KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY

KUMASI-GHANA

STUDIES ON THE INHERITANCE OF SEED QUALITY TRAITS IN GROUNDNUT (*Arachis hypogaea* L.)

BY

MILTON KABBA KABBIA

AUGUST, 2013

KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY

COLLEGE OF AGRICULTURE AND NATURAL RESOURCES

DEPARTMENT OF CROP AND SOIL SCIENCES

STUDIES ON THE INHERITANCE OF SEED QUALITY TRAITS IN GROUNDNUT (*ARACHIS HYPOGAEA* L.)

A THESIS SUBMITTED TO THE SCHOOL OF GRADUATE STUDIES, KWAME NKRUMAH UNIVERSITY OF SCIENCE AND TECHNOLOGY, IN PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE DEGREE OF MASTER OF SCIENCE IN AGRONOMY (PLANT BREEDING)

BY

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B.Sc. (Hons) Crop science

AUGUST, 2013

DECLARATION

I hereby declare that I have, under supervision, undertaken the study and except for specific references which have been duly and appropriately acknowledged, this is the result of my own research and has not been submitted either in part or whole for other degree elsewhere.

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DEDICATION

This thesis is dedicated to the memory of my parents, Pa Robert T. Kabbia and Yea Fattu Lombeh Kabbia (Kinie Ngie-jaay). May their souls rest in perfect peace. Amen.

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ABSTRACT

Development of groundnut genotypes with large seed size and seed weight and improved

seed quality attracts consumers' immediate attention. Knowledge of the genetics system controlling expressions of these traits facilitates the choice of the most efficient breeding and selection procedure. A study of the nature and magnitude of gene effects in groundnut (*Arachis hypogaea* L.), utilizing three parameter additive-dominance model, where a confectionery variety (Oboshie) was crossed with two non confectionery high yielding varieties (Jenkaah and Nkosour). Six generations of parents, first filial and second filial generations, backcrosses 1 and 2 (P_1, P_2, F_1, F_2, B_1 and B_2) were studied for two quantitative traits (seed size and seed weight) in Oboshie x Jenkaah and Oboshie x Nkosour crosses. The study indicated that the additive-dominance model was adequate to explain the mode of inheritance of seed size in both crosses. The net additive gene effect contributed significantly ($P \leq 0.05$) to the inheritance of seed size; therefore, suggesting that selection for improvement of seed size could be accomplished in the F_2 generation in both crosses. The net dominance effect was positive indicating dominance towards the direction of the larger seed parent. Additive gene effects contributed significantly to the inheritance of seed weight per plant in Oboshie x Jenkaah cross, and magnitude of the net additive effect was higher than the dominance gene effect. Dominance value was positive indicating direction towards the heavier seed parent. The simple additive-dominance model was inadequate to explain the mode of inheritance of seed weight per plant for Oboshie x Nkosour cross, and therefore suggested the presence of non-allelic interaction in the inheritance of seed weight per plant. The result suggested that selection for seed weight per plant for Oboshie x Nkosour could be achieved through indirect selection

for a component trait such as seed size than direct selection for seed weight itself. The additive genetic effects observed for both traits will enhance pure line breeding.

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ABBREVIATIONS, ACRONYMS, AND SYMBOLS

ANOVA:	Analysis of Variance
$B_{1:}$	Backcross 1
$B_{2:}$	Backcross 2
bp:	Base pair
Cm:	Centimeter
CRI:	Crops Research Institute
CSIR:	Council for Scientific and Industrial Research
CV:	Co-efficient of Variation
^{o}C:	Degree Celsius
[d]:	Net additive effect
DAP:	Days after planting
df:	Degree of freedom
DNA:	Deoxyribonucleic acid
F_1:	First filial generation
F_2:	Second filial generation
FAO:	Food and Agricultural Organization
FAOSTAT:	Food and Agriculture Organization Statistics
[h]:	Net dominance effect
H_b^2:	Broad sense heritability
H_n^2:	Narrow sense heritability
ICRISAT	International Crop Research Institute for the Semi-Arid Tropics
KNUST	Kwame Nkrumah University of Science and Technology
LSD:	Least Significant Difference
L: W:	Length Width ratio

m:	Mid-parent value
$M = J^{-1}S$:	Estimate of parameters
MoFA:	Ministry of Food and Agriculture
MT:	Metric Tonne
N:	North
No.:	Number
NPK:	Nitrogen, Phosphorus and Potassium
ns:	Not significant
O/L:	Oleic, Linoleic acid ratio
P:	Probability
P_1:	Parent 1 (Female)
$P_{2:}$	Parent 2 (Male)
R:	Replication
RCBD:	Randomized Complete Block Design
SAT:	Semi Arid Tropics
SE:	Standard Error
UNESCO:	United Nations Educational Scientific Cultural Organization
UNICEF:	United Nations International Children Educational Fund
USA:	United States of America
V:	Variance
$1/V_X$	Reciprocal of the Variance of the mean
V_A:	Additive Variance
V_{B1}:	Variance of Backcross 1
V_{B2}:	Variance of Backcross 2
V_D:	Dominance Variance

V_E:	Environmental Variance
V_{F1}:	Variance of Filial generation 1
V_{F2}:	Variance of Filial generation 2
V_G:	Genetic Variance
V_P:	Phenotypic Variance
V_{P1}:	Variance of Parent 1
V_{P2}:	Variance of Parent 2
Vol.:	Volume
W:	West
X^2:	Chi-square

CHAPTER ONE

1.0 INTRODUCTION

Seed quality can have a major impact on potential crop yield and nutritional value. Seeds carry the genetic trait incorporated by years of breeding and selection to create varieties that are adaptable to specific production environments and will produce high yields and quality products. Groundnut seed size is important, as consumers place a high premium on large seeds.

Groundnut is an important oilseed crop around the world. It is ranked as the second most important cultivated grain legume, fourth largest edible oilseed crop and third most important vegetable protein in the world (Shilman *et al*., 2011; Lucas, 1979). It is extensively grown throughout the semi-arid tropics (SAT) of Asia, Africa and North and South America, with its global production of 38 million tons from 24 million hectare area (FAO, 2011).

Groundnut is grown primarily for human consumption and it is a rich source of oil (40–50 per cent), proteins (20–50 per cent) and carbohydrates (10–20 per cent), and also a good source of variety of essential vitamins and minerals (Belamkar *et al.,* 2011). 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.

Ghana is one of the leading producers of groundnut in the world. Ghana ranked 10th (530,887 MT of in-shell groundnut) in production volume in the world and

4th in Africa, behind Nigeria, Senegal and Sudan (FAOSTAT, 2011). Groundnut is the most important legume crop grown in Ghana in terms of the total production and value (Tsibey *et al*., 2003). Agro-ecologically, groundnut is grown mostly in the northern savanna zone, where the highest yield of 1.92 MT/Ha has been recorded (MoFA. 2011). The 2010 agricultural production figures show that the Northern and Upper West Regions produced about 80 percent of the nation's total groundnut production (MoFA. 2011) Groundnut is commonly grown alongside major crops such as maize, yams and millet (Tsibey *et al*., 2003).

Like the rest of Sub-Saharan Africa, groundnut is a valuable cash crop in Ghana and a food staple for millions of Ghanaians (MoFA, 2011). Groundnut is also processed into paste (butter) and widely used by Ghanaians to make soup, stews, and cereal mixtures (Asibuo *et al*., 2008). In the Northern Region, women process the meal into cakes which are consumed as snacks (kulikuli) or further processed into powdered form (kulikuli zim). Groundnut cake from industrial oil processing is mostly used for human and livestock feed especially in the south (Awuah *et al*., 2009).

Despite the recognition of Ghana as one of the leading producers of groundnut in the world, yield on farmers' field continue to be below the attainable yield of 2-3 MT/ha due to biotic and abiotic factors including unstable rainfall patterns, diseases and pest infestation, lack of quality seeds and favourable agronomic practices. These problems have led to low yield and low marketability of groundnut in the international market.

The seed quality aspect of groundnut is gaining importance because of increased use of groundnut as a food crop due to chronic shortage of pulses and increasing protein malnutrition among the burgeoning, undernourished, poverty stricken population in developing countries. Hence, more emphasis is given to improve and exploit groundnut as a food crop to make its farming more competitive and remunerative.

Dwivedi *et al*. (2000) noted that quality of edible groundnut seed is determined by various physical, sensory, chemical and nutritional factors. Physical factors include; integrity of seed testa, seed size, and shape, blanching efficiency and the integrity of the seed at the time of processing. Sensory factors include colour, texture, flavor, and wholesomeness. Chemical and nutritional factors include oil and protein contents, amino acid and fatty acid composition, carbohydrate, minerals and vitamins.

Edible groundnut kernels are generally referred to as confectionery groundnut, export quality groundnut, large/bold seeded groundnut and handpicked selected groundnut.

The quality requirement of confectionery groundnut is more stringent and distinctly different from groundnut as an oilseed crop. Additional efforts to develop confectionery grade varieties with high protein and sugar, low oil and reduced aflatoxin risk, large elongated kernels with tapering ends, pink or tan seed colour, ease of blanching and high oleic/linoleic acid ratio (O/L) is preferred (Nigam, 2000).

The exploitation of genetic control of seed quality traits through hybridization and selection is the primary focus of this work. Knowledge of the genetic systems controlling expressions of these characters facilitates the choice of the most effective breeding and selection procedure.

Objectives of this work were therefore to:

1. Determine the mode of inheritance for seed size, protein and oil contents in groundnut.
2. Estimate the magnitude of heterosis for the various traits and
3. Identify the role of maternal parents in the expression of large seed size, protein and oil content traits in groundnut.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 ORIGIN AND DOMESTICATION OF *Arachis hypogaea*

The cultivated groundnut *(Arachis hypogaea* L.) probably originated in Bolivia at the base of the Andes (Krapovickas, 1968) extending into north Argentina, and in this region many types are found with primitive plant, pod and seed characteristics (Ramanatha Rao, 1988).

Linnaeus, (1753) described the domesticated groundnut as *Arachis* (from Greek "arachus" meaning weed and *hypogaea* meaning underground chamber).

Genus Arachis comprise of 69 species placed in nine sections (Krapovickas and Gregory, 1994). The nine sections include; *Arachis*, *Caulorrhizae*, *Erecttoides, Extranervosae*, *Heteranthae, Procumbentes, Rhizomatosae, Trierectoides* and *Triseminalae*. Hammons, (1994) noted that five species each from different sections are presently cultivated. He further mentioned that *Arachis hypogaea* and *Arachis villosulicarpa* Hoehne are grown for their edible seeds and were improved by the indigenous people of South America. *Arachis glabrata* Benth, *Arachis repen* Handoo, and *Arachis pintoi* Krap. and Greg. were purposely adapted for grazing. *Arachis hypogaea* is widely cultivated throughout the world but, *Arachis villosulicarpa* has limited use only by the Indians of Rondonia area of the Mato Grosso, Brazil (Krapovickas, 1968).

2.2 TAXONOMY

Arachis hypogaea L. is a self-pollinated legumineous crop that belongs to the family *Fabaceaea*, subfamily *Papilionaceae*, tribe *Aeschynomenae* and sub tribe *Stylosanthiae* (Rudd, 1981). The cultivated groundnut (*Arachis hypogaea* L.), an annual herb of indeterminate growth habit, is classified into two subspecies, subsp. *fastigiata* Waldron and subsp. *hypogaea* Krap. and Greg. Subsp. *fastigiata* contains four botanical varieties, var. *vulgaris*, var. *fastigiata*, var. *peruviana*, and var. *aequatoriana*. Subsp. *hypogaea* contains two varieties, var. *hypogaea* and var. *hirsuta*. Sub specific and varietal classifications are mostly based on location of flowers on the plant, patterns of reproductive nodes on branches, numbers of trichomes and pod morphology (Krapovickas and Gregory, 1994). It is morphologically well defined and is clearly delimited from its closest related genera by the development of a 'peg' and geocarpy (Nigam *et al*., 1990).

