# GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS, GENETIC DIVERGENCE AND SELECTION INDICES FOR POD YIELD AND ITS COMPONENT TRAITS IN VIRGINIA GROUNDNUT

## (*Arachis hypogaea* L.)

**BY**


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**B. Sc. (Hons.) Agri.**



**DEPARTMENT OF GENETICS AND PLANT BREEDING**

**COLLEGE OF AGRICULTURE**

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**JUNAGADH– 362 001**



**JULY- 2019**

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## (*Arachis hypogaea* L.)

**THESIS SUBMITTED TO**

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**(Agriculture)**

**IN**

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*Dedicated To*

*My Beloved Parents &*

*My Family for their dreams, hopes*

*and endless prayer*

*SONALI ...* 

**DEPARTMENT OF GENETICS AND PLANT BREEDING**
**COLLEGE OF AGRICULTURE**
**JUNAGADH AGRICULTURAL UNIVERSITY**
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**Name of Student:** **Major Guide:**
**Solanki Sonali M.** **Dr. S. B. Chaudhari**

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## ABSTRACT

Key words: *Arachis hypogaea* L., Variability, Correlation, Path analysis, $D^2$-statistic and Selection indices.

The present study was carried-out to assess genetic variability, correlation coefficient, path coefficient analysis, selection indices and genetic divergence in 60 genotypes of groundnut. These genotypes grown in a Randomized Block Design with three replications at the Instructional Farm, College of Agriculture, J.A.U., Junagadh during *kharif* 2018. The observations were recorded on 14 characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant (g), sound mature kernel (%), 100-kernel weight (g), shelling out-turn (%), biological yield per plant (g), harvest index (%) and oil content (%).

Analysis of variance revealed highly significant differences among the genotypes for all the fourteen characters studied which revealed presence of sufficient variability for all the characters studied. A wide range of variation was observed for important yield components. The high genotypic coefficient of variation was observed for plant height. Moderate values of GCV were observed for number of matured pods per plant, pod yield per plant, number of immature pods per plant, number of pods per plant, biological yield per plant, harvest index, 100-kernel weight, days to 50% flowering and shelling out-turn. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for days to 50%

flowering, plant height, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant, 100-kernel weight, shelling out-turn, biological yield and harvest index.

The narrow differences between GCV and PCV estimates of respective characters indicated that environmental factors had little role for the expression of the characters. Pod yield per plant was significantly and positively correlated at both genotypic and phenotypic levels with number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, biological yield per plant and harvest index.

Path analysis revealed that number of matured pods per plant, 100-kernel weight, biological yield and harvest index exhibited high and positive direct effect on pod yield per plant. Thus, these characters turned-out to be the major components of pod yield. The direct effects of the remaining characters were lower in magnitude. An appreciable indirect influences were exerted by number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, shelling out-turn, biological yield per plant and harvest index. Thus, number of matured pods per plant, 100-kernel weight, biological yield and harvest index were identified as the most important yield components.

The genetic divergence measured by Mahalanobis's $D^2$-statistic grouped 60 genotypes into 13 clusters. The clustering pattern of the genotypes did not confirm to the geographical distribution. The lowest intra-cluster distance was in cluster X whereas the highest intra-cluster distance was in cluster XIII. The maximum inter-cluster distance found between cluster between cluster XIII and V. The minimum inter-cluster distance found between cluster VI and V.

Among all the 31 selection indices, the index based on five component characters *viz*., pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index possessed the highest genetic gain and relative efficiency followed by an index based on four characters *viz.*, pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant possessed the highest genetic gain and relative efficiency.

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## CERTIFICATE - I

This is to certify that the thesis entitled **"GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS, GENETIC DIVERGENCE AND SELECTION INDICES FOR POD YIELD AND ITS COMPONENT TRAITS IN VIRGINIA GROUNDNUT (*Arachis hypogaea* L.)"** submitted by **Ms. SOLANKI SONALI MAHENDRAKUMAR** in partial fulfilment 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 or other similar title. The candidate had fulfilled all prescribe requirements. The assistance and help received during the course of investigation has been fully acknowledged. She has successfully completed the preliminary examination held on March 16, 2019 as required under the regulation for post-graduate studies. She has submitted kachcha bound thesis on July 31, 2019.

**Place:** Junagadh
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## C E R T I F I C A T E - II

**Date:** 04/10/2019

This is to certify that the thesis entitled **"GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS, GENETIC DIVERGENCE AND SELECTION INDICES FOR POD YIELD AND ITS COMPONENT TRAITS IN VIRGINIA GROUNDNUT (*Arachis hypogaea L.*)"** submitted by **Ms. Solanki Sonali Mahendrakumar (Reg. No. 2010117128)** 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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encouragement, sincere prayer, expectations and blessing have always been a vital source of inspiration in my life.

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**Place** : Junagadh

**Date** : - -2019 **(Solanki Sonali M.)**

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# CHAPTER-I

## INTRODUCTION

Cultivated groundnut (*Arachis hypogaea* L.) is a self-pollinated crop. Groundnut is an important oilseed crop, with oil content around 40-50% and is extensively used for cooking purposes. Oil is a rich source of vitamin A, B and E. Besides being an important source of vegetable oil, it is also used as an important source of food, feed, nutrition and fodder. Groundnut is also known as the "King" of oilseeds or "Wonder nut" or "Poor man's cashew nut". It contains on an average 40.1% fat and 25.3% protein, which is about 1.3 times higher than meat, 2.5 times higher than eggs and 8 times higher than fruits. Groundnut is relatively day length insensitive crop. Therefore, most of the varieties developed anywhere in the world can be evaluated at any latitude, where favourable temperature exists. It is also an ideal crop for both crop rotation and intercropping being a leguminous crop; the crop can also be grown in summer as catch crop.

Groundnut (*Arachis hypogaea* L.) is an allotetraploid (2n=4x=40) legume crop and belongs to the subtribe stylosanthinae of tribe aeschynomeneae in family Fabaceae. The groundnut flowers are characterized as cleistogamous, therefore, crop is highly self-pollinated in nature; however, extent of out-crossing has been reported up to 3.9%, which is mainly because of small insects like different types of ant. After fertilization, stalk of ovary elongates and forms peg, which contains fertilized ovules at the tip. The growth of peg is positively geotropic and ovary starts to develop as pod, which contains kernel, each enclosed in a papery testa. Kernels are without endosperm and contain up to 50% oil (Ramanathan, 2001).

The cultivated groundnut has produced in the course of its evolutionary history a large number of morphological variant forms. Botanically, cultivated groundnut can be classified into two sub-species, which mainly differed in their branching pattern (sub-species *hypogaea* with alternate branching habit and sub-species *fastigiata* with sequential branching habit). Each sub-species is again divided into two botanical varieties, sub-species *hypogaea* into *var. hypogaea* (virginia) and *var. hirsuta* (peruvian runner) where, sub-species *fastigiata* into *var. fastigiata* (valencia) and *var. vulgaris* (spanish). In trade, bold seeded types are referred to as

Virginia, the small seeded as spanish and third type runner is also recognized (Ramanathan, 2001).

In India, Five states, Gujarat, Andhra Pradesh, Rajasthan, Karnataka and Maharashtra jointly accounted for 83.7% of groundnut area of the country. The total groundnut production in India during the year 2018-19 was about 5.20 million tones with 3.89 million hectares area and 1336 kg/ha productivity. Groundnut is the major oilseed crop of Gujarat with 1.47 million hectares area and 2.08 million tones of production with 1421 kg/ha productivity (Annon, 2018). One of the main reasons for the low yield groundnut in the country is the large scale poor adoption of newer varieties and their inconsistent performance over range of environments, as the crop is largely cultivated as rainfed crop. Therefore, it has become necessary to develop varieties with attributes such as wide adaptability, fertilizer responsiveness, biotic and abiotic stress resistance and short seed dormancy so as to obtain yield levels of greater than 30 q/ha.

Presence of genetic variability is a pre-requisite for the success of plant breeding programme. Greater the diversity in the materials, better are the chances for evolving promising genotypes. The importance to study genetic variance was realized for the first time by Fisher (1918). He partitioned total genetic variance into additive, dominant and epistasis components. Additive genetic variance can be exploited for genetic advance through selection. The genetic inferences are obtained from phenotypic observations, which are the results interaction of genotype with the environment. Therefore, the observed variability can be grouped under heritable and non heritable components and this can be estimated by parameters like genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic gain. This helps the breeder in developing and formulating selection programme for the genetic improvement of crop plants.

Assessment of genetic variability in the base population is the first step in any breeding programme. The variability parameters certainly determine the extent and quality of variability. The yield is a complex character resulting from inter play of various yield contributing characters, which have positive or negative association with yield and among themselves also. To assess the magnitude of characters association of various quantitative characters with pod yield and their direct and indirect influence on yield would give clue for favouring the character in selection.

Genetic diversity plays a pivotal role in survival and adaptability of a species. When a specific environment changes, slight genetic variation is necessary for it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variation.

The knowledge of association between yield and its component characters is of immense value for breeder, because it forms the basis for selection. It is well known phenomenon that different components of yield very often exhibit considerable degree of association in both positive and negative directions among themselves and with yield as well. A positive correlation between desirable characteristics favorable to the plant breeder because it helps in simultaneous improvement of both the characters. A negative correlation, on the other hand, will hinder the simultaneous expression of both the characters with high values. In such situations some economic compromise has to be made.

Path analysis measures the direct and indirect contribution of various independent characters to a dependent character and is based on all possible simple correlations among various characters (Singh and Narayanan, 2000).

The amount of variability for important economic attributes in any crop determines the progress that can be achieved through selection. An assessment of the variability is required to judge its potential as base material for crop improvement programme. Yield is a polygenically controlled complex character and highly influenced by environment. This necessitates deeper insight into the nature of genetic variation that is heritable in the progeny and genetic advance that can be achieved through selection. Mahalanobis' $D^2$ statistics is a powerful tool for quantifying genetic divergence among germplasm collections with respect to characters considered together.

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 and 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.

Selection index is one of the most beneficial tools for breeders to select the best genotype. On the base of these indices, synchronic selection was done on the base of number of traits according to their phenotypic and genotypic value, phenotypic and genotypic correlations among these traits and a figure that called trait economic value. Yield is a trait that is controlled by a number of genes and so indirect selection would relate to improvement. One of the effective ways for indirect selection is using selection index.

Keeping in a view all these aspects, the present study in groundnut is under taken with following objectives:

**10. Objectives**

1. To study nature and magnitude of genetic variation of pod yield and its component traits.
2. To find out the association between pod yield and yield contributing characters.
3. To determine the direct and indirect effect of different characters on pod yield using path coefficient analysis.
4. To find out the extent of genetic diversity among genotypes through Mahalanobis $D^2$ technique.
5. To construct the selection indices using pod yield and its component traits.

# CHAPTER-II

## REVIEW OF LITERATURE

In the present investigation genetic variability, correlation, path analysis, genetic divergence and selection indices for pod yield and its component traits have been studied in groundnut. The literature pertaining to objectives of this investigation have been reviewed briefly under the following sub-heads.

2.1 Genetic variability

2.2 Correlation coefficients

2.3 Path analysis

2.4 Genetic divergence

2.5 Selection indices

### 2.1 GENETIC VARIABILITY

The existence of genetic variability is prerequisite for any crop improvement programme; however, loss of locally adopted variable material has been rapid and thus, loss of variability is almost universal, which need to be maintained. Information regarding genetic variability present in a population, and estimation of variability parameters including heritability is pre-requisite for planning an effective breeding programme for improvement of any crop. The variability existing among homozygous genotypes/ population is generally considered as free variability which can be exploited for genetic advance selection. This together with information on heritability and genetic advance would be rewarding in designing an effective breeding programme. The genetic variability is determined with the help of certain genetic parameters *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability estimates. The review of literature pertaining to variability parameters in groundnut is presented in the subsequent paragraphs.

Venkataramana (2001) evaluated thirty groundnut genotypes as 20 spanish bunch and 10 virginia bunch for genetic variability parameter and reported that estimates of PCV were higher than GCV for all the characters under study. However, both PCV and GCV estimates were high for 100-kernel weight, kernel yield and oil yield. Whereas, estimates of heritability in broad sense were high for oil content, 100-kernel weight and sound mature kernels percentage. Moderate heritability couples

with high genetic advance as per cent of mean was observed for kernel yield and oil yield. Additive gene effect could be proponed for 100-kernel weight as it had high heritability estimate along with high genetic advance.

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 percent of mean for days to 50% flowering, days to maturity, shelling out-turn, 100-kernel weight and oil content revealing preponderance of non-additive gene effect.

Nath and Alam (2002) conducted the experiment to evaluate 15 exotic groundnut genotypes to study yield and yield contributing characters. High to moderate PCV was observed for plant height, pods per plant, harvest index, pod yield per plant and shelling out-turn. High GCV were observed for plant height. High genetic advance was observed for shelling out-turn. High genetic advance as percentage of mean was observed for pod yield per plant, plant height, 100-kernel weight, shelling out-turn, harvest index and number of pods per plant. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for plant height, number of pods per plant, 100-kernel weight, shelling out-turn, pod yield per plant and harvest index.

Korat *et al.* (2009a) studied components of variation, heritability and genetic advance by using 80 diverse genotypes of bunch groundnut and reported that values of GCV and PCV were high for number of secondary branches per plant. High to moderate GCV were observed for plant height, pod yield per plant, biological yield per plant, harvest index and 100-kernel weight. Moderate PCV was observed for biological yield per plant and harvest index.

Thakur *et al.* (2011) evaluated 25 groundnut genotypes along with local checks (B-4, Jota and Jayanti) to study genetic variability, heritability and genetic advance of pod yield and yield component traits. Highly significant variations were observed for all the characters in all the genotypes used in the experiment. High PCV were observed for days to maturity, plant height, pods per plant, 100-seed weight, shelling out-turn and sound mature kernel. The character 100-seed weight showed high heritability with high genetic advance and high genetic advance as percentage of

mean. Considerable high heritability, low genetic advance and genetic advances as percentage of mean were found for days to maturity.

Zaman *et al.* (2011) tested thirty four groundnut genotypes in the experiment and observed highly significant variations among the genotypes for all the characters studied. Moderate GCV was observed for number of matured pods per plant, 100-kernel weight and shelling out-turn. High to moderate PCV was observed for number of matured pods per plant, shelling out-turn and 100-kernel weight. High heritability was observed for number of branches pods per plant, number of matured pods per plant, number of immature pods per plant, 100-kernel weight and number of pods per plant. Genetic advance was found to be moderate for shelling out-turn and low for days to 50% flowering and days to maturity.

Vishnuvardhan *et al.* (2012) evaluated 28 $F_2$ populations of groundnut for variability, heritability and genetic advance. Analysis of variance revealed highly significant differences among the genotypes for all the characters except number of mature pods per plant and pod yield per plant. Moderate GCV was observed for number of matured pods per plant, pod yield per plant and harvest index. High to moderate PCV was observed for number of matured pods per plant, shelling out-turn and harvest index. Genetic advance was low for days to 50% flowering, days to maturity, plant height, number of matured pods per plant, number of immature pods per plant. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for harvest index.

John *et al.* (2013) observed significant differences among 37 genotypes for all the traits studied. High heritability and high genetic advance as percent of mean was recorded for plant height and pod yield per plant. These characters could be further improved through single plant selection. Moderate heritability and high genetic advance as per cent of mean was observed for 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.

Mukri *et al.* (2014) revealed that low GCV and PCV were recorded with medium to high heritability for days to 50% flowering. However, plant height and number of mature pods per plant recorded moderate GCV and high PCV; whereas 100-seed weight recorded moderate GCV and moderate PCV coupled with high genetic advance and heritability. Moderate GCV and heritability coupled with high

PCV were estimated for pod yield. Moderate estimates of PCV were observed for 100-kernel weight.

Maurya *et al.* (2014) evaluated 15 groundnut genotypes. The analysis of variance revealed the prevalence of significant differences among the genotypes for all the characters studied. Moderate to low estimate of GCV were observed for days to 50% flowering, days to maturity and number of sound mature kernels. Low values of PCV were observed for days to maturity and sound mature kernel. High magnitude of heritability was observed for days to 50% flowering and plant height, pod yield per plant and sound mature kernel. The genetic advance expressed as percentage of mean was high to moderate for days to 50% flowering, plant height, pod yield per plant, sound mature kernels, 100-kernel weight and shelling out-turn.

