mediated by one or several of well-characterized plant hormones including jasmonate (JA), salicylic acid (SA), and ethylene. There is significant cross-talk, both synergistic and antagonistic between these defence pathways, which allows the plant to optimize its defence strategy to particular threats (Koornneef and Pieterse, 2008). However, the intricate

interplay between plant defence responses provides the opportunity for insects to manipulate the pathways in order to enhance their own success and there is a growing evidence to show that this is the case (Walling, 2008).

2.9.3 Resistance gene-mediated aphid resistance

Plant-encoded resistance (R) genes are involved in gene-for-gene resistance and recognize (directly or indirectly) avirulence (Avr) gene products in attacking parasites (Flor, 1971).Traditionally, this type of resistance has been associated with defence against plant pathogens; however, it is now widely accepted that R genes play a role in the recognition and defence against insect pests, including aphids. Gene-for-gene resistance was first identified in the flax/flax rust fungus system (Flor, 1955) but it has since been shown to be a highly conserved mechanism in conferring resistance to many pathogenic organisms. The majority of R genes encode R-proteins that are highly conserved across species, and share major structural similarity. They are characterized by the presence of both nucleotide binding (NB) and leucine-rich repeat (LRR) motifs (Dangl and Jones, 2001; Jones and Dangl, 2006; Takken et al., 2006). R genes form part of molecular surveillance system allowing plants to specifically recognize pathogens that are able to overcome the basal resistance mechanisms (Jones and Dangl, 2006). R genes associated with aphid resistance have been identified and mapped in several species including lettuce, soybean, and Medicago (Klingler et al., 2007; Li *et al*., 2007; Wroblewski *et al*., 2007). However, as yet the only aphid R genes to be cloned and characterized are two from tomato and melon (DeIlarduya *et al*., 2003;Villada *et al*., 2009). The NB-LRR Mi-1 (resistance to *Meloidogyne incognita*) gene, cloned from tomato confers resistance to a number of insects including the phloem-feeding potato aphid (*Macrosiphum euphorbiae)*, tomato psyllids

(*Bactericera cockerelli*), two biotypes of whitefly (*Bemisia tabaci*) and root-knot nematodes (M. incognita; Casteel *et al*., 2006; Milligan *et al*., 1998; Nombela *et al*., 2003; Rossi *et al*.,1998).

2.9.4 Volatile-mediated plant defence

Through modification and induction of plant defensive signalling pathways as outlined above, aphid feeding often results in the release and synthesis of volatile compounds by the host plant (Arimura *et al*., 2005). Compounds emitted include methylsalicylate, ethylene, C6 volatiles, cis-jasmone, MeJA, terpenoids and of particular interest, (E)-b-farnesene (EBF). Such volatiles may either act directly or indirectly defence against aphids. Acting directly; plant volatiles may work as insect repellents, decrease fecundity, deter feeding, or provide information to colonizing aphids about the population density on a particular host. EBF is a common aphid alarm pheromone which is released by aphids under stress and causes other aphids in close proximity to cease feeding and find a new host (Beale *et al*., 2006; De Vos *et al*., 2007; Unsicker *et al*., 2009).

2.10 Combining Ability and Gene Action

Sprague and Tatum (1942) formulated the concepts of combining abilities. General combining ability is the average performance of a strain in series of cross combinations, estimated from the performance of F_{1s} from the crosses, whereas specific combining ability is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of average performance of lines involved. Fisher (1918) partitioned the total genetic variance ($\sigma^2 a$) into (i) additive genetic variance ($\sigma^2 A$), which is the sum of additive genetic variances contributed by individual loci (ii) Dominance variance ($\sigma^2 D$) component which results from intra allelic interaction of genes

at segregating loci (iii) epistatic variance ($\sigma^2 I$) results from inter allelic interaction of genes at segregating loci.

2.10.1 Line x tester mating design

The most common designs used by geneticist to study the genetic parameters and their interpretations are line x tester, diallel, triallel, and quadriallel. These designs give estimates of gene effects and general and specific combining ability effects for the parents and crosses involving the parents. The general combining ability (GCA) effect is attributed to additive gene effect and additive x additive gene interactions that are fixable and could be easily exploited through selection. On the other hand, a specific combining ability (SCA) effect is due to dominance and epistasis (additive x dominance and dominance x dominance) that is not fixable.

The implication of gene effects in plant breeding has been dealt with as follows; when the additive gene effect for a trait is high, the character under consideration could be improved using simple selection procedures. Therefore, plants with desirable traits could be selected even in the early generations. Thus procedures like pure line selection, pedigree selection, and their modification are useful. When dominance or over dominance gene effects are predominant, the best way is to utilize F_{1S} as commercial hybrids. This option is not available to groundnut breeders, because it is a cleistogamous crop. However, recurrent selection procedures could be used to bring the desirable additive genes into broad based populations. When epistasis is involved, all selections should be deferred until the F_5 generation. However, on the basis of early generation testing one can discard the low-yielding and undesirable crosses for economic traits (poor seed quality) or those susceptible to biotic and abiotic factors. Therefore, use of bulk population selection and/or its

modifications like bulk-pedigree and single seed descent selection procedures are recommended. However, additive x additive epistasis, being an interaction of fixable gene effects, could be fixed and thus provide an opportunity to select desirable plants.Hayman (1958) partitioned epistatic variance into additive × additive ($\sigma^2 AA$), additive × dominance ($\sigma^2 AD$) and dominance × dominance ($\sigma^2 DD$) components for two loci, three loci in ($\sigma^2 AAA$, $\sigma^2 DDD$, $\sigma^2 ADD$ etc.) or more.

2.10.2 Heritability

Lush (1940) defined heritability in both broad sense and narrow sense. In broad sense, heritability refers to the functioning of the whole genotype as a unit and is used in contrast with the environmental effects. In the narrow sense, heritability largely includes only the average effect of genes transmitted additively from parent to off spring. Warner (1952) has suggested different technique for estimating the degree of heritability in crop plant which is based on parent offspring regression variance component from an analysis of variance and approximation of non-heritable variance from genetically uniform population to estimate the total genetic variance.

2.10.3 Correlation

This is a measure of the strength and direction of the linear relationship between two variables that is defined as the (sample) covariance of the variables divided by the product of their (sample) standard deviations. Comstock (1955) reported that phenotype associated with a given genotype varies with the environment. This leads to complete inconsistency of genotypic value, a different value of a given genotype relative to every variance of environment major or minor.. Long quist (1964) reported that phenotype of a quantitative character was mainly due to the joint action of genotype and environment.

2.10.4 Genetics of aphid resistance

The aphid vector *A. craccivora* (Homoptera, Aphididae;) is the principal aphid vector of groundnut rosette disease agents. *A. craccivora* is widely distributed in many countries around the world In the tropics, only females have been recorded, and these reproduce parthenogenetically throughout the year. The adults have a black, shiny body with a prominent tail-end and are either winged (alatae) or wingless (apterae). The development of these different morphs is due to a combination of factors: tactile stimulation, host plant quality, and climatic conditions. Alatae produce only about half the progeny produced by apterae. The nymphs undergo four nymphal stages before developing into adults; under favourable conditions the development of one generation takes 6 to 8 days (an average of 5.5 days). An adult can produce larvae for 6 to 7 days at the rate of 2 to 3 per day or a total fertility of 13 to 14 descendants. Thus, with each generation, the degree of infestation on affected plants may increase five- to eight fold. This rate of reproduction is largely dependent on climatic factors, especially temperature, and the nutritional status of the plant host.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Description of Genetic Materials

The plant materials for this study comprised three (3) Aphid resistant male parents (testers), six (6) aphid susceptible female parents (lines) and 3 checks. These are indicated in the table below.

