INHERITANCE OF OIL CONTENT AND OTHER AGRONOMIC TRAITS IN GROUNDNUT GENOTYPES(*ARACHIS HYPOGAEA*L.)

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BY

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A DISSERTATION SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES, AHMADU BELLO UNIVERSITY, ZARIA,
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SEPTEMBER, 2016

Declaration

I declare that the work in this dissertation entitled "INHERITANCE OF OIL CONTENT AND OTHER AGRONOMIC TRAITS IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) GENOTYPES" 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.

…….	…….	….....……
Student	Signature	Date

Certification

The dissertationentitled “INHERITANCE OF OIL CONTENT AND OTHER AGRONOMIC TRAITS IN GROUNDNUT (*ARACHIS HYPOGAEA* L.) GENOTYPES” by Mohammed Shamsideen JIBRIN meets the regulations governing the award of the degree of Masters of Science in Plant Breeding of Ahmadu Bello University, and is approved for its contribution to knowledge and literary presentation.

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Dedication

This dissertation it dedicated to my wonderful and beloved parents, Alh. A.O. Jibrin and Hajia A. Risikat for their love and care at all times and to the past, present and future Plant Breeders.

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Abstract

This study was carried out to determine the inheritance of oil content using eight (three male and five females)parents, that were mated in a North Carolina Design II (NC II) mating design that generated 15 progenies,to determine mode of gene action, estimate heritability and the association of the measured traits. The parents, the resultant $F_1$and two checks were evaluated at Samaru ((11 ^{0}11^{l}N, 7^0 38^l E), 600m above sea level in the Northern Guinea Savanna and I.A.R Irrigation Research Station Kadawa (11^{o}39^l N latitude, 08^o 02^l E longitude with an altitude of 469m above sea level)during 2014/2015 dry season. Significant differences were observed among the studied genotypes, signifying variation among the genotypes. Genotype performance across location was significant ($P \leq 0.05$) forplant height and highly significant ($P \leq 0.01$) for oil content, protein and carbohydrate content.The genotype performance across locations showed thatthe parent; SAMNUT 24 (52.63%) and cross SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 (52.63%) recorded the highest mean performance foroil content. This study also revealed thatboth additive and non-additive gene action were important in controlling oil content and other agronomictraits.However, the ratio of GCA variance to SCA variance was less than unity indicating the preponderance of non-additive gene action for all the traits except plant height. Broad sense heritability estimates were moderate for oil(43.46), protein(46.30) and carbohydrate content (45.03). Narrow sense heritability is low for most traits. The PCV and GCV were low to moderate. The male parentSAMNUT 24 is a good general combiner for plant height (3.74**) and carbohydrate content (2.79**). SAMNUT 23 is good general combiner for protein content. SAMNUT 21 is good combiner for haulm weight (215.21**), pod weight per plant (17.53**) and 100-seed weight (4.50**). The female parent SAMNUT 22 was a good general combiner for Protein content (2.95**). ICGX-SM-00020/5/P_4/$P_1$was a good

general combiner for oil content (0.87*). The crosses; SAMNUT 21 x SAMNUT 10,SAMNUT 21 x ICGX-SM-00020/5/P_4/$P_1$and SAMNUT 21 x ICGV-IS-07903 were good specific combiners for 100-seed eight, whereasSAMNUT 21 x SAMNUT 14,SAMNUT 21 x SAMNUT10 and SAMNUT 21 x ICGV-IS-07903 were the best specific combiners for oil, protein and carbohydrate content. Haulm weight and protein content were significantly negatively correlated with oil content. Haulm weight was significant and positively correlated with 100-seed weight and pod weight per plant. Path coefficient analysis revealed thatpod weight per plant,shelling percentage, carbohydrate content and protein content were the direct positive contributors to oil content.

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List of Abbreviations

FAO	Food and Agricultural Organization
U.S.A	United State of America
UNICEF	United Nations International Children Educational Fund
ICRISAT	International Crop Research Institute for Semi-Arid Tropics
SAMNUT	Samaru Groundnut
IAR	Institute for Agricultural Research
P	Parent
AOAC	Association of Official Analytical Chemist
NaOH	Sodium hydroxide
HCl	Hydrochloric acid
M	Molar
GLM	Generalised Linear Model
ANOVA	Analysis of Variance
SAS	Statistical Analysis System
Df	Degree of Freedom
MS	Means Square
EMS	Error Means Square
GCA	General Combining Ability
SCA	Specific Combining Ability
h_b^2	Broad Sense Heritability
$\mathbf{F_1}$	First Filial Generation

CHAPTER ONE

1.0 INTRODUCTION

Cultivated groundnut originated from South America Wiess (2000). It is one of the most important oil crops cultivated in more than 100 countries of the tropical, subtropical and the warm temperate regions of the world (Upadhayaya *et al*., 2012). About 38.38 million metric tonnes of groundnuts in shell are produced globally from 23.52 million hectares with an average yield of 1634 kg ha^{-1} (FAO, 2011). Its cultivation is mostly confined to the tropical countries ranging from 40^{o}N to 40^{o}S. The major groundnut producing countries are: China (18.7 Mt), India (6.8 Mt), U.S.A (4.1 Mt) Nigeria (3.8 Mt), Burma (1.9 Mt), Indonesia (1.9 Mt), Argentina (1.1 Mt), Chad (0.8Mt), Senegal (0.6Mt) and Ghana (0.4Mt) www.perfectinsider.com (2015). The species is an annual herb with two subspecies that are primarily distinguished by branching pattern and distribution of vegetative and reproductive nodes along the main stem and lateral branches. Subspecies,*hypogaea* has two botanical varieties (*hypogaea* and *hirsuta*) and subspecies *fastigiata* has four botanical varieties (*Fastigiata*, *vulgaris*, *peruviana* and *aequatoriana*) (Krapovickas and Gregory, 1994).

Groundnut (*Arachis hypogaea* L.) is the 13^{th} most important food crop and 5^{th} most important oilseed crop in the world Mondal,*et al*., (2009). The kernel is rich in oil (48-50 %) and protein (25-28 %) Pasupuleti,*et al*. (2013). Groundnut seeds are nutritional sources of vitamin E, niacin, falcin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium Stigter,*et al*. (2006). Groundnut kernels are consumed directly as raw, roasted or boiled kernels or oil extracted from the kernel is used as culinary oil. It is also used as animal feed (oil pressings, seeds, green material and straw) and industrial raw material (oil, cake and fertilizer)Tapheeand Jongur (2014). Groundnut has potential as a source of bio-fuel, but because it must compete as a source offood relative to source of oil, increase in oil production on per acre basis is essential if the crop is to be used as a source of oil for bio-fuel conversion(Wilson, 2013). Every part of the groundnut plant is used in some way: kernels for

human consumption, branches and leaves as fodder for cattle, and nitrogen fixed from its root as nutrient for the soil (Milton, 2013). Groundnut is a high value crop that can be marketed with little processing.However, it is extremely versatile and can be used in a wide range of products. Groundnut is used to make oils and it is second largest source of vegetable oils next to soybeans (Savage and Keenan, 1994). The oil can be used for cooking, as a base for confectioneries and to make groundnut butter which is used as spread for bread, biscuits, or cookies, sandwiches, candies and frostings or icings. These multiple uses of groundnut plant make it an excellent cash crop for domestic markets as well as for foreign trade in several countries (Vijaya,*et al*., 1997).

Despite the potentials of groundnut in solving hunger, malnutrition and improving the economic base of farmers and processors, poor remunerations from its cultivation and processing, due to poor quantitative and qualitative traits such as low oil content, low protein content, small seed with low oil content and other seed quality traits tends to discourage farmers and processors.Some of these constraints are social and political while others are pests, diseases and climate change. As stated by Mudenda (2013), the main constraints hampering higher yields and quality of groundnut in Africa are intermittent drought due to erratic rainfall patterns and terminal drought during maturation, with drought-related yield losses running to millions of dollars each year. It is also affected by heavy weed pressure and calcium deficiency (causing unfilled shells or pods).Mudenda (2013). The groundnut crop is affected by several diseases like leaf spots, collar rot, rust, bud necrosis, stem necrosis rosette virus*(*Reddy,*et al.,* 2011).

Groundnut oil is an excellent cooking medium because of its high smoking point (231^{o}C) (Singh and Diwakar, 1993). Vegetable oils are in high demand due to diseases associated with fat from animal origin. About two-thirds of the total groundnut production is crushed for oil and the remaining one-third is used in confectionery products,thus improvement in oil

content and quality is of interest to plant breeders and millers (Sarvamangala,*et al.*, 2011).With increasing consumer demand for edible oil of good quality, there is a need to investigate and understand various factors that influence groundnut oil content and quality (Dwivedi,*et al.,* 1993). Average protein content is higher than that of eggs, dairy products, meat and fish and the digestibility of groundnut protein is very high (Singh and Singh, 1991). Kernel protein is an important factor affecting seed quality and thus a key determinant of both end use and market value in confectionery groundnut (Wang,*et al*., 2011) and (Atasie,*et al*., 2009). Groundnut protein is increasingly becoming important as food and feed sources, especially in developing countries where protein from animal sources are not within the means of the majority of the populace.

Most works on groundnut oil are on the quality parameters such as fatty acid profile, high oleic/linoleic acid ratio (O/L), while information on the inheritance of oil content and other seed quality traits such as protein and carbohydrate content are scanty. Information on the mode of inheritance of oil content will provide an important guidance for breeding of high oil groundnut cultivar. Information on the genetic makeup of seed quality traits and their exploration through hybridization and selection is vital. Therefore considerable effort should be geared towards identifying germplasmwith good oil, protein and carbohydrate content, with a view of introgressing these traits (oil, protein and carbohydrate content) into cultivated genotypes with good and desirable agronomic traits for improved productivity and acceptability of Nigerian groundnut in the world market for a sustainable agricultural development.

In the light of the aforementioned, the research was carried out with the following objectives:

1. To determine the mode of gene action controlling the inheritance of oil content and other agronomic traits in groundnut
2. To estimate the heritability of oil content and other agronomic traits in groundnut

3. To assess the association betweenoil content and other agronomictraits.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Origin, Domestication and Distributionof Groundnut

Groundnut is native to the Western Hemisphere. It probably originated in South America, the centre of origin most likely being Brazil, where about 15 wild species are found (Acquaah, 2007). The Spanish explorers are credited with its spread throughout the New World. They introduced it to Europe from where traders spread it to Asia and Africa. Groundnut reached North America via the slave trade. Commercial production of groundnuts in the USA began in about 1876. The demand for the crop increased after the civil war, transforming it from a regional (southern) food to a national food. Production came to the Cotton Belt after 1900 (Acquaah, 2007). The expansion of the groundnut industry was driven by advances in technology that resulted in the development of equipment and machinery for planting, harvesting, and processing the crop. (Acquaah, 2007).

The genus *Arachis* is naturally restricted to Argentina, Bolivia, Brazil, Paraguay and Uruguay in South America. Both Krapovickas (1969) and Gregory,*et al* (1980) postulated a planalto profile from Corumba to Joazeiro, Brazil as the centre from which distribution of *Arachis* occurred. Cultivated groundnut most probably originated in the region of southern Bolivia and northwestern Argentina (Krapovickas, 1969), which is an important centre of diversity of subsp. *hypogaea*. A few forms of subsp. *fastigiata*, certain wild diploid annuals such as *A. duranensis*. *A. monticola*, considered to be the probable ancestors of *A. hypogaea* Singh (1988) also occur naturally in this area. It has been suggested that *A. duranensis* (with A genome) and *A. batizocoi* (with B genome) initially evolved into the wild tetraploid *A. monticola* through amphidiplodization, which on domestication gave rise to the cultivated *A. hypogaea*(Smartt,*et al*., 1978 and Singh 1986).

In South America, where the greatest diversity is found, Krapovickas (1969) and Gregory and Gregory (1976) recognized the Chaco region between southern Bolivia and north-western Argentina as the primary centre of diversity and another six regions as secondary centres of diversity for cultivated groundnut.

On the basis of presence of distinct landraces found during further exploration in Ecuador, Singh and Simpson (1994) recently have added Ecuador as another secondary centre of diversity. Most authorities believe that in the late 15th century the Portuguese carried two-seeded groundnut varieties from the east coast of South America (Brazil) to Africa, to the Malabar Coast of south-eastern India and possibly to the Far East(Fuccillo,*et al.* 2007). The Spaniards in the early 16th century took three-seeded Peruvian types (including *hirsuta*) to Indonesia and China up to Madagascar from the west coast of South America via the western Pacific. By the middle of the 16th century, groundnut made its way to North America from Africa as well as from the Caribbean islands, Central America and Mexico and was distributed worldwide. By the 19th century, groundnut became an important crop in West Africa, India, China and the USA(Fuccillo,*et al.* 2007). Among these new areas of introduction, Africa is considered a tertiary centre of diversity. Although various types of groundnut introduced into Africa came from a single centre in South America, near Bolivia, there exists a significant variability in the continent. Similarly, India and China, with long histories of groundnut cultivation and landraces, are considered as important centres of diversity (Fuccillo,*et al.*2007).

2.2 Botany

Groundnut (*Arachis hypogaea)* belongs to the family *fabaceae,* subfamily *papilionacea,* tribe *aeschynomeneae,* subtribe *Stylosanthinae.* This genus is morphologically well defined and distinguished from other genera by having a peg and geocarpic reproductive growth. The genus *Arachis* has more than 70 wild species, of which only *Arachis hypogaea* L. is

domesticated and cultivated (*Encyclopaedia of life Support System* (EOLSS)). Groundnut is an allotetraploid (2n = 2x = 40) with "AA" and "BB" genomes. All species, except the cultivated species (*A. hypogaea* and *A. monticola*) in section *Arachis*, and certain species in section *Rhizomatosae*, are diploid (2n = 2x = 20). The diploid progenitors, *A. duranensis* and *A. ipaensis*, contributed "AA" and "BB" genomes, respectively, to the cultivated groundnut (Kochert,*et al*., 1996). The phylogenetic analyses based on intron sequences and microsatellite markers also provide evidence for this hypothesis (Moretzsohn,*et al*., 2012).

2.3Variation in Oil and Protein Content,of Groundnut Kernel

About two-third of world production is crushed for oil and the remaining one-third is consumedas food. In Indiaabout 80 per cent of total groundnut production is crushed for the extraction of oil. Hence, improvement in oil yield and quality is of interest to plant breeders and millers (Motagi *et al.*, 2000). The oil content of groundnut has been reported to range from 35.8 % to 54.2 % and average near 45 %(Jambunathan,*et al.*, 1985), Dwivedi,*et al.*(1990), and (Pancholy *et al*, 1978). Rajgopal,*et al.* (2000) evaluated 118 bold seeded accessions for 2 years at The National Research Centre on Groundnut (NRCG), Gujarat, India and reported range of oil content form 48 % (M 13) to 51.4 % (NRCG 839). Significant difference for oil content was observed among test genotypes (Manivel,*et al.*, 2000), oil content was highest in PBS -11039(53.8) and thelowestinPBS-29036(47.3).Gupta,*et al.* (1982) tested twenty-five varieties of groundnut in different advanced trials and analysed for oil content. There was very little variation in oil content. The variety 'Sel 6' recorded the highest oil content of 48.60 % followed by 13-10 (48.54%). But, the lowest oil content of 44.52 % was recorded in OG 52-1.The quality requirement of confectionery groundnut is more stringent and distinctly different from groundnut as oil seed crop like bold seed, high protein and low oil (Wang,*et al*., 2011). Kernel protein is important factor affecting quality and thus a key determinant of both end use and market value in confectionery groundnut.

