# "GENETIC VARIATION, SELECTION INDICES AND DIVERSITY ANALYSIS FOR POD YIELD AND ITS COMPONENTS IN RILs OF GROUNDNUT (*Arachis hypogaea* L.)"

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**JUNAGADH – 362 001**


**AUGUST - 2019**

*DEDICATED*

*TO*

*MY*

*BELOVED PARENTS*

*&*

*Respected Guide*

***Without whom none of my success would be possible.***

***HETAL…***

# GENETIC VARIATION, SELECTION INDICES AND DIVERSITY ANALYSIS FOR POD YIELD AND ITS COMPONENTS IN RILs OF GROUNDNUT
**(*Arachis hypogaea* L.)**


| Name of Student | Major Guide |
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## ABSTRACT


***Key words*:** Groundnut, Genetic variability, Correlation, Path analysis, Selection indices, Genetic divergence



An investigation was carried-out on genetic variability, correlation, path analysis, selection indices and genetic divergence in groundnut using 68 genotypes comprising 64 Recombinant Inbred Lines, two parents and two checks. The genotypes were evaluated in a Randomized Block Design with three replications at the Main Oilseeds Research Station, J.A.U., Junagadh during *kharif* 2018.

The observations were recorded on five randomly selected plants from each replication and their mean values were used for statistical analysis. The characters studied were days to 50% flowering, days to maturity, plant height (cm), SCMR, number of mature pods per plant, number of immature pods per plant, shelling percentage (%), 100-kernel weight (g), sound mature kernels (%), kernel yield per plant, biological yield per plant (g), pod yield per plant (g), harvest index (%) and oil content (%).

Analysis of variance revealed significant differences among the genotypes for all the 14 characters studied. Wide to moderate range of variation was observed for majority of the characters. Wide range of variation was observed for biological yield per plant, number of mature pods per plant, SCMR, plant height, 100-kernel weight and harvest index.

The values of PCV were slightly higher than that of GCV for all the traits. The highest GCV and PCV were observed for number of immature pods per plant. The values were observed to be moderate for biological yield per plant, number of mature pods per plant, 100-kernel weight, kernel yield per plant and pod yield per plant.

High estimates of heritability were observed for all the 14 characters, while high heritability along with high genetic advance was observed for number of immature pods per plant, biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant.

The values of genotypic correlations were higher than their corresponding phenotypic correlations. The pod yield per plant exhibited significant and positive correlation with days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant at both genotypic and phenotypic levels. The path coefficient analysis showed the highest positive direct as well as appreciable indirect influences on pod yield per plant through kernel yield per plant and biological yield per plant.

A total of 63 selection indices were constructed involving pod yield per plant and five yield components using the discriminant function technique. The discriminant function selection had higher genetic gain and selection efficiency over straight selection for pod yield alone. The efficiency of selection increased with the inclusion of more number of characters in the index. A selection index consisting of pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant and an index involving pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant could be advantageously exploited in groundnut breeding.

Sixty eight genotypes were grouped into 5 clusters by Mahalanobis's $D^2$ statistic. The maximum inter-cluster distance was found between clusters IV and V followed by that between clusters III and V, I and V, II and V and II and IV. The cluster V was superior for pod yield per plant, kernel yield per plant, number of mature pods per plant, number of immature pods per plant, plant height, SCMR, 100-kernel weight, shelling out-turn, biological yield per plant and oil content, while cluster III was the best for harvest index, sound mature kernels and days to 50% flowering. Cluster IV was good for days to maturity. The number of immature pods per plant, days to maturity and biological yield per plant contributed maximum towards the total divergence. Based on high yielding genotypes and large inter-cluster distances, it would be advantageous to attempt crossing of the genotypes from cluster V with the genotypes of clusters IV, III, II and I which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in groundnut.

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# CERTIFICATE – I

This is to certify that the thesis work report entitled **"GENETIC VARIATION, SELECTION INDICES AND DIVERSITY ANALYSIS FOR POD YIELD AND ITS COMPONENTS IN RILs OF GROUNDNUT (*Arachis hypogaea* L.)"** submitted by **HETALBEN RAMANI** (Reg. No. 2010117045) in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** to the Junagadh Agricultural University is a record of bonafide research work carried out by her under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title. The candidate had fulfilled all prescribed requirements. The assistance and help received during the course of investigation have been fully acknowledged. She has successfully completed the comprehensive preliminary examination held on F**ebruary 19, 2019** as required under the regulation for post-graduate studies. She has submitted kachcha bound thesis on **June 28, 2019.**

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## CERTIFICATE-II

**Date: 05/08/2019**

This is to certify that the thesis/project work report entitled **"GENETIC VARIATION, SELECTION INDICES AND DIVERSITY ANALYSIS FOR POD YIELD AND ITS COMPONENTS IN RILs OF GROUNDNUT (*Arachis hypogaea* L.)"** submitted by **HETALBEN RAMANI** to Junagadh Agricultural University, Junagadh in partial fulfillment of the requirements for award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** after recommendation by the external examiners were defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination was satisfactory. We, therefore, forward with recommendation.

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Place: Junagadh

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# CHAPTER I
# INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is one of the principal economic oilseed crops of the world. It is commercially cultivated in more than 100 countries located in between 40ºN and 40ºS latitudes. Groundnut is considered as the world's fourth largest source of edible oil and third most important source of vegetable protein. It is also a major oilseed legume crop in India and meets about 30% of the edible oil requirements in the country. The botanical name for groundnut, *Arachis hypogaea* L. is derived from two Greek words, *Arachis* means a legume and *hypogaea* means below ground, referring to the formation of pods in the soil. It is widely grown annual crop with dicotyledonous behavior. The groundnut is generally distributed in the tropical, sub-tropical and warm temperate regions of the world.

Groundnut has a wide range of adaptability in varying agro-climatic conditions and soils, which has made its cultivation possible in most of the tropical and sub-tropical countries in the world. Groundnut is grown on an area of 25.92 million ha worldwide with a total production of 44.93 million metric tonnes and average productivity of 1730 kg/ha (Anon, 2018). Developing countries contribute about 97% of global area and 94% of the global production of the crop. In India, groundnut is grown on an area of 4.90 million ha with a production of 8.21 million metric tonnes and the productivity of 1674 kg/ha (Anon, 2018). The principal groundnut growing states in India are Gujarat, Andhra Pradesh, Karnataka, Tamil Nadu, Rajasthan and Maharashtra, which accounts for more than 85% of the Indian production as well as an area. The rest of the area and production is distributed mainly in the states of Odisha, Uttar Pradesh and Madhya Pradesh. In Gujarat, groundnut is grown on an area of 1.69 million ha with production of 4.06 million metric tonnes and a productivity of 2422 kg/ha (Anon. 2018).

Species of the genus *Arachis* are native of South America. Krapovickas (1969) postulated that the cultivated groundnut, (*Arachis hypogaea* L.) is believed to have originated in Northern Argentina and South Bolivia. Bolivia has the second largest number of species followed by Paraguay, Argentina and Uruguay. It is an allotetraploid (2n=4x=40) with basic chromosome number, x =10 (Stalker, 1997). The groundnut is characterized by cleistogamy and hence, it is highly self-pollinated in nature (Knauft

and Wynne, 1995). The cultivated groundnut has produced, in the course of its evolutionary history, a great number of morphological variant forms. The gene pool of cultivated groundnut has been divided into two subspecies and each subspecies is divided into two botanical varieties. The subspecific classification of *Arachis hypogaea* L. is described elsewhere (Krapovickas, 1973, Gregory *et al.,* 1980 and Weiss, 2000) and have been given in short as under:

- *Arachis hypogaea* L. subspecies *hypogaea*: Semi-spreading or spreading in habit, branching alternate, inflorescence simple and absent on main axis, seed dormancy usually present, foliage dark green and first branch on cotyledonary lateral always vegetative. It includes two varieties, i) var. *hypogaea*: Virginia bunch and Virginia runner and ii) var. *hirsute*: Peruvian runner
- *Arachis hypogaea* L. subspecies *fastigiata*: Erect and bunch in habit, branching sequential, inflorescence usually present on the main axis and first branching on the cotyledonary laterals are reproductive, seed dormancy usually absent and foliage light green. It includes two varieties i) var. *fastigiata*: Valencia and ii) var. *vulgaris* : Spanish

Groundnut has a distinct position among the oilseeds as it can be consumed and utilized in diverse ways. It is a rich source of edible oil (44-55%), high quality protein (22-32%) and carbohydrates (8-14%) and hence, it is valued both for edible oil and confectionery purposes. Groundnut kernels are consumed as raw, boiled, roasted or fried products and also used in a variety of culinary preparations like peanut candies, peanut butter, peanut milk and chocolates (Desai *et al.*, 1999). Cake left after extraction of the oil is an excellent feed for livestock. Vegetative parts of groundnut like leaves and stems are good source of nutritionally high quality fodder for farm animals. Dry roasted, salted peanuts are also marketed in significant quantities. Groundnut is also used in cosmetics, nitroglycerin, plastics, dyes and paints.

Assessment of variability in the germplasm forms the basis for any crop improvement programme. The choice of suitable parents is of paramount importance for a planned and successful hybridization programme. Hence, efforts have to be made to identify the best parents with wide genetic variation from germplasm pool for the characters of economic importance, so as to utilize them in hybridization programme. The phenotypic expression of a character is the resultant of interactions between genotype and environment. Hence, the total variation needs to be partitioned into variance due to genotype (heritable) and variance due to environment (non-heritable)

for assessing the true breeding behaviour of the phenotype. In groundnut crop, it is obligatory to accumulate information on the variability existed among the polygenic characters and degree of association between them. Since the economic part of groundnut known as pod is developed under the soil, prediction of its performance based on aerial morphological characters is almost difficult (Weiss, 2000). Therefore, the critical assessment of nature and magnitude of genetic variability is pre-requisite in groundnut breeding programme. Heritability is an important parameter which determines the extent of expressivity of a trait in a set of environments or agro-climatic conditions. Therefore, heritability estimates are useful in predicting genetic advance under different intensities of selection. High heritability estimates together with high genetic advance are more valid for selection than heritability estimates alone (Johnson *et al.,* 1955). Estimation of genetic variability in conjunction with heritability and genetic advance gives an idea of the possible improvement of the character through selection.

Yield being a complex character is influenced by various component characters, which are polygenically inherited and highly subjected to environmental variation. Hence direct selection for yield may not be a reliable approach. More emphasis should be placed on the selection of yield attributes which are less influenced by the environment. Therefore, it becomes essential to identify the component characters through which yield improvement could be obtained. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its component characters and also among various component characters. Correlations though give information about the characters influencing yield, it would not provide an exact picture of relative importance of the direct and indirect contribution of the component characters to yield. In this context, path analysis is an important tool to partition the correlation coefficient into direct and indirect effects (Dewey and Lu, 1959). Path analysis is essential to know optimum combination of yield contributing characters and the implication of interrelationships of various characters in a single genotype. Thus, correlation in conjunction with path analysis would give a better insight into cause and effect relationship between different pairs of characters.

Pod yield is governed by a polygenic system and is highly influenced by the fluctuations in the environment. Hence, selection of plants based directly on yield would not be very reliable in many cases. The effectiveness of component approach to selection breeding is well appreciated (Shettar, 1974; Bandyopadhyay *et al*., 1985;

Dobariya *et al*., 2008). An application of discriminant function developed by Smith (1936) helps to identify important combination of yield components useful for selection by formulating suitable selection indices. The simultaneous selection of traits, which can be performed effectively by the use of selection indices, increases the chances for the success of breeding programmes. The selection indices make a combination of the multiple information of the experimental unit possible and enable selection based on a complex of variables of economic interest.

The choice of genetically divergent parents for hybridization under transgressive breeding programme is also dependent upon categorization of breeding materials on the basis of appropriate criteria. Systematic classification rests exclusively upon easily distinguishable qualitative attributes. This represents phylogenetic hierarchy or descriptive account of individuals or groups of individuals. But, it does not consider quantitative traits showing continuous variation, which constitutes the backbone of plant breeding practices. On the other hand, quantitative classification offers a quantified degree of divergence among genotypes or populations. This serves as a sound basis of grouping any two or more genotypes based on minimum divergence or resemblance between them. The models of multivariate analysis which satisfy this proposition are more than one, e.g., Duncon's multiple range test, metroglyph and index score method, $D^2$-statistic and canonical analysis. Among these methods, Mahalanobis's (1936) $D^2$-technique is the most efficient tool for estimating genetic divergence. Genetic diversity plays an important role because hybrids between lines of diverse genetic background generally display a greater heterosis than those between closely related parents and may generate broad-spectrum genetic variability in segregating generations (Arunachalam, 1981; Sharma, 1998).

Keeping all the facts in view, the present study was, therefore, planned in groundnut with the following objectives:

i. To assess genetic variation for pod yield and its component characters in RILs derived from the cross AG-2006-6 x ICGV-05155.
ii. To assess association among pod yield and its component characters in RIL population.
iii. To study path coefficients for pod yield and its components through direct and indirect effects in RIL population.
iv. To determine the selection indices.
v. To assess the extent of genetic diversity present among the RILs.

# CHAPTER II

## REVIEW OF LITERATURE

Groundnut (*Arachis hypogaea* L.) is an important legume cum oilseed crop which is cultivated on large scale throughout the world. In the present investigation, the Recombinant Inbred Lines of groundnut were evaluated to assess genetic variability, correlation coefficient, path coefficient analysis, selection indices and genetic divergence for yield and its components. The literature pertaining to this investigation has been reviewed briefly under the following sub-heads:

2.1 Variability parameters

2.2 Correlation coefficient

2.3 Path coefficient analysis

2.4 Selection indices

2.5 Genetic divergence

### 2.1 GENETIC VARIABILITY

The success of breeding programme depends upon the extent and magnitude of variability existing in the germplasm or segregating population. A comprehensive summary of methods for estimating genetic variance is presented by Cockerham (1963). Phenotypic variability is observable and it includes both genotypic and environmental variation and therefore, it is also called as total variation. Genotypic variation refers to genetic or inherent variability which remains unaltered by environmental conditions. It is measured in terms of genotypic variance and consists of additive, dominance and epistatic components. Environmental variance is measured in terms of error mean variance. Generally, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are used to assess the extent of variation between two different contrasting characters.

Heritability is the transmissibility of characters from parents to offspring. Heritability in broad sense is the ratio of genotypic variance to total phenotypic variance in percentage. Effectiveness of selection of genotype depends on heritability. Genetic advance (GA) is the improvement over the base population that can be potentially achieved from selection. It is a function of heritability of the trait, the amount of phenotypic variation and the selection differential that the breeder uses. When high heritability is accompanied with high genetic advance, it indicates additive gene effect

and selection may be effective. When low heritability accompanied with low genetic advance, it indicates predominance of environmental effect and selection would be ineffective. High heritability with low genetic advance indicates the importance of non-additive gene effect, while low heritability with high genetic advance indicates the importance of additive gene effect.

Venkataramana (2001) from the evaluation of 30 groundnut genotypes stated that the genotypic coefficient of variation was high for oil content, pod yield, 100-kernel weight and kernel yield. Heritability (broad sense) estimates were high for oil content, 100-kernel weight and sound mature kernel percentage. High heritability coupled with high genetic advance was observed for 100-kernel weight.

Information on genetic variability was derived from data on 144 groundnut germplasm lines by Venkataramana *et al.* (2001). High genotypic and phenotypic coefficients of variation were observed for plant height, oil percentage, 100-kernel weight, haulm yield per plant and kernel yield per plant. High estimates of heritability with high genetic advance were observed for plant weight, pod yield per plant, 100-kernel weight and oil percentage.

Dashora and Nagda (2002) evaluated 22 germplasm lines with one local check (TAG-24) to estimate variability parameters and revealed that dry pod yield, 100-kernel weight and kernel yield had high genetic advance, genetic gain and heritability estimates, suggesting preponderance of additive gene effect. High heritability was accompanied with low genetic advance as per cent of mean for days to 50% flowering, days to maturity, shelling per cent, 100-kernel weight and oil content revealing preponderance of non-additive gene effect.

Nath and Alam (2002) evaluated 15 exotic groundnut genotypes along with local check to study their performance, genetic variability, heritability and genetic advance for yield and yield contributing characters. Higher phenotypic coefficient of variation was observed for plant height, primary branches per plant, pods per plant, harvest index and pod yield per plant. Characters like plant height, pods per plant, 100-pods weight, shelling percentage, harvest index and pod yield per plant showed high heritability. Considerably high genetic advance as percentage of mean was found for plant height, pods per plant, harvest index and pod yield per plant.

Prasad *et al.* (2002) reported that phenotypic and genotypic coefficients of variation were high for harvest index and moderate for pod yield per plant, number of primary branches, height of main axis, number of pods per plant and 100-kernel weight.

High values of heritability were accompanied with high genetic advance for harvest index, pod yield per plant, height of main axis and number of pods per plant.

Parameshwarappa *et al*. (2004) evaluated 48 diverse large seeded groundnut genotypes and reported the presence of high genetic variability for number of primary branches, pod yield per plant, kernel yield and plant height. Considerable variability was also noticed for number of pods, 100-kemel weight, seed size and protein content. However, variability observed for oil content and sound mature kernels was low. High heritability coupled with genetic advance was noticed in respect of kernel yield, sound mature kernels and 100-kemel weight. The extent of genetic advance was quite low for kernel size, protein content and oil content.

Suneetha *et al.* (2004) studied 23 genotypes of groundnut for genetic variability and reported high heritability coupled with high genetic advance as percentage of mean for number of mature pods, number of immature pods and number of secondary branches. High heritability coupled with moderate genetic advance was observed for days to 50% flowering, plant height, total dry matter per plant, 100-pod weight, 100-kernel weight and pod yield per plant, while the characters like days to maturity, number of primary branches, sound mature kernels, shelling percentage and oil content registered high heritability with low genetic advance.

Wani *et al*. (2004) studied variability parameters through advanced generation lines of groundnut and reported high values of genotypic coefficient of variation for mature pods per plant and harvest index. High heritability was observed for days to maturity, number of branches per plant, 100-kernel weight, days to first flowering, 100-pod weight and shelling out-turn. High heritability coupled with high genetic advance as per cent of mean was observed for days to maturity, 100-pod weight and 100-kernel weight revealing that selection would be effective for improvement in these characters.

Mahalakshmi *et al.* (2005) studied genetic variability parameters in 57 genotypes of groundnut. They reported higher value of PCV than GCV for all the characters under study. However, estimates of PCV and GCV were high for number of mature as well as immature pods, pod yield per plant and oil content; whereas, low for plant height, shelling percentage and 100-kernel weight. The heritability estimates were high for all the characters except oil content. All the characters except days to first flowering, days to 50% flowering, plant height, number of primary branches and oil content registered high heritability along with high values of GA as per cent of mean.

John *et al.* (2006) reported that the estimates of phenotypic coefficient of

variation were higher than those of the genotypic coefficient of variation for the characters evaluated. The estimates of heritability in the broad sense ranged from 21.39 (shelling out-turn) to 76.03 (number of secondary branches per plant). High heritability values were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant, pod width and kernel weight. Genetic advance as percentage of the mean was also high for number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant and pod width.

Kadam *et al.* (2007) studied 40 groundnut genotypes of different botanical groups to assess the amount of genetic variation, heritability and genetic advance with respect to pod yield and other agronomic characters. The genotypic coefficient of variation was high for kernel yield, pod yield, number of pods, number of branches, plant height and harvest index. High heritability coupled with high genetic advance was observed for pod yield and kernel yield.

Kumar *et al.* (2008) evaluated 64 genotypes of groundnut (39 accessions and 25 advance breeding lines) for fourteen quantitative characters and revealed wide range of variability. The estimates of PCV and GCV were moderate for plant height, matured pods per plants, pod yield per plant, kernel yield per plant, shelling percentage, 100-kernel weight, harvest index and specific leaf area. High heritability coupled with high genetic advance was noticed for all the characters under study except for days to 50% flowering, days to maturity, sound mature kernel percent and oil content.

John *et al.* (2009) studied 60 genotypes of groundnut for variability parameters for 17 characters. They reported high GCV and PCV values for all the characters except for plant height, shelling percentage and 100-kernel weight. Low GCV and PCV values were observed for days to initial flowering, days to 50% flowering and number of primary branches. The broad sense heritability estimates were high for all the characters and estimates of GA as per cent of mean were high for all the characters except growth attributes, days to initial flowering as well as 50% flowering, plant height and number of primary branches per plant.

Khote *et al.* (2009) studied 56 groundnut genotypes for genetic variability, heritability and genetic advance for yield and yield contributing characters. Higher phenotypic and genotypic coefficients of variation were observed for dry fodder yield per plant followed by dry pod yield per plant. High heritability values were recorded in respect of 100 dry pod weights, number of days to maturity, oil per cent in kernels, pod

length and dry fodder yield per plant. The characters which showed high genetic advance as per cent of mean were dry fodder yield per plant, dry pod yield per plant, leaf area, number of pods per plant, number of sound mature kernels and 100 dry pod weight.

Korat *et al.* (2009) studied components of variation, heritability and genetic advance by using 65 confectionary groundnut genotypes and reported that values of GCV and PCV were high for number of secondary branches per plant and number of aerial pegs per plant. High heritability along with high genetic advance as per cent of mean was observed for number of secondary branches per plant and number of aerial pegs per plant, while moderate genetic advance as per cent of mean was observed for biological yield per plant and harvest index.

Dolma *et al.* (2010a) studied the variability parameters like variability, heritability and genetic advance in 33 groundnut genotypes. High GCV and PCV were observed for kernel yield per plant, plant height, pod yield per plant and test weight. Moderate estimates of PCV and GCV were observed for harvest index, number of primary branches per plant and shelling out-turn. Lowest differences between PCV and GCV were observed for days to maturity and kernel yield per plant. The estimates of heritability were very high for days to maturity, harvest index, shelling out-turn and number of primary branches per plant.

Saraswathi *et al.* (2010) reported high phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent of mean for number of secondary branches per plant, plant height, pod yield and kernel yield per plant. It indicated the role of additive gene action and hence, the usefulness of phenotypic selection for bringing improvement. High heritability was observed for all thirteen characters. High genetic advance as per cent of mean was observed for number of secondary branches per plant, plant height, number of filled pods per plant, harvest index, shelling percentage, sound mature kernels (%), 100-kernel weight, protein content, pod yield and kernel yield along with high heritability. The characters days to maturity and oil percentage recorded moderate genetic advance as per cent of mean along with high heritability.

Shinde *et al.* (2010) studied 50 elite genotypes of Virginia bunch groundnut for ten characters. Phenotypic and genotypic coefficients of variation were higher for pod yield per plant, number of immature pods per plant, number of mature pods per plant and biological yield per plant. High heritability was associated with high genetic

advance and high GCV for pod yield per plant and number of mature pods per plant only. However, in most of the cases, high genetic advance was not accompanied with high heritability.

Zaman *et al.* (2011) assessed genetic variability, heritability and genetic advance in 34 groundnut genotypes and stated that high values of GCV, PCV and genetic advance were observed for number of branches per plant, number of immature and mature nuts per plant, 100 kernel weight and plant height whereas, these values were low for days to 50% flowering, oil content and days to maturity.

Nandini *et al.* (2011) investigated 196 recombinant inbred lines of groundnut and reported that maximum GCV and PCV were observed for pod yield followed by kernel yield per plant, number of pods per plant, sound mature kernel percentage, specific leaf area, number of branches per plant, shelling percentage, plant height, SCMR and days to 50% flowering. The results indicated moderate to high degree of heritability and genetic advance for pod yield per plant, kernel yield per plant, pods per plant, sound mature kernel percentage, plant height, number of branches per plant and SLA. Low heritability and moderate genetic advance as percentage of mean was observed for SCMR.

Vekariya *et al.* (2011) evaluated 50 diverse genotypes of bunch groundnut for genetic parameters viz., variability, heritability and genetic advance. The estimates of PCV and GCV were high for number of mature pods per plant, protein content, kernel yield per plant, harvest index, biological yield per plant and 100-kernel weight. High heritability coupled with high genetic advance expressed as percentage of mean was observed for number of matured pod per plants, kernel yield per plant and pod yield per plant indicating that these traits were mainly governed by additive gene action and responsive for further improvement of these traits.

Babariya (2012) evaluated 100 genotypes of groundnut to estimate variability for pod yield and its component character and reported that high values of GCV and PCV were observed for number of pods per plant, number of mature pods per plant, number of immature pods per plant, biological yield per plant and number of pegs per plant, while moderate values were observed for plant height, shelling out turn and 100-kernel weight whereas these values were low for days to 50% flowering, days to maturity and oil content. High heritability along with high genetic advance was observed for biological yield per plant, kernel yield per plant, number of secondary branches per plant, number of pods per plant, pod yield per plant, sound mature kernels,

number of mature pods per plant and harvest index.

John *et al.* (2013) assessed genetic variability, heritability and genetic advance in 37 genotypes of groundnut and reported high heritability and high genetic advance as percentage of mean was recorded for plant height, haulm yield per plant, pod yield per plant and kernel yield per plant. Moderate heritability and high genetic advance as per cent of mean was observed for number of primary branches per plant, number of secondary branches per plant, number of mature pods per plant and 100-pod weight indicating the importance of both additive and non-additive gene actions in the inheritance of these characters.

Toprope *et al.*, (2013) recorded high GCV, high heritability with high genetic advance as percentage of mean for pod yield per plant, kernel yield per plant, number of pods per plant and harvest index. The SCMR had moderate heritability with low genetic advance as percentage of mean.

Savita *et al.* (2014) evaluated 100 groundnut genotypes for drought tolerance during *kharif* 2011 under normal rainfed condition at two different locations, the same genotypes were tested to confirm the drought tolerance during *rabi*/summer season 2012 at third location and reported moderate values of GCV and PCV for SCMR with high genetic advance as percentage of mean and heritability, while shelling percentage, sound mature kernel percentage and oil content recorded high heritability and high genetic advance as percentage of mean with low GCV and PCV under all environments.

Patil *et al.* (2014) evaluated 58 Spanish bunch groundnut genotypes for variability studies for 16 characters. The maximum heritability was recorded for days to 50% flowering, plant height and 100-kernel weight. The maximum genetic advance was observed for 100-kernel weight and plant height. Moderate to high heritability coupled with moderate to high genetic advance was recorded for days to 50% flowering, plant height, 100-pod weight, 100-kernel weight, shelling percentage and harvest index.

Rao *et al.* (2014) studied genetic variability in important agronomic characters in set of 50 groundnut genotypes and reported that the magnitudes of PCV and GCV were moderate to high for number of pods per plant, plant height, kernel yield, dry pod yield, hundred kernel weight and dry haulm yield. High heritability coupled with high genetic advance as per cent of mean was observed for 100-kernel weight, dry pod yield, kernel yield, plant height and number of pods per plant indicating the role of additive gene in expressing these traits.

Yadav *et al.* (2014) studied genetic variability in 60 genotypes of groundnut. The magnitude of GCV, PCV, heritability and genetic advance as per cent of mean were recorded high for pod yield per plant, 100-kernel weight, harvest index, plant height and shelling out-turn. High broad sense heritability estimates were recorded for most of traits *viz.,* 100-kernel weight, days to maturity, shelling out-turn, pod yield per plant and harvest index, indicating that these traits were less influenced by the environment.

Gupta *et al.* (2015a) evaluated 60 diverse genotypes of groundnut. The PCV and GCV values were high for plant height, number of mature pods per plant and kernel yield per plant and moderate for harvest index, 100-kenel weight and biological yield per plant and low for days to 50% flowering, days to maturity, shelling out turn, sound mature kernel percentage and oil content. High heritability coupled with high genetic advance was observed for 100-kernel weight, biological yield per plant and kernel yield per plant. Moderate to low genetic advance was observed for shelling out turn, oil content, number of mature pods per plant, harvest index plant height, days to 50% flowering and days to maturity.

Sanjeevakumar *et al.* **(**2015) assessed 49 genotypes of groundnut to study genetic variability for yield and its related traits. The high values of GCV were observed for secondary branches per plant, immature pods, mature pods and pod yield, while the values were low for days to 50% flowering, days to maturity, shelling out turn and oil content. The high heritability was observed for number of matured pods per plant, days to 50% flowering, 100-kernel weight, number of immature pods per plant, plant height and oil content. Moderate to low genetic advance was observed for shelling out turn, days to 50% flowering, days to maturity, number of primary branches per plant, number of immature pods per plant and oil content. Low genetic advance as percentage of mean was observed for days to maturity.

Venkataramana *et al*. (2015) studied 21 genotypes of groundnut to assess genetic variability for yield and yield component and reported that GCV and PCV were high for number of secondary branches per plant, kernel yield per plant, pod yield per plant and harvest index, while this values were low for days 50% flowering, days to maturity, shelling out turn and SCMR. High heritability coupled with high genetic advance as percentage of mean was observed for days to 50% flowering and harvest index whereas, moderate heritability coupled with moderate genetic advance as percentage of mean was observed for 100-kernel weight. High genetic advance was

reported for harvest index while moderate to low genetic advance was recorded for days to 50% flowering, days to maturity, number of branches per plant, shelling out-turn, SCMR and pod yield per plant.

Thirumal (2016) assessed genetic variability between yield and its contributing traits in 30 groundnut genotypes under drought. Analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The results showed the magnitude of PCV and GCV was moderate to high for pods per plants, haulm yield, kernel yield, plant height, SCMR and dry pod yield. High heritability coupled with high genetic advance was observed for kernel yield, plant height, dry pod yield and hundred kernel weight. Moderate to low genetic advance was observed for days to flowering, days to maturity, shelling out turn, SCMR and number of pods per plant.

Bhargavi *et al.* (2016) evaluated 20 diverse genotypes of Spanish bunch groundnut to assess the variability, heritability and genetic advance for various characters. The results revealed high PCV and GCV for harvest index and pod yield per hectare, respectively, while low values for GCV and PCV were observed for days to 50% flowering, SCMR, days to maturity, shelling out-turn and oil content. High heritability accompanied with high genetic advance was recorded for number of mature pods per plant, biological yield per plant, pod yield per plant, harvest index, kernel yield per plant and 100-kernel weight. Moderate to low genetic advance was observed for days to 50% flowering, SCMR, shelling out turn and oil content.

Namrata *et al.* (2016) evaluated 30 genotypes of groundnut to study the variability for different component characters. Higher estimates of GCV were observed for number of mature pods per plant and dry pod yield per plant, while moderate GCV were observed for biological yield per plant and low estimates were observed for plant height, number of branches per plant, shelling out turn, sound mature kernels and oil content. Maximum heritability was found for 100-kernel weight, oil content and sound mature kernels. While, maximum genetic gain was observed for dry pod yield per plant, 100-kernel weight and number of mature pods per plant. Thus, the traits *viz.*, number of mature pods per plant, dry pod yield per plant and 100-kernel weight indicated the presence of additive gene effects as they showed high GCV, heritability and genetic gain.

Bhargavi *et al.* (2017) evaluated ten genotypes of groundnut to assess genetic variability, heritability and genetic advance as per cent of mean for nineteen characters.

The components of variance revealed that the estimates of PCV were higher than GCV for all the characters *viz*, days to 50% flowering, SCMR, days to maturity, number of mature pods per plant, biological yield per plant, pod yield per plant, harvest index, 100-kernel weight, shelling percentage and oil content indicating the role of environmental variance in the total variance. The results revealed that high PCV and GCV were observed for number of mature pods per plant, biological yield per plant and pod yield per plant. High heritability accompanied with high genetic advance as percentage of mean was recorded for kernel yield per plant, 100-kernel weight and oil yield. High genetic advance was recorded for 100-kernel weight, while moderate to low values of genetic advanced were observed for harvest index, biological yield per plant, shelling out turn, number of mature pods per plant, SCMR, days to 50% flowering, pod yield per plant and oil content.

Mukesh and Lal (2017a) assessed variability for yield and its contributing traits in 40 genotypes of groundnut. High PCV and GCV values were observed for plant height, pod yield per plant and 100-kernel weight. High genetic advance was observed for 100-kerenel weight and sound mature kernels, moderate for shelling out turn, while low value were observed for days to 50% flowering, days to maturity, number of branches per plant and pod yield per plant.

Sushree *et al*. (2017) evaluated 32 $F_6$ progenies of groundnut along with four released varieties as parents to assess variability, heritability and genetic advance for various characters. The PCV and GCV estimates were high for haulm yield per plant and low for harvest index and shelling per cent. The moderate values for PCV and GCV were reported for plant height, number of branches per plant, number of pods per plant, 100-kernel weight and pod yield per plant. Moderate heritability and genetic advance as per cent of mean was recorded for plant height, pod number per plant, kernel number per plant, kernel yield and pod yield.

Chavadhari *et al.* (2017) evaluated 70 groundnut genotypes for various yield parameters. High estimates of the GCV were observed for kernel yield per plant, number of branches per plant, harvest index and biological yield per plant. The estimates of heritability were observed to be high for harvest index followed by biological yield per plant, kernel yield per plant, 100-kernel weight, plant height, 100-pod weight and number of branches per plant, which indicated that these characters were less influenced by the environmental fluctuations. High heritability along with high genetic advance was observed for 100-pod weight. High heritability along with

moderate genetic advance was observed for biological yield per plant, 100-kernel weight and harvest index.

Mahesh *et al.* (2018) evaluated 144 genotypes of groundnut for 13 characters to assess the variability, heritability and genetic advance. Plant height, number of primary branches per plant, number of mature and immature pods per plant, kernel yield per plant, 100-kernel weight, haulm yield per plant and dry pod yield per plant had high GCV, PCV, heritability and genetic advance as percentage of mean. Low variability was observed for days to 50% flowering, shelling out-turn, sound mature kernel percentage and oil content.

Wadikar *et al.* (2018) evaluated 40 diverse genotypes of groundnut to measure genetic variability. Higher PCV, GCV and high heritability coupled with high genetic advance as percentage of mean were observed for kernel yield per plant, pod yield per plant and number of pods per plant, while low variability was recorded for days to 50% flowering, days to maturity, shelling percentage and oil content. High genetic advance was recorded for shelling out turn, sound mature kernel and 100-kernel weight, while moderate to low genetic advance was observed for harvest index, days to 50% flowering, days to maturity, number of branches per plant, pod yield per plant and oil content.

Kadam *et al.* (2018) evaluated variability for 15 characters in 30 elite groundnut genotypes. The results revealed that PCV and GCV were higher for number of mature pods per plant, dry pod yield per plant, fresh pod yield per plant and fresh fodder yield per plant, while days to 50% flowering, shelling percentage and oil content had very low GCV and PCV value. High heritability coupled with high genetic advance was observed for fresh biomass per pant, fresh fodder yield per plant, fresh pod yield per plant and dry biomass yield per plant.

Lunagariya (2018) evaluated 90 genotypes of groundnut (18 parents and 72 advance breeding lines) for variability and drought tolerance under different four stress conditions. Analysis of variances revealed that estimates of GCV, PCV and genetic advance as per cent of mean were high for number of hanging pegs per plant, number of immature pods per plant, number of mature pods per plant and plant height for well-watered condition, While moderate values of GCV, PCV and high value of GAM were observed for number of pods per plant, 100-kernel weight, biological yield per plant and harvest index under well-watered, High heritability was observed for all sixteen characters except for oil content and number of branches per plant under well-watered

and imposed drought condition.

Syed *et al.* (2018) evaluated genetic variation and for nine characters in 34 advanced breeding lines of groundnut. Higher estimates of PCV and GCV were recorded for pod yield per plant, kernel yield per plant and pods per plant. High heritability with high genetic advance as per cent of mean was observed for yield related traits and specific leaf area, whereas high heritability and low genetic advance as per cent of mean was recorded for SCMR, days to first flowering and primary branches per plant.

Nayak *et al.* (2018) evaluated 20 genotypes of groundnut to measure genetic variability, heritability and genetic advance. The components of variance revealed that the estimates of PCV were higher than GCV for all the characters *viz*, final plant stand, days to initial flowering, days to 50% flowering, days to maturity, 100-kernel weight, 100-pod weight, shelling percentage, sound mature kernels, dry pod yield and kernel yield, indicating the role of environmental variance in the total variance. Higher GCV, PCV and genetic advance as percentage of mean were observed for the characters *viz,* 100-kernel weight, 100-pod weight, dry pod yield and kernel yield. High heritability was observed for sound mature kernels percentage, shelling per cent, dry pod yield per ha, 100-pod weight, 100-kernel weight and kernel yield, while moderate heritability was recorded for days to maturity.

Aparna *et al*. (2018) evaluated 168 germplasm lines of groundnut to estimates genetic variability. Higher GCV and PCV were observed for number of immature pods per plant, kernel yield per plant, number of primary branches per plant, number of mature pods per plant, pod yield per plant, number of pegs per plant and number of pods per plant. High heritability coupled with high genetic advance as per cent of mean was recorded by number of immature pods per plant, days to 50% flowering, number of primary branches per plant, shelling percentage, number of pods per plant, number of mature pods per plant, plant height and 100-kernel weight.