Table 3.1 Description of the groundnut genotypes used in this study

No.	Plant materials	Origin	Description
	Resistant lines		
1.	ICGX-SM 00020/5/9	ICRISAT	Aphid resistant
2.	ICGX-SM 00017/5/P10/P1	ICRISAT	Aphid resistant
3.	ICGX-SM 00020/5/P4/P1	ICRISAT	Aphid resistant
	Susceptible lines		
1.	ICGV IS 07890	ICRISAT	Aphid Susceptible
2.	ICGV IS 07899	ICRISAT	Aphid Susceptible
3.	ICIAR 19BT IS 07899	ICRISAT	Aphid Susceptible
	Aphid Tolerant lines		
4.	SAMNUT 14	I.A.R	Aphid Tolerant
5.	KWANKWASO	LOCAL VARIETY	Aphid Tolerant
6.	MANIPENTA	LOCAL VARIETY	Aphid Tolerant
	Checks		
1.	SAMNUT 22	IAR	Aphid Tolerant
2.	SAMNUT 23	IAR	Aphid Tolerant
3.	SAMNUT 24	IAR	Aphid Tolerant

3.2 Population Development and Evaluation

Eighteen F_1 hybrids were developed by hand pollination in a line x tester mating scheme at IAR groundnut screen house in Samaru, Zaria, Nigeria in the year 2010. The progenies and their parents were evaluated in 2012 at the IAR groundnut screen-house to study their performance and reaction to *Aphis craccivora* infestation.

3.3 Experimental Design and Procedures

The 18 F_1 seeds along with their parents were laid in a completely randomized design (CRD) with two repetitions in screen house. Each genotype was assigned two soil filled plastic pots of 25cm in diameter with three seeds per pot. The pots were watered once daily and hand weeding was carried out four and eight after planting.

3.4 Source of Pest

Aphis cracccivora were isolated from an infected groundnut plant variety and were cultured on a susceptible groundnut variety (ICGV IS 07890).

3.4.1 Infestation Method

Thirty days after sowing, five aphids from a culture maintained on a susceptible groundnut variety (ICGV IS 07890) were introduced onto the tender leaf of each seedling using a paint brush. After confirming that each aphid was moving about on the area of placement, each pot was covered with a crisp bag and secured in place. Aphids were left to move freely along plants and feed. Aphid resistance was visually rated for each plant 3 and 4 weeks after infestation using a scale of 0–4 developed by Mensah *et al*. (2008). Care was taken to avoid disturbance.

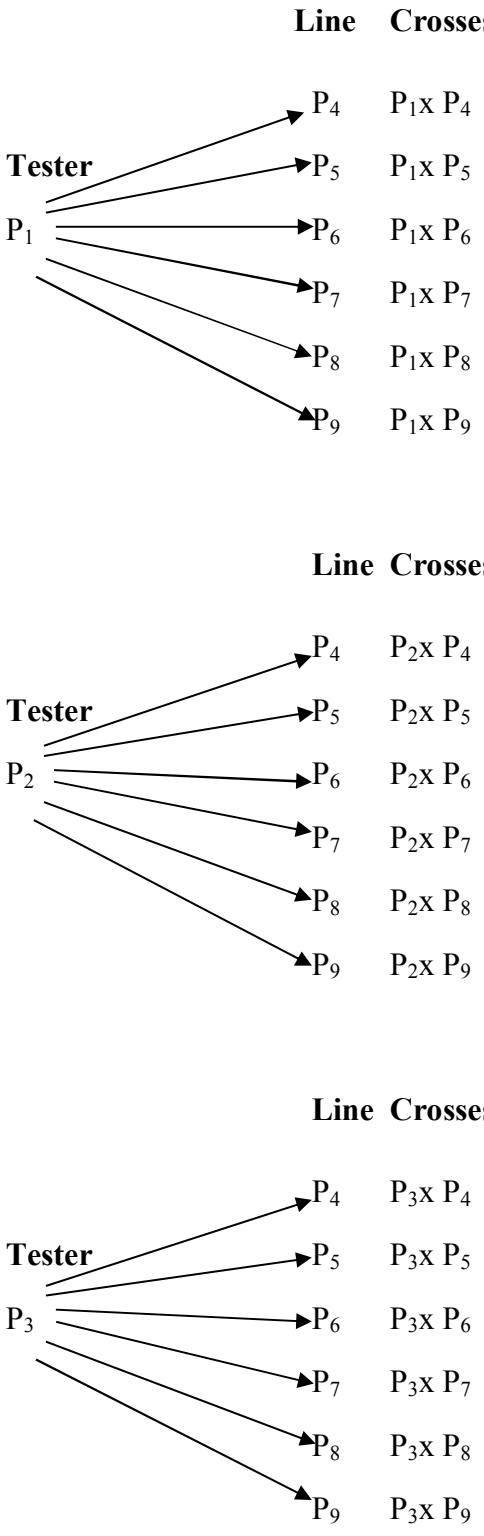


Figure 1 Schematic representation of line x tester mating design used to develop the F_1 Hybrid

3.5 Data Collection

Data for the following agronomic characters were obtained for analysis.

- Plant height (cm) at flowering (20-25 days after planting): Taken as the distance from ground to the top of the main axis.
- Days to 50% flowering: The days after emergence when 50% of the plants have at least one flower.
- Days to maturity: the number of days after emergence to when the pods are matured.
- Number of mature pod per plant: The average of mature pods on five plants at harvest.
- Pod yield (g): The weight in (g) of stripped, dried and cleaned mature pods at harvest.
- 100 seed weight (g): a random sample of 100 seeds was taken from the harvested bulk and weighed.
- Shelling percentage: the ratio of the weight of seed obtained to the weight of pod randomly drawn from the bulk sample.
- Infestation index: The aphid damage index (D.I) for each line
- Formula for DI = $\sum$ **(Scale value x no. of aphids in the category)/ (4 x total no. of plants) x 100.** Mensah *et al.* (2008)

Table 3. 2 Aphid Damage index (D.I) based on four point scale

Scores		symptoms description	No. of Aphids
0	----------	No aphid.	< 1
0.5	----------	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 stunted	301 - 500
3.0	----------	Plants appear stunted, 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 mold and few cast skin.	>800
4.0	----------	Plants appear stunted, leaves appear severely curled and yellow and are covered with soothy mold and cast skin.	>800

The DI ranges between 0 for no infestation and 100 for the most severe damage (Mensah *et al*., 2008). The DI was applied in the analysis.

3.6 Statistical Analysis

Data collected were subjected to Analysis of variance (ANOVA) using the generalised linear model (GLM) procedure of the Statistical Analysis System (SAS 9.1 SAS Institute, 2004).

The model used is as follows;

$$y_{ijk} = \mu + m_i + f_j + (mxf)_{ij} + e_{ijk}$$

Where:

y_{ijk} = observation made.