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

Patil *et al.* (2015) assessed 49 genotypes of groundnut to study genetic variability for yield and its related traits. Moderate values of GCV were observed for days to 50% flowering, 100-kernel weight and shelling out-turn. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for days to 50% flowering, plant height, number of matured pods per plant, number of immature pods per plant, pod yield per plant, 100-kernel weight and shelling out-turn.

Ashutosh *et al.* (2016) evaluated 29 breeding lines of groundnut to estimate genetic variability, heritability and genetic advance for various characters. The PCV and GCV values were high for pod yield per plant. High heritability was observed for number of pods per plant, pod yield per plant, harvest index and shelling out-turn. GCV values were moderate for number of pods per plant, pod yield per plant, harvest index and 100-kernel weight.

Bhargavi *et al.* (2016) evaluated 20 diverse genotypes of spanish bunch groundnut to assess the variability, heritability and genetic advance as per cent of

mean for 19 characters. The results revealed high values of PCV and GCV for harvest index and pod yield, respectively. High heritability accompanied with high genetic advance as per cent of mean was recorded for number of matured pods per plant, biological yield per plant, pod yield per plant, biological yield per hectare, harvest index and 100-kernel weight.

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 number of matured pods per plant and harvest index. Moderate to low estimates of PCV were observed for biological yield per plant, harvest index 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.

Rao (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 were moderate to high for pods per plants, kernel yield, plant height and dry pod yield. High heritability coupled with high genetic advance was observed for plant height, dry pod yield and 100-kernel weight. High magnitude of heritability was observed for days to 50% flowering, plant height and days to maturity.

Ashutosh *et al.* (2016) assessed variability for yield and its contributing traits in 29 breeding lines of groundnut. PCV and GCV were high for pod yield per plant, kernel yield per plant, number of pods per plant, number of kernels per plant and 100-kernel weight. Moderate values of GCV were observed for number of pods per plant, pod yield per plant, harvest index and 100-kernel weight.

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

branches per plant and pod yield per plant. High genetic advance as percentage of mean was recorded for 100-kernel weight and pod yield per plant, moderate for sound mature kernels and low value was recorded for days to maturity. Moderate estimates of PCV were observed for shelling out-turn and 100-kernel weight. High estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for plant height, pod yield per plant and 100-kernel weight.

Mahesh *et al.* (2018) evaluated 144 genotypes of groundnut for 13 characters to assess the variability, heritability and genetic advance. Plant height, number of mature and immature pods per plant, 100-kernel weight, and dry pod yield per plant had high GCV, PCV, heritability and genetic advance as percentage of mean. Low values of GCV were observed for sound mature kernels and oil content. High heritability coupled with high genetic advance expressed as percentage of mean was observed for plant height, number of matured pods per plant, number of immature pods per plant and 100-kernel weight.

Omima *et al.* (2018) studied genetic variability, heritability and genetic advance for yield and yield contributing characters in eight genotypes of groundnut. High GCV and PCV were observed for number of branches per plant, number of pods per plant and pod yield per plant. High heritability estimates coupled with high genetic advance were obtained for number of pod per plant, pod yield per plant and 100-seed weight. The genetic advance expressed as percentage of mean was the high for number of pods per plant.

## 2.2 CORRELATION COEFFICIENTS

Correlation analysis provides the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. The concept of correlation was first given by Galton (1889) and later it was elaborated by Fisher (1918). A brief review of work related to correlation analysis in groundnut has been reviewed as under;

Nagda and Joshi (2004) carried out correlation analysis in 52 genotypes of groundnut for seven characters. They reported that genotypic correlations were higher than the phenotypic correlations. Dry pod yield exhibited positive and significant correlation with harvest index at both the genotypic and phenotypic levels.

Mane *et al.* (2008) carried out correlation analysis to evaluate the relationship among different characters in bunch groundnut. They reported that pod yield per plant

exhibited significant and positive correlation with sound mature kernel, number of pods per plant and shelling out-turn. However, it showed negative and non-significant correlation with 100-kernel weight and days to 50% flowering.

Jogloy *et al.* (2011) evaluated 200 lines of 10 crosses to study correlation for maturity and pod yield in peanut. Maturity was negatively correlated with pod yield and harvest index, suggesting the possibility to select for early mature genotypes without detrimental effect on pod yield and harvest index. Pod yield was well associated with 100-seed weight and harvest index, suggesting that selection for large seeds and good partitioning would improve yield.

Babariya and Dobariya (2012) evaluated 100 genotypes of spanish bunch groundnut to estimate correlation coefficients for pod yield and its component character and reported that pod yield per plant had positive and significant association with number of pods per pant, number of mature pods per pant, 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. Matured pods per plant had positive and significant association with sound mature kernel and biological yield per plant. Number of pods per plant had highly significant and strong positive correlation with number of mature pods per pant and biological yield per plant.

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 out-turn and sound mature kernel at both genotypic and phenotypic levels.

Kumar *et al.* (2014) evaluated 66 genotypes of groundnut for correlation studies and revealed that pod yield per plant was strong positively correlated at both genotypic and phenotypic level with sound mature kernels. Harvest index was highly significant and positively correlated with number of matured pods per plant.

Yadlapalli (2014) estimated correlation coefficients among different yield components. Pod yield exhibited significant and positive genotypic correlations with all the characters *viz.*, number of pods per plant, pod yield, 100-seed weight, number of branches per plant and days to 50% flowering except plant height. Plant height exhibited significant and positive genotypic correlations with number of branches per plant.

Bhargavi *et al.* (2015) evaluated 20 spanish bunch genotypes of groundnut for correlation studies. The result indicated that days to maturity, number of mature pods per plant, biological yield per plant, biological yield per hectare, harvest index, 100-kernel weight, kernel yield per plant, kernel yield per hectare, oil yield per hectare and pod yield per hectare showed significant positive association with pod yield per plant both at phenotypic and genotypic levels.

Patil *et al.* (2015) assessed 49 genotypes of groundnut to study genetic variability for yield and its related traits. The association study among characters revealed that the pod yield per plant showed highly significant and positive association with number of pod bearing nodes, number of matured pods per plant, kernel weight per plant and days to 50% flowering at phenotypic level. Plant height showed significant and positive association with days to maturity at phenotypic level.

Vasanthi *et al.* (2015) evaluated 29 groundnut cultures for correlation studies for yield and yield attributes. The result indicated that the characters; number of mature pods per plant, number of primary branches per plant and 100-seed weight should be given due emphasis for the development of high yielding genotypes.

Ashutosh *et al.* (2016) evaluated 29 breeding lines of groundnut to accomplish correlation coefficients for pod yield and its component characters. Pod yield per plant exhibited significant positive correlation with 100-kernel weight and harvest index at both genotypic and phenotypic levels. Number of branches per plant exhibited significant positive correlation with shelling out-turn at both levels.

Choudhary *et al.* (2016) studied correlation in 27 genotypes for 15 characters in groundnut. The association study among characters revealed that dry pod yield was positively and significantly correlated with number of mature pods per plant and biological yield per plant and harvest index. Days to 50% flowering exhibited negative and significantly correlated with number of branches per plant. Plant height was positively and significantly correlated with number of branches per plant. Number of branches per plant was positively and significantly correlated with sound mature kernel at both levels. Biological yield per plant and harvest index were found to be positive and significantly correlated with number of matured pods per plant.

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.

Rao (2016) assessed correlation coefficients among different yield and its contributing traits in 30 groundnut genotypes under drought. The results of genotypic correlation analysis revealed that dry pod yield was significant positively correlated with kernel yield, number of pods per plant and 100-kernel weight.

Mukesh and Lal (2017) assessed correlation coefficients among different yield and its contributing traits in 40 genotypes groundnut. The results of phenotypic and genotypic correlation analysis revealed that pod yield was significantly and positively correlated with plant height and 100-kernel weight.

Trivikrama *et al.* (2017) studied character association for kernel yield and its component characters in six parents and their 15 $F_1$ crosses in groundnut. The genotypic correlation coefficients were observed to be relatively of higher magnitude than the corresponding genotypic and phenotypic correlation coefficients indicating strong inherent association between the characters. Kernel yield per plant possessed significant positive association with pod yield per plant, mature pods per plant, 100-kernel weight, pods per plant, harvest index and shelling out-turn at both the genotypic and phenotypic levels. Pod yield per plant was positively correlated at both genotypic and phenotypic level with number of matured pods per plant. Number of pods per plant was positively correlated with number of matured pods per plant.

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 number of matured pods per plant, sound mature kernel, 100-kernel weight, biological yield per plant and harvest index. Number of matured pods per plant had strong positive and highly significant correlation with sound mature kernel, biological yield per plant and harvest index at both genotypic and phenotypic level. Number of branches per plant registered positive genotypic and phenotypic associations with sound mature kernel and biological yield per plant. Biological yield and harvest index showed highly significant and strong positive correlation with sound mature kernel.

Mahesh *et al.* (2018) evaluated 144 genotypes of groundnut for 13 characters assess the correlation analysis. The pod yield per plant had significant positive correlation with mature pods per plant and sound mature kernel at phenotypic and genotypic levels. They also reported that significant and positive correlation was

observed 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 oil content. Number of matured pods per plant had strong positive and highly significant correlation with sound mature kernel at both genotypic and phenotypic level.

## 2.3 PATH ANALYSIS

Path analysis splits the correlation coefficient into direct and indirect effects. Path analysis showing direct and indirect effects is effective to get high selection response simultaneously for several characters from the diverse population and analysis could provide a more realistic picture of the interrelationship. The concept of partitioning of correlation into direct and indirect effects through path analysis was originally developed by Wright (1921), but the technique was first used for plant selection by Dewey and Lu (1959).

Methews *et al.* (2001) assessed path coefficient analysis for different component characters in groundnut. They reported that maximum direct effect on pod yield was exhibited by kernel yield per plant followed by plant height. The days to 50% flowering and plant height had positive indirect effect through kernel yield per plant.

Nagda and Joshi (2004) assessed path coefficient analysis and reported that the harvest index had positive and the highest direct effect followed by haulm yield. Among the indirect effects, the influence of 100-kernel weight through harvest index was positive and strong followed by indirect effect of shelling out-turn through haulm yield.

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.* (2008) performed path coefficient analysis to assess the relationship among different characters in summer bunch groundnut. The characters sound mature kernel, shelling out-turn and number of pods per plant recorded high

magnitude of direct effect. The direct negative effects were observed for number of pegs per plant and days to 50% flowering.

Giri *et al.* (2009) performed path coefficient analysis to assess the relationship among different characters in 20 genotypes of groundnut and stated that kernel yield exerted the highest positive direct effect on pod yield per plant, while other characters *viz.*, oil content, strong mature kernel, days to 50% flowering, test weight and days to maturity exhibited high indirect effect on dry pod yield *via* kernel yield.

Khanpara *et al.* (2010) evaluated ten genotypes of groundnut to accomplish path coefficient analysis for pod yield and its component characters. Number of mature pods per plant manifested maximum direct effect towards the pod yield per plant followed by days to maturity, biological yield per plant and 100-kernel weight.

Zaman *et al.* (2011) assessed path coefficient analysis for different yield and yield component characters. The number of mature pods per plant had high positive direct effect on seed yield per hectare followed by shelling out-turn and days to 50% flowering. The days to 50% flowering, number of branches per plant and 100-kernel weight had positive indirect effect through shelling out-turn.

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, number of pods per plant and days to maturity showed moderate and positive direct effect on pod yield per plant. The biological yield per plant had positive indirect effect through plant height, number of mature pods per plant and number of pods 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.

Kumar *et al.* (2014) used 66 genotypes of groundnut to study the path analysis. Pod yield per plant and shelling out-turn had high positive direct effect on kernel yield signifying the importance of these traits in the improvement of pod yield.

Yadlapalli (2014) performed path coefficient analysis to assess the relationship among different characters in groundnut. Number of pods per plant showed positive direct effect on pod yield per plant followed by 100-seed weight, number of branches per plant and days to 50% flowering. Number of pods per plant

and pod yield per plant had positive indirect effect through number of branches per plant.

Patil *et al.* (2015) conducted an experiment on 49 genotypes of groundnut for 16 plant characters to study path analysis for yield and its related traits and reported that number of immature pods per plant, number of mature pods per plant, 100-kernel weight and oil content exhibited positive direct effect on pod yield per plant, while days to maturity exhibited negative direct effect on pod yield per plant.

Rathod *et al.* (2015) evaluated 18 genotypes of groundnut to accomplish path coefficient analysis for pod yield and its component characters. The results revealed that days to maturity and oil content exhibited positive direct effect on pod yield per plant, while number of pods per plant exhibited positive indirect effect through harvest index, shelling out-turn and 100-kernel weight. Number of pods per plant, harvest index and 100-kernel weight revealed the highly significant positive phenotypic correlation with pod yield per plant.

Vasanthi *et al.* (2015) evaluated 29 groundnut cultures to study path association for yield and its related traits and reported that the number of pods per plant revealed the highly significant positive phenotypic correlation with number of matured pods per plant and positive direct effect towards pod yield observed for days to 50% flowering, number of immature pods per plant and shelling out-turn.

Vinutha *et al.* (2015) evaluated 6 $F_2$ crosses of groundnut genotypes to investigate the interrelationship among the yield attributing traits and physiological traits. Phenotypic path coefficient analysis further delineated that the direct effect for pod yield per plant was mainly accelerated by kernel yield per plant in all six crosses, while other characters had very low direct effects on pod yield and thus kernel yield is the important trait for enhancing pod yield in groundnut.

Ashutosh *et al.* (2016) 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, 100-kernel weight, number of pods per plant and plant height were observed to be the major indirect contributor towards pod yield through harvest index. Number of pods per plant, harvest index and 100-kernel weight revealed the highly significant positive phenotypic correlation with pod yield per plant. Positive direct effect towards pod yield was also observed for days to 50% flowering and shelling out-turn.

Choudhary *et al.* (2016) studied path analysis in 27 genotypes of 15 characters in groundnut. Path coefficient analysis revealed that kernel yield per plant, biological yield per plant and harvest index had maximum positive direct effect on dry pod yield per plant. Therefore, greater emphasis should be given on these characters while selecting for higher yield and related traits.

Namrata *et al.* (2016) evaluated 30 genotypes of groundnut to study the path coefficient analysis for different component characters. Path coefficient analysis revealed direct effect biological yield per plant and 100-kernel weight of 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.

Rao (2016) evaluated 30 groundnut genotypes under drought to study path coefficient analysis. Path coefficient analysis indicated that number of pods per plant and 100-kernel weight were essential traits to be considered for realizing the improvement in yield, as they exhibited positive direct effect toward pod yield. Shelling out turn had negative direct effect toward pod yield per plant. Kernel yield exhibited high and positive indirect effect *via* 100-kernel weight and shelling out-turn.

Bhargavi *et al.* (2017) evaluated 10 genotypes of virginia bunch groundnut to accomplish path coefficients for pod yield and its component characters. Path analysis studies revealed that days to 50% flowering and 100-kernel weight exerted high positive direct effect on pod yield per plant. Number of mature pods per plant exhibited positive indirect effect through biological yield per plant and shelling out-turn. Number of matured pods per plant, biological yield per plant and 100-kernel weight exerted highly significant positive phenotypic correlation with pod yield per plant.

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 kernel had negative direct effect toward pod yield per plant. Days to maturity, plant height and mature pod per plant were observed to be the positive indirect contributor towards pod yield through pods per plant.

Trivikrama *et al.* (2017) studied path analysis for kernel yield and its component characters in six parents and their 15 $F_1$ crosses in groundnut. The result revealed the importance of trait like pod yield per plant, mature pods per plant, 100-

kernel weight, pods per plant, harvest index and shelling out-turn as they had direct effects on kernel yield. Therefore, selection based on these characters will lead to simultaneous improvement in kernel yield in groundnut. Days to maturity were observed to be the positive indirect contributor towards pod yield through days to 50% flowering and plant height.

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. Number of branches per plant, number of mature pod per plant, sound mature kernel and dry pod yield per plant were observed to be the positive indirect contributor towards pod yield through biological yield per plant.

Mahesh *et al.* (2018) evaluated 144 genotypes of groundnut for 13 different characters to assess the path analysis and reported that the biological yield per plant, sound mature kernel, 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. Shelling percentage was observed to be the positive indirect contributor towards pod yield through plant height and positive direct effect towards pod yield observed for days to 50% flowering.