Classification done by Gregory *et al*. (1951) divided groundnut into two large botanical groups, Virginia and Spanish-Valencia (Ramanatha Rao and Murty, 1994). The most important criteria were the presence or absence of reproductive axes (inflorescence) on the main stem and the arrangement of reproductive and vegetative axes on the primary laterals.

The Virginia group is characterized by the absence of reproductive axes on the main stem. It has an alternate branching pattern. The first two branches on the primary lateral are always vegetative. The spanish-valencia group is characterized by the presence of reproductive axes in a continuous series on successive nodes of lateral

branches, on which the first branch is always reproductive. It has a sequential branching pattern.

2.3 PHYLOGENY OF THE CULTIVATED GROUNDNUT

Groundnut is an allotetraploid (2n = 4x = 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 the "AA" and "BB" genomes, respectively, to the cultivated groundnut (Kochert *et al*., 1996). Young *et al*. (1996) reported that groundnut originated through a single hybridization and recent polyploidization event, followed by a successive selection which resulted in a highly conserved genome. Although cultivated peanut is a tetraploid, genetically it behaves as diploid (Stalker *et al*., 1991). Singh *et al*. (1996) concluded that the A and B-genomes contributed nearly equal amounts of DNA to the domesticated peanut. The phylogenetic analyses based on intron sequences and microsatellite markers also provide evidence for this hypothesis (Moretzsohn *et al*., 2012). A single hybridization event between the diploid progenitors followed by chromosome doubling (Kochert *et al*., 1996) about 3500 years ago lead to origin of cultivated groundnut. Cytogenetic evidence for two genomes in *A. hypogaea* came first from Husted (1936) who observed one significantly smaller chromosome pair, and later from Stalker and Dalmacio (1986) who karyotyped accessions in both subspecies.

2.4 FLORAL BIOLOGY OF GROUNDNUT

Groundnut is a self-pollinated crop with cleistogamous flowers, but natural outcrossing can occur to small extent where bee activity is high (Nigam *et al*., 1983).

Flowering begins 17–35 days after seedling emergence depending on the cultivar and environmental conditions. Flowers, simple or compound, are born in the axils of leaves and never at the same node as vegetative branch. One or more flowers may be present at a node. The stigma becomes receptive to pollen about 24 hours before anthesis and remains so for about 12 hours after anthesis (Hassan and Srivastava, 1966) and the dehiscence of anthers takes place 7 - 8 hours prior to opening of the flower in some varieties whereas in others they may not do so even at flower opening in the morning (Bolhuis *et al*., 1965). Fertilization occurs about 6 hours after pollination. Depending upon the prevailing temperatures, the peg or gynophore carrying the ovary and fertilized ovule on its tip appears in 6 –10 days and grows to enter the soil (positively geotropic) where it develops into pods. The tip orients itself horizontally away from tap root (Nigam *et al*., 1990).

2.5 HYBRIDIZATION IN GROUNDNUT

In self-fertilized crops, hybridization stands as a conventional methodology by which favourable genes available in different genotypes could be combined in a single genotype through genetic recombination.

Nigam *et al*. (1990) described artificial hybridization as an integral part of groundnut breeding. They further noted that the success rate in artificial hybridization in groundnut depends largely on the proper understanding of the flower structure and its biology, adoption of an appropriate hybridization procedure, adequately trained personnel and a careful pollination control during and after the pollination stage.

The conventional technique for hybridization in groundnut was described by Norden, (1973) but, some modification has been described by Nigam *et al*. (1980).

For convenience of operation, hybridization in groundnut is normally carried out on plants grown in pots or boxes. These pots are placed on raised benches or tables inside a greenhouse or outside in the open. Hybridization should be restricted to the early phase of flowering because of higher success rates in the production of mature pods from early-formed flowers (Ramanatha Rao, 1988).

Acquaah (2007) considered certain factors in preparation for hybridization which include viz: The parents to be crossed should be unidentical but reproductively compatible and should be obtained from the same species; the parents together supply the critical genes needed to accomplish the breeding objective; one parent should be designated as female and the other male, and the female parent need some special preparation called emasculation (removal of the anthers before anthesis).

Temperature and humidity are very important in groundnut hybridization, emasculation is carried out in the afternoon or evening depending on location and environmental condition. During emasculation a well-developed flower bud on a sufficiently elongated hypanthium is selected, and all other buds at that node should be removed with a forceps to ensure one peg set at a node. The bud should be treated with care to avoid injury. The bud is held gently between the thumb and index finger during which the sepal opposite the standard petal is pulled down. The fused sepal is also folded down and held back. The standard is gently and carefully opened with a forceps and is held back with the thumb and index finger. The wing petals are pulled down locking them with the standard. The keel is pulled outwards by its ridge with

forceps to expose the anthers. All the anthers and filament are removed from their bases. This leaves the stigma and style well exposed for pollination. The standard, wing petals and keel are usually returned to their normal positions after emasculation to cover the style and stigma to prevent desiccation or damage. The internode just above the emasculated bud is marked with a date-coded nylon thread. Thread of a different colour is used every day to help identify the buds for pollination the next day.

Pollination is carried out the day after emasculation as soon as buds start opening in the early hours of the morning (0600 hrs), and should not exceed 0900 hrs. For pollination, a healthy flower from a pre-identified male plant is removed by breaking the hypanthium. The calyx, standard, and wing petals are detached for ease of operation. The keel is pressed between the thumb and index finger to squeeze the pollen mass out from the anthers. The pollen is deposited on the tip of the stigma of the emasculated flower. All flowers except those that are artificially pollinated should be removed every day soon after pollination from the base of the hypanthium, to help prolong the duration of flowering of the female plant. The flower removal operation should continue for at least two weeks after the last pollination for the season. This reduces competition for the development of the hybrid pods.

If the operation is successful a peg will be seen emerging from the axil of the leaf just below the coloured thread 4 – 6 days after pollination. Routine checking should therefore be done to remove new buds or flowers.

2.6 PRODUCTION REQUIREMENT FOR GROUNDNUT

Groundnut grows well in well-distributed rainfall of at least 500 mm. The growth and development is largely influenced by temperature in groundnut and the optimum air temperature is between 25 and 30°C (Weiss, 2000). Groundnut thrives best in well-drained sandy loam soils, as light soil helps in easy penetration of pegs and their development and their harvesting. The productivity of groundnut is higher in soils with pH between 6.0 - 6.5. The nutritional requirement of groundnut is different as the pods develop in the soil. Calcium is an important nutrient required for pod and kernel development. It is unique to groundnuts that the pods directly absorb most of the calcium, and therefore calcium fertilizers are applied in the pod zone at the peak flowering stage to ensure its availability to the pods (Nigam *et al*., 1990).

Ono *et al*. (1974) reported optimum soil moisture content in the podding zone to be about 40% of the total soil volume, regardless of the soil moisture content in the rooting zone. They further noted that soil moisture content lower than 40% reduced the podding percentage and pod enlargement.

2.7 ECONOMIC IMPORTANCE AND USES OF GROUNDNUT

Groundnut is an important oil, food, and feed legume crop grown in over 100 countries. It covered 24 million ha area worldwide with a total production of 38 million tons in 2010 (FAOSTAT, 2010). Asia and Africa account for 95% of global groundnut area where it is cultivated under rainfed conditions with low inputs by resource poor farmers. Groundnut is a cash crop providing income and livelihoods to the farmer. It also contributes to nutrition of farm families through consumption of energy- and protein-rich groundnut kernels and provides nutritious fodder (haulms) to

livestock. Thus groundnut cultivation contributes to the sustainability to mixed crop-livestock production systems, the most predominant system of the semi-arid areas.

Groundnut is valued as a rich source of energy contributed by oil (48–50%) and protein (25–28%) in the kernels. They provide 564 kcal of energy from 100 g of kernels (Jambunathan, 1991). In addition, the groundnut kernels contain many health enhancing nutrients such as minerals, antioxidants, and vitamins and are rich in mono-unsaturated fatty acids. As they are highly nutritious, groundnut and products based on groundnut can be promoted as nutritional foods to fight energy, protein, and micronutrient malnutrition among the poor. Groundnut-based Plumpy'nut, a ready to use therapeutic food, has helped save the lives of thousands of malnourished children (UNICEF, 2007).

Groundnut oil is an excellent cooking medium because of its high smoking point (Singh and Diwakar, 1993). Asibuo *et al*. (2008) reported that the cake obtained after extraction of oil is used in animal feed industry, in preparing enriched easily digestible food for children and aged persons, and as soil amendment.

In Europe, North and South America about 75% of the production is used as food, while only 35% is used for the same purpose in Asia (Birthal *et al*., 2010). Peanut butter is the most popular groundnut product in the USA, Canada, and Australia. Groundnut seed can be consumed raw (non-heated), boiled, and roasted and also used to make confections and its flour to make baked products. The groundnut shells are used for making particle boards or used as fuel or filler in fertilizer and feed industry. Groundnut haulms constitute nutritious fodder for livestock. Being a legume crop,

groundnut helps in improving soil health and fertility by leaving behind N_2 and organic matter in the soil.

2.8 STRUCTURE OF GROUNDNUT SEED

The seed has two cotyledons, a hypocotyl, epicotyl and radicle. The cotyledons comprise nearly 96% of the seed weight and are the major storage tissue for the developing seedlings (Moss and Ramanatha Rao, 1995). All primordial leaves and above-ground structures appearing within the first few weeks after germination are already present in the seed. Generally the seed coat constitutes three unicellular layers; the epidermis or sclerenchyma, the middle parenchyma and the inner parenchyma. These layers represent the integument of the maturing ovule and are maternal in origin (Glueck *et al*., 1979). The mature seeds resemble other legume seeds such as beans, but they have paper-thin seed coats as opposed to the usual, hard legume seed coat (Chaturvedi *et al*., 2011).

2.9 SIZE AND SHAPE OF GROUNDNUT SEED AND POD

Seed size is the most notable characteristics of confectionery groundnut varieties. It is fairly stable for any given cultivar and is highly diagnostic in nature (Ramanatha Rao and Murty, 1994). The size (length and width) and shape (length: width ratio) of seeds are important features of cultivated groundnut. Vanuprasad *et al*. (2011) noted that development of groundnut genotype with large seed size and improved seed quality attracts consumers' immediate attention. The international market (USA, Canada etc.) prefers long and bigger sized seed. This is reflected in the high price they are exchanged for. Information on the inheritance of these traits using adaptive varieties

which is lacking will enhance breeding efforts aimed at developing varieties that are acceptable to both the local and international market.

2.10 VARIATION IN SEED AND POD OF GROUNDNUT

Groundnut seeds and pods show large variation for their size and shape. Seed size together with the seed mass, has been used extensively in the classification of groundnut. The size of seed is one of the important factors for export. Retamal *et al*. (1990) reported seed lengths ranges from 7 to 21 mm and seed diameters from 5 to 13 mm. Normally varieties with 100 seed mass of 60 g or more are considered as large seeded groundnut and are preferred for confectionery purpose, while most of the oil types have medium to small seeds (Ramanatha Rao and Murty, 1994). Seed mass is an important as well as diagnostic character. Generally cultivars belonging to var. *hypogaea* have larger and heavier seeds and those belonging to var. *fastigiata* have smaller and lighter seeds (Varisai *et al*., 1973). Depending on the material studied and site of evaluation various ranges have been reported; 0.17 - 1.24 g (Ramanatha Rao, 1988); and 0.54-2.38 g (Retamal *et al*., 1990). Rajgopal *et al*. (2000) evaluated 118 groundnut accessions for two years and reported 100 seed mass to range from 46.8 g - 69.9g. Manivel *et al*. (2000) evaluated 12 advanced breeding lines and found 100 seeds mass to range from 53.9 g - 76.7 g. Seeds and pods of cultivated groundnut observed at ICRISAT, Patancheru ranges from 4-23 mm (length), from 5-13 mm (width) and from 14-65 mm (length), from 7-20 mm (width) respectively (Singh and Simpson, 1994).

2.11 CORRELATION BETWEEN POD AND SEED SIZE AND OTHER QUALITY TRAITS

Correlation is a measure of the degree of association between traits. This association may be on the basis of genetics or may be non-genetic. 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 pleotrophy, 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.