Since groundnut is gaining importance as a snack food, improving nutritional qualities like protein content along with yield will have added benefits and may improve income of farming community.

Variability for oil and protein in kernel had been reported in groundnut by many authors; Evaluating 17 groundnut cultivars of Karnataka for nutritional traits(Ajay,*et al*. 2012) noted that average oil content was 46% and it ranged from 40.9 to 51.5%, while the mean of protein content was 25.5% and it ranged from 22.2 to 30.3%. Quality analysis of seed samples of 152 groundnut genotypes showed that the protein and oil content ranged from 18.93 % to 30.22% and 55.66% respectively (Wang, *et al*., 2011). (Atasie,*et al.*, 2009) recorded a crude protein of 38.61% in defatted groundnut.

2.4 Combining Ability and Gene Action

Combining ability of inbred lines is the ultimate factor determining future usefulness and commercial potential of the lines for hybrids. Combining ability initially was a general concept considered collectively for classifying an inbred line relative to its cross performance. Sprague and Tatum (1942) refined the concept of combining ability, and the two expressions of general (GCA) and specific (SCA) combining ability have had a significant impact on inbred line evaluation and population improvement in maize breeding.

Combining Ability refers to the ability of a parent to transmit desirable performance to its progeny or crosses. The term 'general combining ability' is used to designate theaverage performance of a line in hybrid combination. The term 'specific combining ability' is used to designate those cases in which certain combinations dorelatively better or worse than would be expected on the basis of the average performance of the lines involved. Combining Ability analysis helps in the evaluation of inbred in terms of their genetic value and in the selection of suitable parents for hybridization Griffing (1956).

Several works have been conducted on combining ability and gene action on groundnut indicating thatboth additive effects (GCA) and non-additive effects (SCA) were important indetermining oil content, in studies measuring F_1 populations (Sykes and Michaels, 1986; Isleib,*et al*., 2004) and an F_2 population (Layrisse,*et al*., 1980). The performance of parental lines was generally a good predictor of hybrid oil content (Layrisse,*et al*., 1980; Isleib,*et al*., 2004).Makne and Bhale (1987) in a 10 x 10 diallelcombining ability analysis in groundnut showed predominantrole of additive gene action in the inheritance of pod yieldper plant and non-additive gene action in the inheritance ofoil per cent. Bansal,*et al.* (1992) and Skyes and Michaels (1986)in combining ability studies in groundnut observedimportance of additive gene action in the inheritance of oilper cent. Contrary to this Reddy and Murthy (1994) reportedthe importance of both additive and non-additive gene actionsin the inheritance of oil per cent. Francies andRamalingam (1999) revealed the predominance of non-additive gene action for number of pegs, number of maturepods, pod yield and kernel yield and the role of both additiveand non-additive gene action for oil per cent in 24 F_1s ofinter-specific crosses. Manivel,*et al.* (2000) studied geneaction in crosses made by line x tester analysis fashion withfour Virginia genotypes and reported the predominance ofnon-additive gene action in the inheritance of number andweight of mature pods and sound kernel. Parmar,*et al.* (2000)revealed the significance of both gcaand scavariance forpod yield, shelling percentage and 100-kernel weight. Varman and Raveendran (1996) studied combining ability in 30 F_1sfor five traits and reported the predominance ofsca variancethan gcavariance for number of mature pods, pod yield,shelling out turn and oil content whereas reverse is the truefor kernel weight. Ali,*et al.* (2001) reported significant roleof sca estimates for oil content and pod length, but themagnitude of gca was greater for maturity index and 100-seed weight. Dasaradha and Suneetha (2004) reported thathigher specific combining ability variance than generalcombining ability variance for oil per cent and kernel yieldper plant. They also

observed higher gcavariance for numberof pods per plant, pod yield per plant and harvest index. Hariprasanna,*et al.* (2008) reported thatin the F_1 hybrids including reciprocals from a six parentdiallel cross along with parents on five quality traits in groundnut*viz.* shelling out turn, 100-pod weight, 100-seed weight,count and proportion of sound mature seeds were regulatedpredominantly by additive gene action suggestingpossibility of early generation selection, while non-additivegene action also plays an equally important role in thecontrol of seed size. Jivani *et al.* (2012) in a combining ability study of 8 x 8diallel set reported significant estimates of gca and sca forall the traits *viz.* , 100-kernel weight, number of pods, soundmature kernel, shelling out turn, kernel yield per plant, podyield per plant.

2.5 Heritability

Genes are not expressed in a vacuum but in an environment. A phenotype observed is an interaction between the genes that encode it and the environment in which the genes are being expressed. Plant breeders typically select plants based on the phenotype of the desired trait, according to the breeding objective. Sometimes, a genetically inferior plant may appear superior to other plants only because it is located in a more favourable region of the soil. This may mislead the breeder. In other words, the selected phenotype will not give rise to the same progeny. If the genetic variance is high and the environmental variance is low, the progeny will be like the selected phenotype. The converse is also true. (Acquaah, 2007). Narrow sense heritability is a measure of the ratio of additive genetic variation to phenotypic variation in a given population for a given trait. While Broad sense heritability is estimated using the total genetic variance.Mohammed (2010) stated that broad sense heritability is based on all kinds of gene action while narrow sense heritability is estimated based on additive portion of genen action only. While heritability in the broad sense indicates whether there is sufficient genetic variation in the population to allow for selection, narrow sense heritability determines the degree of resemblance between relatives or individuals related by descent.As a rule, traits

with greater heritability can be modified more easily by selection and breeding than traits with lower heritability.

Several studies have been conducted on heritability in groundnut. Previous reports on the inheritance of oil concentration in groundnut have been variable with respect to the importance of genetic effects and heritability, likely due to genetic differences in genotypes used in these experiments and environmental effects. Oil content was highly heritable in studies by Martin (1967) while Tai and Young (1975) were only able to measure heritability in 5 of 11 F_2 populations. Additive effects (general combining ability) were more important than non-additive effects (specific combining ability) for determining oil concentration on a dry weight basis in studies measuring F_1 populations (Sykes and Michaels, 1986; Isleib,*et al*., 2004) and percentage oil content in an F_2 population (Layrisse,*et al*., 1980). The performance of parental lines was generally a good predictor of oil content in hybrids (Layrisse,*et al*., 1980; Isleib,*et al*,. 2004). Wilson (2013) reported that broad-sense heritability (H^2) estimates were 0.78 for cross I and 0.85 for cross II. These broad-sense heritability values are much higher than those reported by Tai and Young (1975). Isleib,*et al*. (2006) observed that most of the variation in oil content of groundnut grown in the uniform groundnut performance test was overwhelmingly environmental rather than genetic. Narrow-sense heritability (h^2) estimates were 0.53 and 0.55 for crosses I and II, respectively, indicating that additive effects and variation account for the majority of genetic control for oil concentration in these populations. A recent report indicated that narrow-sense heritabilities for oil content were very low in runner crosses (Singkham,*et al.*, 2010). Differences in heritability estimates between studies may be a function of environment, experimental or mating design, and perhaps most importantly genetic background.In diallel study by Wilson (2013) indicated that the broad-sense heritability estimates were 0.85 and 0.78 and narrow-sense heritability estimates were 0.55 and 0.53 for each of the crosses. Wilson (2013) reported a high $h^2$for oil concentration and the

trait exhibited continuous variation in a normal distribution in F_2generations. Genetic studies by Parameshwarappa, *et al*., (2008) obtained high broad sense heritability for protein content, seed size, pod yield per plant and 100-kernel weight and moderate heritability for oil content, plant height, number of primary branches, sound matured kernel, shelling percentage. Patil, *et al*., (2015) reported high broad sense heritability for oil content (96 %), days to 50 % flowering (99 %), height of main axis (96 %), number of primary branches (79 %), number of secondary branches (96 %), days to maturity (96 %), number of matured pod per plant (99 %), number of inmatured pod per plant (97 %), pod per plant (98 %), total number of kernel per plant (95 %), kernel weight per plant (98 %), 100-kernel weight per plant (98 %) and shelling percentage (91 %). Shukla and Rai (2014) evaluation of groundnut genotypes indicated broad sense heritability for oil content, oleic acid and protein content were 91.38 %, 99.45 % and 59.57 % respectively.Genetic studies of F2 population by John, et al., (2011) obtained high broad sense heritability for; oil content (45.63 %), protein content (3.91 %), sound matured kernel (20.21 %), 100-kernel weight (29.24 %), dry haulm weight (51.96 %), kernel yield (19.86 %) days to maturity (60.13 %), plant height (29.05 %), water use efficiency at 60 days after sowing (1.89 %), shelling percentage (9.17 %)and pod yield (24.95 %). The estimates of heritability in broad sense for 13quantitative traits ranged from shelling percentage(27.44%) to Seed index (98.11 %). Higher estimates ofheritability were observed for characters like Seed index(98.11 %), Days to 50% flowering (82.63%), Sound matured kernels (81.80%), Plant height (80.00%), Seed yield per plant (72.73%), Kernel yield (72.63%), Pod yield per plant (70.56%), Pod yield (67.03%). Moderate estimates of heritability were observed for characters like Kernel uniformity (57.46%), Days to maturity (54.89%), Number of primary branches (51.34%), Field emergence (33.59%). The low estimate of heritability was observed for character like shelling percentage (27.44%), as reported by Maurya, *et al.* (2014). Azharudheen and Gowda (2013) indicated that genetic

variability components revealed lowto moderate magnitude of variation (PCV, GCV) andgenetic advance with very high heritability for protein but lower magnitude of variation with higherheritability andlower genetic advance for oil contentin individual seasons.

2.6 Correlation between Oil Content, Yield and other Agronomic Traits

Correlation coefficient analysis helps to determine the nature and degree ofrelationship between any two or more measurable characters. In terms of response to selection, genetic correlation is what is useful. When it exists, selection for one trait will cause a corresponding change in other traits that are correlated (Acquaah 2007). He further explained that correlation between characters may exist due to various reasons such as pleiotropy, and genetic linkage. An understanding of the direction and extent of association of the component characters with economic yield is an essential prerequisite for formulating best selection strategy in breeding programme. Kotzamanidis,*et al*. (2006) noted that correlation between the most important traits showed that the most significant correlation was found between 100-seed weight and 100-pod weight in total plants (0.86) and in cross type virginia x Spanish (0.89). Assessment of genetic variability and correlation of important nutritional quality traits in recombinant inbred lines of groundnut, by Azharudheen, *et al*., (2013) reported positive correlation between oil content and protein content. Thakur, *et al*. (2013) reported pod per plant, sound matured kernel and kernel yield per pod were positively correlated with oil content. studies on correlation and path coefficient for traits related to water use efficiency and pod yield and its components in groundnut by, Kumara, *et al*. (2015) reported that in all the three crosses pod yield per plant was found to have high significant positive association with kernel yield per plant, oil yield, matured pod per plant, total pod per plant, shelling percentage and sound mature kernel. Sadeghi and Niyaki (2012) studied on relationship between oil yield and some seed related and agronomic traits non-drought stress and drought stress condition reported that all characters were positively correlated with oil

yield inboth conditions. Seed yield showed the highestcorrelation value with oil yield compared to other characters (r = 0.751) in both conditions.A high and positive and significant correlation (P < 0.01) was observed total number of kernels per plant, plant height and oil yield underboth conditions (r = 0.447and r = 0.457 in non-drought stress, r = 0.520 and r = 0.358 in drought stresscondition, respectively). Savaliya *et al*. (2008) and Painawadee,*et al*. (2009) observed positive and highlysignificant correlations of oil yield with total number of kernels per plant in drought stress condition. Gomes andLopez (2005),recordedpositiveandhighly significant correlation between plant height, total number of kernels per plant, total number of pods per plant andoil yield in non-drought stress condition. Positive and significant correlation (P < 0.01) wasrecorded between 100-seed weight and oil yield only in non-drought stress (r = 0.305). In both conditions,correlation between total number of kernels per plant and seed yield was a statistically significant and positive (P <0.01). Positiverelationship between 100-seed weight and oil content was statistically significant (P < 0.01) in both conditions. They also obtained statistically significant and negative correlation between oil content and seed yield in non-drought stress, while in drought stress was a statistically significantand positive. In addition, correlation betweenproteincontent and oil content was positive only in drought stress condition. Kumar,*et al*. (2013) reported that the genotypic correlation were higher than their corresponding phenotypic counterpart on all traits combination studied. It showed that oil content was positive and significantly correlated with number of matured kernel per plant (0.2420) at genotypic level. Oil content is positive and significantly correlated with pod yield per plant (0.2806 and 0.2955), shelling percentage (0.3063 and 0.3275), and sound mature kernel (0.3417 and 0.3477) at phenotypic and genotypic levels respectively. However showed no significant correlation with days to maturity, plant height, primary and secondary branches, 100-kernel weight, protein content and sucrose content respectively. Jivani, *et al*.

(2012) reported that the inter relationship estimate between pod yield and protein content, indicated a significant positive (r = 0.56), while it was negative (r = - 0.60) and significant between pod yield and oil content. In an earlier study by Dwevide, *et al*. (1990), found a highly significant negative correlation was observed between oil and protein content. Layrisee, *et al*. (1980) reported a significant but low positive genotypic association between oil and protein content. However the phenotypic correlation between these two traits in their study was non-significant. Dwevide, *et al*. (1990) also reported no association between 100-seed mass and oil or protein content. However in a post-rainy season, a significant positive phenotypic correlation between 100-seed mass and oil, and significant negative phenotypic correlation between 100-seed mass and protein content were found. Study conducted by Rao, *et al*. (1988) and Layrisse, *et al*.(1980) also reported no correlation between 100-seed mass and oil or protein content. Dwevide, *et al*. (1990) reported highly significant positive correlation (r = 0.88** to 0.99**) were observed between 100 seed mass and oil content over graded/season among 33 genotypes when analysed separately or combined over genotypes/grades/season (r = 0.98**). Noubissie, *et al*. (2012) studied heritability of protein and oil content in groundnut genotypes reported significant positive correlation (r = 0.67) between oil content and seed weight.(Narasimhulu,*et al*. 2012) and (Abhay,*et al*., 2002). revealed that pod yield per plant had significant positive association with kernel yield per plant, shelling percentage and sound mature kernel (SMK) percent Narasimhulu,*et al*., 2012). Pod yield also showed positive correlation with number and mass of seed per plant (Phadnis,*et al*., 1973); (Dholaria,*et al*., 1973), 100 seed mass (Alam,*et al*., 1985); (Chandola,*et al*., 1973) and(Liao,*et al*., 1989). Abraham (1990) reported significant positive correlation of kernel yield with pods per plant, kernels per plant, 100-kernel weight and shelling per cent in a study involving 42 bunch type groundnut varieties. Reddi, *et al*. (1991) reported a strong and positive correlation of pod yield with kernel yield, sound mature

kernels and 100-kernel weight. Correlation studies on 18 varieties of groundnut indicated significant and positive correlation of pod yield with pods per plant, shelling per cent, kernel weight and harvest index (Sharma and Varshney1995). In a study involving 35 groundnut genotypes, a strong positive correlation of pod yield and 100-kernel weight but weak negative association with shelling per cent was observed(Vasanthi,*et al*., 1998).In a study involving 15 Valencia groundnut, genotypes showed significant positive association of pod yield and kernel yield with kernels per plant and 100-kernel weight (Kavani*etal*., 2004). Chiow and Wynne, (1983) reported that fruit size was highly correlated with seed weight and both were significantly correlated with yield suggesting that selection for large fruits in this population would result in higher yield.The relationship between pod size and shelling outturn is not always positive and thus there is limited success in developing varieties bearing large pods with shelling outturn (de Godoy and Norden1981). Correlations between protein content and yield were low. Oil content was negatively correlated with yield indicating improvement in oil content could result in lower yield. Oil is the final major reserve to accumulate in seed Pattee *et al*., 1974), therefore maturity directly affects oil concentration (Baring,*et al*., 2013). Correlation study by Kwaga (2014),showed that kernel yield related significantly positive with plant height, crop vigour, number of pods plantshelling percentage and 100 Kernels weight, (r=0.399**, 0.549**, 0.695**, 0.625** and 0.283** respectively.) Plant height associated significantly and positively with crop vigour score and *Alectra* shoots number at 12 WAS (r=0.441** and 0.164* respectively). Also crop vigour exhibited appreciably positive correlation with number of Pods per plant, shelling percentage, 100 Kernels weight and haulm yield (r=0.238**, 0.325**, 0.141** and 0.189** respectively). Similarly there was significant positive correlation between number of pods per plant and shelling percentage and then 100kernels weight (r=0.461** and 0.137* respectively). Significantly positive relationship was also exhibited between shelling percentage and 100 kernels. In combined

analysis of heritability by Mohammed (2010) reported that plant height had the highest heritability score (76.68 %) followed by 100-kernel weight (64.50 %) while the least heritability estimate (6.94 %) was recorded by the number of shelling percentage and for kernel composition Lipid content (53.19 %), protein (36.95) and carbohydrate content (5.58 %).