## 2.2 CORRELATION COEFFICIENTS

The knowledge of association of yield and its components is of immense value to breeder and forms a basis for selection. It is well known that different components of yield very often exhibit considerable degree of association among themselves and with yield. Therefore, to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the

interrelationship of various characters. The concept of correlation was first given by Galton (1889) and later it was elaborated by Fisher (1918). The interrelationship of yield and its components as worked-out by various workers in groundnut is reviewed here under.

Venkataravana *et al*. (2000) carried out correlation analysis in 144 germplasm lines of groundnut in 15 characters. The genotypic correlation coefficients were observed to be relatively of higher magnitude than the corresponding phenotypic correlation coefficients, indicating strong inherent association between the characters. Pod yield had positive and significant association with plant height, number of branches per plant, total number of pods per plant, number of matured pods per plant, shelling out-turn, haulm yield, 100-kernel weight, sound matured kernel percentage, harvest index, kernel yield and oil yield.

Jayalakshmi and Reddy (2003) evaluated 21 diverse genotypes of groundnut to study character association for yield and its related traits. Pod yield per plant had significant and positive correlation with specific leaf area, number of mature pods per plant, number of immature pods per plant and harvest index.

Golakia *et al.* (2004) studied 35 genotypes of Virginia runner groundnut and reported that the genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients. Pod yield was strongly associated with kernel yield and developed pods per plant. Pod yield was also associated with biomass yield per plant and harvest index. The characters like oil content, 100-kernel weight and days to maturity were found to be correlated among them as well as with pod yield.

Parameshwarappa *et al.* (2004) studied 48 diverse large seeded groundnut genotypes for correlation and reported that pod yield had positive and significant association with shelling per cent, sound mature kernels, 100-kernel weight and oil content. Among the yield traits, number of pods per plant exhibited positive association with shelling per cent, sound mature kernels and oil content. Sound mature kernels were found to be associated with 100-kernel weight. It was observed that days to 50% flowering had significant positive association with plant height, primary branches and number of pods. Further, the association of kernel weight with oil content was positive but, negative with protein content indicating that large kernels possess higher oil content but not the protein.

Suneetha *et al.* (2004) studied 23 genotypes of groundnut for correlation and reported that the values of genotypic correlation were higher than phenotypic ones.

Yield per plant had significant positive association with number of mature pods, total dry matter per plant and harvest index. The character pairs *viz*., days to 50% flowering with days to maturity, number of mature pods with total dry matter per plant and 100-pod weight with 100-kernel weight also showed significant and positive correlations among themselves. Days to 50% flowering and height of the main axis were negatively correlated with pod yield per plant.

John *et al.* (2007) carried-out an experiment to assess the correlation coefficient for pod yield and its component characters and reported that pod yield was significantly and positively correlated with number of mature pods per plant, SCMR, kernel yield per plant and harvest index. They also reported that significant and negative correlation was observed for SCMR with plant height; days to maturity with harvest index and number of immature pods per plant; days to 50% flowering with harvest index whereas, it displayed significant and positive correlation with days to maturity and number of branches per plant.

Kadam *et al.* (2009) evaluated 40 germplasm accessions of groundnut to determine the degree of association between pod yield and its components. Pod yield was positively and significantly correlated with number of matured pods per plant, harvest index, 100-kernel weight, numbers of branches per plant, plant height and oil content. These traits also possessed positive and highly significant association between themselves indicating that selection for these traits would be effective in improving the pod yield in groundnut.

Sumathi and Muralidharan (2007) studied 48 diverse genotypes of groundnut and reported that the pod yield per plant had significant positive association with kernel yield, sound mature kernel and 100-seed weight both at genotypic and phenotypic levels. The shelling percentage and oil content had negative association with pod yield per plant both at genotypic and phenotypic levels. In general, the genotypic correlations in most characters were higher than the phenotypic correlation coefficients thereby suggesting strong inherent association between characters. The inter correlations of kernel yield with sound mature kernel weight and 100-seed weight were also positive and significant at both genotypic and phenotypic levels. The number of mature pods per plant exhibited positive and significant association with total number of kernels per plant and sound mature kernel number.

Raut *et al.* (2010) studied the correlation coefficients among 11 yield and yield contributing traits in $F_2$ generation of six crosses of groundnut. The values of correlation

coefficient of pod yield per plant were found positive and highly significant with kernel yield per plant, number of mature pods per plant and shelling out-turn.

Meta and Monpara (2010) evaluated 50 elite genotypes of bunch groundnut to determine the degree of association between different characters. The pod yield per plant was associated strongly and positively with kernel yield per plant, pods per plant, shelling out-turn and oil content but, its correlation was significant and negative with 100-pod weight, days to 50% flowering and days to maturity.

Vekariya *et al.* (2010) studied 50 diverse genotypes of bunch groundnut for correlation coefficients. They reported that the magnitude of genotypic correlation coefficient was higher as compared to the corresponding phenotypic correlation coefficients. The pod yield per plant had highly significant and positive correlation at phenotypic level with number of mature pods per plant, 100-pod weight, 100-kernel weight, kernel yield per plant, biological yield per plant and harvest index.

Bhosale (2011) studied 108 different genotypes of groundnut and reported that the pod yield per plant exhibited significant and positive association with number of pods per plant, kernel yield per plant, number of pegs per plant, number of mature pods per plant, 100-pod weight, 100-kernel weight and harvest index at both genotypic and phenotypic levels, while pod yield per plant exhibited highly significant and negative correlation with days to maturity, plant height, number of secondary branches per plant and haulm yield per plant at both the genotypic and phenotypic levels. The pod yield per plant also showed positive and highly significant correlation with days to 50% flowering and shelling out-turn at genotypic level.

Channayya *et al.* (2011) studied 50 elite genotypes of bunch groundnut for different characters and reported that the pod yield was positively and significantly associated with number of primary branches, pod weight per plant, 100-kernel weight, sound matured kernels percentage and oil yield. These results clearly indicated that indirect selection for yield in groundnut is possible through simultaneous improvement of these yield components.

Babariya and Dobariya (2012) evaluated 100 genotypes of Spanish bunch groundnut to estimate correlation coefficients for pod yield and its component characters and reported that pod yield per plant had positive and significant association with number of pods per plant, number of mature pods per plant, biological yield per plant, harvest index and 100-kernel weight. They also reported that plant height had significant and negative correlation with days to 50% flowering and significant and

positive correlation with days to maturity.

Narasimhulu *et al.* (2012) carried-out association analysis among nine characters in 18 selected groundnut genotypes. The correlation study revealed that pod yield per plant had significant positive association with kernel yield per plant, shelling percentage and sound mature kernel percentage at both genotypic and phenotypic levels.

Ravikumar and Reddi Sekhar (2012) reported significant and positive association of kernel yield per plant, mature pods per plant, total pods per plant, harvest index, 100-seed weight, plant height and shoot weight with pod yield and also observed higher genotypic correlation coefficients than phenotypic correlation coefficients. Hence, they opined that there is strong inherent association between these characters.

Choudhary *et al.* (2013) assessed correlation in 27 groundnut genotypes for 13 characters. Pod yield was positively and significantly correlated with number of pegs per plant, number of mature pods per plant, kernel yield per plant, biological yield per plant and harvest index.

Makinde and Ariyo (2013) reported positive and significant correlation of pod yield with number of pods per plant and non-significant positive correlation with plant height at flowering, days to maturity and sample seed weight. Positive genotypic correlation between yield per plant and stem girth at maturity, number of leaves per plant, 100-seed weight and number of branches per plant at flowering indicated that direct selection for these characters in the early segregating generations will be effective.

Spandana (2014) evaluated 289 recombinant inbred lines of groundnut to accomplish correlation coefficients for pod yield and its component characters. Correlations coefficients indicated that SCMR, pods per plant, kernels per plant had strong positive association with pod yield per plant.

Kumar *et al.* (2014) evaluated 66 elite genotypes of groundnut to determine the degree of association between different characters. The results revealed that kernel yield was significantly and positively associated with pod yield per plant, number of mature pods per plant, shelling percentage, harvest index, sound mature kernel percentage and oil content.

Bhargavi *et al.* (2015) evaluated 20 genotypes of groundnut for correlation studies. Pod yield showed significant and positive association with days to maturity,

number of mature pods per plant, biological yield per plant, harvest index, 100-kernel weight and oil content both at phenotypic and genotypic levels.

Thirumala *et al.* (2016) assessed correlation for yield and its contributing traits in 30 groundnut genotypes under drought. Dry pod yield was significant positively correlated with kernel yield, number of pods per plant, hundred kernel weight and SCMR. The SCMR had positive association with 100-kernel weight, number of pods per plant and dry haulm yield. They also reported that significant positive correlation for days to 50% flowering with days to maturity, shelling outturn with 100-kernel weight whereas plant height showed significant negative correlation with number of pods per plant.

Jain *et al*. (2016) evaluated 24 diverse genotypes of groundnut to accomplish correlation coefficients for pod yield and its component characters. The genotypic correlation coefficients were found to be of relatively higher magnitude than the corresponding phenotypic correlation coefficients, indicating strong inherent association between the characters. Pod yield per plant displayed significant and positive association with kernel yield per plant, mature pods per plant and plant height. They also reported significant negative correlation of plant height with oil content.

Shashikumara *et al.* (2016) carried out an experiment to assess the correlation coefficient for pod yield and its component characters and reported that the pod yield was significantly and positively correlated with SCMR, number of matured pods per plant, harvest index, kernel yield, oil yield and sound mature kernels. Specific leaf area had significant negative correlation with SCMR, total pods per plant, number of matured pods per plant and pod yield per plant. They also reported that days to 50% flowering had significant and negative correlation with plant height and harvest index.

Namrata *et al.* (2016) evaluated 30 genotypes of groundnut to study the character association for different component characters. Association estimates revealed that dry pod yield per plant was positively correlated at both genotypic and phenotypic levels with biological yield per plant, harvest index, 100-kernel weight, sound mature kernels and oil content.

Tulsi *et al*. (2017) evaluated 90 genotypes of groundnut for association analysis. Association estimates revealed that dry pod yield per plant showed positive and significant correlation at both genotypic and phenotypic levels with kernel yield per plant, 100-kernel weight, sound mature kernels and biological yield per plant.

Ashutosh *et al*. (2017) evaluated 29 breeding lines of groundnut to accomplish correlation coefficients for pod yield and its component characters. Pod yield per plant exhibited significant and positive correlation with 100- kernel weight, number of pods per plant and harvest index at both genotypic and phenotypic levels.

Anusha and Savithramma (2017) evaluated 230 RILs of groundnut to accomplish correlation coefficients for pod yield and its component characters. The results reveled that pod yield per plant had significant positive association with primary branches per plant, SCMR, pods per plant and kernel yield per plant, while significant negative association was noticed with SLA and sound mature kernel per cent. SCMR displayed significant positive association with number of branches per plant and kernel yield per plant, while significant negative correlation was observed with SLA.

Sushree *et al*. (2017) evaluated 32 genotypes of groundnut for association analysis. Association estimates revealed that the values of genotypic correlation were higher than their corresponding phenotypic correlation indicating that there was high degree of association between two variables. Pod yield per plant exhibited highly significant and positive correlation with number of branches per plant, haulm yield per plant, number of pods and 100-kernel weight at both phenotypic and genotypic levels.

Mahesh *et al.* (2018) evaluated 144 genotypes of groundnut for 13 characters to perform the correlation analysis. The pod yield per plant had significant and positive correlation with kernel yield per plant, mature pods per plant and sound mature kernel percentage at phenotypic and genotypic levels. They also reported significant and positive correlation for days to 50% flowering with days to maturity, number of branches per plant with shelling out-turn and biological yield per plant; days to maturity with plant height and biological yield per plant while, plant height was significantly and negatively correlated with SCMR and oil content.

Wadikar *et al.* (2018) evaluated 40 diverse genotypes of groundnut to measure character association and reported highly significant and positive association of pod yield with kernel yield per plant, harvest index, test weight and number of pod per plant at both genotypic and phenotypic levels.

Kadam *et al.* (2018) studied character association among 15 characters of 30 elite groundnut genotypes. The number of mature pods per plant, dry biomass per plant, number of pegs per plant, fresh pod yield per plant, fresh biomass per plant and immature pods per plant showed highly significant and positive correlation with dry pod yield per plant.

Lunagariya (2018) evaluated 90 genotypes of groundnut (18 parents and 72 advance breeding lines) for character association and drought tolerance under four different stress condition. Association estimates revealed that pod yield per plant exhibited significant and positive correlation with number of pods per plant, number of mature pods per plant, shelling out-turn, 100-kernel weight, harvest index, oil content and sound mature kernels at genotypic and phenotypic levels under all four conditions except for sound mature kernel in well-watered condition.

Syed *et al.* (2018) carried out association analysis among nine characters of 34 advanced breeding lines of groundnut for WUE and yield related traits. The results revealed that SCMR and yield related traits had strong positive association with pod yield per plant where SLA exhibited strong negative association with pod yield per plant.

Ganvit and Jagpat (2018) studied character association among 10 characters in 40 genotypes of groundnut. Study revealed that pod yield per plant was significantly and positively correlated with number of mature pods per plant, kernel yield per plant, shelling per cent, days to 50% flowering and oil content at both phenotypic and genotypic levels.

Rathod and Toprope (2018) evaluated 18 Spanish bunch groundnut genotypes for character association in 19 plant characters. Association estimates revealed that pod yield per plant exhibited positive and significant association with number of pods per plant, kernel yield, test weight, SCMR, harvest index, oil content and shelling per cent.

Belay *et al.* (2018) attempted association analysis for pod yield and yield related traits by using seven released groundnut varieties. The association results revealed that the kernel yield per plant had significant and positive association with dry pod yield, harvest index, shelling percentage and biomass yield, while highly significant negative association was observed for days to flowering and days to maturity.

Shankar *et al.* (2018) evaluated 49 genotypes of groundnut for correlation analysis for pod yield and its component traits. The correlation study revealed that pod yield per plant had positive and significant association with kernel yield per plant, number of pods per plant, number of mature pods per plant, pod yield per plot, plant height at 90 days after sowing, plant height at 60 days after sowing, number of immature pods per plant, harvest index, test weight, number of primary branches per plant and plant height at 30 days after sowing.

John and Reddy (2018) attempted association analysis for pod yield and yield related traits. The results revealed that pod yield per plant had significant and positive association with plant height, shelling per cent and sound mature kernel per cent, while number of mature pods per plant and kernel yield per plant showed positive but non-significant association with pod yield per plant.

Saritha *et al.* (2018) evaluated 32 genotypes of groundnut for association analysis. The correlation study revealed that genotypic correlation coefficient were higher than phenotypic correlation. The number of primary branches per plant, number of secondary branches per plant, number of pegs per plant, number of mature pods per plant, number of immature pods per plant and harvest index had positive and significant association with pod yield per plant at both genotypic and phenotypic level.

## 2.3 PATH COEFFICIENT ANALYSIS

Pod yield is the ultimate result of interactions involving a number of component factors, which are interrelated. The knowledge of such interrelationship is useful in knowing the magnitude and direction of association. However, study of correlation alone for ascertaining the importance of characters may be misleading when several characters are associated with yield. Therefore, path analysis is helpful in partitioning the total effects of yield related characters into direct and indirect effects. The concept of path coefficient analysis was originally developed by Wright (1921) but, the technique was first used by Dewey and Lu (1959). A brief review of work related to path coefficient analysis in groundnut is presented as under:

Suneetha *et al.* (2004) assessed path coefficient analysis for different component characters and stated that harvest index exerted the highest positive direct effect on pod yield per plant followed by total dry matter per plant, sound mature kernels and 100-kernel weight. Days to maturity, number of primary branches, number of mature pods, shelling percentage and 100-pod weight also exhibited low direct effect on pod yield, while days to 50% flowering and plant height had high and negative direct effect.

Siddiquey *et al.* (2006) evaluated 74 genotypes of groundnut to determine the path coefficient for nine yield contributing characters and reported that number of pods per plant, 100-pod weight and oil content had the highest direct positive effects on pod yield per plant and contributed the highest variation in pod yield of groundnut. The other direct positive effects were observed from days to maturity and plant height.

Mane *et al.* (2008a) performed path coefficient analysis to assess the relationship among different characters in summer bunch groundnut. The characters sound mature kernels percentage, shelling percentage and number of pods per plant recorded high magnitude of direct effect. The direct effect was negative for number of pegs per plant and days to 50% flowering.

Meta and Monpara (2010) studied 50 elite genotypes of bunch groundnut for different characters and reported that the pods per plant manifested maximum direct effect towards pod yield per plant followed by 100-pod weight and 100-kernel weight. Pods per plant and kernel yield per plant also contributed major share to pod yield per plant indirectly through other traits. Thus, pods per plant and kernel yield per plant would be the important component traits of pod yield and should be considered as selection criteria for enhancing yield in summer groundnut.

Raut *et al.* (2010) studied path coefficient analysis among eleven yield and yield contributing traits in $F_2$ generation of six crosses of groundnut. The results revealed that kernel yield per plant had the highest positive direct effect on pod yield per plant followed by mature pods per plant. While, shelling out-turn showed high negative direct effect towards pod yield per plant but, it expressed high indirect effect via kernel yield per plant.

Vekariya *et al.* (2010) studied 50 diverse genotypes of bunch groundnut for path analysis. The results that the kernel yield per plant, biological yield per plant and harvest index had high and positive direct effect on pod yield per plant.

Bhosale (2011) 108 diverse genotypes of groundnut for path analysis. The result showed high positive direct effect for days to 50% flowering, number of pods per plant, kernel yield per plant, haulm yield per plant and harvest index towards pod yield per plant. The indirect effects through days to 50% flowering, number of pegs per plant and harvest index were higher and positive for most of the characters.

Babariya and Dobariya (2012) evaluated 100 genotypes of groundnut to study direct and indirect effects by path analysis for pod yield per plant and its components. Biological yield per plant and harvest index exhibited high and positive direct effect on pod yield per plant. Whereas, kernel yield per plant, number of pods per plant and days to maturity showed moderate and positive direct effect on pod yield per plant.

Choudhary *et al.* (2013) evaluated 27 genotypes of groundnut to determine the path coefficient for 13 yield contributing characters and reported that kernel yield per plant, biological yield per plant and harvest index has maximum positive direct effect

on dry pod yield per plant.

Thakur *et al*. (2013) evaluated 25 groundnut genotypes to study path analysis. Days to maturity, shelling out-turn and oil content recorded positive direct effect on pod yield per plant, while days to 50% flowering, number of pods per plant and 100-kernel weight recorded negative direct effect on pod yield per plant.

Rao *et al*. (2013) performed path analysis under drought in groundnut for yield and yield components. Partitioning of phenotypic correlation coefficients of various component characters with pod yield into direct and indirect contribution revealed that the direct effect was high and positive for pods per plant, SCMR and 100-kernel weight.

Makinde and Ariyo (2013) reported positive direct effect of days to 50% flowering, plant height at flowering, number of branches at flowering, number of pods per plant and sample seed weight on yield and these form important selection criteria in groundnut. They observed negative direct effect of days to maturity, nodes on the main stem at maturity and stem girth at maturity on yield

Bhargavi *et al.* (2015) evaluated 20 Spanish bunch genotypes of groundnut for path analysis and results revealed that 100-kernel weight, biological yield per plant, harvest index, oil content, number of mature pods per plant and kernel yield per plant exerted positive direct effect on pod yield per plant, while negative direct effect on pod yield per plant was exerted by SCMR and shelling out turn.

Gupta *et al.* (2015) evaluated 60 diverse genotypes of groundnut to assess the path coefficient analysis for pod yield and its component characters. Number of mature pods per plant, sound mature kernels, biological yield per plant, days to maturity and number of branches per plant exhibited positive direct effect on pod yield per plant.

Jain *et al*. (2016) evaluated 24 diverse genotypes of groundnut to study path coefficient analysis for pod yield and its component characters. Analysis revealed positive direct effect of kernel yield per plant, plant height, days to maturity, number of pods per plant and matured pods per plant on pod yield per plant.

Namrata *et al.* (2016) evaluated 30 genotypes of groundnut to study the path coefficient analysis for different component characters. Path coefficient analysis revealed positive and direct effect of biological yield per plant and 100-kernel weight of on pod yield, while other characters *viz.*, biological yield per plant, number of branches per plant and 100-kernel weight exhibited high indirect effect on dry pod yield *via* kernel yield per plant.

Shashikumara *et al.* (2016) carried-out an experiment to assess the path

coefficient analysis for pod yield and its component characters. The results revealed positive direct effect of harvest index, SCMR and oil content on pod yield per plant, while number of pods per plant and specific leaf area had negative direct effect on pod yield.

Anusha and Savithramma (2017) studied the path coefficient analysis related to water use efficiency in 230 $RIL_S$ of groundnut. Path coefficient analysis indicated that plant height, kernel yield and primary branches per plant had positive direct effect toward pod yield per plant, while specific leaf area, sound mature kernels and number of pods per plant had negative direct effect on pod yield per plant.

Ashutosh *et al*. (2017) evaluated 29 breeding lines of groundnut to accomplish path coefficients for pod yield and its component characters. Harvest index and haulm yield had high positive direct effect toward pod yield per plant. Kernel yield per plant, hundred kernel weight, number of pods per plant and plant height were observed to be the major indirect contributors towards pod yield through harvest index.

Mukesh and Lal (2017) assessed path coefficient analysis for yield and its contributing traits in 40 genotypes of groundnut. Days to 50% flowering, number of branches per plant, days to maturity, shelling out turn, 100-kernel weight and sound mature kernels had negative direct effect toward pod yield per plant.

Tulsi *et al*. (2017) evaluated 90 genotypes of groundnut for path coefficient analysis. The highest positive direct effect on dry pod yield was exhibited by kernel yield per plant, days to maturity, oil content and days to 50% flowering.

Sushree *et al*. (2017) evaluated 32 $F_6$ progenies along with four released varieties as parents to assess path coefficient analysis for pod yield and its component characters in groundnut. Path analysis revealed that the kernel yield per plant had the highest direct positive effect on pod yield per plant followed by number of kernels per plant and 100-kernel weight. All other characters made major indirect contribution towards pod yield through these three characters. Plant height, number of branches per plant and number of pods per plant exhibited greater influence on pod yield per plant.

Mahesh *et al*. (2018) evaluated 144 genotypes of groundnut for 13 characters to assess the path analysis and reported that the kernel yield, biological yield per plant, sound mature kernels, number of mature pods per plant, 100-kernel weight and harvest index exhibited high and positive direct effect on pod yield per plant whereas, shelling out turn and number of immature pods per plant had low and negative direct effect toward pod yield per plant.

Lunagariya (2018) evaluated 90 genotypes of groundnut (18 parents and 72 advance breeding lines) for path coefficient analysis and drought tolerance under four different drought conditions. The results revealed that high and positive direct effect of number of mature pods per plant on pod yield per plant in three conditions (well-watered, stress-I and stress-III), while biological yield per plant and harvest index showed high and positive direct effect on pod yield per plant in all four conditions. pods per plants showed positive and high direct effect on pod yield per plant in stress III condition only.

Ganvit and Jagpat (2018) performed path coefficient analysis among 10 characters in 40 genotypes of groundnut. The results revealed that kernel yield per plant and number of mature pods per plant exhibited high and positive direct effect on pod yield per plant. Whereas, 100-kernel weight, plant height and days to 50% flowering exhibited low and positive direct effect towards pod yield.

Rathod and Toprope (2018) evaluated 18 Spanish bunch groundnut genotypes for path analysis studies for 19 plant characters. The kernel yield, test weight, SCMR, days to maturity and oil content exerted high and positive direct effect on pod yield whereas, shelling per cent and harvest index had low and negative direct effect on pod yield per plant.

Shankar *et al.* (2018) evaluated 49 genotypes of groundnut for path co-efficient analysis for pod yield and its component traits. The results revealed that kernel yield per plant had the highest direct positive effect on pod yield followed by number of pods per plant, number of mature pods per plant, pod yield per plot, plant height at 60 days after sowing, number of immature pods per plant, harvest index, test weight, number of primary branches per plant, plant height at 30 days after sowing and shelling out turn.

John and Reddy (2018) performed path analysis in groundnut for yield and yield components. The results showed high positive direct effect for kernel yield per plant, number of mature pods per plant, plant height and sound mature kernels per cen towards pod yield per plant, while number of secondary branches per plant and shelling percentage showed negative and high direct effect on pod yield per plant.

**2.4 SELECTOIN INDICES**

Yield is a complex character influenced by number of factors. Direct selection on the basis of yield may not be effective because many component traits affect it. To make an effective selection for higher yield, it is necessary to determine the relative efficiency of selection through discriminant function technique over straight selection.

This discriminant function technique over suitable selection indices was developed by Fisher (1936) and was first time successfully employed in plant breeding selection programme by Smith (1936). The literature related to the selection indices in groundnut has been reviewed here under.

Abraham (1990) constructed selection indices for kernel yield and their efficiency were assessed in terms of predicted genetic gains using 42 varieties of bunch groundnut. 8 characters cumulatively accounted for 65% of genetic gain in kernel yield, while kernels per plant and 100-kernel weight alone showed 58% genetic gain on the basis of discriminant function.

Dobariya *et al.* (2008) construted selection indices in groundnut involving pod yield and its five components using the discriminant function technique. The efficiency of selection increased with inclusion of more number of characters in the index. The index based on five characters *viz*., pod yield per plant, number of mature pods per plant, biological yield per plant, 100-seed weight and harvest index recorded the highest genetic advance and relative efficiency followed by an index based on four characters *viz*., pod yield per plant, biological yield per plant, 100-seed weight and harvest index.

Bhosale (2011) evaluated 108 genotypes of groundnut to study selection indices. A total of 63 indices were constructed involving pod yield and five yield components using the discriminant function technique. In a single character index, the maximum efficiency was exhibited by harvest index followed by haulm yield per plant, number of pods per plant and kernel yield per plant. The efficiency of selection increased with the inclusion of more number of characters in the index. The highest relative efficiency was exhibited by a selection index involving five component characters *viz.*, pod yield per plant, days to 50% flowering, number of pods per plant, kernel yield per plant and harvest index followed by an index based on four characters *viz*., pod yield per plant, number of pods per plant, kernel yield per plant and harvest index.

Safari *et al.* (2013) evaluated 39 genotypes of groundnut and studied 100-kernel weight, 100-pod weight, plant height, pods per plant and oil content. They reported that selection index efficiency was increased over direct selection for oil yield when four oil yield contributing traits were included along with oil content and showed that correlation coefficients between genotypic worth and each of the base indices were less than that for the optimum indices. Selection index for increased oil content and 100-

kernel weight of groundnut genotypes would be between 5 and 62% more efficient than direct selection, depending on the trait and selection method.

Babariya *et al.* (2014) evaluated 100 genotypes of groundnut and constructed selection indices involving pod yield and five components using discriminate function analysis. The efficiency of selection increased with inclusion of more number of characters in the index. A selection index consisting of five characters *viz.* pod yield per plant, days to maturity, number of pods per plant, kernel yield per plant and biological yield per plant and an index involving four characters *viz.* pod yield per plant, number of pods per plant, kernel yield per plant and biological yield per plant registered higher genetic gain and relative efficiency.

Raghuvanshi *et al.* (2015) evaluated 50 diverse genotypes of groundnut for selection indices involving pod yield per plant and four yield components using discriminate function analysis. The efficiency of selection increased with inclusion of more number of characters in the index. A selection index consisting of five characters viz., pod yield per plant, kernel yield per plant, harvest index, number of mature pods per plant and biological yield per plant recorded the highest genetic advance as well as relative efficiency and selection efficiency. Among the single character indices, biological yield per plant showed higher genetic advance and relative efficiency over straight selection for pod yield per plant.

Vachhani *et al.* (2016) evaluated 50 diverse genotypes of Virginia bunch groundnut for selection indices and reported that the biological yield per plant exhibited higher genetic advance and relative efficiency over straight selection for pod yield per plant. The index based on five characters *viz;* pod yield per plant, kernel yield per plant, harvest index, number of matured pods per plant and biological yield per plant recorded the highest genetic advance as well as selection efficiency.

## 2.5 GENETIC DIVERGENCE

The selection of parents for breeding programmes is based usually on their adaptation, yield potential, genetic diversity and other useful agronomic characters. The crosses among diverse parents are accepted to produce a broad spectrum of genetic variability thereby providing a greater probability of isolating high yielding segregates in advance generations (Murty and Arunachalam, 1966). Several methods have been developed for measuring divergence between populations using multivariate analysis such as coefficient of racial likeness (Pearson 1926), multiple regression (Hotelling,

1936) discriminant function (Fisher, 1936) and $D^2$-statistic (Mahalanobis, 1936). Out of these methods, $D^2$-statistic is a potential tool for obtaining quantitative estimates of divergence among biological populations and has extensively been applied to assess diversity. The concept of generalized distance as given by Mahalanobis (1936) is based on multivariate analysis of quantitative traits and has been successfully used by several workers for measuring the genetic divergence in several field crops including groundnut. The importance of genetic diversity in breeding high yielding varieties has obvious importance (Joshi and Dhawan, 1966; Murty and Arunachalum, 1966; Bhatt, 1970). The literature pertaining to the genetic divergence in groundnut has been reviewed here under:

Venkataramana *et al*. (2000) studied genetic divergence among 144 germplasm accessions of groundnut. The germplasm accessions were grouped into six clusters each in two environments ($E_1$ and $E_2$). Cluster I was the largest and consisted of 67 ($E_1$) and 98 ($E_2$) genotypes followed by cluster II which consisted of 30 ($E_1$) and 28 ($E_2$) and cluster III with 26 ($E_1$) and 11 ($E_2$). Maximum intra-cluster values were observed in cluster V (191.83) followed by cluster III (133.93) and cluster I (131.81) in $E_1$ and cluster V (230.67) followed by cluster IV (90.68) and cluster I (70.84) in $E_2$, revealing some intra-cluster diversity. Maximum inter-cluster $D^2$ values were observed between clusters III and VI in $E_1$ (699.86) and $E_2$ (1390.23), indicating that the genotypes included in these clusters had maximum divergence.

Dashora and Nagda (2004) studied genetic divergence in groundnut by using 52 genotypes from different regions. The 52 genotypes were grouped into 11 clusters on the basis of $D^2$ value of genotypes. The cluster I was the largest containing 23 genotypes followed by cluster II (14 genotypes) and cluster VII (7 genotypes). The remaining eight clusters had a single genotype each. The genotypes included in the largest cluster I originated from different eco-geographic regions of India indicating that the geographic distribution and genetic divergence did not follow the same trend. The maximum contribution to the total genetic divergence was from haulm yield per plant followed by dry pod yield per plant and 100-kernel weight.

Mahalakshmi *et al.* (2005) investigated the divergence among 57 groundnut accessions for 19 characters. The genotypes were grouped into 7 clusters. Maximum divergence was obtained between clusters II and VII followed by clusters VI and VII. Among the traits, days to first flowering contributed the most to total divergence (32.64%) followed by shelling percentage (16.85%) and reproductive efficiency

(11.28%). The genotypes VRI 2 (cluster II), ICG 3063 (cluster VI) and ICG 3254 (cluster VII) were potential parents based on cluster mean and genetic diversity and performance in terms of shelling percentage and oil content; sound mature kernel number and pod number; and maturity index and reproductive efficiency, respectively.

Laxmidevamma *et al.* (2006) studied genetic divergence in 81 genotypes of groundnut which revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Based on relative magnitude of values, all the genotypes were grouped into 16 clusters in which cluster I was the largest having 47 genotypes followed by cluster II with 10 genotypes. Days to maturity and oil content were the most potential traits contributing to the total divergence. Cluster Xl and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing the accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII had genotypes with most favourable characters and hence can be involved as potential parent for development of superior genotypes.

Siddiquey *et al.* (2006) studied genetic diversity among 74 genotypes of groundnut using Mahalanobis's $D^2$ statistic. The genotypes were grouped into 7 clusters. In inter cluster mean analysis, it was revealed that cluster I had the highest mean value for pod length, 100-seed weight, harvest index, 100-pod weight and yield per plant. The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters I and III (11.58) followed by clusters III and VII (11.06). In cluster analysis, it was found that pod length, shelling percentage, mature pods per plant, seeds per plant, protein content and 100-pod weight contributed maximum towards the total genetic divergence in groundnut genotypes.

Venkataramana (2008) carried out genetic divergence analysis in 100 accessions of water use efficient groundnut germplasm. The germplasm lines were grouped into seven clusters. Among the 15 characters, the contribution of chlorophyll content was maximum (24.2%) followed by 100-kernel weight (19.8%), haulm yield per plant (12.6%) and shelling per cent (11.6%). The maximum inter-cluster distance was between the cluster IV and VI (D-694.0). The maximum intra-cluster distance was reported in cluster VI (D-123.7) followed by cluster VII (D-104.4). The cluster VII showed the highest cluster mean for six characters *viz*., pod yield per plant, shelling per cent, kernel yield per plant, haulm yield per plant, oil content and oil yield per plant.

Odedra *et al*. (2008) grouped 112 genotypes of groundnut into eight clusters. No parallelism was observed between geographical distribution and genetic diversity. The inter-cluster distances ranged from 5.699 between clusters II and VIII to 21.293 between VII and VIII. The different clusters were superior in respect of different characters. Cluster VII showed highest mean values for pod yield per plant, number of primary branches per plant, number of pegs per plant, number of mature pods per plant and biological yield per plant. Cluster IV was good for days to 50% flowering, plant height, 100-seed weight and harvest index. The cluster II showed desirable rating in respect of days to maturity and shelling percentage. The cluster VIII possessed the highest mean values for oil content and number of kernels per pod, while cluster III was good for number of secondary branches per plant. It may be fruitful to intercross the genotypes from clusters VII and IV with those of cluster VIII for generation of promising derivatives and wide spectrum genetic variability for yield improvement in groundnut.

Mane *et al.* (2008b) grouped 40 genotypes of groundnut into three clusters. The cluster I with 37 genotypes emerged as the largest cluster followed by cluster II with 2 genotypes. The third cluster was solitary type. The mean $D^2$ values for the cluster ranged between 187.80 and 1171.75 indicating the good genetic diversity in the material studied. The clustering pattern showed absence of parallelism between geographical and genetic diversity. The maximum intra-cluster distance was observed for cluster II (D =17.55) followed by cluster I (D = 13.74) indicating that the genotypes of these cluster differed marginally in their genetic architecture.

Sumathi and Muralidharan (2009) studied genetic divergence in 48 groundnut genotypes, which were grouped into 13 clusters revealing the presence of considerable amount of genetic diversity. Cluster I was the largest with 19 genotypes followed by cluster II with 10 genotypes and cluster IV with 6 genotypes. The highest intra-cluster distance was observed for cluster IV (12.34) followed by cluster I and II. The inter-cluster $D^2$ values ranged from 11.41-89.42, the maximum inter-cluster distance was observed between the clusters VII and XII (89.42) followed by II and XII (78.81) and VI and VII (77.93), which indicated that the genotypes included in these clusters will give high heterotic response and thus better segregants. Among the 12 characters studied 100-seed weight contributed the most (75%) towards the divergence of genotypes.

Korat *et al.* (2009) studied 80 genotypes of groundnut and grouped into 9

clusters. The maximum inter-cluster distance was observed between clusters I and VIII followed by clusters IV and VIII, clusters III and VIII and clusters II and VIII. The cluster VII showed high mean in respect to pod yield per plant, number of secondary branches per plant, number of kernels per pod, 100-kernel weight and harvest index. The cluster I had desirable value for days to 50% flowering and days to maturity.

Khote *et al.* (2009) studied genetic divergence among 30 groundnut genotypes using Mahalanobis' $D^2$ statistic. Based on genetic distance, these genotypes were grouped into 6 different clusters. Maximum intra-cluster distance was observed in cluster V comprising two groundnut genotypes *viz.*, RCM-556 and MS-48-1. Inter-cluster distance was found to be maximum between clusters II and V followed by clusters I and V, clusters V and VI, III and VI, II and VI, II and V and I and VI. The genotypes from the genetically diverse clusters could be used for hybridization programme in groundnut.

In a study carried out by Awatade *et al.* (2009) 40 genotypes of groundnut were grouped into 12 clusters. Cluster I was the largest comprising of 17 genotypes followed by cluster II and cluster III having 9 and 5 genotypes, respectively. The clusters IV and XII were solitary. The average inter-cluster distance was maximum between clusters X and XII (25.37) followed by clusters X and XI (24.43) and clusters IV and X (23.62) indicating that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial differences in the mean for important yield contributing characters suggesting that the genotypes belonging to these clusters may be ideal parents for improvement in groundnut.

Dolma *et al.* (2010b) studied 33 genotypes of groundnut belonging to different eco-geographical regions by using Mahalanobis's $D^2$ statistic. The analysis of variance revealed significant differences among the genotypes for all the traits. The 33 genotypes were grouped into six clusters, where the cluster I was the largest containing 18 genotypes followed by cluster II with 10 genotypes. The inter-cluster distance was maximum between clusters IV and V followed by clusters III and V. Based on inter-cluster distance and *per se* performance of genotypes, ISK-04-26, ISK-05-20 (cluster IV), ISK-04-11 (cluster V) and ISK-04-15 (cluster III) were suggested for inclusion in the hybridization programme to evolve high yielding and late leaf spot resistant genotypes.

