VARIABILITY AND ASSOCIATIONS OF YIELD AND ITS COMPONENTS IN SOME GROUNDNUT (*Arachis hypogaea* L.) GENOTYPES

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DEDICATION

TO MY DEAREST FATHER …

COMPASSIONATE MOTHER…

LOVING SISTERS & BROTHERS …

SWEETEST FRIENDS & COMPANIONS…

FOR ALL, I PRESENT MY LOVE AND APPRECIATION FOR THEIR HELP AND ENCOURAGEMENT

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Abstract

An investigation was conducted in the Demonstration Farm, Faculty of Agriculture, University of Khartoum, Shambat. for one season (2002/2003) to assess the variation in kernel and pod yield and their components in 19 groundnut genotypes . The layout of the experiment was a complete randomized block design with three replicates. Genotypic and phenotypic variances, genetic coefficient of variation (G.C.V.), heritability, genetic advance and genotypic and phenotypic correlation coefficients between 12 traits were estimated. Significant differences for all traits were obtained, except number of seeds/pod. High genotypic coefficient of variation accompanied with high genetic advance was exhibited by number of branches/plant. Days to 50% flowering days to maturity, number of branches/ plant and number of pods/ plant had high estimates of heritability. Kernel yield/plant was significantly and positively associated, at the genotypic and phenotypic levels, with days to 50% flowering, pod yield/plant and number of pods/ plant.

خلاصة الأطروحة

أجريت تجربة فى المزرعة الإيضاحية بكلية الزراعة ، جامعة الخرطوم ، شمبات لموسم واحد (2003/2002) باستخدام تصميم القطاعات الكاملة العشوائية بثلاثة مكررات لدراسة التباين فى الإنتاجية ومكوناتها لتسعة عشر طرازاً وراثيا من محصول الفول السوداني . تم تقدير التباين الوراثي والتباين المظهري ، ومعامل التباين الوراثي ، ودرجة التوريث ، والتقدم الوراثي ، ومعامل الارتباط المظهري والوراثي . أظهرت النتائج فروقات معنوية بين الطرز الوراثية لكل الصفات المدروسة عدا عدد البذور/القرن . كما دلت النتائج على أن لعدد الأفرع/النبات أعلى معامل تباين وراثي وتقدم وراثي . سجلت أعلى درجة توريث لعدد الأيام لـ 50 % إزهار وعدد الأيام للنضج وعدد الأفرع/ النبات وعدد القرون/النبات . كما أظهرت النتائج أن إنتاجية النبات من البذور ارتبطت إرتباطاً مظهريا ووراثيا موجبا ومعنويا بعدد الأيام لـ 50% إزهار وعدد وزن القرون فى النبات .

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CHAPTER ONE

INTRODUCTION

Groundnut or peanut (*Arachis hypogaea* L.) belongs to the family Leguminosae. It is a highly self – pollinated crop and appears to have originated in Brazil. It is one of the most wide –spread and important food legumes in the world. The total annual world production amounts to about 25 million tons of unshelled nuts, 70% of which is contributed by India, China and U.S.A. (Khidir 1997).

The groundnut plant and its products found varied uses both in day–to–day life and in industries. The seed contains 42%– 55% edible non–drying oil and 25%–32 %. protein as well as appreciable quantities of phosphorus, calcium and vitamins. The oil is used as table oil and for the manufacture of soap, margarine and other products. Groundnut haulms and seed cake are fed to livestock. The seeds are crushed to make peanut butter, which is very popular in the U.S.A. and the Sudan. The shell maybe used as manure, animal feed, a source of heat and row source of many products (Venkatanarayana 1952).

In the Sudan, groundnut is one of the main cash crops, and Sudan used to be the major African producting and exporting country. However, its production and export decreased during the 1980's and early 1990's. As an average for 1979-81, Sudan produced 4% and 16% of the production of the world and Africa, respectively (Khidir 1997). However, its contribution decreased to 0.8% and 3.9%, respectively, by 1991, but started to increase in recent years. The total harvested area, production and yield on average for the last decade of the previous century (1990 – 99) were, respectively, 2.126 million feddans, 0.0631 metric tons and 860 kg/fed. (1 fed = 0.42 ha) in irrigated areas and 214 kg/fed in rainfed areas (Khidir 2003).

The crop is, produced in Sudan under irrigation and rainfed conditions (only about 12% of the area is irrigated), and its production is facing many problems. These include: policy issues, lack of high yielding adapted genotypes, poor cultural practices with limited use of fertilizers, weakness of research and extension services, fluctuation in the amount of rainfall and its irregular distribution during the growing season, lack of good seed of improved varieties and use of untreated seeds for planting, delay in sowing date, weed control and harvesting and increasing cost of production especially in the irrigated areas.

The objectives of groundnut breeding programme in the Sudan has been to (i) develop high yielding, early maturing, spreading bunch types adapted to the irrigated Vertisols, (ii) develop early maturing, drought tolerant cultivars for the rainfed sandy soils of western Sudan, (iii) select large-seeded Virginia types for production in northern Sudan, (iv) develop genotypes with increased resistance to infection by *Aspergillus flavus* and (v) look for genotypes with high oil content and high kernel yield. (Mokhtar and Ali 1998).

Due to the narrow genetic base of groundnut in the Sudan, the objectives of the present work were to study variability and correlation between yield and its components in 14 newly introduced and 5 improved local groundnut genotypes.

CHAPTER TWO
LITERATURE REVIEW

2.1 Classification of groundnut

Groundnut or peanut (*Arachis hypogaea* L.) is a member of the family Leguminosae, subfamily Paplionaceae. It is an annual tetraploid

plant having 20 pairs of chromosomes (2n = 4 X = 40). The genus *Arachis* consists of four diploid (2n = 2 X = 20) annual species, five tertraploid (2n= 4 X = 40) perennial species and two tetraploid annual species; one of them is the cultivated groundnut (Khidir 1997). Groundnut is very variable morphologically, and there are many distinct varieties. Variants of *A. hypogaea* have frequently been described as distinct species, subspecies or botanical varieties.