2.7 Path Coefficient Analysis

Path analysis has been used to look at the direct and indirect relationship between different traits in groundnut as reported by several authors.Sadeghi and Niyaki (2012) reported thatconsideringrates of direct effect on oilyield,the highest value was taken from total number of kernels per plant (0.321) in non-drought stress, after that the directeffect of seed yield and 100-pod weight on oil yield were the highest and positive (0.217, 0.125, respectively).Similar results were reported in normal condition by Songsri,*et al*. (2008). In drought stress condition the highest value was taken from 100-seed weight (0.425)and after that the direct effect of seed yield and biomass were the highest and positive (0.285, 0.110,respectively). The direct effects of all characters under study were positive on oil yield in both conditions.The indirect effect total number of kernels per plant via seed yield, biomass and plant height was high and positive innon-drought stress, while in drought stress, the indirect effect 100-seed weight via alltraitswashighandpositive. However, itmay be emphasized that direct effect of total number of kernels per plant and 100- pods weight was low in droughtstress but indirect effect of this traits via seed yield and 100-seed weight was as high as its genotype correlationwith oil yield.In non-drought stress, Higher and significant correlation of oil yield with total number of kernels per plantand 100-seed weight and the highest direct contribution of total number of kernels per plant and 100-seed weight tooil yield and great indirect contribution of most of the traits via total number of kernels per plant and 100-seedweight.Patra,*et al*.(1995) reported that LAI at 50 at 70 DAS had positive andsignificant influence on number of pods per plant,

shellingpercentage, 100-kernel weight, pod yield and oil content.Varman and Raveendran (1996) in 63 F_1 populationsobserved that kernel yield had high positive direct effect onoil content and significant positive correlation. The highestdirect effect of pod yield was nullified by indirect effect ofoil content. Patil,*et al.* (2006) reported the relationship between oil content and pod yield of groundnut; oil content had negative direct effect on pod yield per plant, which indicate its inverse relation with pod yield per plant. So selection for improvement of oil content will lead to reduction in pod yield. Sah,*et al*. (2000) reported that seed yield perplant had high direct effect on pod as well as oil yield perplant. Number of mature pods per plant, 100-seed weightand oil yield per plant had high and positive association withpod yield but their direct effects were very low and theycontribute mainly through seed yield per plant.Kalmeshwer,*et al*. (2006) observed that number ofpods per plant, shelling percentage and sound mature kernelper cent had the maximum direct effect on pod yield perplant. Venkateswarlu,*et al*. (2007) revealed high positivedirect effects of kernel yield per plant, followed by specificleaf nitrogen, root length, shelling per cent, number of wellfilled and mature pods per plant on pod yield per plant.Studies of Bera and Das (2000) in 44 genotypes ofgroundnut for path coefficient analysis showed positive directcontribution of pods per plant and harvest index to the seedyield. Their correlation with seed yield is also significantand positive .So pod yield per plant and harvest index canbe used directly as selection criteria for improvement of seedyield in groundnut. Mathews,*et al.* (2000) revealed maximumdirect effect of kernel yield per plant followed by plant heighton dry pod yield per plant; hence emphasis should be givenon these characters while breeding for high yield ingroundnut.Kalmeshwer,*et al*. (2006) observed that number ofpods per plant, shelling percentage and sound mature kernelper cent had the maximum direct effect on pod yield perplant. Babariya and Dobariya (2012) reported that the path coefficient analysis revealed that the biological yield per plant (0.8497) and harvest index (0.6600) exhibited high and

positive direct effects on pod yield per plant. Whereas, kernel yield per plant (0.0949), number of pods per plant (0.0699) and days to maturity (0.0293) showed moderate and positive direct effects on pod yield per plant. Thus, these characters turned-out to be the major components of pod yield and direct selection for these traits may be rewarding for yield improvement. Similar results were also reported by Vekariya,*et al.*(2010) and Raut,*et al.*(2010). The number of mature pods per plant (- 0.0826) and 100-kernel weight (-0.0050) exerted negative direct effects towards pod yield per plant as observed earlier by Patel and Shelke (1992).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted at two locations; Institute for Agricultural Research (I.A.R) Farm, Ahmadu Bello University Samaru, Zaria (11 ^{0}11^{l}N, 7^{0} 38^{l} E), 600m above sea level in the Northern Guinea Savanna and I.A.R Irrigation Research Station Kadawa (11^{o}39^{l} N latitude, 08^{o} 02^{l} E longitude with an altitude of 469m above sea level) situated in Sudan Savannah.

3.2 Genetic Background and Description of Materials

A total of 8 genotypes with three high oil content lines as males and five high yielding but low oil content lines as femaleswere selected as parents.The genotypes were obtained from the I.A.R, Ahmadu Bello University Zaria. Detailed description of the Parental materials used in this study is given in Table 3.1. Genotypes with oil content of 50% and above are considered high oil content parents as given by Asibuo,*et. al.* (2008).

Table 3.1: Characteristics of the parents used in the study

S/No.	Variety	Oil Content	Seed source
1	SAMNUT 24	High	SAMARU
2	SAMNUT 23	High	SAMARU
3	SAMNUT 21	High	SAMARU
4	SAMNUT 22	Low	SAMARU
5	SAMNUT 14	Low	SAMARU
6	SAMNUT 10	Low	SAMARU
7	ICGX-SM-00020/5/P_4/P_1	Low	ICRISAT
8	ICGV-IS-07903	Low	ICRISAT

Source: Institute for Agricultural Research (IAR).

3.2.1 Population development

TheF_1 progenies were developed by hand pollination using North Carolina mating (NC II) (Design II mating scheme) as described by (Comstock and Robinson, 1948) at the IAR

groundnut screen house in Samaru, Zaria, Nigeria.Male and female genotypes were allocated three and six pots initially and later increasedto five and ten respectively in order to have enough crosses to generate more F_1 progenies over a period of 10-13 months. The first set of planting was done on 9thSeptember, 2013 and were staggered at 10-15 days intervals toensure synchronization of flower for hybridization.At flowering, the female parents were emasculated with forcepsin the evening, and crossings were made the following morning.

Table 3.2: Hybridization Scheme, using North Carolina design II.

♀ \ ♂	PARENT (MALES)		
PARENT(FEMALES)	1	2	3
4	X_{14}	X_{24}	X_{34}
5	X_{15}	X_{25}	X_{35}
6	X_{16}	X_{26}	X_{36}
7	X_{17}	X_{27}	X_{37}
8	X_{18}	X_{28}	X_{38}

3.2.2 Field evaluations

The fifteen F_1 hybrids, their Parents and two checks (SAMNUT 25 and SAMNUT 26) were laid out in 5 x 5 lattice design with three replications, on a single row plot of 5m long at inter and intra row spacings of 0.50m X 0.25m at the two locations;I.A.R, Ahmadu Bello University Samaru, Zariaand Kadawa during 2014/2015 dry season. All cultural practices were carried out according to I.A.R recommendations.

3.2.3 Data collection

Data were collected from five randomly selected plants per plot on the following traits:

Days to maturity (DMT): The number of days after emergence when 50% of plants have reached physiological maturity (leaves start to turn brown).

Plant height (cm): The distance from the base of the plant (ground) to the topmost leaf on the plant.

Haulm weight per plant (g): The weight ofthe plant after picking the pods from each plant after drying the plant for five days.

Number of matured pods per plant: Thenumber of healthy filled pod picked from the five randomly selected plants were counted during harvest to calculate the mean number of pods per plant.

Pod weight per plant (g): The average weight of thepods collected from five sampled plants from each plot.

Seed Yield per plant (g): The average weight of theseed collected from five sampled plants from each plot.

Pod size: Ratio of pod length to pod width on ten mature pod selected at random.

Seed size: Ratio of seed length to seed width on ten mature seed selected at random.

100 seed weight (g): This is the weight of 100-kernel for each plant

Shelling percentage: This is the ratio of kernel weight of the dry pod weight expressed as a percentage of the sampled plant.

$$\text{Shelling (\%)} = \frac{\text{Kernel weight (g)}}{\text{Pod weight (g)}} \times 100$$

Kernel yield (g/ha): Kernel yield was calculated by using the following formula;

$$\text{Kernel yield (g/ha)} = \frac{\text{Pod yield (g/ha)} \times \text{shelling (\%)}}{100}$$

Protein (%): The amountof protein per unitweight of kernelwas determined based on micro Kjeldahl method as explained below:

Carbohydrate (%): The carbohydrate content was determined as nitrogen free extract in each sample using the AOAC (1990) procedure.

Crude protein (CP) was calculated by Multiplying total percentage N by a factor as in the formular: Crude protein = 6.25 X %N (AOAC. 1990).
Where Tv = Titre value, M = Concentration of HCl (0.1M) and Sw = Sample weight
14 Atomic weight of Nitrogen and 100 = Total volume of digest.

Oil content (%): The amount of oil content was determined from 100 seed sample for each genotype.

The protein and oil content were determined by proximate analysis of groundnut kernel using AOAC (1990) procedure as explained below.

The organic matter was digested with sulphuric acid in the presence of catalyst, which rendered the action alkaline, then distilled and titrated the liberated ammonia, the digestion involves the oxidation of organic matter with sulphuric acid and reduction of nitrogen to ammonia sulphate, the distillation involves the liberation of ammonia by sodium hydroxide. The ammonia was trapped in an employed where the ammonia reacted with the boric acid in the receiving flask and the amount of excess NaOH was determined by titration with 0.1 M HCl. The resulted ammonia borate was titrated with the standard hydrochloric acid. The total percentage of N for each sample was calculated using the formular below:

$$\%N = \frac{Tv \times M \times 14 \times 100}{Sw \times aliquotVolume} \times 100$$

Lipid (Oil content) was estimated by the Soxhlet method as given by Jambunathan,*et al*. (1985) but with some modification. 5g of groundnut seeds for each sample was into fine powder with pestle and mortar, the groundnut meal was extracted with petroleum ether (60-80^{o}C) boiling point for 8 hours in Soxhlet was taken, the difference between the two determined and expressed in terms of oil percentage and the extractable was calculated using the following formular given below: % Lipids = (Weight of lipids extracted /Weight of direct sample) x 100

The weight of lipids extracted was obtained by the loss in weight of container with sample and weight of empty container.

3.3Data Analysis

3.3.1 Analyses of variances

The data collected was subjected to both separate and combined analysis of variance (ANONA) using the Generalised linear model (GLM) procedure of Statistical Analysis

system (SAS).Pairwise comparisons of means were made using Least Significant Differences (LSD).

Table 3.3: Form of ANOVA and Expected Means Square for one Location

Sources of variation	df	Mean Squares	Expected Mean Squares
Block(Replication)	$r(b-1)$		
Replication	$(r-1)$		
Genotype	$(g-1)$	M_2	$\sigma^2_e + r\sigma^2_e$
Error	$(g-1)(r-1)$	M_1	σ^2_e

$$\sigma^2_g = \frac{MS_2 - MS_1}{r}, \qquad \sigma^2_e = MS_1, \qquad \sigma^2_{ph} = \sigma^2_g + \frac{\sigma^2_e}{r}$$

Table 3.4: Form of ANOVA and Expected Means Square Combined across Locations.

Sources of variation	df	Mean Squares	Expected Mean Squares
Location	$(l-1)$		
Replication	$(r-1)$		
Replication (Location)	$l(r-1)$		
Block (Location x Replication)	$rl(b-1)$		
Genotype	$(g-1)$	M_3	$\sigma^2_e + r\sigma^2_{gl} + rl\sigma^2_g$
Genotype x Location	$(g-1)(l-1)$	M_2	$\sigma^2_e + r\sigma^2_{gl}$
Error	$l(g-1)(r-1)$	M_1	σ^2_e
Total	$rgl-1$		

Where; l = number of locations r = number of replications, σ^2_e = error variance

σ^2_g = genetic variance, σ^2_{gl} = genotype x location interaction

EMS= expected means squares, MS= observed sum of squares, df = degree of freedom.

$$\sigma_g^2 = \frac{M_3 - M_2}{rl}, \qquad \sigma_{gl}^2 = \frac{M_2 - M_1}{r}, \qquad \sigma_e^2 = MS_1, \qquad \sigma_{ph}^2 = \sigma_g^2 + \frac{\sigma_{gl}^2}{l} + \frac{\sigma_e^2}{rl}$$

3.3.2 Proportional contributions of males, females and crosses

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

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

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

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

3.3.3Estimates of variance components

The phenotypic and genotypic coefficient of variation as well as broad sense heritability were computed using the formulae given by Singh and Chaudhary (1985).

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

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

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

(c) Broad sense heritability (h_b^2 %) $= \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$

The heritability values were classified as low (<30%), moderate (30-60%) and high (>60%) according to Johnson,*et al*. (1955).

Table 3.5: Form of ANOVA for North Carolina mating design for one location.