Dwivedi *et al*. (1990) studied genetic variation and character association of 64 genotypes and found that there was no significant association for seed weight with oil or protein contents. They further noted that oil content variation with a genotype showed a significant linear increase as seed weight increased, but no such relationship was observed for protein content. 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). Narasimhulu*et al*. (2012) 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; Abhay-Darshora *et al*., 2002; Vasanthi *et al*.,1998). Pod yield show positive correlation with number and mass of seed plant^{-1} (Phadnis *et al*., 1973; Dholaria*et al*., 1973), 100 seed mass (Deshmukh *et al*., 1986), number of mature pods plant^{-1} (Alam *et al*., 1985; Chandola *et al*., 1973; 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 Varshney, 1995). 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 reported (Vasanthi *et al*., 1998).

Pod yield had significant positive correlation with plant height, number of branches per plant, number of mature pods per plant, shelling per cent, 100-kernel weight and kernel yield per plant at genotypic and phenotypic level (Venkataravana *et al*., 2000). 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 *et al*., 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 fruit 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 Norden, 1981). 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.

Nigam *et al*. (1984) reported that, association among morphological and reproductive traits including pod yield in peanut is of special interest because of the subterranean nature of pod development. Also he noted that morphological traits are often highly heritable and, if directly associated with pod yield, this would help to accelerate the selection of high yielding plants in segregating populations before harvest.

2.12 INHERITANCE OF SEED AND POD SIZE IN GROUNDNUT

The phenotype of a plant is determined by its genetic composition, the environment in which the plant is grown, and the interaction of genotype with environment. The challenge in plant breeding is to identify and select those plants that have genotypes conferring desirable phenotypes, rather than plants with favorable phenotypes due to environmental effects. Narrow sense heritability is a measure of the ratio of additive genetic variation to phenotypic variation in a given population for a given trait. As a rule, traits with greater heritability can be modified more easily by selection and breeding than traits with lower heritability.

Many studies have been done on the inheritance of seed and pod size in groundnut. It is difficult to judge what proportion of the observed variability is heritable and what proportion is non-heritable i.e. environmental. However, it was reported that heritability values were highly influenced by the environment in groundnut (Lin *et al*., 1971). High broad sense heritability estimates were observed for 100 pod mass (Cahaner, 1978; Basu and Ashokraj, 1969; Dixit *et al*.,1970), 100 seed mass (Basu and Ashokraj, 1969; Dixit *et al*., 1970; Sangha, 1973), pod length (Kushwaha and Tawar, 1973), pod width (Kushwaha and Tawar, 1973), primary branches (Kulkarni and Albuquerque, 1967; Raman and Sreerangaswamy, 1970) and plant height

(Kulkarni and Albuquerque, 1967; Alam *et al*., 1985; Basu *et al*., 1986). Coffelt and Hammons (1974) reported high broad sense heritability estimates (0.71-0.90) for 100 seed weight, pod length, pod breadth and pod length-breadth ratio. High heritability for fruit size has also been shown by Wynne, (1975). High heritability estimates have been found for seed weight, grams/100 seed, pod length, pod breadth and number of seeds/pod (Dixit *et al*., 1970; Majumdar *et al*., 1969). Negative/zero narrow sense heritability estimates have been obtained for shelling percentage computed from variance components (Naazar *et al*., 1999)

The expression of majority of quality traits in groundnut is predominantly by additive gene action and seed size is controlled by non-additive gene action (Hariprasanna *et al*., 2008). Large pod and seed size is reported to be dominant over small pod and seed (Balaiah *et al*., 1977; Layrisse *et al*., 1980). Cahaner (1978) reported small pods to be dominant over large pods. Seed size was reported to be controlled by single gene (Balaiah *et al*., 1977), three genes (Pattanashetti *et al*., 2008) and also five genes (Martin, 1967). Report by some workers showed predominant additive gene action for pod and seed traits (Garet, 1976; Mohammed *et al*., 1978; Layrisse *et al*., 1980; Swe and Branch, 1986; Anderson *et al*., 1993). However, relative importances of additive, non-additive and epistatic effects in determining seed size are reported (Upadhyaya *et al*., 1992; Nadaf *et al*., 1988; Vindhiya Varman and Thangavelu, 1999). Report by Jayalakshmi and Lakshmikantha, (2003) revealed adequacy of additive-dominance model to explain variation in kennel yield (seed weight) in groundnut. They further noted that additive gene effects were highly significant for kernel yield. Naazar *et al*. (1999) reported additive gene effects for seed weight in groundnut. Isleib *et al*, (1978) indicated significant dominance effects for pod and seed yield in peanut. Alake *et al*.

(2012) reported inadequacy of the additive-dominance model for log transformed data on seed yield in okra.

2.13 HETEROSIS IN GROUNDNUT

Commercial production of F1 seeds is not currently feasible in groundnut because it is a self-pollinated and tetraploid. Heterosis however provides a genetic diversity to select desirable parents for developing superior F1 hybrids to exploit hybrid vigor and are building gene pool to be exploited in breeding programmes. Heterosis in F1 generation expressed in terms of superiority over better parent/mid-parent/standard parent is of relevance not only for developing hybrids in cross-pollinated crops, but also in self-pollinated crops because heterotic crosses help the breeder to select appropriate crosses which lead to desirable transgressive segregants in advanced generation (Arunachalam *et al*., 1982). John and Vasanthi, (2006) reported high heterosis over better parent for seed yield in groundnut. John *et al*. (2012) studied 28 crosses involving 8 parents to get information on the extent of heterosis over mid parent, better parent or standard parent for yield and physiological attributes. Negative heterosis was observed for kernel yield in groundnut (Venkateswarlu *et al*., 2007; Jayalakshmi *et al*., 2000). The maximum better parent heterosis for pod yield was observed to be 97.3% and that of mid parent and standard parent was found to be 101.52 and 108.54% respectively.

2.14 MATERNAL EFFECT AND SEED QUALITY

Variation in an individual's phenotype may be determined not only by the genotype and environment of that individual but also by maternal effects, i.e. the contribution of the maternal parent to the phenotype of its offspring beyond the equal chromosomal

contribution expected from each parent (Roach and Wulff, 1987). Three classes of maternal effects include; cytoplasmic genetic, endosperm nuclear, and maternal phenotypic. Cytoplasmic genetic maternal effects are derived from the fact that organelles such as plastids and mitochondria can be directly transferred from the maternal plant to the offspring during ovule formation and development, and this transmission is independent of nuclear genes. Molecular and quantitative genetic studies have shown that cytoplasmic factors contribute to heritable variation in both qualitative and quantitative traits in plants (Gillham, 1978). A second class of maternal effects in plants originate via the endosperm. During angiosperm development, multiple fertilization usually results in 3N endosperm with two nuclei from the maternal and only one from the paternal parent. Although the endosperm is not always triploid, it always contains more doses of maternal than paternal genes (Roach and Wulff, 1987). The endosperm contains enzymes important for germination (Harvey and Oaks, 1974) and is also the source of nutrients for the developing embryo. As a consequence of the differential dosage of male and female genes, the female parent may have a more important role in determining the characteristics of this nutrient source. A third class of maternal effects is phenotypic, resulting from the environment or genotype of the maternal parent. These influences may occur via structure or physiology. The tissues immediately surrounding the developing embryo and endosperm are all maternal. These tissues, the integuments of the ovule and the wall of the ovary, eventually form the seed coat, fruit, and accessory seed structures such as the hairs, awns, and barbs.

Roach and Wulff, (1987) concluded that at the seed stage, a large proportion of the variation is under maternal control, and this maternal control appears to have a large

environmental component. These effects carry through to the early seedling stages, but at the late seedling stage, the genotype of the offspring itself begins to contribute significantly to the variation. Endosperm maternal effects and most phenotypic maternal effects have their major influence via the seed or seed structure. Cytoplasmic inheritance is the only mechanism for direct maternal effects on adult traits, although there may be indirect carryover effects from the seed or seedling stage.

Vanuprasad *et al*. (2011) suggested that seed size traits (seed length, seed width and seed: width ratio) were controlled by a combination of both maternal and nuclear gene effect. He further stated that in a breeding programme for confectionery traits, it is essential to include a large-seeded genotype as the female to exploit the maternal effects.

2.15 OIL AND PROTEIN CONTENT IN GROUNDNUT

Besides physical (seed mass and shape, integrity of seed taste and blanching efficiency) and sensory (seed color, texture, flavor) factors, nutritional (oil and protein contents, fatty acid and amino acid composition) factors are important in the food trade.

Groundnut seeds contain 44-56% oil and 22-30% protein on a dry seed basis (Savage and Keenan, 1994). Jambunathan *et al*. (1985) reported protein to range between 16 to 34%. After analysis of twenty groundnut varieties Asibuo *et al*. (2008) reported oil content ranged from 33.6 to 54.95%. Five varieties had oil content higher than 50%. Groundnut varieties belonging to subspecies hypogaea had slightly more oil than the fastigiata varieties. Quality analysis of seed samples of 152 groundnut genotypes from

China showed that the protein, oil and sucrose content, oleic acid and linoleic acid content, as percentage of total fatty acids, ranged from 18.93 to 30.22%, 37.42 to 55.69%, 2.73 to 14.65%, 20 to 80.51% and 2.91 to 41.82%, respectively (Wang *et al*., 2011).

The oil content of groundnut has been reported to range from 35.8 to 54.2 per cent and average near 45 per cent (Jambunathan *et al.*, 1985; Dwivedi *et al.*, 1990). Pancholy *et al.* (1978) reported that per cent oil ranged from 46 to 52.6 per cent. Gupta *et al*. (1982) analyzed twenty-five varieties of groundnut for oil content. Highest oil content of 48.60 per cent and lowest of 44.52 was observed. Rajgopal *et al*. (2000) evaluated 118 bold seeded accessions for 2 years and reported range of oil content from 48 per cent to 51.4 per cent. Significant difference for oil content was observed among test genotypes, highest was 53.8 and lowest 47.3. (Manivel *et al*., 2000).

Dwivedi *et al*. (1993) reported a range of 16 to 34 per cent protein observed in 8000-germplasm accession analyzed at ICRISAT. However, these ranges of variation were not maintained when selected genotypes with such variation were tested over season and locations. Pancholy *et al*. (1978) reported crude protein content of whole seed groundnuts ranges between 22 and 30 per cent showing a large variation, which is greatly influenced by genotype and environments.

Shelf-life and nutritional quality of the oil and other groundnut products are influenced by fatty acid composition. Oleic (O) and linoleic (L) acids are nutritionally important and together account for 75 to 80 percent of the total fatty acids in groundnut oil (Dwivedi *et al*., 1993).

2.16 INHERITANCE AND BREEDING OF OIL AND PROTEIN CHARACTERS

Inheritance of oil and protein contents has been reported by many workers;

Tai and Young (1975) reported that oil content is quantitatively inherited, while Martin (1967) estimated that only two pairs of major genes control oil content in peanut seeds. Martin (1967) and Patil (1972) obtained high heritability estimates for oil content.

Gaurav *et al*. (2010) carried out genetic analysis of four yield components and four confectionery traits on two interspecific crosses involving two bold seeded and two Spanish genotypes of groundnut and revealed that both additive and non-additive gene effects were prominent in the case of quality traits viz; protein content, oil content, sugar content and oleic/linoleic ratio.

The O/L ratio determines the shelf-life of oil and other groundnut products. High oleic groundnut rather than normal groundnuts have increased shelf life and thus improve the oxidative stability of groundnut products (Isleib *et al*., 2006). Two recessive genes controls high oleic character and is therefore easily transferable to existing cultivars through backcross method (Moore and Knauft, 1989).

Shany, (1977) indicated that high protein content is dominant to low protein content, and low oil content dominant to high oil content. Both oil and protein contents showed a non-additive genetic variance (Basu *et al*., 1988).

Wang *et al*. (2011) analyzed correlations between quality attributes in 152 genotypes of groundnut and reported that protein content was not correlated with oil content however; both of them were negatively related to sucrose content.

Sogut, (2009) observed Oil and protein yields to change with cropping systems and he concluded that the main cropping increased oil and protein yield as a result of higher pod yield. His results showed that late planting dates negatively affect groundnut pod yield through reductions in all yield components except for protein concentration.