## 2.4 GENETIC DIVERGENCE

The breeding programme is based usually on their adaptation, yield potential, genetic diversity and other useful agronomic characters. The crosses among diverse parents are being expected 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). The review of literature pertaining to genetic divergence in groundnut is presented in the subsequent paragraphs;

Dashora and Nagda (2004) studied genetic divergence in groundnut by using 52 genotypes from different regions. The 52 genotypes were grouped into eleven clusters on the basis of $D^2$-values 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-graphic regions of India indicated 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 phenotypes were grouped into seven clusters. Maximum divergence was obtained between cluster I and cluster VII, followed by cluster VI and VII. Among the characters, day to first flowering contributed the most to total divergence (32.64%) followed by shelling percentage (16.85%) and reproductive efficiency (11.28%). The genotypes VR12 (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.

Venkataramana (2008) carried out genetic divergence analysis in 100 accessions of groundnut germplasm. The germplasm were grouped into seven clusters. Among the 15 characters considered the contribution was maximum of 100-kernel weight (19.8%) followed by haulm yield per plant (12.6%) and shelling out-turn percent (11.6%). The maximum inter-cluster distance was between the cluster IV and VI (0694.0). 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 out-turn, kernel yield per plant, oil content and oil yield per plant.

Korat *et al.* (2009b) studied 80 genotypes of groundnut and grouped into 9 clusters. The clustering pattern of the genotypes did not conform to the geographical distribution. The maximum inter cluster distance was observed between cluster I and VIII followed by cluster IV and VIII, cluster III and VIII and cluster II and VIII. The cluster VII showed high mean in respect to pod yield per plant, number of kernels per pods, 100-kernel weight and harvest index. The cluster I showed desirable value for days to 50% flowering and days to maturity. While higher number of primary branches was found in cluster V. The cluster VII was the best for plant height and biological yield per plant. The cluster IV and III had desirable values for shelling percentage and oil content, respectively. The cluster IX was the best for number of underground pegs per plant. It will advisable to inter cross among the genotypes from cluster I, II, III, IV and VIII for generation of transgressive segregates and wide spectrum genetic variability for improvement of pod yield in groundnut.

Sonone and Thaware (2009) studied 40 groundnut genotypes of different geographical origin for genetic diversity and reported that all these genotypes were grouped into 10 distinct for genetic clusters irrespective of their geographical origins. The cluster I was the largest cluster consisting of 23 genotypes followed by cluster V with 6 genotypes and cluster VI with 4 genotypes. Out of fifteen characters studied, oil content, number of pods per plant, and 100-seed weight contributed the maximum towards total divergence in the material.

Venkateswarlu *et al.* (2011) studied 74 groundnut genotypes using Mahalanobis's $D^2$ statistics and were grouped into 12 clusters. Maximum inter cluster distance was observed between cluster VII and X followed by cluster VI and XII indicating wide diversity among these genotypes. The characters 100-kernel weight, shelling out-turn and harvest index contributed maximum towards genetic divergence in both $D^2$ analysis and canonical root analysis.

Nirmala *et al.* (2013) studied 30 groundnut genotypes using Mahalanobis's $D^2$ statistics and were grouped in to 14 clusters. Maximum inter cluster distance was observed between cluster III and cluster XII followed by cluster V and cluster XIII indicating maximum divergence between the genotypes included these clusters. The characters weight of pods per plant, kernel weight per plant and plant height contributed maximum towards genetic divergence.

Yadav *et al.* (2014) evaluated 60 genotypes for 14 traits for variability with regards to yield, yield components and quality parameters. Based on $D^2$ analysis, the genotypes were grouped into 12 clusters. Maximum inter cluster distance was observed between cluster III and X. Therefore it is advisable to make crossing between the genotypes from cluster I with cluster X, cluster III, cluster V and cluster VIII for the generation of wide spectrum genetic variability and isolation of transgressive segregates for enhancement of pod yield in groundnut.

Gupta *et al.* (2015b) evaluated 60 groundnut genotypes using Mahalanobis's $D^2$-statistics and were grouped in to 13 clusters. Maximum inter cluster distance was found between cluster III and V followed by cluster IV and V and II and IV indicated that these groups of genotypes were highly divergent from each other. The genotypes in the above clusters reveled substantial difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters form ideal parents for yield improvement in groundnut.

Bhakhal and Lal (2015) studied genetic divergence using $D^2$ analysis of 40 genotypes of groundnut of different geographic origins which revealed existence of considerable diversity for eleven quantitative and qualitative characters. The genotypes were grouped into 7 clusters. The cluster VI was the largest containing 12 genotypes each 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 diversity among the genotypes measured by intra-cluster and inter-cluster distance was adequate for improvement of groundnut by hybridization and selection. The genotype included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in groundnut.

Vivekananda *et al.* (2015) evaluated 31 groundnut genotypes using Mahalanobis's $D^2$ statistics and were grouped in to seven clusters, where cluster I was largest containing eleven genotypes. Maximum inter cluster distance was found between cluster I and VI followed by cluster I and V, cluster III and VI and cluster I and IV. Considering the inter cluster distances and cluster means the genotypes from cluster I, III, V and VI could be selected for hybridization programme.

## 2.5 SELECTION 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 discriminate function technique over straight selection. This discriminant function technique over suitable selection indices was developed by Fisher (1936). The literature related to the selection indices in groundnut has been reviewed here under.

Chandra *et al.* (2003) evaluated 192 genotypes of groundnut to study suitable index of secondary traits that may be relatively less sensitive to genotype by environment interaction than yield and found that the selection index, based on median and semi inter-quartile range, which was actually used in identifying high yielding genotypes, had an efficiency that is comparable to the best index.

Dobariya *et al.* (2008) constituted selection indices in groundnut involving pod yield and its five components were constructed using the discriminant function techniques. 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.

Babariya *et al.* (2014) constituted selection indices in groundnut involving pod yield and its five components were constructed 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, days to maturity, number of pods per plant, kernel yield per plant and biological yield per plant recorded the highest genetic advance and relative efficiency followed by an index based on four characters *viz.*, pod yield per plant, number of pods per plant, kernel yield per plant and biological yield per plant.

Raghuwanshi *et al.* (2016) evaluated fifty diverse genotypes of groundnut for selection indices. Thirty-one selection indices involving pod yield per plant and four yield components *viz*., kernel yield per plant, harvest index, number of mature pods per plant and biological yield per plant were constructed using the discriminant function technique. Discriminant function analysis indicated that selection efficiency of the function was improved by increasing the number of characters in the index. Among the single character indices, 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 mature pods per plant and biological yield per plant recorded the highest genetic advance as well as relative efficiency and selection efficiency. These characters could be advantageously exploited in the groundnut breeding programmes.

# CHAPTER-III

## MATERIALS AND METHODS

The present experiment was conducted to assess the genetic variability, correlation, path analysis, genetic divergence and selection indices for pod yield and its component traits of virginia groundnut. The study was conducted during *kharif* 2018 at Instructional farm, College of Agriculture, J.A.U., Junagadh. Geographically Junagadh is situated at $21^0$.50' N latitude and $70^0$.00' E longitude with an altitude of 60 meters above the mean sea level. The soil of experimental site was medium black, alluvial in origin and medium in organic matter. The climate of the area represents tropical and semi-arid. The details of material used and the methods adopted in the investigation which was carried out at Instructional farm, College of Agriculture, J.A.U., Junagadh during *kharif* season of 2018 are described under the following heads. The details of weather parameters recorded for the year 2018 during which the experiment was conducted is presented in Appendix I.

### 3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of 60 genotypes of groundnut derived from different origins. The genotypes were obtained from the Main Oilseeds Research Station, Junagadh Agricultural University, Junagadh. List of genotypes used in the present study and their source are mentioned in Table 3.1.

### 3.2 EXPERIMENTAL DETAILS

Sixty genotypes of groundnut were sown in a Randomized Block Design (RBD) with three replications on 27, July-2018. Each genotype was accommodated in a single row of 3.0 meter length with a spacing of 60 cm between rows and 15 cm between plants within the row. The experiment was surrounded by two guard rows to avoid damage and border effects. The fertilizers in the experimental area was applied at the rate of 12.50 kg/ha $N_2$ and 25.0 kg/ha $P_2O_5$ as it is a recommended dose for *kharif* cultivation of groundnut in the region. Other recommended agronomical practices in vogue were followed for reaping good crop.

### 3.3 CHARACTERS STUDIED

The observations were recorded on five randomly selected and tagged plants

**Table 3.1 List of genotypes used in the present study and their source**

| Sr. No. | Name of genotypes | Source | Sr. No. | Name of genotypes | Source |
|---|---|---|---|---|---|
| 1 | 4343 | Patancheru, ICRISAT | 31 | ICGS-05 | Patancheru, ICRISAT |
| 2 | 4896 | Patancheru, ICRISAT | 32 | ICGV- 91026 | Patancheru, ICRISAT |
| 3 | 48-114 | Patancheru, ICRISAT | 33 | ICGV-00350 | Patancheru, ICRISAT |
| 4 | 59-112 | Patancheru, ICRISAT | 34 | ICGV-86325 | Patancheru, ICRISAT |
| 5 | 59-239 | Patancheru, ICRISAT | 35 | ICGV-86564 | Patancheru, ICRISAT |
| 6 | 72-39 | Patancheru, ICRISAT | 36 | ICGV-86590 | Patancheru, ICRISAT |
| 7 | AK 143 | PDVK, Akola | 37 | ICGV-87846 | Patancheru, ICRISAT |
| 8 | ALG-05-253 | Patancheru, ICRISAT | 38 | ICGV-89955 | Patancheru, ICRISAT |
| 9 | AMR-174 | Patancheru, ICRISAT | 39 | ICGV-9001 | Patancheru, ICRISAT |
| 10 | BAV-18 | Patancheru, ICRISAT | 40 | JVB- 154 | Junagadh (Gujarat) |
| 11 | C-156 | Patancheru, ICRISAT | 41 | JVB-147 | Junagadh (Gujarat) |
| 12 | CGC-07 | Patancheru, ICRISAT | 42 | JVB-49 | Junagadh (Gujarat) |
| 13 | CGC-1-19 | Patancheru, ICRISAT | 43 | JVR- HOC- 3 | Junagadh (Gujarat) |
| 14 | CSMG-2005-18 | CSAUA & T, Mainpuri | 44 | JVR-308 | Junagadh (Gujarat) |
| 15 | CSMG-884 | CSAUA & T, Mainpuri | 45 | JVR-309 | Junagadh (Gujarat) |
| 16 | CSMG-9101 | CSAUA & T, Mainpuri | 46 | JVR-HPS-2284 | Junagadh (Gujarat) |
| 17 | CSMG-9708 | CSAUA & T, Mainpuri | 47 | JVR-HPS-2289 | Junagadh (Gujarat) |
| 18 | CSMG-9907 | CSAUA & T, Mainpuri | 48 | K-1574 | ANGRAU (AP) |
| 19 | CSMG-HPS-9101 | CSAUA & T, Mainpuri | 49 | K-1577 | ANGRAU (AP) |
| 20 | EC-146615 | Exotic collection | 50 | K-1643 | ANGRAU (AP) |
| 21 | GG 11 | Junagadh (Gujarat) | 51 | KADIRI-7 | ANGRAU (AP) |
| 22 | GG 13 | Junagadh (Gujarat) | 52 | KAUSHAL | ANGRAU (AP) |
| 23 | GG 20 (C) | Junagadh (Gujarat) | 53 | KDG-123 | ANGRAU (AP) |
| 24 | GG 21 | Junagadh (Gujarat) | 54 | KDG-128 | ANGRAU (AP) |
| 25 | GG14 | Junagadh (Gujarat) | 55 | KDG-213 | ANGRAU (AP) |
| 26 | GJG 22 (C) | Junagadh (Gujarat) | 56 | NRCG-8 | Junagadh (Gujarat) |
| 27 | HNG-36 | Hanumangrah (RJ) | 57 | RG-382 | Durgapura (RJ) |
| 28 | HNG-56 B | Hanumangrah (RJ) | 58 | RG-438-2 | Durgapura (RJ) |
| 29 | HNG-57(A) | Hanumangrah (RJ) | 59 | RG-559-3 | Durgapura (RJ) |
| 30 | HNG-HPS-2 | Hanumangrah (RJ) | 60 | SOMNATH | Junagadh (Gujarat) |

from each genotype and average values were used for the statistical analysis. The procedure adopted for data collection of individual character is described below; Days to 50% flowering and days to maturity were recorded on plot basis. The technique/method used for measuring the characters is described as below;

**3.3.1 Quantitative characters**

**3.3.1.1 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.

**3.3.1.2 Days to maturity**

The total numbers of days was calculated from date of sowing to maturity in all plants in the plot at the time of harvesting.

**3.3.1.3 Plant height (cm)**

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

**3.3.1.4 Number of branches per plant**

The numbers of branches arising on main axis of each selected plant were counted at the time of harvesting.

**3.3.1.5 Number of matured pods per plant**

The numbers of fully developed seed bearing mature pods were counted at the time of harvest.

**3.3.1.6 Number of immature pods per plant**

The numbers of immature pods (undeveloped pods) were counted from each selected plant at the time of harvesting.

**3.3.1.7 Number of pods per plant**

The total number of pods (developed and undeveloped) of each selected plant were counted at the time of harvesting.

**3.3.1.8 Pod yield per plant (g)**

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

**3.3.1.9 Sound Mature Kernel (SMK) %**

The observations were made on the randomly selected kernels. From 100 kernels, mature sound and healthy kernels were separated, counted and recorded as sound mature kernel percentage according to the following formula.

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

**3.3.1.10 100-kernel weight (g)**

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

**3.3.1.11 Shelling out turn (%)**

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

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

**3.3.1.12 Biological yield per plant (g)**

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

**3.3.1.13 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.

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

**3.3.1.14 Oil content (%)**

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

**3.3.2 Qualitative characters**

**3.3.2.1 Leaflet size**

States:

Small < 4.0 cm

Medium < 4.0- 6.0 cm

Large > 6.0 cm

Stage of observation: Flowering

**3.3.2.2 Leaflet color**

States: Light green, green, dark green

Stage of observation: Flowering

**3.3.2.3 Stem: Pubescence**

State: Absent, sparse, medium, dense

Stage of observation: Flowering

**3.3.2.4 Inflorescence**

State: Simple, complicated

Stage of observation: Flowering

**3.3.2.5 Pod: Constriction**

State: Absent, shallow, medium, deep, very deep

Stage of observation: Within a month of harvest

**3.3.2.6 Pod: Texture (reticulation)**

State: Absent, slight, medium, prominent, very prominent

Stage of observation: Within a month of harvest

**3.3.2.7 Pod: Prominence of beak**

State: Absent, slight, medium, prominent, very prominent

Stage of observation**:** Within a month of harvest

**3.3.2.8 Pod: Shape of beak**

State: Straight, curved

Stage of observation**:** Within a month of harvest

**3.3.2.9 Pod: Number of kernels (on 100 pod basis)**

State:

> 60% 1 seeded

> 60% 2 seeded

> 60% 3 seeded

> 60% 4 seeded

Stage of observation: Within a month of harvest

**3.3.2.10 Varieties with monochrome testa only: Kernel: Color of testa**

State: White, off-white, tan, rose, salmon, red, dark red, purple, dark purple

Stage of observation: Within a month of harvest

**3.3.2.11 Kernel: Color**

State: Monochrome, variegated

Stage of observation: Within a month of harvest

**3.3.2.12 Kernel: Shape**

State: Spheroidal, cylindrical and fusiform

Stage of observation: Within a month of harvest

## 3.4 STATASTICAL ANALYSIS

The replication wise mean values of five randomly selected plants were used for the statistical analysis for fourteen characters studied.

### 3.4.1 Analysis of variance

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, path analysis, genetic divergence and selection indices. The analysis of variance for RBD was based on following linear model;

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

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:

| **Sources** | **d. f.** | **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

$M_g$ = Mean sum of squares for genotype

$M_r$ = Mean sum of squares for replication

$M_e$ = 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).