Sources of variation	Degree of freedom	Mean squares	Expected means square
Replications	$(r-1)$		
Males	$(m-1)$	M_5	$\sigma^2_e + r\sigma^2_{fm} + rf\sigma^2_m$
Females	$(f-1)$	M_4	$\sigma^2_e + r\sigma^2_{fm} + rm\sigma^2_f$
Males x Females	$(m-1)(f-1)$	M_3	$\sigma^2_e + r\sigma^2_{fm}$
Pooled error	$(r-1)(mf-1)$	M_2	σ^2_e
Total	$(rmf-1)$	M_1	

Where; σ^2_{fm} = Variance male x female σ^2_m = Variance male σ^2_f = Variance female m = male f = female

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

$$\sigma^2_m = \frac{M_5 - M_3}{rf} \qquad \sigma^2_f = \frac{M_4 - M_3}{rm} \qquad \sigma^2_{fm} = \frac{M_3 - M_2}{r}$$

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

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

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

μ = general mean; m_i = effect of the ith male;

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

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

The linear model for analysis of variance for combined location

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

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

m_i = effect of the ith male; f_i = effect of the jth female;

$(m \times f)_{ij}$ = interaction effect; m_{ie} = male effect with environment

f_{ie} = female effect with environment e_{ijk} = error associated with each observation.

i = number of males and j = number of females.

Table 3.6: Combined analysis of variance for North Carolina mating designacross locations.

Sources of Variation	Degree of Freedom	MeanSquares	Expected Mean Square
Location	$(l-1)$		
Replication(Location)	$l(r-1)$		
Males	$(m-1)$	M_7	$\sigma^2_e + r\sigma^2_{mfl} + rf\sigma^2 ml + rl\sigma^2_{mf} + rlf\sigma^2_m$
Females	$(f-1)$	M_6	$\sigma^2_e + r\sigma^2_{mfl} + rm\sigma^2 fl + rl\sigma^2_{mf} + rlm\sigma^2_f$
Males x Females	$(m-1)(f-1)$	M_5	$\sigma^2_e + r\sigma^2_{mfl} + rl\sigma^2_{fm}$
Malesx Locations	$(m-1)(l-1)$	M_4	$\sigma^2_e + r\sigma^2_{mfl} + rf\sigma^2_{ml}$
Females x Locations	$(f-1)(l-1)$	M_3	$\sigma^2_e + r\sigma^2_{mfl} + rm\sigma^2_{fl}$
Males x Females x Locations	$(m-1)(f-1)(l-1)$	M_2	$\sigma^2_e + \sigma^2_{mfl}$
Error	$l(r-1)(mf-1)$	M_1	σ^2_e
Total	$lsrmf-1$		

l, *s*, *r*, *m*, and *f* refer to the number of locations, sets within an locations, replications,males, and females, respectively.

Where; σ^2_{fml} = Variance males x females x location σ^2_{fm} =Variance males x females, σ^2_{fl} = Variance females x males, l =Location

From the ANOVA, components of variance and their interaction with location would be estimated from the following equations:

$$\sigma^2_{fml} = \frac{M_2 - M_1}{r} \qquad \sigma^2_{ml} = \frac{M_4 - M_2}{fr} \qquad \sigma^2_{fl} = \frac{M_3 - M_2}{mr}$$

$$\sigma^2_{fm} = \frac{M_5 - M_2}{rl} \qquad \sigma^2_{m} = \frac{M_7 - M_5}{rlf} \qquad \sigma^2_{f} = \frac{M_3 - M_2}{rlm}$$

3.3.4. Estimation of general combining ability (GCA) and specific combining ability (SCA) variances

$$\sigma^2_f = \text{COV (H.S) females} = \frac{MS_f - MS_{fm}}{rlm}$$

$$\sigma^2_m = \text{COV (H.S) males} = \frac{MS_m - MS_{fm}}{rlf}$$

$$\sigma^2_{mf} = \text{COV (F.S) females} = \frac{MS_{fm} - MS_{lfm}}{rl}$$

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

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

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

σ^2_{GCA} = 2COV (H.S) average

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

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

3.3.5 Estimation of general combining ability (GCA) and specific combining ability (SCA) effects

Estimation of GCA effect

(a) females:

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

Where: $x_i..$ = Total of i^{th} females over males,

$x...$ = Ground total,

l = Number of females,

t = Number of males,

r = Number of replications

(b) males:

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

Where $x._i$ = Total of the j^{th} males over females,

$x...$ = ground total,

l = number of females

t = number of males

r = number of replications

Estimation of SCA effect

(a) male x females

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

Where; s_{ij} = Specific combining ability,

l = number of lines,

t = number of testers

r = number of replications,

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

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

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

$x...$ = Ground total of crosses

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

(a) General combining ability effect:

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

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

Where: Me = error mean square,

r = number of replications,

f = number of females,

m = number of males, $S.E$ = Standard error

(b) Similarly, significance of SCA effect:

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

Where: $Me =$ error mean square,

$r =$ number of replications

3.3.6Estimation of correlation coefficients.

Pearson's correlation coefficient were estimated using the formular given by Singh and Chaudhary (1985).

Correlation coefficient $r_{xy} = \frac{Cov(xy)}{\sqrt{\text{var}(x) \times \text{var}(y)}}$

Where: $\text{cov}(xy) =$ Correlation coefficient of character x and y

$\text{var}(x) =$ Variance of trait x,

$\text{var}(y) =$ Variance of trait y.

3.3.7Path coefficient analysis

Indicates the direct and the indirect effects of the various traits measured on oil content. The path analysis was obtained using matrix method.

CHAPTER FOUR

4.0 RESULTS

4.1 Mean Performance and analysis of variance

4.1.1 The mean performance

The mean performance of groundnut genotypes for oil content and other agronomic traits at Samaru, Kadawa and for combined data during 2014/2015 dry season are presented in Tables 4.1, 4.2 and 4.3 respectively.

At Samaru,plant height among the parents ranged from 13.05 cm to 25.46 cm with a mean height of 19.58 cm. Among the crosses, plant height ranged from 15.71 cm to 33.65 cm and SAMNUT 24 x SAMNUT 10 recorded the highest plant height(33.65 cm). Days to maturity among the parents ranged from 106 days to 124 days, with a mean of 114 days and SAMNUT 23 and SAMNUT 24 recorded the least number of days to maturity.Among the crosses, SAMNUT 24 x SAMNUT 10 recorded the shortest maturation period of 102 days and SAMNUT 21 x SAMNUT 10 recorded the longest days to maturity of 116 days with a mean of 108 days recorded by the crosses. The shortest period to maturity was recorded by the cross SAMNUT 24 x SAMNUT 10.The cross (SAMNUT 24 x SAMNUT 10) matured earlier than the early maturing check SAMNUT 26 with 109 days to maturity.Haulm weight among the parents ranged from 462.30g to 1296.00g with a mean of 714.34g. Among crosses, SAMNUT 21 x ICGV-IS-07903 recorded the highest haulm weight (1440.00g) followed by SAMNUT 21 x SAMNUT 10 (1097.3g) and least weight was recorded by SAMNUT 23 x ICGV-IS-07903 (513.70g). Pod weight per plant among the parents ranged from 40.00g to 68.33g with a mean of 51.63g. The cross SAMNUT 21 x ICGV-IS-07903 recorded the highest mean weight of 83.27g and the least was recorded by SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1 (39.29g). The crosses mean weightwas higher than the mean weight of the checks. The values for shellingpercentage, indicated that the parents SAMNUT 24 (63.35%) recorded the highest value followed by SAMNUT 23 (55.11%) and the

least was recordedby ICGX-SM-00020/5/P_4/P_1 (36.40%). Among the crosses, the shelling percentage ranged from 34.19% to 76.90% with a mean of 52.63%. 100-seed weight among the parents varied from 21.67g to 57.08g with a mean of 50.97g.Shelling percentage of the crosses ranged from 49.67g to 77.67g with a mean of 61.09g. The cross SAMNUT 21 x SAMNUT 10 gave the highest 100-seed weight that was higher than that of the best check SAMNUT 26 (54.33g). Oil content among the parental varied from 47.37% to 52.63% and SAMNUT 24 registered the highest Oil content. Among the progenies the highest oil content was recorded by SAMNUT 23 x SAMNUT 22. The best check (SAMNUT 25) recorded low oil content compared to the cross (SAMNUT 23 x SAMNUT 22). The highest protein content for the parental was recorded by SAMNUT 21 and the least by ICGX-SM-00020/5/P_4/P_1, with a mean of 29.79 %. Among the crosses,protein content ranged from 16.81 % to 37.06% and the best cross (SAMNUT 24 x SAMNUT 22) had more protein content than the best check (SAMNUT 26). Carbohydrate content varied from 1.01 % to 19.15 % among the parental with a mean of 8.58 %. The progenies,carbohydrate content ranged from 2.63 % to 25.39 % with a mean of 11.08 %.

Table 4.1 Mean performance of parents, F_1 progenies and checks for growth and yield parameters of groundnut genotypes at Samaru during 2014/2015 dry season.

Genotypes									
Parents	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant(g)	Shelling Percentage (%)	100seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 24	19.53	107	462.30	40.00	63.35	49.00	52.63	32.19	5.77
SAMNUT 23	19.85	106	526.50	45.60	55.11	53.75	51.60	25.70	9.33
SAMNUT 21	18.30	117	775.30	68.33	54.04	55.33	47.37	40.25	1.01
SAMNUT 22	20.92	114	829.70	55.67	40.27	52.33	47.37	33.25	8.35
SAMNUT 14	19.43	115	474.70	48.47	40.15	41.67	50.88	25.67	8.88
SAMNUT 10	13.05	124	563.50	44.00	41.88	52.00	50.75	21.75	13.70
ICGX-SM-00020/5/P_4/P_1	25.46	114	1296.00	49.20	36.40	46.58	47.37	21.58	19.15
ICGV-IS-07903	20.13	114	786.70	61.73	38.82	57.08	47.37	37.95	2.45
Crosses									
SAMNUT 24 x SAMNUT 22	29.63	107	651.00	50.93	48.92	49.67	47.37	37.06	4.21
SAMNUT 24 x SAMNUT 14	27.75	107	619.70	49.73	54.11	63.33	50.00	17.50	17.11
SAMNUT 24 x SAMNUT 10	33.65	102	810.00	47.20	55.92	57.67	47.37	16.81	25.39
SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1	29.08	109	769.00	39.27	76.90	53.00	47.37	23.81	18.91
SAMNUT 24 x ICGV-IS-07903	31.57	106	746.00	55.27	48.82	63.67	47.37	32.19	9.67
SAMNUT 23 x SAMNUT 22	23.29	107	633.00	52.20	34.19	56.33	52.63	32.81	2.63
SAMNUT 23 x SAMNUT 14	24.25	106	734.00	40.00	60.24	60.00	47.37	33.25	7.50

Table 4.1 Continue.

Parents	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant(g)	Shelling percentage(%)	100seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 23 x SAMNUT 10	24.18	107	617.30	45.47	53.17	61.33	47.37	36.00	5.04
SAMNUT 23 x ICGX-SM-00020/5/P_4/P_1	26.00	106	843.70	44.33	52.46	60.33	50.00	26.25	7.83
SAMNUT 23 x ICGV-IS-07903	23.43	106	513.70	49.47	43.74	58.33	50.00	20.31	14.01
SAMNUT 21 x SAMNUT 22	21.73	112	581.30	68.60	45.16	60.33	45.00	28.75	9.69
SAMNUT 21 x SAMNUT 14	22.98	108	1018.30	82.33	49.24	68.00	47.37	30.06	10.59
SAMNUT 21 x SAMNUT 10	21.21	116	1097.30	64.40	60.96	77.67	47.37	30.69	10.19
SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1	15.71	112	799.00	60.80	63.28	62.67	52.63	22.75	13.13
SAMNUT 21 x ICGV-IS-07903	24.77	110	1440.00	83.27	42.33	64.00	49.12	29.23	10.31
Checks									
SAMNUT 25	22.55	111	741.70	48.27	42.87	51.75	50.00	30.81	3.13
SAMNUT 26	20.68	109	507.70	50.33	39.28	54.33	47.37	35.25	5.87
Mean	23.26	110	753.00	53.82	49.84	57.23	48.85	28.93	9.70
LSD ($P < 0.05$)	5.83	7.00	264.00	20.25	21.98	10.86	1.18	4.87	4.33
CV (%)	15.19	4.00	21.25	22.80	26.73	11.5	1.46	10.20	27.08

Table 4.2. Presents the mean performance at Kadawa, the mean performance for plant height of parents varied from 12.78 cm to 20.00 cm and SAMNUT 10 recorded the highest value for plant height. The progenies plant height ranged from 15.11 cm to 25.33 cm. Days to maturity of the parents ranged from 106 days to 124 days with a mean of 114 days, and SAMNUT 24 recorded the lowest days to maturity.Among the progenies, days to maturity ranged from 110 days to 119 days, with a progeny mean of 114 days. Haulm weight among the parents ranged from 706.70g to 1009.00g with a mean of 844.94g.Among the crosses it varied from 648.00g to 1638.00g with a mean of 996.40g. Pod weight per plant ranged from 38.47g to 67.80g with mean pod weight of 51.12g among the parents. The cross SAMNUT 21 x SAMNUT 14 recorded the highest pod weight of 111.13g followed by SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 (105.93g) and the least pod weight was recorded by SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1 (27.40g).Shelling percentage among the parents varied from 39.18% to 99.86%, with a mean of 63.81% and SAMNUT 14 recorded the highest shelling percentage.Among the crosses it ranged from 47.72% to 86.00%, with a mean of 61.64%. 100-seed weight among the parents varied from 47.33g to 57.33g, with a mean of 51.39g and ICGX-SM-00020/5/P_4/P_1 recorded the highestvalue.The progenies had a 100-seed weight that ranged from 51.00g to 68.00g, with mean 100-seed weight of 59.48g.The best cross (SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1) outperformed the best check SAMNUT 26 (55.67g). The highest oil content among the parental was recorded by SAMNUT 24 and least value was recorded by ICGX-SM-00020/5/P_4/P_1 with a mean of 48.26. Oil content of the crosses, ranged from 45.79 % to 52.63 % and the best cross (SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1) had more oil content than the best check (SAMNUT 25). Protein content of the parents ranged from 25.94 % to 41.00 %. Among the progenies, protein content varied from 21.31 % to 34.22 % with a mean of 27.84%. The carbohydrate content among the parents ranged from 1.81 % to 14.87 % with the best parent ICGX-SM-00020/5/P_4/P_1 outperformed the best

check. While the progenies,carbohydrate content varied from 4 29 % to 19.19 % and a mean of 11.15 %.

Table 4.2 Mean performance of parents, F_1 progenies and checks for growth and yield parameters of groundnut genotypes at Kadawa during 2014/2015 dry season.