2.17 GROUNDNUT IMPROVEMENT IN GHANA

One of the major reasons for low export market of groundnut in Ghana is that little or no hybridization work has been done to develop and release high yielding varieties that have local and international acceptable characteristics suited for the confectionery market. Information on groundnut hybridization in Ghana is scarce and there is no record of a groundnut variety that has been released from a groundnut hybridization programme.

Tremendous work on the evaluation of confectionery groundnut varieties is on-going at the Council for Scientific and Industrial Research (CSIR)-Crop Research Institute (CRI), Kumasi, and a few has been released in 2012. Confectionery varieties presently released by CRI include; Oboshie, and Obolo. Non confectionery varieties were also released by CRI in 2004. They are resistant to the rosette virus and other

field diseases and are also high yielding, but have high oil, low protein and smaller seed size, they include; Adepa, Nkosour, Jenkaah, and Azivivi.

To improve the marketability of both types of groundnut (confectionery and non-confectionery), crosses between one of the confectionery (Oboshie) and two non-confectionery (Nkosour and Jenkaah) and their reciprocals had been made. This study, therefore, forms an integral part of the ongoing groundnut breeding work at CRI. The information provided on the inheritance of seed size, protein and oil contents would help choose appropriate breeding strategies for development of confectionery varieties which will attract both local and foreign consumers.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 SITE OF EXPERIMENT

The study was conducted at both the Faculty of Agriculture of Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, and Centre for Scientific and Industrial Research (CSIR)- Crop Research Institute (CRI), Fumesua, Kumasi (6° 45´ N, 1° 25´ W) from February 2012 to May, 2013. Two stages of hybridization trials were conducted in pots at KNUST, whilst an evaluation experiment was done on the upland research field at CSIR-CRI, Fumesua.

The upland research field area falls within the semi-deciduous rain forest zone and is characterized by a bimodal rainfall pattern, from April to July and then from September to December, with an average annual rainfall of 1500 mm. The soil is Ferric Acrisol (FAO/UNESCO legend, 1986).

3.1.1 CROPPING HISTORY OF STUDY AREA

The upland evaluation study area was previously planted to rice

3.2 PARENTAL PLANTS

The basic material for the present study consisted of three groundnut varieties, Oboshie, Nkosour and Jenkaah. These were bred at the International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, India. Oboshie was screened and evaluated for confectionary purposes, and was released in 2012 at CSIR-CRI, Kumasi. Nkosour and Jenkaah were screened and evaluated for resistance to

rosette virus and other field diseases and are also high yielding. They were released in 2004 at CSIR-CRI, Kumasi. The three parents Oboshie, Nkosour and Jenkaah were mostly referred to as Obo, Nko and Jen respectively in this report.

Detailed description of the three parents is given below:

3.2.1 OBOSHIE

Oboshie with accession number ICGV 98412 is a confectionery variety bred at the International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, India. It has been screened and evaluated for its confectionery attributes and adaptation at the CSIR-CRI, and was released in 2012.

Oboshie belongs to subspecies fastigiata with a semi-erect growth habit. It exhibits a sequential branching pattern. It has a dark green leaf colour, elliptic leaf shape and light green petiole and mid vein colour. The plant flowers in 26 days after planting (DAP) and matures within 105-110 DAP with yield potential of 2.6 tons/ha. The pod measures 3.565 cm in length and 1.7 cm in width. It has a brown seed colour, with a length of 1.855 cm and width of 1. 0 cm. Has a shelling outturn of 67 %. The dry seed contains 34.13% protein, 46.49% oil and 6.78% carbohydrate.

It is moderately tolerant to rosette virus disease, resistant to early leaf spot and moderately resistant to late leaf spot.

3.2.2 NKOSOUR (M578-79)

Following the devastating effect of rosette virus in 1993, Nkosour (M578-79) and Jenkaah (MDR-8-19) were among 40 accessions received from ICRISAT to be evaluated at CSIR-CRI for resistance to the rosette virus.

It is semi-erect and has pubescence on both the stem and the leaf. The flower colour is orange-yellow. The plant bears an average of 40 pods and grows to a height of 18.1cm. The leaf is dark green in colour and elliptic in shape. The petiole and mid vein are light green in colour. The pod has two seeds with a moderate pod beak and measures 2.9cm in length and 1.4cm in width. The pod is moderately constricted. The seed is slightly dark brown and measures 1.401 cm in length and0.782 cm in width. Seed coat thickness and 1000 seeds weight are 0.004 cm and 473.1 g respectively. The seed contain 27.53 % protein, 48.84 % oil and 21.13 % carbohydrate.

It is resistant to the rosette virus and tolerant to the *Cercospora* leaf spot. It flowers in 29 days after planting and matures within 120 days after planting with yield potential of 2282kg/ha. The variety is well identified by its bold seed and uniformity in colour, making it a potential premium in the confectionery market. It is also tolerant to drought.

3.2.3 JENKAAH (MDR-8-19)

It is semi-erect and has pubescence on both the stem and the leaf. The flower colour is orange-yellow. The plant bears an average of 43 pods and can grow to a height of 19.1cm. The leaf is dark green in colour and oblong-elliptic in shape, with both the petiole and mid vein being light green in colour. The pod has two seeds with a

moderate pod beak and measures 3.1cm in length and 1.3cm in width. The pod has a moderate constriction. The seed is light brown in colour and measures 1.354 in length and 0.803 in width. Seed coat thickness and 1000 seeds measures 0.002 cm and 469.1 gm. respectively. The dry seed contains protein 27.82 %, oil 51.13 % and carbohydrate 18.08 %.

It is resistant to the rosette virus and the *Cercospora* leaf spot. It flowers in 28 days after planting and requires about 120 days from planting to maturity with yield potential of 2456kg/ha, about 18% more than that of F.MIX and 26% more than that of Schitaochi, the recommended varieties farmers are currently using. It has shelling percentage of 73.

Among parents, the boldness of Oboshie is clearly distinct from the others, and is therefore referred to in this study as the higher parent for the studied traits.

3.3 SEEDLING ESTABLISHMENT

Seeds were sown in plastic bowls/ pots measuring 45 cm (top diameter) x 39 cm (base diameter) x 12 cm (height) with drainage holes. The pots were filled with 16.5 kg sterilized soil in the ratio of two parts top soil or black soil to one part river sand. Two seeds were planted into each pot and thinned to one plant per pot one week after germination. Sowing of parents was staggered over a period of three days to synchronize flowering. Pots were placed on a platform constructed to facilitate appropriate agronomic practices and ease hybridization activities.

3.4 EXPERIMENTS CONDUCTED

3.4.1 Experiment 1: Hybridization of parents and F1's to develop progenies for F1, F_2 and backcrosses.

Hybrids were generated using manual emasculation and pollination techniques. Equipment used for hybridization included; a pair of forceps with fine points, different coloured nylon threads, petri dishes and alcohol for rinsing forceps and fingers between pollination.

This operation was done in two stages as follows:

3.4.1.1 Stage 1: Crosses of parents to develop F1 population.

This included both straight and reciprocals. Two straight crosses viz.;

Oboshie x Nkosour, Oboshie x Jenkaah and their reciprocals i.e., Nkosour x Oboshie, Jenkaah x Oboshie were done.

3.4.1.2 Stage 2: Crosses of F1's with either parents to develop backcrossed progenies and selfing of F1's to develop F2 population.

Eight backcrosses viz.; (Nkosour x Oboshie) x Nkosour, (Nkosour x Oboshie) x Oboshie, (Jenkaah x Oboshie) x Jenkaah, (Jenkaah x Oboshie) x Oboshie, (Oboshie x Nkosour) x Oboshie, (Oboshie x Nkosour) x Nkosour, (Oboshie x Jenkaah) x Oboshie, (Oboshie x Jenkaah) x Jenkaah. F1's of the four crosses were selfed to obtain F2 generation.

3.4.2 Experiment 2: Evaluation of parents, F1's, F_2's and backcrosses

A field experiment was conducted during the dry season on 14th December, 2012 at the CSIR-CRI, Kumasi, to study the genetic control of seed quality traits in

groundnut. The experiment consisted of three parents (Nko, Jen and Obo), four F1's (Nko x Obo, Obo x Nko, Jen x Obo and Obo x Jen), eight backcrosses (Nko x Obo) x Nko, (Nko x Obo) x Obo, (Obo x Nko) x Obo, (Obo x Nko) x Nko, (Jen x Obo) x Jen, (Jen x Obo) x Obo, (Obo x Jen) x Obo, (Obo x Jen) x Jen and four F2's (Nko x Obo) selfed, (Obo x Nko) selfed, (Jen x Obo) selfed, and (Obo x Jen) selfed.

3.5 EXPERIMENTAL DESIGN AND AGRONOMIC PRACTICES

The experimental area was prepared to fine tilth before planting was done. Experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Plot size varied by generation. Each plot was a single row for F1 and backcross generations, and six rows for parent and F2 generations. Rows were 2.0 m long with a between and within row spacing of 30 x 20 cm respectively. NPK-15:15:15 (40kgha^{-1}) was applied two weeks after germination and gypsum (40kgha^{-1}) applied at 50% flowering. Mechanical and manual irrigation was done on a regular basis. Other field agronomic practices were done as and when necessary.

3.6 DATA COLLECTION AND DESCRIPTION OF OBSERVATION

3.6.1 PHYSIOLOGICAL DATA

3.6.1.1 Days to 50% flowering:

This was achieved by counting the number of days after planting (DAP) that 50% of the total number of plants had opened flowers.

3.6.1.2 Plant height:

Length of main axil from ground level to the tip of the closed apical leaflet, measured in cm. Mean of five tagged plants was recorded at 50% flowering and at maturity.

3.6.1.3 Number of primary branches per plant:

Number of n + 1 branch borne on the main axis was counted and mean of five tagged plants was recorded at 50% flowering and at maturity.

3.6.1.4 Number of leaves per plant:

Number of fully opened leaves was counted and mean on five tagged plants was recorded at 50% flowering and at maturity.

3.6.2 YIELD DATA

3.6.2.1 Number of filled and unfilled pods per plant:

Numbers of filled and empty/pop pods were counted separately on five tagged plants and mean recorded.

3.6.2.2 Number of aborted pegs per plant:

Number of pegs that did not swell to form pod were counted on five tagged plants and mean recorded.

3.6.2.3 Total number of pegs per plant:

Total number of filled pods, unfilled pods and aborted pegs were counted on five tagged plants and mean recorded.

3.6.2.4 Shelling percentage:

Fifty mature pods were selected at random and weight recorded in grams. Seeds from the fifty pods were weighed in grams. The shelling percentage was calculated as:

$$\text{Shelling \%} = \frac{\text{Seed mass}}{\text{Pod mass}} \times 100$$

3.6.2.5 Pod yield per plant:

Pod yield per plant was calculated by dividing total pod dry yield by the number of plants harvested.

3.6.2.6 Seed yield per plant:

The mean weights of the total seeds shelled from mature pod of ten plants were recorded in grams.

3.6.3 Pod and Seed character data:

3.6.3.1 Pod length and width:

Ten dried mature pods were selected at random and pod length and width were measured in millimeters (mm) using a venier caliper.

3.6.3.2 Seed length and width:

Ten dried mature seeds were selected at random and seed length and width were measured in mm using a venier caliper.

3.6.3.3 100-seed weight:

100 well dried mature seeds were selected at random from a seed lot of each treatment and weight recorded in grams.

3.6.3.4 Seed size:

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

3.7 PROXIMATE ANALYSIS

3.7.1 OIL CONTENT

Oil content was determined using soxhlet method as described by Jambunathan *et al*., (1985). 5 g of groundnut seeds were made into fine powder in a pestle and mortar and groundnut meal was extracted with petroleum ether (60-80°C bp) for 5 hours in soxhlet apparatus. Petroleum ether was evaporated. Powder weight before and after extraction was taken, the difference between the two was expressed in terms of percentage.