Zaman *et al.* (2010) studied genetic diversity among 34 groundnut genotypes. The genotypes were grouped into five clusters. Cluster III was the largest containing 12

genotypes followed by cluster II with 2 genotypes. The highest intra-cluster distance was observed in cluster V and the lowest in II. The highest inter-cluster distance was observed between the cluster IV and III followed by V and III and the lowest between cluster V and I.

Kumar *et al.* (2010) studied the genetic diversity among 16 advanced breeding lines along with two varieties of groundnut for yield attributing traits and oil content by using $D^2$ analysis. 18 genotypes were grouped into 4 clusters by Tocher's method. The average inter-cluster distance was maximum between clusters II and III (22.28) followed by clusters I and III (20.74) and clusters II and IV (19.73) suggesting wide diversity between groups. The test weight, days to maturity, pod yield and mature pods per plant together contributed for 81.99% of total divergence, indicating their importance in choice of parents for hybridization. Based on inter-cluster distance values (D), *per se* performance and disease reaction, the genotypes of cluster III (ICGV0 3157, ICGV0 3063), cluster I (ICGV0 4148, ICGV0 4122), cluster II (ICGV0 3206) and cluster IV (TDG 56) were identified as most potential donors for generating materials suitable for agro-climatic condition of NEH region.

Bhosale (2011) evaluated 108 genotypes which were grouped into 13 clusters by Mahalanobis's $D^2$-statistic. The clustering pattern of the genotypes did not confirm to the geographical distribution. The maximum inter-cluster distance was found between clusters VIII and XII followed by that between clusters IV and XII, VIII and XI, XI and XIII, XII and XIII, V and VIII, IV and XI and VI and XII. The cluster XI was superior for haulm yield per plant, number of pegs per plant, 100-pod weight and protein content, while cluster I was the best for number of pods per plant, number of mature pods per plant and harvest index. Cluster XII was good for plant height and sound mature kernel, while the cluster II was good for pod yield per plant and kernel yield per plant. Based on high yielding genotypes and large inter-cluster distances, it was proposed to attempt crossing of the genotypes from cluster XI with the genotypes of cluster XII and I, which may lead to broad spectrum of favourable genetic variability for yield improvement in groundnut.

Venkateswarlu *et al.* (2011) studied 74 genotypes of groundnut representing diverse geographic origin for genetic divergence using Mahalanobis's $D^2$ statistic. These genotypes were grouped into 12 clusters. The mode of distribution of genotypes to various clusters was at random suggesting that there is no relationship between geographical distribution and genetic diversity. Based on inter-cluster distances, the

clusters VII vs X, VI vs XII and X vs XII were found as divergent. Hence, selection of genotypes from these clusters for hybridization programme may result into good recombinants. The characters 100-kernel weight, shelling percentage and harvest index contributed maximum towards genetic divergence in both $D^2$ analysis and canonical root analysis. The canonical root analysis confirmed the clustering pattern obtained by $D^2$ analysis.

Babariya *et al*. (2012) evaluated 100 genotypes of groundnut which were grouped in to 10 clusters by Mahalanobis's $D^2$ statistic. Cluster III was the largest with 38 genotypes followed by clusters II and IV with 14 genotypes each and cluster I and V with 13 genotypes in each. The clusters VI, VIII and X were solitary with one genotype only. The maximum inter-cluster distance was found between clusters IV and VII followed by that between clusters VII and X, VII and III, VII and VI. High intra-cluster distance was observed in cluster V followed by cluster IV, cluster III, while minimum intra-cluster distance was observed in cluster VII. Based on the inter-cluster distance and cluster means, the genotypes involved in the clusters III, IV, VI, VII and X were widely diverse and considered as ideal parent for groundnut breeding programmes.

Suneetha *et al.* (2013) evaluated the genetic diversity among 29 released and pre-released cultures of groundnut. The magnitude of $D^2$ values suggested that there was considerable diversity in the released and pre-released groundnut cultures. The range of variation allowed for cultivars into 9 clusters based on data of yield and yield attributes. Intra- cluster $D^2$ values (26.83) and distances (5.81) were high within the group V and inter-cluster average $D^2$ values ranged from 11.02 (between group IV and VIII) to 57.76 (between group V and IX). Maximum intra-cluster distance was observed in clusters V, III and I and selection of maximum number of 13 genotypes from cluster I might be fruitful to produce good recombinants.

Yadav *et al.* (2014) studied genetic divergence in 60 groundnut genotypes. These genotypes were grouped into 12 clusters, based on their inter-cluster distance. The maximum inter-cluster distance (D = 7.044) was found between clusters III and X carrying one and two genotypes from each cluster, respectively followed by that between clusters V and X (D = 6.447) and clusters III and XII (D = 5.943). The minimum inter-cluster distance was observed between clusters VII and XI (D = 2.770). The inra-cluster distance (D) ranged from 1.909 to 2.863, the maximum being in cluster V (2.863) and minimum in cluster II (1.909) which includes 8 genotypes. Cluster III

showed high genetic divergence with cluster X followed by cluster V.

Gupta *et al.* (2015) studied divergence analysis by using Mahalanobis's $D^2$ statistic among 60 groundnut genotypes. The genotypes were grouped into 13 clusters. The maximum inter-cluster distance (D = 36.51) was found between clusters III and V followed by clusters IV and V (D = 32.67) and II and IV (D = 24.21), which indicated that these genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial differences in the mean values for important yield contributing characters suggesting that the genotypes belonging to these clusters from ideal parents for yield improvement in groundnut.

Mukesh and Lal (2015) evaluated 40 genotypes of groundnut of different geographic origins for genetic divergence using Mahalanobis's $D^2$ statistic. The genotypes were grouped into 7 clusters. The cluster VI was the largest containing 12 genotypes followed by cluster V consisted 7 genotypes, cluster I and cluster VII consisted 6 genotypes, cluster III consisted 4 genotypes, cluster II consisted 3 genotypes and cluster IV consisted 2 genotypes. The maximum inter-cluster distance was found between clusters IV and VII followed by I and V, II and V, V and VII, I and IV. Cluster IV was superior in 100-kernel weight, pod yield per plant and cluster I was superior in sound mature kernels and shelling out-turn. Based on high yielding genotypes and large inter-cluster distance it was proposed to crossing between the genotype of cluster I with cluster IV and V in hybridizing programme.

Vivekananda *et al.* (2015) studied genetic diversity among 31 groundnut genotypes using Mahalanobis's $D^2$ statistic for five agro-morphological characters. Based on Trocher's method, 31 genotypes were grouped into 7 clusters, where cluster I was the largest containing 11 genotypes followed by cluster II and III with 7 genotypes each. The inter-cluster distance was maximum between clusters I and VI followed by clusters I and V, clusters III and VI and clusters I and IV. Considering the cluster distances and cluster means the genotypes from clusters I, III, V and VI could be selected for hybridization programme.

Sushree *et al.* (2017) evaluated 36 genotypes of groundnut which were grouped into 10 clusters by Mahalanobis's $D^2$ statistic. The cluster X was the largest containing 10 genotypes followed by cluster IX with 8 genotypes, III with 4 genotypes and rest of the clusters with 2 genotypes in each. Maximum inter-cluster distance was found between clusters III and X followed by clusters III and IX. The highest intra-cluster distance was observed in cluster III followed by X and lowest in cluster I. The cluster

X was superior for haulm yield per plant and 100-kernel weight, while cluster VI good for pod yield per plant, kernel yield per plant, kernels per plant and number of pods per plant.

Dhakar *et al.* (2017) studied genetic divergence using $D^2$ analysis of 93 genotypes of groundnut for 15 characters. The genotypes were grouped into 8 clusters. The cluster VI was the largest containing 18 followed by 16 in cluster VII, 15 in cluster I, 12 in cluster V and VIII, 10 in cluster IV, 7 in cluster III and 3 in cluster II. Maximum intra-cluster values were recorded for cluster V ($D^2$ = 101.80) followed by cluster IV (D = 93.89), cluster VII (D = 83.72), cluster VIII (D = 82.62), cluster I (D = 80.82), cluster VI (D = 80.46), cluster II ($D^2$ = 65.93) and cluster III (D = 58.06). While, maximum average inter-cluster value was obtained between clusters III and VIII. The genotypes from cluster III and VIII were promoted for hybridization programme.

Mohammad *et al.* (2018) studied divergence analysis by using Mahalanobis's $D^2$ statistic among 40 groundnut genotypes. The genotypes were grouped into 8 clusters. Cluster VII was the largest comprising of 25 genotypes followed by cluster I having 4 genotypes, clusters II, III, IV, V and VI comprised of two genotypes each. The cluster VII was solitary. The average inter-cluster distance was maximum between clusters II and VII followed by clusters VI and VIII, IV and VIII, III and VIII and I and VIII. cluster I had the maximum intra-cluster distance (88.8) followed by cluster VII (82.36), cluster VI (24.12), cluster V (21.67), cluster IV (20.57), cluster III (19.38) and cluster II (17.02), while the clusters VIII recorded zero values.

Mahesh and Hasan (2018) evaluated genetic diversity among 144 groundnut genotypes for 13 characters by using $D^2$ statistic. The genotypes were grouped into 16 clusters, where cluster IV was the largest with comprising 24 genotypes followed by clusters I and II with 22 genotypes in each, clusters III and VII comprising 15 genotypes, cluster IV with 14, cluster VI with 12, cluster VII with 7 and cluster X with 6 genotypes. The average inter-cluster distance was maximum in between clusters XI and XVI (241.24) followed by between clusters IV and XVI (223.43). The haulm yield and oil percentage had maximum contribution of 33.39% and 30.99%, respectively to the total divergence of genotypes.

Saritha *et al* (2018) studied divergence analysis by using Mahalanobis's $D^2$ statistic among 32 groundnut genotypes. The genotypes were grouped into 7 clusters. The cluster I had maximum number of 14 genotypes followed by cluster II with seven genotypes, cluster III with five genotypes, cluster IV with three genotypes, while

clusters V, VI and VII had one genotype each. The inter-cluster distance was larger than the intra-cluster distance. Maximum intra-cluster distance recorded by cluster I (112.90) followed by cluster IV (111.91), while minimum distance was obtained in clusters V, VI, and VII. Maximum inter-cluster distance was observed between clusters III and VII (3316.04), followed by clusters III and IV (2539.13) and VI and VII (2047.55).

Jain *et al.* (2018) evaluated genetic divergence among 35 genotypes of Spanish bunch groundnut by using Mahalanobis's $D^2$ statistic for 14 characters. Based on Tocher's method, the genotypes were grouped into 8 clusters, where cluster I was the largest containing 9 genotypes followed by clusters II and IV with 8 and 6 genotypes, respectively. The cluster VIII was having maximum inter-cluster distance with cluster I, cluster VI and cluster VII followed by clusters V and VII, clusters II and VI and clusters II and III. The intra-cluster distance was maximum in cluster VII followed by II and IV. Considering the cluster distance and cluster mean, the genotypes of clusters VIII, V, VI and III could be selected for hybridization programme.

# CHAPTER III

# MATERIAL AND METHODS

The present investigation was conducted to assess the genetic variability, correlation coefficients, path coefficients, selection indices and genetic divergence for pod yield and it's components in Recombinant Inbred Lines (RILs) of groundnut. The study was conducted during the *Kharif*- 2018 at the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh. The station is situated on Arabian Sea coast with longitude East $70^{0}$-$33^{0}$, Latitude North $21^{0}$-$31^{0}$ and elevation above M. S. L. 61m soil is medium black calcareous. The meteorological data during cropping season are given in Appendix I.

## 3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of 68 genotypes of Spanish bunch groundnut consisting 64 diverse Recombinant Inbred Lines (RILs), RIL-1 to RIL-64 derived from the cross AG-2006-6 x ICGV-05155, two parents and two checks (GJG-32 and GJG-9). The required quantity of pure seeds of these RILs populations, parents of the cross and checks were obtained from the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh.

## 3.2 EXPERIMENTAL DETAILS

Sixty eight genotypes of groundnut were sown in a Randomized Block Design with three replications during *kharif*- 2018. Each entry was accommodated in a single row of 3.0 m length with a spacing of 45 x 15 cm. The recommended agronomical practices and plant protection measures were followed for the successful raising of the crop. The observations were recorded on five randomly selected plants in each entry and replication and their mean values were used for the statistical analysis.

## 3.3 OBSERVATIONS RECORDED

The observations were recorded on five randomly selected plants from each entry and replication from all the characters. Days to 50% flowering and days to maturity were recorded on plot basis. The technique/method used for measuring the character is described as below;

### 3.3.1 Days to 50% flowering

Number of days from the date of sowing to date on which flowers appeared in 50% of the plants in the line was recorded.

**3.3.2 Days to maturity**

The total numbers of days was calculated from sowing to physiological maturity of all plants in the line.

**3.3.3 Plant height (cm)**

Plant height was measured in centimeters from ground level to the tip of the main axis at the time of harvesting.

**3.3.4 SCMR (SPAD Chlorophyll meter reading)**

The fully expanded third leaf from terminal bud of the main stem of each selected five plant was measured for SPAD chlorophyll meter reading (SCMR) during morning hours (9:00 to 10:00am) at 65-70 days after sowing by hand held portable SPAD meter (SPAD-502 Minolta, Tokyo, Japan) using four leaflets per sample. Since the groundnut has tetra-foliate leaf, SCMR was recorded in all four leaflets of selected plant and average value was computed. Care was taken to ensure that the SPAD meter sensor fully covered leaf lamina and the interference from veins and midribs could be avoided.

**3.3.5 Number of mature pods per plant**

Number of fully developed kernel bearing mature pods was counted from each selected plant at the time of harvesting.

**3.3.6 Number of immature pods per plant**

Number of immature pods (undeveloped pods) was counted from each selected plant at the time of harvesting.

**3.3.7 Shelling percentage (%)**

The shelling out-turn based on the weight of kernels recovered after shelling the pods was calculated as per formula given below;

$$\text{Shelling percentage (\%)} = \frac{\text{Weight of kernels (g)}}{\text{Weight of pod sample (g)}} \text{ x } 100$$

**3.3.8 100-kernel weight (g)**

One hundred kernels were counted from random sample from each line and weigh in grams on an electronic balance.

**3.3.9 Sound mature kernels (SMK)%**

Fully mature and immature kernels counted from representative sample were obtained from each plot and were expressed as per cent sound mature kernel.

$$\text{SMK(\%)} = \frac{\text{Number of well mature kernels}}{\text{Total number of kernels}} \text{ x } 100$$

### 3.3.10 Kernel yield per plant (g)

The kernels obtained by shelling of pods were weigh in grams.

### 3.3.11 Biological yield per plant (g)

After harvesting and sun drying the selected plants were weigh in grams.

### 3.3.12 Pod yield per plant (g)

The fully mature pods were separated from the individual selected plant, sun dried, cleaned and weigh in grams on an electronic balance.

### 3.3.13 Harvest index (%)

The biological yield (total dry matter after harvesting and sun drying) and pod yield of each plant was recorded in grams and the harvest index was calculated as under.

$$\text{Harvest Index}(\%) = \frac{\text{Pod yield per plant (g)}}{\text{Biological yield per plant (g)}} \text{ x } 100$$

### 3.3.14 Oil content (%)

A sample of kernels from each entry was subjected to oil estimation by using Nuclear Magnetic Resonance Spectrometer (NMR).

## 3.4 STATASTICAL ANALYSIS

The mean values of five randomly selected plants were used for the statistical analysis of different characters under study. The data recorded for various characters were statistically analyzed at the Computer Cell, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh for various parameters *viz*., genetic variability, genotypic and phenotypic correlations and path coefficient analysis, selection indices and genetic divergence.

### 3.4.1 Analysis of variance

The data collected on randomly selected five plants in each line and replication for individual character were arranged and mean values were used for statistical analysis according to Panse and Sukhatme (1985).

The statistical model used for the analysis of variance in the present investigation is described below.

$$Y_{ij} = \mu + g_i + r_j + \varepsilon_{ij}$$

Where,

$Y_{ij}$ = Value of $i^{th}$ genotype in $j^{th}$ replication

M = General mean

$g_i$ = Effect of $i^{th}$ genotype ( j = 1,2…..,g)

$r_j$ = Effect of $j^{th}$ replication (i = 1,2,....,r)

$\varepsilon_{ij}$ = Uncontrolled random error associated with $i^{th}$ genotype and $j^{th}$ replication

The format of analysis of variance is given as under:

**Analysis of variance for experimental design**

| Sources | DF | Mean squares | Expected Mean Square |
|---|---|---|---|
| Replications | (r-1) | $M_r$ | $\sigma_e^2 + g\sigma_r^2$ |
| Genotypes | (g-1) | $M_g$ | $\sigma_e^2 + r\sigma_g^2$ |
| Error | (r-1) (g-1) | $M_e$ | $\sigma_e^2$ |

Significance of replication mean sum of square ($M_r$) and genotype mean sum of square ($M_g$) was tested against error mean sum of square ($M_e$).

**Phenotypic and genotypic variances:**

The phenotypic, genotypic and error variances were computed according to formula dealt by Singh and Chaudhary (1977) for each trait separately using the mean sum of squares from the ANOVA table.

Error variance $(\sigma_e^2)$ = $M_e$

Genotypic variance $(\sigma_g^2)$ = $(M_g - M_e)/r$

Phenotypic variance $(\sigma_p^2)$ = $\sigma_g^2 + \sigma_e^2$

Where,

r = Number of replications

g = Number of genotypes

Mg = Mean sum of squares for genotype

Mr = Mean sum of squares for replication

Me = Mean sum of squares for error

### 3.4.2 Measures of genetic variability

**a) Phenotypic coefficient of variance (PCV %)**

The phenotypic coefficient of variation which measures the magnitude of phenotypic variation present in a particular character was estimated as per the formula suggested by Burton (1952).

$$\text{PCV}(\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma_p^2$ = Phenotypic variance

$\bar{X}$ = Mean of the character

The PCV values were categorized as low (0 – 10%), moderate (10 – 20%) and high (20% and above) values as suggested by Shivsubramanian and Madhav Menon (1973).

**b) Genotypic coefficient of variance (GCV %)**

The genotypic coefficient of variation which measures the magnitude of genotypic variation present in a particular character was estimated as per the formula suggested by Burton (1952).

$$GCV(\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

$\sigma_g^2$ = Genotypic variance

$\bar{X}$ = Mean of the genotype

The GCV values were categorized as low (0 – 10%), moderate (10 – 20%) and high (20% and above) values as suggested by Shivsubramanian and Madhav Menon (1973).

**Heritability ($h^2$)**

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance as suggested by Allard (1960) and expressed as percentage.

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$h^2$ = Heritability in broad sense

$\sigma_p^2$ = Phenotypic variance

$\sigma_g^2$ = Genotypic variance

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

**d) Genetic advance (GA)**

The expected genetic advance at 5% selection intensity was computed by using the formula elucidated by Johnson *et al.*(1955a)

$$GA = k \times \sigma_p \times h^2$$

Where,

GA = Genetic advance under selection

k = Selection differential (value of k at 5% selection intensity = 2.06)

$\sigma_p$ = Phenotypic standard deviation

$h^2$ = Heritability in broad sense

**e) Genetic advance expressed as percentage of mean (GAM):**

The genetic advance expressed as percentage of mean was calculated as under:

$$\text{GA as percentage of mean} = \frac{\text{Genetic Advance(GA)}}{\text{Mean of character}(\bar{X})} \times 100$$

Genetic advance as per cent of mean was categorized as low (0–10%), moderate (10–20%) and high (20% and above) as suggested by Johnson *et al.* (1955a).

**3.4.3 Correlation coefficients**

Correlation coefficients measure the degree and direction of association between two or more series of variables. The inherent or heritable association between two variables is referred to as genotypic correlation, while observable correlation between two variables is called phenotypic correlation.

The phenotypic and genotypic correlation coefficients of all the characters were worked-out as per Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis as follow from which different components of mean sum of products were estimated.

**Analysis of covariance**

| Source | d. f. | Mean sum of products | Expected mean sum of products |
|---|---|---|---|
| Replications | (r-1) | $M_r$ | - |
| Genotypes | (g-1) | $M_g$ | $Covg_{1.2} + Cove_{1.2}$ |
| Error | (r-1) (g-1) | $M_e$ | $Cov\ e_{1.2}$ |

Where,

r = Number of replications

g = Number of genotypes

Cov = Covariance

**(i) Genotypic covariance**

Genotypic covariance (Cov $g_{1.2}$) = (Mg-Me)/r

Where,

$M_g$ = Mean sum of products due to genotypes between character first and second

$M_e$ = Mean sum of products due to error between character first and second

r = Number of replications

**(ii) Phenotypic covariance**

Phenotypic covariance (Cov $p_{1.2}$) = (Cov $g_{1.2}$ + Me)/r

Where,

$M_e$ = Mean sum of products due to error between character first and second

R = Number of replications

**(iii) Error covariance**

Error covariance (Cov $e_{1.2}$) = Me

Where,

$M_e$ = Mean sum of products due to error between character first and second

The genotypic, phenotypic and error variances and covariances were used for calculating the genotypic and phenotypic correlation coefficients, respectively as suggested by Al-Jibouri *et al.* (1958).

**(a) Genotypic correlation coefficient**

Genotypic correlation coefficient ($r_{g_{1.2}}$) = $\frac{Cov_{g\ 1.2}}{\sqrt{\sigma^2_{g1}\sigma^2_{g2}}}$

Where,

$Cov_{g_{1.2}}$ = Genotypic covariance for character first and second

$\sigma^2{}_{g_1}$ = Genotypic variance for character first

$\sigma^2{}_{g_2}$ = Genotypic variance for character second

**(b) Phenotypic correlation coefficient**

Phenotypic correlation coefficient ($r_{p_{1.2}}$) = $\frac{Cov_{p\ 1.2}}{\sqrt{\sigma^2_{p1}\sigma^2_{p2}}}$

Where,

$Cov_{p_{1.2}}$ = Phenotypic covariance for character first and second

$\sigma^2_{p_1}$ = Phenotypic variance for character first

$\sigma^2_{p_2}$ = Phenotypic variance for character second

**Test of significance**

The test of significance for correlation coefficient was done by calculating 't' value using following formula as described by Panse and Sukhatme (1985).

$$t = \frac{r}{\sqrt{(1 - r^2)}} \times \sqrt{(n - 2)}$$

Where,

't' = Calculated value of 't'

R = Correlation coefficient

N = Number of observations

The calculated 't' value was compared with table 't' value at n-2 degrees of freedom to test the significance of correlation coefficient.

**3.4.4 Path coefficient analysis**

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects. In other way, it measures the direct and indirect contribution of various independent characters on dependent characters. The path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959). Phenotypic correlation coefficients of 14 variables with yield were used to estimate the path coefficient for the direct effect of various independent characters on yield. The direct effect designated as 'p' were calculated by increasing the underlying correlation matrix as per Doolittle method described by Steel and Torrie (1960).

$r_{1y} = P_{1y} + P_{2y}r_{12} + \ldots,\ldots + P_{1.3y}\, r_{1.13}$

$r_{2y} = P_{1y}\, r_{12} + P_{2y} + \ldots,\ldots + P_{13y}\, r_{2.13}$

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$r_{13y} = P_{1y}\, r_{1.13} + P_{2y}\, r_{2.13} + \ldots,\ldots + P_{13y}$

Where,

$r_{1y}$, $r_{2y}$, $r_{3y}$,……., $r_{13y}$ are the genotypic correlations of days to 50% flowering, days to maturity, plant height, SCMR, number of mature pods per plant, number of immature pods per plant, shelling out-turn, 100-kernel weight, sound mature kernels, kernel yield per plant, biological yield per plant, harvest index and oil content with pod yield per plant, respectively.

$P_{1y}$, $P_{2y}$, $P_{3y}$,……., $P_{13y}$ are the direct effects of characters *viz*., days to 50% flowering, days to maturity, plant height, SCMR, number of mature pods per plant, number of immature pods per plant, shelling out-turn, 100-kernel weight, sound mature kernels, kernel yield per plant, biological yield per plant, harvest index and oil content on pod yield per plant, respectively.

The coefficient of determination was calculated by using the following relationship.

$$1= P^2_{1.y} + 2P_{1.y}\, r_{1.2}\, P_{2.y} + 2P_{1.y}\, r_{1.3}\, P_{3.y} + 2P_{1.y}\, r_{1.4}\, P_{4.y} + 2P_{1.y}\, r_{1.5}\, P_{5.y} + 2P_{1.y}\, r_{1.6}\, P_{6.y} + 2P_{1.y}\, r_{1.7}\, P_{7.y} + 2P_{1.y}\, r_{1.8}\, P_{8.y} + 2P_{1.y}\, r_{1.9}\, P_{9.y} + 2P_{1.y}\, r_{1.10}\, P_{10.y} + 2P_{1.y}\, r_{1.11}\, P_{11.y} + 2P_{1.y}\, r_{1.12}\, P_{12.y} + 2P_{1.y}\, r_{1.13}\, P_{13.y} + P^2_{2.y} +\ldots\ldots\ldots\ldots + P^2_{12.y} + 2P_{12.y}\, r_{12.13}\, P_{13.y} + P^2_{13.y} + R$$

The residual variation (R) i.e. variation in dependent character yield due to unexplained causes was estimated by subtracting this vale from unity.

Path coefficient analysis was categorized as very low (0.00–0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-0.99) and very high (>1.0).

**3.4.5 Selection indices**

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. Selection index was proposed for the first time by Smith (1936) on the basis discriminant function of Fisher (1936). The model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and the development of a required discriminant function. Smith (1936) defined the genetic worth (H) of an individual as:

$$H = a_1G_1 + a_2G_2 + \ldots,..,+ a_nG_n$$

Where,

$G_1$, $G_2$,…,$G_n$ are genotypic values of individual character and $a_1$, $a_2$,…,$a_n$ signify their relative economic importance.

Another function (I), based on the phenotypic performance of various characters, was defined as

$$I = b_1p_1 + b_2p_2 + \ldots,+ b_np_n.$$

Where,

$b_1$, $b_2$….,$b_n$ are to be estimated such that the correlation between H and I i.e. $r_{(H.I)}$ becomes maximum. Once such function is obtained, discrimination of good genotypes/characters from the undesirable ones may be possible on the basis of phenotypic performance i.e. $p_1$, $p_2$,……,$p_n$ directly.

The maximization of $r_{(H.I)}$ leads to a set of simultaneous equations which upon solving give the desired estimate of 'bi' values. Considering three characters as an example, the simultaneous equations look like as follows

$$b_1x_{11} + b_2x_{12} + b_3x_{13} = a_1G_{11} + a_2G_{12} + a_3G_{13}$$

$$b_1x_{21} + b_2x_{22} + b_3x_{23} = a_1G_{21} + a_2G_{22} + a_3G_{23}$$

$$b_1x_{31} + b_2x_{32} + b_3x_{33} = a_1G_{31} + a_2G_{32} + a_3G_{33}$$

Which in matrix form become

$$\begin{bmatrix} x_{11} & x_{12} & x_{13} \\ x_{21} & x_{22} & x_{23} \\ x_{31} & x_{32} & x_{23} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} & G_{13} \\ G_{21} & G_{22} & G_{23} \\ G_{31} & G_{32} & G_{33} \end{bmatrix} . \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

X b G a

Where,

x = Phenotypic variance-covariance matrix

b = Discriminant function coefficient

G = Genotypic variance-covariance matrix

a = Economic weightage

The solution of these equations gives the estimate of 'bi' values in the following manner

$$bi = X^{-1}. G. A$$

Where,

$X^{-1}$= Inverse matrix of X

G = Genotypic variance-covariance matrix

a = Economic weightage

The mathematical description of the function (I) is known a selection index

$$I = b_1p_1 + b_2p_2 + \ldots\ldots,\ldots,+ b_np_n$$

Using this function it is possible to discriminate among the superior and inferior characters or combination of characters. Selection index or score is calculated for all the combination of characters and those with the highest values are considered.

**i) Expected genetic advance**

The expected genetic advance through selection may be calculated by the following formula suggested by Robinson *et al*. (1951).

$$G = \frac{Z}{P} \frac{\sum\sum a_i b_j G_{ij}}{\sqrt{\sum\sum a_i b_j P_{ij}}}$$

Where,

Z/P = Standardized selection differential (s)

indicating the intensity of selection (i) at 5% i.e.

k = 2.06

$a_i$ = Economic weightage

$b_j$ = The regression coefficient

$G_{ij}$ = The genotypic variance-covariance matrix

$P_{ij}$ = The phenotypic variance-covariance matrix

**ii) Relative efficiency**

The relative efficiency of different discriminant functions was calculated according to Robinson *et al.* (1951) assuming the efficiency of selection for pod yield as 100%.

$$RI\ (\%) = \frac{GA(D)}{GA(S)} x100$$

Where,

RI = Relative efficiency

GA (D) = Genetic advance through discriminant function

GA (S) = Genetic advance through straight selection

**3.4.6 Genetic divergence**

Rao (1952) described the multivariate analysis of genetic divergence using Mahalanobis's $D^2$-statistic. Transformation of original mean of various characters ($X_1$ to $X_{14}$) to uncorrelated variates ($Y_1$ to $Y_{14}$) was carried-out by pivotal condensation method as the common dispersion matrix by using the computer. This made $D^2$-values as simple sum of squares of differences in transformed values for various characters.

With $X_1$, $X_2$, $X_3$,….., $X_p$ as the multiple measurements available on each individual and $d_1$, $d_2$,…, $d_p$ as $\overline{X}1^1 - \overline{X}1^2, \overline{X}2^1 - \overline{X}2^2, \ldots\ldots\ldots \overline{X}p^1 - \overline{X}p^2$, respectively being the differences in the means of two populations, Mahalanobis's D-statistic can be defined as follows:

$$pD^2 = b_1 d_1 + b_2 d_2 + \ldots\ldots\ldots\ldots + b_p d_p$$

Here, the '$b_i$' values are to be estimated such that the ratio of variance between the populations is maximized. In terms of variances and covariances, the $D^2$ value is obtained as follow:

$$pD^2 = W^{ij} (\overline{X}i^1 - \overline{X}i^2) (\overline{X}j^1 - \overline{X}j^2)$$

Where,

$W^{ij}$ is the inverse of estimated variance-covariance matrix

For formation of clusters, the general criteria of grouping as suggested by Tocher were followed in the present study (Rao, 1952). The criteria for clustering were that, any two populations in the same cluster should show a smaller $D^2$-value than those belonging to different clusters. The first step of grouping the genotypes into distinct clusters was to arrange them in order of their relative distance from each other. After arranging the $D^2$-values in this manner, the two populations having the smallest distance from each other were considered first, to which a third population was added having a smallest average $D^2$-value but higher than the previous two. Similarly, the next population was added and the process continued till the average $D^2$-value increased considerably with the next addition. Generally, this level should be approximately near to the maximum $D^2$-value shown by a population to the nearest population. At certain stage, when it was felt that after adding a particular population, if there was an abrupt increase in the average $D^2$, this population was not added in that cluster. Similarly, a second cluster was formed and this process was continued till all the populations were included into one or the other clusters. After formation of clusters, average inter- and intra-cluster distance values were calculated.

Average intra-cluster and inter-cluster distances were measured as under

**i) Average intra-cluster distance ($D = \sqrt{D^2}$)**

$$D^2 = \frac{\sum D_i^2}{n}$$

Where ,

$\Sigma D_i^2$ = Sum of distances between all possible combinations of the populations included in cluster

n = Number of populations in the cluster

**ii) Average inter-cluster distance ($D=\sqrt{D^2}$ )**

$$D^2 = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\Sigma D_{ij}^2$ = Sum of distance between all possible combinations of the two clusters

$N_i$ = Number of populations in cluster i

$N_j$ = Number of populations in cluster j

The inter-cluster distance was calculated by measuring the distance between clusters I and II, between I and III, between I and IV and so on. Likewise, one by one cluster was taken and their distances from each other were calculated.

The cluster mean values for all the 14 characters were computed using character means for the genotypes included in the clusters.

# CHAPTER IV

# EXPERIMENTAL RESULTS

The results obtained on the present investigation on "Genetic variation, selection indices and diversity analysis for pod yield and its components in RILs of groundnut (*Arachis hypogaea* L.)" are presented under the following sub-heads:

4.1 Analysis of variance

4.2 Genetic variability

4.3 Correlation coefficients

4.4 Path coefficient analysis

4.5 Selection indices

4.6 Genetic diversity

## 4.1 ANALYSIS OF VARIANCE

The analysis of variance as presented in Table 4.1 revealed highly significant differences among the genotypes for all the characters studied.

## 4.2 GENETIC VARIABILITY

The results obtained on various parameters of genetic variability have been presented here under:

### 4.2.1 Mean performance and range of variation

The mean values of 68 genotypes of groundnut for all the 14 characters along with the standard error of mean (SEm.), critical difference (CD) and coefficient of variation (CV%) are given in Appendix II, the summary of which is also presented in Table 4.2.

The mean recorded for days to 50% flowering was 25.50 with a range of 22.00 to 29.67. Maximum value was observed in RIL-35 and RIL-19 (29.67) followed by RIL-38 (29.33), RIL-58 (29.00) and AG-2006-6 (29.00) and RIL-36 (28.67). The lowest days to 50% flowering was recorded in RIL-25 (22.00) followed by RIL-18 (22.33), RIL-3 (22.67) and RIL-13(23.00).

The overall mean of the genotypes for days to maturity was 114.26 with a range of 107.33 to 120.33. The genotype ICGV-05155 (120.33) had maximum value followed by RIL-51 (119.67), RIL-26 (119.33) and RIL-38 (118.67). The minimum value was recorded in RIL-55 (107.33) followed by RIL-3(107.67), RIL-13(108.00) and RIL-54(108.67).

**Table 4.1. Analysis of variance for various characters in groundnut**

| Source | df | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | Number of mature pods per plant | Number of immature pods per plant | Shelling out-turn (%) |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| **Replications** | 2 | 5.06** | 11.66** | 134.77** | 0.37 | 3.99* | 2.10 | 0.58 |
| **Genotypes** | 67 | 14.91** | 40.77** | 16.58** | 16.62** | 14.88** | 1.98* | 31.99** |
| **Error** | 134 | 1.91 | 1.57 | 4.15 | 5.49 | 1.88 | 0.10 | 10.60 |

| Source | df | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Pod yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| **Replications** | 2 | 66.02** | 31.32** | 3.09 | 432.26** | 6.54** | 267.22** | 0.01 |
| **Genotypes** | 67 | 128.12** | 32.58** | 9.27** | 179.20** | 15.95** | 64.02** | 5.07** |
| **Error** | 134 | 17.26 | 9.42 | 2.23 | 26.37 | 4.11 | 10.51 | 1.15 |

*, ** Significant at 5% and 1% levels, respectively

The plant height ranged from 19.53 cm to 30.46 cm with a mean of 23.74 cm. The line RIL-56 recorded maximum value (30.46 cm) followed by RIL-2 (29.26 cm), RIL-36 (28.80 cm) and GJG-9 (28.00 cm), while minimum value was recorded in RIL-7 (19.53 cm) followed by RIL-64 (19.80 cm), RIL-4 (20.33 cm) and RIL-11 (20.80 cm).

The mean of SCMR was 34.76 with a range of 28.33 to 41.56. The maximum value was observed in RIL-12 (41.56) followed by RIL-43 (38.76), RIL-46 (38.62) and RIL-30 (38.11), while minimum value was observed in AG-2006-6 (28.33) followed by RIL-8 (29.37) and RIL-16 (29.82).

The number of mature pods per plant varied from 8.93 to 22.13 with a mean of 12.53. The genotype GJG-32 (22.13) recorded maximum value followed by RIL-58 (18.60), RIL-63 (16.06) and ICGV-05155 (15.80), while minimum value was recorded in RIL-15 (8.93) followed by RIL-32 (9.20), RIL-27 (9.60) and RIL-30 (9.86).

The number of immature pods per plant varied from 1.27 to 4.86 with a mean value of 2.58. Maximum value was observed in RIL-44 (4.86) followed by RIL-60 (4.46), GJG-32 (4.20) and RIL-63 (4.13), while minimum value was recorded in RIL-24 (1.26) followed by RIL-39 (1.40) and RIL-54 (1.46).

The mean recorded for shelling percentage was 68.51% with a range of 62.04 to 78.08%. Maximum value was observed in RIL-16 (78.08%) followed by RIL-11 (74.12%), RIL-12 (73.95%) and RIL-62 (73.37%). The minimum value was recorded in RIL-31 (62.04%) followed by RIL-40 (62.53%), RIL-32 (62.73%) and RIL-52 (63.29%).

The overall mean of the genotypes for 100-kernel weight was 44.40 g with a range of 33.33 to 58.67 g. The line RIL-61 (58.67 g) recorded maximum value followed by RIL-28 (58.33 g), RIL-16 (57.67 g), RIL-3 (56.00 g) and RIL-2 (55.33g), while minimum value was recorded in RIL-58 (33.33 g) followed by RIL-53 (34.67 g) and RIL-5 (35.33 g).