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

Where,

$\sigma_p^2$ = Phenotypic variance

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

**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 PCV and GCV values were categorized as described by Sivasubramanian and Menon (1973).

| GCV and PCV values | Classification |
|---|---|
| 0-10 | Low |
| 10-20 | Medium |
| 20 and above | High |

**c) 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 given by Hanson *et al.* (1956).

| Heritability (%) | Classification |
|---|---|
| 0-30 | Low |
| 30-60 | Medium |
| 60 and above | High |

**d) Genetic advance (GA)**

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

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

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:

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

Classification of expected genetic advance as per cent of mean followed as described by Johnson *et al.* (1955).

| GAM | Classification |
|---|---|
| 0-10 | Low |
| 10-20 | Medium |
| 20 and above | High |

### 3.4.3 Correlation coefficients

Correlation coefficients measure the relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences.

The phenotypic and genotypic correlation coefficients of all the pair of characters were worked-out as per Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis. Phenotypic and genotypic covariances for pair of characters were calculated in the similar fashion as variance for individual character. The format of analysis of covariance is given as under.

| 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) | $M_e$ | $Cove_{1.2}$ |

Where,

r = Number of replications

g = Number of genotypes

Cov = Covariance

**(i) Genotypic covariance**

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

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**

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

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). Now, genotypic and phenotypic correlation coefficients were worked out according to formula described below;

**(a) Genotypic correlation coefficient**

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

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**

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

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

**(c) 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 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).

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

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

, , , , ,

, , , , ,

, , , , ,

, , , , ,

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

Where,

$r_{1y}$, $r_{2y}$, $r_{3y}$,……., $r_{13y}$ are the genotypic correlations of days to 50% flowering, days to maturity, plant height, number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, shelling out-turn, 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, number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of

pods per plant, sound mature kernel, 100-kernel weight, shelling out-turn, 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 (pod yield per plant) due to uncontrolled causes was estimated by subtracting this value of coefficient of determination from unity. Path coefficient was rated as suggested by Lenka and Mishra (1973).

| Scales | Classification |
|---|---|
| > 1.0 | Very high |
| 0.30 – 0.99 | High |
| 0.20 – 0.29 | Moderate |
| 0.10 – 0.19 | Low |
| 0.00 – 0.09 | Very low |

**3.4.5 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 $d_1, d_2,\ldots, d_p$ as $\overline{X}^1_1 - \overline{X}^2_1$, $\overline{X}^1_2 - \overline{X}^2_2$ ,……$\overline{X}^1_p - \overline{X}^2_p$ , respectively being the differences in the means of two genotypes, Mahalanobis's $D^2$ statistician be defined as follows:

$$pD^2 = b_1d_1 + b_2d_2 + \ldots\ldots\ldots\ldots + b_pd_p$$

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 genotypes 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 distances between all possible combinations of the two clusters

$n_i$ = Number of genotypes in $i^{th}$ cluster

$n_j$ = Number of genotypes in $j^{th}$ cluster

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.

**3.4.6 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

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

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

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

The matrix form of above simultaneous equation is as under:

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

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 '$b_i$' values in the following manner

$$b_i = X^{-1}. G. a$$

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% (k = 2.06)

$a_i$ = Economic weightage

$b_i$ = Regression coefficient

$G_{ij}$ = Genotypic variance-covariance matrix

$P_{ij}$ = 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%.

$$RI\ \% = \left[\frac{GA(D)}{GA(S)}\right] \times 100$$

Where,

RI = Relative efficiency

GA (D) = Genetic advance through discriminant function

GA (S) = Genetic advance through straight selection

# CHAPTER-IV

## EXPERIMENTAL RESULTS

The results presented in this chapter comprise different aspects undertaken during the present study on "Genetic variability, correlation, path analysis, genetic divergence and selection indices for pod yield and its component traits in virginia groundnut (*Arachis hypogaea* L.)". These aspects are:

4.1 Analysis of variance

4.2 Genetic variability

4.3 Correlation coefficients

4.4 Path analysis

4.5 Genetic divergence

4.6 Selection indices

4.7 Classification of qualitative characters

### 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 taken under study. Highly significant differences among the replications was observed for days to maturity and sound mature kernel, while significant difference among the replications was observed for number of matured pods per plant.

### 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 60 genotypes of virginia groundnut for all the 14 characters are given in Appendix II. The standard error of mean (S.Em.±), critical difference (C.D.) and coefficient of variation (C.V.%) are presented in Table 4.2.

##### 4.2.1.1 Days to 50% flowering

The mean values for days to 50% flowering ranged from 31.01 days (ICGV-

87846) to 52.33 days (ICGV-00350). The genotype ICGV-87846 was the earliest to 50% flowering appearance (31.01 days) followed by JVB-49 (32.55 days), ICGV-86590 (32.66 days) and CGC-07 (34.80 days) while, ICGV-00350 registered maximum number of days to 50% flowering (52.33 days) followed by JVB-147 (51.73 days), 48-114 (50.52 days) and EC-146615 (50.4 days). The overall mean for days to 50 % flowering was 43.28 days.

#### 4.2.1.2 Days to maturity

The mean values for days to maturity ranged from 117.41 days (KDG-128) to 139.20 days (ICGV-00350). The genotype KDG-128 was the earliest in maturity (117.41 days) followed by ICGV-87846 (120.00 days), SOMNATH (122.00 days) and JVB-49 (122.85 days). ICGV-00350 (139.20 days) registered maximum number of days to maturity followed by JVB-147 (139.00 days), EC-146615 (137.00 days) and RG-438-2 (136.79 days). The overall mean for days to maturity was 128.88 days.

#### 4.2.1.3 Plant height (cm)

The mean values for plant height ranged from 12.71 cm (JVR-HPS-2289) to 33.30 cm (CGC-1-19). The genotype CGC-1-19 exhibited maximum plant height 33.30 cm followed by the EC-146615 (30.93 cm), ICGV-86564 (29.35 cm) and RG-382 (27.93 cm). Genotype JVR-HPS-2289 was having lowest plant height (12.71 cm) followed by ICGV-9001 (13.22 cm), RG-438-2 (13.27 cm), CGC-07 (14.97 cm). The overall mean for plant height was 21.13 cm.

#### 4.2.1.4 Number of branches per plant

The mean values for numbers of branches per plant ranged from 2.37 (GG 11) to 3.63 (AK 143). The genotype AK 143 (3.63) was exhibited maximum numbers of branches per plant followed by CSMG-9101 (3.40), NRCG-8 (3.40) and JVR-309 (3.37). The genotype GG 11 (2.37) exhibited minimum numbers of branches per plant followed by GG13 (2.63), GG 14 (2.67) and ICGV-00350 (2.70). The overall mean for this character was 3.05 branches per plant.

#### 4.2.1.5 Number of matured pods per plant

The numbers of matured pods per plant ranged from 2.70 (AMR-174) to 20.50 (ICGS-05). Among the genotypes, the maximum number of matured pods per plant (20.50) was observed in ICGS-05 followed by K-1577 (19.00), 48-114 (17.30) and

HNG-36 (15.73). The genotype AMR-174 (2.70) was exhibited minimum numbers of matured pods per plant followed by ICGV-86564 (6.07), CSMG-9907 (8.27) and BAV-18 (8.43). The overall mean for this character was 12.25 matured pods per plant.

**4.2.1.6 Number of immature pods per plant**

The numbers of immature pods per plant ranged from 3.44 (59-112) to 8.03 (BAV-18). Among the genotypes, the minimum number of immature pods per plant (3.44) was observed in 59-112 followed by 59-239 (3.57), JVB-154 (3.61) and ICGV-86564 (3.63). Among the genotypes, the maximum number of immature pods per plant (8.03) was observed in BAV-18 followed by CSMG-2005-18 (7.08), EC-146615 (6.99) and 4896 (6.40). The overall mean for this character was 4.91 immature pods per plant.

**4.2.1.7 Number of pods per plant**

The numbers of pods per plant ranged from 10.08 (ICGV-86564) to 25.30 (ICGS-05). Among the genotypes, ICGS-05 possessed maximum number of pods per plant (25.30) followed by 48-11 and JVR- HOC- 3 (22.59), GJG 22 (20.85) and HNG-57(A) (20.61). The minimum number of pods per plant (10.08) was observed in ICGV-86564 followed by HNG-HPS-2 (11.87), 59-112 and JVR-308 (12.4) and CSMG-9907 and RG-438-2 (13.05). The overall mean for this character was 17.10 pods per plant.

**4.2.1.8 Pod yield per plant (g)**

The pod yield per plant ranged from 9.00 g (ICGV-86564) to 20.76 g (ICGS-05). The genotype ICGS-05 performed the highest pod yield per plant (20.76 g) followed by ALG-05-253 (19.00 g), K-1577 (18.95 g) and KDG-128 (18.8 g). Among the genotypes, low pod yield per plant (9.00 g) was observed in ICGV-86564 followed by CGC-1-19 (9.11 g), 59-112 (9.80 g) and RG-438-2 (9.85 g). The overall mean for this character was 14.17 g.

**4.2.1.9 Sound mature kernel (%)**

The sound mature kernel percentage ranged from 56.05% (ICGV-86564) to 89.99% (ICGS-05). The highest value of sound mature kernel (%) was exhibited by

**Table 4.1 Analysis of variance for 14 characters in 60 genotypes of virginia groundnut**

| Source | d.f. | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of branches per plant | Number of matured pods per plant | Number of immature pods per plant | Number of pods per plant |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| **Replications** | 2 | 11.9341 | 135.9747** | 11.6094 | 0.1905 | 5.1981* | 0.4522 | 3.0805 |
| **Genotypes** | 59 | 65.2339** | 54.2191** | 58.7761** | 0.1598** | 19.2737** | 2.4095** | 43.3282** |
| **Error** | 118 | 4.0525 | 16.8116 | 4..8102 | 0.0639 | 1.4917 | 0.4714 | 3.4944 |

| Source | d.f. | Pod yield per plant (g) | Sound mature kernel (SMK) % | 100-kernel weight (g) | Shelling out-turn (%) | Biological yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| **Replications** | 2 | 4.5252 | 199.4029** | 2.8742 | 1.2184 | 23.6520 | 26.7481 | 18.0535 |
| **Genotypes** | 59 | 25.0756** | 73.7528** | 82.9483** | 195.8598** | 244.7947** | 49.3096** | 10.5515** |
| **Error** | 118 | 2.2926 | 16.9077 | 17.4661 | 15.6735 | 17.2297 | 12.3493 | 5.8857 |

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

ICGS-05 (89.99%) followed by 48-114 (87.16%), K-1577 (86.63%) and ICGV-86590 (85.18%). Among the genotypes, the minimum number of sound mature kernel (%) was exhibited by ICGV-86564 (56.05%) followed by CSMG-9907 (66.23%), BAV-18 (68.53%) and 59-112 (70.88%). The mean for sound mature kernel was 77.62%.

#### 4.2.1.10 100-kernel weight (g)

The magnitude of 100-kernel weight ranged from 52.56 g (JVR-HPS-2289) to 31.20 g (CSMG-2005-18). The genotype JVR-HPS-2289 was having maximum 100-kernel weight (52.56 g) followed by KADIRI-7 (51.97 g), GJG 22 (51.8 g) and ICGV-00350 (50.63 g). Among the genotypes, the minimum number of 100-kernel weight was exhibited by CSMG-2005-18 (31.20 g), 59-239(32.20 g) and ICGV-86590 (32.52 g). The mean for 100-kernel weight was 42.72 g.

#### 4.2.1.11 Shelling out-turn (%)

The shelling out-turn (%) ranged from 56.16% (CSMG-2005-18) to 88.26% (ICGV-89955). The genotype CSMG-2005-18 (56.16%) showed the minimum shelling out-turn percentage followed by 59-239 (57.96%), ICGV-86590 (58.54%) and CSMG-HPS-9101 (62.16%). Among the genotypes, the maximum number of shelling out-turn percentage exhibited by ICGV-89955 (88.26%), ICGV-00350 (88.20%), KDG-128 (87.79%) and RG-438-2 (87.72%). The overall mean for shelling out-turn was 75.17%.

#### 4.2.1.12 Biological yield per plant (g)

The biological yield per plant ranged from 39.73 g (4343) to 72.00 g (ICGS-05). The genotype ICGS-05 (72.00 g) observed with maximum biological yield per plant followed by both EC-146615 and K-1577 (71.00 g), GJG 21 (70.95 g) and KDG-123 (70.52 g). The genotype 4343 (39.73 g) showed the minimum biological yield per plant followed by JVR-309 (40.15 g), 59-112 (41.22 g) and GG 21 (42.33 g). The overall mean for biological yield per plant was 59.33 g.

#### 4.2.1.13 Harvest index (%)

The harvest index ranged from 15.16% (CGC-1-19) to 33.94% (ICGS-05). The genotype ICGS-05 (33.94%) had the highest harvest index followed by 48-114 (33.03%), ALG-05-253 (32.82%) and CSMG-9708 (31.65%).The genotype CGC-1-19 (15.16%) showed the minimum harvest index followed by ICGV-86564 (17.41%),

**Table 4.2 Mean, range of variation, phenotypic (PCV%) and genotypic (GCV%) coefficients of variation, heritability (broad sense), genetic advance and genetic advance expressed as percentage of mean for 14 characters in virginia groundnut**

| Character | Mean | Range | PCV (%) | GCV (%) | Heritability (broad sense) $h^2_{(bs)}$ (%) | Genetic advance (Gs) | Genetic advance expressed as percentage of mean GAM (%) |
|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | 43.28 | 31.01-52.33 | 10.77 | 10.43 | 93.79 | 9.01 | 20.81 |
| **Days to maturity** | 128.88 | 117.41-139.20 | 3.30 | 2.74 | 68.99 | 6.04 | 4.69 |
| **Plant height (cm)** | 21.13 | 12.71-33.30 | 20.95 | 20.07 | 91.82 | 8.37 | 39.62 |
| **No. of branches per plant** | 3.05 | 2.37-3.63 | 7.56 | 5.86 | 60.02 | 0.28 | 9.35 |
| **No. of matured pods per plant** | 12.25 | 6.07-20.50 | 20.69 | 19.87 | 92.26 | 4.82 | 39.32 |
| **No. of immature pods per plant** | 4.91 | 3.43-8.03 | 18.25 | 16.37 | 80.44 | 1.49 | 30.24 |
| **No. of pods per plant** | 17.09 | 10.08-25.30 | 16.13 | 14.88 | 85.03 | 4.83 | 28.26 |
| **Pod yield per plant (g)** | 14.17 | 9.00-20.76 | 20.59 | 19.66 | 91.21 | 5.48 | 38.68 |
| **Sound mature kernel (SMK) %** | 77.62 | 56.05-89.99 | 6.39 | 5.61 | 77.08 | 7.87 | 10.14 |
| **100-kernel weight (g)** | 42.72 | 31.20-51.97 | 12.31 | 10.94 | 78.94 | 8.55 | 20.02 |
| **Shelling out-turn (%)** | 75.17 | 56.16-88.26 | 10.75 | 10.31 | 92.00 | 15.31 | 20.37 |
| **Biological yield per plant (g)** | 59.33 | 39.73-72.00 | 15.22 | 14.68 | 92.96 | 17.30 | 29.16 |
| **Harvest index (%)** | 24.85 | 15.16-33.94 | 16.31 | 14.12 | 74.96 | 6.26 | 25.19 |
| **Oil content (%)** | 45.88 | 41.40-50.18 | 4.09 | 2.72 | 44.22 | 1.71 | 3.72 |

RG-438-2 (17.46%) and BAV-18 (18.51%). The overall mean was 24.85% for harvest index.

#### 4.2.1.14 Oil content (%)

The oil content ranged from 41.40% (RG-559-3) to 50.18% (JVB-49). The genotype JVB-49 registered maximum oil content 50.18% followed by 59-112 (49.30%), AK 143 (48.80%) and ICGV-86590 (48.78%). The genotype RG-559-3 (41.40%) showed the minimum oil content followed by GG 14 (41.58%), GG 20 (42.40%) and GG 11 (42.78%). The overall mean for oil content was 45.88%.