3.7.2 CRUDE PROTEIN ESTIMATE

To estimate protein content, nitrogen concentration was determined using Technicon auto analyzer (Singh and Jambunathan, 1980). 0.5 g of defatted sample was taken and 12.5 ml of distilled water was added and kept it for extraction for 8-10 hours. Sample was centrifuged for 15 minutes at 10000 rpm by using centrifuge. Supernatant was decanted into separate test tube and made up to known volume. The extracted sample was further used for estimation of proteins. A factor of 5.46 was used to convert nitrogen into crude protein content.

3.8 STATISTICAL ANALYSIS

Data for traits were subjected to Analysis of Variance (ANOVA) using Genstat statistical package (Discovery Edition 4). Least Significant Difference (LSD) at 5% was used to determine the significant differences among the means of the various generations.

Generation mean analysis using scaling test A, B and C proposed by Mather (1949) and joint scaling test of Cavalli (Cavalli, 1952) was followed using Microsoft Excel to determine the genetic control of seed size, and seed weight.

The A, B and C scaling tests were solved individually to check the adequacy of the additive-dominance model by their deviation or equality to zero. The model was adequate when all of each individual value equal to zero. A corresponding standard error (SE) for each test was used as a denominator to determine the calculated t-test. Significance of the values of A, B, and C was determined by comparing the calculated and tabulated t values, at a degree of freedom (df) determined by summing up the individual df of each parameter. Formulas to determine individual A, B and C values, their corresponding standard errors and test of significance were as follows:

Table 3.1 Determination of A, B, C scaling value, standard error and calculated t value

Scaling test	Value for deviation from zero	Standard Error	tcal.
A	$2B_1 - F_1 - P_1 = 0 = A$	$SE_A = \sqrt{V_A}$ $V_A = 4V_{B1} + V_{F1} + V_{P1}$	$t_A = A/SE_A$
B	$2B_2 - F_1 - P_2 = 0 = B$	$SE_B = \sqrt{V_B}$ $V_B = 4V_{B2} + V_{F1} + V_{P2}$	$t_B = B/SE_B$
C	$4F_2 - 2F_1 - P_1 - P_2 = 0 = C$	$SE_C = \sqrt{V_C}$ $V_C = 16V_{P1} + 4V_{F1} + V_{P1} + V_{P2}$	$t_C = C/SE_C$

Where; P_1, P_2, F_1, F_2, B_1 and $B_2$are the generation mean, V_{P1}, V_{P2}, V_{F1}, V_{F2}, V_{B1} and V_{B2} are variances of the mean of the generations involved in the test, t_A, t_B and t_C are the calculated t values and SE the standard error.

Significance of each parameter (A, B and C) from zero is concluded when the t calculated is higher than the t tabulated.

Cavalli's joint scaling test has the advantage of testing goodness of fit once instead of in three separate instances and of making clear at once, if the fit is bad which part of the data is responsible for it. The generation means was influenced by three parameters: m, the mid-parent value; [d], the additive components and [h], the dominance components in a generalized inverse matrix equation ($M = J^{-1}S$). It estimates the weighted least squared value of m, [d] and [h] from the generation means. The weights are the reciprocals of the variance of the generation means (1/Vx). Expected generation means are then calculated using the weighted m, [d] and [h] values. The comparison between the observed and expected can be effected by assuming the sum of squares minimized in the fitting process to be distributed as X^2 (Chi square) with the degree of freedom equal to the number of generation means (P_1, P_2, F_1, F_2, B_1 and B_2) minus the number of parameters which has been fitted (m, [d] and [h]).

Inadequacy of the additive-dominance model was tested utilizing one or more of the individual scaling test (A, B and C) showing a significant departure from zero, and by a significant X^2, inadequacy of the additive-dominance model indicates the expression of complex genetic factors (non-allelic interaction or epistasis, linkage and multiplication effects) present in the inheritance of the trait (Mather and Jinks, 1982). A log transformation is used to normalize the distribution in the non-segregating populations (Mather and Jinks, 1982).

Table 3.2 Significance estimates and interpretation of the 3 genetic parameters are as follows:

Parameters	Gene effects	Interpretation
m	Common genes and the environment	Common genes the parents share are significant if m is significant from zero.
[d]	Additive genes	Additive gene effect is significant if [d] is significant from zero.
[h]	Dominance gene	Dominance gene effect is significant, significant net directional dominance if [h] is significant from zero. Sign of [h] tells the direction of dominance for the trait.

3.9 ESTIMATE OF HETEROSIS

Estimates of heterosis were done using mid-parent values as the percent deviation of the mean F_1 value from the mid-parent. Mean components of seed quality traits were utilized to estimate heterosis.

CHAPTER FOUR

4.0 RESULTS

4.1 CROSSES AND SUCCESS RATE

The number of crosses and the success rates are presented in Table 4.1. The success rates were different for the crosses. Mean success rate was 58.4%.

Table 4.1: Type of crosses, number of flowers, number of pods and percent success

Type of cross	Number of Flowers pollinated	Number of pods obtained	Percent (%) success
Obo x Nko	65	38	58.5
Nko x Obo	69	51	73.9
Obo x Jen	70	43	61.4
Jen x Obo	52	28	53.8
(Obo x Nko) x Obo	47	24	51.1
(Nko x Obo) x Obo	51	24	47.1
(Obo x Jen) x Obo	50	33	66.0
(Jen x Obo) x Obo	47	32	68.1
(Obo x Nko) x Nko	52	24	46.2
(Nko x Obo) x Nko	42	19	45.2
(Obo x Jen) x Jen	45	26	57.8
(Jen x Obo) x Jen	35	23	65.7
Total	625	365	

The highest success rate was obtained from the reciprocal cross between Nkosour x Oboshie (73.9) and the least from (Nkosour x Oboshie) x Nkosour (45.2).

Backcross 1 (hybrid crossed with higher parent) for direct and reciprocal (Oboshie x Jenkaah) x Oboshie and (Jenkaah x Oboshie) x Obshie had higher success rate than

backcross 1 for (Oboshie x Nkosour) x Obshie and (Nkosour x Oboshie) x Oboshie. The same was maintained for backcross 2 (hybrid crossed with lower parent) (Table 4.1).

4.2 CROP ESTABLISHMENT AND POD YIELDING COMPONENTS

Seed emergence of parents, direct and reciprocal crosses are presented in Table 4.2.

Seed emergence was very low at 21 days after planting (DAP). It however, improved significantly after 42 DAP. Erratic emergence pattern greatly affected the results.

High seed emergence mean was recorded for Jenkaah (parent) while the least emergence mean was recorded for Oboshie (parent) among the parents at 21 and 42 DAP. No seed emergence occurred during the first 21 DAP for F_1 Oboshie x Jenkaah cross.

The highest emergence proportion at 21 and 42 DAP was recorded for hybrids Jenkaah x Oboshie and Nkosour x Oboshie respectively.

The segregating generation (F_2) Oboshie x Nkosour and Oboshie x Jenkaah had a higher emergence mean value than their corresponding mid-parent values at 21 DAP. Among the segregating generation (F_2), the direct and reciprocals (Oboshie x Jenkaah and Jenkaah x Oboshie) gained the highest and similar emergence means at 42 DAP.

Table 4.2: Number of seeds planted and emergence at 21 and 42 days after planting (DAP).

Parent/cross (Generation)	No. of seed planted	21 DAP	42 DAP
Parents			
Oboshie (Obo)	60	2.7 ± 4.62	32.3 ± 19.73
Nkosour (Nko)	60	3.7 ± 2.08	35.7 ± 11.15
Jenkaah (Jen)	60	8.3 ± 4.93	45.7 ± 9.71
F_1 generation			
Obo x Nko	10	1.0 ± 1.00	5.3 ± 0.58
Nko x Obo	10	1.7 ± 2.08	9.3 ± 1.15
Obo x Jen	10	0.0 ± 0.00	5.0 ± 0.00
Jen x Obo	10	5.0 ± 1.73	7.3 ± 1.15
F_2 generation			
Obo x Nko	60	7.3 ± 4.51	26.7 ± 10.12
Nko x Obo	60	1.7 ±1.53	25.0 ± 14.18
Obo x Jen	60	7.3 ± 3.06	28.0 ± 7.94
Jen x Obo	60	3.3 ± 0.58	28.0 ± 11.79
Backcross 1			
(Obo x Nko) x Obo	10	1.0 ± 1.00	5.0 ± 0.00
(Nko x Obo) x Obo	10	1.7 ± 1.15	6.0 ± 1.00
(Obo x Jen) x Obo	10	0.7 ± 0.58	7.0 ± 2.65
(Jen x Obo) x Obo	10	1.7 ± 1.53	6.0 ± 1.10
Backcross 2			
(Obo x Nko) x Nko	10	1.0 ± 1.00	5.3 ± 0.58
(Nko x Obo) x Nko	10	0.3 ± 0.58	4.3 ± 1.15
(Obo x Jen) x Jen	10	0.7 ± 0.58	4.0 ± 1.00
(Jen x Obo) x Jen	10	1.0 ± 1.00	5.7 ± 1.15

Yield components including days to 50% flowering, number of filled and unfilled pods, number of aborted and total number of pegs are presented on Table 4.3.

Days to 50 % flowering, number of filled and unfilled pods per plant, number of aborted pegs and total number of pegs produced per plant were affected by seed dormancy (Table 4.3).

Mean days to 50% flowering and number of aborted pegs were higher for Oboshie (parent) than the other parents. Oboshie also recorded the least number of filled pods and the highest number of total pegs produced among parents (Table 4.3)

Mean days to flowering were higher in the hybrids than their corresponding parents except for Jenkaah x Oboshie cross, and the highest number of days to 50% flowering among hybrids was recorded for Oboshie x Nkosour cross. The segregating generation (F_2) for Oboshie x Nkosour and Oboshie x Jenkaah recorded a lower number of days to 50% flowering than their corresponding hybrids (Table 4.3)

The highest and least number of days to 50% flowering were recorded for backcross two, (Nko x Obo) x Nko (52) and segregating generation (F_2) Oboshie x Jenkaah (33) respectively (Table 4.3).

Segregating generation (F_2) Oboshie x Nkosour and backcross two (Obo x Nko) xNko recorded the highest (41) and least (11) number of filled pods per plant respectively.

In general, more total number of pegs were produced by the segregating generation (F_2) Oboshie x Nkosour (136) and the least number of pegs was produced by the hybrid (F_1) Nkosour x Oboshie (Table 4.3)

Table 4.3: Mean days to 50 % flowering, number of filled and unfilled pods per plant, number of aborted pegs and total number of pegs per plant for 19 groundnut generations

Parent/cross (Generation)	Days to 50 % flowering	No. of filled pods per plant	No. of unfilled pod per plant	No. of aborted pegs per plant	Total number of peg per plant
Parents					
Oboshie (Obo)	44	20	26	97	143
Nkosour (Nko)	34	31	33	34	98
Jenkaah (Jen)	39	25	32	34	91
F_1 generation					
Obo x Nko	47	29	32	24	85
Nko x Obo	38	22	21	24	67
Obo x Jen	46	34	40	31	105
Jen x Obo	34	27	41	52	119
F_2 generation					
Obo x Nko	36	41	38	58	136
Nko x Obo	42	24	31	32	86
Obo x Jen	33	28	50	46	124
Jen x Obo	34	28	33	35	96
Backcross 1					
(Obo x Nko) x Obo	41	22	29	21	71
(Nko x Obo) x Obo	34	28	41	27	96
(Obo x Jen) x Obo	48	16	17	17	50
(Jen x Obo) x Obo	35	26	26	25	77
Backcross 2					
(Obo x Nko) x Nko	47	11	31	36	78
(Nko x Obo) x Nko	52	17	34	23	74
(Obo x Jen) x Jen	38	21	31	33	84
(Jen x Obo) x Jen	42	25	30	28	83
Mean	40.1	24.9	32.3	35.5	89.2
Lsd (0.05)	ns	ns	ns	ns	ns
CV (%)	18.2	43.0	38.9	78.4	35.3

ns = Not significant at $P < 0.05$

4.3 POD AND SEED CHARACTERS

Analysis of variance indicated significant differences ($p< 0.05$) for dry pod weight per plant, seed weight per plant, and pod width. Significant differences ($p < 0.01$) were recorded for 100 seed weight, pod length, seed length, seed width and seed size (Table 4.4).