The general taxonomic position was reviewed by Gregory *et al.* (1951), who also proposed a classification of some of the varieties. It was based on an important distinction in branching pattern between two groups. According to their notations, the main axis is denoted n, and first, second and higher order branching are designated n+1, n+2 etc. In their first group, Virginia, alternating pairs of vegetative and reproductive branches are borne on the cotyledonary and other n+1 branches. The first two branches on an n+1 lateral are always vegetative, and the main axis produces vegetative branches only. The alternating branching pattern is repeated in the higher orders of branching (n+3, n+4….). In their second group, Spanish– Valencia, reproductive branches are borne in a continuous series on successive nodes on the cotyledonary and other n+1 branches, on which the first branch is always reproductive. Reproductive branches are also borne directly on the main axis at higher nodes. Most n+2 and all n+3 branches are reproductive. The Spanish and Valencia sub groups differ in the pattern of production of n+2 vegetative branches. Spanish varieties produce such branches irregularly, but Valencias frequently have none; if any are produced they are formed in sequence distal to 5-8th node of n+1 branches.

Bunting (1955, 1958) accepted the main division of species based on branching pattern and added a number of new variety groups to the classification.

Krapovickas (1968) suggested a taxonomic treatment of the main subdivisions of the species. He classified *Arachis hypogaea* into two subspecies; namely, *hypogaea* (alternately–branched) and *fastigiata* (sequentially– branched), each was again classified into two botanical varities.

Gibbons *et al.* (1972) attempted to establish a systematic scheme by combining the systems of Gregory *et al.* (1951) and Bunting (1955, 1958) with the taxonomic treatment of Krapovickas (1968). The primary division of the species was into two subspecies; namely, *hypogaea* (alternately–branched) and *fastigiata* (sequentially–branched). The subspecies *hypogaea* consists of two distinct botanical varieties *hirsuta* and *hypogaea*, and these are divided into variety groups, according to pod characters, number of seeds/ pod and general appearance, and subsequently into variety cluster based on habit (bunch and runner). Within these variety clusters, testa colour distinguishes individual varieties.

The subspecies *fastigiata* (all upright forms) consists of the botanical varieties *fastigiata* (the very distinct Valencia forms) and *vulgaris* (the Spanish –Natal-Manyema complex), separation depends on the habit and characters of the inflorescence. These varieties are further divided, according to pod and seed characters, into variety groups and clusters. Finally, as in the subspecies *hypogaea*, the individual varieties may be distinguished according to testa colour.

2.2 Phenotypic variability

2.2.1 Days to flowering

Groundnut has an indeterminate growth habit, and both vegetative and reproductive phases go side by side. The flowering commences 20-30 days after emergence, depending on genotype and

environment (Ramanatha 1988). The production of flowers is cyclic, characterized by two distinct peaks in the normally sown crop, the first flush lasting up to 2-3 weeks after commencement of flowering. The maximum flowering period occurs 38 – 44 days after sowing in the first flush. The second spell of flowering occurs 12-15 days after the first flush, and lasts for longer duration than the first flush; the flowering is maximum 50-62 days after sowing (Reddy *et al.* 1990). The duration of flowering in the bunch varieties varies from 35 to 63 days and in the spreading and runner varieties from 42 to 78 days (Smith 1950).

2.2.2 Days to maturity

The maturation of groundnut pods requires about 60 days, but the length of the growing season varies with the variety; it ranges from 90 to 110 days for up-right bunch varieties and from 110 to 160 days for spreading and runner varieties (Purseglove 1974). Pods are mature when the kernels are fully developed, the testa assuming the varietal colour and the inside of pods darkens to brown. In some runner varieties, pods become brittle and crack open when pressed. The indicator of harvest is that the plant leaves become yellowish in colour and begin to fall (Khidir 1997).

2.2.3 Branching pattern

The branching pattern in groundnut is considered one of the important features used to help in the classification of the species (Gregory *et al.* 1951). In all subspecies, the main axes (n) is upright and the two principal n+1 order are vegetative axes arising in the axils of the alternately arranged cotyledons.

The subspecies *A. hypogaea hypogaea* produces a pair (or three) of n+2 order vegetative axes from the cotyledonary nodes of the n+1 axes, followed by a pair (or three) of n+2 order reproductive axes to establish along the length of the n+1 laterals an alternating pattern of paired vegetative with paired reproductive n+2 axes. With rare exceptions, all n+1 order axes are vegetative and no flowering axes occur along the main stem. In axes of higher order (n+4, n+5), reproductive and vegetative axes tend to arise. The subspecies *A. hypogaea fastigiata* produces n+2 reproductive axes from their cotyledonary nodes, and produces n+1 order reproductive axes along the n axis above the fourth node. The n+2 reproductive axes succeed each other along the n+1 vegetative axes uninterrupted by an n+2 vegetative axis (sequential branching pattern) to terminate all further branching in *A. hypogaea fastigiata* var. *fastigiata*, or occur in large sequential runs, interrupted by

shorter runs of n+2 vegetative axes in *A. hypogaea fastigata* var. *vulgaris* (Duke 1983).

2.2.4 Pod and kernel features

Pod and kernel features, such as size and shape of the pods and number and colour of the kernels, are useful characters in classifying groundnut (Bunting 1958; Smartt 1961; Gibbons *et al.* 1972). The characters of pods are studied in mature specimens from older nodes. Groundnut pods vary considerably in size, from the very large pods of certain Virginia types (over 20 mm in diameter) to large (15 – 20 mm), medium (10 – 15 mm) and small pods (less than 10 mm). The pods maybe more or less markedly constricted between the kernels, and their distal ends maybe smooth or keeled and beaked.

The number of kernels in a fully developed pod is commonly two, but in some varieties it is three or four. Kernel testa colour is determined in kernels which have been stored in shell for several weeks after harvest; during this time, the colour deepens as the kernel dries. In most alternately – branched varieties, the testa colour is russet–brown, but white, red and purple colours have also been found. In sequentially – branched plants, the same range of colours is found, except that light–brown is common (Badwal *et al.* 1967; Gibbons *et al.* 1972; Thomas *et al.* 1974). Sometimes, the features of kernels maybe affected by the environment; Kaleemullah (1992) found that the moisture content affects the physical properties of groundnut kernel; however, in general, pod and kernel features depend more on the genotype than the environment.

2.2.5 Pod and kernel yields

The pod and kernel yields in groundnut depend on genotype as well as environment. It was found, at ICRISAT (1983), that the partition of the total assimilates into pod yield provides an indication of yield improvement. Hago and Salama (1987) reported that pod

maturation is influenced by elemental sulphur. The agricultural practices, like sowing date, spacing and mineral fertilization, significantly affect the production of pods and kernels (Munda and Patel 1989). Ishag (2000) found that pod initiation differs due to the differences in temperature.