μ =general mean;

m_i = the effect of ith male;

f_j = the effect of jth female;

mf_{ij} = the interaction effect;

e_{ijk} = the error associated with each observation.

All the effects in the model were considered fixed.

3.6.1 Combining ability analysis

3.6.1.1 GCA effect

The GCA and SCA effects were estimated using the formula suggested by Singh and Chaudhary (1985).

GCA effect of lines

$$\text{gi} = \frac{x_{i..}}{tr} - \frac{x\cdots}{ltr}$$

Where;

x_i = total of ith lines over testers,

$x\cdots\cdot$ = grand total,

l = number of lines,

t = number of testers,

r = number of replications.

GCA effects of testers:-

$$\text{g}_\text{t} = \frac{x_{.j}}{lr} - \frac{x\cdots}{ltr}$$

Where;

$x_{.j}$ = total of jth lines over testers,

$x\cdots\cdot$ = grand total,

l = number of lines,

t = number of testers,

$r =$ number of replications.

3.6.1.2 SCA effects

$$S_{ij} = \frac{x_{ij}}{r} - \frac{x_{i.}}{tr} - \frac{x_{.j}}{rl} + \frac{x\cdots}{ltr}$$

Where;

$x_{ij} =$ Value of the jth lines with ith testers,

$x_{i.} =$ Total of ith over all testers,

$x_{.j} =$ Total of jth testers over all lines,

$x_{..} =$ grand total ,

$l =$ number of lines,

$t =$ number of testers; and

$r =$ number of replication.

3.6.2 Genetic Components of Variance

Genetic components of variance were estimated according to Singh and Chaudhary (1985);

Cov H.S (line) = $\frac{m_l - m_{lxt}}{rxt}$

Cov H.S (testers) = $\frac{m_t - m_{lxt}}{rxl}$

Cov H.S average = $\frac{l}{r(2lt - l - t)}\left(\frac{(l-1)(m_t) + (t-1)(m_t) + m_{l-t}}{l + t + 2}\right)$

$$\text{Cov F.S} = \left(\frac{(m_t - m_e) + (m_t - m_t) + (t-1)(m_{txt} - m_t)}{3xr} \right) + \frac{6rCovHS - r(l+t)CovHS}{3r}$$

Where;

m_l = Mean square lines,

m_t = Mean square testers,

m_{lxt} = Line x tester interaction mean square,

r = Number of replication,

t = Number of testers,

l = Number of lines,

3.6.3 Phenotypic and genotypic variance

These were calculated according to the formular given by Lush (1940), Chaudhary and Prasad (1968)

Genotypic variance = $\sigma_g^2 = \frac{m_2 - m_1}{r}$

Error Variance = σ_e^2

Phenotypic Variance = $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where,

M_2 = Mean sum square for treatment

M_1= Mean square for error

r = Number of repetition.

3.6.4 Estimation of phenotypic and genotypic coefficient of variation

Phenotypic and genotypic coefficient of variation were computed using the formulae outlined by Singh and Chaudhary (1985)

(a) Phenotypic coefficient of variation (P.C.V) $= \sqrt{\delta_p^2} \Big/ \bar{x} \; x100$

(b) Genotypic coefficient of variation (G.C.V) $= \sqrt{\delta_g^2} \Big/ \bar{x} \; x100$

Where;

$\sigma_p =$ Phenotypic standard deviation,

$\sigma_g =$ Genotypic standard deviation,

$\bar{x} =$ Grand mean

GCV and PCV values were categorised as low (0 – 10 %), moderate (10 – 20 %) and high (> 20%) as indicated by Siva Subramanian and Menon (1973)

3.6.5 Estimation of genotypic and phenotypic correlations

Genotypic and phenotypic correlation were estimated from the component of variance using the formular suggested by Singh and Chaudhary (1985).

Genotypic correlation coefficient

$$r_{gxgy} = \frac{\sigma^2{}_{gxgy}}{\sqrt{\sigma^2{}_{gx} * \sigma^2{}_{gy}}}$$

Where;

r_{gxgy} = genetypic correlation coefficient of character X and Y,

σ^2_{gxgy} = genotypic covariance of character X and Y,

σ^2_{gx} = genotypic variance of character X,

σ^2_{gy} = genotypic variance of character Y,

Phenotypic correlation coefficient;

$$r_{ph} = \frac{m_{gxgy}}{\sqrt{m_{gx} * m_{gy}}}$$

Where;

r_{ph} = phenotypic correlation between character X and Y,

m_{gx} = entry mean square of the character X,

m_{gy} = entry mean square of the character Y,

m_{gxgy} = entry mean product of the character X and Y

3.6.6 Heritability

Estimation of Narrow and Broad sense heritability was done according to (Hanson *et.al.,*1956). Broad sense heritability estimate as a ratio of genotypic variance to phenotypic variance and Narrow sense heritability estimate as the ratio of additive genetic variance to phenotypic variance as follows;

$$h^2_{n.s} = \frac{\sigma^2 A}{\sigma^2 P} x100$$

$$H^2_{b.s} = = \frac{\sigma^2 G}{\sigma^2 P} x100$$

Where;

h^2 = Heritability estimate,

σ^2_A = Additive variance,

σ^2_P = Phenotypic variance,

σ^2_G = Genotypic variance,

The heritability percentage was categorized as low (0 – 20%) moderate (30 -60 %) and high (>60 %) as given by Robinson *et. al.,* (1949

3.6.7 Genetic Advance

This was computed according to the methods suggested by Johnson *et al.,* (1955). As follows;

Genetic Advance (GA) = I. σ_P. h^2

Where

I = Selection intensity = 10% = 1.775,

σ_P = Phenotypic standard deviation,

h^2 = Heritability estimate in narrow sense,

Genetic advance as a percentage of mean (GAM), this was calculated by using the formular given below.

GAM = $\frac{GA}{\overline{X}} X100$

Where,

GA = Genetic advance,

$\overline{X}$ = General mean.

Genetic advance as percent of mean was categorized as low (0- 10%), moderate (10 – 20%) by Johnson *et al.* (1955).

CHAPTER FOUR

4.0 RESULTS

4.1 Mean Performance of Groundnut Lines, Testers, Hybrids and Checks Evaluated For Resistance to Aphids (*Aphis craccivora*) Koch

Mean performance of lines, testers, hybrid and checks are presented in table 4.1 and table 4.2.

4.1.1 Days to maturity

The mean was 92 (ICGX – SM 0020/5/9, ICGX – SM 00017/5/P10/P1 and ICGX 00020/5/P4/P1) in males, ranged from 93 (ICGV IS 07899) to 100 days (SAMNUT 14) in females, 92 (ICGX – SM 000017/5/P10/P1 x ICGV IS 07899, ICGX – SM 000020/5/9 x SAMNU 14) to 105 days (ICGX – SM 000017/5/P10/P1 x KWANKWASO) in hybrids and 98 (SAMNUT 22) to 110 days (SAMNUT 23) in checks. Among hybrids, ICGX – SM 000020/5/9 x SAMNU 14 and ICGX – SM 0020/ /9 x MANIPENTA (92 days) showed earliness in maturity.