The mean value recorded for sound mature kernels was 89.67% with a range of 80.67 to 96.67%. The line RIL-56 had maximum value (96.67%) followed by RIL-39 (96.00%), RIL-49 (95.33%) and RIL-22 (95.00%). The lowest value was recorded in RIL-60 (80.67%) followed by RIL-64 (83.33), RIL-11 (83.67%) and RIL-13 (84.00%).

The mean kernel yield per plant was 12.69 g with a range of 8.56 to 17.56 g. The genotype GJG-32 (17.56 g) showed maximum value followed by RIL-28 (16.23 g), RIL-19 (15.76 g), RIL-58 (15.50 g) and RIL-16 (15.26 g). The line RIL-40 (8.56 g)

followed by RIL-30 (8.70 g) and RIL-52 (10.00 g) recorded the lowest kernel yield per plant.

The biological yield per plant varied from 29.13 to 79.16 g with a mean value of 42.19 g. Maximum value was observed in GJG-32 (79.16 g) followed by RIL-35 (62.70) and RIL-2 (62.13 g), while minimum value was recorded in RIL-62 (29.13 g) followed RIL-13 (31.86 g), RIL-27 (32.46 g) and RIL-7(32.96 g).

The mean pod yield per plant was 18.51 g with a range of 13.20 to 24.40 g. The genotype GJG-32 (24.40 g) showed maximum value followed by RIL-35 (23.67 g), RIL-28 (23.00 g) and RIL-19 (21.86 g). The line RIL-30 (13.20 g) followed by RIL-40 (13.67 g) and RIL-62 (14.06 g) recorded the lowest kernel yield per plant.

The harvest index showed minimum value of 30.80% and maximum value of 53.73% with a mean of 44.56%. The line RIL-18 (53.73%) showed maximum value, which was followed by RIL-26 (52.33%), RIL-21(51.67%) and RIL-64 (51.13%). The lowest harvest index was recorded in GJG-32 (30.80%) followed by RIL-2 (34.46%) and RIL-33 (34.83%).

The mean oil content was 50.58% exhibiting minimum value of 40.23% and a maximum value of 53.12%. The maximum value was observed in RIL-4 (53.12%), followed by RIL-37 (52.64%), RIL-2 (52.62%), ICGV-05155 (52.36%) and RIL-58 (52.36%), while minimum value was recorded in RIL-13 (40.23%) followed by RIL-39 (47.57%).

**4.2.2 Phenotypic coefficient of variation**

Phenotypic coefficients of variation for all the characters are given in Table 4.2. High phenotypic coefficient of variation was observed for number of immature pods per plant (31.53%). The plant height (9.90%), days to 50% flowering (8.73%), SCMR (6.76%), shelling percentage (4.76%), sound mature kernels (3.67%), days to maturity (3.22%) and oil content (2.56%) had low phenotypic coefficient of variation. The biological yield per plant (18.31%), number of mature pods per plant (17.77%), 100-kernel weight (14.71%), kernel yield per plant (13.84%), pod yield per plant (12.45%) and harvest index (10.36%) exhibited moderate values for phenotypic coefficient of variation.

**4.2.3 Genotypic coefficient of variation**

Genotypic coefficients of variation for different characters are also presented in Table 4.2. High genotypic coefficient of variation was observed for number of immature pods per plant (30.66%). The biological yield per plant (16.91%), number of

mature pods per plant (16.61%), 100-kernel weight (13.69%), kernel yield per plant (12.06%) and pod yield per plant (10.73%) had moderate values, while harvest index (9.47%), plant height (8.57%), days to 50% flowering (8.16%), SCMR (5.53%), shelling percentage (3.89%), days to maturity (3.16%), sound mature kernelS (3.09%) and oil content (2.25%) exhibited very low genotypic coefficient of variation.

**4.2.4 Heritability**

The broad sense heritability estimates for different characters are given in Table 4.2. High heritability estimates were observed for all the characters under study *viz.*, days to maturity (96.14%), number of immature pods per plant (94.73%), number of mature pods per plant (87.36%), days to 50% flowering (87.19%), 100-kernel weight (86.53%), biological yield per plant (85.28%), harvest index (83.58%), oil content (77.28%), kernel yield per plant (75.91%), plant height (74.93%), pod yield per plant (74.24%), sound mature kernels (71.07%), SCMR (66.96%) and shelling percentage (66.85%).

**4.2.5 Genetic advance**

Genetic advance at 5% selection intensity (k=2.06) was estimated for different characters (Table 4.2). High genetic advance was observed for biological yield per plant (13.57), 100-kernel weight (11.64), harvest index (7.95) and days to maturity (7.30). The values were moderate for sound mature kernels (4.82), shelling percentage (4.49), days to 50% flowering, number of mature pods per plant (4.00), plant height (3.62), pods yield per plant (3.52) and SCMR (3.24). Low values of genetic advance were observed for kernel yield per plant (2.74), oil content (2.06) and number of immature pods per plant (1.58).

**4.2.6 Genetic advance expressed as percentage of mean**

The estimates of genetic advance expressed as percentage of mean (Table 4.2) were found high for number immature pods per plant (61.47%), biological yield per plant (32.17%), number of mature pods per plant (31.98%), 100-kernel weight (26.23%) and kernel yield per plant (21.65%). The values were moderate for pod yield per plant (19.04%), harvest index (17.84%), days to 50% flowering (15.69%) and plant height (15.28%). The values were low for SCMR (9.33%), shelling percentage (6.56%), days to maturity (6.38%), sound mature kernels (5.38%) and oil content (4.09%).

**Table 4.2. Phenotypic and genotypic coefficients of variation, heritability and genetic advance for various characters in groundnut**

| Characters | Range of variation | Mean | Phenotypic coefficient of variation (%) | Genotypic coefficient of variation (%) | Heritability in broad sense | Genetic advance | Genetic advance expressed as percentage of mean |
|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | 22.00 – 29.67 | 25.50 | 08.73 | 08.16 | 87.19 | 04.00 | 15.69 |
| **Days to maturity** | 107.33-120.33 | 114.26 | 03.22 | 03.16 | 96.14 | 07.30 | 06.38 |
| **Plant height (cm)** | 19.53-30.46 | 23.74 | 9.90 | 8.57 | 74.93 | 03.62 | 15.28 |
| **SCMR** | 28.33-41.56 | 34.76 | 06.76 | 05.53 | 66.96 | 03.24 | 09.33 |
| **Number of mature pods per plant** | 8.93-22.13 | 12.53 | 17.77 | 16.61 | 87.36 | 04.00 | 31.98 |
| **Number of immature pods per plant** | 1.26-4.86 | 2.58 | 31.53 | 30.66 | 94.73 | 01.58 | 61.47 |
| **Shelling percentage (%)** | 62.04-78.08 | 68.51 | 04.76 | 03.89 | 66.85 | 04.49 | 06.56 |
| **100-kernel weight (g)** | 33.33-58.67 | 44.40 | 14.71 | 13.69 | 86.53 | 11.64 | 26.23 |
| **Sound mature kernels (%)** | 80.67-96.67 | 89.67 | 03.67 | 03.09 | 71.07 | 04.82 | 05.38 |
| **Kernel yield per plant (g)** | 8.56-17.56 | 12.69 | 13.84 | 12.06 | 75.91 | 02.74 | 21.65 |
| **Biological yield per plant (g)** | 29.13-79.16 | 42.19 | 18.31 | 16.91 | 85.28 | 13.57 | 32.17 |
| **Pod yield per plant (g)** | 13.20-24.40 | 18.51 | 12.45 | 10.73 | 74.24 | 03.52 | 19.04 |
| **Harvest index (%)** | 30.80-53.73 | 44.56 | 10.36 | 09.47 | 83.58 | 07.95 | 17.84 |
| **Oil content (%)** | 47.58-53.12 | 50.58 | 02.56 | 02.25 | 77.28 | 02.06 | 04.09 |

## 4.3 CORRELATION COEFFICIENTS

The correlation coefficients were worked out among 14 characters to find out association of pod yield per plant with its components as well as association among yield components at genotypic ($r_g$) and phenotypic ($r_p$) levels. The data given in Table 4.3 revealed that, in general the genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlations. The results on correlation coefficients between different pairs of characters are presented below:

### 4.3.1 Pod yield per plant

The pod yield per plant had significant and positive correlation both at genotypic and phenotypic levels with days to 50% flowering ($r_g$=0.4460, $r_p$=0.3347), days to maturity ($r_g$=0.5451, $r_p$=0.4635), number of mature pods per plant ($r_g$=0.5568, $r_p$=0.5803), kernel yield per plant ($r_g$=0.9521, $r_p$=0.9419) and biological yield per plant ($r_g$=0.7362, $r_p$=0.7387), while with SCMR (0.2630) at genotypic level only.

### 4.3.2 Days to 50% flowering

The days to 50% flowering had positive and significant correlation both at genotypic and phenotypic levels with days to maturity ($r_g$=0.4362, $r_p$=0.4000), number of mature pods per plant ($r_g$=0.3680, $r_p$=0.3125), kernel yield per plant ($r_g$=0.4460, $r_p$=0.3362) and biological yield per plant ($r_g$=0.5011, $r_p$=0.4117). Days to 50% flowering had negative significant correlation at genotypic and phenotypic levels ($r_g$=-0.3069, $r_p$=-2584) with harvest index.

### 4.3.3 Days to maturity

The days to maturity had positive and significant association with SCMR ($r_g$=0.3060, $r_p$=0.2419), number of mature pods per plant ($r_g$=0.3710, $r_p$=0.3426), kernel yield per plant ($r_g$=0.4860, $r_p$=0.4144), biological yield per plant ($r_g$=0.4938, $r_p$=0.4536) and oil content ($r_g$=0.3575, $r_p$=0.3122) at both genotypic and phenotypic levels.

### 4.3.4 Plant height

The plant height was positively and significantly associated at both genotypic and phenotypic levels with 100-kernel weight ($r_g$=0.4118, $r_p$=0.3400) and sound mature kernels ($r_g$=0.4425, $r_p$=0.2956). Plant height showed significant and negative correlation with SCMR ($r_g$=-0.3335, $r_p$=-0.2659) and number of immature pods per plant ($r_g$=-0.3003, $r_p$=-0.2588) at both genotypic and phenotypic levels whereas, with number of mature pods per plant ($r_g$=-0.3137) at genotypic level only.

**Table 4.3. Genotypic ($r_g$) and phenotypic ($r_p$) correlation coefficients among 14 characters in groundnut**

| Characters | | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling percentage (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Pod yield per plant (g)** | $r_g$ | 0.4460** | 0.5451** | 0.1256 | 0.2630* | 0.5568** | 0.1897 | 0.1817 | 0.0603 | -0.0256 | 0.9521** | 0.7362** | -0.0171 | 0.0170 |
| | $r_p$ | 0.3347** | 0.4635** | 0.1261 | 0.1958 | 0.5803** | 0.1666 | 0.1126 | 0.0770 | -0.0443 | 0.9419** | 0.7387** | 0.0148 | 0.0338 |
| **Days to 50% flowering** | $r_g$ | | 0.4362** | -0.0868 | 0.1570 | 0.3680** | 0.0562 | 0.1391 | -0.2256 | -0.2259 | 0.4460** | 0.5011** | -0.3069** | 0.1160 |
| | $r_p$ | | 0.4000** | -0.1131 | 0.1088 | 0.3125* | 0.0645 | 0.0978 | -0.1823 | -0.1692 | 0.3362** | 0.4117** | -0.2584* | 0.0821 |
| **Days to maturity** | $r_g$ | | | 0.0049 | 0.3060** | 0.3710** | 0.2376 | -0.0011 | -0.0998 | -0.0399 | 0.4860** | 0.4938** | -0.2141 | 0.3575** |
| | $r_p$ | | | -0.0117 | 0.2419* | 0.3426** | 0.2299 | -0.0083 | -0.0924 | -0.0354 | 0.4144** | 0.4536** | -0.1980 | 0.3122* |
| **Plant height (cm)** | $r_g$ | | | | -0.3335** | -0.3137** | -0.3003* | -0.1778 | 0.4118** | 0.4425** | 0.0497 | 0.0499 | 0.0184 | -0.0736 |
| | $r_p$ | | | | -0.2659* | -0.2314 | -0.2588* | -0.0779 | 0.3400** | 0.2956* | 0.0864 | 0.0697 | 0.0054 | -0.0606 |
| **SCMR** | $r_g$ | | | | | 0.2196 | 0.3733** | -0.0258 | -0.2827* | -0.3527** | 0.2288 | 0.1520 | 0.0576 | 0.2846* |
| | $r_p$ | | | | | 0.1629 | 0.2957* | -0.0147 | -0.1915 | -0.2473* | 0.1741 | 0.1212 | 0.0512 | 0.2084 |
| **No. of mature pods per plant** | $r_g$ | | | | | | 0.5321** | 0.1731 | -0.6196** | -0.1636 | 0.5607** | 0.5001** | -0.0698 | 0.2076 |
| | $r_p$ | | | | | | 0.4900** | 0.1551 | -0.5361** | -0.1699 | 0.5831** | 0.5098** | -0.0424 | 0.1656 |
| **No. of immature pods per plant** | $r_g$ | | | | | | | 0.0762 | -0.3560** | -0.2720* | 0.2048 | 0.2679* | -0.2025 | 0.2035 |
| | $r_p$ | | | | | | | 0.0541 | -0.3233** | -0.2393 | 0.1775 | 0.2513* | -0.1936 | 0.1848 |
| **Shelling percentage (%)** | $r_g$ | | | | | | | | -0.0814 | 0.0169 | 0.4717** | 0.0368 | 0.2030 | -0.0764 |
| | $r_p$ | | | | | | | | -0.0403 | 0.0069 | 0.4364** | 0.0028 | 0.1738 | -0.0912 |
| **100-kernel weight (g)** | $r_g$ | | | | | | | | | 0.0968 | 0.0267 | 0.1110 | -0.1284 | -0.2917* |
| | $r_p$ | | | | | | | | | 0.1273 | 0.0556 | 0.0897 | -0.0701 | -0.2429* |
| **Sound mature kernels (%)** | $r_g$ | | | | | | | | | | -0.0150 | -0.0723 | 0.0835 | -0.0317 |
| | $r_p$ | | | | | | | | | | -0.0351 | -0.0912 | 0.0917 | -0.0216 |
| **Kernel yield per plant (g)** | $r_g$ | | | | | | | | | | | 0.6815** | 0.0313 | -0.0119 |
| | $r_p$ | | | | | | | | | | | 0.6772** | 0.0592 | -0.0044 |
| **Biological yield per plant(g)** | $r_g$ | | | | | | | | | | | | -0.6757** | 0.0766 |
| | $r_p$ | | | | | | | | | | | | -0.6427** | 0.0781 |
| **Harvest index (%)** | $r_g$ | | | | | | | | | | | | | -0.0765 |
| | $r_p$ | | | | | | | | | | | | | -0.0651 |

***, ** Significant at 5 % and 1% levels, respectively**

### 4.3.5 SCMR

The SCMR was significantly and positively correlated with number of immature pods per plant ($r_g$ =0.3733, $r_p$=0.2957) at genotypic and phenotypic levels and with oil content ($r_g$=0.2846) at genotypic level. The SCMR had significant and negative correlation at both levels with sound mature kernels ($r_g$ =-0.3527, $r_p$ =-0.2473), while it's association was found significant and negative with 100-kernel weight ($r_g$ =-0.2827) at genotypic level only.

### 4.3.6 Number of mature pods per plant

Number of mature pods per plant exhibited significant and positive correlation with number of immature pods per plant ($r_g$=0.5321, $r_p$=0.4900), kernel yield per plant ($r_g$=0.5607, $r_p$=5831) and biological yield per plant ($r_g$=0.5001, $r_p$=0.5098) at both genotypic and phenotypic levels. This character showed negative and significant correlation both at genotypic and phenotypic levels with 100-kernel weight ($r_g$=-0.6196, $r_p$=-5361).

### 4.3.7 Number of immature pods per plant

Number of immature pods per plant exhibited significant and positive correlation with biological yield per plant ($r_g$=0.2679, $r_p$=0.2513) at both genotypic and phenotypic levels. Number of immature pods per plant showed negative and significant correlation with 100-kernel weight ($r_g$=-0.3560, $r_p$=-3233) both at genotypic and phenotypic levels and with sound mature kernels ($r_g$=-0.2720) at genotypic level only.

### 4.3.8 Shelling percentage

The shelling percentage had significant and positive correlation at genotypic and phenotypic levels with kernel yield per plant ($r_g$ =0.4717, $r_p$ =0.4364).

### 4.3.9 100-kernel weight

The 100-kernel weight displayed negative and significant association with oil content ($r_g$ =-0.2917, $r_p$ =-0.2429) at both genotypic and phenotypic levels.

### 4.3.10 Sound mature kernels

No significant association was observed between sound mature kernels and kernel yield per plant, biological yield per plant, harvest index and oil content.

### 4.3.11 Kernel yield per plant

The kernel yield per plant had significant and positive association with biological yield per plant ($r_g$=0.6815, $r_p$=6772) at both genotypic and phenotypic levels.

### 4.3.12 Biological yield per plant

The biological yield per plant was significantly and negatively correlated both at genotypic and phenotypic levels with harvest index ($r_g$ =-0.6757, $r_p$ =-0.6427).

### 4.3.13 harvest index

The harvest index had non-significant and negative correlation with oil content ($r_g$=-0.0765, $r_p$=-0.0651) at genotypic and phenotypic level.

## 4.4 PATH COEFFICIENT ANALYSIS

The phenotypic correlation coefficients calculated for different pairs of character were subjected to path coefficient analysis for partitioning these values into the direct and indirect effects. The results obtained for direct and indirect effects of different characters on pod yield per plant are presented in Table 4.4 and diagrammatically represented in Figure 4.1.

### 4.4.1. Days to 50% flowering vs pod yield per plant

The phenotypic correlation between days to 50% flowering and pod yield per plant was significant and positive ($r_p$=0.3347), while its direct effect was positive and low in magnitude (0.0024). The days to 50% flowering exhibited very high and positive indirect effect *via* kernel yield per plant (0.3451). This trait exhibited moderate and positive indirect effect *via* biological yield per plant (0.0449) and low effect *via* days to maturity (0,0044). It showed negative and moderate indirect effect *via* shelling out-turn (-0.0339) and harvest index (-0.0224).

### 4.4.2 Days to maturity vs pod yield per plant

Days to maturity exhibited positive and significant phenotypic correlation with pod yield per plant ($r_p$=0.4635). This character exerted positive and moderate direct effect (0.0109) on pod yield per plant but, it exhibited positive and very high indirect effect *via* kernel yield per plant (0.4255) and moderate effect *via* biological yield per plant (0.0494). The days to maturity exhibited negative and moderate indirect effect *via* harvest index (-0.0172) and number of mature pods per plant (-0.0092).

### 4.4.3 Plant height vs pod yield per plant

The correlation coefficient between pod yield per plant and plant height was positive and non-significant ($r_p$=0.1261) and its direct effect was also found to be positive but negligible (0.0004) in magnitude. This character exhibited positive and moderate indirect effect *via* kernel yield per plant (0.0887) and shelling percentage (0.0270), while low indirect effect *via* biological yield per plant (0.0076) and number of

mature pods per plant (0.0062). Plant height exhibited negative and low indirect effect through 100-kernel weight (-0.0036) and sound mature kernels (-0.0026).

**4.4.4 SCMR vs pod yield per plant**

The SCMR had non-significant and positive correlation with pod yield per plant ($r_p$=0.1958) and also manifested negative and low direct effect (-0.0088). This character exhibited positive and high indirect effect *via* kernel yield per plant (0.1787), moderate indirect effect through biological yield per plant (0.0132) and low *via* shelling percentage (0.0051), harvest index (0.0044) and days to maturity (0.0026).

**4.4.5 Number of mature pods per plant vs pod yield per plant**

The number of mature pods per plant had significant and positive correlation with pod yield per plant ($r_p$=0.5803) and its direct effect was negative and moderate in magnitude (-0.0269). Its negative contribution was also *via* shelling out-turn (-0.0538). This character contributed towards pod yield per plant mainly through positive and very high indirect effect *via* kernel yield per plant (0.5986), moderate indirect effect *via* biological yield per plant (0.0556) and low effect *via* 100-kernel weight (0.0057) and days to maturity (0.0037).

**4.4.6 Number of immature pods per plant vs pod yield per plant**

The correlation coefficient between pod yield per plant and number of immature pods per plant was non-significant and positive ($r_p$=0.1666). Its direct effect on pod yield per plant was found negative and negligible in magnitude (-0.0005). The harvest index (-0.0168), shelling out-turn (-0.0188) and number of mature pods per plant (0.0132) also exhibited moderate and negative indirect effect on pod yield per plant. This trait contributed through positive and high indirect effect *via* kernel yield per plant (0.1822), moderate effect *via* biological yield per plant (0.0274) and low effect *via* 100-kernel weight (0.0035) and days to maturity (0.0025).

**4.4.7 Shelling percentage vs pod yield per plant**

The shelling out-turn exhibited non-significant and positive phenotypic association with pod yield ($r_p$=0.1126) but, exerted negative and very high direct effect (-0.3469) on pod yield per plant. This trait contributed towards pod yield per plant indirectly through positive and very high indirect effect by kernel yield per plant (0.4480) and moderate and positive indirect effect through harvest index (0.0151).

**Table 4.4. Phenotypic path coefficient analysis showing direct(diagonal) and indirect effects of different characters on pod yield per plant in groundnut**

| Characters | Days to 50 % flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling percentage (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Harvest Index (%) | Oil content (%) | phenotypic correlation with pod yield/plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50 % flowering** | **0.0024** | 0.0044 | 0.0000 | -0.0010 | -0.0084 | 0.0000 | -0.0339 | 0.0020 | 0.0015 | 0.3451 | 0.0449 | -0.0224 | 0.0003 | 0.3347** |
| **Days to maturity** | 0.0009 | **0.0109** | 0.0000 | -0.0021 | -0.0092 | -0.0001 | 0.0029 | 0.0010 | 0.0003 | 0.4255 | 0.0494 | -0.0172 | 0.0012 | 0.4635** |
| **Plant height (cm)** | -0.0003 | -0.0001 | **0.0004** | 0.0024 | 0.0062 | 0.0001 | 0.0270 | -0.0036 | -0.0026 | 0.0887 | 0.0076 | 0.0005 | -0.0002 | 0.1261 |
| **SCMR** | 0.0003 | 0.0026 | -0.0001 | **-0.0088** | -0.0044 | -0.0001 | 0.0051 | 0.0021 | 0.0021 | 0.1787 | 0.0132 | 0.0044 | 0.0008 | 0.1958 |
| **No. of mature pods per plant** | 0.0007 | 0.0037 | -0.0001 | -0.0014 | **-0.0269** | -0.0002 | -0.0538 | 0.0057 | 0.0015 | 0.5986 | 0.0556 | -0.0037 | 0.0006 | 0.5803** |
| **No. of immature pods per plant** | 0.0002 | 0.0025 | -0.0001 | -0.0026 | -0.0132 | **-0.0005** | -0.0188 | 0.0035 | 0.0021 | 0.1822 | 0.0274 | -0.0168 | 0.0007 | 0.1666 |
| **Shelling percentage (%)** | 0.0002 | -0.0001 | 0.0000 | 0.0001 | -0.0042 | 0.0000 | **-0.3469** | 0.0004 | -0.0001 | 0.4480 | 0.0003 | 0.0151 | -0.0003 | 0.1126 |
| **100-kernel weight (g)** | -0.0004 | -0.0010 | 0.0001 | 0.0017 | 0.0144 | 0.0002 | 0.0140 | **-0.0107** | -0.0011 | 0.0571 | 0.0098 | -0.0061 | -0.0009 | 0.0770 |
| **Sound mature kernels (%)** | -0.0004 | -0.0004 | 0.0001 | 0.0022 | 0.0046 | 0.0001 | -0.0024 | -0.0014 | **-0.0086** | -0.0361 | -0.0099 | 0.0079 | -0.0001 | -0.0443 |
| **Kernel yield per plant (g)** | 0.0008 | 0.0045 | 0.0000 | -0.0015 | -0.0157 | -0.0001 | -0.1514 | -0.0006 | 0.0003 | **1.0266** | 0.0738 | 0.0051 | 0.0000 | 0.9419** |
| **Biological yield per plant (g)** | 0.0010 | 0.0049 | 0.0000 | -0.0011 | -0.0137 | -0.0001 | -0.0010 | -0.0010 | 0.0008 | 0.6952 | **0.1090** | -0.0557 | 0.0003 | 0.7387** |
| **Harvest Index (%)** | -0.0006 | -0.0022 | 0.0000 | -0.0005 | 0.0011 | 0.0001 | -0.0603 | 0.0008 | -0.0008 | 0.0608 | -0.0701 | **0.0867** | -0.0002 | 0.0148 |
| **Oil content (%)** | 0.0002 | 0.0034 | 0.0000 | -0.0018 | -0.0045 | -0.0001 | 0.0316 | 0.0026 | 0.0002 | -0.0045 | 0.0085 | -0.0056 | **0.0038** | 0.0338 |

***, ** significant at 5% and 1% levels, respectively**
**Residual effect, R= 0.046**

**4.4.8 100-kernel weight vs pod yield per plant**

At phenotypic level, 100-kernel weight had non-significant and positive association with pod yield per plant ($r_p$=0.0770), while its direct effect was negative and moderate in magnitude (-0.0107). This trait had also negative contribution *via* harvest index (-0.0061). Its indirect effect was moderate towards pod yield per plant through kernel yield per plant (0.0571), shelling percentage (0.0140), number of mature pods per plant (0.0144) and biological yield per plant (0.0098) in positive direction.

**4.4.9 Sound mature kernels vs pod yield per plant**

The correlation value of sound mature kernels was observed non-significant and negative with pod yield per plant ($r_p$=-0.0443) and its direct effect was also negative and low in magnitude (-0.0086). Its negative contribution was also from kernel yield per plant (-0.0361), biological yield per plant (-0.0099) and shelling out-turn (-0.0024). This trait exhibited positive and low indirect effect through harvest index (0.0079), number of mature pods per plant (0.0046) and SCMR (0.0022) towards pod yield per plant.

**4.4.10 kernel yield per plant vs pod yield per plant**

At phenotypic level, kernel yield per plant had highly significant and positive association with pod yield per plant ($r_p$=0.9419) and its direct effect was also found positive and very high in magnitude (1.0266). Its positive contribution towards pod yield per plant was also through biological yield per plant (0.0738), harvest index (0.0051) and days to maturity (0.0045). However, its indirect contribution towards pod yield per plant was negative and high through shelling out-turn (-0.1514) and moderate *via* number of mature pods per plant (-0.0157).

**4.4.11 Biological yield per plant vs pod yield per plant**

The phenotypic correlation between biological yield per plant and pod yield per plant was positive and highly significant ($r_p$=0.7387) and also showed high and positive (0.1090) direct effect on pod yield per plant. This trait also exhibited positive and very high indirect effect *via* kernel yield per plant (0.6952) and low effect *via* days to maturity (0.0049). This trait however, had negative contribution through moderate indirect effect from harvest index (-0.0557).

**4.4.12 Harvest index vs pod yield per plant**

The harvest index had non-significant and positive correlation with pod yield per plant ($r_p$=0.0148) and also displayed positive and moderate direct effect (0.0867) on pod yield per plant. This trait also exhibited moderate and positive indirect effect

*via* kernel yield per plant (0.0608). Harvest index displayed negative and moderate indirect effect *via* biological yield per plant (-0.0701) and shelling out-turn (-0.0603), while low effect *via* days to maturity (-0.0022).

**4.4.13 Oil content vs pod yield per plant**

The oil content had non-significant and positive correlation with pod yield per plant ($r_p$=0.0338) and its direct effect was also found positive and low in magnitude (0.0038). This trait exhibited positive and moderate indirect effect *via* shelling percentage (0.0316) and low effect *via* biological yield per plant (0.0085), days to maturity (0.0034) and 100-kernel weight (0.0026). Its indirect contribution was negative through kernel yield per plant (-0.0045) and number of mature pods per plant (-0.0045).

## 4.5 SELECTION INDICES

For the construction of selection indices, the characters, which had desirable correlation as well as moderate to high direct effect on pod yield per plant, were considered. In this context, the pod yield per plant (X1) along with its five components *viz*., days to 50% flowering (X2), days to maturity (X3), number of mature pods per plant (X4), kernel yield per plant (X5) and biological yield per plant (X6) were identified and considered for the construction of selection indices.

Sixty-three selection indices were constructed in all possible combinations of the five yield contributing characters and pod yield per plant. Their respective genetic advances were calculated and relative efficiency of different discriminant functions in relation to the straight selection for pod yield was compared. The data on selection indices, discriminant functions, genetic gain and relative efficiency are given in Table 4.5, assuming the efficiency of straight selection for pod yield as 100%.

The results suggested that the selection efficiency was higher, in general, over straight selection when the selection was based on component character, which further increased with the inclusion of two or more characters. The highest efficiency was noted when five or six characters were considered together.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of 178.21% was exhibited by number of mature pods per plant followed by days to 50% flowering (145.18%), biological yield per plant (90.59%), days to maturity (65.64%) and kernel yield per plant (36.37%).

**Table 4.5. Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in groundnut**

| Sr. No. | Selection index | Discriminant function | Expected genetic advance | Relative efficiency (%) |
|---|---|---|---|---|
| | (1) | (2) | (3) | (4) |
| **1** | X1 Pod yield per plant | 0.945X1 | 6.98 | 100.00 |
| **2** | X2 Days to 50% flowering | 0.946X2 | 10.13 | 145.18 |
| **3** | X3 Days to maturity | 0.980X3 | 4.58 | 65.64 |
| **4** | X4 No. of mature pods/plant | 0.959X4 | 12.43 | 178.21 |
| **5** | X5 Kernel yield per plant | 0.737X5 | 2.54 | 36.37 |
| **6** | X6 Biological yield per plant | 0.990X6 | 6.32 | 90.59 |
| **7** | X1.X2 | 0.774X1 + 0.975X2 | 6.68 | 95.91 |
| **8** | X1.X3 | 0.704X1 + 1.045X3 | 9.94 | 142.49 |
| **9** | X1.X4 | 0.642X1 + 0.952X4 | 6.62 | 94.90 |
| **10** | X1.X5 | 0.612X1 + 0.941X5 | 6.22 | 89.16 |
| **11** | X1.X6 | 0.356X1 + 0.949X6 | 16.40 | 235.07 |
| **12** | X2.X3 | 0.877X2 + 0.991X3 | 9.85 | 141.23 |
| **13** | X2.X4 | 0.908X2 + 0.911X4 | 6.77 | 96.97 |
| **14** | X2.X5 | 0.941 X2 +0.818X5 | 6.01 | 86.08 |
| **15** | X2.X6 | 1.174X2 + 0.838X6 | 16.32 | 233.91 |
| **16** | X3.X4 | 1.982 X3 +0.859X4 | 9.55 | 136.91 |
| **17** | X3.X5 | 1.000X3 + 0.468X5 | 8.44 | 121.00 |
| **18** | X3.X6 | 1.114X3 + 0.825X6 | 18.57 | 266.23 |
| **19** | X4.X5 | 0.937X4 + 0.645X5 | 5.97 | 85.58 |
| **20** | X4.X6 | 0.868X4 + 0.850X6 | 15.93 | 228.35 |
| **21** | X5.X6 | 0.480X5 + 0.904X6 | 15.62 | 223.83 |
| **22** | X1.X2.X3 | 0.743X1 + 0.955X2 + 1.045X3 | 12.60 | 180.61 |
| **23** | X1.X2.X4 | 0.660X1 + 1.043X2 + 0.936X4 | 9.48 | 135.82 |
| **24** | X1.X2.X5 | 0.593X1 + 1.067X2 + 0.969X5 | 9.15 | 131.12 |
| **25** | X1.X2.X6 | 0.356X1 + 1.307X2 + 0.919X6 | 19.19 | 275.09 |
| **26** | X1.X3.X4 | 0.578X1 + 1.094X3 + 0.932X4 | 12.41 | 177.94 |
| **27** | X1.X3.X5 | 0.446X1 + 1.110X3 + 1.051X5 | 12.18 | 174.63 |
| **28** | X1.X3.X6 | 0.253X1 + 1.242X3 + 0.916X6 | 21.55 | 308.94 |
| **29** | X1.X4.X5 | 0.513X1 + 0.962X4 + 0.932X5 | 9.06 | 129.83 |
| **30** | X1.X4.X6 | 0.188X1 + 1.024X4 + 0.960X6 | 18.84 | 269.98 |
| **31** | X1.X5.X6 | -0.245X1 + 1.513X5 + 0.973X6 | 18.65 | 267.31 |
| **32** | X2.X3.X4 | 0.908X2 + 1.001X3 + 0.906X4 | 12.26 | 175.74 |
| **33** | X2.X3.X5 | 0.932X2 + 1.015X3 + 0.810X5 | 11.83 | 169.58 |
| **34** | X2.X3.X6 | 1.142X2 + 1.084X3 + 0.821X6 | 21.32 | 305.57 |
| **35** | X2.X4.X5 | 1.009X2 + 0.925X4 + 0.684X5 | 8.82 | 126.49 |
| **36** | X2.X4.X6 | 1.234X2 + 0.832X4 + 0.832X6 | 16.71 | 268.19 |
| **37** | X2.X5.X6 | 2.247X2 + 4.072X5 + -0.470X6 | 18.41 | 235.16 |
| **38** | X3.X4.X5 | 1.053X3 + 0.916X4 + 0.616X5 | 11.64 | 166.77 |
| **39** | X3.X4.X6 | 1.154X3 + 0.831X4 + 0.819X6 | 20.94 | 300.12 |

| | | | | |
|---|---|---|---|---|
| **40** | X3.X5.X6 | 1.187X3 + 0.422X5 + 0.869X6 | 20.69 | 296.61 |
| **41** | X4.X5.X6 | 0.976X4 + 0.321X5 + 0.909X6 | 18.05 | 258.72 |
| **42** | X1.X2.X3.X4 | 0.611X1 + 1.007X2 + 1.084X3 + 0.925X4 | 15.09 | 216.30 |
| **43** | X1.X2.X3.X5 | 0.448X1 +1.021X2 + 1.098X3 + 1.085X5 | 14.87 | 213.13 |
| **44** | X1.X2.X3.X6 | 0.277X1 + 0.996X2 + 1.233X3 + 0.919X6 | 24.21 | 347.00 |
| **45** | X1.X2.X4.X5 | 0.492X1 + 1.136X2 + 0.928X4 + 0.957X5 | 11.88 | 170.24 |
| **46** | X1.X2.X4.X6 | 0.209X1 + 1.366X2 + 0.965X4 + 0.927X6 | 21.65 | 310.28 |
| **47** | X1.X2.X5.X6 | -0.196X1 + 1.379X2 + 1.440X5 + 0.935X6 | 21.47 | 307.71 |
| **48** | X1.X3.X4.X5 | 0.306X1 + 1.160X3 + 0.923X4 + 1.078X5 | 14.69 | 210.62 |
| **49** | X1.X3.X4.X6 | 0.082X1 + 1.286X3 + 0.984X4 + 0.924X6 | 23.98 | 343.67 |
| **50** | X1.X3.X5.X6 | -0.501X1 + 1.310X3 + 1.677X5 + 0.934X6 | 23.83 | 341.61 |
| **51** | X1.X4.X5.X6 | -0.391X1 + 0.998X4 + 1.498X5 + 0.986X6 | 21.11 | 302.57 |
| **52** | X2.X3.X4.X5 | 0.986X2 + 1.048X3 + 0.909X4 + 0.666X5 | 14.33 | 205.42 |
| **53** | X2.X3.X4.X6 | 1.201X2 + 1.115X3 + 0.811X4 + 0.812X6 | 23.71 | 339.81 |
| **54** | X2.X3.X5.X6 | 1.223X2 + 1.142X3 + 0.441X5 + 0.855X6 | 23.47 | 336.38 |
| **55** | X2.X4.X5.X6 | 1.344X2 + 0.922X4 + 0.335X5 + 0.880X6 | 20.87 | 299.18 |
| **56** | X3.X4.X5.X6 | 1.227X3 + 0.933X4 + 0.270X5 + 0.871X6 | 23.12 | 331.35 |
| **57** | X1.X2.X3.X4.X5 | 0.313X1 + 1.074X2 + 1.138X3 + 0.905X4 + 1.104X6 | 17.39 | 249.25 |
| **58** | X1.X2.X3.X4.X6 | 0.162X1 + 1.286X2 + 1.236X3 + 0.950X4+ 0.887X6 | 26.71 | 382.86 |
| **59** | X1.X2.X3.X5.X6 | -0.431X1 + 1.274X2 + 1.255X3 + 1.619X5 + 0.913X6 | 26.60 | 381.22 |
| **60** | X1.X2.X4.X5.X6 | 1.045X1 + 1.483X2 + 1.018X4 + -0.469X5 + -0.917X6 | 23.86 | 342.03 |
| **61** | X1.X3.X4.X5.X6 | -0.672X1 + 1.356X3 + 0.939X4 + 1.704X5 + 0.944X6 | 26.28 | 376.68 |
| **62** | X2.X3.X4.X5.X6 | 1.278X2 + 1.176X3 + 0.896X4 + 0.305X5 + 0.855X6 | 25.91 | 371.32 |
| **63** | X1.X2.X3.X4.X5.X6 | -0.585X1 + 1.324X2 + 1.294X3 + 0.897X4 + 1.647X5 + 0.921X6 | 29.06 | 416.46 |

Among the combinations involving two component characters, days to maturity and biological yield per plant (X3.X6) exhibited maximum relative efficiency of 266.23% followed by pod yield per plant and biological yield per plant (X1.X6), days to 50% flowering and biological yield per plant (X2.X6), number of mature pods per plant and biological yield per plant (X4.X6), kernel yield per plant and biological yield per plant (X5.X6), pod yield per plant and days to maturity (X1.X3) and days to 50% flowering and days to maturity (X2.X3) having relative efficiency of 235.07, 233.91, 228.35, 223.83, 142.49 and 141.23 %, respectively.