Mean values of hybrids (F_1) of Oboshie x Jenkaah cross and their reciprocals were higher than their respective mid-parents for all traits, while mean values of Oboshie x Nkosour (direct) cross were higher than their corresponding mid-parents for all traits except pod width (Table 4.4). Among the hybrids, Oboshie x Nkosour cross recorded highest mean values of 26.4, 86.4, 33.30, 17.99, 9.92 and 1.82 for dry pod weight per plant, 100 seeds weight, pod length, seed length, seed width and seed size respectively.

Segregating population (F_2) mean values for both direct crosses (i.e. Oboshie x Nkosour and Oboshie x Jenkaah) were higher than their corresponding mid-parent values except seed size for Oboshie x Jenkaah cross (Table 4.4).Backcross one (B_1) values of reciprocal crosses were higher than values of their corresponding direct crosses for all traits except seed width for (Nkosour x Oboshie) x Oboshie and seed size for (Jenkaah x Oboshie) x Oboshie crosses (Table 4.4).

There was no significance difference between the direct, reciprocals and back crosses, pooled values were computed to estimate the genetic control of seed size and seed weight per plant in two crosses.

4.4 CHEMICAL COMPOSITION

Means and their respective standard errors for 19 generations of groundnut composite analyses are presented in Table 4.5.

Table 4.4: Mean pod weight, weight of seed per plant, 100 seed weight, shelling percentage, pod length, pod width, seed length, seed width, seed length and width ratio for the crosses Oboshie x Nkosour and Oboshie x Jenkaah and their reciprocals

Parents/crosses (Generation)	Dry pods weight per plant (g)	Weight of seeds per plant (g)	100 seeds weight (g)	Pod length (mm)	Pod width (mm)	Seed length (mm)	Seed width (mm)	L:W seed (Seed size)
Parents								
Oboshie (Obo)	22.3	14.73	86.9	34.20	12.05	18.08	9.87	1.83
Nkosour (Nko)	24.0	15.43	59.8	29.09	11.11	14.88	9.07	1.64
Jenkaah (Jen)	15.6	9.50	55.3	27.13	10.49	14.74	8.79	1.68
F_1 generation								
Nko x Obo (F_1)	19.5	13.00	82.9	32.89	11.43	17.80	9.78	1.82
Obo x Nko (F_1)	26.4	17.07	86.4	33.30	11.52	17.99	9.92	1.82
Jen x Obo (F1)	24.7	15.57	81.3	33.18	11.89	17.29	9.80	1.76
Obo x Jen (F1)	27.2	17.23	75.6	32.54	11.46	16.85	9.59	1.76
F_2 generation								
Nko x Obo (F2)	23.4	15.17	74.0	31.73	11.34	16.99	9.33	1.83
Obo x Nko (F2)	36.0	23.40	82.5	32.23	11.77	17.55	10.18	1.73
Jen x Obo (F2)	22.0	13.77	70.4	30.50	10.83	16.21	9.32	1.74
Obo x Jen (F2)	26.3	17.53	81.1	31.11	11.61	17.23	10.06	1.71
Backcross 1								
(Obo x Nko) x Obo	14.9	9.43	64.5	30.95	11.77	15.85	8.96	1.77
(Nko x Obo) x Obo	24.1	14.83	68.3	31.50	11.90	17.24	8.84	1.95
(Obo x Jen) x Obo	11.3	7.33	66.4	31.69	11.79	16.44	8.88	1.85
(Jen x Obo) x Obo	23.3	15.40	75.7	32.71	12.46	17.18	9.65	1.78
Backcross 2								
(Obo x Nko) x Nko	6.5	4.07	50.4	27.46	10.65	13.78	8.58	1.61
(Nko x Obo) x Nko	8.0	5.03	50.9	28.50	10.40	14.80	8.32	1.78
(Obo x Jen) x Jen	9.8	5.67	51.2	27.47	11.01	14.39	8.45	1.70
(Jen x Obo) x Jen	18.6	11.17	62.4	28.72	11.72	15.36	9.28	1.66
Mean	20.2	12.91	69.8	30.89	11.43	16.35	9.30	1.76
Lsd	14.89*	9.99*	15.36**	2.41**	0.90*	1.20**	0.89**	0.15**
CV (%)	44.5	46.7	13.3	4.7	4.8	4.4	5.8	5.2

*---Significant at P < 0.05 **---Significant at P < 0.01

Table 4.5 Means and standard errors of protein (%), oil (%), carbohydrate (%) and ash content for proximate composition of 19 generations of parents, direct and reciprocal crosses in groundnut

Generation	Protein (%)	Oil (%)	Carbohydrate (%)	Ash (%)
Parents				
Oboshie (Obo)	31.20 ± 0.248	47.17 ± 0.078	17.99 ± 0.307	3.64 ± 0.050
Nkosour (Nko)	28 61 ± 0.121	47.56 ± 0.010	19.84 ± 0.128	3.96 ± 0.029
Jenkaah (Jen)	27.81 ± 0.127	51.22 ± 0.010	16.84 ± 0.127	4.13 ± 0.050
F1 generation				
Obo x Nko	26.67 ± 0.127	47.21 ± 0.032	22.41 ± 0.085	3.72 ± 0.126
Nko x Obo	26.86 ± 0.121	47.24 ± 0.006	22.14 ± 0.191	3.75 ± 0.145
Obo x Jen	26 43 ± 0.127	48.85 ± 0.006	20.85 ± 0.140	3.87 ± 0.076
Jen x Obo	26.07 ± 0.127	48.79 ± 0.010	21.44 ± 0.272	3.70 ± 0.145
F2 generation				
Obo x Nko	27.33 ± 0.127	47.28 ± 0.006	21.20 ± 0.182	4.19 ± 0.071
Nko x Obo	27.47 ± 0.00	47.28 ± 0.006	21.10 ± 0.140	4.16 ± 0.145
Obo x Jen	26.51 ± 1.097	48.84 ± 0.010	19.93 ± 0.156	4.05 ± 0.100
Jen x Obo	26.97 ± 0.127	48.82 ± 0.006	20.21 ± 0.221	4.00 ± 0.100
Backcross 1				
(Obo x Nko) x Obo	28.05 ± 0.121	47.23 ± 0.006	20.68 ± 0.182	4.05 ± 0.076
(Nko x Obo) x Obo	28.10 ± 0.000	47.20 ± 0.010	20.67 ± 0.067	4.03 ± 0.076
(Obo x Jen) x Obo	28.33 ± 0.000	49.10 ± 0.010	18.80 ± 0.120	3.77 ± 0.121
(Jen x Obo) x Obo	28.18 ± 0.121	49.15 ± 0.010	18.96 ± 0.058	3.71 ± 0.095
Backcross 2				
(Obo x Nko) x Nko	27.81 ± 0.127	47.69 ±0.010	20.54 ± 0.184	3.97 ± 0.076
(Nko x Obo) x Nko	27.67 ± 0.000	47.70 ± 0.006	20.65 ± 0.026	3.98 ± 0.029
(Obo x Jen) x Jen	27.90 ± 0.000	49.25 ± 0.006	19.12 ± 0.095	3.74 ± 0.098
(Jen x Obo) x Jen	27.99 ± 0.121	49.35 ± 0.006	18.49 ± 0.207	4.17 ± 0.098

Values are means of triplicate determination expressed on dry weight basis

Protein content ranged from 26.07 % for the cross Jenkaah x Oboshie (F_1) to 31.20 % for Oboshie (parent) on a dry weight basis. Among the crosses, backcross 1 (B_1) in both direct and reciprocal crosses recorded the highest protein content ranging from 28.05 % for (Obo x Nko) x Obo to 28.33 % for (Obo x Jen) x Obo. Mean protein values for B_1 (Oboshie x Jenkaah) x Oboshie and B_1 (Jenkaah x Oboshie) x Oboshie were higher than the lower parent (Jenkaah) and their mean oil values are lower than the higher mean parent (Jenkaah) value. Oil content ranged from 47.17 % to 51.22 %

with Oboshie (parent) and Jenkaah (parent) recording the least and the highest respectively. Carbohydrate content ranged from 16.84% for Nkosour (parent) to 22.41% for Oboshie x Nkosour (F_1), and ash content on a dry weight basis ranged from 3.64% to 4.19% with Oboshie (parent) and Oboshie x Nkosour (F_2) recording the least and highest respectively.

4.5 GENETIC CONTROL FOR SEED SIZE AND SEED WEIGHT PER PLANT

4.5.1 Generation mean analysis of seed size

The generation means and their standard errors, variances, variances of means, weights (reciprocal of variance of generation mean) and expected generation means for seed size in six generations of two crosses (Oboshie x Jenkaah and Oboshie x Nkosour) are presented in Tables 4.6. The estimate of gene effect as per additive-dominance model with their standard errors, degree of freedom and chi square values for the scaling and joint scaling tests for seed size are reported in Tables 4.7.

Table 4.6: Estimates of six generation means based on three parameters (m, [d], [h]) for seed size in the crosses between Oboshie x Jenkaah and Oboshie x Nkosour

Generation	No. of plants	Mean (x) ± SE	Variance (V)	Variance of mean (V_x)	Wt ($1/V_x$)	m	d	h	Expected mean
OBOSHIE X JENKAAH									
Oboshie	10	1.78 ± 0.151	0.023	0.002	434.48	1	1	0	1.80
Jenkaah	10	1.58 ± 0.258	0.066	0.007	151.52	1	-1	0	1.50
F_1	20	1.81 ± 0.166	0.028	0.001	714.25	1	0	1	1.82
F_2	60	1.73 ± 0.195	0.038	0.001	1578.95	1	0	0.5	1.75
B_1	60	1.82 ± 0.180	0.032	0.001	1875.00	1	0.5	0.5	1.81
B_2	60	1.69 ± 0.215	0.046	0.001	1304.35	1	-0.5	0.5	1.69
OBOSHIE X NKOSOUR									
Oboshie	10	1.78 ± 0.151	0.023	0.002	434.48	1	1	0	1.82
Nkosour	10	1.68 ±0.133	0.018	0.002	555.56	1	-1	0	1.62
F_1	20	1.90 ± 0.285	0.081	0.004	246.91	1	0	1	1.85
F_2	60	1.79 ± 0.202	0.041	0.001	1463.41	1	0	0.5	1.74
B_1	60	1.87 ± 0.239	0.057	0.001	1052.63	1	0.5	0.5	1.84
B_2	60	1.70 ± 0.181	0.033	0.001	1818.18	1	-0.5	0.5	1.74

Mid – parent value for Oboshie x Jenkaah cross = 1.68

Mid- parent value for Oboshie x Nkosour cross = 1.73

The result of the scaling tests of Mather (1949) showed no significant difference from zero at $P \leq 0.05$ (Table 4.7) for seed size in scaling test A, B and C in both crosses (Oboshie x Jenkaah and Oboshie x Nkosour). Value for scaling test B and C in both crosses were negative whiles values for scaling test A in both crosses was positive.

Table 4.7 Estimates of scaling and joint scaling test for seed size in two groundnut crosses

	df	Oboshie x Jenkaah	df	Oboshie x Nkosour
Scaling test				
A	87	$0.63^{ns} \pm 0.076$	87	$0.60^{ns} \pm 0.100$
B	87	$-0.10^{ns} \pm 0.105$	87	$-2.00^{ns} \pm 0.089$
C	96	$-0.38^{ns} \pm 0.158$	96	$-0.56^{ns} \pm 0.177$
Parameters		**Joint scaling test**		
m	3	1.68** ± 0.032	3	1.72** ± 0.029
[d]	3	0.12* ± 0.028	3	0.10* ± 0.025
[h]	3	0.14^{ns} ±0.057	3	0.12^{ns} ± 0.059
X^2		1.02^{ns}		6.87^{ns}

*---- Significant at P = 0.05

**---Significant at P = 0.01

ns---Not significant at P = 0.05

Result for the joint scaling tests of Cavalli (1952) showed that values of calculated chi square in both crosses were not significantly different from zero at P = 0.05 (Table 4.7), which clearly indicates an adequacy for the additive dominance model. Both net additive [d] and dominance [h] effects were positive for the two crosses, but the magnitude of [h] in both crosses were higher than that of [d]. The net dominance [h] effect was however not significant ($P \geq 0.05$) in both crosses (Table 4.7).