4.1.2 Plant height (cm)

The range for plant height was from 20.5 (ICGX – SM 00017/5/P10/P1) to 21.5cm (ICGX – SM 00020/5/9) in males, 12.5 (MANIPENTA) to 23cm (ICGV IS 07899) in females, 16.3 (ICGX – SM 00017/5/P10/P1 x ICIAR – 19BT IS 07899) to 24cm (ICGX – SM 00020/5/9 x KWANKWASO) in hybrids and 15 (SAMNUT 23) to 21cm (SAMNUT 22) in checks. Among hybrids, ICGX – SM 00020/5/9 x KWANKWASO were taller than the checks.

4.1.3 Pod yield per plant (g)

Ranged from 16.5 (ICGX – SM 00020/5/9) to 21g (ICGX – SM 00020/5/P4/P1) in males, 12 (SAMNUT 14) to 21.5g (ICIAR – 19BT –IS 07899) in females, 13 (ICGX – SM 00017/5/P10/P1 x ICGV IS 07890) to 43.5g (ICGX – SM 0017/5/P10/P1 x KWANKWASO) in hybrids and 22.3 (SAMNUT 22) to 34g (SAMNUT 23) in checks.

Hybrid ICGX – SM 0017/5/P10/P1 x KWANKWASO (43.5g) had higher pod yield per plant than check SAMNUT 23 (34g) which was the highest among checks.

4.1.4 Number of pods per plant

Mean for number of pods per plant is 9 (ICGX – SM 00020/5/9) in males and ranged from 14 (MANIPENTA) to 20 (ICIAR - 19BT IS 07890) in females, 14 (ICGX - SM 00017/5/P10/P1 x ICGV IS 07890) to 35 (ICGX – SM 00017/5/P10/P1 x KWANKWASO) in hybrids and 25 (SMANUT 22) to 34 (SAMNUT 24) in checks. Hybrid ICGX – SM 00017/5/P10/P1 x KWANKWASO (35) had higher number of pods per plant than check SAMNUT 23 which was the highest among checks.

4.1.5 Seed weight per plant (g**)**

Seed weight per plant ranged from 5.5 (ICGX –SM 00020/5/P4/P1) to 8g in males, 6 (ICGV IS 07899) to 10.5g (ICIAR – 19BT IS 07899) in females, 5 (ICGX – SM 00017/5/P10/P1 x ICGV IS 07890) to 24g (ICGX – SM 00017/5/P10/P1 x KWANKWASO) in hybrids and 13.5 (SAMNUT 22) to 17.5g (SAMNUT 23 and SAMNUT 24) in checks.

4.1.6 Shelling percentage

Ranged from 26.2 (ICGX – SM 00020/5/P4/P1) to 53.3 % (ICGX – SM 0020/5/9) in males, 32.2 (ICGV IS 07899) to 85.2% (SAMNUT 14) in females, 33.9 (ICGX – SM 00020/5/P4/P1 x SAMNUT 14) to 66.9 % (ICGX – SM 00017/P10/P1 x KWANKWASO) in hybrids and 36.3 (SAMNUT 22) to 66% (SAMNUT 24) in checks.

4.1.7 Aphid damage index (%)

The mean for aphid damage index ranged from 13.8 (ICGX – SM 00020/5/P14/P1) to 24.7% (ICGX – SM 00020/5/9) in males, 13.8 (KWANKWASO) to 40.5% (ICGV IS 07899) in females, Six hybrids had 13.8% while ICGX –SM 00017/P10/P1 x KWANKWASO had 40.5%, for the checks, the range is from 14.5 (SAMNUT 24) to 22.3% (SAMNUT 22 and SAMNUT 23)

Table 4.1 Mean performance of 6 groundnut lines and 3 testers evaluated for resistance to Aphid (*Aphis craccivora*) Koch

GENOTYPE	DTM	PHT	PY	NPD	SW	HSW	SP	DI
ICGX - SM 00020/5/9	92.00	21.50	16.50	9.00	8.00	27.00	53.25	24.70
ICGX - SM 00017/5/P10/P1	92.00	20.50	19.00	9.00	6.00	20.50	35.45	18.68
ICGX - SM 00020/5/P4/P1	92.00	21.00	21.00	9.00	5.50	18.50	26.15	13.78
ICGV IS 07890	92.00	23.00	20.00	19.00	9.00	30.50	44.10	23.59
ICGV IS 07899	93.00	21.30	14.50	10.00	6.00	20.50	32.15	40.53
ICIAR-19BT IS 07899	96.00	16.90	21.50	20.00	10.50	35.50	48.20	22.64
SAMNUT 14	100.00	23.00	12.00	13.00	10.00	33.50	85.35	33.96
KWANKWASO	96.00	21.00	16.00	15.00	8.50	28.50	53.60	13.78
MANIPENTA	96.00	12.50	17.50	14.00	8.50	28.50	50.90	21.69

DTM (days) = days to maturity, PHT (cm) = Plant height, SW (g) = Seed weight per plant, HSW (%) = 100 seed weight, SP (%) = Shelling percentage, NPD (no) Number of pods per plant, PY (g) = Pod yield per plant, DI (%) =Aphid damage index

Table 4.2 Mean performance of 18 hybrids evaluated for resistance to Aphids (*Aphis craccivora*) koch

GENOTYPES	DTM	PHT	PY	NPD	SW	HSW	SP	DI
ICGX - SM 00020/5/9 X ICGV IS 07890	100.00	21.50	25.00	30.00	16.00	54.00	64.00	13.78
ICGX - SM 00020/5/9 X ICGV IS 07899	97.00	17.75	25.00	20.00	12.00	40.00	48.75	16.63
ICGX - SM 00020/5/9 X ICIAR-19BT IS 07899	96.00	21.25	24.50	22.00	14.00	47.00	57.10	24.70
ICGX - SM 00020/5/9 X SAMNUT 14	92.00	22.50	23.00	20.00	11.50	38.50	47.35	21.69
ICGX - SM 00020/5/9 X KWANKWASO	96.00	24.00	25.00	16.00	9.00	30.00	37.50	13.78
ICGX - SM 00020/5/9 X MANIPENTA	92.00	21.50	23.50	21.00	11.00	37.00	46.90	35.63
ICGX - SM 00017/5/P10/P1 X ICGV IS 07890	92.00	22.50	13.00	14.00	5.00	17.00	38.75	15.68
ICGX - SM 00017/5/P10/P1 X ICGV IS 07899	92.00	21.00	21.50	19.00	12.00	40.00	55.90	13.78
ICGX - SM 00017/5/P10/P1X ICIAR-19BT IS 07899	94.00	16.25	26.00	32.00	13.50	45.50	52.10	13.78
ICGX - SM 00017/5/P10/P1 X SAMNUT 14	94.00	18.25	28.50	29.00	19.00	64.00	66.90	24.70
ICGX - SM 00017/5/P10/P1 X KWANKWASO	105.00	19.50	43.50	35.00	24.00	80.50	55.25	40.53
ICGX - SM 00017/5/P10/P1 X MANIPENTA	95.00	22.50	21.50	19.00	11.00	37.00	51.00	24.70
ICGX - SM 00020/5/P4/P1 X ICGV IS 07890	94.00	21.00	34.00	23.0	20.00	67.00	59.05	13.78
ICGX - SM 00020/5/P4/P1 X ICGV IS 07899	102.00	23.00	26.00	17.00	14.00	47.00	54.45	17.73
ICGX - SM 00020/5/P4/P1 X ICIAR-19BT IS 07899	102.00	21.75	27.00	21.00	14.00	47.00	52.15	35.63
ICGX - SM 00020/5/P4/P1 X SAMNUT 14	102.0	19.50	30.50	26.00	11.00	37.00	33.95	13.78
ICGX - SM 00020/5/P4/P1 X KWANKWASO	95.50	20.00	33.00	34.00	18.00	60.50	54.55	15.68
ICGX - SM 00020/5/P4/P1 X MANIPENTA	100.00	20.00	26.00	18.00	10.50	35.50	41.40	24.70
SAMNUT 22	100.00	21.00	22.50	25.00	13.50	55.50	36.25	20.25
SAMNUT 23	110.00	15.00	34.00	32.00	17.50	55.50	51.60	20.25