### 4.2.2 Phenotypic coefficient of variation

Phenotypic coefficients of variation for all the characters are given in Table 4.2. The highest phenotypic coefficient of variation was observed for plant height (20.95%) followed by number of matured pods per plant (20.69%), pod yield per plant (20.59%). The number of immature pods per plant (18.25%), harvest index (16.31%), biological yield per plant (15.22%), 100-kernel weight (12.31%), days to 50% flowering (10.77%) and shelling out-turn (10.75%) expressed moderate phenotypic coefficient of variation. The number of branches per plant (7.56%), sound mature kernel (6.39%), oil content (4.09%) and days to maturity (3.30%) exhibited low 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. The highest genotypic coefficient of variation was observed for plant height (20.07%). Number of matured pods per plant (19.87%), pod yield per plant (19.66%), number of immature pods per plant (16.37%), number of pods per plant (14.88%), biological yield per plant (14.68%), harvest index (14.12%), 100-kernel weight (10.94%), days to 50% flowering (10.43%) and shelling out-turn (10.31%) reported moderate genotypic coefficient of variation. The number of branches per plant (5.86%), sound mature kernel (5.61%), days to maturity (2.74%) and oil content (2.72%) registered low value for genotypic coefficient of variation.

### 4.2.4 Heritability

The estimate of heritability for different characters is presented in Table 4.2. The highest heritability was observed for days to 50% flowering (93.79%) followed

by biological yield per plant (92.96%), number of matured pods per plant (92.26%), shelling out-turn (92.00%), plant height (91.82%), pod yield per plant (91.21%), number of pods per plant (85.03%), number of immature pods per plant (80.44%), 100-kernel weight (78.94%), sound mature kernel (77.08%), harvest index (74.96%), days to maturity (68.99%) and number of branches per plant (60.02%). The moderate heritability estimates were recorded for oil content (44.22%).

### 4.2.5 Genetic advance

The value of genetic advance was high for biological yield per plant (17.3 g), shelling out-turn (15.31%). The estimates were moderate for days to 50% flowering (9.01 days), 100-kernel weight (8.55 g), plant height (8.37 cm), sound mature kernel (7.87%), harvest index (6.26%), days to maturity (6.04 days), pod yield per plant (5.48 g), number of pods per plant (4.83), number of mature pods per plant (4.82), number of immature pods per plant (1.49) and oil content (1.71%). The value was low for number of branches per plant (0.28).

### 4.2.6 Genetic advance expressed as percentage of mean

Genetic advance expressed as percentage of mean is presented in Table 4.2. The highest genetic advance as percentage of mean was observed for plant height (39.62%) followed by number of matured pods per plant (39.32%), pod yield per plant (38.68%), number of immature pods per plant (30.24%), biological yield per plant (29.16%), number of pods per plant (28.26%), harvest index (25.19%), days to 50% flowering (20.81%), shelling out-turn (20.37%) and 100-kernel weight (20.02%). The values were moderate for sound mature kernel (10.14%). Low values of genetic advance expressed as percentage of mean were observed for number of branches per plant (9.35%), days to maturity (4.69%) and oil content (3.72%).

## 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 correlation coefficients.

### 4.3.1 Pod yield per plant (g)

The pod yield per plant had highly significant and positive correlations both at genotypic and phenotypic levels with number of matured pods per plant ($r_g$=0.8216, $r_p$=0.7457), number of pods per plant ($r_g$=0.8660, $r_p$=0.7568), sound mature kernels ($r_g$=0.7618, $r_p$=0.6317), 100-kernel weight ($r_g$=0.4728, $r_p$=0.4128), shelling out-turn ($r_g$=0.3565, $r_p$=0.3388), biological yield ($r_g$=0.6113, $r_p$=0.5748) and harvest index ($r_g$=0.7083, $r_p$=0.6051), while significant and positive correlations with number of immature pods per plant only at genotypic level ($r_g$=0.3246). The pod yield per plant had non-significant and positive correlation both at genotypic and phenotypic levels with days to 50% flowering ($r_g$=0.2044, $r_p$=0.1689) and days to maturity ($r_g$=0.0281, $r_p$=0.0195). The pod yield per plant had non-significant and negative correlation both at genotypic and phenotypic levels with plant height ($r_g$=-0.1195, $r_p$=-0.1176), number of branches per plant ($r_g$=-0.1432, $r_p$=-0.0829) and oil content ($r_g$=-0.0077, $r_p$=-0.0002).

### 4.3.2 Days to 50% flowering

The days to 50% flowering had positive and highly significant correlations at both genotypic and phenotypic levels with days to maturity ($r_g$=1.0510, $r_p$=0.8347) and number of immature pods per plant ($r_g$=0.3769, $r_p$=0.3226).

### 4.3.3 Days to maturity

The days to maturity had positive and highly significant genotypic and phenotypic associations with days to 50% flowering ($r_g$=1.0510, $r_p$=0.8347). All the characters except days to 50% flowering were found to be non-significant with days to maturity.

### 4.3.4 Plant height (cm)

Plant height had positive genotypic and phenotypic associations with days to 50% flowering ($r_g$=0.2070, $r_p$=0.1894), days to maturity ($r_g$=0.1733, $r_p$=0.1355), number of branches per plant ($r_g$=0.0254, $r_p$=0.0016), number of immature pods per plant ($r_g$=0.1671, $r_p$=0.1303). Plant height had significant and highly significant negative significant negative correlation both at genotypic and phenotypic levels with 100-kernel weight ($r_g$=-0.3394, $r_p$=-0.3301) and shelling out-turn ($r_g$=-0.4608, $r_p$=-0.4091), respectively.

**Table 4.3 Genotypic ($r_g$) and phenotypic ($r_p$) correlation coefficients among 14 characters in 60 genotypes of virginia groundnut**

| Character | Corr. | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of branches per plant | Number of matured pods per plant | Number of immature pods per plant | Number of pods per plant | SMK % | 100-kernel weight (g) | Shelling out-turn (%) | Biological yield (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Pod yield per plant (g)** | $r_g$ | 0.2044 | 0.0281 | -0.1195 | -0.1432 | 0.8216** | 0.3246* | 0.8660** | 0.7618** | 0.4728** | 0.3565** | 0.6113** | 0.7083** | -0.0077 |
| | $r_p$ | 0.1689 | 0.0195 | -0.1176 | -0.0829 | 0.7457** | 0.2590 | 0.7568** | 0.6317** | 0.4128** | 0.3388* | 0.5748** | 0.6051** | -0.0002 |
| **Days to 50% flowering** | $r_g$ | **1.0000** | 1.0510** | 0.2070 | -0.2307 | 0.1207 | 0.3769** | 0.1822 | 0.1726 | 0.0617 | 0.0989 | 0.1218 | 0.2132 | -0.1005 |
| | $r_p$ | **1.0000** | 0.8347** | 0.1894 | -0.1645 | 0.1146 | 0.3226* | 0.1911 | 0.1511 | 0.0639 | 0.0887 | 0.1135 | 0.1647 | -0.1053 |
| **Days to maturity** | $r_g$ | | **1.0000** | 0.1733 | -0.2383 | -0.0139 | 0.2604 | 0.0433 | 0.0497 | 0.1242 | 0.0709 | 0.0241 | 0.0479 | -0.2417 |
| | $r_p$ | | **1.0000** | 0.1355 | -0.1396 | -0.0093 | 0.1873 | 0.0271 | 0.0289 | 0.0629 | 0.0646 | 0.0241 | 0.0414 | -0.1562 |
| **Plant height (cm)** | $r_g$ | | | **1.0000** | 0.0254 | -0.0554 | 0.1671 | -0.0238 | -0.0763 | -0.3394* | -0.4608** | -0.0203 | -0.0657 | -0.1261 |
| | $r_p$ | | | **1.0000** | 0.0016 | -0.0437 | 0.1303 | -0.0069 | -0.0542 | -0.3301* | -0.4091** | -0.0092 | -0.0718 | -0.0555 |
| **Number of branches per plant** | $r_g$ | | | | **1.0000** | -0.0266 | -0.0326 | -0.0038 | 0.0847 | -0.1178 | 0.0032 | 0.0860 | -0.2243 | 0.4471** |
| | $r_p$ | | | | **1.0000** | -0.0087 | 0.0119 | -0.0133 | 0.0439 | -0.0369 | 0.0010 | 0.0901 | -0.1102 | 0.2284 |
| **Number of matured pods per plant** | $r_g$ | | | | | **1.0000** | 0.1338 | 1.0588** | 0.9532** | -0.0048 | -0.0610 | 0.5962** | 0.6607** | 0.1203 |
| | $r_p$ | | | | | **1.0000** | 0.1134 | 0.9520** | 0.8782** | -0.0054 | -0.0624 | 0.5709** | 0.5475** | 0.0634 |
| **Number of immature pods per plant** | $r_g$ | | | | | | **1.0000** | 0.4817** | 0.1990 | -0.0547 | 0.0359 | 0.4248** | 0.1285 | -0.2443 |
| | $r_p$ | | | | | | **1.0000** | 0.3792** | 0.1474 | -0.0301 | 0.0152 | 0.3556** | 0.1003 | -0.1374 |
| **Number of pods per plant** | $r_g$ | | | | | | | **1.0000** | 0.9985** | 0.0142 | -0.0345 | 0.6707** | 0.7007** | 0.0625 |
| | $r_p$ | | | | | | | **1.0000** | 0.8425** | 0.0076 | -0.0186 | 0.6002** | 0.5453** | 0.0097 |
| **Sound mature kernel (SMK%)** | $r_g$ | | | | | | | | **1.0000** | 0.0312 | 0.0029 | 0.5222** | 0.6479** | 0.2284 |
| | $r_p$ | | | | | | | | **1.0000** | 0.0152 | 0.0022 | 0.4776** | 0.5106** | 0.1011 |
| **100-kernel weight (g)** | $r_g$ | | | | | | | | | **1.0000** | 0.9818** | 0.2458 | -0.1134 | 0.0874 |
| | $r_p$ | | | | | | | | | **1.0000** | 0.8354** | 0.2247 | -0.0223 | 0.0241 |
| **Shelling out-turn (%)** | $r_g$ | | | | | | | | | | **1.0000** | 0.1429 | 0.0849 | -0.0895 |
| | $r_p$ | | | | | | | | | | **1.0000** | 0.1382 | 0.0651 | -0.0241 |
| **Biological yield per plant (g)** | $r_g$ | | | | | | | | | | | **1.0000** | -0.1246 | -0.0287 |
| | $r_p$ | | | | | | | | | | | **1.0000** | -0.1010 | -0.0345 |
| **Harvest index (%)** | $r_g$ | | | | | | | | | | | | **1.0000** | 0.0105 |
| | $r_p$ | | | | | | | | | | | | **1.0000** | 0.0237 |
| **Oil content (%)** | $r_g$ | | | | | | | | | | | | | **1.0000** |
| | $r_p$ | | | | | | | | | | | | | **1.0000** |

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

### 4.3.5 Number of branches per plant

Number of branches per plant exhibited positive and non-significant genotypic and phenotypic associations with plant height ($r_g$=0.0254, $r_p$=0.0016), sound mature kernel ($r_g$=0.0847, $r_p$=0.0439), shelling out-turn ($r_g$=0.0032, $r_p$=0.0010) and biological yield per plant ($r_g$=0.0860, $r_p$=0.0901). Number of branches per plant exhibited highly significant and positive genotypic associations with oil content ($r_g$=0.4471).

### 4.3.6 Number of matured pods per plant

Number of matured pods per plant was found to be highly significant and positively correlated with number of pods per plant ($r_g$=1.0588, $r_p$=0.9520), pod yield per plant ($r_g$=0.8216,$r_p$=0.7457), sound mature kernel ($r_g$=0.9532, $r_p$=0.8782), biological yield per plant ($r_g$=0.5962, $r_p$=0.5709) and harvest index ($r_g$=0.6607, $r_p$=0.5475) both at genotypic and phenotypic levels.

### 4.3.7 Number of immature pods per plant

Number of immature pods per plant was found to be highly significant and positively correlated with number of pods per plant ($r_g$=0.4817, $r_p$=0.3792) and biological yield per plant ($r_g$=0.4248, $r_p$=0.3556) at both genotypic and phenotypic levels. Number of immature pods per plant was found to be highly significant and positively correlated with days to 50% flowering ($r_g$=0.3769) at genotypic level; significant and positively correlated with pod yield per plant ($r_g$=0.3246) at genotypic level and days to 50% flowering ($r_p$=0.3226) at phenotypic level.

### 4.3.8 Number of pods per plant

Number of pods per plant exhibited highly significant and positive correlations at both genotypic and phenotypic levels with number of matured pods per plant ($r_g$=1.0588, $r_p$=0.9520), number of immature pods per plant ($r_g$=0.4817, $r_p$=0.3792), pod yield per plant ($r_g$=0.8660, $r_p$=0.7568), sound mature kernel ($r_g$=0.9985, $r_p$=0.8425), biological yield per plant ($r_g$=0.6707, $r_p$=0.6002) and harvest index ($r_g$=0.7007, $r_p$=0.5453).

### 4.3.9 Sound mature kernel (SMK) %

This character showed highly significant and positive correlations both at genotypic and phenotypic levels with number of matured pods per plant ($r_g$=0.9532, $r_p$=0.8782), number of pods per plant ($r_g$=0.9985, $r_p$=0.8425), pod yield per plant ($r_g$=0.7618,

$r_p$=0.6317), biological yield per plant ($r_g$=0.5222, $r_p$=0.4776) and harvest index ($r_g$=0.6479, $r_p$=0.5106).

**4.3.10 100-kernel weight (g)**

100-kernel weight had highly significant and positive genotypic and phenotypic associations only with pod yield per plant ($r_g$=0.4728, $r_p$=0.4128) and shelling out-turn ($r_g$=0.9818, $r_p$=0.8354). 100-kernel weight had significant and negative genotypic and phenotypic associations only with plant height ($r_g$=-0.3394, $r_p$=-0.3301).

**4.3.11 Shelling out-turn (%)**

Shelling out-turn had highly significant and positive genotypic and phenotypic associations with pod yield per plant ($r_g$=0.3565, $r_p$=0.3388) and 100-kernel weight ($r_g$=0.9818, $r_p$=0.8354). Shelling out-turn had highly significant and negative association with plant height ($r_g$=-0.4608, $r_p$=-0.4091) at both genotypic and phenotypic levels.

**4.3.12 Biological yield per plant (g)**

Biological yield per plant had highly significant and positive associations with number of matured pods per plant ($r_g$=0.5962, $r_p$=0.5709), number of immature pods per plant ($r_g$=0.4248, $r_p$=0.3556), number of pods per plant ($r_g$=0.6707, $r_p$=0.6002), pod yield per plant ($r_g$=0.6113, $r_p$=0.5748) and sound mature kernel ($r_g$=0.5222, $r_p$=0.4776) at both genotypic and phenotypic levels.

**4.3.13 Harvest index (%)**

Harvest index had highly significant and positive genotypic and phenotypic associations with number of matured pods per plant ($r_g$=0.6607, $r_p$=0.5475), number of pods per plant ($r_g$=0.7007, $r_p$=0.5453), pod yield per plant ($r_g$=0.7083, $r_p$=0.6051) and sound mature kernel ($r_g$=0.6479, $r_p$=0.5106).

**4.3.14 Oil content (%)**

Oil content registered non-significant and negative correlation with days to 50% flowering ($r_g$=-0.1005, $r_p$=-0.1053), days to maturity ($r_g$=-0.2417, $r_p$= -0.1562), plant height ($r_g$=-0.1261, $r_p$=-0.0555), number of immature pods per plant($r_g$= -0.2443, $r_p$= -0.1374), shelling out-turn ($r_g$=-0.0895, $r_p$=-0.0241) and biological yield per plant

($r_g$=-0.0287, $r_p$=-0.0345). Oil content had highly significant and positive association with number of branches per plant ($r_g$=0.4471) at only genotypic level.

## 4.4 PATH ANALYSIS

The phenotypic correlation coefficients calculated for different pairs of character were subjected to path coefficient analysis for partitioning these values into 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. The path coefficient analysis revealed the cause and effect relationship which is shown in Figure 4.1.

### 4.4.1 Days to 50% flowering v/s pod yield per plant

Days to 50% flowering had non-significant and positive correlation with pod yield per plant ($r_p$=0.1689) and its direct effect was also positive and very low in magnitude (0.0250). The indirect contributions through other characters were found negligible indirect.

### 4.4.2 Days to maturity v/s pod yield per plant

The correlation coefficient between pod yield per plant and days to maturity was positive and non-significant ($r_p$= 0.0195). Its direct effect on pod yield per plant was found to be negative and very low in magnitude (-0.0841). Days to maturity had negligible indirect effects on pod yield per plant *via* other traits.