The selection index based on three character combinations indicated that a discriminant function with pod yield per plant, days to maturity and biological yield per plant (X1.X3.X6) possessed maximum relative efficiency of 308.94% followed by days to 50% flowering, days to maturity and biological yield per plant (X2.X3.X6). Similarly, days to maturity, number of mature pods per plant and biological yield per plant (X3.X4.X6); days to maturity, kernel yield per plant and biological yield per plant (X3.X5.X6); pod yield per plant, days to 50% flowering and biological yield per plant (X1.X2.X6); pod yield per plant, number of mature pods plant and biological yield per plant (X1.X4.X6); days to 50% flowering, number of mature pods per plant and biological yield per plant (X2.X4.X6); pod yield per plant, kernel yield per plant and biological yield per plant (X1.X5.X6), number of mature pods per plant kernel yield per plant and biological yield per plant (X4.X5.X6) and days to 50% flowering, kernel yield per plant and biological yield per plant (X2.X5.X6) exhibited high relative efficiency of 305.57, 300.12, 296.61, 275.09, 269.98, 268.19, 267.31, 258.72 and 235.16, respectively in respect of three component combinations.

In four character selection index, a function involving pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) exerted maximum relative efficiency of 347.00% followed by pod yield per plant, days to maturity, number of mature pods per plant and biological yield per plant (X1.X3.X4.X6); pod yield per plant, days to maturity, kernel yield per plant and biological yield per plant (X1.X3.X5.X6); days to 50% flowering, days to maturity, number of pods per plant and biological yield per plant (X2.X3.X4.X6); days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X2.X3.X5.X6); days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X3.X4.X5.X6); pod yield per plant, days to 50% flowering, number of mature pods per plant and biological yield per plant

(X1.X2.X4.X6) and pod yield per plant, days to 50% flowering, kernel yield per plant and biological yield per plant (X1.X2.X5.X6) consisting of 343.67, 341.61, 339.81, 336.38, 331.35, 310.28 and 307.71% relative efficiency, respectively.

The highest relative efficiency of 382.86% was exhibited by a selection index involving five component characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) followed by an index consisting of pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X1.X2.X3.X5.X6); pod yield per plant, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X3.X4.X5.X6); days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X2.X3.X4.X5.X6) consisting of 381.22, 376.68 and 371.32% relative efficiency, respectively.

The selection index based on all the six characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X2.X3.X4.X5.X6) exerted 416.46% relative efficiency.

Among all the 63 selection indices (Table 4.5), the index based on six characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X2.X3.X4.X5.X6) possessed the highest genetic gain and relative efficiency (29.06g and 416.46%) as compared to straight selection for pod yield per plant. Other two important index based on five characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) possessed the highest genetic gain and relative efficiency (26.71g and 382.86%), while the other possessing, pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X1.X2.X3.X5.X6) exerted the high genetic gain and relative efficiency of 26.60g and 381.22% respectively as compared to straight selection for pod yield per plant. Other two important selection indices identified were with the inclusion of four characters. Of these, one included pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) with genetic advance of 24.21g and 347.00% relative efficiency, while the other had pod yield per plant, days to maturity, number of mature pods per plant and biological yield per plant (X1.X3.X4.X6) showing expected

genetic gain of 23.98g and a relative efficiency of 343.67% as compared to the straight selection for pod yield. The best selection index identified for three characters combination included pod yield per plant, days to maturity and biological yield per plant (X1.X3.X6) having expected genetic gain of 21.55g and a relative efficiency of 308.94% as compared to the straight selection for pod yield per plant.

## 4.6 GENETIC DIVERGENCE

The significant mean squares due to genotypes for all the traits suggested the presence of considerable genetic variability for all the traits studied. Based upon 14 characters, the Mahalanobis's $D^2$ statistic was computed for all possible pairs of 68 genotypes in order to assess the genetic divergence present among the genotypes under the study.

### 4.6.1 Composition of clusters

Grouping of the genotypes was carried-out by following Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller $D^2$-values among themselves than those from groups belonging to different clusters. In all, 5 clusters were formed from 68 genotypes. The composition of cluster is given in Table 4.6 and diagrammatically has been represented in Figure 4.2.

The cluster I was the largest having 30 genotypes. The cluster III was the second largest which contained 19 genotypes followed by cluster IV with 13 genotypes, cluster II with 5 genotypes. The cluster V was the last and the smallest cluster having only one genotype.

### 4.6.2 Inter and intra-cluster distances

The inter and intra-cluster distance values are given in Table 4.7. The maximum inter-cluster distance (D=49.89) was found between clusters IV and V followed by that between clusters III and V (D=47.38), I and V (D=40.52), II and V (D=34.61), II and IV (D=26.66), I and II (D=18.39), II and III (D=17.65) The minimum inter-cluster distance was observed between clusters I and IV (D=10.84).

The intra-cluster distance ranged from 8.34 to 11.29, the maximum being in cluster II (11.30). The minimum intra-cluster distance was found in cluster IV (8.35). The clusters V contained single genotype and therefore, its intra-cluster distance was zero (0.00).

**Table 4.6. Grouping of 68 genotypes of groundnut in various clusters on the basis of $D^2$ statistic**

| Cluster | No. of Genotypes | Name of the genotypes |
|---|---|---|
| **I** | **30** | RIL-1, RIL-6, RIL-8, RIL-17, RIL-55, RIL-59, RIL-31, RIL-38, RIL-57, RIL-44, RIL-46, RIL-18, RIL-21, RIL-47, RIL-53, RIL-9, RIL-41, RIL-42, RIL-45, RIL-60, RIL-19, RIL-37, RIL-43, RIL-11, RIL-58, RIL-29, RIL-36, RIL-51, RIL-63 and ICGV-05155 |
| **II** | **5** | RIL-2, RIL-35, RIL-15, RIL-28 and RIL-16 |
| **III** | **19** | RIL-3, RIL-24, RIL-48, RIL-13, RIL-64, RIL-12, RIL-14, RIL-23, GJG-9, RIL-26, RIL-50, RIL-39, RIL-49, RIL-56, RIL-25, RIL-34, RIL-32, RIL-33 and RIL-61 |
| **IV** | **13** | RIL-4, RIL-54, RIL-20, RIL-7, RIL-10, RIL-62, AG-2006-6, RIL-22, RIL-27, RIL-5 RIL-52, RIL-30 and RIL-40 |
| **V** | **1** | GJG-32 |

**Table 4.7 Average inter and intra-cluster distance ($D=\sqrt{D^2}$) values in groundnut**

| | **I** | **II** | **III** | **IV** | **V** |
|---|---|---|---|---|---|
| **I** | 9.62 | 18.39 | 11.04 | 10.84 | 40.52 |
| **II** | | 11.30 | 17.65 | 26.66 | 34.61 |
| **III** | | | 10.32 | 12.53 | 47.38 |
| **IV** | | | | 8.35 | 49.89 |
| **V** | | | | | 0.0000 |

**Table 4.8. Cluster means for 14 different characters in groundnut**

| Clusters | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling out-turn (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Pod yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 25.83 | 115.05 | 23.32 | 35.26 | 13.60 | 2.87 | 67.88 | 41.28 | 88.54 | 13.10 | 43.67 | 19.29 | 44.51 | 50.81 |
| **II** | 27.86 | 115.86 | 25.26 | 34.33 | 11.70 | 2.26 | 69.73 | 54.66 | 88.73 | 15.04 | 54.41 | 21.62 | 40.33 | 50.09 |
| **III** | 24.15 | 113.64 | 24.91 | 34.17 | 11.34 | 2.21 | 68.33 | 50.28 | 91.22 | 12.37 | 39.79 | 18.08 | 45.97 | 50.22 |
| **IV** | 25.61 | 112.30 | 22.60 | 34.53 | 11.37 | 2.40 | 69.49 | 39.64 | 90.38 | 10.92 | 34.92 | 15.69 | 45.29 | 50.70 |
| **V** | 28.33 | 119.66 | 21.00 | 36.11 | 22.13 | 4,20 | 72.10 | 36.66 | 89.33 | 17.56 | 79.16 | 24.40 | 30.80 | 51.33 |
| **Mean** | 25.50 | 114.26 | 23.74 | 34.76 | 12.53 | 2.58 | 68.51 | 44.40 | 89.67 | 12.69 | 42.19 | 18.51 | 44.56 | 50.58 |
| **SEm ±** | 0.79 | 0.72 | 1.17 | 1.35 | 0.79 | 0.18 | 1.87 | 2.39 | 1.77 | 0.86 | 2.96 | 1.17 | 1.87 | 0.61 |
| **C.V.%** | 5.41 | 1.09 | 8.58 | 6.73 | 10.94 | 12.52 | 4.75 | 9.35 | 3.42 | 11.77 | 12.16 | 10.94 | 7.27 | 2.12 |
| **Percentage contribution of characters towards total divergence** | | | | | | | | | | | | | | |
| **Number of times appearing first** | 143 | 821 | 57 | 39 | 92 | 513 | 28 | 148 | 73 | 85 | 164 | 28 | 26 | 61 |
| **% contribution** | 6.28 | 36.04 | 2.50 | 1.71 | 4.04 | 22.52 | 1.23 | 6.50 | 3.20 | 3.73 | 7.20 | 1.23 | 1.14 | 2.68 |

### 4.6.3 Cluster means for various characters

The cluster means for 14 characters are presented in Table 4.8. The coefficient of variation (CV %) was calculated for all the attributes. The maximum coefficient of variation was recorded for number of immature pods per plant (12.52%) followed by biological yield per plant (12.16%), kernel yield per plant (11.77%), number of mature pods per plant (10.94) and pod yield per plant (10.94%). The lowest coefficient of variation was noted for days to maturity (1.09%) followed by oil content (2.12%), sound mature kernels (3.42%) and shelling out-turn (4.75%), while the days to 50% flowering (5.41%), SCMR (6.73%), harvest index (7.27%), plant height (8.58%) and 100-kernel weight (9.35%) had moderate coefficient of variation. Greater range of mean values among the clusters was recorded for different traits. The cluster V had the highest mean values for most off all characters like pod yield per plant (24.40g), kernel yield per plant (17.56g), biological yield per plant (79.16), shelling out-turn (72.10%), number of mature pods per plant (22.13), number of immature pods per plant (4.20%), days to 50% flowering (28.33), days to maturity (119.66), SCMR (36.11) and oil content (51.33%). The cluster II was good for plant height (25.26cm) and 100-kernel weight (54.66g). The cluster III was good for sound mature kernels (91.22%) and harvest index (45.97%).

The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that days to maturity (36.04%) followed by number of immature pods per plant (22.52%) and biological yield per plant (7.20%) contributed maximum towards total genetic divergence in the present study (Table 4.9). These characters accounted for more than 60.00% of total divergence in the material studied.

# CHAPTER IV

# EXPERIMENTAL RESULTS

The results obtained on the present investigation on "Genetic variation, selection indices and diversity analysis for pod yield and its components in RILs of groundnut (*Arachis hypogaea* L.)" are presented under the following sub-heads:

4.1 Analysis of variance

4.2 Genetic variability

4.3 Correlation coefficients

4.4 Path coefficient analysis

4.5 Selection indices

4.6 Genetic diversity

## 4.1 ANALYSIS OF VARIANCE

The analysis of variance as presented in Table 4.1 revealed highly significant differences among the genotypes for all the characters studied.

## 4.2 GENETIC VARIABILITY

The results obtained on various parameters of genetic variability have been presented here under:

### 4.2.1 Mean performance and range of variation

The mean values of 68 genotypes of groundnut for all the 14 characters along with the standard error of mean (SEm.), critical difference (CD) and coefficient of variation (CV%) are given in Appendix II, the summary of which is also presented in Table 4.2.

The mean recorded for days to 50% flowering was 25.50 with a range of 22.00 to 29.67. Maximum value was observed in RIL-35 and RIL-19 (29.67) followed by RIL-38 (29.33), RIL-58 (29.00) and AG-2006-6 (29.00) and RIL-36 (28.67). The lowest days to 50% flowering was recorded in RIL-25 (22.00) followed by RIL-18 (22.33), RIL-3 (22.67) and RIL-13(23.00).

The overall mean of the genotypes for days to maturity was 114.26 with a range of 107.33 to 120.33. The genotype ICGV-05155 (120.33) had maximum value followed by RIL-51 (119.67), RIL-26 (119.33) and RIL-38 (118.67). The minimum value was recorded in RIL-55 (107.33) followed by RIL-3(107.67), RIL-13(108.00) and RIL-54(108.67).

**Table 4.1. Analysis of variance for various characters in groundnut**

| Source | df | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | Number of mature pods per plant | Number of immature pods per plant | Shelling out-turn (%) |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| **Replications** | 2 | 5.06** | 11.66** | 134.77** | 0.37 | 3.99* | 2.10 | 0.58 |
| **Genotypes** | 67 | 14.91** | 40.77** | 16.58** | 16.62** | 14.88** | 1.98* | 31.99** |
| **Error** | 134 | 1.91 | 1.57 | 4.15 | 5.49 | 1.88 | 0.10 | 10.60 |

| Source | df | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Pod yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| **Replications** | 2 | 66.02** | 31.32** | 3.09 | 432.26** | 6.54** | 267.22** | 0.01 |
| **Genotypes** | 67 | 128.12** | 32.58** | 9.27** | 179.20** | 15.95** | 64.02** | 5.07** |
| **Error** | 134 | 17.26 | 9.42 | 2.23 | 26.37 | 4.11 | 10.51 | 1.15 |

*, ** Significant at 5% and 1% levels, respectively

The plant height ranged from 19.53 cm to 30.46 cm with a mean of 23.74 cm. The line RIL-56 recorded maximum value (30.46 cm) followed by RIL-2 (29.26 cm), RIL-36 (28.80 cm) and GJG-9 (28.00 cm), while minimum value was recorded in RIL-7 (19.53 cm) followed by RIL-64 (19.80 cm), RIL-4 (20.33 cm) and RIL-11 (20.80 cm).

The mean of SCMR was 34.76 with a range of 28.33 to 41.56. The maximum value was observed in RIL-12 (41.56) followed by RIL-43 (38.76), RIL-46 (38.62), and RIL-30 (38.11), while minimum value was observed in AG-2006-6 (28.33) followed by RIL-8 (29.37) and RIL-16 (29.82).

The number of mature pods per plant varied from 8.93 to 22.13 with a mean of 12.53. The genotype GJG-32 (22.13) recorded maximum value followed by RIL-58 (18.60), RIL-63 (16.06) and ICGV-05155 (15.80), while minimum value was recorded in RIL-15 (8.93) followed by RIL-32 (9.20), RIL-27 (9.60) and RIL-30 (9.86).

The number of immature pods per plant varied from 1.27 to 4.86 with a mean value of 2.58. Maximum value was observed in RIL-44 (4.86) followed by RIL-60 (4.46), GJG-32 (4.20) and RIL-63 (4.13), while minimum value was recorded in RIL-24 (1.26) followed by RIL-39 (1.40) and RIL-54 (1.46).

The mean recorded for shelling out turn was 68.51% with a range of 62.04 to 78.08%. Maximum value was observed in RIL-16 (78.08%) followed by RIL-11 (74.12%), RIL-12 (73.95%) and RIL-62 (73.37%). The minimum value was recorded in RIL-31 (62.04%) followed by RIL-40 (62.53%), RIL-32 (62.73%) and RIL-52 (63.29%).

The overall mean of the genotypes for 100-kernel weight was 44.40 g with a range of 33.33 to 58.67 g. The line RIL-61 (58.67 g) recorded maximum value followed by RIL-28 (58.33 g), RIL-16 (57.67 g), RIL-3 (56.00 g) and RIL-2 (55.33g), while minimum value was recorded in RIL-58 (33.33 g) followed by RIL-53 (34.67 g) and RIL-5 (35.33 g).

The mean value recorded for sound mature kernels was 89.67% with a range of 80.67 to 96.67%. The line RIL-56 had maximum value (96.67%) followed by RIL-39 (96.00%), RIL-49 (95.33%) and RIL-22 (95.00%). The lowest value was recorded in RIL-60 (80.67%) followed by RIL-64 (83.33), RIL-11 (83.67%) and RIL-13 (84.00%).

The mean kernel yield per plant was 12.69 g with a range of 8.56 to 17.56 g. The genotype GJG-32 (17.56 g) showed maximum value followed by RIL-28 (16.23 g), RIL-19 (15.76 g), RIL-58 (15.50 g) and RIL-16 (15.26 g). The line RIL-40 (8.56 g)

followed by RIL-30 (8.70 g) and RIL-52 (10.00 g) recorded the lowest kernel yield per plant.

The biological yield per plant varied from 29.13 to 79.16 g with a mean value of 42.19 g. Maximum value was observed in GJG-32 (79.16 g) followed by RIL-35 (62.70) and RIL-2 (62.13 g), while minimum value was recorded in RIL-62 (29.13 g) followed RIL-13 (31.86 g), RIL-27 (32.46 g) and RIL-7(32.96 g).

The mean pod yield per plant was 18.51 g with a range of 13.20 to 24.40 g. The genotype GJG-32 (24.40 g) showed maximum value followed by RIL-35 (23.67 g), RIL-28 (23.00 g) and RIL-19 (21.86 g). The line RIL-30 (13.20 g) followed by RIL-40 (13.67 g) and RIL-62 (14.06g) recorded the lowest kernel yield per plant.

The harvest index showed minimum value of 30.80% and maximum value of 53.73% with a mean of 44.56%. The line RIL-18 (53.73%) showed maximum value, which was followed by RIL-26 (52.33%), RIL-21(51.67%) and RIL-64 (51.13%). The lowest harvest index was recorded in GJG-32 (30.80%) followed by RIL-2 (34.46%) and RIL-33 (34.83%).

The mean oil content was 50.58% exhibiting minimum value of 40.23% and a maximum value of 53.12%. The maximum value was observed in RIL-4 (53.12%), followed by RIL-37 (52.64%), RIL-2 (52.62%), ICGV-05155 (52.36%) and RIL-58 (52.36%), while minimum value was recorded in RIL-13 (40.23%) followed by RIL-39 (47.57%).

**4.2.2 Phenotypic coefficient of variation**

Phenotypic coefficients of variation for all the characters are given in Table 4.2. High phenotypic coefficient of variation was observed for number of immature pods per plant (31.53%). The plant height (9.90%), days to 50% flowering (8.73%), SCMR (6.76%), shelling out-turn (4.76%), sound mature kernels (3.67%), days to maturity (3.22%) and oil content (2.56%) had low phenotypic coefficient of variation. The biological yield per plant (18.31%), number of mature pods per plant (17.77%), 100-kernel weight (14.71%), kernel yield per plant (13.84%), pod yield per plant (12.45%) and harvest index (10.36%) exhibited moderate values for phenotypic coefficient of variation.

**4.2.3 Genotypic coefficient of variation**

Genotypic coefficients of variation for different characters are also presented in Table 4.2. High genotypic coefficient of variation was observed for number of immature pods per plant (30.66%). The biological yield per plant (16.91%), number of

**Table 4.2. Phenotypic and genotypic coefficients of variation, heritability and genetic advance for various characters in groundnut**

| Characters | Range of variation | Mean | Phenotypic coefficient of variation (%) | Genotypic coefficient of variation (%) | Heritability in broad sense | Genetic advance | Genetic advance expressed as percentage of mean |
|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | 22.00 – 29.67 | 25.50 | 08.73 | 08.16 | 87.19 | 04.00 | 15.69 |
| **Days to maturity** | 107.33-120.33 | 114.26 | 03.22 | 03.16 | 96.14 | 07.30 | 06.38 |
| **Plant height (cm)** | 19.53-30.46 | 23.74 | 9.90 | 8.57 | 74.93 | 03.62 | 15.28 |
| **SCMR** | 28.33-41.56 | 34.76 | 06.76 | 05.53 | 66.96 | 03.24 | 09.33 |
| **Number of mature pods per plant** | 8.93-22.13 | 12.53 | 17.77 | 16.61 | 87.36 | 04.00 | 31.98 |
| **Number of immature pods per plant** | 1.26-4.86 | 2.58 | 31.53 | 30.66 | 94.73 | 01.58 | 61.47 |
| **Shelling out-turn (%)** | 62.04-78.08 | 68.51 | 04.76 | 03.89 | 66.85 | 04.49 | 06.56 |
| **100-kernel weight (g)** | 33.33-58.67 | 44.40 | 14.71 | 13.69 | 86.53 | 11.64 | 26.23 |
| **Sound mature kernels (%)** | 80.67-96.67 | 89.67 | 03.67 | 03.09 | 71.07 | 04.82 | 05.38 |
| **Kernel yield per plant (g)** | 8.56-17.56 | 12.69 | 13.84 | 12.06 | 75.91 | 02.74 | 21.65 |
| **Biological yield per plant (g)** | 29.13-79.16 | 42.19 | 18.31 | 16.91 | 85.28 | 13.57 | 32.17 |
| **Pod yield per plant (g)** | 13.20-24.40 | 18.51 | 12.45 | 10.73 | 74.24 | 03.52 | 19.04 |
| **Harvest index (%)** | 30.80-53.73 | 44.56 | 10.36 | 09.47 | 83.58 | 07.95 | 17.84 |
| **Oil content (%)** | 47.58-53.12 | 50.58 | 02.56 | 02.25 | 77.28 | 02.06 | 04.09 |

mature pods per plant (16.61%), 100-kernel weight (13.69%), kernel yield per plant (12.06%) and pod yield per plant (10.73%) had moderate values, while harvest index (9.47%), plant height (8.57%), days to 50% flowering (8.16%), SCMR (5.53%), shelling out-turn (3.89%), days to maturity (3.16%), sound mature kernelS (3.09%) and oil content (2.25%) exhibited very low genotypic coefficient of variation.

**4.2.4 Heritability**

The broad sense heritability estimates for different characters are given in Table 4.2. High heritability estimates were observed for all the characters under study *viz.*, days to maturity (96.14%), number of immature pods per plant (94.73%), number of mature pods per plant (87.36%), days to 50% flowering (87.19%), 100-kernel weight (86.53%), biological yield per plant (85.28%), harvest index (83.58%), oil content (77.28%), kernel yield per plant (75.91%), plant height (74.93%), pod yield per plant (74.24%), sound mature kernels (71.07%), SCMR (66.96%) and shelling out-turn (66.85%).

**4.2.5 Genetic advance**

Genetic advance at 5% selection intensity (k=2.06) was estimated for different characters (Table 4.2). High genetic advance was observed for biological yield per plant (13.57), 100-kernel weight (11.64), harvest index (7.95) and days to maturity (7.30). The values were moderate for sound mature kernels (4.82), shelling out-turn (4.49), days to 50% flowering, number of mature pods per plant (4.00), plant height (3.62), pods yield per plant (3.52) and SCMR (3.24). Low values of genetic advance were observed for kernel yield per plant (2.74), oil content (2.06) and number of immature pods per plant (1.58).

**4.2.6 Genetic advance expressed as percentage of mean**

The estimates of genetic advance expressed as percentage of mean (Table 4.2) were found high for number immature pods per plant (61.47%), biological yield per plant (32.17%), number of mature pods per plant (31.98%), 100-kernel weight (26.23%) and kernel yield per plant (21.65%). The values were moderate for pod yield per plant (19.04%), harvest index (17.84%), days to 50% flowering (15.69%) and plant height (15.28%). The values were low for SCMR (9.33%), shelling out-turn (6.56%), days to maturity (6.38%), sound mature kernels (5.38%) and oil content (4.09%).

## 4.3 CORRELATION COEFFICIENTS

The correlation coefficients were worked-out among 14 characters to find out association of pod yield per plant with its components as well as association among yield components at genotypic ($r_g$) and phenotypic ($r_p$) levels. The data given in Table 4.3 revealed that, in general the genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlations. The results on correlation coefficients between different pairs of characters are presented below:

### 4.3.1 Pod yield per plant

The pod yield per plant had significant and positive correlation both at genotypic and phenotypic levels with days to 50% flowering ($r_g$=0.4460, $r_p$=0.3347), days to maturity ($r_g$=0.5451, $r_p$=0.4635), number of mature pods per plant ($r_g$=0.5568, $r_p$=0.5803), kernel yield per plant ($r_g$=0.9521, $r_p$=0.9419) and biological yield per plant ($r_g$=0.7362, $r_p$=0.7387), while with SCMR (0.2630) at genotypic level only.

### 4.3.2 Days to 50% flowering

The days to 50% flowering had positive and significant correlation both at genotypic and phenotypic levels with days to maturity ($r_g$=0.4362, $r_p$=0.4000), number of mature pods per plant ($r_g$=0.3680, $r_p$=0.3125), kernel yield per plant ($r_g$=0.4460, $r_p$=0.3362) and biological yield per plant ($r_g$=0.5011, $r_p$=0.4117). Days to 50% flowering had negative significant correlation at genotypic and phenotypic levels ($r_g$=-0.3069, $r_p$=-2584) with harvest index.

### 4.3.3 Days to maturity

The days to maturity had positive and significant association with SCMR ($r_g$=0.3060, $r_p$=0.2419), number of mature pods per plant ($r_g$=0.3710, $r_p$=0.3426), kernel yield per plant ($r_g$=0.4860, $r_p$=0.4144), biological yield per plant ($r_g$=0.4938, $r_p$=0.4536) and oil content ($r_g$=0.3575, $r_p$=0.3122) at both genotypic and phenotypic levels.

### 4.3.4 Plant height

The plant height was positively and significantly associated at both genotypic and phenotypic levels with 100-kernel weight ($r_g$=0.4118, $r_p$=0.3400) and sound mature kernels ($r_g$=0.4425, $r_p$=0.2956). Plant height showed significant and negative correlation with SCMR ($r_g$=-0.3335, $r_p$=-0.2659) and number of immature pods per plant ($r_g$=-0.3003, $r_p$=-0.2588) at both genotypic and phenotypic levels whereas, with number of mature pods per plant ($r_g$=-0.3137) at genotypic level only.

**Table 4.3. Genotypic ($r_g$) and phenotypic ($r_p$) correlation coefficients among 14 characters in groundnut**

| Characters | | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling percentage (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Pod yield per plant (g)** | $r_g$ | 0.4460** | 0.5451** | 0.1256 | 0.2630* | 0.5568** | 0.1897 | 0.1817 | 0.0603 | -0.0256 | 0.9521** | 0.7362** | -0.0171 | 0.0170 |
| | $r_p$ | 0.3347** | 0.4635** | 0.1261 | 0.1958 | 0.5803** | 0.1666 | 0.1126 | 0.0770 | -0.0443 | 0.9419** | 0.7387** | 0.0148 | 0.0338 |
| **Days to 50% flowering** | $r_g$ | | 0.4362** | -0.0868 | 0.1570 | 0.3680** | 0.0562 | 0.1391 | -0.2256 | -0.2259 | 0.4460** | 0.5011** | -0.3069** | 0.1160 |
| | $r_p$ | | 0.4000** | -0.1131 | 0.1088 | 0.3125* | 0.0645 | 0.0978 | -0.1823 | -0.1692 | 0.3362** | 0.4117** | -0.2584* | 0.0821 |
| **Days to maturity** | $r_g$ | | | 0.0049 | 0.3060** | 0.3710** | 0.2376 | -0.0011 | -0.0998 | -0.0399 | 0.4860** | 0.4938** | -0.2141 | 0.3575** |
| | $r_p$ | | | -0.0117 | 0.2419* | 0.3426** | 0.2299 | -0.0083 | -0.0924 | -0.0354 | 0.4144** | 0.4536** | -0.1980 | 0.3122* |
| **Plant height (cm)** | $r_g$ | | | | -0.3335** | -0.3137** | -0.3003* | -0.1778 | 0.4118** | 0.4425** | 0.0497 | 0.0499 | 0.0184 | -0.0736 |
| | $r_p$ | | | | -0.2659* | -0.2314 | -0.2588* | -0.0779 | 0.3400** | 0.2956* | 0.0864 | 0.0697 | 0.0054 | -0.0606 |
| **SCMR** | $r_g$ | | | | | 0.2196 | 0.3733** | -0.0258 | -0.2827* | -0.3527** | 0.2288 | 0.1520 | 0.0576 | 0.2846* |
| | $r_p$ | | | | | 0.1629 | 0.2957* | -0.0147 | -0.1915 | -0.2473* | 0.1741 | 0.1212 | 0.0512 | 0.2084 |
| **No. of mature pods per plant** | $r_g$ | | | | | | 0.5321** | 0.1731 | -0.6196** | -0.1636 | 0.5607** | 0.5001** | -0.0698 | 0.2076 |
| | $r_p$ | | | | | | 0.4900** | 0.1551 | -0.5361** | -0.1699 | 0.5831** | 0.5098** | -0.0424 | 0.1656 |
| **No. of immature pods per plant** | $r_g$ | | | | | | | 0.0762 | -0.3560** | -0.2720* | 0.2048 | 0.2679* | -0.2025 | 0.2035 |
| | $r_p$ | | | | | | | 0.0541 | -0.3233** | -0.2393 | 0.1775 | 0.2513* | -0.1936 | 0.1848 |
| **Shelling percentage (%)** | $r_g$ | | | | | | | | -0.0814 | 0.0169 | 0.4717** | 0.0368 | 0.2030 | -0.0764 |
| | $r_p$ | | | | | | | | -0.0403 | 0.0069 | 0.4364** | 0.0028 | 0.1738 | -0.0912 |
| **100-kernel weight (g)** | $r_g$ | | | | | | | | | 0.0968 | 0.0267 | 0.1110 | -0.1284 | -0.2917* |
| | $r_p$ | | | | | | | | | 0.1273 | 0.0556 | 0.0897 | -0.0701 | -0.2429* |
| **Sound mature kernels (%)** | $r_g$ | | | | | | | | | | -0.0150 | -0.0723 | 0.0835 | -0.0317 |
| | $r_p$ | | | | | | | | | | -0.0351 | -0.0912 | 0.0917 | -0.0216 |
| **Kernel yield per plant (g)** | $r_g$ | | | | | | | | | | | 0.6815** | 0.0313 | -0.0119 |
| | $r_p$ | | | | | | | | | | | 0.6772** | 0.0592 | -0.0044 |
| **Biological yield per plant(g)** | $r_g$ | | | | | | | | | | | | -0.6757** | 0.0766 |
| | $r_p$ | | | | | | | | | | | | -0.6427** | 0.0781 |
| **Harvest index (%)** | $r_g$ | | | | | | | | | | | | | -0.0765 |
| | $r_p$ | | | | | | | | | | | | | -0.0651 |

***, ** Significant at 5 % and 1% levels, respectively**

### 4.3.5 SCMR

The SCMR was significantly and positively correlated with number of immature pods per plant ($r_g$ =0.3733, $r_p$=0.2957) at genotypic and phenotypic levels and with oil content ($r_g$=0.2846) at genotypic level. The SCMR had significant and negative correlation at both levels with sound mature kernels ($r_g$ =-0.3527, $r_p$ =-0.2473), while it's association was found significant and negative with 100-kernel weight ($r_g$ =-0.2827) at genotypic level only.

### 4.3.6 Number of mature pods per plant

Number of mature pods per plant exhibited significant and positive correlation with number of immature pods per plant ($r_g$=0.5321, $r_p$=0.4900), kernel yield per plant ($r_g$=0.5607, $r_p$=5831) and biological yield per plant ($r_g$=0.5001, $r_p$=0.5098) at both genotypic and phenotypic levels. This character showed negative and significant correlation both at genotypic and phenotypic levels with 100-kernel weight ($r_g$=-0.6196, $r_p$=-5361).

### 4.3.7 Number of immature pods per plant

Number of immature pods per plant exhibited significant and positive correlation with biological yield per plant ($r_g$=0.2679, $r_p$=0.2513) at both genotypic and phenotypic levels. Number of immature pods per plant showed negative and significant correlation with 100-kernel weight ($r_g$=-0.3560, $r_p$=-3233) both at genotypic and phenotypic levels and with sound mature kernels ($r_g$=-0.2720) at genotypic level only.

### 4.3.8 Shelling out turn

The shelling out-turn had significant and positive correlation at genotypic and phenotypic levels with kernel yield per plant ($r_g$ =0.4717, $r_p$ =0.4364).

### 4.3.9 100-kernel weight

The 100-kernel weight displayed negative and significant association with oil content ($r_g$ =-0.2917, $r_p$ =-0.2429) at both genotypic and phenotypic levels.

### 4.3.10 Sound mature kernels

No significant association was observed between sound mature kernels and kernel yield per plant, biological yield per plant, harvest index and oil content.

### 4.3.11 Kernel yield per plant

The kernel yield per plant had significant and positive association with biological yield per plant ($r_g$=0.6815, $r_p$=6772) at both genotypic and phenotypic levels.

### 4.3.12 Biological yield per plant

The biological yield per plant was significantly and negatively correlated both at genotypic and phenotypic levels with harvest index ($r_g$ =-0.6757, $r_p$ =-0.6427).

### 4.3.13 harvest index

The harvest index had non-significant and negative correlation with oil content ($r_g$=-0.0765, $r_p$=-0.0651) at genotypic and phenotypic level.

## 4.4 PATH COEFFICIENT ANALYSIS

The phenotypic correlation coefficients calculated for different pairs of character were subjected to path coefficient analysis for partitioning these values into the direct and indirect effects. The results obtained for direct and indirect effects of different characters on pod yield per plant are presented in Table 4.4

### 4.4.1. Days to 50% flowering vs pod yield per plant

The phenotypic correlation between days to 50% flowering and pod yield per plant was significant and positive ($r_p$=0.3347), while its direct effect was positive and low in magnitude (0.0024). The days to 50% flowering exhibited very high and positive indirect effect *via* kernel yield per plant (0.3451). This trait exhibited moderate and positive indirect effect *via* biological yield per plant (0.0449) and low effect *via* days to maturity (0,0044). It showed negative and moderate indirect effect *via* shelling out-turn (-0.0339) and harvest index (-0.0224).

### 4.4.2 Days to maturity vs pod yield per plant

Days to maturity exhibited positive and significant phenotypic correlation with pod yield per plant ($r_p$=0.4635). This character exerted positive and moderate direct effect (0.0109) on pod yield per plant but, it exhibited positive and very high indirect effect *via* kernel yield per plant (0.4255) and moderate effect *via* biological yield per plant (0.0494). The days to maturity exhibited negative and moderate indirect effect *via* harvest index (-0.0172) and number of mature pods per plant (-0.0092).

### 4.4.3 Plant height vs pod yield per plant

The correlation coefficient between pod yield per plant and plant height was positive and non-significant ($r_p$=0.1261) and its direct effect was also found to be positive but negligible (0.0004) in magnitude. This character exhibited positive and moderate indirect effect *via* kernel yield per plant (0.0887) and shelling out-turn (0.0270), while low indirect effect *via* biological yield per plant (0.0076) and number of mature pods

per plant (0.0062). Plant height exhibited negative and low indirect effect through 100-kernel weight (-0.0036) and sound mature kernels (-0.0026).

**4.4.4 SCMR vs pod yield per plant**

The SCMR had non-significant and positive correlation with pod yield per plant ($r_p$=0.1958) and also manifested negative and low direct effect (-0.0088). This character exhibited positive and high indirect effect *via* kernel yield per plant (0.1787), moderate indirect effect through biological yield per plant (0.0132) and low *via* shelling out-turn (0.0051), harvest index (0.0044) and days to maturity (0.0026).

**4.4.5 Number of mature pods per plant vs pod yield per plant**

The number of mature pods per plant had significant and positive correlation with pod yield per plant ($r_p$=0.5803) and its direct effect was negative and moderate in magnitude (-0.0269). Its negative contribution was also *via* shelling out-turn (-0.0538). This character contributed towards pod yield per plant mainly through positive and very high indirect effect *via* kernel yield per plant (0.5986), moderate indirect effect *via* biological yield per plant (0.0556) and low effect *via* 100-kernel weight (0.0057) and days to maturity (0.0037).