GENOTYPES	DTM	PHT	PY	NPD	SW	HSW	SP	DI
SAMNUT 24	98.00	16.50	27.50	32.00	17.50	53.50	66.05	14.50
Means	97	20.23	23.95	21	12.20	41.07	50.00	21.63
Range	92.0 - 110	12.5 - 24.0	12.0 - 43.5	9.0 - 35.0	5.0 - 24.0	17.0 - 80.5	26.2 - 85.4	13.8 - 40.5
LSD	5.10	6.90	12.70	10.60	8.10	26.70	31.50	5.20
CV (%)	2.80	16.60	25.90	25.00	32.30	32.10	30.70	11.70

DTM (days) = days to maturity, PHT (cm) = Plant height, SW (g) = Seed weight per plant, HSW (%) = 100 seed weight, SP (%) = Shelling percentage, NPD (no) Number of pods per plant, PY (g) = Pod yield per plant, DI (%) =Aphid damage index, LSD =Least significant difference, CV(%) = Coefficient of variation.

4.2 Analysis of Variance for Combining Ability

Analysis of variances for females, males and female x male interaction with respect to 8 quantitative traits are presented in Table 4.3. Mean squares due male and female were non-significant for all the traits except D.I. The female x male interaction mean squares were highly significant for DTM, SW, HSW, NPD and D.I.

4.3 Variances due to GCA and SCA

Variance due to general and specific combining ability (σ^2_{gca} and σ^2_{sca}), ratio of GCA: SCA variances, additive variance (σ^2_A), and dominance variance (σ^2_D) for different traits are presented in Table 4.4. It is evident from the table that the hybrids in general were superior to parents for most of the indicated traits studied during the investigation. Table 4.4 also depicts that variance due to specific combining ability was more important than the variance due to general combining ability as well as the additive variance for most of the traits. It is evident from the Table that the variance due to SCA wherein dominance variance was more important for most of the plant traits. Preponderance of dominance gene action is declared by the degree of dominance less than one for all the traits.

Table 4.3 Analysis of variance for combining ability for 8 traits of 6 groundnut lines and 3 testers evaluated for resistance to Aphid

		Mean squares							
Source of variation	Df	DTM	PH	SW	HSW	SP	NPD	PY	D.I
Replication	1	0.000^{NS}	15.34*	5.64^{NS}	42.61^{NS}	438.84^{NS}	0.53	1.26^{NS}	65.16**
Genotypes(G)	29	40.54**	14.35*	41.92**	427.12**	291.98^{NS}	120.35**	92.94**	136.45**
Parents (P)	8	16.00*	22.49^{NS}	6.50^{NS}	72.00^{NS}	94.03^{NS}	36.81^{NS}	19.80^{NS}	154.26**
P vs crosses	1	65.33**	5.64^{NS}	381.57**	4243.79**	4.36^{NS}	42.39**	954.08**	78.62**
Crosses	17	33.45**	8.31^{NS}	37.48*	421.99*	325.79^{NS}	83.89**	78.95^{NS}	148.69**
Line (L)	5	10.47^{NS}	3.39^{NS}	24.23^{NS}	269.96^{NS}	458.15^{NS}	81.71^{NS}	89.56^{NS}	170.14**
Tester (T)	2	56.33^{NS}	6.13^{NS}	18.11^{NS}	209.03^{NS}	485.76^{NS}	30.11^{NS}	83.36^{NS}	11.87**
L x T	10	40.60**	10.49^{NS}	51.94**	585.33**	227.86^{NS}	94.61**	73.09^{NS}	165.34**
Error	17	6.46	11.45	16.30	184.84	248.59	27.68	40.67	5.18

DTM (days) = days to maturity, PHT (cm) = Plant height, SW (g) = Seed weight per plant, HSW (%) = 100 seed weight, SP (%) = Shelling percentage, NPD (no) Number of pods per plant, PY (g) = Pod yield per plant, DI (%) =Aphid damage index, * = Significant (P<0.05), ** = Highly significant (<0.001) NS = non-significant.

Table 4. 4 Estimate of variance due to GCA variance due SCA, additive variance, dominance variance, heritability and ratio of additive to dominance variance of groundnut genotypes evaluated at samaru in 2012

Crosses	DTM	PHT	SW	HSW	SP	NPD	PY	D.I
Cov H.S(line)	-5.02	-1.18	-4.62	-52.56	38.38	-2.15	2.74	196507.08
CovH.S(testers)	1.31	-0.36	-2.82	-31.36	21.49	-5.38	0.85	-16890.76
Cov H.S average	-0.31	-0.12	-0.55	-6.16	4.41	-0.51	0.27	10769.05
Cov F.S	14.98	-2.27	8.11	91.13	66.59	21.08	20.39	537426.40
σ^2_{gca} with F= 0, $\sigma^{\hat{}}_A$,	5.04	-1.87	8.73	98.60	70.57	8.19	4.35	172304.74
σ^2_{sca} with F= 0, $\sigma^{\hat{}}_D$,	273.09	-7.67	285.11	3203.93	165.84	535.41	259.36	5324434.53
σ^2_A/σ^2_D	0.02	0.24	0.03	0.03	0.43	0.02	0.02	0.03

DTM (days) = days to maturity, PHT(cm)= Plant height, SW(g)= Seed weight, HSW(%)= 100 seed weight, SP(%)= Shelling percentage, NPD = Number of pods per plant, PY(g)= Pod yield per plant, DI(%) =Aphid damage index

4.4 Proportional Contribution of Lines, Testers and their Interaction to the Total Variance and Genetic Advance

A line x tester analysis of groundnut with 3 resistant male lines and 6 female lines as tester were carried out to obtain the proportional contribution of lines, testers and lines x testers to the total variance for different plant traits (Table 4.5). The contribution of maternal and paternal interaction (line x tester) was very high for all traits studied It revealed preponderance of paternal and maternal interaction (line x tester) influence for all these traits. Genetic advance as percentage of mean is presented in table 4.8. The range of genetic advance as a percentage of mean is from (0.22 – 10.68) however, the genetic advance was generally low for all the characters studied.