### 4.4.3 Plant height v/s pod yield per plant

The correlation coefficient between pod yield per plant and plant height was low and negative ($r_p$=-0.1176). Its direct effect was positive and very low in magnitude (0.0555). Plant height had negligible indirect effects on pod yield per plant *via* other traits.

### 4.4.4 Number of branches per plant v/s pod yield per plant

The negative correlation coefficient between pod yield per plant and number of branches per plant ($r_p$=-0.0829) and its direct effect on pod yield per plant was very low and negative (-0.0448). Other characters were found to be having negligible indirect effect on pod yield per plant through number of branches per plant.

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

| Characters | Days to 50% Flowering | Days to maturity | Plant height (cm) | No. of branches per plant | No. of matured pods per plant | No. of Immature pods per cluster | No. of pods per plant | SMK (%) | 100-kernel weight | Shelling out-turn (%) | Biological yield per plant (gm) | Harvest index (%) | Oil content (%) | Phenotypic correlation with pod yield per plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Days to 50% flowering** | **0.0250** | -0.0702 | 0.0105 | 0.0074 | 0.1059 | 0.0723 | -0.1068 | -0.0264 | 0.0234 | 0.0017 | 0.0405 | 0.0843 | 0.0011 | 0.1689 |
| **Days to maturity** | 0.0209 | **-0.0841** | 0.0075 | 0.0063 | -0.0086 | 0.0420 | -0.0152 | -0.0050 | 0.0231 | 0.0013 | 0.0086 | 0.0212 | 0.0016 | 0.0195 |
| **Plant height (cm)** | 0.0047 | -0.0114 | **0.0555** | -0.0001 | -0.0404 | 0.0292 | 0.0039 | 0.0094 | -0.1212 | -0.0080 | -0.0033 | -0.0368 | 0.0006 | -0.1176 |
| **No. of branches per plant** | -0.0041 | 0.0117 | 0.0001 | **-0.0448** | -0.0081 | 0.0027 | 0.0075 | -0.0077 | -0.0135 | 0.0000 | 0.0321 | -0.0565 | -0.0024 | -0.0829 |
| **No. of matured pods per plant** | 0.0029 | 0.0008 | -0.0024 | 0.0004 | **0.9241** | 0.0254 | -0.5324 | -0.1532 | -0.0020 | -0.0012 | 0.2035 | 0.2804 | -0.0007 | 0.7457** |
| **No. of immature pods per plant** | 0.0081 | -0.0158 | 0.0072 | -0.0005 | 0.1048 | **0.2242** | -0.2121 | -0.0257 | -0.0111 | 0.0003 | 0.1267 | 0.0514 | 0.0014 | 0.2590 |
| **No. of pods per plant** | 0.0048 | -0.0023 | -0.0004 | 0.0006 | 0.8797 | 0.0850 | **-0.5592** | -0.1470 | 0.0028 | -0.0004 | 0.2139 | 0.2793 | -0.0001 | 0.7568** |
| **SMK (%)** | 0.0038 | -0.0024 | -0.0030 | -0.0020 | 0.8115 | 0.0330 | -0.4712 | **-0.1744** | 0.0056 | 0.0000 | 0.1702 | 0.2615 | -0.0010 | 0.6317** |
| **100-kernel weight** | 0.0016 | -0.0053 | -0.0183 | 0.0017 | -0.0050 | -0.0068 | -0.0042 | -0.0027 | **0.3670** | 0.0163 | 0.0801 | -0.0114 | -0.0020 | 0.4128** |
| **Shelling out-turn (%)** | 0.0022 | -0.0054 | -0.0227 | 0.0000 | -0.0576 | 0.0034 | 0.0104 | -0.0004 | 0.3066 | **0.0195** | 0.0493 | 0.0333 | 0.0002 | 0.3388** |
| **Biological yield per plant** | 0.0028 | -0.0020 | -0.0005 | -0.0040 | 0.5275 | 0.0797 | -0.3356 | -0.0833 | 0.0825 | 0.0027 | **0.3564** | -0.0517 | 0.0004 | 0.5748** |
| **Harvest index (%)** | 0.0041 | -0.0035 | -0.0040 | 0.0049 | 0.5060 | 0.0225 | -0.3050 | -0.0891 | -0.0082 | 0.0013 | -0.0360 | **0.5122** | -0.0002 | 0.6051** |
| **Oil content (%)** | -0.0026 | 0.0131 | -0.0031 | -0.0102 | 0.0586 | -0.0308 | -0.0054 | -0.0176 | 0.0088 | -0.0005 | -0.0123 | 0.0121 | **-0.0103** | -0.0002 |

*, ** Significant at 5% and 1% levels, respectively
Residual effect, R = 0.3370

### 4.4.5 Number of matured pods per plant v/s pod yield per plant

Number of mature pods per plant v/s pod yield per plant exhibited positive and highly significant phenotypic correlation ($r_p$=0.7457) and also exerted positive direct effect (0.9241) on pod yield per plant. This character contributed moderate and positive indirect effect towards the pod yield mainly through biological yield per plant (0.2035) and harvest index (0.2804). This trait exhibited negative and high indirect effect *via* number of pods per plant (-0.5324).

### 4.4.6 Number of immature pods per plant v/s pod yield per plant

Number of immature pods per plant v/s pod yield per plant exhibited positive and highly significant genotypic correlation ($r_p$=0.2590) and also exerted moderate and positive direct effect (0.2242) on pod yield per plant. Other characters were found negligible indirect effects.

### 4.4.7 Number of pods per plant v/s pod yield per plant

The number of pods per plant was positively and high significantly correlated with pod yield per plant ($r_p$=0.7568) and its direct effect on pod yield per plant was high and negative (-0.5592). This trait exhibited high and positive indirect effect *via* number of matured pods per plant (0.8797). This trait exhibited moderate and positive indirect effect *via* harvest index (0.2793) and biological yield per plant (0.2139), while number of pods per plant had negligible indirect effects on pod yield per plant through other traits except number of matured pods per plant, harvest index and biological yield per plant.

### 4.4.8 Sound mature kernel v/s pod yield per plant

Sound mature kernel v/s pod yield per plant exhibited positive and highly significant phenotypic correlation ($r_p$= 0.6317) and also exerted negative direct effect (-0.1744) on pod yield per plant. This trait exhibited positive and high indirect effect *via* number of matured pods per plant (0.8115) and moderate indirect effect *via* harvest index (0.2615). This trait exhibited high and negative indirect effect *via* number of pods per plant (-0.4712). The indirect effect of sound mature kernel on pod yield per plant *via* all other characters except number of matured pods per plant, harvest index and number of pods per plant were found to be low in magnitude.

### 4.4.9 100-kernel weight v/s pod yield per plant

100-kernel weight v/s pod yield per plant was positively and high significantly correlated ($r_p$=0.4128) with pod yield and also exerted high and positive direct effect (0.3670) on pod yield per plant. Other characters were found negligible indirect effects.

### 4.4.10 Shelling out-tern v/s pod yield per plant

Shelling out-tern v/s pod yield per plant exhibited positive and significant phenotypic correlation ($r_p$=0.3388) with pod yield and also exerted very low and positive direct effect (0.0195) on pod yield per plant. This trait showed high and positive indirect effect *via* 100-kernel weight (0.3066). While, indirect effect *via* all other characters found to be low in magnitude.

### 4.4.11 Biological yield per plant v/s pod yield per plant

The phenotypic correlation between biological yield per plant and pod yield per plant was positive and highly significant ($r_p$=0.5748) and exerted high and positive direct effect (0.3564) on pod yield per plant. This trait showed high and positive indirect effect *via* number of matured pods per plant (0.5275). This trait showed high and negative indirect effect *via* number of pods per plant (-0.3356).

### 4.4.12 Harvest index v/s pod yield per plant

Harvest index exhibited significant positive phenotypic correlation ($r_p$=0.6051) with pod yield and also exerted high and positive direct effect (0.5122) on pod yield per plant. This trait showed high and positive indirect effect *via* number of matured pods per plant (0.5060). This trait showed high and negative indirect effect *via* number of pods per plant (-0.3050). The indirect effect of harvest index on pod yield per plant *via* all other characters except number of matured pods per plant and number of pods per plant were found to be low in magnitude and negligible.

### 4.4.13 Oil content v/s pod yield per plant

The phenotypic correlation between oil content and pod yield per plant was found to be negative ($r_p$= -0.0002). The direct effect on pod yield was found to be very low in magnitude and negative (-0.0103). The oil content had negligible indirect effects on pod yield per plant *via* other traits.

## 4.5 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 60 genotypes in order to assess the genetic divergence present among the genotypes understudy.

### 4.5.1 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, 13 clusters were formed from 60 genotypes. The composition of cluster is given in Table 4.5; diagrammatically has been represented in Figure 4.2 and clustering pattern is shown in Table 4.6.

The cluster I was the largest having 29 genotypes from different geographical regions comprising 9 from Junagadh, 8 from ICRISAT, 5 from ANGRAU, 4 from CSAUA & T, 2 from Rajasthan and 1 from PDVK, Akola (Table 4.5). The cluster IV contained 9 genotypes comprising 3 from Junagadh, 3 from ICRISAT, 1 from CSAUA & T and 2 from Rajasthan. The cluster V, X and XII contained 9, 2 and 3 genotypes respectively from different geographical regions. Eight clusters *viz.*, II, III, VI, VII, VIII, IX, XI and XIII contained single genotype each from different geographical regions. Thus, the observed clustering pattern of genotypes was independent of their geographical origin.

**Table 4.5 Grouping of 60 genotypes of virginia groundnut in various clusters on the basis of $D^2$-statistic**

| Cluster | No. of genotypes | Name of genotypes | Source |
|---|---|---|---|
| **I** | **29** | ICGV- 9001, C-156, ICGV- 89955, AMR-174, ICGV-86325, 72-39, 4896, ICGV- 91026 | ICRISAT |
| | | KDG-123, K-1574, KDG-213, KADIRI-7, K-1643 | ANGRAU |
| | | KAUSHAL, CSMG- 9101, CSMG-9708, CSMG-884 | CSAUA & T |
| | | NRCG-8, JVR-HPS-2289, GG-13, GG-14, JVR-HPS-2284, GG-20, JVB-49, SOMNATH, GG-11 | Junagadh |
| | | RG-559-3, HNG-36 | Rajasthan |
| | | AK-143 | PDVK, Akola |
| **II** | **1** | CSMG-HPS- 9101 | CSAUA & T |
| **III** | **1** | GJG-22 | Junagadh |
| **IV** | **9** | 59-112, 4343, 59-239, | ICRISAT |
| | | CSMG-9907 | CSAUA & T |
| | | JVR-309, GG-21, JVR-HOC-3, | Junagadh |
| | | HNG-HPS-2, RG-382 | Rajasthan |
| **V** | **9** | 48-114, ALG-05-253, ICGS-5, ICGV-00350 | ICRISAT |
| | | K-1577 | ANGRAU |
| | | JVR-308, JVB-147 | Junagadh |
| | | HNG-57A, HNG-56B | Rajasthan |
| **VI** | **1** | CGC-07 | ICRISAT |
| **VII** | **1** | KDG-128 | ANGRAU |
| **VIII** | **1** | RG-438-2 | Rajasthan |
| **IX** | **1** | JVB-154 | Junagadh |
| **X** | **2** | ICGV- 86590, ICGV-87846 | ICRISAT |
| **XI** | **1** | CGC-1-19 | ICRISAT |
| **XII** | **3** | BAV-18 | ICRISAT |
| | | CSMG-2005-18 | CSAUA & T |
| | | EC-146615 | Exotic collection |
| **XIII** | **1** | ICGV-86564 | ICRISAT |

**Table 4.6 Source and clustering pattern of 60 genotypes of virginia groundnut**

| Source | ICRISAT | ANGRAU | CSAUA & T | Junagadh | Rajasthan | PDVK, Akola | Exotic collection | Total |
|---|---|---|---|---|---|---|---|---|
| **I** | 8 | 5 | 4 | 9 | 2 | 1 | - | 29 |
| **II** | - | - | 1 | - | - | - | - | 1 |
| **III** | - | - | - | 1 | - | - | - | 1 |
| **IV** | 3 | | 1 | 3 | 2 | - | - | 9 |
| **V** | 4 | 1 | - | 2 | 2 | - | - | 9 |
| **VI** | 1 | - | - | - | - | - | - | 1 |
| **VII** | - | 1 | - | - | - | - | - | 1 |
| **VIII** | - | - | - | - | 1 | - | - | 1 |
| **IX** | - | - | - | 1 | - | - | - | 1 |
| **X** | 2 | - | - | - | - | - | - | 2 |
| **XI** | 1 | - | - | - | - | - | - | 1 |
| **XII** | 1 | - | 1 | - | - | - | 1 | 3 |
| **XIII** | 1 | - | - | - | - | - | - | 1 |

### 4.5.2 Inter and intra-cluster distance ($D = \sqrt{D^2}$)

The intra and inter-cluster distance values are given in Table 4.7. The maximum inter-cluster distance (D=16.79) was found between clusters XIII and V followed by that between clusters VI and XII (D=15.03), X and XII (D=15.01), XIII and VII (D=14.79), III and XIII (D=14.74). The minimum inter-cluster distance was observed between clusters IV and II (D=6.71). The intra-cluster distance ranged from 5.90 to 9.34, the maximum being in cluster XII (9.34). The minimum intra-cluster distance was found in cluster X (5.90). The clusters II, III, VI, VII, VIII, IX, XI and XIII contained single genotype and therefore, their intra-cluster distance was zero.

### 4.5.3 Cluster means for various characters

The cluster means for 14 characters are presented in Table 4.8. The coefficient of variation (C.V.%) was calculated for all the attributes. The maximum coefficient of variation was recorded for harvest index (14.14%) followed by number of immature pods per plant (13.98%), number of pods per plant (10.81%), pod yield per plant (10.57%), plant height (10.38%), while it was low for number of matured pods per plant (9.97%), 100-kermel weight (9.78%), number of branches per plant (8.28%), biological yield per plant (7.00%), sound mature kernel (5.30%), oil content (5.29%), shelling out-turn (5.27%), days to 50% flowering (4.65%) and days to maturity (3.18 %).

The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that pod yield per plant (19.77%) followed by days to 50% flowering (16.78%), biological yield per plant (16.05%), shelling out-turn (15.31%), plant height (11.02%) and number of matured pods per plant (10.00%) contributed maximum towards total genetic divergence in the present study (Table 4.8). These six characters accounted for more than 85% of total divergence in the material studied.