**4.4.6 Number of immature pods per plant vs pod yield per plant**

The correlation coefficient between pod yield per plant and number of immature pods per plant was non-significant and positive ($r_p$=0.1666). Its direct effect on pod yield per plant was found negative and negligible in magnitude (-0.0005). The harvest index (-0.0168), shelling out-turn (-0.0188) and number of mature pods per plant (-0.0132) also exhibited moderate and negative indirect effect on pod yield per plant. This trait contributed through positive and high indirect effect *via* kernel yield per plant (0.1822), moderate effect *via* biological yield per plant (0.0274) and low effect *via* 100-kernel weight (0.0035) and days to maturity (0.0025).

**4.4.7 Shelling out turn vs pod yield per plant**

The shelling out-turn exhibited non-significant and positive phenotypic association with pod yield ($r_p$=0.1126) but, exerted negative and very high direct effect (-0.3469) on pod yield per plant. This trait contributed towards pod yield per plant indirectly through positive and very high indirect effect by kernel yield per plant (0.4480) and moderate and positive indirect effect through harvest index (0.0151).

**Table 4.4. Phenotypic path coefficient analysis showing direct(diagonal) and indirect effects of different characters on pod yield per plant in groundnut**

| Characters | Days to 50 % flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling percentage (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Harvest Index (%) | Oil content (%) | phenotypic correlation with pod yield/plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50 % flowering** | **0.0024** | 0.0044 | 0.0000 | -0.0010 | -0.0084 | 0.0000 | -0.0339 | 0.0020 | 0.0015 | 0.3451 | 0.0449 | -0.0224 | 0.0003 | 0.3347** |
| **Days to maturity** | 0.0009 | **0.0109** | 0.0000 | -0.0021 | -0.0092 | -0.0001 | 0.0029 | 0.0010 | 0.0003 | 0.4255 | 0.0494 | -0.0172 | 0.0012 | 0.4635** |
| **Plant height (cm)** | -0.0003 | -0.0001 | **0.0004** | 0.0024 | 0.0062 | 0.0001 | 0.0270 | -0.0036 | -0.0026 | 0.0887 | 0.0076 | 0.0005 | -0.0002 | 0.1261 |
| **SCMR** | 0.0003 | 0.0026 | -0.0001 | **-0.0088** | -0.0044 | -0.0001 | 0.0051 | 0.0021 | 0.0021 | 0.1787 | 0.0132 | 0.0044 | 0.0008 | 0.1958 |
| **No. of mature pods per plant** | 0.0007 | 0.0037 | -0.0001 | -0.0014 | **-0.0269** | -0.0002 | -0.0538 | 0.0057 | 0.0015 | 0.5986 | 0.0556 | -0.0037 | 0.0006 | 0.5803** |
| **No. of immature pods per plant** | 0.0002 | 0.0025 | -0.0001 | -0.0026 | -0.0132 | **-0.0005** | -0.0188 | 0.0035 | 0.0021 | 0.1822 | 0.0274 | -0.0168 | 0.0007 | 0.1666 |
| **Shelling percentage (%)** | 0.0002 | -0.0001 | 0.0000 | 0.0001 | -0.0042 | 0.0000 | **-0.3469** | 0.0004 | -0.0001 | 0.4480 | 0.0003 | 0.0151 | -0.0003 | 0.1126 |
| **100-kernel weight (g)** | -0.0004 | -0.0010 | 0.0001 | 0.0017 | 0.0144 | 0.0002 | 0.0140 | **-0.0107** | -0.0011 | 0.0571 | 0.0098 | -0.0061 | -0.0009 | 0.0770 |
| **Sound mature kernels (%)** | -0.0004 | -0.0004 | 0.0001 | 0.0022 | 0.0046 | 0.0001 | -0.0024 | -0.0014 | **-0.0086** | -0.0361 | -0.0099 | 0.0079 | -0.0001 | -0.0443 |
| **Kernel yield per plant (g)** | 0.0008 | 0.0045 | 0.0000 | -0.0015 | -0.0157 | -0.0001 | -0.1514 | -0.0006 | 0.0003 | **1.0266** | 0.0738 | 0.0051 | 0.0000 | 0.9419** |
| **Biological yield per plant (g)** | 0.0010 | 0.0049 | 0.0000 | -0.0011 | -0.0137 | -0.0001 | -0.0010 | -0.0010 | 0.0008 | 0.6952 | **0.1090** | -0.0557 | 0.0003 | 0.7387** |
| **Harvest Index (%)** | -0.0006 | -0.0022 | 0.0000 | -0.0005 | 0.0011 | 0.0001 | -0.0603 | 0.0008 | -0.0008 | 0.0608 | -0.0701 | **0.0867** | -0.0002 | 0.0148 |
| **Oil content (%)** | 0.0002 | 0.0034 | 0.0000 | -0.0018 | -0.0045 | -0.0001 | 0.0316 | 0.0026 | 0.0002 | -0.0045 | 0.0085 | -0.0056 | **0.0038** | 0.0338 |

***, ** significant at 5% and 1% levels, respectively**

**Residual effect, R= 0.046**

**4.4.8 100-kernel weight vs pod yield per plant**

At phenotypic level, 100-kernel weight had non-significant and positive association with pod yield per plant ($r_p$=0.0770), while its direct effect was negative and moderate in magnitude (-0.0107). This trait had also negative contribution *via* harvest index (-0.0061). Its indirect effect was moderate towards pod yield per plant through kernel yield per plant (0.0571), shelling out-turn (0.0140), number of mature pods per plant (0.0144) and biological yield per plant (0.0098) in positive direction.

**4.4.9 Sound mature kernels vs pod yield per plant**

The correlation value of sound mature kernels was observed non-significant and negative with pod yield per plant ($r_p$=-0.0443) and its direct effect was also negative and low in magnitude (-0.0086). Its negative contribution was also from kernel yield per plant (-0.0361), biological yield per plant (-0.0099) and shelling out-turn (-0.0024). This trait exhibited positive and low indirect effect through harvest index (0.0079), number of mature pods per plant (0.0046) and SCMR (0.0022) towards pod yield per plant.

**4.4.10 kernel yield per plant vs pod yield per plant**

At phenotypic level, kernel yield per plant had highly significant and positive association with pod yield per plant ($r_p$=0.9419) and its direct effect was also found positive and very high in magnitude (1.0266). Its positive contribution towards pod yield per plant was also through biological yield per plant (0.0738), harvest index (0.0051) and days to maturity (0.0045). However, its indirect contribution toward pod yield per plant was negative and high through shelling out-turn (-0.1514) and moderate *via* number of mature pods per plant (-0.0157).

**4.4.11 Biological yield per plant vs pod yield per plant**

The phenotypic correlation between biological yield per plant and pod yield per plant was positive and highly significant ($r_p$=0.7387) and also showed high and positive (0.1090) direct effect on pod yield per plant. This trait also exhibited positive and very high indirect effect *via* kernel yield per plant (0.6952) and low effect *via* days to maturity (0.0049). This trait however, had negative contribution through moderate indirect effect from harvest index (-0.0557) and number of mature pods per plant (-0.0137).

**4.4.12 Harvest index vs pod yield per plant**

The harvest index had non-significant and positive correlation with pod yield per plant ($r_p$=0.0148) and also displayed positive and moderate direct effect (0.0867)

on pod yield per plant. This trait also exhibited moderate and positive indirect effect *via* kernel yield per plant (0.0608). Harvest index displayed negative and moderate indirect effect *via* biological yield per plant (-0.0701) and shelling out-turn (-0.0603), while low effect *via* days to maturity (-0.0022).

**4.4.13 Oil content vs pod yield per plant**

The oil content had non-significant and positive correlation with pod yield per plant ($r_p$=0.0338) and its direct effect was also found positive and low in magnitude (0.0038). This trait exhibited positive and moderate indirect effect *via* shelling out-turn (0.0316) and low effect *via* biological yield per plant (0.0085), days to maturity (0.0034) and 100-kernel weight (0.0026). Its indirect contribution was negative through kernel yield per plant (-0.0045) and number of mature pods per plant (-0.0045).

## 4.5 SELECTION INDICES

For the construction of selection indices, the characters, which had desirable correlation as well as moderate to high direct effect on pod yield per plant, were considered. In this context, the pod yield per plant (X1) along with its five components *viz*., days to 50% flowering (X2), days to maturity (X3), number of mature pods per plant (X4), kernel yield per plant (X5) and biological yield per plant (X6) were identified and considered for the construction of selection indices.

Sixty-three selection indices were constructed in all possible combinations of the five yield contributing characters and pod yield per plant. Their respective genetic advances were calculated and relative efficiency of different discriminant functions in relation to the straight selection for pod yield was compared. The data on selection indices, discriminant functions, genetic gain and relative efficiency are given in Table 4.5, assuming the efficiency of straight selection for pod yield as 100%.

The results suggested that the selection efficiency was higher, in general, over straight selection when the selection was based on component character, which further increased with the inclusion of two or more characters. The highest efficiency was noted when five or six characters were considered together.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of 178.21% was exhibited by number of mature pods per plant followed by days to 50% flowering (145.18%), biological yield per plant (90.59%), days to maturity (65.64%) and kernel yield per plant (36.37%).

**Table 4.5. Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in groundnut**

| Sr. No. | Selection index | Discriminant function | Expected genetic advance | Relative efficiency (%) |
|---|---|---|---|---|
| | (1) | (2) | (3) | (4) |
| **1** | X1 Pod yield per plant | 0.945X1 | 6.98 | 100.00 |
| **2** | X2 Days to 50% flowering | 0.946X2 | 10.13 | 145.18 |
| **3** | X3 Days to maturity | 0.980X3 | 4.58 | 65.64 |
| **4** | X4 No. of mature pods/plant | 0.959X4 | 12.43 | 178.21 |
| **5** | X5 Kernel yield per plant | 0.737X5 | 2.54 | 36.37 |
| **6** | X6 Biological yield per plant | 0.990X6 | 6.32 | 90.59 |
| **7** | X1.X2 | 0.774X1 + 0.975X2 | 6.68 | 95.91 |
| **8** | X1.X3 | 0.704X1 + 1.045X3 | 9.94 | 142.49 |
| **9** | X1.X4 | 0.642X1 + 0.952X4 | 6.62 | 94.90 |
| **10** | X1.X5 | 0.612X1 + 0.941X5 | 6.22 | 89.16 |
| **11** | X1.X6 | 0.356X1 + 0.949X6 | 16.40 | 235.07 |
| **12** | X2.X3 | 0.877X2 + 0.991X3 | 9.85 | 141.23 |
| **13** | X2.X4 | 0.908X2 + 0.911X4 | 6.77 | 96.97 |
| **14** | X2.X5 | 0.941 X2 +0.818X5 | 6.01 | 86.08 |
| **15** | X2.X6 | 1.174X2 + 0.838X6 | 16.32 | 233.91 |
| **16** | X3.X4 | 1.982 X3 +0.859X4 | 9.55 | 136.91 |
| **17** | X3.X5 | 1.000X3 + 0.468X5 | 8.44 | 121.00 |
| **18** | X3.X6 | 1.114X3 + 0.825X6 | 18.57 | 266.23 |
| **19** | X4.X5 | 0.937X4 + 0.645X5 | 5.97 | 85.58 |
| **20** | X4.X6 | 0.868X4 + 0.850X6 | 15.93 | 228.35 |
| **21** | X5.X6 | 0.480X5 + 0.904X6 | 15.62 | 223.83 |
| **22** | X1.X2.X3 | 0.743X1 + 0.955X2 + 1.045X3 | 12.60 | 180.61 |
| **23** | X1.X2.X4 | 0.660X1 + 1.043X2 + 0.936X4 | 9.48 | 135.82 |
| **24** | X1.X2.X5 | 0.593X1 + 1.067X2 + 0.969X5 | 9.15 | 131.12 |
| **25** | X1.X2.X6 | 0.356X1 + 1.307X2 + 0.919X6 | 19.19 | 275.09 |
| **26** | X1.X3.X4 | 0.578X1 + 1.094X3 + 0.932X4 | 12.41 | 177.94 |
| **27** | X1.X3.X5 | 0.446X1 + 1.110X3 + 1.051X5 | 12.18 | 174.63 |
| **28** | X1.X3.X6 | 0.253X1 + 1.242X3 + 0.916X6 | 21.55 | 308.94 |
| **29** | X1.X4.X5 | 0.513X1 + 0.962X4 + 0.932X5 | 9.06 | 129.83 |
| **30** | X1.X4.X6 | 0.188X1 + 1.024X4 + 0.960X6 | 18.84 | 269.98 |
| **31** | X1.X5.X6 | -0.245X1 + 1.513X5 + 0.973X6 | 18.65 | 267.31 |
| **32** | X2.X3.X4 | 0.908X2 + 1.001X3 + 0.906X4 | 12.26 | 175.74 |
| **33** | X2.X3.X5 | 0.932X2 + 1.015X3 + 0.810X5 | 11.83 | 169.58 |
| **34** | X2.X3.X6 | 1.142X2 + 1.084X3 + 0.821X6 | 21.32 | 305.57 |
| **35** | X2.X4.X5 | 1.009X2 + 0.925X4 + 0.684X5 | 8.82 | 126.49 |
| **36** | X2.X4.X6 | 1.234X2 + 0.832X4 + 0.832X6 | 16.71 | 268.19 |
| **37** | X2.X5.X6 | 2.247X2 + 4.072X5 + -0.470X6 | 18.41 | 235.16 |
| **38** | X3.X4.X5 | 1.053X3 + 0.916X4 + 0.616X5 | 11.64 | 166.77 |
| **39** | X3.X4.X6 | 1.154X3 + 0.831X4 + 0.819X6 | 20.94 | 300.12 |

| | | | | |
|---|---|---|---|---|
| **40** | X3.X5.X6 | 1.187X3 + 0.422X5 + 0.869X6 | 20.69 | 296.61 |
| **41** | X4.X5.X6 | 0.976X4 + 0.321X5 + 0.909X6 | 18.05 | 258.72 |
| **42** | X1.X2.X3.X4 | 0.611X1 + 1.007X2 + 1.084X3 + 0.925X4 | 15.09 | 216.30 |
| **43** | X1.X2.X3.X5 | 0.448X1 +1.021X2 + 1.098X3 + 1.085X5 | 14.87 | 213.13 |
| **44** | X1.X2.X3.X6 | 0.277X1 + 0.996X2 + 1.233X3 + 0.919X6 | 24.21 | 347.00 |
| **45** | X1.X2.X4.X5 | 0.492X1 + 1.136X2 + 0.928X4 + 0.957X5 | 11.88 | 170.24 |
| **46** | X1.X2.X4.X6 | 0.209X1 + 1.366X2 + 0.965X4 + 0.927X6 | 21.65 | 310.28 |
| **47** | X1.X2.X5.X6 | -0.196X1 + 1.379X2 + 1.440X5 + 0.935X6 | 21.47 | 307.71 |
| **48** | X1.X3.X4.X5 | 0.306X1 + 1.160X3 + 0.923X4 + 1.078X5 | 14.69 | 210.62 |
| **49** | X1.X3.X4.X6 | 0.082X1 + 1.286X3 + 0.984X4 + 0.924X6 | 23.98 | 343.67 |
| **50** | X1.X3.X5.X6 | -0.501X1 + 1.310X3 + 1.677X5 + 0.934X6 | 23.83 | 341.61 |
| **51** | X1.X4.X5.X6 | -0.391X1 + 0.998X4 + 1.498X5 + 0.986X6 | 21.11 | 302.57 |
| **52** | X2.X3.X4.X5 | 0.986X2 + 1.048X3 + 0.909X4 + 0.666X5 | 14.33 | 205.42 |
| **53** | X2.X3.X4.X6 | 1.201X2 + 1.115X3 + 0.811X4 + 0.812X6 | 23.71 | 339.81 |
| **54** | X2.X3.X5.X6 | 1.223X2 + 1.142X3 + 0.441X5 + 0.855X6 | 23.47 | 336.38 |
| **55** | X2.X4.X5.X6 | 1.344X2 + 0.922X4 + 0.335X5 + 0.880X6 | 20.87 | 299.18 |
| **56** | X3.X4.X5.X6 | 1.227X3 + 0.933X4 + 0.270X5 + 0.871X6 | 23.12 | 331.35 |
| **57** | X1.X2.X3.X4.X5 | 0.313X1 + 1.074X2 + 1.138X3 + 0.905X4 + 1.104X6 | 17.39 | 249.25 |
| **58** | X1.X2.X3.X4.X6 | 0.162X1 + 1.286X2 + 1.236X3 + 0.950X4+ 0.887X6 | 26.71 | 382.86 |
| **59** | X1.X2.X3.X5.X6 | -0.431X1 + 1.274X2 + 1.255X3 + 1.619X5 + 0.913X6 | 26.60 | 381.22 |
| **60** | X1.X2.X4.X5.X6 | 1.045X1 + 1.483X2 + 1.018X4 + -0.469X5 + -0.917X6 | 23.86 | 342.03 |
| **61** | X1.X3.X4.X5.X6 | -0.672X1 + 1.356X3 + 0.939X4 + 1.704X5 + 0.944X6 | 26.28 | 376.68 |
| **62** | X2.X3.X4.X5.X6 | 1.278X2 + 1.176X3 + 0.896X4 + 0.305X5 + 0.855X6 | 25.91 | 371.32 |
| **63** | X1.X2.X3.X4.X5.X6 | -0.585X1 + 1.324X2 + 1.294X3 + 0.897X4 + 1.647X5 + 0.921X6 | 29.06 | 416.46 |

Among the combinations involving two component characters, days to maturity and biological yield per plant (X3.X6) exhibited maximum relative efficiency of 266.23% followed by pod yield per plant and biological yield per plant (X1.X6), days to 50% flowering and biological yield per plant (X2.X6), number of mature pods per plant and biological yield per plant (X4.X6), kernel yield per plant and biological yield per plant (X5.X6), pod yield per plant and days to maturity (X1.X3) and days to 50% flowering and days to maturity (X2.X3) having relative efficiency of 235.07, 233.91, 228.35, 223.83, 142.49 and 141.23 %, respectively.

The selection index based on three character combinations indicated that a discriminant function with pod yield per plant, days to maturity and biological yield per plant (X1.X3.X6) possessed maximum relative efficiency of 308.94% followed by days to 50% flowering, days to maturity and biological yield per plant (X2.X3.X6) Similarly, days to maturity, number of mature pods per plant and biological yield per plant (X3.X4.X6); days to maturity, kernel yield per plant and biological yield per plant (X3.X5.X6); pod yield per plant, days to 50% flowering and biological yield per plant (X1.X2.X6); pod yield per plant, number of mature pods plant and biological yield per plant (X1.X4.X6); days to 50% flowering, number of mature pods per plant and biological yield per plant (X2.X4.X6); pod yield per plant, kernel yield per plant and biological yield per plant (X1.X5.X6), number of mature pods per plant kernel yield per plant and biological yield per plant (X4.X5.X6) and days to 50% flowering, kernel yield per plant and biological yield per plant (X2.X5.X6) exhibited high relative efficiency of 305.57, 300.12, 296.61, 275.09, 269.98, 268.19, 267.31, 258.72 and 235.16 respectively in respect of three component combinations.

In four character selection index, a function involving pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) exerted maximum relative efficiency of 347.00% followed by pod yield per plant, days to maturity, number of mature pods per plant and biological yield per plant (X1.X3.X4.X6); pod yield per plant, days to maturity, kernel yield per plant and biological yield per plant (X1.X3.X5.X6); days to 50% flowering, days to maturity, number of pods per plant and biological yield per plant (X2.X3.X4.X6); days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X2.X3.X5.X6); days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X3.X4.X5.X6); pod yield per plant, days to 50% flowering, number of mature pods per plant and biological yield per plant

(X1.X2.X4.X6) and pod yield per plant, days to 50% flowering, kernel yield per plant and biological yield per plant (X1.X2.X5.X6) consisting of 343.67, 341.61, 339.81, 336.38, 331.35, 310.28 and 307.71% relative efficiency, respectively.

The highest relative efficiency of 382.86% was exhibited by a selection index involving five component characters viz., pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) followed by an index consisting of pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X1.X2.X3.X5.X6); pod yield per plant, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X3.X4.X5.X6); days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X2.X3.X4.X5.X6) consisting of 381.22, 376.68 and 371.32% relative efficiency, respectively.

The selection index based on all the six characters viz., pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X2.X3.X4.X5.X6) exerted 416.46% relative efficiency.

Among all the 63 selection indices (Table 4.5), the index based on six characters viz., pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant (X1.X2.X3.X4.X5.X6) possessed the highest genetic gain and relative efficiency (29.06g and 416.46%) as compared to straight selection for pod yield per plant. Other two important index based on five characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) possessed the highest genetic gain and relative efficiency (26.71g and 382.86%), while the other possessing, pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant (X1.X2.X3.X5.X6) exerted the high genetic gain and relative efficiency of 26.60g and 381.22% respectively as compared to straight selection for pod yield per plant. Other two important selection indices identified were with the inclusion of four characters. Of these, one included pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) with genetic advance of 24.21g and 347.00% relative efficiency, while the other had pod yield per plant, days to maturity, number of mature pods per plant and biological yield per plant (X1.X3.X4.X6) showing expected

genetic gain of 23.98g and a relative efficiency of 343.67% as compared to the straight selection for pod yield. The best selection index identified for three characters combination included pod yield per plant, days to maturity and biological yield per plant (X1.X3.X6) having expected genetic gain of 21.55g and a relative efficiency of 308.94% as compared to the straight selection for pod yield per plant.

## 4.6 GENETIC DIVERGENCE

The significant mean squares due to genotypes for all the traits suggested the presence of considerable genetic variability for all the traits studied. Based upon 14 characters, the Mahalanobis's $D^2$ statistic was computed for all possible pairs of 68 genotypes in order to assess the genetic divergence present among the genotypes under the study.

### 4.6.1 Composition of clusters

Grouping of the genotypes was carried-out by following Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller $D^2$-values among themselves than those from groups belonging to different clusters. In all, 5 clusters were formed from 68 genotypes. The composition of cluster is given in Table 4.6 and diagrammatically has been represented in Figure 4.1.

The cluster I was the largest having 30 genotypes. The cluster III was the second largest which contained 19 genotypes followed by cluster IV with 13 genotypes, cluster II with 5 genotypes. The cluster V was the last and the smallest cluster having only one genotype.

### 4.6.2 Inter and intra-cluster distances

The inter and intra-cluster distance values are given in Table 4.7. The maximum inter-cluster distance (D=49.89) was found between clusters IV and V followed by that between clusters III and V (D=47.38), I and V (D=40.52), II and V (D=34.61), II and IV (D=26.66), I and II (D=18.39), II and III (D=17.65) The minimum inter-cluster distance was observed between clusters I and IV (D=10.84).

The intra-cluster distance ranged from 8.34 to 11.29, the maximum being in cluster II (11.30). The minimum intra-cluster distance was found in cluster IV (8.35). The clusters V contained single genotype and therefore, its intra-cluster distance was zero (0.00).

**Table 4.6. Grouping of 68 genotypes of groundnut in various clusters on the basis of $D^2$ statistic**

| Cluster | No. of Genotypes | Name of the genotypes |
|---|---|---|
| **I** | **30** | RIL-1, RIL-6, RIL-8, RIL-17, RIL-55, RIL-59, RIL-31, RIL-38, RIL-57, RIL-44, RIL-46, RIL-18, RIL-21, RIL-47, RIL-53, RIL-9, RIL-41, RIL-42, RIL-45, RIL-60, RIL-19, RIL-37, RIL-43, RIL-11, RIL-58, RIL-29, RIL-36, RIL-51, RIL-63 and ICGV-05155 |
| **II** | **5** | RIL-2, RIL-35, RIL-15, RIL-28 and RIL-16 |
| **III** | **19** | RIL-3, RIL-24, RIL-48, RIL-13, RIL-64, RIL-12, RIL-14, RIL-23, GJG-9, RIL-26, RIL-50, RIL-39, RIL-49, RIL-56, RIL-25, RIL-34, RIL-32, RIL-33 and RIL-61 |
| **IV** | **13** | RIL-4, RIL-54, RIL-20, RIL-7, RIL-10, RIL-62, AG-2006-6, RIL-22, RIL-27, RIL-5 RIL-52, RIL-30 and RIL-40 |
| **V** | **1** | GJG-32 |

**Table 4.7 Average inter and intra-cluster distance ($D=\sqrt{D^2}$) values in groundnut**

| | **I** | **II** | **III** | **IV** | **V** |
|---|---|---|---|---|---|
| **I** | 9.62 | 18.39 | 11.04 | 10.84 | 40.52 |
| **II** | | 11.30 | 17.65 | 26.66 | 34.61 |
| **III** | | | 10.32 | 12.53 | 47.38 |
| **IV** | | | | 8.35 | 49.89 |
| **V** | | | | | 0.0000 |

**Table 4.8. Cluster means for 14 different characters in groundnut**

| Clusters | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods per plant | No. of immature pods per plant | Shelling out-turn (%) | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield per plant (g) | Pod yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 25.83 | 115.05 | 23.32 | 35.26 | 13.60 | 2.87 | 67.88 | 41.28 | 88.54 | 13.10 | 43.67 | 19.29 | 44.51 | 50.81 |
| **II** | 27.86 | 115.86 | 25.26 | 34.33 | 11.70 | 2.26 | 69.73 | 54.66 | 88.73 | 15.04 | 54.41 | 21.62 | 40.33 | 50.09 |
| **III** | 24.15 | 113.64 | 24.91 | 34.17 | 11.34 | 2.21 | 68.33 | 50.28 | 91.22 | 12.37 | 39.79 | 18.08 | 45.97 | 50.22 |
| **IV** | 25.61 | 112.30 | 22.60 | 34.53 | 11.37 | 2.40 | 69.49 | 39.64 | 90.38 | 10.92 | 34.92 | 15.69 | 45.29 | 50.70 |
| **V** | 28.33 | 119.66 | 21.00 | 36.11 | 22.13 | 4,20 | 72.10 | 36.66 | 89.33 | 17.56 | 79.16 | 24.40 | 30.80 | 51.33 |
| **Mean** | 25.50 | 114.26 | 23.74 | 34.76 | 12.53 | 2.58 | 68.51 | 44.40 | 89.67 | 12.69 | 42.19 | 18.51 | 44.56 | 50.58 |
| **SEm ±** | 0.79 | 0.72 | 1.17 | 1.35 | 0.79 | 0.18 | 1.87 | 2.39 | 1.77 | 0.86 | 2.96 | 1.17 | 1.87 | 0.61 |
| **C.V.%** | 5.41 | 1.09 | 8.58 | 6.73 | 10.94 | 12.52 | 4.75 | 9.35 | 3.42 | 11.77 | 12.16 | 10.94 | 7.27 | 2.12 |
| **Percentage contribution of characters towards total divergence** | | | | | | | | | | | | | | |
| **Number of times appearing first** | 143 | 821 | 57 | 39 | 92 | 513 | 28 | 148 | 73 | 85 | 164 | 28 | 26 | 61 |
| **% contribution** | 6.28 | 36.04 | 2.50 | 1.71 | 4.04 | 22.52 | 1.23 | 6.50 | 3.20 | 3.73 | 7.20 | 1.23 | 1.14 | 2.68 |

### 4.6.3 Cluster means for various characters

The cluster means for 14 characters are presented in Table 4.8. The coefficient of variation (CV %) was calculated for all the attributes. The maximum coefficient of variation was recorded for number of immature pods per plant (12.52%) followed by biological yield per plant (12.16%), kernel yield per plant (11.77%), number of mature pods per plant (10.94) and pod yield per plant (10.94%). The lowest coefficient of variation was noted for days to maturity (1.09%) followed by oil content (2.12%), sound mature kernels (3.42%) and shelling out-turn (4.75%), while the days to 50% flowering (5.41%), SCMR (6.73%), harvest index (7.27%), plant height (8.58%) and 100-kernel weight (9.35%) had moderate coefficient of variation. Greater range of mean values among the clusters was recorded for different traits. The cluster V had the highest mean values for most off all characters like pod yield per plant (24.40g), kernel yield per plant (17.56g), biological yield per plant (79.16), shelling out-turn (72.10%), number of mature pods per plant (22.13), number of immature pods per plant (4.20%), days to 50% flowering (28.33), days to maturity (119.66), SCMR (36.11) and oil content (51.33%). The cluster II was good for plant height (25.26cm) and 100-kernel weight (54.66g). The cluster III was good for sound mature kernels (91.22%) and harvest index (45.97%).

The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that days to maturity (36.04%) followed by number of immature pods per plant (22.52%) and biological yield per plant (7.20%) contributed maximum towards total genetic divergence in the present study (Table 4.9). These characters accounted for more than 60.00% of total divergence in the material studied.

# CHAPTER V
# DISCUSSION

Groundnut (*Arachis hypogaea* L.) is grown over a vast area in the country as well as world and a little increase in its yield potential would make a tremendous impact on the total production. The improvement of pod yield largely depends on magnitude of genetic variability present and the extent to which pod yield determining characters are heritable. It is also important to understand the association of important characters with pod yield for effective selection in the segregating population.

To step up groundnut yield levels per unit area, there is a need to develop high yielding varieties with resistant to biotic and abiotic stresses. Information on the phenotypic and genotypic relationships of pod yield in the groundnut with its component characters and also among the characters themselves would be very useful to the breeders in developing an appropriate breeding strategy since pod yield is a complex character and is influenced by number of traits as well as the of environmental factors. Hence, selection of genotype with desirable characters would be greatly enhanced if significant correlations between pod yield and its component characters are established. In order to improve pod yield by accumulating optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various characters. The information on correlation and path coefficient provides an opportunity to know the magnitude and direction of association of yield with its direct and indirect components. Yield is a complex character influenced by the number of factors. Direct selection on the basis of yield may not be beneficial because many morphological traits affect it. Therefore, to make effective selection for higher yield, it is necessary to determine the relative efficiency of selection through discriminant function over straight selection.

Further, it is well known that the success of any breeding programme depends upon the availability of adequate genetic diversity. The major factor responsible for limited success in increasing the groundnut pod yield has been the narrow genetic base of the material available. It has been observed that genetically diverse parents show maximum heterosis and offer the maximum chances of isolating transgressive segregates. Mahalanobis's (1936) $D^2$ statistic is being used as an efficient tool in

quantitative estimation of genetic diversity and for choice of parents in hybridization programme (Sharma, 1998).

In the present study, analysis of variance revealed the presence of sufficient amount of genetic variability among the genotypes for all the 14 characters studied.

## 5.1 ANALYSIS OF VARIANCE

Analysis of variance revealed that all the characters were found to be highly significant among all the lines suggesting the existence of high genetic variability among the genotypes. This indicated that there is ample scope for selection of promising lines from the present material for pod yield and its components. These results are in accordance with those reported by Korat *et al.* (2009), Shinde *et al.* (2010), Nandini *et al.* (2011), Babariya (2012), Thirumala *et al.* (2014), Gupta *et al.* (2015a), Bhargavi *et al.* (2016), Bhargavi *et al.* (2017), Chavadhari *et al.* (2017), Mahesh *et al.* (2018). Syed *et al.* (2018), Rathod and Toprope (2018), Aparna *et al*. (2018) and Lunagariya (2018).

## 5.2 GENETIC VARIABILITY

Genetic variability is the pre-requisites for genetic improvement in a systematic breeding programme. There is more genetic potentiality in the genetically variable populations and thus the chances to achieve the desired types are increased. The estimates of genetic parameters are helpful to plant breeders to predict the performance of genotypes in the subsequent generations. So, it is necessary to spilt the phenotypic variability into heritable and non-heritable components.

The total variance in the material cannot be inferred only by the range and mean values. Therefore, it is important to estimate the actual variance for the characters to learn about the extent of variability present. The phenotypic variance indicates the amount of variance which is due to the differences in phenotypic value due to genotype, environment and interaction of genotype and environment whereas, the genotypic variance indicates the magnitude of variance arising due to differences in genotypic values.

### 5.2.1. Mean and range of variation

In this present study, wide range of variation was observed for biological yield per plant, number of mature pods per plant, SCMR, plant height, 100-kernel weight and harvest index. The range observed was of moderate magnitude for number of immature

pods per plant, selling out-turn, sound mature kernels percentage, kernel yield per plant and pod yield per plant. In case of days to 50% flowering, days to maturity and oil content a narrow range of variation was recorded.

**5.2.2 Genotypic and phenotypic coefficients of variation**

The estimates of genotypic (GCV) and phenotypic (PCV) coefficients of variability indicated that the values of PCV were higher than GCV for all the traits due partly to interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters. Narrow differences observed between the PCV and GCV in all the traits indicated greater role of genetic components and less influence by the environment. Similar results were obtained by Nath and Alam (2002), Suneetha *et al*. (2004), John *et al*. (2006), John *et al.* (2009), Korat *et al.* (2010), Meta and Monpara (2010), Nandini *et al.* (2011), Thirumala *et al.* (2014), Sanjeevakumar *et al.* (2015), Shashikumara *et al.* (2016), Bhargavi *et al.* (2016), Bhargavi *et al.* (2017), Harkesh and Sharma (2018), Rathod and Toprope *et al.* (2018), Syed *et al.* (2018), Mahesh *et al.* (2018), Aparna *et al.* (2018) and Lunagariya (2018) for pod yield and its components in groundnut.

The high values of GCV and PCV were observed for number of immature pods per plant. High magnitude of GCV indicated the presence of wide variation for the character under study to allow further improvement by selection of the individual trait. High estimates of GCV and PCV in groundnut for immature pods per plant have been reported by Mahalakshmi *et al.* (2005), Shinde *et al.* (2010), Zaman *et al.* (2011), Babariya *et al.* (2012), Sanjeevakumar *et al.* **(**2015), Mahesh *et al.* (2018), Lunagariya (2018) and Aparna *et al*. (2018).

In the present study, moderate values of GCV and PCV were observed for biological yield per plant, number of mature pods per plant, 100-kernel weight, kernel yield per plant and pod yield per plant. The moderate GCV and PCV have been reported in groundnut by Kumar *et al.* (2008), Bhargavi *et al.* (2017), Mahesh *et al.* (2018), Rathod and Toprope, (2018) and Nayak *et al.* (2018) for kernel yield per plant; Kumar *et al.* (2008), Korat *et al*. (2009), Rao *et al.* (2014), Gupta *et al.* (2015a), Bhargavi *et al.* (2017), Sushree *et al*. (2017), Mahesh *et al.* (2018), Nayak *et al.* (2018) and Rathod and Toprope (2018) for pod yield per plant; Kumar *et al.* (2008), Zaman *et al.* (2011) and Bhargavi *et al.* (2017) for mature pods per plant; Kumar *et al.* (2008), John *et al.* (2009), Zaman *et al.* (2011), Babariya (2012), Rao *et al.* (2014), Gupta *et al.* (2015a), Sanjeevakumar *et al.* (2015), Bhargavi *et al.* (2017), Mukesh and Lal (2017), Sushree

*et al*. (2017), Nayak *et al.* (2018) and Lunagariya (2018) for 100-kernel weight and Korat *et al*. (2009), Gupta *et al.* (2015a), Namrata *et al.* (2016) and Lunagariya (2018) for biological yield per plant.

The low estimates of GCV and PCV were observed for harvest index, plant height, days to 50% flowering, SCMR, shelling percentage, days to maturity, sound mature kernels and oil content. Sound mature kernels, days to 50% flowering, days to maturity and oil content there by indicating narrow genetic variability for these characters in the material studied. Similar results were reported in groundnut by John *et al.* (2009), Korat *et al*. (2009), Meta and Monapara, (2010), Zaman *et al.* (2011), Nandini *et al*. (2011), Babariya (2012), Gupta *et al.* (2015a), Bhargavi *et al.* (2017), Mukesh and Lal (2017), Wadikar *et al.* (2018), Kadam *et al.* (2018), Harkesh and Sharma (2018), Syed *et al*. (2018), Mahesh *et al.* (2018), Nayak *et al.* (2018) and Lunagariya (2018) for days to 50% flowering; Korat *et al*. (2009), Meta and Monapara, (2010), Zaman *et al.* (2011), Babariya (2012), Gupta *et al.* (2015a), Sanjeevakumar *et al.* (2015), Mukesh and Lal (2017), Bhargavi *et al.* (2017), Nayak *et al.* (2018), Rathod and Toprope (2018), Harkesh and Sharma (2018), Wadikar *et al.* (2018) and Lunagariya (2018) for days to maturity; Korat *et al*. (2009), Gupta *et al.* (2015a), Namrata *et al.* (2016), Mukesh and Lal (2017), Mahesh *et al.* (2018), Syed *et al.* (2018), Nayak *et al.* (2018) and Lunagariya (2018) for sound mature kernels; Mahalakshmi *et al.* (2005), Gupta *et al.* (2015a), Sanjeevakumar *et al*. (2015), Namrata *et al.* (2016), Bhargavi *et al.* (2017), Mukesh and Lal (2017), Mahesh *et al.* (2018), Kadam *et al.* (2018), Thirumala *et al.* (2018), Wadikar *et al.* (2018), Rathod and Toprope (2018) and Lunagariya (2018) for shelling percentage; Bhargavi *et al.* (2017), Wadikar *et al.* (2018) and Rathod and Toprope (2018) for harvest index; Nandini *et al*. (2011), Bhargavi *et al.* (2016), Syed *et al.* (2018), Rathod and Toprope (2018) and Lunagariya (2018) for SCMR; Korat *et al*. (2009), Babariya (2012), Gupta *et al.* (2015a), Sanjeevakumar *et al*. (2015), Bhargavi *et al.* (2017), Mukesh and Lal (2017), Wadikar *et al.* (2018), Mahesh *et al.* (2018), Kadam *et al.* (2018), Harkesh and Sharma (2018), Rathod and Toprope (2018), Wadikar *et al.* (2018) and Lunagariya (2018) for oil percentage and Mahalakshmi *et al.* (2005), Namrata *et al.* (2016), Mukesh and Lal (2017) for plant height.