Genotypes									
Parents	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 24	17.11	113	825.70	38.47	74.59	47.33	52.63	32.25	4.58
SAMNUT 23	17.00	106	824.70	67.80	39.18	51.67	49.45	27.45	12.40
SAMNUT 21	18.22	119	883.70	67.67	62.04	55.67	45.56	41.00	1.81
SAMNUT 22	15.67	115	906.00	46.60	60.21	51.77	47.37	33.12	6.50
SAMNUT 14	15.11	115	706.70	38.62	99.86	46.33	49.12	24.50	14.84
SAMNUT 10	20.00	121	759.00	54.06	41.59	52.00	47.57	32.19	4.11
ICGX-SM-00020/5/P_4/P_1	12.78	113	844.70	45.53	62.34	57.33	47.04	25.94	14.87
ICGV-IS-07903	15.00	113	1009.00	50.20	70.69	49.00	47.37	35.25	5.87
Crosses									
SAMNUT 24 x SAMNUT 22	20.56	110	979.00	71.97	63.48	61.00	50.00	30.06	4.29
SAMNUT 24 x SAMNUT 14	25.33	113	648.00	53.60	86.00	61.00	49.12	22.83	17.22
SAMNUT 24 x SAMNUT 10	22.78	113	1233.30	53.27	45.91	52.00	50.00	20.63	19.19
SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1	25.11	114	844.70	27.40	62.71	43.63	46.58	27.99	11.55
SAMNUT 24 x ICGV-IS-07903	21.56	116	605.30	33.20	73.52	51.00	50.00	29.32	11.49
SAMNUT 23 x SAMNUT 22	22.89	110	1112.30	72.47	62.43	60.33	50.00	30.81	7.20
SAMNUT 23 x SAMNUT 14	17.78	114	972.30	70.40	60.59	66.33	47.37	29.87	5.41
SAMNUT 23 x SAMNUT 10	20.78	114	933.70	64.17	84.57	63.33	50.00	34.22	4.19

Table 4.2 Continued.

Parents	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 23 x ICGX-SM-00020/5/P_4/P_1	23.44	110	772.70	71.33	57.16	57.10	46.82	28.89	10.44
SAMNUT 23 x ICGV-IS-07903	21.89	111	880.30	62.60	70.77	61.33	47.37	21.31	13.81
SAMNUT 21 x SAMNUT 22	19.11	118	824.30	54.73	54.19	57.56	47.37	23.74	18.90
SAMNUT 21 x SAMNUT 14	18.13	113	1638.00	111.13	47.72	63.00	45.00	30.25	7.40
SAMNUT 21 x SAMNUT 10	16.00	119	1253.00	78.67	52.79	61.33	45.79	31.21	11.50
SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1	19.00	119	1252.70	105.93	49.21	68.00	52.63	23.89	11.16
SAMNUT 21 x ICGV-IS-07903	15.11	111	1283.70	80.27	53.57	65.33	47.64	25.05	13.54
Checks									
SAMNUT 25	12.78	111	772.00	58.20	52.72	54.43	50.00	30.25	3.76
SAMNUT 26	17.11	108	876.00	62.53	54.77	55.67	45.56	30.18	13.24
Mean	18.81	114	945.63	61.63	61.70	56.54	48.30	28.89	9.97
LSD ($P < 0.05$)	5.14	7.78	514.28	31.97	39.44	10.56	2.29	3.91	3.30
CV (%)	16.56	4.15	32.96	31.44	38.73	11.31	2.87	8.20	20.06

Means performance from the combined data were presented in Table 4.3.Plant height among the parents ranged from 16.53 cm to 19.12 cm with a mean of 17.98 cm. Among the crosses, plant height ranged from 17.36 cm to 28.29 cm and SAMNUT 24 x SAMNUT 10 recorded the highest plant height with a mean of 16.36 cm. Days to maturity mean performance among the parents ranged from 106 days to 124 days with a mean of 114days. The progenies, number of days to maturity ranged from 108 days to 118 days with a mean of 111 days. Haulm weight among the parents ranged from 590.70g to 1070.00g with IGCV-IS-07903 being the highest in terms of haulmyield. Among the crosses, haulm weight varied from 633.80g to 1361.80g, with a mean of 756.8 g and most ofthe crosses outperformed the best check SAMNUT 25 (756.80g). Pod weight per plant, among the parents, ranged from 39.32g to 68.00g with mean of 51.30g. Thecross SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1 (33.33g) recorded the least pod weight and highest pod weight was recorded by SAMNUT 21 x SAMNUT 14 (96.73g). Shelling percentage for the parents varied from 41.70% to 70.00%. SAMNUT 14 recorded the highest shelling percentage. The crosses shelling percentage ranged from 47.95% to 70.05%, with a mean of 57.79%. The cross SAMNUT 21 x ICGV-IS-07903 recorded high shelling percentage compared to the best checks SAMNUT 25 (47.80%). 100-seed weight among the parents, varied from 44.00g to 55.50g and highest 100-seed weight was recorded by SAMNUT 21 (55.50 g).100-seed weight of the crosses, varied from 48.32g to 69.50g with a mean of 59.97g. The cross SAMNUT 21 x SAMNUT 10 gave the highest 100-seed weight (69.50 g) that was higher than that of the best check SAMNUT 26 (55.00g). Oil content of the parental varied from 47.21 % to 52.63 % and SAMNUT 24 gave the highest oil content (52.63 %). Among the progenies, the highest oil content was recorded by SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1(52.63 %) which outperformed the best check (SAMNUT 25). SAMNUT 21 (40.63%) recorded the highest protein content and the least was recorded by ICGX-SM-00020/5/P_4/P_1(23.76 %), with a mean of 30.63%. The crosses protein content ranged from 18.78 % to 33.56 %. The best cross (SAMNUT

x SAMNUT 22) had more protein content than the best check (SAMNUT 26). Carbohydrate content varied from 1.41 % to 17.01 % among the parental with a mean of 8.35 %. Among the progenies carbohydrate content ranged from 4.25 % to 22.29 % with a mean of 11.12 %.

Table 4.3 Mean performance of parents, F_1 progenies and checks for growth and yield parameters from combined data during 2014/2015 dry season.

Genotypes									
Parents	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 24	18.32	110	644.00	39.23	68.97	48.17	52.63	32.22	5.18
SAMNUT 23	18.43	106	654.30	55.11	48.28	52.86	50.53	26.58	10.86
SAMNUT 21	18.26	118	829.50	68.00	58.04	55.50	46.47	40.63	1.41
SAMNUT 22	18.30	115	867.80	51.13	50.24	52.05	47.37	33.19	7.43
SAMNUT 14	17.27	115	590.70	43.54	70.00	44.00	50.00	25.08	11.86
SAMNUT 10	16.53	122	680.80	50.04	41.70	52.00	49.16	26.97	8.91
ICGX-SM-00020/5/P4/P1	19.12	113	1070.30	47.37	49.37	51.96	47.21	23.76	17.01
ICGV-IS-07903	17.57	113	897.80	55.97	54.76	53.04	47.37	36.60	4.16
Crosses									
SAMNUT 24 x SAMNUT 22	25.10	108	815.00	61.45	56.20	55.33	48.69	33.56	4.25
SAMNUT 24 x SAMNUT 14	26.54	110	633.80	51.67	70.05	62.17	49.56	20.17	17.16
SAMNUT 24 x SAMNUT 10	28.22	108	1021.70	50.23	50.91	54.83	48.69	18.72	22.29
SAMNUT 24 x ICGX-SM-00020/5/P4/P1	27.10	112	806.80	33.33	69.81	48.32	46.98	25.90	15.23
SAMNUT 24 x ICGV-IS-07903	26.57	111	675.70	44.23	61.17	57.33	48.69	30.75	10.58
SAMNUT 23 x SAMNUT 22	23.09	109	872.70	62.33	48.31	58.33	51.32	31.81	4.92
SAMNUT 23 x SAMNUT 14	21.02	110	853.20	55.20	60.42	63.17	47.37	31.56	6.45
SAMNUT 23 x SAMNUT 10	22.48	111	775.50	54.82	68.87	62.33	48.69	35.11	4.62
SAMNUT 23 x ICGX-SM-00020/5/P4/P1	24.72	108	808.20	57.83	54.81	58.72	48.41	27.57	9.13

SAMNUT 23 x ICGV-IS-07903	22.66	109	697.00	56.03	57.26	59.83	48.69	20.81	13.91

Table 4.3 Continued.

Parents	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 21 x SAMNUT 22	20.42	115	702.80	61.67	49.67	58.95	46.19	26.25	14.30
SAMNUT 21 x SAMNUT 14	20.56	111	1328.20	96.73	48.48	65.50	46.19	30.16	9.00
SAMNUT 21 x SAMNUT 10	18.61	118	1175.20	71.53	56.87	69.50	46.58	30.95	10.85
SAMNUT 21 x ICGX-SM-00020/5/P4/P1	17.36	116	1025.80	83.37	56.25	65.33	52.63	23.32	12.15
SAMNUT 21 x ICGV-IS-07903	19.94	111	1361.80	81.77	47.95	64.67	48.38	27.14	11.93
Check									
SAMNUT 25	17.67	111	756.80	53.23	47.80	53.09	50.00	30.53	3.45
SAMNUT 26	18.90	108	691.80	56.43	47.03	55.00	46.47	32.72	9.56
Mean	21.04	112	849.31	57.72	30.24	56.88	48.57	28.91	9.83
LSD ($P < 0.05$)	5.485	7.26	408.77	26.76	31.93	10.71	1.82	4.42	3.85
CV (%)	15.88	3.94	29.17	28.09	34.69	11.41	2.28	9.26	23.73

Table 4.4 presents the resultsacross locations.Plant height, showed that the parent ICGX-SM-00020/5/P_4/P_1 (25.46cm)is the best performing genotype at Samaru while at Kadawa SAMNUT 10 (20.00cm) is the best. Among the crosses, it ranged from 15.11cm to 33.65cm and the tallestcross at Samaru was SAMNUT 24 x SAMNUT 10 (33.65 cm) and at Kadawa, it was SAMNUT 24 x SAMNUT 14 (25.53 cm).Oil content of the parents ranged from 45.56% to 52.63% and SAMNUT 24 is the best performing parent at both locations with a mean value of 52.63%.Amongthe crosses, plant height ranged from 45.00% to 52.63%, and the best crosses at Samaru were SAMNUT 23 x SAMNUT 22 and SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 (52.63%). At Kadawa the progeny with the highest oil content was SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 (52.63). The best check SAMNUT 25 across locations gave low oil content compared to the best parent and cross.Protein content, SAMNUT 21,has the highest protein content among the parents at both locations with a range and mean of 21.58% to 40.25% and 30.63% respectively.Among the progenies protein content ranged from 21.58% to 41.00%. Carbohydrate content of the parents ranged from 1.01% to 19.15%,and ICGX-SM-00020/5/P_4/P_1 recorded the highest carbohydrate contentacrossthe two locations.Carbohydrate content of the crosses ranged from 2.63% to 25.39%.

Table 4.4. Mean performance of parents, F_1 progenies and checks for growth and yield parameters across locations during 2014/2015 dry season.

Genotypes	Plant height (cm)			Oil content (%)			Protein content (%)			Carbohydratecontent (%)		
Parents	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean
SAMNUT 24	19.53	17.11	18.32	52.63	52.63	52.63	32.19	32.25	32.22	5.77	4.58	5.18
SAMNUT 23	19.85	17.00	18.43	51.60	49.45	50.53	25.70	27.45	26.58	9.33	12.40	10.86
SAMNUT 21	18.30	18.22	18.26	47.37	45.56	46.47	40.25	41.00	40.63	1.01	1.81	1.41
SAMNUT 22	20.92	15.67	18.30	47.37	47.37	47.37	33.25	33.12	33.19	8.35	6.50	7.43
SAMNUT 14	19.43	15.11	17.27	50.88	49.12	50.00	25.67	24.50	25.08	8.88	14.84	11.86
SAMNUT 10	13.05	20.00	16.53	50.75	47.57	49.16	21.75	32.19	26.97	13.70	4.11	8.91
ICGX-SM-00020/5/P_4/P_1	25.46	12.78	19.12	47.37	47.04	47.21	21.58	25.94	23.76	19.15	14.87	17.01
ICGV-IS-07903	20.13	15.00	17.57	47.37	47.37	47.37	37.95	35.25	36.60	2.45	5.87	4.16
Crosses												
SAMNUT 24 x SAMNUT 22	29.63	20.56	25.10	47.37	50.00	48.69	37.06	30.06	33.56	4.21	4.29	4.25
SAMNUT 24 x SAMNUT 14	27.75	25.33	26.54	50.00	49.12	49.56	17.50	22.83	20.17	17.11	17.22	17.16
SAMNUT 24 x SAMNUT 10	33.65	22.78	28.22	47.37	50.00	48.69	16.81	20.63	18.72	25.39	19.19	22.29
SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1	29.08	25.11	27.10	47.37	46.58	46.98	23.81	27.99	25.90	18.91	11.55	15.23
SAMNUT 24 x ICGV-IS-07903	31.57	21.56	26.57	47.37	50.00	48.69	32.19	29.32	30.75	9.67	11.49	10.58
SAMNUT 23 x SAMNUT 22	23.29	22.89	23.09	52.63	50.00	51.32	32.81	30.81	31.81	2.63	7.20	4.92
SAMNUT 23 x SAMNUT 14	24.25	17.78	21.02	47.37	47.37	47.37	33.25	29.87	31.56	7.50	5.41	6.45
SAMNUT 23 x SAMNUT 10	24.18	20.78	22.48	47.37	50.00	48.69	36.00	34.22	35.11	5.04	4.19	4.62

Table 4.4. Continued…

Genotypes	Plant height (cm)			Oil content (%)			Protein content (%)			Carbohydrate content (%)		
Parents	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean	Samaru	Kadawa	Mean
SAMNUT 23 x ICGX-SM-00020/5/P_4/P_1	26.00	23.44	24.72	50.00	46.82	48.41	26.25	28.89	27.57	7.83	10.44	9.13
SAMNUT 23 x ICGV-IS-07903	23.43	21.89	22.66	50.00	47.37	48.69	20.31	21.31	20.81	14.01	13.81	13.91
SAMNUT 21 x SAMNUT 22	21.73	19.11	20.42	45.00	47.37	46.19	28.75	23.74	26.25	9.69	18.90	14.30
SAMNUT 21 x SAMNUT 14	22.98	18.13	20.56	47.37	45.00	46.19	30.06	30.25	30.16	10.59	7.40	9.00
SAMNUT 21 x SAMNUT 10	21.21	16.00	18.61	47.37	45.79	46.58	30.69	31.21	30.95	10.19	11.50	10.85
SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1	15.71	19.00	17.36	52.63	52.63	52.63	22.75	23.89	23.32	13.13	11.16	12.15
SAMNUT 21 x ICGV-IS-07903	24.77	15.11	19.94	49.12	47.64	48.38	29.23	25.05	27.14	10.31	13.54	11.93
Checks												
SAMNUT 25	22.55	12.78	17.67	50.00	50.00	50.00	30.81	30.25	30.53	3.13	3.76	3.45
SAMNUT 26	20.68	17.11	18.90	47.37	45.56	46.47	35.25	30.18	32.72	5.87	13.24	9.56
Mean	23.26	18.81	21.04	48.85	48.30	48.57	28.93	28.89	28.91	9.70	9.97	9.83
LSD ($P < 0.05$)	5.83	5.14	5.485	1.18	2.29	1.82	4.87	3.91	4.42	4.33	3.30	3.85
CV (%)	15.19	16.56	15.88	1.46	2.87	2.28	10.20	8.20	9.26	27.08	20.06	23.73

4.1.2 Analysis of variance for groundnut genotypes during 2014/2015 dry season.

The analysis of variance for data from Samaru, Kadawa and combined data are presented in Tables 4.5, 4.6 and 4.7 respectively. At Samaru the means squares from the genotypes showed highly significant difference ($P \leq 0.01$) for all traits except,shelling percentage was not significant. At Kadawa highly significant differences ($P \leq 0.01$) were observed among the genotypes for plant height, 100-seed weight, oil content, protein content and carbohydrate content. Significant difference ($P \leq 0.05$) was shown for pod weight per plant.From combined data highly significant difference ($P \leq 0.01$) were observed among the traits studied exceptshellingpercentage.