The number of pods seems to be a yield constraint in the Valencia types (Ashle 1978). More fruiting nodes near the base of the plant would help to ensure penetration of a greater number of pegs in the soil, and perhaps more pods would form as a result. This implies the need for more branches with short basal internodes, and in Valencia types shorter internodes on the main stem (Ishag 1970). The results of some experiments suggest that in Valencia the supply of assimilates exceeds the requirements of the normal pod load, and there is scope to increase yield, as Duncan *et al.* (1978) suggest, by partitioning more of the assimilates to pods. In the sequentially – branched Spanish and Valencia types, the assimilates produced after flowering go to pods and kernels. These forms are more determinate than the alternately–branched Virginia types in which pairs of new vegetative and production buds continue to alternate on the branches after flowering (Bunting and Elston 1980). At ICRISAT (1980), it was found that pod yield, shelling percentage and pod maturity are best in varieties which produce 60% or more of their flowers about eight weeks before harvest.

2.3 Genetic coefficient of variation, heritability and genetic advance

Estimates of heritability give an indication of the portion of the phenotypic variability that is due to genetic causes. Heritability estimates coupled with genetic coefficient of variation are usually useful in predicting the result of selection than heritability value alone (Johnson *et al.* 1955a).

Vaddoria and Patel (1990) carried out an investigation to assess the variation in Virginia runner groundnut for pod yield and nine

component characters. They reported high heritability, genetic coefficient of variation and genetic advance estimates for the most important direct components of pod yield (100-seed weight, harvest index and number of mature pods). Similar results were obtained by Reddy (1994) in a Spanish groundnut collection.

Uddin *et al.* (1995) studied the variability of seven yield components in 23 divergent groundnut genotypes (seed yield/ plant, seed/ plant, primary branches/ plant, plant height, 100- seed weight, days to maturity and shelling percentage). They obtained high estimates of heritability and genetic coefficient of variation for all traits and moderate to high genetic advance for all traits except days to maturity and shelling percentage.

Working on Spanish bunch groundnut, Abhay *et al.* (2002) and Prasad *et al.* (2002), studied the variability, heritability, genetic coefficient of variation and genetic advance for yield and its components. They reported the importance of additive gene action for these traits, and suggested that phenotypic selection for the improvement of these traits will be effective.

Azad and Hamid (2000) studied nine breeding lines and their parental varieties, and obtained high genotypic coefficient of variation with high heritability and genetic advance for plant height, pod number and kernel and pod yields.

2.4 Interrelationships between the different characters

Developing high yielding varieties is regarded as the ultimate objective in many groundnut breeding programmes. However, the selection of superior genotypes based on yield will be less efficient because yield is a complex character. Therefore, if reliable selection criteria are to be established for the breeding of high yielding varieties, the breeder must know the magnitude of the relationships of yield components (Ibrahim 1983).

2.4.1 Phenotypic and genotypic correlations

Phenotypic and genotypic correlations among characters give an indication of the useful characters, which maybe used as indicators in selection for other traits (Johnson *et al.* 1955b). Yassin (1973) attributed the association among characters to pleiotropy or linkage, while Adams (1967) reported that it is due to developmentally induced relationship among components that are only indirectly the consequence of gene action.

The interrelationships among characters in groundnut were studied by many workers. Ibrahim (1983) found that yield is positively and significantly correlated with number of mature pods, flowers, pegs and branches and weight of hay. Uddin *et al.* (1995) reported that, at the genotypic level, seed yield/plant is significantly and positively correlated with days to maturity, number of seeds/plant, plant height and number of primary branches/plant, but was negatively associated with shelling percentage and 100 – seed weight.

In Spanish bunch groundnut, Abhay *et al.* (2002) found a significant association of dry pod yield with shelling percentage and kernel yield. Azad and Hamid (2000), in a study of character association in groundnut, reported that the number of pods, kernel yield and 100–pod weight demonstrated, mostly significant positive genotypic and phenotypic correlation coefficients with pod yield. Moreover, genotypic correlation coefficients of the characters were always higher than that of their phenotypic ones.

Salara and Gowda (1998) studied the variability and correlation in segregating generations of sub-specific crosses of groundnut, and reported that pod number and testa weight are highly correlated with pod yield. Reddy and Gupta (1992) estimated correlation coefficients among nine characters in 46 diverse groundnut genotypes (15 Virginia bunch and 31 Spanish bunch types), grown under three environments

(rainfed, rainfed with supplementary irrigation and irrigation). They indicated that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Pod yield was significantly and positively associated with number of mature pods, grain yield, shelling out–turn and harvest index in all environments. Mishra and Yadav (1992) reported that kernel yield is positively and significantly associated with dry pod yield. Reddy *et al.* (1993) showed that there are significant negative associations between days to flowering and other yield components. El-Ashry *et al.* (1986) analyzed data from 211 indigenous and exotic varieties of groundnut and reported that pod yield/plant was positively associated with 100 – seed weight, number of branches and number of pods/ plant at the phenotypic and genotypic levels.

CHAPTER THREE
MATERIALS AND METHODS

3.1 Trial and planting material

An experiment was conducted for one season (2002/2003) in the Demonstration Farm, Faculty of Agriculture, University of Khartoum, Shambat (altitude 375 m above sea level, latitude 15° 40′ N, longitude 32° 32′E). The soil of the site is heavy clay (more than 50% clay) and alkaline (pH8.5). The layout of the experiment was a randomized complete block design with three replications. The material tested consisted of 19 genotypes of groundnut (*Arachis hypogaea* L.). The source of the genotypes and some of their important characteristics are depicted in Table 1.

The genotypes were sown on 16 June 2003 on ridges at the rate of two seeds per hole and a spacing of 70 cm between ridges and 15 cm between holes. Each genotype was sown on two ridges. Re-sowing was carried out after two weeks from sowing. Surface irrigation was applied a week before sowing, at sowing and every two weeks thereafter. Hand weeding was carried out three times: three weeks, five weeks and eight weeks after sowing. Dursban was sprayed at the rate of 4 ml/litre of water against white ants (*Microtermes thoracalis*), a week before sowing and a month and two months after sowing.