Table 4.5 Proportional contribution of lines, testers, and their interaction to total variance and Expected genetic advance for studied characters

Characters	Contribution of lines (%)	Contribution of testers (%)	Contribution of *(l* x*t)* (%)	Genetic Advance	Genetic Advance as % of mean
DTM	9.20	19.81	71.39	0.21	0.22
PHT	12.00	8.68	74.23	1.48	7.32
SW	19.01	5.68	81.52	0.39	1.63
HSW	18.82	5.83	81.59	1.29	6.24
SP	41.36	17.54	41.14	25.56	208.65
NPD	28.64	4.22	66.33	0.31	0.76
PY	33.37	12.42	54.46	1.14	2.27
DI	47.83	5.37	46.79	2.31	10.68

DTM (days) = days to maturity, PHT(cm)= Plant height, SW(g)= Seed weight, HSW(%)= 100 seed weight, SP(%)= Shelling percentage, NPD = Number of pods per plant, PY(g)= Pod yield per plant, DI(%) =Aphid damage index

4.5 General Combining Ability Effects

The results of general combining ability effects of lines and testers are presented in Tables 4.6. Negative GCA effect were exhibited by parents (lines) ICGV IS 07890 (-1.333), SAMNUT 14 (-0.8333) and MANIPENTA (-1.000) for days to maturity. Female parents KWANKWASO, revealed positive and significant GCA effect for 100 seeds weight, number of pods per plant and pod yield while male parent ICGX – SM 00020/5/P4/P1 depicted positive and significant GCA effect for these traits . Lines with high positive GCA estimates for seeds weight, and pod yield are good candidates to be used as parents for the development of desirable hybrids. Among the testers ICGX – SM 00020/5/9 for 100 seed weight and days to maturity exhibited negative GCA effect and such was desirable male parent for earliness. Male parents ICGX – SM 00020/5/P4/P1 demonstrated positive and significant GCA effect for seeds weight, number of pods per plant and pod yield however as for the Aphid Damage index (D.I), All the lines and testers show significantly higher positive GCA except lines; KWANKWASO (-273.2738), MANIPENTA (-609.1071) and tester ICGX-SM0020/5/P4P1 (-235.3095) which show significantly higher negative GCA.

Table 4. 6 General combining ability effects for indicated traits in 6 groundnut lines and 3 testers at Samaru 2012

Trait	DTM	PHT	SW	HSW	SP	NPD	PY	D.I
Female parent(Lines)								
ICGV IS 07890	-1.3333	0.9028	0.0278	0.1944	2.5250	-0.9444	-2.4722	635.3571
ICGV IS 07899	0.3333	-0.1806	-0.9722	-3.4722	-7.3917	-4.4444	-2.3056	369.2262
ICIAR-19BT IS 07899	0.6667	-1.0139	0.1944	0.6944	-3.7250	1.8889	-0.6389	760.8929
SAMNUT 14	-0.8333	-0.6806	0.1944	0.6944	12.3083	1.8889	0.8611	428.1429
KWANKWASO	2.1667	0.4028	3.3611	11.1944	-10.4750	5.2222	7.3611	-273.2738
MANIPENTA	-1.0000	0.5694	-2.8056	-9.3056	6.7583	5.2222	-2.8056	-609.1071
Male parents (testers)								
ICGX – SM 00020/5/9	-1.1667	0.6528	-1.3889	-4.7222	3.2833	-1.6111	-2.1389	228.2143
ICGX – SM 00017/5/P10/P1	-1.3333	-0.7639	0.4444	1.5278	-7.3333	1.5556	-0.8056	52.8810
ICGX – SM 00020/5/P4/P1	2.5000	0.1111	0.9444	3.1944	4.0500	0.0556	2.9444	-235.3095
SE(GCA for lines)	1.0380	1.3814	1.6485	5.5503	6.4367	2.1480	2.6037	109.0833
SE (gi-gj) for lines	1.4679	1.9535	2.3314	7.8494	9.1029	3.0378	3.6821	109.0833
SE (GCA for testers)	0.7340	0.9768	1.1657	3.9247	4.5515	1.5189	1.8411	82.4592
SE(gi-gj)for testers	1.0380	1.3814	1.6485	5.5503	6.4367	2.1480	2.6037	116.6149

DTM (days) = days to maturity, PHT (cm) = Plant height, SW (g) = Seed weight per plant, HSW (%) = 100 seed weight, SP (%) = Shelling percentage, NPD (no) Number of pods per plant= PY (g) = Pod yield per plant, DI (%) =Aphid damage index

4.6 Specific Combining Ability Effects

Cross combination ICGX – SM 00020/5/P4/P1 X ICGV IS 07890, ICGX – SM 00017/5/P10/P1 X KWANKWASO and ICGX – SM 00017/5/P10/P1 X SAMNUT 14 revealed maximum positive and significant SCA effects for higher SW. Similarly, potential crosses showing significantly high positive SCA effects for NPD were six (Table 4.7). However all the potential crosses show lower negative SCA, for Aphid infestation index (D.I) except six of the crosses which show significantly higher positive SCA as presented in the table below. Higher PY and lower D.I is an ultimate objective of groundnut breeding and hybrid development programs. Positive and highly significant specific combining ability effects for pod yield were revealed by four crosses (ICGX – SM 00017/5/P10/P1 x KWANKWASO, ICGX – SM 0020/5/P4/P1 x ICGV IS 07890, ICGX SM 00020/5/9 x ICGV IS 07890, and ICGX –SM 00020/5/9 x ICGV IS 07899).

Table 4.7 Estimation of specific combining ability effects for indicated plant traits of 18 groundnut crosses derived from 6 female and 3 male parents evaluated at samaru in 2012

Crosses	DTM	PHT	SW	HSW	SP	NPD	PY	D.I
ICGX – SM 00020/5/9 X ICGV IS 07890	5.8333	-0.8194	3.7222,	12.7222	9.3833	9.6111	3.1389	1.7857
ICGX – SM 00020/5/9 X ICGV IS 07899	1.1667	-3.4861	0.7222	2.3889	5.9000	3.1111	2.9722	-249.4643
ICGX – SM 00020/5/9 X ICIAR-19BT IS 07899	-0.1667	0.8472	1.5556	5.2222	-13.6667	-1.2222	0.8056	117.8690
ICGX – SM 00020/5/9 X SAMNUT 14	-2.6667	1.7639	-0.9444	-3.2778	-11.2000	-3.7222	-2.1944	-174.7143
ICGX – SM 00020/5/9 X KWANKWASO	-1.6667	2.1806	-6.6111	-22.2778	4.4333	-11.0556	-6.6944	497.0357
ICGX – SM 00020/5/9 X MANIPENTA	-2.5000	-0.4861	1.5556	5.2222	5.1500	3.2778	1.9722	-224.4643
ICGX – SM 00017/5/P10/P1 X ICGV IS 07890	-2.0000	1.5972	-9.1111	-30.5278	-7.5000	-10.0556	-10.1944	31.9524
ICGX – SM 00017/5/P10/P1 X ICGV IS 07899	-3.6667	1.1806	-1.1111	-3.8611	-7.3833	-1.0556	-1.8611	70.4524
ICGX – SM 00017/5/P10/P1X ICIAR-19BT IS 07899	-2.0000	-2.7361	-0.7778	-2.5278	6.1500	5.1111	0.9722	212.5357
ICGX – SM 00017/5/P10/P1 X SAMNUT 14	-2.0000	-1.0694	4.7222	15.9722	2.2667	2.6111	1.9722	-2.7976
ICGX – SM 00017/5/P10/P1 X KWANKWASO	7.5000	-0.9028	6.5556	21.9722	10.7000	5.2778	10.4722	792.9524
ICGX – SM 00017/5/P10/P1 X MANIPENTA	0.6667	1.9306	-0.2778,	-1.0278	-4.2333	-1.8889	-1.3611	-36.9643
ICGX – SM 00020/5/P4/P1 X ICGV IS 07890	-3.8333	-0.7778	5.3889	17.8056	-1.8833	0.4444	7.0556	-394.7976
ICGX – SM 00020/5/P4/P1 X ICGV IS 07899	2.5000	2.3056	0.3889	1.4722	1.4833	-2.0556	-1.1111	-641.3810
ICGX – SM 00020/5/P4/P1 X ICIAR-19BT IS 07899	2.1667,	1.8889	-0.7778	-2.6944	7.5167	-3.8889	-1.7778	-215.6905
ICGX – SM 00020/5/P4/P1 X SAMNUT 14	3.1667	-0.6944	-3.7778	-12.6944	8.9333	1.1111	0.2222	-120.9405
ICGX – SM 00020/5/P4/P1 X KWANKWASO	-5.8333	-1.2778	0.0556	0.3056	-15.1333	5.7778	-3.7778	-325.9405
ICGX – SM 00020/5/P4/P1 X MANIPENTA	1.8333	-1.4444	-1.2778	-4.1944	-0.9167	-1.3889	-0.6111	-900.8571
SE (SCA effect)	1.7978	2.3926	2.8554	9.6135	11.1487	3.7205	4.5097	218.1666
SE (Sij-Sk1)	2.5425	3.3836	4.0381	13.5955	15.7667	5.2616	6.3777	308.5341