The F_1 values, that is, 1.81 and 1.91 for Oboshie x Jenkaah and Oboshie x Nkosour crosses respectively were higher than their corresponding higher parent (Oboshie) and

mid-parental values (Table 4.6). The highest generation mean for seed size in the two crosses was recorded for B_1 (progeny of cross between F_1 and higher parent) in Oboshie x Jenkaah cross (1.82) and F_1 in Oboshie x Nkosour cross (1.90). Jenkaah (parent) and Nkosour (parent) recorded the least mean values for seed size in both crosses.

4.5.2 Generation mean analysis of seed weight per plant

The generation means and their standard errors, variances, variances of means, weights (reciprocal of variance of generation mean) and expected generation means for seed weight per plant in six generations of two crosses (Oboshie x Jenkaah and Oboshie x Nkosour) are presented in Tables 4.8. The estimate of gene effect as per additive-dominance model with their standard errors, degree of freedom and chi square values for the scaling and joint scaling tests for seed size are reported in Tables 4.9.

The highest mean seed weight per plant was recorded for Oboshie (19.58) and lowest for Jenkaah (4.78) in Oboshie x Jenkaah cross, but their hybrid seed weight value (12.05) was lower than their mid-parent value (12.18). Segregation generation (F_2) mean seed weight per plant value (13.82) was higher than corresponding hybrid (12.05), backcross 1 (11.37) and backcross 2 (9.33) in Oboshie x Jenkaah cross (Table 4.8)

Hybrids mean seed weight per plant (14.22) for Oboshie x Nkosour corss was higher than its mid-parent mean value (12.68). F_2 segregating generation mean value (18.87) was higher than it corresponding hybrid and backcrosses (Table 4.8).

Table 4.8: Estimates of six generation means based on three parameters (m, [d], [h]) for seed weight per plant in the crosses between Oboshie x Jenkaah and Oboshie x Nkosour

Generation	No. of plants	Mean (x) ± SE	Variance (V)	Variance of mean (V_x)	Wt ($1/V_x$)	m	d	h	Expected mean
OBOSHIE X JENKAAH									
Oboshie	5	19.58 ± 3.992	19.92	3.98	0.25	1	1	0	18.30
Jenkaah	5	4.78 ± 3.435	11.80	2.36	0.42	1	-1	0	5.53
F_1	10	12.05 ± 9.582	91.82	9.18	0.11	1	0	1	12.03
F_2	30	13.82 ± 8.885	78.94	2.63	0.38	1	0	0.5	11.97
B_1	30	11.37 ±10.596	112.27	3.74	0.27	1	0.5	0.5	15.17
B_2	27	9.33 ± 6.953	48.34	1.79	0.56	1	-0.5	0.5	8.78
OBOSHIE X NKOSOUR									
Oboshie	5	19.58 ± 3.992	19.92	3.98	0.25	1	1	0	19.49
Nkosour	5	5.78 ±2.224	4.95	0.99	1.10	1	-1	0	4.98
F_1	10	14.22 ± 8.080	65.29	6.53	0.15	1	0	1	9.43
F_2	30	18.87 ± 9.109	82.97	2.77	0.36	1	0	0.5	10.83
B_1	30	10.91 ±6.939	48.15	1.61	0.62	1	0.5	0.5	14.46
B_2	28	5.07 ± 4.682	21.92	0.78	1.28	1	-0.5	0.5	7.21

Mid parent value for Oboshie x Jenkaah (seed weight per plant) = 12.18

Mid parent value for Oboshie x Nkosour (seed weight per plant) = 12.68

Result of the scaling test of Mather (1949) showed that scaling test A, B and C were not significantly different from zero at P = 0.05 for the cross between Oboshie and Jenkaah, however the value for scaling test A was negative, while that for scaling test B and C were positive (Table 4.9)

The joint scaling test of Cavalli (1952) estimated a non significant Chi-square value for Oboshie x Jenkaah cross at P = 0.05 indicating that the additive- dominance model was adequate for the trait (Table 4.9). The mid-parent value m and net additive [d] were significantly different at P = 0.05 and the net dominance effect [h] was not significant at P = 0.05. Both net additive [d] and dominance [h] effects were positive, but the magnitude of [d] was greater than [h] (Table 4.9).

For the Oboshie x Nkosour cross for seed weight, results of Mather's (1949) scaling test showed that scaling test A, B and C were significantly different from zero at P = 0.05. Values for scaling test A and B were negative, while C was positive (Table4.9).

Chi-square estimate of the Cavalli (1952) joint scaling test for the cross Oboshie x Nkosour was significantly different from zero at P = 0.05 (Table 4.9). The mid-parent value m and net additive effect [d] were significant at P = 0.01 and the net dominance effect was not significant at P = 0.05. The net additive effect [d] value was positive and [h] negative. The magnitude of the additive effect was greater than the dominance effect (Table 4.9).

Since all of the scaling test of Mather (1949) and the joint scaling test of Cavalli (1952) were significant in the cross Oboshie x Nkosour for seed weight, a log transformation of the original data was done to remove the multiplicative effects of genes. The generation mean analysis procedure was repeated using the log-transformed data.(Table 4.10).

Table 4.9 Estimates of scaling and joint scaling test for seed weight per plant in two groundnut crosses

	df	Oboshie x Jenkaah	df	Oboshie x Nkosour
Scaling test				
A	42	$-1.75^{ns} \pm 5.304$	42	$-2.91^{**} \pm 4.117$
B	39	$0.42^{ns} \pm 4.324$	40	$-3.02^{**} \pm 3.262$
C	46	$0.74^{ns} \pm 9.229$	46	$2.50^{*} \pm 8.684$
Parameters		**Joint scaling test**		
m	3	$10.31^{**} \pm 1.229$	3	$12.24^{**} \pm 0.988$
[d]	3	$5.46^{*} \pm 1.135$	3	$7.25^{**} \pm 0.897$
[h]	3	$4.20^{ns} \pm 2.609$	3	$-2.81^{ns} \pm 2.037$
X^2		5.96^{ns}		41.19^{**}

*---Significant at P = 0.05 **--Significant at P = 0.01

ns—Not significant at P = 0.05 X^2 = Calculated Chi square

Table 4.10: Estimate of six generation means based on three parameter model (m, [d], [h]) for seed weight per plant in the cross between Oboshie x Nkosour (Log transformed)

Generation	No. of plants	Mean (x) ± SE	Variance (V)	Variance of mean (V_x)	Wt ($1/V_x$)	m	d	h	Expected mean
OBOSHIE X NKOSOUR									
Oboshie	5	1.28 ± 0.105	0.0109	0.0022	458.72	1	1	0	1.27
Nkosour	5	0.73 ± 0.180	0.0323	0.0065	154.80	1	-1	0	0.74
F_1	10	1.09 ± 0.253	0.0641	0.0064	156.01	1	0	1	1.08
F_2	30	1.23 ± 0.219	0.0481	0.0016	623.70	1	0	0.5	1.04
B_1	30	0.93 ±0.335	0.1121	0.0037	267.62	1	0.5	0.5	1.18
B_2	27	0.52 ± 0.452	0.2045	0.0073	136.92	1	-0.5	0.5	0.91

Mid-parent value for Oboshie x Nkosour-Log (seed weight per plant) = 1.01

Table 4.11: Estimates of scaling and joint scaling test for seed weight per plant in the cross Oboshie x Nkosour (Log transformed)

	Parameters		
Scaling test	A	B	C
	-1.28^{ns} ± 0.397	-3.80** ± 0.205	2.98** ±0.245
df	42	40	46
Joint scaling test	m	[d]	[h]
	1.01** ± 0.042	0.26** ± 0.042	0.07^{ns} ± 0.083
df	3	3	3
$\mathbf{X^2}$	58.89**		

**---Significant at P = 0.01 ns---Not significant at P = 0.05

After log transformation of original data, Mather (1949) scaling test B and C were significantly different from zero at P = 0.01. Values for scaling Test C was positive while those for A and B were negative. The joint scaling test of Cavalli (1952) estimated a Chi square that was significantly different from zero at P = 0.01. The mid-parent value(m) and net additive effect, [d] were significantly different from zero at P = 0.01 while the net dominance effect was not significantly different from zero at P = 0.05 (Table 4.11). Values for parameters m, [d] and [h] were positive and the magnitude of the net additive effect [d] was greater than the net dominance effect [h]. The significance of both scaling test indicated that the additive-dominance model is not adequate for the trait.

4.6 ESTIMATION OF HETEROSIS

Heterosis estimates were calculated based on mid parent values of the two crosses for seed size and seed weight per plant.(Table 4.12).

Table 4.12 Estimates of heterosis for seed size and seed weight per plant in two groundnut crosses

CROSS	HETEROSIS (%)
Seed size	
Oboshie x Jenkaah	7.74
Oboshie x Nkosour	9.83
Seed weight per plant	
Oboshie x Jenkaah	a
Oboshie x Nkosour	42.43
Oboshie x Nkosour (log)	7.92

a = Generation mean of F_1< mid-parent variance.

Heterosis value for Oboshie x Nkosour cross was higher than Oboshie x Jenkaah cross and the highest heterosis value over mid-parent was noticed in Oboshie x Nkosour cross (42.43%).

CHAPTER FIVE

5.0 DISCUSSION

The field establishment of groundnut has a lot to do with its seed quality. Slow or delayed germination greatly affect yield and seed quality in particular. High seed dormancy was observed in all generations in the present study probably due to an innate trait in some parents, duration of storage and other environmental factors. Koornneef *et al*. (2002) observed seed dormancy to be controlled by complex adaptive traits influenced by large number of genes, environmental factors and storage duration. The seed dormancy effect caused a lot of variability, which gave cause to tag early germinated plants that were used for all data collection rather than the entire population within a plot. Nkosour and Jenkaah belong to subspecies *hypogaea* which possess seed dormancy ranging from 30 to 360 days (Gregory *et al*., 1951; Zade *et al*., 1986).

The low mean number of filled pods per plant and longer days to 50% flowering for parents obtained in the present study, were in contrast with results of CRI, (2001) for Nkosour and Jenkaah and CRI, (2011) for Oboshie due to high environmental effects. The seeds were sown in the dry season (December, 2012) under irrigation. Even though soil moisture might have been adequate, the low humidity and temperature and other environmental factors like diseases adversely affected the results.

Other yield and quality reducers like *Sclerotium rolfsii* and rosette diseases were observed to a lesser degree than seed dormancy. Mayee (1995) noted that among the

soil-borne fungal diseases of groundnut, stem rot caused by *Sclerotium rolfsii* is a potential threat to groundnut production practiced under irrigated condition.

There were indications of the (F_2) segregating generations to have inherited bolded seed trait, since their 100-seeds weight were higher than 60 g, which is in conformity with confectionery varieties (Ramanatha Rao and Murty, 1994).

Composite analysis mean values for protein and oil contents were in agreement with (Dwivedi *et al*., 1993; Jambunathan *et al*., 1985; Asibuo *et al*., 2008; Wang *et al*., 2011). Mean values of protein content for direct and reciprocal of (Oboshie x Jenkaah) x Oboshie and (Jenkaah x Oboshie) x Oboshie backcrosses were higher than lower parent (Jenkaah), and their corresponding oil contents were lower than the higher mean parent (Jenkaah) for the trait. This finding is in agreement with earlier report of Dwivedi *et al*. (1990), who recorded negative correlation between protein and oil. This is a common trend of confectionery groundnut varieties, increased protein content and decreased oil content.

There was no significant difference between direct and reciprocal crosses to account for maternal effects. Mean of direct and reciprocals were pooled to develop a six generation mean using a three parameter component additive-dominance model to investigate the gene effects of seed size and seed weight in two groundnut crosses.