3.2 Data collection

Ten plants from each genotype in each replication were chosen randomly for collecting data on the following parameters, except days to 50% flowering and days to maturity

i. Days to 50% flowering: The number of days after sowing when 50% of the plants bear at least one flower each.
ii. Days to maturity: Recorded when the lower leaves became yellowish in most of the plants.

iii. Plant height (cm): The main stem of each of the ten plants was measured at harvest, and the average was recorded.

iv. Number of braches/plant: Average of the number of all types of branches/ plant at harvest.

v. Number of pods/plant: Average of the number of pods / plant of ten plants.

vi. Pod yield / plant (g)

vii. Kernel yield /plant (g)

viii. Number of seeds/ pod: Average of the number of seeds in 100 randomly selected pods from the ten randomly selected plants.

ix. 100 – seed weight (g): One hundred seeds were taken at random from the ten randomly selected plants and weighed.

x. Shelling out – turn % (SOT): Calculated as follows:

$$SOT = \frac{\text{Weight of- kernels plants-(g)}}{\text{Weight of-pods1 plant(g)}} \times 100$$

xi. Pod yield/ha (kg):

xii. Kernel yield/ha (kg)

Pod yield/ha and kernel yield/ha were calculated from the yield per one metre length (0.7 m^2) of the middle ridge in grammes as follows:

$$\frac{\text{Yield of kernel or pod per one metre length x 10 000}}{1000 \times 0.7} \quad \textbf{3.3}$$

Statistical analysis

Data were analysed according to the standard statistical procedure (Gomez and Gomez 1984). Analysis of variance was carried out for each character as for a randomized complete block design (Table 2). The means were seprated using the least significant difference (LSD). The estimates obtained from the analysis of variance were used to compute the following.

3.3.1 Coefficient of variation (CV%):

The coefficient of variation for each character was determined according to following formula:

$$CV\% = \sqrt{\frac{MSE}{\bar{X}}} \times 100$$

where

MSE = Error mean square

$\bar{X}$ = Grand mean of the character

3.3.2 Phenotypic and genotypic variances: Phenotypic ($\sigma^2 ph$) and genotypic ($\sigma^2 g$) variances were estimated as follows:

$\sigma^2 ph = \sigma^2 g + \sigma^2 e = M_2/r$

$\sigma^2 g = (M_2 - M_3/r)/ r$

$\sigma^2 e$ = The error variance (M_3)

3.3.3 Heritability (h^2): Heritability in broad sense was estimated for each character according to Johnson *et al.* (1955a) as follows .

$$h^2 = \frac{\text{Genotypic variance } (\delta^2 g)}{\text{Phenotypic variance } (\delta^2 ph)}$$

3.3.4 Genetic coefficient of variation (GCV): was determined following Burton and De Vane (1953) as follows:

$$GCV = \frac{\sqrt{\delta^2 g}}{\overline{X}} x100$$

3.3.5 Expected genetic advance (G.A.): For one cycle of selection,GA was determined using the formula suggested by Robinson *et al.* (1949)

$$\text{Genetic advance} = \frac{K\,\delta^2 g\,(g)}{\sqrt{\delta^2 ph}}$$

where

κ = Selection differential for 5% selection intensity equals = 2.06

3.3.6 Genotypic and phenotypic correlations: Covariance analysis between pairs of different traits was worked out on the basis of the formula suggested by Gomes and Gomez (1984). Then, estimates of the genotypic (gxy) and phenotypic (phxy) covariances between every two traits (x and y) were used to compute the genotypic and the phenotypic correlation coefficients between pairs of various characters, according to the procedure described by Singh and Chaudhary (1985), as follows:

$$\text{Genotypic correlation coefficient (rg)} = \frac{\delta g\ x\ y}{\sqrt{(\delta^2 gx).\ (\delta^2 gy)}}$$

$$\text{Phenotypic correlation coefficient (rph)} = \frac{\delta ph\ x\ y}{\sqrt{\delta^2 ph\ x).\ (\delta^2 phy)}}$$

where:

- σgxy = The genotypic covariance between two traits, x and y
- σphxy = The phenotypic covariance between two traits, x and y
- σ^2gx and σ^2gy = The genotypic variances for traits x and y, respectively
- σ^2phx and σ^2 phy = The phenotypic variances for traits x and y, respectively.

The genotypic and phenotypic correlation coefficients were estimated for all possible pair-wise combinations between all characters.

Table 1. Source of the groundnut genotypes used in the study and some of their main features

Serial number	Name	Source*	Growth habit	Branching form	Pod characteristics
1	ICGV-97040	ICRISAT	Upright	Sequential	Large, 1–2–3 seeds, beaked shallow constriction, shell thick, testa red turning brown.
2	ICGV-97045	ICRISAT	Upright	Sequential	Large, 1–2–3 seeds, beaked, shallow constriction, shell medium thick, testa light brown
3	ICGV-97047	ICRISAT	Spreading	Sequential	Large, 1–2–3 seeds, beaked, shallow constriction sheel thick, light brown
4	ICGV-97049	ICRISAT	Spreading	Sequential	Large, 1–2–3 seeds, beaked medium constriction, shell thick, testa rose
5	ICGV-97051	ICRISAT	Spreading	Sequential	Large, 1–2–3 seeds, beaked shallow to medium constriction, shell medium thick testa dark brown
6	ICGV-97058	ICRISAT	Spreading		
7	ICGV-98061	ICRISAT	Semi–spreading	Sequential	Large, 1–2–3 seeds beaked, shallow constriction, shell medium thick, testa rose
8	ICGV-98396	ICRISAT	Spreading	Sequential	Large, 1–2–3 seeds, shallow to medium constriction, shell medium thick testa dark brown
9	ICGV-98397	ICRISAT	Upright	Sequential	Large, 1–2–3 seeds, beaked medium constriction, shell medium thick, testa light brown
10	ICGV-98402	ICRISAT	Upright	Sequential	Large, 1–2–3 sees beaked, medium to deep constriction, shell thick, testa rose.

Table 1. Cont.