DTM (days) = days to maturity, PHT (cm) = Plant height, SW (g) = Seed weight per plant, HSW (%) = 100 seed weight, SP (%) = Shelling percentage, NPD (no) Number of pods per plant= PY (g) = Pod yield per plant, DI (%) =Aphid damage index

4.7 Genetic Parameters

The results pertaining to genetic variability parameters viz., genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, broad and narrow sense heritability, genetic advance and genetic advance as percent of mean for eight characters of groundnut lines are presented in Table 4.8. The heritability in Broad and Narrow sense was determined depending on variance of general and specific combining abilities.

It is apparent from the Table that most of the characters manifested higher magnitude of both genotypic and phenotypic coefficient of variation. The characters viz., HSW (95.2 and 114.67%), SP (107.68 and 165.85%), SW (24.66 and 29.95 g), NPD (25.15 and 28.12) and DI (53.36 and 54.64 %) respectively Two characters showed moderate magnitude viz., plant height (14.36 and 21.9) and pod yield per plant (17.15 and 21.16). As for low magnitude of both GCV and PCV, only days to maturity recorded (6.34 and 6.85). Broad and narrow sense heritability for the studied characters are also presented in Table 4.6. Moderate to high estimates of broad sense heritability were recorded for all the characters. Broad sense heritability ranged from 0.42 for SP to 0.95 for DI. The characters DTM (0.80), SW (0.69), HSW (0.69), NPD (0.80) and PY (0.66) indicated high heritability. However, as for narrow sense heritability the trend was generally low for all the characters studied except for SP (0.74).

Table 4.8 Estimate of genetic variance components broad sense, narrow sense heritability, PCV and GCV for 8 characters of 30 genotypes grown at samaru 2012

Character	σ_g^2	σ_{ph}^2	σ_e^2	$H^2{}_b$	h^2n	PCV	GCV
DTM	37.49	43.73	6.24	0.86	0.019	6.85	6.34
PHT	8.40	19.74	11.30	0.43	0.196	21.96	14.36
SW	34.88	50.40	15.52	0.69	0.032	29.95	24.66
HSW	385.83	559.66	173.83	0.69	0.032	114.67	95.21
SP	172.59	409.45	236.86	0.42	0.74	165.85	107.68
NPD	106.70	133.35	26.65	0.80	0.016	28.12	25.15
PY	73.82	112.43	38.61	0.66	0.063	21.16	17.15
DI	133.20	139.71	6.51	0.95	0.115	54.64	53.36

DTM (days) = days to maturity, PHT(cm)= Plant height, SW(g)= Seed weight, HSW(%)= 100 seed weight, SP(%)= Shelling percentage, NPD = Number of pods per plant, PY(g)= Pod yield per plant, DI(%) =Aphid damage index, σ_g^2 =genetic variance, σ_p^2 = phenotypic variance, σ_e^2 = error variance, $H^2{}_b$ = broad sense heritability, h^2n = narrow sense heritability, PCV= phenotypic coefficient of variation, GCV= genotypic coefficient of variation.

4.8 Inter-character Correlations

Analysis of simple phenotypic and genotypic correlation coefficient between aphid damage index, yield and yield component characters are presented in table 4.9. The data for correlation studies for the genotypes showed that, days to maturity was positively significantly correlated with pod yield (0.56 and 0.81), number of pods per plant (0.9 and 0.7), plant height (0.82 and 0.65) both at phenotypic and genotypic level respectively. Pod yield showed positive significant genotypic correlation (0.92) with number of pod per plant and a negative significant correlation (-0.76) with the same character. Damage index was poorly correlated with all agronomic traits.

Table 4.9 Phenotypic (upper diagonal) and genotypic (lower diagonal) correlation coefficients for five characters of groundnut evaluated in 2012

Traits	DI	DTM	NPD	PHT	PY
DI		0.02	-0.09	0.28	- 0.21
DTM	0.25		0.9	0.82**	0.56*
NPD	-0.06	0.70**		-0.28	-0.76**
PHT	0.16	0.65**	-1.00		0.33
PY	0.05	0.81**	0.92**	-1.00	

DTM (days) = days to maturity, PHT(cm)= Plant height, SW(g)= Seed weight, HSW(%)= 100 seed weight, SP(%)= Shelling percentage, NPD = Number of pods per plant, PY(g)= Pod yield per plant, DI(%) =Aphid damage index

CHAPTER FIVE

5.0 DISCUSSION

5.1 Analysis of Variance for Combining Ability

The analysis of variance for all entries, including parents, hybrids, checks for eight characters were highly significant except for shelling percentage. This indicates the presence of variability among genotypes, which is pre-requisite for any crop improvement programme.

From the analysis of variance of parents and hybrids, it was clear that the mean sum of squares for parents and females were non-significant for all the traits except for days to maturity and aphid damage index while for males the mean sum of square were also non-significant indicating insufficient variability among parents. Earlier workers Wright *et al*. (1971) and Atkins (1972) reported similar results

The mean sum of squares of females versus males was not-significant for all traits except days to maturity, pod yield per plant and plant height. This implies less divergence among testers compared to lines with respect to all characters.

The mean sum of squares for hybrids were highly significant for all traits except for Plant height, yield per plant and shelling percentage indicating diverse performance of different cross combinations for the remaining traits.

The parent versus hybrids mean sum of squares were significant for days to maturity, seed weight, 100-seed weight, number of pods per plant ,pod yield per plant and aphid damage index revealing the presence of average heterosis due to the significant difference in the mean performance of hybrids and parent.