Seed size is an important trait for quality purpose. Large-seeded varieties are likely to attract premium price in the world market of edible nuts. The fact that values obtained for seed size of F_1 for Oboshie x Jenkaah and Oboshie x Nkosour crosses were higher than those in the two parents indicated dominance towards parent with larger seed

size, and further implies heterosis for larger seed size. This is in agreement with the work of Balaiah *et al*, (1977) and Layrisse *et al*, (1980).

The non-significance of A, B and C scaling tests of Mather (1949) and joint scaling test of Cavalli (1952), indicates the adequacy of the simple additive-dominance model in explaining the genetic control of seed size for Oboshie x Jenkaah and Oboshie x Nkosour crosses.

The generation mean analysis revealed that additive genes contributed significantly to the inheritance of larger seed size in the two crosses. This was in contrast with the report of Hariprasanna *et al*. (2008) that seed size was controlled by non-additive gene action. According to Vanuprasad *et al.* (2011) significance of additive effects suggests that effective selection could be practised in early generation. The positive signs of the dominance effects indicated dominance in the direction of the higher parent for seed size trait.

The lower mean seed weight of F_1 for Oboshie x Jenkaah cross in comparism with the mid-parent value implies dominance towards lower seed weight per plant. Result of Mather (1949) and Cavalli, (1952) scaling and joint-scaling tests for seed weight per plant revealed the adequacy of the additive-dominance model in explaining the mode of inheritance of seed weight per plant in Oboshie x Jenkaah cross. Jayalakshmi and Lakshmikantha, (2003) also reported adequacy of additive-dominance model to explain variation in kernel yield (seed weight) in groundnut. The generation mean analysis of seed weight per plant also revealed that net additive effect contributed significantly to the inheritance of seed weight per plant in the Oboshie x Jenkaah

cross. This is consistent with the findings of Naazar *et al*. (1999) that only additive gene effects were important for seed weight in groundnut. Various workers revealed predominant additive gene action for seed traits (Garet, 1976; Mohammed *et al*., 1978; Layrisse *et al*., 1980; Swe and Branch, 1986; Anderson *et al*., 1993). The net dominance effect, [h] was not significant for Oboshie x Jenkaah cross, and the magnitude of the net additive effect, [d] was higher than the net dominance effect, [h]. The positive sign of the net dominance value indicated dominance in the direction of the higher parent for seed weight per plant.

The generation mean analysis for seed weight per plant in the Oboshie x Nkosour cross, showed the inadequacy of the additive-dominance model in explaining its mode of inheritance. This may be due to multiplicative effects of the genes, digenic interaction or non-allelic interaction like epistasis or correlated factors like linkage of genes.

To verify whether the significant Chi-square was due to multiplicative effect of genes, a log transformation suggested by Mather and Jinks (1982) was performed. The significance of the Chi-square for the transformed data reveals that digenic interactions or non-allelic interaction (epistasis) or correlated factors (linkage) was responsible for the inheritance of seed weight per plant in Oboshie x Nkosour cross. Alake *et al*. (2012) had similar experience in their work on West African okra.

The low heterosis values estimated for seed size in Oboshie x Jenkaah and Oboshie x Nkosour crosses could probably be due to environmental effects as noted by Acquaah, (2007), who reported that phenotypic variability of the F_1 is generally less than the

variability of either parent. This indicates that the heterozygotes are less subjected to environmental influences than the homozygotes.

The negative heterosis observed in the cross Oboshie x Jenkaah may be attributed to non-allelic interactions which can either increase or decrease the expression of heterosis. The result is akin to the findings of Venkateswarlu *et al*. (2007); Jayalakshmi *et al*. (2000).

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATION

6.1 CONCLUSION

The present study showed that genetic recombination for seed quality traits could be achieved through hybridization. For instance, mean values for most quantitative traits measured for F_2 generations were higher than their corresponding lower parents or intermediate between the two parents.

Generation mean analysis showed traits were highly influenced by environmental variation.

The study showed that the additive-dominance model was adequate to explain the mode of inheritance of seed size in both crosses. The net additive effect contributed significantly to the inheritance of seed size, therefore, suggesting that selection for improvement of seed size could be accomplished in the F_2 generation in both crosses.

The additive-dominance model was inadequate to explain the mode of inheritance of seed weight per plant for Oboshie x Nkosour cross. Therefore genetic improvement of seed weight (yield) per plant will be easier through indirect selection for a component trait such as seed size than through direct selection for seed weight itself. This selection criterion is suggested because of character association between seed weight and seed size as observed by Chiow and Wynne (1983).

6.2 RECOMMENDATION

Pure line breeding with selection at early generation is suggested for improvement of both traits studied, because the net additive genetic effect contributed significantly in controlling the inheritance of both seed size and seed weight per plant.

To reduce environmental variation in future suggesting that optimal environmental factors be carefully selected and larger sample sizes used in the prediction of genetic parameters for improvement of seed size and seed weight per plant.

Since the simple additive-dominance model was inadequate to explain the mode of inheritance of seed weight per plant in Oboshie x Nkosour cross, the model should be extended to a six parameter model indicating three interaction terms [i], [j] and [l] using the methodology of Jinks and Jones (1958) in which net additive [d], dominance [h], additive x additive [i], additive x dominance [j] and dominance x dominance [l] effects will be calculated.

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APPENDICES

Analysis of variance

Variate: %100SedWt

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	391.02	195.51	2.27	
Rep.*Units* stratum					
T_ment	18	8195.93	455.33	5.29	<.001
Residual	36	3096.38	86.01		
Total	56	11683.33			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	5.35

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	7.57

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	15.36

Stratum standard errors and coefficients of variation

Variate: %100SedWt

Stratum	d.f.	s.e.	cv%
Rep	2	3.21	4.6
Rep.*Units*	36	9.27	13.3

Analysis of variance

Variate: %50%_flow

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	70.56	35.28	0.66	
Rep.*Units* stratum					
T_ment	18	1751.47	97.30	1.83	0.060
Residual	36	1912.11	53.11		
Total	56	3734.14			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	4.208

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	5.951

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	12.068

Stratum standard errors and coefficients of variation

Variate: %50%_flow

Stratum	d.f.	s.e.	cv%
Rep	2	1.363	3.4
Rep.*Units*	36	7.288	18.2

Analysis of variance

Variate: DryPodWt

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	2945.	1472.	0.73	
Rep.*Units* stratum					
T_ment	18	76932.	4274.	2.11	0.028
Residual	36	72783.	2022.		
Total	56	152660.			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	25.96

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	36.71

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	74.46

Stratum standard errors and coefficients of variation

Variate: DryPodWt

Stratum	d.f.	s.e.	cv%
Rep	2	8.80	8.7
Rep.*Units*	36	44.96	44.5

Analysis of variance

Variate: FilledPod

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	104.3	52.1	0.46	
Rep.*Units* stratum					
T_ment	18	2517.8	139.9	1.22	0.294
Residual	36	4111.7	114.2		
Total	56	6733.9			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	6.17

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	8.73

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	17.70

Stratum standard errors and coefficients of variation

Variate: FilledPod

Stratum	d.f.	s.e.	cv%
Rep	2	1.66	6.7
Rep.*Units*	36	10.69	43.0

Analysis of variance

Variate: L_W_seed

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	0.017193	0.008596	0.89	
Rep.*Units* stratum					
T_ment	18	0.440000	0.024444	2.52	0.009
Residual	36	0.349474	0.009708		
Total	56	0.806667			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	0.0569

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	0.0804

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	0.1632

Stratum standard errors and coefficients of variation

Variate: L_W_seed

Stratum	d.f.	s.e.	cv%
Rep	2	0.0213	1.2
Rep.*Units*	36	0.0985	5.6

Analysis of variance

Variate: No_Pegs

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	5268.7	2634.3	3.39	
Rep.*Units* stratum					
T_ment	18	17739.1	985.5	1.27	0.265
Residual	36	27992.0	777.6		
Total	56	50999.8			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	16.10

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	22.77

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	46.18

Stratum standard errors and coefficients of variation

Variate: No_Pegs

Stratum	d.f.	s.e.	cv%
Rep	2	11.77	33.1
Rep.*Units*	36	27.88	78.4

Analysis of variance

Variate: PodLengt

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	11.982	5.991	2.82	
Rep.*Units* stratum					
T_ment	18	261.113	14.506	6.83	<.001
Residual	36	76.466	2.124		
Total	56	349.560			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	0.841

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	1.190

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	2.413

Stratum standard errors and coefficients of variation

Variate: PodLengt

Stratum	d.f.	s.e.	cv%
Rep	2	0.562	1.8
Rep.*Units*	36	1.457	4.7

Analysis of variance

Variate: PodWidth

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	2.2211	1.1106	3.74	
Rep.*Units* stratum					
T_ment	18	16.6659	0.9259	3.12	0.002
Residual	36	10.6857	0.2968		
Total	56	29.5727			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	0.3145

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	0.4448

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	0.9022

Stratum standard errors and coefficients of variation

Variate: PodWidth

Stratum	d.f.	s.e.	cv%
Rep	2	0.2418	2.1
Rep.*Units*	36	0.5448	4.8

Analysis of variance

Variate: SedLengt

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	1.3080	0.6540	1.24	
Rep.*Units* stratum					
T_ment	18	95.7059	5.3170	10.11	<.001
Residual	36	18.9318	0.5259		
Total	56	115.9457			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	0.4187

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	0.5921

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	1.2008

Stratum standard errors and coefficients of variation

Variate: SedLengt

Stratum	d.f.	s.e.	cv%
Rep	2	0.1855	1.1
Rep.*Units*	36	0.7252	4.4

Analysis of variance

Variate: SedWidth

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	0.9588	0.4794	1.68	
Rep.*Units* stratum					
T_ment	18	17.2701	0.9595	3.35	<.001
Residual	36	10.2975	0.2860		
Total	56	28.5264			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	0.3088

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	0.4367

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	0.8856

Stratum standard errors and coefficients of variation

Variate: SedWidth

Stratum	d.f.	s.e.	cv%
Rep	2	0.1588	1.7
Rep.*Units*	36	0.5348	5.8

Analysis of variance

Variate: SeedWt

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	1645.1	822.5	0.90	
Rep.*Units* stratum					
T_ment	18	33782.5	1876.8	2.06	0.032
Residual	36	32733.9	909.3		
Total	56	68161.5			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	17.41

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	24.62

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	49.93

Stratum standard errors and coefficients of variation

Variate: SeedWt

Stratum	d.f.	s.e.	cv%
Rep	2	6.58	10.2
Rep.*Units*	36	30.15	46.7

Analysis of variance

Variate: Shling%

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	78.30	39.15	2.93	
Rep.*Units* stratum					
T_ment	18	311.03	17.28	1.29	0.250
Residual	36	481.48	13.37		
Total	56	870.80			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	2.111

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	2.986

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	6.056

Stratum standard errors and coefficients of variation

Variate: Shling%

Stratum	d.f.	s.e.	cv%
Rep	2	1.435	2.3
Rep.*Units*	36	3.657	5.8

Analysis of variance

Variate: TotalPegs

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	3338.7	1669.4	1.68	
Rep.*Units* stratum					
T_ment	18	23808.8	1322.7	1.33	0.226
Residual	36	35725.7	992.4		
Total	56	62873.2			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	18.19

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	25.72

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	52.17

Stratum standard errors and coefficients of variation

Variate: TotalPegs

Stratum	d.f.	s.e.	cv%
Rep	2	9.37	10.5
Rep.*Units*	36	31.50	35.3

Analysis of variance

Variate: Unfilled

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	2	247.6	123.8	0.78	
Rep.*Units* stratum					
T_ment	18	2974.5	165.2	1.04	0.442
Residual	36	5709.3	158.6		
Total	56	8931.4			

Standard errors of means

Table	T_ment
rep.	3
d.f.	36
e.s.e.	7.27

Standard errors of differences of means

Table	T_ment
rep.	3
d.f.	36
s.e.d.	10.28

Least significant differences of means (5% level)

Table	T_ment
rep.	3
d.f.	36
l.s.d.	20.85

Stratum standard errors and coefficients of variation

Variate: Unfilled

Stratum	d.f.	s.e.	cv%
Rep	2	2.55	7.9
Rep.*Units*	36	12.59	38.9