11	ICGV-98404	ICRISAT	Spreading	Sequential	Large, 1–2–3 seeds, beaked, shallow to medium constriction, shell medium thick, testa light brown
12	ICGV-98412	ICRISAT	Upright	Sequential	Large, 1–2–3 seeds, beaked, shallow to medium constriction, shell thick, testa light brown
13	ICGV-98426	ICRISAT	Upright	Sequential	Large, 1–2–3 seeds, beaked shallow to medium constriction, shell thick, testa red turning brown
14	ICGV-98432	ICRISAT	Upright	Sequential	Large, 1–2–3, seeds, beaked, shallow constriction, shell medium thick, testa light brown
15	Medani	ARC	Spreading	Alternate	Medium to shall, beaked, 1–2–3 seeds, shallow to medium constriction, shell medium thin, testa light brown
16	Keriz	ARC	Spreading	Sequential	Medium to large, 1–2–3 seeds, beaked, shallow to medium constriction, shell medium thick, testa dark brown.
17	Ahmadi	ARC	Spreading	Alternate	Medium, 1–2–3 seeds, beaked medium constriction, shell medium thick, testa light brown
18	MH383	ARC	Spreading	Alternate	Medium, 1–2–3 seeds, beaked, medium constriction, shell medium thick, testa dark brown
19	Gebeish	ARC	Upright	Sequential	Small, 1–2 seeds, beaked, medium to deep constriction, shell thin, testa light brown

*ARC= Agriculture Research Corporation, Sudan
ICRISAT = International Crop Research Institute for the Semi – arid Tropics, Hyderabad, India

Table 2. The form of analysis of variance and expected mean squares (E.M.S.) in a randomised complete block design

Source of variation	D.F.	M.S.	E.M.S.
Replications (Blocks)	r-1	M1	
Treatments (Genotypes)	t-1	M2	$\sigma^2 e + r \sigma^2 g$
Error	(r-1) (t-1)	M_3	$\sigma^2 e$
Total	rt-1		

where

r= Number of replications

t= Number of treatments (genotypes)

M_1, M2, M3 = Mean squares for replications, genotypes and error, respectively

$\sigma^2 e$ = Environmental variance

$\sigma^2 g$ = Genotypic variance

CHAPTER FOUR
RESULTS

4.1 Phenotypic variability

The individual analysis of variance (Table 3) showed significant differences among the evaluated genotypes in all the studied characters, except the number of seeds/pod.

4.1.1 Days to 50% flowering: The analysis of variance, (Table 3) showed highly significant (P≤0.01) differences among the genotypes for the number of days to 50% flowering. It ranged from 23.0 days, recorded for Gebeish (19) to 34.7 days recorded for Keriz (16), with an overall mean of 30.9 days (Table 4). The coefficient of variation for this character was 4.6%.

4.1.2 Days to maturity: Highly significant (P≤0.01) differences were detected, among the evaluated genotypes, for this trait (Table 3). The overall mean of days to maturity was 106.5. Gebeish (19) was the first to mature, while ICGV-97058 (6) was the latest (Table 4). The coefficient of variation for this character was 1.0%.

4.1.3 Plant height (cm): Differences in this trait, among the 19 genotypes, was significant (P≤0.05) (Table 3). The highest value of plant height was obtained for ICGV-97049 (3) and the lowest one for ICGV-98396 (8). The overall mean was 26.5 cm (Table 4), and the coefficient of variation was14.0%.

4.1.4 Number of branches/plant: The analysis of variance (Table 3) revealed highly significant (P≤0.01) differences among the 19 genotypes. ICGV-98396 (8) had the lowest number of branches/plant (7.3), while Medani (15) had the highest number (38.5) (Table 4). The overall mean was 20.0, and the coefficient of variation was 13.4%.

4.1.5 Number of pods/plant: Differences in this character, among the evaluated genotypes, were highly significant (P≤0.01) (Table 3). The number of pods/ plant ranged from 16.3 for ICGV- 98396 (8) to 44.0 for Ahmadi (17) (Table 4). The overall mean was 27.6, and the coefficient of variation was 14.4%.

4.1.6 Pod yield/plant (g): Significant (P≤0.05) differences were detected among the evaluated genotypes in pod yield/plant (Table 3), and the overall mean was 34.6 g. ICGV-98396 (8) produced the lowest pod yield/plant, while Ahmadi (17) produced the highest (Table 4). The coefficient of variation was 19.8%.

4.1.7 Kernel yield/plant (g): The analysis of variance of the data showed significant (P≤0.05) differences among the genotypes under study in the kernel yield/plant (Table 3). The overall mean was 22.0g . Gebeish (19) produced the lowest kernel yield/plant, whereas ICGV-97058 (6) produced the highest (Table 4). The coefficient of variation was 23.5%.

4.1.8 Number of seeds/pod: The analysis of variance (Table 3) indicated that the difference in the number of seeds/pod among the means of the evaluated genotypes was not significant. The overall mean was 1.7, and the coefficient of variation was 0.08%.

4.1.9 Hundred–seed weight (g): Highly significant (P≤0.01) differences in this trait were detected among the 19 genotypes (Table 3). Gebeish (19) gave the lowest 100 – seed weight, and ICGV-98397 (9) produced the highest one (Table 4). The overall mean was 57.95, and the coefficient of variation was 17.3%.

4.1.10 Shelling out-turn (%): For this character, differences among the evaluated genotypes were highly significant (P≤0.01) (Table 3). SOT ranged from 52.3% for ICGV-98404 (10) to 72.0% for Medani (15) with

an overall mean of 63.5% (Table 4). The coefficient of variation for this character was 8.3%.

4.1.11 Pod yield/ha (kg): The analysis of variance indicated that the means of the 19 genotypes were significantly (P≤0.05) different (Table 3). The overall mean was 5935.79 kg/ha, and the highest value of pod yield/ha was produced by Ahmadi (17), while the lowest value was given by ICGV-9836 (8) (Table 4). The coefficient of variation was 19.8%.

4.1.12 Kernel yield/ha (kg): Significant (P≤0.05) differences were detected in this trait among the means of the genotypes under study (Table 3). The overall mean was 3774.5 kg/ha. Gebeish (19) produced the lowest kernel yield per ha, whereas ICGV-97058 (6) produced the highest one (Table 4). The coefficient of variation was 23.5%.