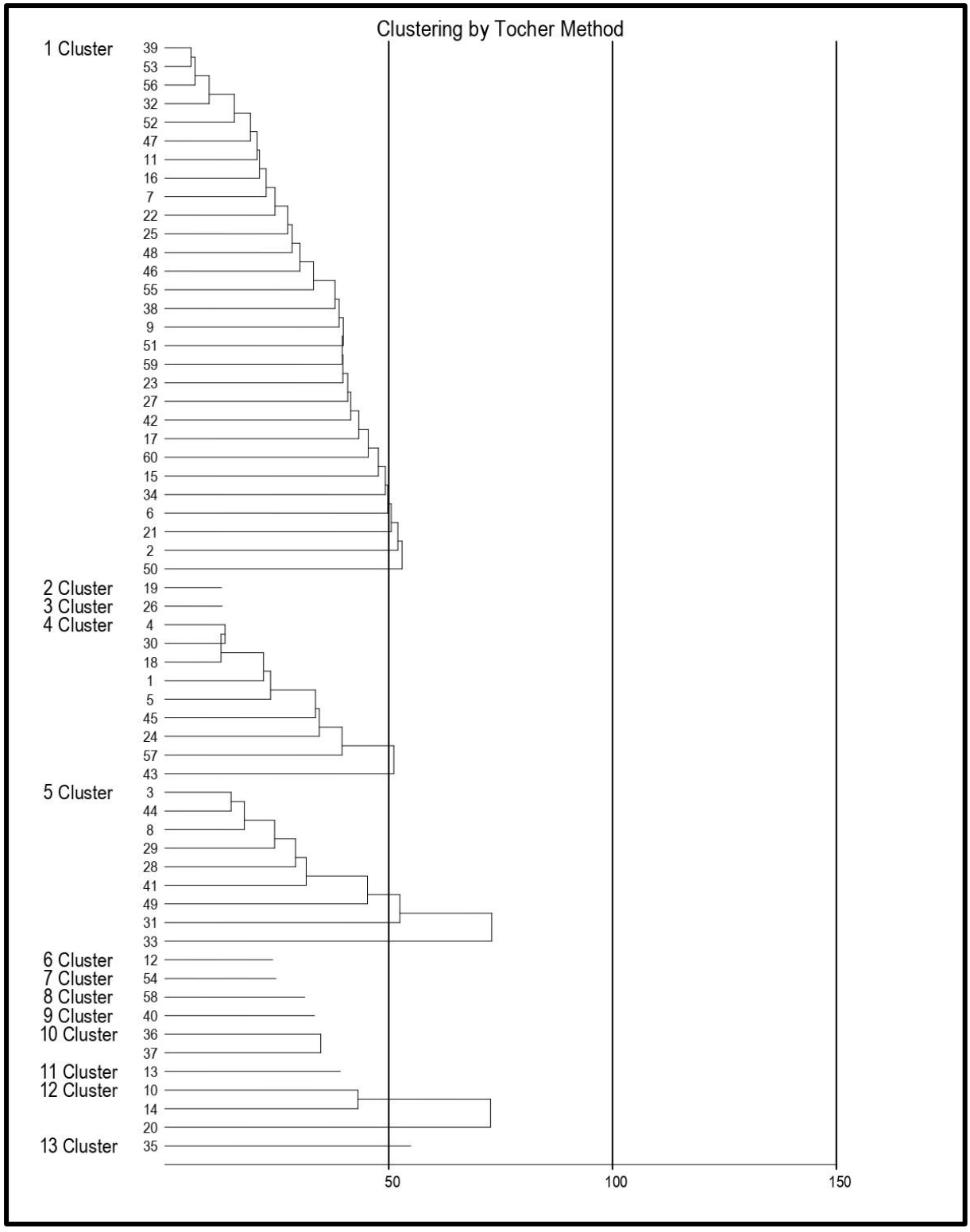


**Figure 4.2 Dendrogram showing relationship among 60 genotypes of virginia groundnut**

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

| Cluster | I | II | III | IV | V | VI | VII | VIII | IX | X | XI | XII | XIII |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | **6.58** | 7.63 | 7.71 | 8.51 | 9.07 | 8.74 | 8.05 | 9.07 | 8.54 | 10.31 | 10.08 | 10.12 | 12.57 |
| **II** | | **0.00** | 10.28 | 6.71 | 10.21 | 9.98 | 11.91 | 9.17 | 7.69 | 9.16 | 6.98 | 9.57 | 9.68 |
| **III** | | | **0.00** | 11.40 | 7.42 | 12.32 | 7.84 | 12.73 | 8.50 | 11.99 | 10.07 | 9.68 | 14.74 |
| **IV** | | | | **6.41** | 11.54 | 8.54 | 11.93 | 9.23 | 8.72 | 10.58 | 9.87 | 11.75 | 10.30 |
| **V** | | | | | **7.26** | 13.50 | 11.17 | 12.39 | 9.55 | 14.10 | 11.86 | 10.21 | 16.79 |
| **VI** | | | | | | **0.00** | 8.32 | 9.27 | 12.77 | 8.57 | 13.79 | 15.03 | 12.07 |
| **VII** | | | | | | | **0.00** | 12.15 | 12.28 | 10.30 | 13.42 | 13.48 | 14.79 |
| **VIII** | | | | | | | | **0.00** | 9.44 | 13.94 | 12.43 | 11.83 | 14.03 |
| **IX** | | | | | | | | | **0.00** | 13.94 | 7.25 | 8.93 | 12.23 |
| **X** | | | | | | | | | | **5.90** | 11.72 | 15.01 | 10.61 |
| **XI** | | | | | | | | | | | **0.00** | 9.46 | 9.30 |
| **XII** | | | | | | | | | | | | **9.34** | 14.67 |
| **XIII** | | | | | | | | | | | | | **0.00** |

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

| Cluster | Days to 50% Flowering | Days to maturity | Plant height (cm) | Number of branches per plant | Number of matured pods per plant | Number of immature pods per plant | Number of pods per plant | Pod yield per plant (gm) | Sound mature kernel (%) | 100-kernel weight | Shelling out-turn | Biological yield per plant | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **I** | 42.24 | 127.40 | 19.92 | 3.04 | 12.29 | 5.03 | 17.27 | 14.80 | 78.17 | 44.32 | 77.46 | 61.38 | 24.89 | 45.79 |
| **II** | 45.29 | 130.19 | 20.70 | 3.23 | 10.60 | 4.45 | 15.23 | 10.70 | 78.27 | 34.53 | 62.12 | 57.68 | 23.25 | 44.06 |
| **III** | 41.99 | 130.00 | 24.45 | 3.00 | 15.47 | 5.45 | 20.85 | 18.52 | 80.87 | 51.80 | 73.22 | 70.95 | 26.87 | 47.77 |
| **IV** | 43.15 | 129.61 | 21.91 | 3.07 | 9.88 | 4.14 | 13.96 | 11.04 | 73.20 | 40.86 | 73.54 | 45.16 | 24.77 | 45.89 |
| **V** | 48.47 | 133.20 | 21.55 | 2.95 | 15.58 | 5.05 | 20.58 | 17.26 | 82.70 | 41.20 | 74.16 | 62.88 | 29.03 | 46.06 |
| **VI** | 34.80 | 124.88 | 14.97 | 3.00 | 11.27 | 3.88 | 15.47 | 12.00 | 75.80 | 46.66 | 83.98 | 48.63 | 27.23 | 44.73 |
| **VII** | 34.94 | 117.41 | 19.95 | 3.07 | 14.80 | 4.85 | 19.74 | 18.80 | 82.00 | 48.77 | 87.79 | 70.00 | 25.70 | 45.35 |
| **VIII** | 48.32 | 136.79 | 13.27 | 3.23 | 9.43 | 4.72 | 14.27 | 9.85 | 71.84 | 48.73 | 87.72 | 58.74 | 17.46 | 43.46 |
| **IX** | 49.52 | 133.00 | 25.98 | 3.20 | 11.03 | 3.61 | 14.54 | 15.00 | 76.01 | 50.00 | 74.17 | 65.24 | 19.61 | 45.00 |
| **X** | 31.83 | 121.48 | 20.21 | 3.27 | 13.23 | 4.47 | 17.88 | 11.49 | 81.08 | 34.66 | 62.39 | 55.46 | 23.42 | 48.76 |
| **XI** | 46.12 | 130.00 | 33.30 | 3.17 | 12.23 | 4.55 | 16.94 | 9.11 | 78.18 | 35.45 | 63.81 | 69.25 | 15.16 | 45.70 |
| **XII** | 49.30 | 134.56 | 25.52 | 3.06 | 10.77 | 7.37 | 17.17 | 13.42 | 75.35 | 39.66 | 71.39 | 67.32 | 21.89 | 45.65 |
| **XIII** | 35.00 | 124.07 | 29.35 | 3.10 | 6.07 | 3.63 | 10.08 | 9.00 | 56.05 | 35.00 | 63.00 | 54.09 | 17.41 | 47.20 |
| **Mean** | **42.38** | **128.66** | **22.39** | **3.11** | **11.74** | **4.71** | **16.46** | **13.15** | **76.12** | **42.43** | **73.44** | **60.52** | **22.82** | **45.80** |
| **S.Em.±** | **1.15** | **2.35** | **1.26** | **0.14** | **0.70** | **0.39** | **1.06** | **0.86** | **2.35** | **2.39** | **2.27** | **2.38** | **2.01** | **1.39** |
| **C. V. %** | **4.65** | **3.18** | **10.38** | **8.28** | **9.97** | **13.98** | **10.81** | **10.57** | **5.30** | **9.78** | **5.27** | **7.00** | **14.14** | **5.29** |
| **Percentage contribution of characters towards total divergence** | | | | | | | | | | | | | | |
| **Number of times appearing first** | 297 | 9 | 195 | 30 | 177 | 69 | 11 | 350 | 2 | 33 | 271 | 284 | 23 | 19 |
| **% contribution** | 16.78 | 0.51 | 11.02 | 1.69 | 10.00 | 3.90 | 0.62 | 19.77 | 0.11 | 1.86 | 15.31 | 16.05 | 1.30 | 1.07 |

## 4.6 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, pod yield per plant ($X_1$) along with its four components *viz.*, number of matured pods per plant ($X_2$), 100-kernel weight ($X_3$), biological yield per plant ($X_4$) and harvest index ($X_5$) were identified and considered for the construction of selection indices.

Thirty-one selection indices were constructed in all possible combinations of the four 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 4.9, assuming the efficiency of straight selection for pod yield per plant 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 four or five characters were considered together.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of 315.65% was exhibited by biological yield per plant followed by 100-kernel weight (156.03%), harvest index (114.23%), pod yield per plant (100.00%) and number of matured pods per plant (87.90%).

Among the combinations involving two component characters, pod yield per plant and biological yield per plant ($X_1+X_4$) exhibited maximum relative efficiency of 388.12% followed by number of matured pods per plant and biological yield per plant [($X_2+X_4$), 376.70%], biological yield per plant and harvest index [($X_4+X_5$), 319.27%], 100-kernel weight and biological yield per plant [($X_3+X_4$), 317.03%], pod yield per plant and 100-kernel weight ($X_1+X_3$) and pod yield per plant and harvest index ($X_1+X_5$) having relative efficiency of 226.47% and 205.57%, respectively.

The selection index based on three character combinations indicated that a discriminant function with pod yield per plant, 100-kernel weight and biological yield per plant ($X_1+X_3+X_4$) possessed maximum relative efficiency of 476.79% followed by pod yield per plant, number of matured pods per plant and biological yield per plant [($X_1+X_2+X_4$), 456.98%], number of matured pods per plant, 100-kernel weight

**Table 4.9 Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in virginia groundnut**

| Sr. No. | Selection index | Discriminant function | Expected genetic advance | Relative efficiency (%) |
|---|---|---|---|---|
| 1 | $X_1$: Pod yield per plant (g) | $0.9121X_1$ | 5.48 | 100.00 |
| 2 | $X_2$: No. of matured pods per plant | $0.9226X_2$ | 4.82 | 87.90 |
| 3 | $X_3$: 100-kernel weight (g) | $0.7894X_3$ | 8.55 | 156.03 |
| 4 | $X_4$: Biological yield per plant (g) | $0.9296X_4$ | 17.30 | 315.65 |
| 5 | $X_5$: Harvest index (%) | $0.7496X_5$ | 6.26 | 114.23 |
| 6 | $X_1.X_2$ | $0.9171X_1 + 1.0029X_2$ | 10.04 | 183.22 |
| 7 | $X_1.X_3$ | $1.0635X_1 + 0.7685X_3$ | 12.41 | 226.47 |
| 8 | $X_1.X_4$ | $1.0110X_1 + 0.9237X_4$ | 21.27 | 388.12 |
| 9 | $X_1.X_5$ | $1.1695X_1 + 0.6618X_5$ | 11.27 | 205.57 |
| 10 | $X_2.X_3$ | $0.9230X_2 + 0.7899X_3$ | 9.80 | 178.77 |
| 11 | $X_2.X_4$ | $1.0143X_2 + 0.9221X_4$ | 20.64 | 376.70 |
| 12 | $X_2.X_5$ | $1.2055X_2 + 0.6804X_5$ | 10.54 | 192.31 |
| 13 | $X_3.X_4$ | $0.3920X_3 + 0.8556X_4$ | 17.37 | 317.03 |
| 14 | $X_3.X_5$ | $0.6609X_3 + 0.5370X_5$ | 8.36 | 152.60 |
| 15 | $X_4.X_5$ | $0.9158X_4 + 0.7240X_5$ | 17.50 | 319.27 |
| 16 | $X_1.X_2.X_3$ | $1.3822X_1 + 0.6031X_2 + 0.6951X_3$ | 15.03 | 274.29 |
| 17 | $X_1.X_2.X_4$ | $1.0228X_1 + 1.0232X_2 + 0.9126X_4$ | 25.04 | 456.98 |
| 18 | $X_1.X_2.X_5$ | $1.0730X_1 + 1.1864X_2 + 0.6411X_5$ | 15.69 | 286.35 |
| 19 | $X_1.X_3.X_4$ | $1.0774X_1 + 0.8253X_3 + 0.9478X_4$ | 26.13 | 476.79 |
| 20 | $X_1.X_3.X_5$ | $1.8126X_1 + 0.5346X_3 + 0.2841X_5$ | 15.51 | 282.98 |
| 21 | $X_1.X_4.X_5$ | $2.1138X_1 + 0.6802X_4 + 0.1721X_5$ | 22.95 | 418.81 |
| 22 | $X_2.X_3.X_4$ | $0.9118X_2 + 0.8402X_3 + 0.9729X_4$ | 24.60 | 448.90 |
| 23 | $X_2.X_3.X_5$ | $1.3202X_2 + 0.7331X_3 + 0.5491X_5$ | 12.81 | 233.68 |
| 24 | $X_2.X_4.X_5$ | $1.9291X_2 + 0.7456X_4 + 0.3688X_5$ | 14.16 | 258.40 |
| 25 | $X_3.X_4.X_5$ | $0.7913X_3 + 0.9529X_4 + 0.6420X_5$ | 21.53 | 392.90 |
| 26 | $X_1.X_2.X_3.X_4$ | $1.3230X_1 + 0.6761X_2 + 0.7655X_3 + 0.9566X_4$ | 29.29 | 534.49 |
| 27 | $X_1.X_2.X_3.X_5$ | $2.1763X_1 + 0.5554X_2 + 0.4507X_3 + 0.2767X_5$ | 19.00 | 346.74 |
| 28 | $X_1.X_2.X_4.X_5$ | $2.1406X_1 + 1.9807X_2 + 0.4953X_4 - 0.2158X_5$ | 27.55 | 502.69 |
| 29 | $X_1.X_3.X_4.X_5$ | $3.7776X_1 + 0.3263X_3 + 0.4330X_4 - 0.7116X_5$ | 27.65 | 504.54 |
| 30 | $X_2.X_3.X_4.X_5$ | $1.9818X_1 + 0.8608X_3 + 0.7642X_4 + 0.2667X_5$ | 25.41 | 463.66 |
| 31 | $X_1.X_2.X_3.X_4.X_5$ | $3.7175X_1 + 1.5167X_2 + 0.3742X_3 + 0.3422X_4 - 0.8802X_5$ | 31.49 | 574.67 |

and biological yield per plant [($X_2$+$X_3$+$X_4$), 448.90%], pod yield per plant, biological yield per plant and harvest index [($X_1$+$X_4$+$X_5$), 418.81%], 100-kernel weight, biological yield per plant and harvest index [($X_3$+$X_4$+$X_5$), 392.90%].

The selection index based on four characters combinations indicated that a discriminant function with pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant ($X_1$+$X_2$+$X_3$+$X_4$) exerted 534.49% relative efficiency followed by pod yield per plant, 100-kernel weight, biological yield per plant and harvest index [($X_1$+$X_3$+$X_4$+$X_5$), 504.54%], pod yield per plant, number of matured pods per plant, biological yield per plant and harvest index [($X_1$+$X_2$+$X_4$+$X_5$), 502.69%], number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index [($X_2$+$X_3$+$X_4$+$X_5$),463.66%], pod yield per plant, number of matured pods per plant, 100-kernel weight and harvest index [($X_1$+$X_2$+$X_3$+$X_5$), 346.74%].

Among all the 31 selection indices (Table 4.9), the index based on five characters *viz*., pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1$+$X_2$+$X_3$+$X_4$+$X_5$) possessed the highest genetic gain and relative efficiency (31.49g and 574.67%) as compared to straight selection for pod yield per plant. Other two important index based on four characters *viz.*, pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant ($X_1$+$X_2$+$X_3$+$X_4$) possessed the highest genetic gain and relative efficiency (29.29g and 534.49%), while the other possessing, pod yield per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1$+$X_3$+$X_4$+$X_5$) exerted genetic gain of 27.65g and relative efficiency of 504.54% as compared to straight selection for pod yield per plant.

## 4.7 CLASSIFICATION OF QUALITATIVE CHARACTERS

Classification of qualitative characters is given in Table 4.10. Here, Plate 4.1 shows photographs of leaflet size, leaflet color, stem pubescence and inflorescence; Plate 4.2 shows photographs of pod constriction and pod reticulation; Plate 4.3 shows photographs of prominence of beak, shape of beak and number of kernels; Plate 4.4 shows photographs of color of testa and Plate 4.5 shows photographs of kernel color and kernel shape.