The contribution to total hybrids variance was found to be higher from females (lines) than males (testers) for all characters under study except for days to maturity as females were genetically diverse than males. The contribution of the female × male interaction for the total hybrid variance was also higher than that of males for all characters. On the other hand, the contribution of the female × male interaction was higher than that of female, in respect to days to maturity, plant height, seed weight, 100-seed weight, shelling percentage, number of pods per plant, pod yield per plant and aphid damage index.

5.2 Genetic Components of Different Characters

Heritability and genetic advance is a useful tool for breeders in determining the direction and magnitude of selection. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its components and also among various components.

In the present investigation, an attempt was made to estimate the proportion of variability, broad sense heritability, environmental, genotypic and phenotypic variances, predicted genetic advance, GCV, and PCV with respect to 8 characters. The association among these characters and their direct and indirect effect on pod yield has been studied. The genotypes showed a wide range of variation, which provides ample scope for selection of superior and desired genotypes by the plant breeders for further improvement in groundnut. An assessment of heritable and non-heritable components in the total variability observed is indispensable in adopting suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation such as coefficients of genotypic and phenotypic variability, heritability and predicted genetic advance. Presence of narrow gap between phenotypic coefficient of variability (PCV) and

genotypic coefficient of variability (GCV) for all the characters under study as shown in table 4.3, suggested that the traits studied have low environmental influence.

5.3 General and Specific Combining Abilities

Variation in general combining ability effect was estimated among lines and tester for indicated plant traits to identify the best parent for subsequent hybrid development programme. The results of general combining ability effects of lines and testers are presented in Tables 4.1 and 4.2. Farmers need short duration groundnut hybrids because it reduces the incidence of insect-pest and disease attack due to early maturity. Minimum number of days to 50% flowering is preferred to reduce the crop growth period. Negative GCA effect was exhibited by parents (lines) ICGVIS07890 and MANIPENTA for days to maturity and D.I. ICGVIS07890 and MANIPENTA having significant negative GCA effects can be considered for selection due to shorter number of days to maturity. Female parent KWANKWASO, revealed positive and significant GCA effect for 100 seeds weight, number of pods per plant and pod yield. Lines with high positive GCA estimates for seeds weight, and pod yield are good candidates to be used as parents for the development of desirable hybrids. These results are in accordance to Naik *et al*., (1999) and Ashok *et al*., (2000) who observed significant and positive GCA effects for these traits in their respective studies**.**

The hybrids having negative and significant SCA effects for plant height, D.I and days maturity showed their ability to contribute genes for earliness and reduced level of damage by the aphids. These results are in line with the finding of Ashok *et al*., (2000) who found significant and negative SCA effects for maturity in sunflower hybrids. For 100-seed weight, significantly positive SCA effects were demonstrated by 6 crosses. Higher seed

yield is an ultimate objective of groundnut breeding and hybrid development programmes. Positive and highly significant specific combining ability effects for pod yield were revealed by 6 crosses.

5.4 Proportional contribution of Lines, Testers and their Interaction to the total variance

A line x tester analysis of groundnut with 6 female susceptible lines and 3 male resistant lines as tester were carried out to obtain the proportional contribution of lines, testers and lines x testers to the total variance for different plant traits (Table 4.5). The contribution of maternal and paternal interaction (line x tester) was very high for all traits. It revealed preponderance of paternal and maternal interaction (line x tester) influence for all these traits. These results are partially in agreement with Kannababu and Karivaratharaju (2000)

5.5 Genotypic and Phenotypic Correlation

Genotypic and phenotypic correlation coefficients for five traits were computed using SAS (9.0) as shown in table 4.6. In general, it was observed that estimates of genotypic correlation were higher than their corresponding phenotypic correlations. This agrees with the findings of Johnson *et.al* (1955) Paroda and Joshi (1970), Kamboj and Mani, (1983). Pod yield per plant recorded positive genotypic correlation with days to maturity and number of pods per plants. While on the other hand, D.I was found to be negatively correlated with plant height and pod yield.

CHAPTER SIX

6.0 SUMMARY, CONCLUSION RECOMMENDATIONS.

6.1 Summary

The present investigation was carried out during 2012 growing season at the groundnut screen house of the Institute for Agricultural Research, Ahmadu Bello University, Zaria. Line × tester experiment was conducted to evaluate nine parents and their 18 hybrid of groundnut genotype for their resistance to aphids (*Aphis craccivora Koch*.), which were obtained by crossing six female parents (lines) with three males (testers). An attempt was made to understand the genetic nature of Eight quantitative characters viz., days to maturity, plant height, seed weight, 100 - seed weight, number of pods per plant, shelling percentage, pod yield per plant and aphid damage index. These genotypes were also screened against aphid infestation.

6.2 Conclusion

The salient features of experimental findings are summarized below;

Among the lines, KWANKWASO and SAMNUT 14 were best combiners for all the traits studied , while MANIPENTA also performed best for NPD and D.I. Lines ICGV IS 07890, SAMNUT 14 and MANIPENTA were the best general combiner for early maturity. KWANKWASO was the best line for seed weight .Among testers, ICGX – SM 0002/5/9 was the best general combiner for early maturity. Tester ICGX – SM 00020/5/P4/P1 was the best general combiner for seed weight, D.I and seed yield. For shelling percentage ICGX – SM 00017/5/P10/P1 was found to be the best general combiner. In terms of specific combining ability effects, the best groundnut hybrids were ICGX – SM

00020/5/P4/P1 X KWANKWASO for early maturity, and ICGX – SM 00017/5/P10/P1 X KWANKWASO for pod yield. ICGX – SM 00020/5/9 X ICGV IS 07899 for NPD and ICGX – SM 00020/5/P4/P1 X MANIPENTA for D.I. Dominance gene action was predominant for days to maturity, seed weight, shelling percentage, and pod yield. The relative contribution of line x tester interaction was found more important for all characters under study. Parental lines with high GCA effects for yield and yield components may result in resistant hybrids with better performance for yield and its components. High SCA effects resulting from crosses between higher general combiners can be improved through early selection. High SCA effects resulting from low GCA combiners suggest that such crosses may be utilized for further improvement through single plant selection in the later generations. Higher SCA variances than GCA variances show that the characters were under the control of Dominance gene action. The results obtained are in agreement with the findings of (Hakim khan *et al*., 2008) who studied the magnitude of combining abilities in sunflower and reports similar result.

6.3 Recommendation

The following recommendations are thus made:

- There is a need of collaboration between plant breeders and entomologist towards the identification and characterization of groundnut aphid population in Zaria.
- Further evaluation of the material used in this study should be carried out in the field under natural infestation so that their potential as a new source of resistance can be harnessed.

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Appendix

Appendix 1. Analysis of variance layout for Line x Tester Analysis including parents

Source:	df	M.S	Expected mean square
Replication	$r-1$		
Treatment	$T-1$		
Parent s	$p-1$		
Crosses	$c-1$		
Parent vs crosses	1		
Lines	$l-1$	M_l	$\sigma^2_e + r\sigma^2_{lt} + rt\sigma^2_l$
Testers	$t-1$	M_t	$\sigma^2_e + r\sigma^2_{lt} + rl\sigma^2_t$
L X T	$(l-1)(t-1)$	M_{Lxt}	$\sigma^2_e + r\sigma^2_{lt}$
Error	$(lt-1)(r-1)$	M_e	σ^2_e