Table 3. Mean squares from the analysis of variance for 12 characters in 19 genotypes of groundnut

Character	Source of variation		
	Block (d.f. =2)	Genotype (d.f.=18)	Error (d.f.=36)
Days to 50% flowering	0.75 ns	23.06**	2.03
Days to maturity	3.39 ns	385.01**	1.20
Plant height	49.27 *	27.62*	13.77
No. of branches/plant	2.93 ns	273.75**	7.22
No. of pods/plant	6.84 ns	185.81**	13.76
Shelling out – turn	47.63 ns	88.04**	27.43
No. of seeds/pod	0.02 ns	0.03ns	0.02
100 – seed weight	357.79*	423.26**	100.35
Pod yield/plant	98.26ns	103.28*	46.91
Kernel yield/plant	58.03ns	50.70*	26.71
Pod yield/ha	2887485ns	3035041*	1378603
Kernel yield/ha	1705408ns	1666341*	784954

* = Significant at P≤0.05

** = Significant at P≤0.01

ns = Not significant

Table 4. Means of 12 characters in 19 groundnut genotypes

Serial number	Days to 50% flow-ering	Days to matuirty	Plant height (cm)	No. of branches/ plant	No. of pods/plant	Shelling out — turn (%)
1	28.7	97.7	28.7	16.9	26.1	61.8
2	28.7	98.0	26.1	15.1	26.9	58.0
3	32.0	113.3	31.2	16.5	24.6	54.9
4	32.7	114.7	30.2	17.3	24.3	60.8
5	33.0	116.0	28.9	9.6	16.4	61.0
6	34.0	120.7	29.5	15.1	32.7	65.7
7	32.0	111.0	29.4	18.0	19.7	63.6
8	32.0	115.0	20.3	7.3	16.3	63.7
9	32.7	98.0	28.6	13.7	23.7	67.4
10	28.3	91.0	27.5	16.5	28.1	52.3
11	30.0	117.0	25.6	13.3	22.2	70.6
12	31.7	91.3	23.3	11.6	21.4	71.5
13	30.7	95.0	26.8	16.6	22.0	66.8
14	28.7	94.3	27.4	24.1	28.2	65.2
15	32.3	117.0	25.1	38.5	40.1	72.0
16	34.7	114.0	23.5	23.1	35.6	64.1
17	32.7	112.0	26.5	35.7	44.0	64.6
18	33.3	119.0	22.5	37.8	36.3	66.5
19	23.0	87.7	22.2	33.4	36.0	56.3
Mean	31.0	106.5	26.5	20.0	27.6	63.5
LSD(0.05)	2.4	1.8	6.1	4.4	6.1	8.7
LSD(0.01)	3.2	2.3	-	5.9	8.2	11.6
CV%	4.6	1.0	14.0	13.4	14.4	8.3

Table 4 (Cont.)

Serial number	No. of seeds/pod	100-seed weight (g)	Pod yield/ plant (g)	Kernel yield/ plant (g)	Pod yield/ha (kg)	Kernel yield/ha (kg)
1	1.7	61.9	38.5	23.9	6595.4	4090.3
2	1.6	58.6	38.0	22.2	6514.9	3805.2
3	1.6	63.6	37.9	19.6	6490.3	3362.3
4	1.8	64.7	38.3	22.9	6561.7	3924.0
5	1.7	66.3	32.7	18.1	5605.7	3101.2
6	1.6	67.7	42.6	28.1	7304.6	4818.9
7	1.7	57.0	28.0	18.1	4814.3	3105.2
8	1.6	63.6	21.8	13.9	3730.9	2381.2
9	1.8	71.0	33.6	25.5	5752.6	4362.3
10	1.5	52.0	33.0	17.6	5662.3	3014.3
11	1.8	67.7	32.7	23.2	5609.2	3980.6
12	1.8	70.6	28.7	20.5	4924.0	3514.3
13	1.8	65.3	36.2	24.0	6195.4	4114.3
14	1.7	66.1	39.7	26.1	6804.6	4471.4
15	1.9	38.6	36.2	26.1	6200.0	4471.4
16	1.6	46.9	36.3	23.3	6219.4	3990.3
17	1.6	48.2	42.9	27.7	7356.6	4747.4
18	1.7	41.6	38.0	24.8	6519.4	4247.4
19	1.6	29.6	22.9	12.9	3918.9	2214.3
Mean	1.7	58.0	34.6	22.0	5935.8	3774.5
LSD(0.05)	-	16.6	11.3	8.6	1937.5	1462.0
LSD(0.01)	-	22.1	-	-	-	-
CV%	0.1	17.3	19.8	23.5	19.8	23.5

4.2 Phenotypic, genotypic and environmental variances

The estimated values of the phenotypic, genotypic and environmental variances are shown in Table 5. For all characters, the estimated values of the phenotypic variances were greater than the estimated values of the genotypic and environmental variances. The estimated values of the environmental variances were greater than the genotypic variances for some characters. These were plant height, pod yield/plant, kernel yield/plant, number of seeds/pod, pod yield/ha and kernel yield/ha. The highest values of the phenotypic, genotypic and environmental variances were scored by pod yield/ha, and the lowest values were scored by number of seeds/pod.

Table 5. Phenotypic (σ^2ph), genotypic (σ^2g) and environmental variance (σ^2e) for 12 characters in 19 groundnut genotypes

Character	σ^2ph	σ^2g	σ^2e
Days to 50% flowering	9.04	7.01	2.03
Days to maturity	129.14	127.94	1.20
Plant height	18.39	4.62	13.77
No. of branches/plant	96.07	88.85	7.22
No. of pods/plant	71.11	57.35	13.76
Shelling out-turn	88.04	60.61	27.43
No. of seeds/pod	0.019	0.003	0.016
100-seed weight	207.98	107.63	100.35
Pod yield/plant	65.70	18.79	46.91
Kernel yield/plant	36.71	10.00	26.71
Pod yield/ha	2344329	695726	1378603
Kernel yield/ha	1078750	293796	784954

4.3 Genetic coefficient of variation, heritability and expected genetic advance

Estimates of the genetic coefficient of variation (GCV), heritability in broad sense (h^2) and genetic advance (GA) are depicted in Table 6. The highest value of GCV was obtained for the number of branches per plant (47.13), while the lowest value was given by the number of seeds per pod (3.28).

Awide range of variation in heritability estimates of the different characters was detected (Table 6). It ranged from 15.79 for the number of seeds per pod to 99.07 for days to maturity. Most of the traits had low (<75%) estimates of heritability. These were plant height, pod yield/plant, kernel yield/plant, 100-seed weight, shelling out-turn, number of seeds/pod, pod yield/ha and kernel yield/ha.

A great deal of variation was detected in genetic advance (GA) as percentage of the mean for the different traits (Table 6). GA ranged from 0.24 for number of seeds/pod to 1299.31 for pod yield/ha, whereas GA as a percentage of the mean ranged from 8.38 for plant height to 93.4 for number of branches/plant.