Table 4.5 Mean squares from ANOVA for oil content and agronomic traits of groundnut genotypes at Samaru during 2014/2015 dry season.

Sources of variations	DF	Plant height(cm)	Days to maturity	Haulm weight(g)	Pod weight per plant (g)	Shelling percentage(%)	100seed weight(g)	Oilcontent (%)	Proteins content(%)	Carbohydrate content(%)
Block(Rep)	12	10.66	34.66*	202014.00**	320.09*	74.25	54.05	0.65	7.14	3.95
Rep	2	11.71	9.82	638535.21**	72.70	76.71	39.97	57.46**	63.67**	49.44**
Genotype	24	51.71**	50.61**	89715.57**	406.98**	295.29	130.31**	11.58**	103.49**	83.25**
Error	36	12.48	16.46	25595.58	150.54	177.47	43.34	0.51	8.71	6.89

* and ** = significant at 0.05 and 0.01 probability levels respectively

Table 4.6 Mean squares from ANOVA for oil content and agronomic traits of groundnut genotypes at Kadawa during 2014/2015 dry season.

Sources of variations	DF	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage(%)	100Seed weight (g)	Oilcontent (%)	Proteins content(%)	Carbohydrate content(%)
Block(Rep)	12	13.90	37.71	75803.97	560.03	881.52	23.52	0.75	9.44	9.09
Rep	2	22.69	1.82	1947467.00**	3059.84**	1894.26*	128.52	60.29**	64.98**	46.86**
Genotype	24	40.22**	39.57	151520.60	837.74*	556.76	107.22**	11.78**	59.42**	65.32**
Error	36	9.71	22.24	97131.99	375.41	571.27	40.92	1.92	5.61	4.00

* and ** = significant at 0.05 and 0.01 probability levels respectively.

Table 4.7 Mean squares from ANOVA for Oil content andAgronomic traits of groundnut genotypes from combined analysis during 2014/2015 dry season.

Sources of variation	DF	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Proteins content (%)	Carbohydrate content (%)
Locations	1	665.51**	512.62**	1156970.00**	2431.05**	4866.92**	22.39	10.34**	0.03	3.07
Genotype*Locations	24	24.27*	18.64	69234.97	262.48	510.93	44.64	4.75**	19.77**	22.70**
Genotype	24	68.67**	73.53**	172157.50**	982.86**	364.18	192.99**	18.55**	143.35**	125.57**
Block(Rep*Locations)	24	12.28	36.19*	138909.00**	440.06*	477.89	38.78	0.70	8.29	6.52
Error	72	11.10	19.35	61363.79	262.97	374.37	42.13	1.21	7.16	5.44

* and ** = significant at 0.05 and 0.01 probability levels respectively.

4.2 Variance component estimate.

The variance component estimates are presented in Table 4.8. The Phenotypic variance (σ^2_{ph}) values recorded were higher than the Genotypic variance (σ^2_g) for all the traits studied. Phenotypic coefficient of variation (PCV) is higher than thegenotypic coefficient of variation (GCV). Moderate broad sense heritability estimates were recorded for plant height (39.27), days to maturity (42.74), haulm weight (37.42), podweight per plant (42.29), 100-seed weight (43.46), oil content (42.65), protein content (46.30) and carbohydrate content (45.03). Low broad sense heritability was recorded forshelling percentage (-67.49). Narrow sense heritability, moderate values were recorded for plant height (50.69), haulm weight (38.29) and pod weight per plant (44.69). days to maturity (26.17), shelling percentage (15.07), 100-seed weight (28.78) and oil content, recorded low narrow sense heritability. However protein content (-7.89) and carbohydrate content (-11.63) recorded negative narrow sense heritability respectively.

Table 4.8. Variance components for oil content and agronomic traits of groundnut genotypesfrom combined data during2014/2015 dry season.

Traits	σ_g^2	σ_e^2	σ_{ph}^2	h_b^2	h_n^2	Genotypic coefficient of variation (%)	Phenotypic coefficient ofvariation (%)
Plant height	7.40	11.10	18.84	39.27	50.69	12.93	20.64
Days to maturity	9.15	19.35	21.40	42.74	26.17	2.71	4.14
Haulm weight	17153.76	61363.79	45846.68	37.42	38.29	15.42	25.21
Pod weight per plant	120.06	262.97	283.87	42.29	44.69	18.98	29.19
Shelling percentage	-24.46	374.37	36.24	-67.49	15.07	0.00	10.79
100 seed weight	24.72	42.13	56.89	43.46	28.78	8.74	13.26
Oil content	2.30	1.21	5.39	42.65	14.03	3.12	4.78
Protein content	20.60	7.16	44.49	46.30	-7.89	15.70	23.07
Carbohydrate content	17.14	5.44	38.07	45.03	-11.63	42.11	62.75

σ_g^2 =Genotypic variance, σ_e^2 = Environmental variance, σ_{ph}^2 = phenotypic variance, h_b^2 = Broad sense heritability, h_n^2 = Narrow sense heritability.

4.3 Analysis of Variance for Design IIand Combining ability variances.

Mean squares for Design II are presented in Table 4.9.The general combining ability estimates among the male parents (GCAm), showed highly significantdifference ($P < 0.01$) forhaulm weight. Significant difference($P < 0.05$) of GCAm were shown for days to maturity, pod weight per plant, oil content, protein content and carbohydrate content. The general combining ability estimates among the female parents (GCAf) exhibited significant difference for days to maturity and carbohydrate content only. Highly significant difference ($P < 0.01$)were exhibited for Specific Combining Ability estimates of the crosses for protein and carbohydrate content only. Estimates of specific combining ability (SCA) recorded significant difference fordays to maturity and haulm weight was recorded. The general combining ability estimates among the male parents as influenced by the environment (LOC*GCAm) showed highly significant difference for plant height,while significant difference ($P < 0.05$) was obtained for pod weight per plant. The specific combining ability estimates among the crosses as influenced by the environmentshowed significant difference ($P < 0.05$) for pod weight per plant.However other traits showed no significant difference.

Table 4.9. North Carolina design II means squares for oil content and agronomictraits of groundnut genotypes during 2014/2015 dry season.

Sources of variations	Df	Plant height(cm)	Days to maturity	Haulm weight(%)	Pod weight per plant (%)	Shelling percentage(%)	100 seed weight (g)	Oil content(%)	Protein content(%)	Carbohydrate content(%)
LOC	1	504.66**	522.44**	1465469.99**	1917.93**	2388.45**	14.70	62.57	17.07	10.67
Rep(LOC)	3	18.19**	23.48*	744713.88**	643.21**	402.94*	58.47	45.67*	18.04	23.67**
GCAm	2	140.60	64.36*	461046.82**	2220.92*	143.02	208.64	40.05*	59.66*	89.51*
GCAf	4	3.21	14.47*	34894.65	72.49	283.02	19.50	37.35	59.29	44.51*
SCA	8	5.49	17.75*	68446.14*	181.08	120.60	33.44	26.78	62.40**	63.70**
LOC*GCAm	2	37.46**	4.04	8391.53	342.31*	266.92	72.65	2.63	5.98	8.21
LOC*GCAf	4	9.74	2.47	36373.18	134.76	122.04	29.03	31.26	21.96	11.24
LOC*SCA	8	3.35	4.83	29283.77	78.33*	115.93	34.05	15.38	4.27	6.51
Error	56	4.47	8.90	31829.83	109.35	153.62	27.53	17.44	11.20	5.51

* and ** = significant at 0.05 and 0.01 probability levels respectively.

4.3.1 Component of general combining ability variance (σ^2_{GCA}) and specific combining ability variance (σ^2_{SCA})

The general combining ability variance (σ^2_{GCA})and specific combining ability variance (σ^2_{SCA})are presented in Table 4.10. Thespecific combining ability variance were greater than general combining ability variance for all the traits except plant height. The ratios of general combining ability variance to specific combining ability variance for all the traits were less than unity except for plant height.

4.3.2 Proportional contributions of males and females

The proportional contributions of male parents and female parentsto the variations in total sums of squares of progenies for oil content and agronomic traits is presented in Table 4.11 and pictorially in Figure 1. As shown by the representations, the male parents contributed significantly to the variances observed on plant height, days to maturity, haulm weight, pod weight per plant and 100-seed weight and carbohydrate content indicating the predominance of paternal effects for these traits. The female parentscontributed more variations in shelling percentage, oil content and protein content.

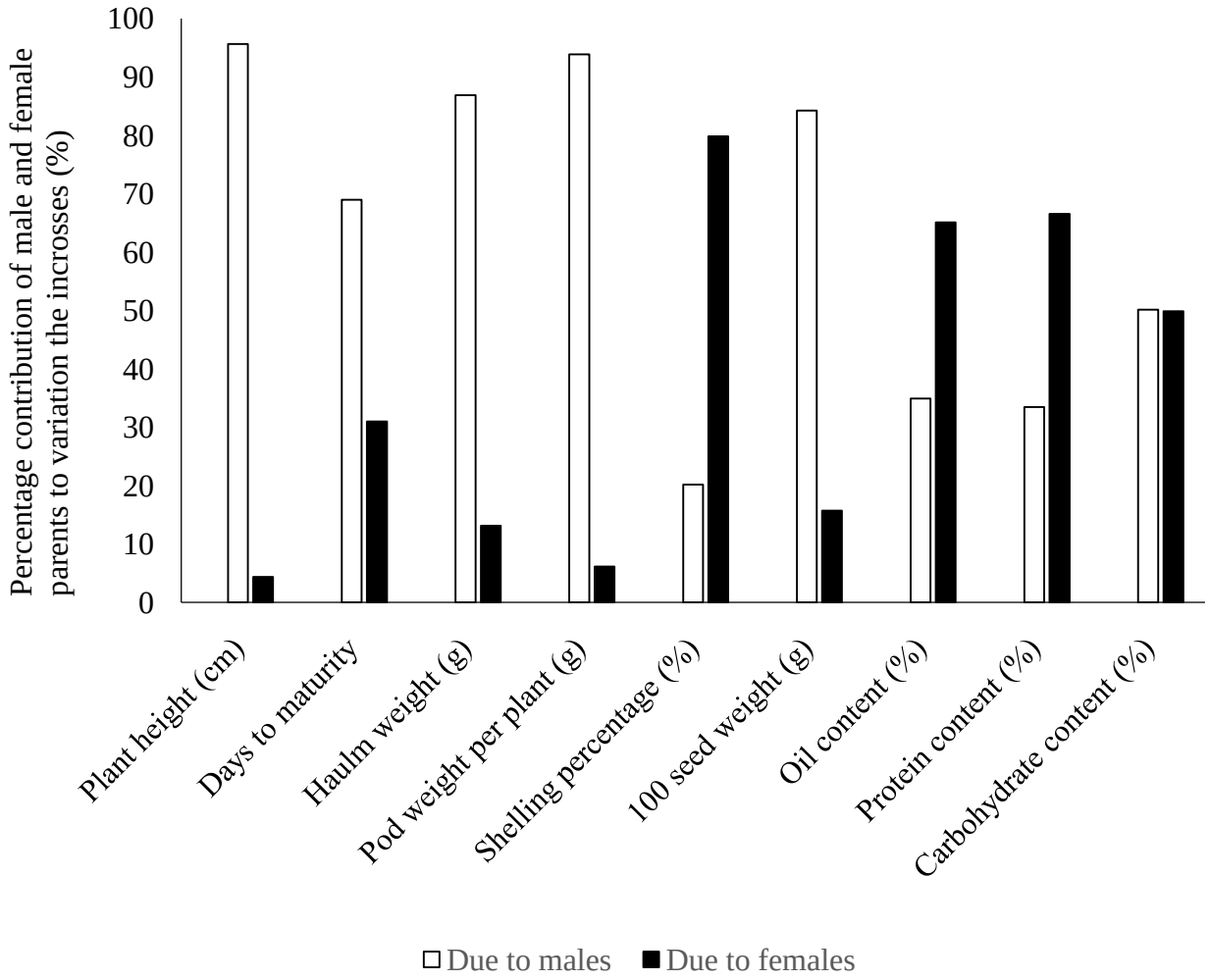
Table 4.10. Component GCA and SCA variance on oil content and agronomic traits of groundnut genotypes during 2014/2015 dry season.

Variance	Plant height (%)	Days to maturity (%)	Haulm weight (%)	Pod weight per plant (%)	Shelling percentage (%)	100 seed weight (%)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
σ^2_{GCA}	5.5346	1.8054	14960.3829	80.4688	7.7017	6.7192	0.9933	-0.2438	0.2758
σ^2_{SCA}	1.4830	13.6197	80124.5373	217.6853	-322.4740	21.6333	-13.9823	45.0647	75.6463
$\frac{\sigma^2_{GCA}}{\sigma^2_{SCA}}$	3.7320	0.1326	0.1867	0.3697	-0.0239	0.3106	-0.0710	-0.0054	0.0036

Table 4.11. Percentage contributions of males and females toprogenyvariation of groundnut genotypes for oil content and agronomictraits during 2014/2015 dry season.

Sources of Variance	Plant height (%)	Days to maturity (%)	Haulm weight (%)	Pod weight per plant (%)	Shelling percentage (%)	100 seed weight (%)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
Due to males	95.63	68.98	86.85	93.87	20.17	84.25	34.90	33.47	50.14
Due to females	4.367	31.02	13.15	6.13	79.83	15.75	65.10	66.53	49.86

Figure1.Percentage contributions of males and females toprogeny variation of groundnut genotypes for oil content and agronomictraits during 2014/2015 dry season



4.4 Combining Ability Effects

4.4.1 General combining ability (GCA) and specific combining ability (SCA) effects.

The estimates of GCA effects of male parents and female parents are presented in Table 4.11. SAMNUT 24 recorded significant positive GCA effects for plant height and carbohydrate content, and significant negative GCA effects for pod weight per plant, 100-seed weight and protein content. SAMNUT 23 as male parent recorded significant positive and negative GCA effects for protein and carbohydrate content respectively. SAMNUT 21 exhibited significant positive GCA effects for days to maturity, haulm weight, pod weight per plant and 100-seed weight. Significant negative GCA effects was recorded by SAMNUT 21 for plant height. Female parent SAMNUT 22 showed significant negative and positive GCA effects for protein content and carbohydrate content respectively. SAMNUT 14 exhibited significant negative GCA effect for Oil content. ICGX-SM-00020/5/P_4/P_1 had significant positive and negative GCA effects for oil content and carbohydrate content respectively.