**5.2.3 Heritability**

The genotypic coefficient of variation measures the amount of variation present in a particular character. However, it does not determine the proportion of heritable

variation present in the total variation. Therefore heritability, which represents the heritable variation existing in the character was calculated. High values of heritability in broad sense are helpful in identifying the appropriate character for selection and in enabling the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits (Johnson *et al.* 1955).

In the present study, high heritability (broad sense) was observed for all the 14 characters under study. The maximum heritability was recorded for days to maturity followed by number of immature pods per plant, number of mature pods per plant, days to 50% flowering, 100-kernel weight, biological yield per plant, harvest index, oil content, kernel yield per plant, plant height, pod yield per plant, sound mature kernels, SCMR and shelling percentage. High heritability estimates indicated that the characters were least influenced by the environmental effects and high capacity of the characters for transmission to subsequent generation. This also suggested that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be reliable. The high magnitude of heritability in groundnut has also been reported by Wani *et al.* (2004), Khote *et al.* (2009), Dolma *et al.* (2010a), Saraswathi *et al.* (2010), Babariya (2012), Bhargavi *et al.* (2016), Wadikar *et al.* (2018) and Lunagariya (2018) for days to maturity; Suneetha *et al.* (2004), John *et al*. (2006), Raut *et al.* (2010), Nandini *et al.* (2011), Babariya (2012), John *et al.* (2013), Rao *et al.* (2014), Yadav *et al.* (2014), Patil *et al.* (2014), Sanjeevakumar *et al.* (2015), Mahesh *et al.* (2018), Aparna *et al.* (2018), Wadikar *et al.* (2018) and Lunagariya (2018) for plant height; Raut *et al.* (2010), Shinde *et al.* (2010), Vekariya *et al*. (2011), Babariya (2012), Sanjeevakumar *et al.* (2015), Bhargavi *et al.* (2016), Mahesh *et al.* (2018), Lunagariya (2018) and Aparna *et al.* (2018) for number of mature pods per plant; John *et al*. (2006), Raut *et al.* (2010), Sanjeevakumar *et al.* (2015), Mahesh *et al.* (2018), Lunagariya (2018) and Aparna *et al.* (2018) for number of immature pods per plant; Wani *et al.* (2004), Dolma *et al.* (2010), Saraswathi *et al.* (2010), Babariya (2012), Kumar *et al*. (2014), Yadav *et al.* (2014), Lunagariya (2018) and Aparna *et al.* (2018) for shelling percentage; Parameshwarappa *et al*. (2004), Saraswathi *et al.* (2010), Nandini *et al.* (2011), Babariya (2012), Namrata *et al.* (2016), Wadikar *et al.* (2018) and Lunagariya (2018) for sound mature kernels; Suneetha *et al.* (2004), Kadam *et al.* (2007), Raut *et al.* (2010), Saraswathi *et al.* (2010), Shinde *et al.* (2010), Nandini *et al.* (2011), Vekariya *et al*. (2011), Babariya (2012), John *et al*. (2013), Kumar *et al*. (2014), Yadav *et al.* (2014), Gupta *et al.* (2015a), Mahesh *et al.* (2018), Wadikar *et al*. (2018),

Lunagariya (2018) and Nayak *et al.* (2018) for pod yield per plant; Parameshwarappa *et al*. (2004), Kadam *et al.* (2007), Raut *et al.* (2010), Nandini *et al.* (2011), Vekariya *et al*. (2011), Babariya (2012), John *et al.* (2013), Rao *et al.* (2014), Gupta *et al.* (2015a), Bhargavi *et al.* (2016), Bhargavi *et al.* (2017), Chavadhari *et al.* (2017) and Wadikar *et al*. (2018) for kernel yield per plant; Suneetha *et al.* (2004), Babariya (2012), Kumar *et al*. (2014), Patil *et al.* (2014), Sanjeevakumar *et al.* (2015), Lunagariya (2018), Wadikar *et al.* (2018) and Aparna *et al.* (2018) for days to 50% flowering; Suneetha *et al.* (2004), Wani *et al.* (2004), Saraswathi *et al.* (2010), Babariya (2012), Rao *et al.* (2014), Yadav *et al.* (2014), Patil *et al.* (2014), Gupta *et al.* (2015a), Sanjeevakumar *et al.* (2015), Bhargavi *et al.* (2016), Namrata *et al.* (2016), Bhargavi *et al.* (2017), Chavadhari *et al.* (2017), Mahesh *et al.* (2018), Nayak *et al.* (2018), Lunagariya (2018) and Aparna *et al.* (2018) for 100-kernel weight; Khote *et al.* (2009), Raut *et al.* (2010), Saraswathi *et al.* (2010), Sanjeevakumar *et al.* (2015), Gupta *et al*. (2015a), Namrata *et al.* (2016), Bhargavi *et al.* (2017) and Wadikar *et al.* (2018) for oil content; Saraswathi *et al.* (2010), Babariya (2012), Yadav *et al.* (2014), Bhargavi *et al.* (2016), Chavadhari *et al.* (2017) and Lunagariya (2018) for harvest index; Babariya (2012), Gupta *et al.* (2015a), Bhargavi *et al.* (2016), Chavadhari *et al.* (2017) and Lunagariya (2018) for biological yield per plant and Syed *et al.* (2018) and Lunagariya (2018) for SCMR.

**5.1.3 Genetic advance**

Heritability value alone cannot provide information on the amount of genetic progress that would result from selection of best individuals. Johnson *et al.* (1955) reported that heritability estimates along with genetic gain would be more useful than alone in predicting the effectiveness of selecting the best individuals. Therefore, it is necessary to consider the predicted genetic advance along with high heritability estimates as a tool in selection programme for better efficiency in the selection. High heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in expression of the trait. But, lower values of genetic advance indicate the prevalence of narrow range of variability, high gene interaction or non-additive gene action. Moderate values of genetic advance indicate both additive and non-additive gene actions might be responsible for their expression.

The expected genetic advance was high for biological yield per plant and 100-kernel weight. High genetic advance has been reported in groundnut by Venkataramana *et al.* (2001), Parmeshwarappa *et al.* (2004), Wani *et al*. (2004), Kumar *et al*. (2008),

Shinde *et al.* (2010), Zaman *et al.* (2011), Gupta *et al.* (2015), Bhargavi *et al.* (2016), Bhargavi *et al*. (2017), Mukesh and Lal (2017), Wadikar *et al.* (2018) and Lunagariya (2018) for 100-kernel weight and Kumar *et al*. (2008), Shinde *et al.* (2010), Babariya (2012), Gupta *et al.* (2015a) and Bhargavi *et al.* (2016) for biological yield per plant.

The expected genetic advance was moderate for days to maturity and harvest index. The present results are in agreement with those reported by Nath and Alam (2002), Gupta *et al.* (2015a), Bhargavi *et al*. (2017), Chavadhari *et al*. (2017), Lunagariya (2018) and Aparna *et al.* (2018) for harvest index and Shinde *et al.* (2010), Sanjeevakumar *et al.* (2015) and Gupta *et al.* (2015a) for days to maturity.

The expected genetic advance was low for number of mature pods per plant, plant height, SCMR, sound mature kernels, kernel yield per plant, shelling percentage, days to 50% flowering, number of immature pods per plant, pod yield per plant and oil content. Similar results were obtained by Bhargavi *et al.* (2017) for all characters *viz*, number of mature pods per plant, plant height, SCMR, sound mature kernels percentage, kernel yield per plant, shelling percentage, days to 50% flowering, number of immature pods per plant, pod yield per plant and oil content. In addition, low genetic advance has also been reported by Suneetha *et al.* (2004), Sanjeevakumar *et al.* (2015) and Bhargavi *et al.* (2016) for shelling percentage; Suneetha *et al.* (2004), Bhargavi *et al.* (2016), Wadikar *et al.* (2018) and Lunagariya (2018) for oil content; Suneetha *et al.* (2004) for sound mature kernel; Mukesh and Lal (2017), Wadikar *et al.* (2018), Lunagariya (2018) and Aparna *et al.* (2018) for days to 50% flowering and Shinde *et al.* (2010), Mukesh and Lal (2017), Aparna *et al.* (2018) and Lunagariya (2018) for pod yield per plant, number of mature pods per plant and number of immature pods per plant.

### 5.1.4 Genetic advance expressed as percentage of mean

The genetic advance expressed as percentage of mean was the maximum for number of immature pods per plant followed by biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant. High estimates of genetic advance expressed as percentage of mean in groundnut have also been reported earlier by Wani *et al.* (2004), Mahalakshmi *et al.* (2005), Korat *et al.* (2009), Sarashwathi *et al.* (2010), Shinde *et al*. (2010), Vekariya *et al.* (2011), Babariya (2012), Rao *et al.* (2014), Yadav *et al*. (2014), Gupta *et al.* (2015a), Sanjeevakumar *et al.* (2015), Bhargavi *et al.* (2016), Bhargavi *et al*. (2017), Chavadhari *et al.* (2017), Wadikar *et al.* (2018), Lunagariya (2018), Nayak *et al.* (2018) and Aparna *et al.* (2018)

for 100-kernel weight; Sarashwathi *et al.* (2010), Nandini *et al.* (2011), Vekariya *et al.* (2011), Babariya (2012), John *et al.* (2013), Rao *et al.* (2014), Gupta *et al.* (2015a), Bhargavi *et al.* (2016), Bhargavi *et al*. (2017), Chavadhari *et al.* (2017), Mahesh *et al.* (2018), Wadikar *et al.* (2018), Syed *et al*. (2018) and Aparna *et al.* (2018) for kernel yield per plant; Mahalakshmi *et al.* (2005), John *et al.* (2009), Shinde *et al*. (2010), Vekariya *et al.* (2011), Babariya (2012), Sanjeevakumar *et al.* (2015), Mahesh *et al.* (2018), Lunagariya (2018) and Aparna *et al.* (2018) for number of mature and immature pods per plant and Shinde *et al*. (2010), Vekariya *et al.* (2011), Babariya (2012), Gupta *et al.* (2015a), Bhargavi *et al.* (2016), Chavadhari *et al.* (2017) and Lunagariya (2018) for biological yield per plant.

The pod yield per plant, harvest index, days to 50% flowering and plant height expressed moderate values of genetic advance expressed as percentage of mean. Moderate genetic advance expressed as percentage of mean has been reported by John *et al.* (2009), Shinde *et al*. (2010), Gupta *et al.* (2015a) and Sushree *et al.* (2017) for plant height; Vekariya *et al.* (2011), Babariya (2012), Gupta *et al.* (2015a), Singh *et al.* (2017), Mahesh *et al.* (2018) and Wadikar *et al.* (2018) for days to 50% flowering; Korat *et al.* (2009) and Wadikar *et al.* (2018) for harvest index and Sushree *et al.* (2017) and Lunagariya (2018) for pod yield per plant.

The values of genetic advance expressed as percentage of mean were low for days to maturity, SCMR, shelling percentage, sound mature kernels percentage and oil content. These results are in agreement with those reported by Korat *et al.* (2009), Shinde *et al*. (2010), Vekariya *et al.* (2011), Rao *et al.* (2014), Gupta *et al.* (2015a), Sanjeevakumar *et al.* (2015), Chavadhari *et al.* (2017), Wadikar *et al.* (2018), Lunagariya (2018) and Nayak *et al.* (2018) for days to maturity; Bhargavi *et al.* (2016) and Chavadhari *et al.* (2017) for SCMR and shelling percentage; Korat *et al.* (2009), Vekariya *et al.* (2011), Babariya (2012), Yadav *et al*. (2014), Bhargavi *et al.* (2016), Chavadhari *et al.* (2017), Wadikar *et al.* (2018) and Lunagariya (2018) for oil content and Mahesh *et al.* (2018) for sound mature kernels and shelling percentage.

Johnson *et al.* (1955) suggested that the heritability and genetic advance when considered together would be more reliable and useful in predicting the resultant effects of selection. Rapid progress in selection can be achieved when high heritability is accompanied with high genetic advance, which forms the most reliable index of selection (Burton, 1952).

In the present study, high estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for number of immature pods per plant, biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant. Similar results were obtained by Dashora and Nagda (2002), Prasad *et al.* (2002), Parameshwarappa *et al.* (2004), Wani *et al.* (2004), John *et al.* (2006), Kadam *et al.* (2007), Shinde *et al.* (2010), Nandini *et al*. (2011), Babariya (2012), Gupta *et al*. (2015a), Bhargavi *et al.* (2016), Thirumal *et al*. (2016), Chavadhari *et al.* (2017), Mahesh *et al.* (2018) and Lunagariya (2018). The present results suggest the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitabaly be applied on these characters for their rationale improvement (Panse, 1957).

High estimates of heritability with moderate or low genetic advance were observed for pod yield per plant, harvest index, days to 50% flowering, plant height, days to maturity, SCMR, shelling percentage, sound mature kernels and oil content. Results are in agreement with those of Dashora and Nagda (2002), Suneetha *et al*. (2004), Korat *et al* (2009), Saraswathi *et al.* (2010), Gupta *et al*. (2015a), Sanjeevakumar *et al.* (2015), Bhargavi *et al*. (2016), Syed et al. (2018) and Mahesh *et al.* (2018). The present results revealed the presence of non-additive gene action and influence of environment in the expression of these characters and thus, the selection should be less effective.

## 5.2 CORRELATION COEFFICIENTS

In plant breeding programmes, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. Several characters are often to be handled together by a breeder as most of the characters especially of fitness are correlated. Thus, the different components of yield very often exhibit considerable degree of association among themselves and yield. Searle (1965) suggested that the average merit of a character in a population could be changed by means of selection programme based on the basis of phenotype of the main trait concerned. However, such an improvement would be more reliable if indirect selection based on another trait correlated with it is made. Unlike many other crops where the economic yield of the plant is visible during the growing season, pod yield in the groundnut is only observable after plants have been harvested. Researchers have

studied the relationship between pod yield and many vegetative characteristics in an attempt to allow breeders the ability to improve selection efficiency by conducting some evaluation before harvest as well as using traits with higher heritability than pod yield (Knauft and Wynne, 1995). Therefore, for rationale improvement of pod yield and its components the understanding of correlations has been observed very useful.

Correlation among traits may result from pleiotrophy, linkage or physiological associations among characters. The linkage is a cause of transit correlations particularly in a population derived from crosses between divergent strains. The correlation is the overall or net effect of the segregating genes; some of the genes may increase both the characters causing the positive correlation, while the others may increase the one and decrease the other causing the negative correlation (Falconer, 1981). Thus, to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various characters.

The study of genotypic correlation gives an idea of the extent of relationship between different variables. This relationship among yield contributing characters as well as their association with pod yield provides information for exercising selection pressure for bringing genetic improvement in pod yield.

In general, the values of genotypic correlation were higher than their corresponding phenotypic correlation in the present investigation. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. It has also indicated that there was an inherent relationship between the characters studied which is in agreement with the conclusions of Venkataravana *et al.* (2000), Suneetha *et al.* (2004), Vekariya *et al.* (2010), Bhosale (2011), Babariya and Dobariya (2012), Gupta *et al.* (2015b), Sanjeevakumar *et al.* **(**2015), Sushree *et al.* (2017) and Lunagariya (2018).

In the present study, the pod yield per plant was found to be significantly and positively correlated with days to 50% flowering, days to maturity, kernel yield per plant, number of mature pods per plant and biological yield per plant at both the genotypic and phenotypic levels. Such positive interrelationship between pod yield and these attributes has also been reported in groundnut by several researchers. The positive genotypic and phenotypic association has been reported between pod yield per plant and kernel yield per plant by Venkataravana *et al*. (2000), Golakia *et al.* (2004), John *et al.* (2007), Sumathi and Muralidharan (2007), Raut *et al.* (2010), Meta and Monpara

(2010), Bhosale (2011), Narasimhulu *et al.* (2012), Babariya and Dobariya (2012), Ravikumar and Reddi Sekhar (2012), Choudhary *et al.* (2013), Jain *et al*. (2016), Shashikumara *et al.* (2016), Tulsi *et al*. (2017), Anusha and Savithramma (2017), Mahesh *et al.* (2018), Wadikar *et al.* (2018), Ganvit and Jagpat (2018), Rathod and Toprope (2018) and Shankar *et al.* (2018); number of mature pods per plant by Venkataravana *et al*. (2000), Jayalakshmi and Reddy (2003), Suneetha *et al.* (2004) John *et al.* (2007), Kadam *et al.* (2009), Raut *et al.* (2010), Bhosale (2011), Babariya and Dobariya (2012), Ravikumar and Reddi Sekhar (2012), Choudhary *et al.* (2013), Bhargavi *et al.* (2015), Jain *et al*. (2016), Shashikumara *et al.* (2016), Mahesh *et al.* (2018), Kadam *et al.* (2018), Lunagariya (2018), Ganvit and Jagpat (2018), Reddy *et al.* (2018) and Shankar *et al.* (2018); biological yield per plant by Golakia *et al.* (2004), Babariya and Dobariya (2012), Choudhary *et al.* (2013), Bhargavi *et al.* (2015), Namrata *et al.* (2016), Tulsi *et al*. (2017) and Lunagariya (2018); days to 50% flowering by Ganvit and Jagpat (2018) and days to maturity by Babariya and Dobariya (2012) and Bhargavi *et al.* (2015). Thus, on the basis of correlations, the days to 50% flowering, days to maturity, kernel yield per plant, number of mature pods per plant and biological yield per plant were proved to be the outstanding characters influencing pod yield in groundnut and needs to be given due importance in selection to achieve higher pod yield.

The days to 50% flowering had positive and significant correlation at both genotypic and phenotypic levels with days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant. The results suggest that the selection for early flowering is likely to provide high kernel yield and biological yield with more number of mature pods per plant in groundnut. This relationship also indicated that the improvement in one character would bring about the improvement of another, which in turn, automatically lead to increase in pod yield. Similar results were reported for days to maturity by Suneetha *et al.* (2004), Korat *et al.* (2010), Ravikumar and Reddi Sekhar (2012), Rao *et al.* (2014), Gupta *et al.* (2015b) and Mahesh *et al.* (2018); number of mature pods per plant by John *et al.* (2009), Kadam *et al*. (2017) and Ganvit and Jagpat (2018); kernel yield per plant and biological yield per plant by Korat *et al.* (2010) and Ganvit and Jagpat (2018). Further, the days to 50% flowering registered significant and negative genotypic and phenotypic relationship with harvest index. These results are in agreement with of those reported by John *et al.* (2007) and

Shashikumara *et al.* (2016) for harvest index. The results suggest that the selection for early flowering will result in lower the harvest index in groundnut.

In the present study, the days to maturity showed positive and significant correlation at both genotypic and phenotypic levels with SCMR, number of mature pods per plant, kernel yield per plant, biological yield per plant and oil content. These results are in agreement with those of Savita *et al.* (2014) for number of mature pods per plant; Babariya and Dobariya (2012) for biological yield per plant and kernel yield per plant and Mahesh *et al.* (2018) for biological yield per plant. Thus, the selection for late maturity will result in increased number of mature pods per plant, kernel yield per plant and biological yield per plant in groundnut.

The association of plant height with 100-kernel weight and sound mature kernels was found to be significant and positive at both genotypic and phenotypic level, while the same was significant but negative with SCMR and number of immature pods per plant.

The SCMR had significant and positive correlation with number of immature pods per plant at both genotypic and phenotypic levels and oil content at genotypic levels. This relationship also indicated that the improvement in one character would bring about the improvement in another. This results are in agreement with those of Savita *et al.* (2014) and Lunagariya (2018). SCMR registered significant and negative association with sound mature kernels at both genotypic and phenotypic levels and with 100-kernel weight at genotypic level. These results are in agreement with those of Savita *et al.* (2014) for sound mature kernels and Lunagariya (2018) for 100-seed weight.

The number of mature pods per plant had significant and positive correlation both at genotypic and phenotypic levels with number of immature pods per plant, kernel yield per plant and biological yield per plant. Similar results were observed by Ravikumar and Reddi Sekhar (2012), Sashikumara *et al.* (2015), Gupta *et al.* (2015b), Tulsi *et al*. (2017) and Ganvit and Jagpat (2018) for kernel yield per plant; Babariya *et al.* (2012), Gupta *et al.* (2015b) and Tulsi *et al*. (2017) for biological yield per plant and Kadam *et al.* (2017) and Shankar *et al.* (2018) for immature pods per plant. A strong association between number of mature pods per plant, number of immature pods per plant, kernel yield per plant and biological yield per plant indicated that the selection toward increased number of mature pods per plant will lead to increase in that character and ultimately increase in pod yield.

The number of immature pods per plant had significant and positive correlation with biological yield per plant at both the levels. Similar results were obtained by Lunagariya (2018). Immature pods per plant showed negative but highly significant association with 100-kernel weight at both genotypic and phenotypic level and with sound mature kernels at genotypic level.

Shelling percentage had significant and positive correlation at both levels with kernel yield per plant, thus selection for high shelling percentage will result in high kernel yield per plant. Similar results were reported by Narsimhulu *et al.* (2012), Gupta *et al.* (2015b), Sashikumara *et al.* (2015), Shankar *et al.* (2018), Nayak *et al.* (2018) and Mahesh *et al.* (2018) for kernel yield per plant. In the present study, 100-kernel weight had significant and negative correlation with oil content at both levels, suggesting that an increase in kernel size will result in decrease in oil content.

A strong relationship was also observed between kernel yield per plant and biological yield per plant at both genotypic and phenotypic levels. As all these two characters are interrelated and also had strong genotypic association with pod yield per plant, the improvement in one component will automatically result in improvement in another component and finally the yield. Similar results were reported by Meta and Monpara (2010), Vekariya *et al.* (2010), Babariya *et al.* (2012), Bhosale (2011), Gupta *et al.* (2015b), Tulsi *et al*. (2017) and Saini and Sharma (2018). In the present study, strong negative relationship was observed between biological yield per plant and harvest index. The results thus, suggest that an increase in biological yield per plant may result in reduced harvest index in groundnut. Similar findings were obtained by Lunagariya (2018).

The present results on correlation coefficient thus, revealed that the days to 50% flowering, days to maturity, number of mature pods per plant, number of immature pods per plant, kernel yield per plant and biological yield per plant were the most important attributes and may contribute considerably towards higher pod yield. The interrelationship among yield components would help in increasing the yield levels and therefore, more emphasis should be given to these components while selecting better types in groundnut.

## 5.3 PATH COEFFICIENT ANALYSIS

Path co-efficient analysis, a biometrical technique developed by Wright (1921) and later elaborated by Dewey and Lu (1959), has been widely used by plant breeders

to separate the effect of particular cause among the characters. Path analysis provides information about the cause and effect situation in understanding the association between two variables. It permits the examination of direct effect of various characters on yield as well as their indirect effects via other component traits. Therefore, it provides basis for selection of superior genotypes from the diverse breeding populations. The results obtained on phenotypic path analysis have been discussed here under.

In the present study, the path coefficient analysis revealed that kernel yield per plant and biological yield per plant exhibited very high and high positive direct effect on pod yield per plant, respectively and both these characters also had significant and positive correlation with pod yield per plant. In addition, majority of the characters studied contributed positively towards pod yield per plant via kernel yield per plant and biological yield per plant. Thus, these two characters were considered as important yield component and could be used in selection programme aiming at improving pod yield in groundnut. In addition, these characters also showed appreciable positive contribution towards pod yield by indirect effect through each other. Similar results have been reported by Raut *et al.* (2010), Vekariya *et al.* (2010), Bhosale (2011), Choudhary *et al.* (2013), Bhargavi *et al.* (2015), Jain *et al*. (2016), Anusha and Savithramma (2017), Sushree *et al*. (2017), Tulsi *et al*. (2017), Mahesh *et al*. (2018), Ganvit and Jagpat (2018), Rathod and Toprope (2018), Shankar *et al.* (2018) and John and Reddy (2018) for kernel yield per plant and Vekariya *et al.* (2010), Korat *et al*. (2010), Babariya and Dobariya (2012), Choudhary *et al.* (2013), Bhargavi *et al.* (2015), Namrata *et al.* (2016), Lunagariya (2018) and Mahesh *et al.* (2018) for biological yield per plant in groundnut.

The characters like days to maturity and harvest index showed positive and moderate direct effect on pod yield per plant. Thus, these characters turned-out to be the important components of pod yield and direct selection for these traits will be rewarding for yield improvement. The results are in accordance with Babariya and Dobariya (2012), Gupta *et al*. (2015b), Bhargavi *et al.* (2015) and Rathod and Toprope (2018) for days to maturity and Shankar *et al.* (2018) for harvest index.

In the present study, the shelling percentage exhibited very high but negative direct effect on pod yield per plant. This character however, contributed toward pod yield per plant through positive indirect effect mainly *via* kernel yield per plant. Raut *et al.* (2010), Bhargavi *et al.* (2015), Mukesh and Lal (2017), John and Reddy (2018),

Mahesh *et al.* (2018) and Shankar *et al.* (2018) reported negative direct effect of shelling out-turn on pod yield per plant.

The days to 50% flowering and oil content exhibited low and positive direct effect towards pod yield. Low and positive direct effect of days to 50% flowering on pod yield has been reported by Bhargavi *et al.* (2015), Kadam *et al.* (2017), Lunagariya (2018), Mahesh *et al.* (2018) and Ganvit and Jagpat (2018), Tulsi *et al*. (2017) and Rathod and Toprope (2018) for oil content.

The characters like number of mature pods per plant and 100-kernel weight exerted moderate and negative direct effect towards pod yield per plant. Their indirect contribution toward pod yield per plant, either positive or negative, was mainly through indirect effect *via* kernel yield per plant. The results are in agreement with Thakur *et al*. (2013) and Mukesh and Lal (2017) for 100-kernel weight; Babariya and Dobariya (2012), Anusha and Savithramma (2017), Mukesh and Lal (2017) and John and Reddy (2018) for sound mature kernels and Babariya and Dobariya (2012) and Choudhary *et al.* (2013) for mature pods per plant.

## 5.4 SELECTION INDICES

The plant breeder has certain desired plant characteristics in his mind while selecting for particular genotypes and for this he applies various weights to different traits for arriving on decisions. The better way of exploiting genetic correlations with several traits having high heritability is to construct an index which combines information on all the characters associated with yield. This suggests the use of selection index, which gives proper weight to each of the two or more characters to be considered.

Breeding programmes attempt to achieve genetic progress through sequential selection of high performance genotypes over a number of selection cycles. For traits such as yield that are highly influenced by Genotypic x Environment interactions, the outcome of such a procedure remains highly unpredictable. Identification of high performance genotypes in a given cycle/generation can sometimes be more accurately done directly on the basis of other associated traits that are less sensitive to environmental variations. These associated traits, rather than being used individually, could be combined into a suitable index that could be used to identify high performance genotypes.

The use of selection index was originally proposed by Smith (1936). He argued that since genotypic worth could not be directly evaluated, it might be best estimated by a linear function of observable phenotypic values. The maximum response to index selection will be achieved if the correlation between genetic worth and the index is maximized (Baker, (1986). Index selection has also become an important concept in plant breeding and has been widely used, implicitly or explicitly, for the selection of superior varieties as well as for the improvement of a complex breeding objectives.

Hazel and Lush (1943) showed that the selection based on such an index is more efficient than selecting individually for the various characters. The basis for the development of the selection indices has been provided by Smith (1936), Hazel (1943), Hazel and Lush (1943) and Robinson *et al.* (1951).

Hazel and Lush (1943) stated that the superiority of selection based on index increases with an increase in the number of characters under selection. In the present study also, the genetic advance and relative efficiency assessed for different indices increased considerably when selection was based on two or more characters. The maximum genetic advance (GA) and relative efficiency (RI) in single character discriminant function were 12.43g and 178.21%, respectively which however, increased to 18.57g and 266.67%, respectively in two character combinations and 21.55g and 308.94%, respectively in three character combinations. Thus, there was an increase in the genetic gain as well as relative efficiency with inclusion of an additional trait in the character combinations. In four-character combinations, the highest genetic advance and relative efficiency were 24.21g and 347.00%, respectively. In five-character combinations, the highest genetic advance and relative efficiency were 26.71g and 382.86%, respectively whereas, the maximum genetic advance and relative efficiency in case of six-character combinations were 29.06g and 416.46%, respectively. Abraham (1990), Dobariya *et al.* (2008), Bhosale (2011), Safari *et al.* (2013), Babariya *et al.* (2014), Raghuvanshi *et al.* (2015) and Vachhani *et al.* (2016) were also with the same opinion that an increase in characters results in an increase in genetic gain and that the selection indices improve the efficiency of selection than the straight selection for yield alone.

In the present study, it was also observed that the straight selection for yield was not that much rewarding (GA=6.98g, RI=100.00%) as it was through its components like number of mature pods per plant (GA=12.43g, RI=178.21%) and days to 50% flowering (GA=10.13g, RI=145.18%) or in their combinations. The maximum

efficiency in selection for pod yield was exhibited by a discriminant function involving pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant which had a genetic advance and relative efficiency of 29.06g and 416.46%, respectively followed by an index of five characters *viz.,* pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant, which had a genetic advance and relative efficiency of 26.71g and 382.86%. The best selection index identified for four characters *viz.,* pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant with 24.27g genetic advance and 347.00% relative efficiency. The best selection index identified for three character combination included pod yield per plant, days to maturity and biological yield per plant (X1.X3.X6) having expected genetic gain of 21.55g and a relative efficiency of 308.94% as compared to the straight selection for pod yield per plant.

Further, there was a consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. However, in practice, the plant breeder might be interested in maximum gain with minimum number of characters. In such a case, selection index consisting of pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) followed by a selection index involving pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) or pod yield per plant, days to maturity, number of mature pods per plant and biological yield per plant (X1.X3.X4.X6) could be advantageously exploited in the groundnut breeding programmes. The results of the present study also revealed that the discriminant function method of making selection in plants appeared to be the most useful than the straight selection for pod yield alone and hence, due weightage should be given to the important selection indices while making selection for yield advancement in groundnut.

## 5.5 GENETIC DIVERGENCE

The progress in breeding for economic characters often depends on the availability of large germplasm representing a diverse genetic variation. For long term improvement programme, a large and diverse germplasm collection is an invaluable source of parental strains for hybridization and subsequent development of improved varieties. Accurate cultivar evaluation and ability to differentiate between cultivars in

respect of genetic parameters associated with adaptedness in cultivated plants and their wild proginators are critical to any breeding programme. The objective of this study therefore, was to evaluate and determine the variation pattern in some RILs of groundnut, identify the characters and differentiae the genotypes into different groups, suggest potential genotypes that could be used in improvement programme and appraise the suitability of the multivariate technique for classification of variation in groundnut. The use of Mahalanobis's $D^2$ statistic for estimating genetic divergence has been emphasized (Murthy and Arunachalam, 1966) because it permits precise comparison among the populations given in any group before effecting actual crosses.

Plant breeders are always interested in assessing the genetic divergence among the varieties or advanced breeding materials available with them so as to utilize them in directed breeding programmes because genetically diverse parents are likely to produce high heterotic effect and the distantly related parents within species, when utilized in cross breeding programme, are likely to produce a wide spectrum of variability (Arunachalm, 1981).

Earlier, geographic diversity among the parents was generally taken as an index of genetic diversity. However, Zaman *et al.* (2010), Venkateswarlu *et al.* (2011), Sushree *et al.* (2017), Jain *et al*. (2018), Saritha *et al.* (2018b) and Namrata *et al.* (2018) did not agree with this view and pointed out that geographical diversity need not result in genetic diversity. To a plant breeder, single character is not of much importance as the combined merit of number of desirable traits becomes more important when he/she is concerned with a complex trait like pod yield. Thus, for improving the pod yield, selection of parents based on number of characters having quantitative divergence is required which can be assessed by $D^2$-statistic developed by Mahalanobis (1936). The $D^2$-statistics estimated on 68 genotypes of groundnut for 14 characters showed that the generalized distance $\sqrt{D^2}$ between two entries varied from 10.84 to 49.89, which was an indicator of considerable diversity available in the material evaluated. On the basis of $D^2$ values, five clusters were formed from 68 genotypes.

The cluster I contained 30 genotypes. On the other hand, the cluster V possessed only one genotype. In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. Similar results were observed by Zaman *et al.* (2010), Babariya (2012), Vivekananda *et al.* (2015), Gupta *et al.* (2015c). The lowest intra-cluster distance was in cluster IV (D=8.35), whereas the highest intra-cluster distance was in cluster II

(D=11.30). The maximum inter-cluster distance (D=49.89) was found between clusters IV and V followed by that between clusters III and V (D=47.38), I and V (D=40.52), II and V (D=34.61). The closest proximity was noticed between the clusters I and IV (D=10.84). The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster V (GJG-32), cluster III (RIL-3, RIL-56, RIL-51, and GJG-9), cluster IV (AG-2006-6, RIL-54, RIL-22, RIL-30 and RIL-5) and cluster II (RIL-2, RIL-35, RIL-15, RIL-28 and RIL-16) could be selected as parents in hybridization programme.

A wide range of variation for several characters among single as well as multi-genotype clusters was observed. However, the differences were clearer for number of immature pods per plant, biological yield per plant, kernel yield per plant, pod yield per plant, number of mature pods per plant and 100-kernel weight. The present findings are in conformity with those reported earlier in groundnut by Dashora and Nagda (2004), Mahalakshmi *et al.* (2005), Siddiquey *et al.* (2006), Odedra *et al*. (2008), Sumathi and Muralidharan (2009), Venkataravana *et al.* (2008), Kumar *et al.* (2010), Venkateswarlu *et al.* (2011), Babariya *et al*. (2012), Suneetha *et al.* (2013), Gupta *et al.* (2015c), Sushree *et al.* (2017), Saritha *et al.* (2018b), Jain *et al.* (2018) and Mohammad *et al.* (2018).

The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high mean values of any cluster can be used in hybridization programme for further selection and improvement. In the present study, the cluster V differed from other clusters in respect of pod yield per plant, shelling percentage, kernel yield per plant, biological yield per plant, number of mature pods per plant, number of immature pods per plant, oil content, SCMR and plant height. For days to maturity cluster IV was the best. The cluster III had desirable value for days to 50% flowering, Harvest index and sound mature kernels. The cluster II was the best for 100-kernel weight. Therefore, intercrossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rationale improvement for increasing the pod yield in groundnut.

The analysis of the per cent contribution of various characters towards the total genetic divergence indicated that days to maturity (36.04%) followed by number of immature pods per plant (22.52%) and biological yield per plant (7.20%) contributed

maximum towards the total divergence in the present study. They accounted for more than 60.00% towards the total divergence in the material studied.

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, in the present investigation, based on high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster VII with the genotypes of cluster X, V, III, IX and IV which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in groundnut.

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* Original not seen

# CHAPTER VI
# SUMMARY AND CONCLUSIONS

The present investigation was carried out to measure the genetic variability, correlation coefficients, path coefficients, genetic divergence and also to construct the selection indices using 68 genotypes comprising 64 Recombinant Inbred Lines, two parents and two checks of groundnut (*Arachis hypogaea* L.). The experiment was layed-out in a Randomized Block Design with three replications at the Main Oilseeds Research Station, JAU, Junagadh during *kharif* -2018.

The observations were recorded on five randomly selected plants in each entry and replication and their mean values were used for statistical analysis. The characters studied were days to 50% flowering, days to maturity, plant height (cm), SCMR, number of mature pods per plant, number of immature pods per plant, shelling percentage (%), 100-kernel weight (g), sound mature kernels (%), kernel yield per plant (g), biological yield per plant (g), pod yield per plant (g), harvest index (%) and oil content (%).

The mean squares due to genotypes were found significant for all the characters indicating the existence of sufficient variability in the experimental material.

The biological yield per plant had wide range of variation followed by number of mature pods per plant, SCMR, plant height, 100-kernel weight and harvest index. In case of days to 50% flowering, days to maturity and oil content, a narrow range of variation was recorded. The range observed was of moderate magnitude for number of immature pods per plant, selling percentage, sound mature kernels percentage, kernel yield per plant and pod yield per plant.

The values of phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the characters indicating the influence of environmental factors.