Table 6. Estimates of genetic coefficient of variation (GCV), heritability (h^2) and expected genetic advance (GA) for 12 traits in 19 groundnut genotypes

Character	GCV (%)	h^2 (%)	GA	GA as a percentage of the mean
Days to 50% flowering	8.56	77.54	4.93	5.94
Days to maturity	10.62	99.07	23.19	21.77
Plant height	8.11	25.12	2.22	8.38
No. of branches/plant	47.13	92.48	18.68	93.4
No. of pods/plant	27.43	80.65	14.01	50.74
Shelling out-turn	12.26	68.84	13.31	20.96
No. of seeds/pod	3.28	15.79	0.24	14.37
100-seed weigh	17.90	51.75	15.37	26.52
Pod yield/plant	12.52	28.6	4.77	13.77
Kernel yield/plant	14.36	27.24	3.4	15.44
Pod yield/ha	16.56	41.19	1299.31	21.89
Kernel yield/ha	14.36	27.23	582.71	15.44

4.4 Phenotypic and genotypic correlations

Table 7 presents the phenotypic and genotypic correlation coefficients between all possible pair-wise combinations of the twelve characters studied in nineteen groundnut genotypes. Phenotypic and genotypic correlation coefficients between the different characters exhibited different patterns. These can be summarized as follows:

4.4.1 Correlation between kernel yield/plant and its components: Significant positive phenotypic correlation coefficients were obtained between kernel yield/plant and days to 50% flowering (r = 0.52), pod yield/ plant (r = 0.81) and number of pods/plant (r = 0.46). At the genotypic level, the kernel yield/plant exhibited significant positive correlation with number of pods/plant (r = 0.49), number of seeds/pod (r = 0.48), 100-seeds weight (r = 0.41) and pod yield/plant (r = 0.89).

4.4.2 Correlation between yield components: Estimates of correlation coefficients among yield components showed different patterns at both phenotypic and genotypic levels. Days to 50% flowering was significantly and positively associated, at both phenotypic and genotypic levels, with days to maturity (r = 0.88, 0.80), and only at the phenotypic level with pod yield/plant (r = 0.53) and kernel yield/plant (r = 0.52). Days to maturity had a significant negative correlation with number of seeds/pod (r = 0.42) at the phenotypic level, and significant positive association with number of seeds/pods (r = 0.54) at the genotypic level.

Number of pods/plant was significantly and positively associated, at the phenotypic level, with shelling out-turn (r = 0.43), pod yield/plant (r = 0.43) and kernel yield/plant (r = 0.43). However, it had significant negative phenotypic association with number of seeds/pod (r = -0.48) and 100-seed weight (r = -0.95). At the genotypic level, the number of pods/plant was significantly and positively correlated with shelling out-turn (r = 0.46), pod yield/plant (r = 0.5) and kernel

yield/plant (r = 0.49), but it was significantly and negatively correlated with 100-seed weight (r = -0.47).

Number of seeds/pod had a significant negative association with pod yield/plant (r = -0.53) and a positive association with shelling out-turn (r = 0.63), at the phenotypic level, as well as positive association at the genotypic level with kernel yield/plant (r = 0.48). Hundred – seed weight was significantly and positively associated at the genotypic level with pod yield/plant (r = 0.41).

4.4.3 Correlation between kernel yield/plant and morphological characters: Kernel yield/plant had non-significant positive association, at both phenotypic and genotypic levels, with days to maturity (r = 0.36, 0.18) and number of branches/plant (r = 0.32, 0.31). However, it had a significant positive association, at the genotypic level, with length of the main stem (r = 0.46) and shelling out-turn (r = 0.45).

Table 7. Phenotypic and genotypic correlation coefficients among 12 characters in 19 groundnut genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X2	0.88**										
	0.80**										
X3	0.3	0.14									
	- 0.05	0.04									
X4	- 0.07	0.09	- 0.26								
	- 0.07	0.09	- 0.13								
X5	0.03	0.11	- 0.38	0.9**							
	0.02	0.10	- 0.08	0.86**							
X6	0.24	0.19	- 0.53*	0.05	0.43*						
	0.11	0.15	0.11	0.12	0.46*						
X7	0.13	- 0.42*	- 0.28	- 0.12	- 0.48*	0.63**					
	0.02	0.54*	0.2	0.1	0.03	0.35					
X8	0.25	0.32	0.45*	0.32	- 0.95**	0.04	0.14				
	0.08	0.4	0.5*	0.21	- 0.47*	0.23	0.32				
X9	0.53*	0.36	0.58**	0.26	0.43*	- 0.19	- 0.53**	- 0.2			
	0.18	0.18	0.49*	0.35	0.50**	0.21	0.30	0.38			
X10	0.52*	0.36	0.02	0.32	0.46*	0.24	0.13	- 0.16	0.81**		
	0.15	0.18	0.46*	0.31	0.49*	0.45*	0.48*	0.41*	0.89**		
X11	0.98**	0.27	0.44*	0.2	0.32	0.12	0.02	- 0.15	0.96**	0.61**	
	- 0.5	0.17	0.45*	0.26	0.45*	- 0.05	0.28	0.35	0.98**	0.81**	
X12	0.52*	0.96**	0.34	0.32	0.46*	0.21	0.13	- 0.14	0.81**	0.95**	0.61*
	0.15	- 0.44*	0.36	0.31	0.49*	0.32	0.49*	0.41*	0.89**	0.97*	0.81**

X1 = days to 50% flowering, X2 = days to maturity, X3 = plant height, X4 = no. of branches/ plant, X5 = no. of pods/plant, X6 = shelling out-turn, X7 = no. of seeds/pod, X8 = 100 – seed weight, X9 = pod yield/plant, X10 = kernel yield/plant, X11 = pod yield/ha, X12 = kernel yield/ha.

Figures in the upper part of each cell are phenotypic correlation coefficients; those in the lower part are the genotypic ones.