Specific combining ability (SCA) effects are presented in Table 4.12.The cross combinationsSAMNUT 24 x SAMNUT 22, SAMNUT 24 x SAMNUT 10, SAMNUT 21 x SAMNUT 10 and SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1recorded significant negative SCA effects for days to maturity. SAMNUT 21 x SAMNUT 22 had significant positive SCA effects for days to maturity. The combination SAMNUT 24 x SAMNUT 14 had significant negative SCA effects for haulm weight. SAMNUT 21 x SAMNUT 14, SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 recorded significant positive SCA effects for haulm weight. Significant negative SCA effects were exhibited by the following progenies (SAMNUT 24 x SAMNUT 14 and SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1) for pod weight per plant. Significant positive SCA effects were shown by SAMNUT 21 x SAMNUT 14, SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 and SAMNUT 21 x ICGV-IS-07903 for pod weight per plant. The crosses SAMNUT 24 x SAMNUT 10, SAMNUT 24 x ICGX-SM-00020/5/P4/P1had

significant negative SCA effects for 100-seed weight. Positive significant SCA effects were recorded by SAMNUT 21 x SAMNUT 10, SAMNUT 21 x ICGV-IS-07903 for 100-seed weight. Significant negative SCA effects were recorded by the following crosses SAMNUT 24 x SAMNUT 22, SAMNUT 24 x SAMNUT 14, SAMNUT 24 x SAMNUT 10, SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1 and SAMNUT 24 x ICGV-IS-07903 for Oil content. However significant positive SCA effects for oil content were exhibited by SAMNUT 23 x SAMNUT 22, SAMNUT 21 x SAMNUT 14, SAMNUT 21 x SAMNUT 10, SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 and ICGV-IS-07903. Significant SCA effects were recorded by the following crosses SAMNUT 24 x SAMNUT 14, SAMNUT 24 x SAMNUT 10, SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1 and SAMNUT 24 x ICGV-IS-07903 for protein content and carbohydrate content. Significant positive SCA effects were exhibited by SAMNUT 23 x SAMNUT 14, SAMNUT 21 x SAMNUT 14, SAMNUT 21 x SAMNUT 10 and SAMNUT 21 x ICGV-IS-07903 for protein content and carbohydrate content.

Table 4.12. Estimate of General combiningability effects for oil content and agronomictraitsof groundnut genotypes in 2014/2015 dry season.

Parents	Plant height(cm)	Days to maturity	Haulm weight (cm)	Pod weight per plant (g)	Shelling percentage (g)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 24	3.74**	-1.18	-112.96	-13.30**	4.49	-4.69*	0.05	-1.76*	2.79**
SAMNUT 23	-0.16	-1.71	-102.26	-4.24	0.80	0.19	0.43	1.79*	-3.31**
SAMNUT 21	-3.58**	2.89*	215.21**	17.53**	-5.29	4.50*	-0.48	-0.02	0.52
SE±	0.86	1.14	63.96	4.19	5.00	1.68	0.28	0.69	0.60
SAMNUT 22	-0.09	-0.27	-106.72	0.34	-5.74	-2.75	0.26	2.95**	-3.30**
SAMNUT 14	-0.25	-0.88	34.83	6.39	2.52	3.32	-0.76*	-0.29	-0.25
SAMNUT 10	0.14	1.07	87.22	-2.62	1.75	1.93	-0.48	0.68	1.47
ICGX-SM-00020/5/P_4/P_1	0.10	0.84	-23.28	-3.30	3.15	-2.83	0.87*	-1.99*	1.05
ICGV-IS-07903	0.10	-0.77	7.94	-0.80	-1.68	0.32	0.12	-1.35	1.02
SE±	1.11	1.47	82.57	5.41	6.45	2.16	0.37	0.89	0.78

* = Significant at P≤0.05; ** = significant at P≤0.01.

Table 4.13. Estimate of Specific combining ability effects for oil content and agronomictraits of groundnut genotypesin 2014/2015 dry season.

Crosses	Plant height (cm)	Days to maturity	Haulm weight(g)	Pod weight per plant(g)	Shelling percentage (%)	100seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content(%)
SAMNUT 24 x SAMNUT 22	-1.52	-6.02*	14.42	-4.11	1.06	-5.95	-3.79**	-0.72	-0.72
SAMNUT 24 x SAMNUT 14	0.09	-3.91	-308.30*	-19.94*	6.66	-5.19	-1.89*	-10.87**	-10.87**
SAMNUT 24 x SAMNUT 10	1.37	-7.86**	27.14	-12.37	-11.72	-11.13*	-3.04**	-13.28**	-13.28**
SAMNUT 24 x ICGX-SM-00020/5/P_4/P_1	0.29	-3.97	-77.19	-28.59**	5.77	-12.88**	-6.11**	-3.44*	-3.44*
SAMNUT 24 x ICGV-IS-07903	-0.23	-2.86	-239.58	-20.19	1.97	-7.02	-3.64**	0.77	0.77
SAMNUT 23 x SAMNUT 22	0.39	-1.61	76.00	0.68	-2.92	0.96	2.75**	1.44	1.44
SAMNUT 23 x SAMNUT 14	-1.53	-0.17	-85.06	-12.50	0.93	-0.28	-0.17	4.43*	4.43**
SAMNUT 23 x SAMNUT 10	-0.46	-1.28	-215.11	-3.88	10.15	0.28	0.87	7.01**	7.01**
SAMNUT 23 x ICGX-SM-00020/5/P_4/P_1	1.83	-3.56	-71.95	-0.18	-5.31	1.43	-0.76	2.14	2.14

Table 4.13. Cont…

Crosses	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage (%)	100 seed weight (g)	Oil content (%)	Protein content (%)	Carbohydrate content (%)
SAMNUT 23 x ICGV-IS-07903	-0.23	-1.11	-214.34	-4.48	1.96	-0.61	0.26	-5.26**	-5.26**
SAMNUT 21 x SAMNUT 22	1.13	7.64**	-90.42	3.43	1.86	4.99	1.04	-0.71	-0.71
SAMNUT 21 x SAMNUT 14	1.43	4.08	393.36*	32.45**	-7.59	5.47	2.06**	6.44**	6.44**
SAMNUT 21 x SAMNUT 10	-0.91	9.14**	187.97	16.25	1.57	10.86*	2.18**	6.27**	6.27**
SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1	-2.12	7.52*	149.14	28.77**	-0.46	11.46**	6.87**	1.30	1.30
SAMNUT 21 x ICGV-IS-07903	0.47	3.97	453.91**	24.67*	-3.93	7.64*	3.38**	4.49**	4.49**
SE±	1.92	2.54	143.02	9.36	11.17	3.75	0.64	1.54	1.35

* = Significant at P≤0.05; ** = significant at P≤0.01.ficant at P≤0.01.

4.5 Correlations

The estimates of correlation among the studied traitsare presented in Table 4.14.The result showed that oil content exhibit negative significant correlation with haulm weight (r = -0.2495*) and protein content (r = 0.2775*) respectively. Plant height showed highly significant and negative association with days to maturity (r = -0.4415**), while the association between plant height and carbohydrate content was significant and positive (0.2843*). Haulm weight was highly significantly positively correlated with pod weight per plant (r = 0.5271**) and 100-seed weight (r = 0.5024**). Pod weight per plant had negative and highly significant association with shelling percentage (r =-0.4498) and highly significant positive association with 100-seed weight (r = 0.6636). The result also showed that protein content had strong negative correlation with carbohydrate content (r = -0.9137).

Table 4.14. Correlation coefficient of oil content and agronomic traits of groundnut genotypes during 2014/2015 dry season.

	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage (%)	100-seed Weight (g)	Protein content (%)	Carbohydrate content (%)
Oil content (%)	-0.1226	-0.2046	-0.2495*	-0.0789	0.1781	-0.1502	-0.2775*	0.0238
Plant height (cm)	**1.0000**	-0.4415**	0.0160	-0.1016	0.0625	0.1314	-0.2126	0.2843*
Days to maturity		**1.0000**	0.0035	0.0260	0.0067	-0.0758	0.1497	-0.1048
Haulm weight (g)			**1.0000**	0.5271**	-0.2140	0.5024**	0.0771	0.0123
Pod weight per plant (g)				**1.0000**	-0.4498**	0.6636**	0.0584	-0.0981
Shelling percentage (%)					**1.0000**	-0.1030	0.0079	-0.0159
100-seed weight (g)						**1.0000**	-0.0586	0.0605
Protein content (%)							**1.0000**	-0.9137**
Carbohydrate content (%)								**1.0000**

* and ** = significant at 0.05 and 0.01 probability levels respectively.

4.6 Path Coefficient Analysis

The results of path coefficient analysis are presentedin Table 4.14.

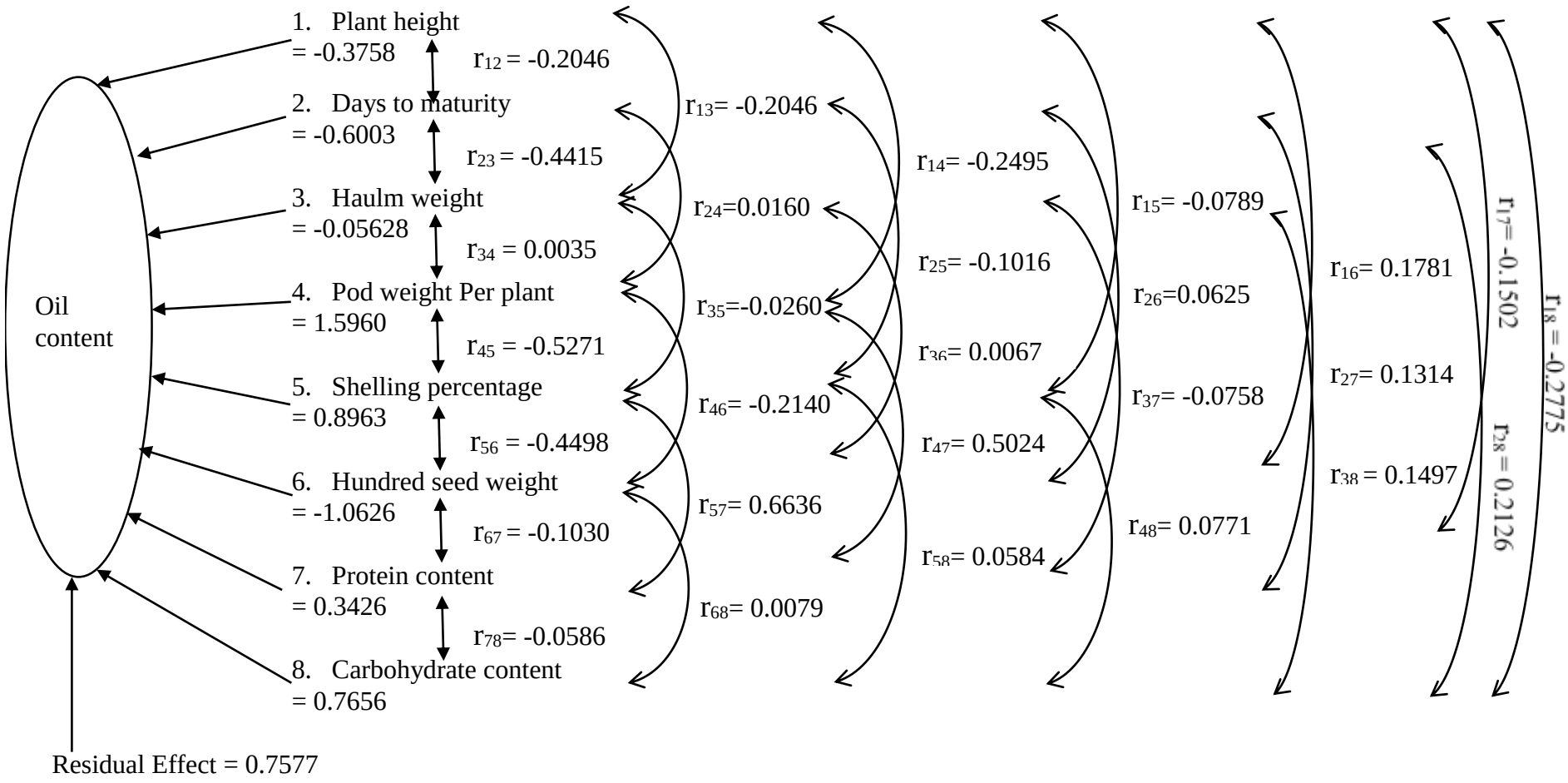
Pod weight per plant (1.5960), shelling percentage (0.8963), carbohydrate content (0.7656) and protein content (0.3426) respectively were the direct positive contributors to groundnut oil content. Other traits showed negative direct contribution to oil content. The positive indirect contributions via pod weight per plant were shelling percentage (0.4725), 100-seed weight (0.2274), protein content (0.1721) and carbohydrate content (0.0590). Plant height and haulm weight were the only negative indirect contributors to oil content via shelling percentage. Pod weight per plant (0.8019) was the highest indirect contributor via protein content. Via carbohydrate content, the highest indirect positive contributor was days to maturity (0.1276).

Table 4.15: Path coefficient analysis showing direct (diagonal) and indirect effects of different characters on oil content of groundnut genotypes in 2014/2015 dry season.

	Plant height (cm)	Days to maturity	Haulm weight (g)	Pod weight per plant (g)	Shelling percentage (%)	100-seed weight (g)	Protein content (%)	Carbohydrate content (%)	Total correlated
Plant height (cm)	**-0.37575**	0.07361	0.115121	-0.12589	0.159665	0.15963	-0.09507	0.018244	-0.07044
Days to maturity	0.07361	**-0.60031**	0.248482	0.025551	-0.09106	-0.06645	0.045028	-0.16277	-0.52791
Haulm weight (g)	0.115121	0.265043	**-0.5628**	0.041479	0.023296	-0.00716	-0.02597	0.11458	-0.03642
Pod weight per plant (g)	-0.39813	-0.00961	-0.00198	**1.59595**	0.472461	0.227384	0.172133	0.059028	2.117243
Shelling percentage (%)	-0.0707	0.060985	-0.01463	0.841225	**0.89634**	0.478007	0.227332	0.04478	2.46334
100-seed weight (g)	-0.18929	-0.03754	-0.00379	-0.3415	-0.4032	**-1.06264**	-0.03529	0.00601	-2.06724
Protein content (%)	-0.05147	-0.0789	0.042666	0.801853	0.594766	0.109463	**0.3426**	0.00601	1.766994
Carbohydrate content (%)	-0.21245	0.127626	-0.08423	0.123048	0.052427	-0.00834	-0.02006	**0.7656**	0.743614

Residual effects = 0.7577

Figure 2: Path coefficient Diagram of oil content and its components on groundnut genotypes in 2014/2015 dry season.



CHAPTER FIVE

5.0 DISCUSSION

The mean performance of the progenies for 100-seed weight for the separate locations and from combined data recorded higher values when compared to the checks for seed weight.This shows that genes controlling seed weight in the parents contributed positively in the cross. It also showed that the parents were different in their genetic background and combined well to produce promising crosses.100-seed weight, for most crosses gave mean weight of 60g and above indicated that for targeting confectionary traits (large seeded) groundnut, such crosses are good hybrids. The findings on 100-seed weight corroborates with the work of Milton (2013), Ramanatha and Murty(1994) whoreported that 100-seed weight higher than 60g were for confectionary varieties. The mean performance result of oil content, revealed that the crosses SAMNUT 23 x SAMNUT 22 and SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 recorded high oil content relative to the bestchecks across locations.This showed thatthese crosses received favourable gene combinations from their parents. However for protein content only the cross SAMNUT 24 x SAMNUT 22 and SAMNUT 23 x SAMNUT 10 recorded higherprotein content when compared to the checks.Carbohydrate content mean performance of most of the progenies were higher than the best check.This signifies the positive contributions of gene controlling carbohydrate content from parents to the progenies and the crosses can be considered as good candidates in future breeding.