The estimates of GCV and PCV were high for number of immature pods per plant. The results indicated the presence of wide variation for the character under study. The biological yield per plant, number of mature pods per plant, 100-kernel weight, kernel yield per plant and pod yield per plant had moderate GCV and PCV, while harvest index, plant height, days to 50% flowering, SCMR, shelling percentage, days to maturity, sound mature kernels and oil content recorded low GCV and PCV.

The estimates of heritability were observed to be high for 14 characters under study *viz*., days to 50% flowering, days to maturity, plant height, SCMR, number of mature pods per plant, number of immature pods per plant, shelling percentage, 100-kernel weight, sound mature kernels, kernel yield per plant, biological yield per plant, pod yield per plant, harvest index and oil content, indicating that these characters were less influenced by the environmental fluctuations and high capacity of the characters for transmission to subsequent generation.

The expected genetic advance was the highest for biological yield per plant followed by 100-kernel weight. The values were moderate for days to maturity and harvest index. The values were low for number of mature pods per plant, plant height, SCMR, sound mature kernels percentage, kernel yield per plant, shelling percentage, days to 50% flowering, number of immature pods per plant, pod yield per plant and oil content. Genetic advance expressed as percentage of mean was found high for number of immature pods per plant, biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant. The genetic advance expressed as percentage of mean was moderate for pod yield per plant, harvest index, days to 50% flowering and plant height, while it was low for days to maturity, SCMR, shelling percentage, sound mature kernels and oil content.

High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for number of immature pods per plant, biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant, while high estimates of heritability with moderate or low genetic advance were observed for pod yield per plant, harvest index, days to 50% flowering, plant height, days to maturity, SCMR, shelling percentage, sound mature kernels and oil content.

The values of genotypic correlation were higher than their corresponding phenotypic correlation in the present investigation. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. It also indicated that there was an inherent relationship between the characters studied. In the present investigation, pod yield per plant exhibited significant and positive correlation with days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant at both the genotypic and phenotypic levels,

whereas its association was found significant and positive with SCMR at phenotypic level only.

The path coefficient analysis revealed high and positive direct effect of kernel yield per plant and biological yield per plant toward pod yield per plant, while the days to maturity and harvest index showed moderate and positive direct effect on pod yield per plant. These characters may be considered as the most important yield contributing characters and due emphasis should be placed on these components while selecting for high yielding types in groundnut.

The discriminant functions based on single character index indicated that the number of mature pods per plant showed maximum relative efficiency followed by days to 50% flowering, biological yield per plant, days to maturity and kernel yield per plant over straight selection for pod yield. Among the combinations involving two component characters, days to maturity and biological yield per plant exhibited maximum relative efficiency followed by pod yield per plant and biological yield per plant and days to 50% flowering and biological yield per plant. Thus, there was an increase in the genetic gain as well as relative efficiency with inclusion of an additional trait in the character combinations. Among all the 63 selection indices, the index based on six characters *viz*., pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant possessed the highest genetic gain and relative efficiency (29.06g and 416.46%) as compared to straight selection for pod yield per plant (6.98g and 100%). Other important selection indices identified were with the inclusion of five as well as four characters. The index involving five characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant (X1.X2.X3.X4.X6) had genetic advance of 26.71g and 382.86% relative efficiency, while the other index with four characters *viz.*, pod yield per plant, days to 50% flowering, days to maturity and biological yield per plant (X1.X2.X3.X6) showed 24.21g genetic advance and 347.00% relative efficiency as compared to the straight selection for pod yield (6.98g, 100%). The results thus, indicated that the maximum weightage should be given to these functions while making selection for isolating high yielding lines in groundnut.

The genetic divergence analysis indicated moderate genetic diversity among the 68 genotypes, which were grouped in to 5 clusters. The maximum inter-cluster distance (D=49.89) was found between clusters IV and V followed by that between clusters III

and V (D=47.38), I and V (D=40.52). The minimum inter-cluster distance was observed between clusters I and III (D=11.04). The intra-cluster distance ranged from 8.35 to 11.30.

The characters like number of immature pods per plant, biological yield per plant, kernel yield per plant, pod yield per plant and number of mature pods per plant showed high genetic divergence. The cluster V differed from other clusters in respect of number of mature pods per plant, number of immature pods per plant, shelling percentage, kernel yield per plant, pod yield per plant, biological yield per plant, oil content, plant height and SCMR. For days to 50% flowering, sound mature kernels and harvest index cluster III was the best. The cluster IV had desirable value for days to maturity. The cluster II was the best for 100-kernel weight. The analysis of the per cent contribution of various characters towards the total genetic divergence indicated that days to maturity, number of immature pods per plant and biological yield per plant contributed maximum towards the divergence in the present study. They accounted for more than 60.00% towards the total divergence in the material studied.

The salient features of the present findings are summarized as under:

1. All the characters exhibited significant differences among the entries, which indicated considerable amount of variability present in the material studied.
2. The wide range of variation was recorded for biological yield per plant followed by number of mature pods per plant, plant height, SCMR, 100-kernel weight and harvest index.
3. The values of phenotypic coefficient of variation were higher than genotypic coefficient of variation indicating the influence of environmental factors.
4. The highest GCV and PCV were observed for number of immature pods per plant.
5. The estimates of heritability were high for the 14 characters *viz.,* days to 50% flowering, days to maturity, plant height, SCMR, number of mature pods per plant, number of immature pods per plant, shelling percentage, 100-kernel weight, sound mature kernels, kernel yield per plant, biological yield per plant, pod yield per plant, harvest index and oil content
6. The expected genetic advance was the highest for biological yield per plant followed by100-kernel weight. Genetic advance expressed as percentage of mean was found high for number of immature pods per plant followed by

biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant.

7. High estimates of heritability along with high genetic advance expressed as percentage of mean were observed for number of immature pods per plant, biological yield per plant, number of mature pods per plant, 100-kernel weight and kernel yield per plant, which may be attributed to the preponderance of additive gene action and these traits possess high selective value.
8. The magnitudes of genotypic correlation were higher as compared to the corresponding phenotypic correlation thereby indicating the presence of an inherent relationship between the variables.
9. The pod yield per plant showed highly significant and positive correlation with days to 50% flowering, days to maturity, number of mature pods per plant, kernel yield per plant and biological yield per plant at both genotypic and phenotypic levels.
10. Path coefficient analysis showed high positive direct effect of kernel yield per plant and biological yield per plant towards pod yield per plant. Whereas, days to maturity and harvest index exhibited moderate positive direct effect on pod yield per plant. These traits were considered as the most important yield contributors and due emphasis should be given while attempting yield improvement in groundnut.
11. The discriminant function selection had higher genetic gain and relative efficiency over straight selection for pod yield alone. There was an increase in genetic gain and relative efficiency with inclusion of an additional trait in the character combination.
12. A selection index consisting of pod yield per plant, days to 50% flowering, days to maturity, number of mature pods per plant and biological yield per plant or an index involving pod yield per plant, days to 50% flowering, days to maturity, kernel yield per plant and biological yield per plant could be advantageously exploited in the groundnut breeding.
13. The formation of five clusters suggested the presence of moderate genetic diversity among the 68 genotypes studied.
14. The days to maturity, number of immature pods per plant and biological yield per plant contributed maximum towards the total genetic divergence in the material studied.

15. Based on the inclusion of high yielding genotypes and large inter-cluster distances, it would be advantageous to attempt crossing of the genotypes from cluster V with the genotypes of clusters IV, III and I which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in groundnut.

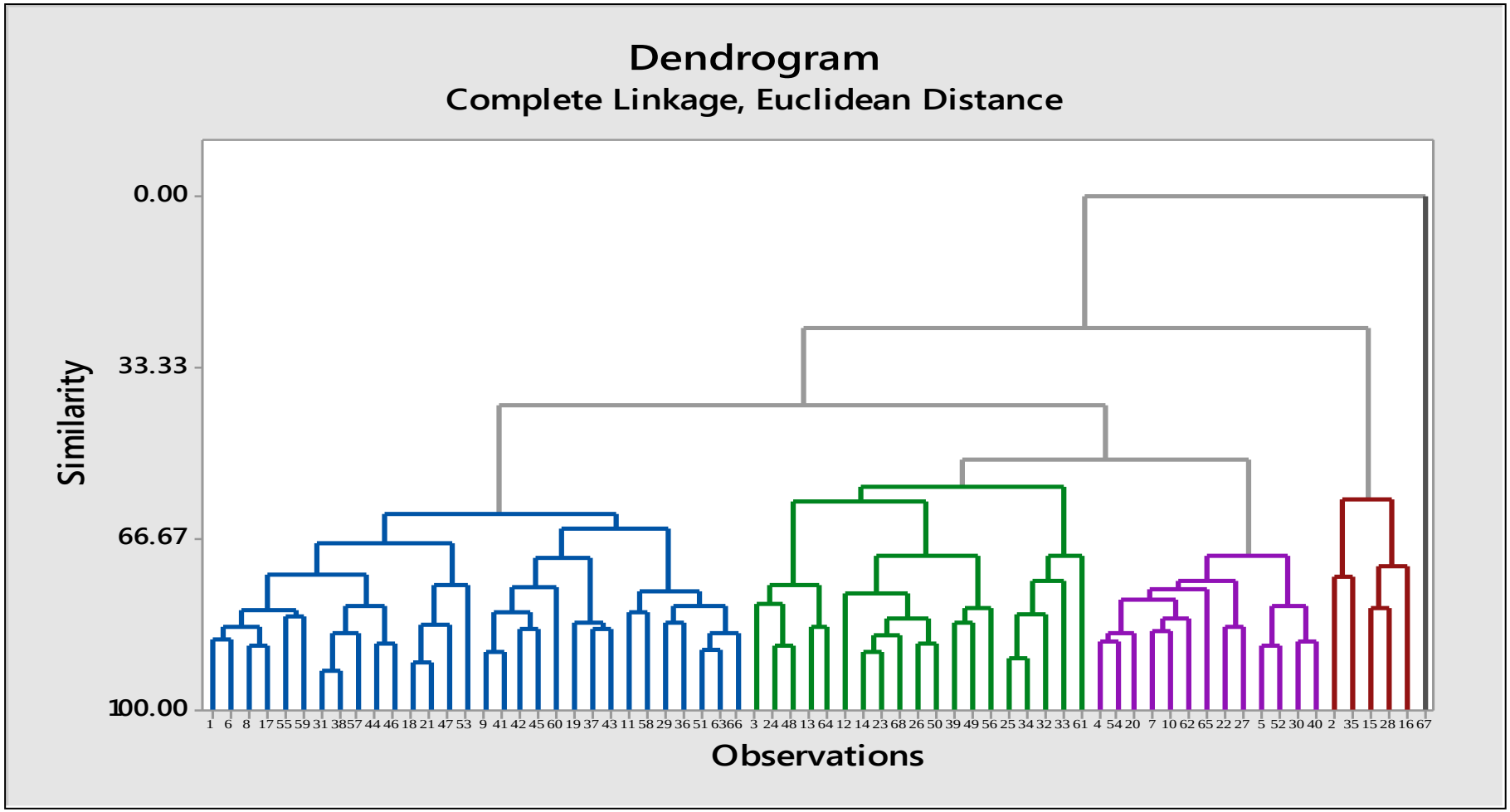



**Figure 4.2:** Diagrammatic representation of dendogram based on 14 characters in 68 genotypes of groundnut

# Appendix-II

**Mean values of 68 genotypes for 14 characters in groundnut.**

| Sr. No. | Genotypes | Days to 50% flowering | Days to maturity | Plant height (cm) | SCMR | No. of mature pods/ plant | No. of immature pods/plant | Shelling percentage (%) |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| **1** | RIL 1 | 24.33 | 111.00 | 27.20 | 34.18 | 13.13 | 2.20 | 65.96 |
| **2** | RIL 2 | 28.00 | 116.00 | 29.26 | 34.59 | 11.33 | 1.60 | 66.02 |
| **3** | RIL 3 | 22.67 | 107.67 | 21.80 | 31.20 | 13.40 | 2.33 | 66.54 |
| **4** | RIL 4 | 26.33 | 112.00 | 20.33 | 35.07 | 14.93 | 2.26 | 69.37 |
| **5** | RIL 5 | 26.67 | 112.67 | 22.50 | 35.48 | 12.93 | 2.80 | 66.02 |
| **6** | RIL 6 | 24.67 | 111.00 | 21.80 | 33.01 | 12.06 | 2.06 | 68.46 |
| **7** | RIL 7 | 25.67 | 113.00 | 19.53 | 33.76 | 10.20 | 1.60 | 71.57 |
| **8** | RIL 8 | 22.67 | 112.00 | 25.60 | 29.37 | 12.60 | 2.13 | 70.09 |
| **9** | RIL 9 | 28.00 | 117.00 | 23.60 | 36.51 | 10.53 | 1.67 | 66.67 |
| **10** | RIL 10 | 26.00 | 113.67 | 24.40 | 35.48 | 12.26 | 3.06 | 71.57 |
| **11** | RIL 11 | 25.67 | 118.67 | 20.80 | 35.73 | 13.67 | 3.40 | 74.12 |
| **12** | RIL 12 | 26.00 | 113.67 | 25.40 | 41.56 | 11.13 | 2.80 | 73.95 |
| **13** | RIL 13 | 23.00 | 108.00 | 25.47 | 37.24 | 11.00 | 1.86 | 71.08 |
| **14** | RIL 14 | 22.67 | 118.00 | 26.73 | 33.36 | 11.93 | 1.67 | 67.93 |
| **15** | RIL 15 | 26.00 | 112.33 | 23.80 | 36.17 | 08.93 | 1.80 | 65.25 |
| **16** | RIL 16 | 28.33 | 114.67 | 26.53 | 29.82 | 10.93 | 2.73 | 78.08 |
| **17** | RIL 17 | 27.33 | 109.33 | 24.86 | 31.32 | 14.80 | 2.53 | 67.59 |
| **18** | RIL 18 | 22.33 | 113.00 | 20.93 | 34.92 | 14.60 | 3.67 | 67.94 |
| **19** | RIL 19 | 29.67 | 118.00 | 22.80 | 37.64 | 13.40 | 1.93 | 72.17 |
| **20** | RIL 20 | 27.67 | 114.33 | 24.13 | 34.12 | 11.60 | 2.86 | 70.01 |
| **21** | RIL 21 | 23.33 | 112.67 | 23.86 | 34.46 | 14.46 | 2.53 | 67.82 |
| **22** | RIL 22 | 22.67 | 110.00 | 24.80 | 33.30 | 10.13 | 3.73 | 71.99 |

| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|---|
| **23** | RIL 23 | 25.67 | 117.33 | 25.80 | 32.74 | 13.13 | 2.26 | 69.24 |
| **24** | RIL 24 | 24.33 | 111.33 | 25.13 | 35.19 | 11.00 | 1.26 | 66.87 |
| **25** | RIL 25 | 22.00 | 115.33 | 24.93 | 32.50 | 11.40 | 2.73 | 67.37 |
| **26** | RIL 26 | 23.67 | 119.33 | 24.80 | 36.79 | 13.40 | 2.60 | 68.78 |
| **27** | RIL 27 | 23.00 | 113.33 | 21.67 | 33.72 | 09.60 | 1.73 | 73.12 |
| **28** | RIL 28 | 27.33 | 118.33 | 23.86 | 34.02 | 12.53 | 2.13 | 70.64 |
| **29** | RIL 29 | 23.00 | 117.00 | 22.33 | 33.18 | 14.33 | 2.33 | 65.36 |
| **30** | RIL 30 | 25.00 | 111.67 | 24.33 | 38.11 | 09.86 | 1.93 | 65.98 |
| **31** | RIL 31 | 28.33 | 119.00 | 22.86 | 34.45 | 13.20 | 2.60 | 62.04 |
| **32** | RIL 32 | 25.33 | 118.00 | 27.73 | 32.74 | 09.20 | 2.67 | 62.73 |
| **33** | RIL 33 | 24.67 | 108.00 | 22.20 | 31.42 | 11.80 | 2.06 | 66.04 |
| **34** | RIL 34 | 23.00 | 117.33 | 22.93 | 32.11 | 10.73 | 2.80 | 65.18 |
| **35** | RIL 35 | 29.67 | 118.00 | 22.86 | 37.08 | 14.80 | 3.13 | 68.65 |
| **36** | RIL 36 | 28.67 | 119.33 | 28.80 | 33.72 | 15.26 | 3.60 | 67.46 |
| **37** | RIL 37 | 27.33 | 119.67 | 22.93 | 35.19 | 12.40 | 3.13 | 72.05 |
| **38** | RIL 38 | 29.33 | 118.67 | 21.86 | 34.73 | 12.67 | 2.06 | 63.43 |
| **39** | RIL 39 | 27.33 | 116.00 | 24.80 | 35.16 | 10.40 | 1.40 | 68.32 |
| **40** | RIL 40 | 25.33 | 113.00 | 22.67 | 34.55 | 10.80 | 3.26 | 62.53 |
| **41** | RIL 41 | 25.00 | 118.33 | 25.80 | 35.92 | 12.53 | 2.20 | 66.19 |
| **42** | RIL 42 | 28.00 | 119.33 | 21.06 | 35.20 | 10.93 | 2.00 | 67.90 |
| **43** | RIL 43 | 26.33 | 118.00 | 21.53 | 38.76 | 13.86 | 3.20 | 67.20 |
| **44** | RIL 44 | 23.67 | 114.00 | 22.06 | 37.88 | 12.60 | 4.86 | 66.03 |
| **45** | RIL 45 | 23.00 | 111.67 | 24.20 | 35.02 | 12.60 | 2.60 | 69.09 |
| **46** | RIL 46 | 22.67 | 113.67 | 23.86 | 38.62 | 12.60 | 3.67 | 67.44 |
| **47** | RIL 47 | 23.33 | 115.33 | 23.26 | 36.29 | 13.73 | 3.26 | 63.88 |
| **48** | RIL 48 | 24.00 | 111.33 | 25.13 | 36.33 | 11.06 | 2.73 | 70.05 |
| **49** | RIL 49 | 22.67 | 114.67 | 23.60 | 32.08 | 10.73 | 2.06 | 71.93 |
| **50** | RIL 50 | 23.00 | 119.67 | 26.46 | 35.52 | 10.53 | 1.86 | 70.66 |
| **51** | RIL 51 | 27.33 | 116.67 | 22.13 | 36.83 | 14.80 | 3.53 | 68.01 |
| **52** | RIL 52 | 24.33 | 115.00 | 21.46 | 36.78 | 10.00 | 2.93 | 63.29 |

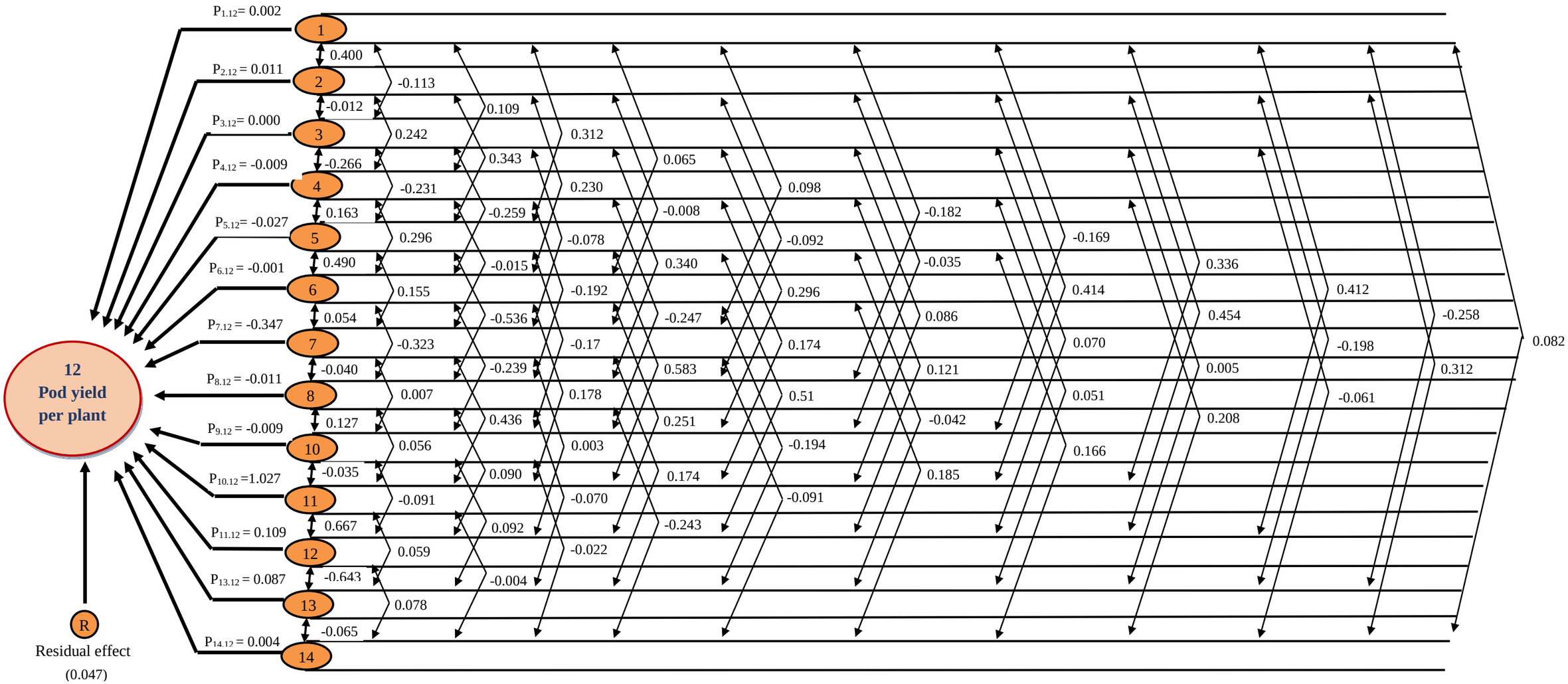
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|---|
| **53** | RIL 53 | 23.67 | 109.00 | 24.06 | 36.93 | 15.60 | 2.13 | 71.43 |
| **54** | RIL 54 | 26.33 | 108.67 | 21.73 | 34.68 | 12.00 | 1.46 | 71.27 |
| **55** | RIL 55 | 23.67 | 107.33 | 27.46 | 33.40 | 12.13 | 2.73 | 63.31 |
| **56** | RIL 56 | 23.67 | 109.67 | 30.46 | 32.64 | 11.60 | 2.46 | 70.10 |
| **57** | RIL 57 | 27.00 | 117.00 | 21.73 | 37.64 | 14.46 | 3.46 | 67.13 |
| **58** | RIL 58 | 29.00 | 119.00 | 22.13 | 36.08 | 18.60 | 3.73 | 72.63 |
| **59** | RIL 59 | 27.33 | 113.67 | 26.00 | 32.82 | 10.67 | 1.93 | 64.16 |
| **60** | RIL 60 | 23.33 | 112.33 | 21.33 | 36.71 | 13.53 | 4.46 | 72.15 |
| **61** | RIL 61 | 22.67 | 109.00 | 22.13 | 32.20 | 09.26 | 1.40 | 66.04 |
| **62** | RIL 62 | 24.67 | 113.00 | 22.13 | 35.49 | 11.60 | 1.40 | 73.37 |
| **63** | RIL 63 | 28.67 | 119.00 | 21.93 | 34.13 | 16.06 | 4.13 | 70.79 |
| **64** | RIL 64 | 26.67 | 109.33 | 19.80 | 36.36 | 10.86 | 3.60 | 67.95 |
| **65** | AG-2006-6 | 29.00 | 109.67 | 24.20 | 28.33 | 12.00 | 2.20 | 73.32 |
| **66** | ICGV-05155 | 28.33 | 120.33 | 20.93 | 37.16 | 15.80 | 2.73 | 67.86 |
| **67** | GJG-32 | 28.33 | 119.67 | 21.00 | 36.11 | 22.13 | 4.20 | 72.10 |
| **68** | GJG-9 | 26.00 | 115.67 | 28.00 | 32.00 | 13.20 | 1.46 | 67.46 |
| | **Mean** | 25.50 | 114.26 | 23.74 | 34.76 | 12.53 | 2.58 | 68.51 |
| | **SEm+** | 0.79 | 0.72 | 1.17 | 1.35 | 0.79 | 0.18 | 1.87 |
| | **C.D. at 5%** | 2.23 | 2.02 | 3.29 | 3.78 | 2.21 | 0.52 | 5.25 |
| | **CV%** | 5.41 | 1.09 | 8.58 | 6.73 | 10.94 | 12.52 | 4.75 |

**Contd...**

| Sr. No. | Genotypes | 100-kernel weight (g) | Sound mature kernels (%) | Kernel yield per plant (g) | Biological yield/ plant (g) | Pod yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | **8** | **9** | **10** | **11** | **12** | **13** | **14** |
| **1** | RIL 1 | 44.00 | 89.67 | 13.46 | 42.90 | 20.40 | 48.13 | 50.65 |
| **2** | RIL 2 | 55.33 | 89.33 | 14.06 | 62.13 | 21.33 | 34.46 | 52.62 |
| **3** | RIL 3 | 56.00 | 92.33 | 11.46 | 34.46 | 17.20 | 50.60 | 47.82 |
| **4** | RIL 4 | 39.33 | 88.67 | 13.00 | 37.06 | 18.67 | 50.40 | 53.12 |
| **5** | RIL 5 | 35.33 | 88.00 | 10.96 | 39.86 | 16.60 | 43.06 | 51.27 |
| **6** | RIL 6 | 41.33 | 92.67 | 13.36 | 43.00 | 19.40 | 45.20 | 50.65 |
| **7** | RIL 7 | 36.67 | 86.33 | 10.26 | 32.96 | 14.40 | 43.67 | 49.22 |
| **8** | RIL 8 | 40.67 | 89.00 | 12.63 | 39.60 | 18.00 | 45.53 | 50.16 |
| **9** | RIL 9 | 48.67 | 84.00 | 12.96 | 42.53 | 19.40 | 45.60 | 51.51 |
| **10** | RIL 10 | 38.00 | 90.67 | 11.63 | 37.30 | 16.26 | 44.13 | 51.35 |
| **11** | RIL 11 | 36.00 | 83.67 | 13.26 | 41.03 | 17.93 | 44.06 | 52.03 |
| **12** | RIL 12 | 45.33 | 92.33 | 14.70 | 39.73 | 19.86 | 50.33 | 50.49 |
| **13** | RIL 13 | 52.67 | 84.00 | 10.86 | 31.86 | 15.33 | 48.00 | 40.23 |
| **14** | RIL 14 | 48.00 | 90.67 | 14.70 | 42.53 | 21.67 | 51.13 | 50.64 |
| **15** | RIL 15 | 56.00 | 88.67 | 13.40 | 46.76 | 20.53 | 43.86 | 50.74 |
| **16** | RIL 16 | 57.67 | 90.00 | 15.26 | 49.13 | 19.60 | 40.40 | 48.66 |
| **17** | RIL 17 | 40.67 | 91.33 | 11.60 | 39.16 | 17.20 | 44.33 | 50.56 |
| **18** | RIL 18 | 39.33 | 90.00 | 14.53 | 40.10 | 21.40 | 53.73 | 49.46 |
| **19** | RIL 19 | 42.67 | 91.00 | 15.76 | 52.53 | 21.86 | 41.60 | 48.62 |
| **20** | RIL 20 | 42.67 | 88.67 | 12.03 | 30.80 | 17.20 | 50.80 | 49.13 |
| **21** | RIL 21 | 38.67 | 91.67 | 13.36 | 37.90 | 19.60 | 51.67 | 49.47 |
| **22** | RIL 22 | 42.67 | 95.00 | 10.67 | 33.93 | 14.80 | 43.86 | 50.22 |
| **23** | RIL 23 | 49.33 | 88.33 | 13.80 | 42.53 | 19.93 | 47.00 | 50.81 |
| **24** | RIL 24 | 50.67 | 87.00 | 12.06 | 35.60 | 18.06 | 50.73 | 50.57 |
| **25** | RIL 25 | 48.67 | 94.33 | 11.70 | 41.93 | 17.33 | 41.33 | 51.15 |
| **26** | RIL 26 | 46.67 | 93.00 | 13.63 | 37.90 | 19.73 | 52.33 | 51.77 |

| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|---|---|---|---|---|---|---|---|---|
| **27** | RIL 27 | 46.67 | 89.67 | 11.26 | 32.46 | 15.40 | 47.40 | 50.69 |
| **28** | RIL 28 | 58.33 | 90.33 | 16.23 | 51.36 | 23.00 | 44.86 | 50.34 |
| **29** | RIL 29 | 35.33 | 88.33 | 12.26 | 43.83 | 18.73 | 43.06 | 50.15 |
| **30** | RIL 30 | 38.67 | 92.33 | 8.70 | 33.10 | 13.20 | 41.20 | 51.47 |
| **31** | RIL 31 | 44.00 | 90.33 | 12.23 | 45.16 | 19.86 | 44.13 | 51.71 |
| **32** | RIL 32 | 51.33 | 90.67 | 10.03 | 44.76 | 16.00 | 35.86 | 50.35 |
| **33** | RIL 33 | 44.00 | 89.67 | 10.53 | 46.10 | 15.93 | 34.83 | 51.36 |
| **34** | RIL 34 | 51.67 | 91.33 | 10.96 | 42.60 | 17.00 | 40.20 | 51.22 |
| **35** | RIL 35 | 46.00 | 85.33 | 16.23 | 62.70 | 23.67 | 38.06 | 48.09 |
| **36** | RIL 36 | 35.33 | 87.67 | 13.30 | 45.90 | 19.80 | 43.40 | 51.15 |
| **37** | RIL 37 | 48.67 | 89.67 | 14.33 | 49.67 | 19.86 | 40.13 | 52.64 |
| **38** | RIL 38 | 41.33 | 91.00 | 11.86 | 45.23 | 18.80 | 41.67 | 51.52 |
| **39** | RIL 39 | 51.67 | 96.00 | 13.13 | 43.13 | 19.20 | 44.60 | 47.57 |
| **40** | RIL 40 | 42.67 | 91.00 | 8.56 | 35.10 | 13.67 | 39.00 | 50.35 |
| **41** | RIL 41 | 47.33 | 86.00 | 12.70 | 45.26 | 19.20 | 42.53 | 51.84 |
| **42** | RIL 42 | 47.33 | 88.33 | 12.93 | 44.46 | 19.06 | 43.20 | 50.98 |
| **43** | RIL 43 | 44.00 | 90.00 | 12.50 | 50.56 | 18..60 | 37.20 | 51.64 |
| **44** | RIL 44 | 47.33 | 87.33 | 12.06 | 43.16 | 18.26 | 42.53 | 52.04 |
| **45** | RIL 45 | 48.00 | 83.67 | 13.40 | 46.76 | 19.33 | 41.46 | 47.64 |
| **46** | RIL 46 | 43.33 | 92.00 | 13.03 | 43.56 | 19.40 | 45.00 | 51.47 |
| **47** | RIL 47 | 40.00 | 85.33 | 12.40 | 39.63 | 19.33 | 48.91 | 51.84 |
| **48** | RIL 48 | 52.67 | 89.33 | 12.63 | 38.80 | 18.06 | 46.67 | 51.50 |
| **49** | RIL 49 | 52.67 | 95.33 | 13.43 | 39.33 | 18.73 | 47.86 | 52.01 |
| **50** | RIL 50 | 46.67 | 94.33 | 12.50 | 37.83 | 17.67 | 47.01 | 50.77 |
| **51** | RIL 51 | 36.67 | 88.33 | 12.90 | 41.13 | 18.93 | 46.06 | 49.28 |
| **52** | RIL 52 | 38.00 | 91.33 | 10.00 | 38.36 | 15.80 | 41.33 | 51.05 |
| **53** | RIL 53 | 34.67 | 92.33 | 14.56 | 42.46 | 20.40 | 48.33 | 51.11 |
| **54** | RIL 54 | 38.67 | 86.00 | 12.30 | 35.30 | 17.26 | 48.93 | 48.74 |
| **55** | RIL 55 | 38.67 | 90.00 | 11.26 | 42.23 | 17.73 | 42.40 | 50.42 |
| **56** | RIL 56 | 52.67 | 96.67 | 14.70 | 45.56 | 21.00 | 46.20 | 49.92 |

| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
|---|---|---|---|---|---|---|---|---|
| **57** | RIL 57 | 40.67 | 93.00 | 13.60 | 45.26 | 20.33 | 45.00 | 49.33 |
| **58** | RIL 58 | 33.33 | 85.67 | 15.50 | 48.40 | 21.33 | 44.08 | 52.36 |
| **59** | RIL 59 | 43.33 | 86.33 | 10.86 | 39.00 | 16.93 | 43.60 | 50.55 |
| **60** | RIL 60 | 42.00 | 80.67 | 12.83 | 43.96 | 17.73 | 40.20 | 49.55 |
| **61** | RIL 61 | 58.67 | 91.00 | 10.00 | 39.73 | 15.13 | 38.53 | 47.73 |
| **62** | RIL 62 | 38.00 | 92.67 | 10.36 | 29.13 | 14.06 | 48.53 | 52.08 |
| **63** | RIL 63 | 38.67 | 87.33 | 13.40 | 43.50 | 18.93 | 43.46 | 51.48 |
| **64** | RIL 64 | 49.33 | 83.33 | 11.43 | 32.93 | 16.80 | 51.13 | 50.48 |
| **65** | AG-2006-6 | 38.00 | 94.67 | 12.23 | 36.16 | 16.67 | 46.53 | 50.41 |
| **66** | ICGV-05155 | 36.67 | 90.00 | 14.20 | 42.46 | 20.93 | 49.29 | 52.36 |
| **67** | GJG-32 | 36.67 | 89.33 | 17.56 | 79.16 | 24.40 | 30.80 | 51.33 |
| **68** | GJG-9 | 46.67 | 93.67 | 12.76 | 38.90 | 18.93 | 49.13 | 48.85 |
| | **Mean** | 44.40 | 89.67 | 12.69 | 42.19 | 18.51 | 44.56 | 50.58 |
| | **SEm±** | 2.39 | 1.77 | 0.86 | 2.96 | 1.17 | 1.87 | 0.61 |
| | **C.D. at 5%** | 6.70 | 4.95 | 2.41 | 8.29 | 3.27 | 5.23 | 1.73 |
| | **CV%** | 9.35 | 3.42 | 11.77 | 12.16 | 10.94 | 7.27 | 2.12 |




**Where, double arrowed lines indicate phenotypic correlation coefficient and single arrowed lines indicate direct effect**

**1)** Days to 50% flowering, **2)** Days to maturity, **3)** Plant height (cm), **4)** SCMR, **5)** Number of mature pods per plant, **6)** Number of immature pods per plant, **7)** Shelling percentage (%)

**8)** 100-kernel weight (g), **9)** Sound mature kernels (%), **10)** Kernel yield per plant (g), **11)** Biological yield per plant (g), **12)** Pod yield per plant (g), **13)** Harvest index (%), **14)** Oil content (%)

**Figure 4.1:- Diagrammatic representation of phenotypic path analysis in groundnut**

# Appendix-I

Mean weekly meteorological data recorded during study period in the Meteorological Observatory, Department of Agronomy, College of Agriculture, JAU, Junagadh.

| Month | Std. weeks | Temperature ($^0$C) | | Humidity (%) | | Rainfall (mm) | Rainy days |
|---|---|---|---|---|---|---|---|
| | | Max. | Min. | Max. | Min. | | |
| July | 30 | 30.2 | 26.1 | 90 | 76 | 1.8 | 0 |
| Aug | 31 | 32.1 | 26.1 | 88 | 63 | 4.5 | 1 |
| | 32 | 31.5 | 25.4 | 87 | 72 | 8.8 | 1 |
| | 33 | 30.1 | 25.1 | 91 | 76 | 10.0 | 3 |
| | 34 | 29.0 | 24.2 | 94 | 84 | 50.3 | 5 |
| Sept | 35 | 29.5 | 24.0 | 92 | 78 | 31.3 | 4 |
| | 36 | 30.1 | 23.4 | 89 | 66 | 27.4 | 1 |
| | 37 | 31.3 | 23.6 | 87 | 59 | 2.1 | 0 |
| | 38 | 33.5 | 23.9 | 84 | 54 | 6.2 | 2 |
| Oct | 39 | 34.7 | 23.1 | 76 | 38 | 0 | 0 |
| | 40 | 37.4 | 22.9 | 76 | 32 | 0 | 0 |
| | 41 | 37.9 | 23.1 | 66 | 29 | 0 | 0 |
| | 42 | 36.7 | 21.1 | 74 | 28 | 0 | 0 |
| | 43 | 37.5 | 20.2 | 64 | 22 | 0 | 0 |
| Nov | 44 | 37.0 | 19.8 | 60 | 23 | 0 | 0 |
| | 45 | 36.7 | 18.0 | 68 | 22 | 0 | 0 |
| | 46 | 35.4 | 18.7 | 75 | 27 | 0 | 0 |
| | 47 | 35.9 | 18.0 | 67 | 21 | 0 | 0 |