* Significant at P≤0.05

** Significant at P≤ 0.01

CHAPTER FIVE
DISCUSSION

5.1 Variability in groundnut

Genetic variability provides a good opportunity for selection of the best genotype (s). In the present investigation, the means of the nineteen genotypes were significantly different for all the studied characters, except the number of seeds/pod. These results are similar to those reported by Vaddoria and Patel (1990) and Uddin *et al.* (1995), except for number of seeds/pod. The variation among genotypes can be attributed to genetic factors as well as to environmental ones. Thus, the phenotypic, genotypic and environmental variances were determined for all characters under study. The results showed that estimates of genotypic variances for days to 50% flowering, days to maturity, number of branches/plant, number of pods/plant, shelling out–turn and 100– seed weight were greater than the estimates of their respective environmental ones. On the other hand, the environmental variances for plant height, pod yield/plant, kernel yield/plant, number of seeds/pod, pod yield/ha and kernel yield/ha were greater than the estimates of their respective genotypic ones. High estimates of genotypic variances for some characters indicate that these characters possess promising genetic variation, unlike characters with low estimates of genotypic variances which are affected more by the environmental conditions.

5.2 Genetic coefficient of variation (G.C.V.), heritability (h^2) and genetic advance (G.A.)

Genetic coefficient of variation (G.C.V.) determines the degree of the genetic variability expressed by a character in a population. In the

present study, the 12 characters showed a wide range of genetic variability among the evaluated genotypes. The highest G.C.V. values were obtained for number of branches/plant, whereas the lowest G.C.V. values were given by days to maturity, days to 50% flowering, number of seeds/pod, pod yield/plant, kernel yield/plant, pod yield/ha, kerned yield/ha, plant height, 100–seed weight and shelling out-turn. Consequently, the highest values of expected genetic advance were obtained for the first group, while the second group exhibited the lowest estimates. The findings of Uddin *et al.* (1995), Azad and Hamid (2000) and Vaddoria and Patel (1990) are at variance with these results. Such contradicting results may be explained by the differences in the varieties and environmental conditions. The association between G.C.V. and G.A. was explained by Allard (1960) as follows: Genetic advance from selection in any character depends mainly on the genetic variability of that character.

In contrast to genetic coefficient of variation, heritability expresses the portion of the total variance that is attributed to the average effects of genes. Its main role is in predicting the reliability of the phenotype as a guide to the genotype. Thus, heritability of a character and its phenotypic performance, in combination with intensity of selection and the amount of genetic variability present in a population, influence the gain to be obtained from selection (Falconer 1980).

In the current investigation, high values of heritability, (above 70%), were obtained for days to 50% flowering, days to maturity, number of branches/plant and number of pods/ plant. Similar results were reported by Uddin *et al.* (1995) and Azad and Hamid (2000). Such findings indicate that most of the variation exhibited by these characters can be attributed to genetic causes. Consequently, improvement in these traits could be achieved using mass selection. On the other hand, low

estimates of heritability were obtained for plant height, pod yield/plant, kernel yield/plant, number of seeds/pod, 100–seed weight, shelling out–turn, pod yield/ha and kernel yield/ha; these characters had low genetic variances and high environmental ones. Johnson *et al.* (1955a) reported that, in soybean, the estimates of heritability in the broad sense may vary greatly depending on the character, the population and the sample for which the variance is estimated. In addition, Falconer (1980) indicated that heritability is a property not only of a character but also of the population and the environmental conditions to which the individuals are subjected.

In the present study, high genetic advance (more than 50%) was given by number of branches/plant, which exhibited high G.C.V. On the other hand, low (less than 50%) estimates were exhibited by the other characters, which had low estimates of G.C.V. This indicated that there was association between the estimates of G.C.V. and the expected G.A. However, no definite trend was obtained between G.C.V. and h^2 estimates or between h^2 and G.A. Similar results were reported by Uddin *et al.* (1995) and Azad and Hamid (2000) in groundnut, Singh and Singh (1969) in lentil, Osman and Khidir (1974) in sesame, Abdelmula (1992) in faba bean and Gasim and Khidir (1998) in roselle. Furthermore, Singh and Singh (1969) indicated that mass selection in lentil may be more effective for characters which express high genetic advance than for those with low genetic advance.

5.3 Phenotypic and genotypic correlations

To improve yield, determination of the degree of association between yield components is very essential. This is because yield is a complex character in inheritance, highly influenced by the environment and is dependent on many component traits; consequently, slow gain is expected from direct selection for yield improvement. Most of the yield components are also not simply inherited but are less influenced by

environmental conditions. Therefore, they could be used as selection criteria for improving yield.

In the present study, kernel yield/plant was significantly and positively correlated, at the phenotypic and genotypic levels, with number of pods/plant and pod yield/plant. On the other hand, the kernel yield had positive significant association at the genotypic level with length of main stem, 100–seed weight, shelling out – turn and number of seeds/pod. Similar results were reported by Ibrahim (1983), Uddin *et al.* (1995) and El – Ashry *et al.* (1986), except for shelling out – turn, length of main stem and number of seeds/pod. The close association among the above mentioned characters could be due to the effect of genes rather than the effect of environmental factors (Falconer 1980), and selection for any of these traits could result in a substantial improvement in yield. On the other hand, kernel yield/plant had no significant association, at both genotypic and phenotypic levels, with days to maturity and number of branches/plant indicating that these characters are not suitable criteria in selection for yield improvement.

Significant positive genotypic and phenotypic correlation coefficients were detected between pod yield/plant, 100 – seed weight, days to 50% flowering, days to maturity and shelling out– turn. Such association may be attributed to pleiotropy or linkage (Yassin 1973) or may be due to developmentally induced relationships between these components that are only indirectly the consequence of gene action (Adams 1967). These positive associations between these traits indicated that selection of one of them will be effective in improving the other.

Negative association between yield components were also detected; such negative correlations occur when the components compete for assimilates during development (Adams 1967).

Summary and Conclusion

1- The present investigation was conducted for one season to estimate the variability, and correlations between yield and its components in 19 groundnut genotypes.

2- Genetic coefficient of variation, genetic advance, heritability, and phenotypic and genotypic association between 12 traits were estimated.

3- The results revealed high estimates of variance among the mean value of genotypes for all characters studied except number of seeds/pod. High estimate of genetic advance coupled with high estimate of genetic coefficient of variation was obtained for number of branches/plant. Kernel yield had significant and positive associations, both at the phenotypic and genotypic levels, with days to 50% flowering, pod yield/plant and number of pods/plant.

4- Effectiveness of selection depends mainly on variability; the amount of variability detected in the studied genotypes offers a better chance to select the best genotype (s).

5- To obtain more reliable results, the experiment should have been carried out for more than one season and more than one location to reduce the effect of the environmental factors.

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