Theperformance across locations revealed that the best performing genotype in terms of plant height at Samaru was SAMNUT 24 x SAMNUT 10 and at Kadawa was SAMNUT 24 x SAMNUT 14, which showed that the genes controlling plant height in the parents have contributed significantly in the crosses. The mean performance result showed that SAMNUT 21 is the best genotype across locations for protein content. SAMNUT 24 x SAMNUT10 is the best genotype across the locations for carbohydrate content.

The significant difference among the genotypes for most of the traits studied in the separate locations and from the combined data as shown by the ANOVA,indicatesthe presences of significant variations among the genotypes, which is the backbone for any crop improvement programme. Falconer (1981), pointed out that the amount of improvement that can be achieved by selection among a number of crosses is dependent on the amount of variation between the crosses and the intensity of selection, since selection is ultimately applied to the crosses. This suggest that the parental lines used to develop these crosses can be used for genetic improvement ofoil content and agronomic traits of groundnut. Similar results were reported by Khote,*et al.* (2009)andKorat, *et al.* (2009). Results from the combined data showed significant difference recorded for plant height, oil content, protein content and carbohydrate content. This shows that difference in the location had influence in the expression of these traits. This therefore indicates that suitable crosses could be developed for each environment for these traits. This corroborates with the work of Hassan,*et al*. (2005) on oil content of groundnut.

The potentials and the genetic worth of a genotype as potential candidate for selection depends on the amount of genetic variability of a target trait. The result of this study showed that the PCV was higher thanGCV for all the studied traits, portraying the importance of environment in the variation exhibited.Similar result was reported by Patil,*et al*.(2015).

Heritability estimates provides the information about index of transmissibility of the quantitative character of economic importance and are essential for an effective crop breeding strategy. The breeder makes rapid progress where heritability is high using selection methods that are dependent solely on phenotype (example, mass selection). However, where heritability is low, the method of selection based on families and progeny testing are more effective and efficient (Acquaah, 2007). Estimate of broad sense heritability were moderate for most traits except, for shelling percentagethat recorded low values. This indicates that

selection forthe improvement of thesetraits at early generation may not be effective. This disagrees with the findings of Patil,*et al*.(2015)who recorded high broad sense heritability for their studied traits. The moderate value of broad sense heritability signifies the preponderance of non-additive gene action in the inheritance of those traits. Hence selection for such traits should be delayed to later generations. This study corroborates with the work of John and Raghava, (2015) who reported moderate broad sense heritability for oilcontent. The low to moderate values of narrow sense heritability observed on this genotypes for the studied traits, can be attributed to high magnitude of dominance or environmental effects, on the traits studied relative to additive effect. Therefore selection should also be postponed till later generation in other to increase the response to selection. Jinks and Pooni (1984) reported that ifselection is delayed further into the inbreedingprogramme, there will be an increase in narrow sense heritability and,hence, increase in response to selection.

The significantgeneral combining ability estimates among the male parents (GCAm) for haulm weight and significant difference for days to maturity, pod weight per plant,oil content, protein and carbohydrate content suggested the prevalence of additive gene action governing the inheritance of these traits. General combining ability estimates among the female parents (GCAf) reveals additive gene action controlling the inheritance ofdays to maturity and carbohydrate content as indicated by their significant difference. The significance of specific combining ability(SCA) for days to maturity,haulm weight,protein and carbohydrate content suggested that dominance gene action was important for the inheritance of these traits. The absence of significance SCA means squares for plant height, pod weight per plant, shelling percentage, 100-seed weight and oil content, indicates the importance of additive gene action. This is in agreement with the findings of Singkham,*et al*. (2010).The presence of both additive and Non-additive type of gene action is an indication of variability among the

genotypes evaluated, confirming the result of Edilbarto and Ricardo (1985) who reported both significant GCA and SCA.

The relative importance of GCA to SCA variance was judged from the ratio of the GCA to SCA variance which help to indicate the predominance presence of either additive or non-additive action. The ratio here revealed the preponderance of σ^2_{SCA} variance over σ^2_{GCA} variance for most ofthe measured traits measured.This may be due to differences in the genotypes use as parents. A stated by AbulKalam, *et al*.(2014); Additionally, higher SCA variance than GCA, can be explained in otherdifferent ways: (i) negative associations between genes,(ii) previous selection that narrowed the genetic base of thelines tested, (iii) directional selection, and (iv) useof closely related parents. This study corroborates with earlier work ofDwivedi,*et al*. (1989)who reported variation in the inheritance of these traits may be due to differences in the method of analysis (random or fixed model) and/or in the parental material that was used in these studies.Non-additivegenetic variance was larger than additive genetic variance for all the traitsexcept plant height, as depicted by ratio of variance of generalto specific combining ability ($\frac{\sigma^2_{gsc}}{\sigma^2_{sca}}$)was less than unity for all measured traits.However this result contradicts the early findings by (Layrisse,*et al*., 1980 and Mohammed,*et al*., 1978). The implication of the preponderance of non-additive gene in the expression of the traits studied, is that identifying good parents would be difficult for these traits. Instead, specific crosses should be looked out for.The results obtained from this study indicated that the male parents contributed more to variation in plant height, days to maturity, haulm weight, pod weight per plant and 100-seed weight and carbohydrate content. The female contribution to variation were more on shelling percentage, oil content and protein content. This indicates that male parents brought more variation to the studied traits.

A detailed genetic study is prerequisite to determining the mode of inheritance of traits which ultimately helps adopt better planning and execution of a plant breeding improvement programme AbulKalam, *et al*.(2014). Combining ability refers to the ability of a parent to transmit desirable performance to its progeny or crosses. Combining Ability analysis helps in the evaluation of inbred in terms of their genetic value and in the selection of suitable parents for hybridization.The result of the GCA effects revealed that SAMNUT 24 is a good general combiner for plant height among the male parents. Days to maturity, negative GCA effects is required for earliness as reported by Vishnuvardhan,*et al*. (2012). However none of the parents showed significance negative GCA for days to maturity. In this study SAMNUT 21 was found to be a good general combiner for haulm weight, pod weight per plant and 100-seed weight. GCA estimates for oil content among the female parent revealed ICG-SM-00020/5/P_4/P_1 as the only good general combiner. The female parent SAMNUT 22 was good general combiner for protein content. This findings corroborates with the works of John and Raghava (2015).

The exploitation of heterosis through useful cross combination is determined by specific combining ability. As reported by Fellahi,*et al.* (2013), that even though SCA effects do not contributes tangibly in the improvement of self-pollinated crops(except in situations where exploitation of heterosis is feasible) best hybrids are expected to generate transgressive segregants which could be selected as potential homozygous lines.SAMNUT 24 x SAMNUT 22 and SAMNUT 24 x SAMNUT 10 were identified as good specific combiners for days to maturity,due to their significant negative SCA effects. Significant negative SCA is desirable for earliness. These result is in conformity with the findings of John,*et al.*(2011). For haulm weight, the cross combination SAMNUT 21 x SAMNUT 14 and SAMNUT 21 x ICGV-IS-07903 were good specific combiners. This result is in agreement with the work of Adamu, *et al.* (2008). SAMNUT 21 x SAMNUT 14, SAMNUT 21 x ICGV-IS-07903 and SAMNUT 21

x ICGV-IS-07903 recorded SCA effects in desirable direction and are therefore identified as good specific combiners for Pod weight per plant. The cross combinations SAMNUT 21 x SAMNUT 10, SAMNUT 21 x ICGV-IS-07903, and SAMNUT 21 x ICGX-SM-00020/5/P_4/P_1 were good specific combiners for 100-seed weight. A perusal at the mean performance, SCA effects and GCA effects showed that the identified specific combiners for Pod weight per plant and 100-seed weight were promising progenies as stated by Arunga,*et al*. (2010).That the SCA effect alone has limited value for parental choice in breeding programs. They, therefore, suggested that the SCA effects should be used in combination with other parameters, such as hybrid means and the GCA of the respective parents.Such that a hybrid combination with both high mean and favourable SCA estimates, involving at least one of the parents with high GCA, would tend to increase the concentration of favourable alleles; which is desired by breeders. The following crosses (SAMNUT 23 x SAMNUT 22, SAMNUT 21 x SAMNUT 14, SAMNUT 21 x SAMNUT 10, SAMNUT 21 x ICGX-SM-00020/5/P_4/$P_1$and SAMNUT 21 x ICGV-IS-07903) were the best specific combiners for oil content. For protein and carbohydrate content, the following progenies SAMNUT 23 x SAMNUT 14, SAMNUT 23 x SAMNUT 10, SAMNUT 21 x SAMNUT 14, SAMNUT 21 x SAMNUT 10, and SAMNUT 21 x ICGV-IS-07903 were the best specific combiners. The results of this findings corroborate with the work of John and Raghava (2015).The superior crosses where from different parental combinations, where both parents are with high GCA effects (high x high, high x low and low x high). The cross combinations showing high SCA effects arising from parents with high and low GCA values for any trait indicates that there is influence of non-additive genes on their expression. Parent of these crosses can be used for bi-parental mating or reciprocal recurrent selection for developing superior varieties with high yield. Crosses with high SCA effects having both parents with good GCA effects could be exploited by pedigree method of breeding to get transgressive segregants.

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters, it resolves the complex relationship between characters into simple form of association Channayya, (2009).When correlation exists between any two traits, a selection for one trait will lead to a corresponding change in the other trait that are correlated, if positively correlated. In this study, the significant negative correlation recorded between oil content and (haulm weight and protein content) indicates that improvement in both haulm weight and protein content would lead to decrease in oil content. This corroborates with the findings of de Godoy and Norden(1981), and contrary to the findinds of Azharudheen, *et al*. (2013) and Dwevide, *et al*. (1990) who reported significant positive association between protein content and oil content. The significant association between 100-seed weight and pod weight per plant, shows that selection of 100-seed weight would lead to a corresponding improvement in pod weight per plant. This is in conformity with the findings of Kotzamanidis, *et al*. (2006) and Narasimhulu, *et al.*(2012)

Knowledge of interaction among the characters is very essential in plant breeding to determine the extent andnature of relationship between a target character and other characters influencing the target. Path coefficient analysisenables a plant breeder to separate direct and indirect effects attributable by partitioning the correlations. In this study pod weight per plant, shelling percentage, protein content and carbohydrate content were identified as the positive direct contribution to oil content. This corroborate with the findings of Patil, *et al.* (2006), who reported pod weight per plant as one of the direct positive contributors to oil content in groundnut.

CHAPTER SIX

6.0 Summary, Conclusion and Recommendations

6.1 Summary

The Research was conducted to study the inheritance of oil content and other agronomictraits in groundnut via genetic variability components for oil content and other agronomictraits. The parental materials used in this study comprised of eight (8) parents (three male and five females) based on their oil content.The parentswere mated in a North Carolina (factorial) mating design II in thescreen house, 15 F_1were generated. The resultant progenies, their parents and two checks (SAMNUT 25 and SAMNUT 26) were evaluated at Samara and Kadawaduring the 2014/2015 dry season, laid out in 5 x 5 lattice design with three replications.

Variations were obtained for most of the studied traits, indicating the presence of appreciable variability in the studied genotypes, which is a key requirement in a crop enhancement programme. The result of this study also showed that hybrid crosses could be developed for specific environment as indicated by significance difference in the performance of genotype across locations particularly, for plant height, oil content and other seed related traits. The best crosses for protein and carbohydrate content at Samaru were obtained. For 100-seed weight, most of the crosses outperformed the best check and gave 100-seed weight of above 60g which are excellent for confectionary groundnut. The low to moderate PCV and GCV for most studied traits indicates the dominance of non-additive gene action in the inheritance of oil and agronomic traits and selection cannot be exercised for most of the studied traits at early generation which has to be delayed to later generations. The estimate of broad sense heritability were moderate. This gives an indication of importance of both additive and non-additive gene effects governing these traits.Narrow sense heritability is low for most traits, which suggested that selection should be delayed till later generations.

Breeding of genotypes for different environments would not be a problem, since confounding effects from genotype performance across environment is absent as indicated by non-significant GCAm x location, GCAf x location and SCA x location for oil content and most traits.

The male parent SAMNUT 21 is a good general combiner for plant height (3.74**) and carbohydrate content (2.79**). SAMNUT 23 is good general combiner for protein content. SAMNUT 21 is good combiner for haulm weight (215.21**), pod weight per plant (17.53**) and 100-seed weight (4.50**). The female parent SAMNUT 22 is a good general combiner for protein content (2.95**). ICGX-SM-00020/5/P_4/P_1 is a good general combiner for oil content (0.87*). The crosses showed great deal of good SCA effects for oil content and other agronomic traits.

The negative significant correlation between oil content and (haulm weight and protein content) indicates that improvement in oil content will cause a decrease in both haulm weight and protein content. The highly significant positive correlation between pod weight per plant and (haulm weight and 100-seed weight), Implies that selection for pod weight per plant would lead to a corresponding increase in haulm weight and 100-seed weight. The positive direct contributors to oil content were pod weight per plant, shelling percentage, carbohydrate content and protein content. This shows that selection for such traits would be effective in influence the oil content.

6.2 Conclusion

In conclusion genetic recombination and improvement of seed quality traits (oil content and 100-seed weight) can be achieved, as depicted by high variability among the genotypes studied,

This study also showed that both additive and non-additive gene action were important in controlling oil content and other agronomic traits, however there is more preponderance of

non-additive gene action in controlling the measured traits. The male parents SAMNUT 24 isidentified as the best General combiner for plant height and carbohydrate content. SAMNUT 23 as male parent and SAMNUT 22 as female parent were the good general combiners for protein content. SAMNUT 21 is regarded as the best parent with good general combining ability for days to maturity, haulm weight, pod weight per plant and 100-seed weight. ICGX-SM-00020/5/P_4/P_1 (female) is the good general combiner for oil content. Cross combinations were also identified with good SCA effects. Moderate values of broad sense heritability particularly for oil(43.46), protein(46.30)and carbohydrate content (45.03). The low to moderate PCV and GCV values for most traits indicates that selection based on these traits should be delayed till later generations. Haulm weight and protein content were negatively correlated with oil content. Positive correlation recorded between pod weight per plant with haulm weightindicates that selection for any of these traits will lead to a corresponding increase in pod weight. Path coefficient analysis further reveals that selection of pod weight per plant shelling percentage, carbohydrate content and protein content should be considered as selection criteria for improvement in oil content, due to their direct positive contribution to oil content.

6.3 Recommendations

Base on the findings of this study the male parents SAMNUT 24 and SAMNUT 21 and the female parents SAMNUT 22, SAMNUT 14 and ICGX-SM-00020/5/P_4/P_1can be considered for hybridization to develop genotype with goodplant height, 100-seed weight, protein content and high oil content by virtue of them been the best good general combiners and SCA effects, showed that the crosses; SAMNUT 21 x SAMNUT 10,SAMNUT 21 x ICGX-SM-00020/5/P_4/$P_1$and SAMNUT 21 x ICGV-IS-07903 are good specific combiners for 100-seed weight. SAMNUT 21 x SAMNUT 14,SAMNUT 21 x SAMNUT10 and SAMNUT 21 x ICGV-IS-07903 were the best specific combiners for oil, protein and carbohydrate content.

Therefore further studies over years and locations should be conducted to ascertain their stability.

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