**Table 4.10 Classification of qualitative characters in 60 genotypes of virginia groundnut**

| Genotypes | Leaflet size | Leaflet color | Stem: Pubescence | Inflorescence | Pod: Constriction | Pod: Texture (reticulation) | Pod: Prominence of beak | Pod: Shape of beak | Pod: Number of kernels | Kernel: Color of testa | Kernel: Color | Kernel: Shape |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **1** | M | DG | SP | SI | S | SL | A | - | 2 | T | MO | CY |
| **2** | M | DG | SP | SI | S | SL | A | - | 2 | T | MO | CY |
| **3** | M | DG | M | SI | VD | SL | M | ST | 2 | T | MO | CY |
| **4** | M | DG | DE | SI | M | SL | A | - | 2 | T | MO | CY |
| **5** | M | DG | DE | SI | M | SL | A | - | 2 | T | MO | CY |
| **6** | M | DG | M | SI | M | SL | A | - | 2 | T | MO | F |
| **7** | M | G | SP | SI | S | SL | P | CU | 2 | R | MO | CY |
| **8** | M | G | SP | SI | M | M | M | CU | 2 | OW | MO | CY |
| **9** | M | G | SP | SI | M | M | SL | ST | 2 | OW | MO | CY |
| **10** | SM | DG | M | SI | S | P | SL | ST | 2 | T | MO | CY |
| **11** | SM | DG | SP | SI | A | SL | A | - | 1 | T | MO | CY |
| **12** | SM | DG | M | SI | A | SL | M | CU | 2 | T | MO | SPH |
| **13** | SM | DG | M | SI | A | SL | SL | ST | 2 | T | MO | CY |
| **14** | M | DG | SP | SI | VD | SL | SL | ST | 2 | - | VA | SPH |
| **15** | SM | G | SP | SI | M | SL | SL | ST | 2 | OW | MO | SPH |
| **16** | M | DG | SP | SI | S | SL | SL | ST | 2 | R | MO | CY |
| **17** | SM | DG | SP | SI | S | SL | SL | ST | 2 | OW | MO | SPH |
| **18** | M | DG | SP | SI | S | M | M | CU | 2 | T | MO | CY |
| **19** | SM | DG | SP | SI | A | SL | A | - | 2 | DR | MO | SPH |

**Table 4.10 Contd..**

| Genotypes | Leaflet size | Leaflet color | Stem: Pubescence | Inflorescence | Pod: Constriction | Pod: Texture (reticulation) | Pod: Prominence of beak | Pod: Shape of beak | Pod: Number of kernels | Kernel: Color of testa | Kernel: Color | Kernel: Shape |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **20** | SM | DG | DE | SI | S | M | A | - | 2 | T | MO | CY |
| **21** | M | DG | SP | SI | S | SL | A | - | 2 | T | MO | CY |
| **22** | M | G | DE | SI | S | M | SL | CU | 2 | T | MO | CY |
| **23** | M | DG | M | SI | A | SL | A | - | 1 | T | MO | SPH |
| **24** | M | DG | M | SI | M | M | A | - | 2 | T | MO | SPH |
| **25** | SM | G | M | SI | A | M | A | - | 2 | T | MO | CY |
| **26** | M | G | M | SI | S | M | M | ST | 2 | T | MO | SPH |
| **27** | M | DG | DE | SI | S | M | SL | ST | 2 | T | MO | CY |
| **28** | SM | G | SP | SI | S | M | A | - | 2 | SA | MO | CY |
| **29** | SM | G | DE | SI | M | P | SL | ST | 2 | T | MO | SPH |
| **30** | SM | DG | DE | SI | A | P | A | - | 2 | T | MO | F |
| **31** | SM | G | DE | SI | S | SL | SL | ST | 2 | T | MO | SPH |
| **32** | SM | G | M | SI | S | SL | SL | ST | 2 | T | MO | SPH |
| **33** | M | DG | SP | SI | D | SL | A | - | 2 | SA | MO | CY |
| **34** | M | DG | SP | SI | S | SL | A | - | 2 | SA | MO | CY |
| **35** | M | DG | SP | SI | S | SL | SL | ST | 2 | T | MO | CY |
| **36** | SM | DG | M | SI | A | SL | A | - | 2 | DP | MO | SPH |
| **37** | SM | DG | SP | SI | D | SL | SL | ST | 2 | T | MO | F |
| **38** | SM | DG | M | SI | A | P | SL | ST | 2 | T | MO | F |
| **39** | SM | DG | SP | SI | M | SL | SL | ST | 2 | T | MO | CY |

**Table 4.10 Contd..**

| Genotypes | Leaflet size | Leaflet color | Stem: Pubescence | Inflorescence | Pod: Constriction | Pod: Texture (reticulation) | Pod: Prominence of beak | Pod: Shape of beak | Pod: Number of kernels | Kernel: Color of testa | Kernel: Color | Kernel: Shape |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **40** | M | DG | SP | SI | A | P | SL | ST | 2 | OW | MO | SPH |
| **41** | M | DG | DE | SI | VD | SL | A | - | 2 | T | MO | CY |
| **42** | SM | DG | SP | SI | S | SL | SL | ST | 2 | T | MO | CY |
| **43** | SM | DG | SP | SI | S | P | P | ST | 2 | DR | MO | CY |
| **44** | M | G | M | SI | D | P | SL | ST | 2 | T | MO | CY |
| **45** | M | G | M | SI | A | SL | A | - | 2 | T | MO | SPH |
| **46** | SM | DG | SP | SI | S | VP | M | ST | 2 | DP | MO | F |
| **47** | SM | G | M | SI | A | M | A | - | 2 | T | MO | SPH |
| **48** | SM | DG | M | SI | S | SL | A | - | 2 | T | MO | SPH |
| **49** | M | DG | DE | SI | D | SL | A | - | 2 | T | MO | CY |
| **50** | SM | DG | M | SI | S | M | A | - | 2 | T | MO | F |
| **51** | SM | DG | SP | SI | A | SL | A | - | 2 | T | MO | SPH |
| **52** | M | DG | SP | SI | S | SL | A | - | 2 | T | MO | F |
| **53** | SM | DG | SP | SI | D | SL | SL | ST | 2 | SA | MO | F |
| **54** | SM | DG | SP | SI | S | P | M | CU | 2 | SA | MO | F |
| **55** | SM | G | SP | SI | A | P | M | ST | 2 | T | MO | CY |
| **56** | M | DG | SP | SI | S | M | SL | ST | 2 | SA | MO | F |
| **57** | M | DG | SP | SI | M | SL | SL | ST | 2 | OW | MO | F |
| **58** | M | DG | SP | SI | A | M | A | - | 2 | T | MO | SPH |
| **59** | M | DG | SP | SI | A | SL | SL | CU | 2 | OW | MO | F |
| **60** | M | DG | SP | SI | A | SL | A | - | 2 | T | MO | F |

Here,

| | | |
|---|---|---|
| **(1) Leaflet size** | : | M-medium and SM-small |
| **(2) Leaflet colour** | : | G-green and DG-dark green |
| **(3) Stem pubescence** | : | DE-dense, M-medium and SP-sparse |
| **(4) Inflorescence** | : | C-complicated and SI-simple |
| **(5) Pod constriction** | : | A-Absent, D-deep, M-medium, S-shallow and VD-very deep |
| **(6) Pod reticulation** | : | M-medium, P-prominent and SL-slight |
| **(7) Prominence of beak** | : | A-Absent, M-medium, P-prominent and SL-slight |
| **(8) Shape of beak** | : | (-) is for absence of beak, CU-curved and ST-straight |
| **(9) Number of kernels** | : | 1 and 2 one seeded and two seeded, respectively |
| **(10) Colour of testa** | : | DP-dark purple, DR-dark red, OW-off-white, R-red, SA-salmon and T-tan |
| **(11) Kernel colour** | : | MO-monochrome and VA-variegated |
| **(12) Kernel shape** | : | CY-cylindrical, F-fusiform and SPH-spheroidal |

# CHAPTER-V

## DISCUSSION

Success of plant breeding programme depends on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. 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 character association with mature pods and pod yield for effective selection in the segregating population. A thorough knowledge of the nature and magnitude of genetic variability and the extent of association between pod yield and its components are essential before launching a breeding program. Similarly, heritability and genetic advance estimates are helpful in selecting superior individuals.

To step up groundnut yields per unit area and per unit time, 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 for pod yield as it is a complex character and is influenced by number of traits as well as the effect of environment. Hence, selection of genotypes with desirable characters would be greatly depends upon significant correlation 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 coefficients provides an opportunity to know the magnitude and direction of association of pod yield with its direct and indirect components.

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 GENETIC VARIABILITY

Genetic variability is the basic requirement for crop improvement as it provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable. The present experimental materials showed a wide range of variation for plant height followed by number of matured pods per plant, pod yield per plant, number of immature pods per plant, biological yield per plant, number of pods per plant, harvest index, days to 50% flowering, shelling out-turn and 100-kernel weight.

### 5.1.1 Genotypic and phenotypic coefficient of variation

The narrow differences between GCV and PCV estimates of respective characters indicated that environmental factors had little role for the expression of the characters.

The highest value of GCV was observed for plant height. High magnitude of GCV indicated the presence of wide variation for the characters under study, which allow further improvement by selection of the individual trait. Nath and Alam (2002), Korat *et al.* (2009a), Devangana *et al*. (2015), Mukesh and Lal (2017), Mahesh *et al.* (2018) had been also found highest value of GCV for plant height.

In the present study moderate values of GCV were observed for number of matured pods per plant, pod yield per plant, number of immature pods per plant, number of pods per plant, biological yield per plant, harvest index, 100-kernel weight, days to 50% flowering and shelling out-turn. Therefore, it is suggested that these characters can be improved. The results of the present study are in agreement with findings of Korat *et al.* (2009a) for pod yield per plant, biological yield per plant, harvest index and 100-kernel weight; Zaman *et al.* (2011) for number of matured pods

per plant, 100-kernel weight and shelling out-turn; Vishnuvardhan *et al*. (2012) for number of matured pods per plant, pod yield per plant, harvest index; Maurya *et al.* (2014) for days to 50% flowering; Gupta *et al.* (2015a) for pod yield per plant, biological yield per plant, harvest index and 100-kernel weight; Patil *et al.* (2015) for days to 50% flowering, 100-kernel weight and shelling out-turn; Namrata *et al.* (2016) for number of matured pods per plant and harvest index and Ashutosh *et al.* (2016) for number of pods per plant, pod yield per plant, harvest index and 100-kernel weight.

The low estimates of GCV were observed for number of branches per plant, sound mature kernels, days to maturity and oil content. Thereby, indicated narrow genetic variability for these characters in the material studied. The results of the present study are in agreement with findings of Korat *et al.* (2009a) for oil content; Maurya *et al.* (2014) and Mukesh and Lal (2017) for days to maturity and number of sound mature kernel; Gupta *et al.* (2015a) for days to maturity, sound mature kernel and oil content; Namrata *et al.* (2016) for number of branches per plant and oil content; Mahesh *et al.* (2018) for sound mature kernels and oil content.

Highest PCV in the present study was observed in plant height followed by number of matured pods per plant and pod yield per plant. The present findings are also in agreement with those obtained by Thakur *et al.* (2011) for plant height; Nath and Alam (2002) , Devangana *et al.* (2015), Mukesh and Lal (2017) for plant height and pod yield per plant; Nath and Alam (2002), Maurya *et al.* (2014), Mukesh and Lal (2017), Omima *et al.* (2018) for pod yield per plant; Mahesh *et al.* (2018) for plant height and number of matured pods per plant; Zaman *et al.* (2011) and Vishnuvardhan *et al*. (2012) for number of matured pods per plant.

Number of immature pods per plant, harvest index, number of pods per plant, biological yield per plant, 100-kernel weight, days to 50% flowering, shelling out-turn had observed moderate PCV in present study. The results of the present findings are accordance with Nath and Alam (2002) for shelling out-turn; Zaman *et al.* (2011), Gupta *et al.* (2015a) and Mukesh and Lal (2017) for shelling out-turn and 100-kernel weight; Korat *et al.* (2009a) and Namrata *et al.* (2016) for biological yield per plant and harvest index; Vishnuvardhan *et al.* (2012) for shelling out-turn and harvest index; Mukri *et al.* (2014) for 100-kernel weight; Gupta *et al.* (2015a) for biological yield per plant.

Low value of PCV was observed for remaining characters *viz.*, days to maturity, number of branches per plant, sound mature kernels and oil content. The

result of present study is in agreement with result of Gupta *et al.* (2015a), Mukesh and Lal (2017), Maurya *et al.* (2014) and Vishnuvardhan *et al.* (2012) for days to maturity and sound mature kernel; Mahesh *et al.* (2018) for sound mature kernel and oil content; Vishnuvardhan *et al.* (2012) for sound mature kernel; Gupta *et al.* (2015a), Patil *et al.* (2015) and Namrata *et al.* (2016) for oil content.

**5.1.3 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 breeders to select superior genotypes on the basis of phenotypic expression of quantitative traits (Johnson *et al.* 1955).

In the present study, maximum heritability (broad sense) was observed for days to 50% flowering followed by biological yield per plant, number of matured pods per plant, shelling out-turn, plant height, pod yield per plant, number of pods per plant, number of immature pods per plant, 100-kernel weight, sound mature kernel, harvest index, days to maturity, number of branches per plant. High heritability estimates indicated that the characters were least influenced by the environmental effects. This also suggested that the phenotypes were the true representative of their genotypes for these traits and selection based on phenotypic value could be more reliable and high capacity of the characters for transmission to subsequent generation.

The high magnitude of heritability has also been earlier reported by Maurya *et al.* (2014), Rao (2016), Mukesh and Lal (2017), Mahesh *et al.* (2018), Patil *et al.* (2015) for days to 50% flowering and plant height; Vishnuvardhan *et al.* (2012) and Gupta *et al*. (2015a) for days to 50% flowering; Vishnuvardhan *et al.* (2012), Patil *et al.* (2015), Rao (2016) for days to maturity; Zaman *et al.* (2011) for number of branches pods per plant; Zaman *et al.* (2011), Patil *et al.* (2015) and Mahesh *et al.* (2018) for number of matured pods per plant, number of immature pods per plant and 100-kernel weight; Nath and Alam (2002) and Ashutosh *et al.* (2016) for number of pods per plant, pod yield per plant, harvest index and shelling out-turn; Mukesh and Lal (2017) for number of matured pods per plant; Zaman *et al.* (2011) for number of pods per plant; Maurya *et al.* (2014), Gupta *et al*. (2015a), Mukesh and Lal (2017) for pod yield per plant and sound mature kernel; Gupta *et al*. (2015a) for biological yield

per plant. The estimates of heritability were moderate for oil content (44.22).

**5.1.4 Genetic advance**

Burton (1952) suggested that genotypic coefficient of variation along with heritability estimate would provide a better idea of the amount of advance expected by phenotypic selection of heritability estimates very often subjected to genotypic selection. Heritability estimates in conjunction with genetic gain are more effective and reliable in predicting the improvement through selection (Johnson *et al*. 1955). Rapid progress in selection can be achieved when high heritability is accompanied with high genetic advance, which form the most reliable index for selection.

In the present study expected genetic advance was moderate for biological yield per plant and shelling out-turn. The result of present study is in akin to findings of Gupta *et al*. (2015a) for biological yield per plant; Nath and Alam (2002) and Zaman *et al.* (2011) for shelling out-turn.

In the present study, the low values of genetic advance were observed for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant, sound mature kernel, 100-kernel weight, harvest index and oil content. Low estimates of genetic advance have been reported by Zaman *et al.* (2011), Vishnuvardhan *et al.* (2012), Maurya *et al.* (2014), Gupta *et al*. (2015a), Patil *et al.* (2015), Mukesh and Lal (2017) for days to 50% flowering and days to maturity; Vishnuvardhan *et al.* (2012) and Patil *et al.* (2015) for plant height and number of immature pods per plant; Maurya *et al.* (2014) for sound mature kernel and pod yield per plant; Vishnuvardhan *et al.* (2012) for number of matured pods per plant and sound mature kernel; Rao (2016) for number of pods per plant and 100-kernel weight; Gupta *et al*. (2015a) for plant height, number of matured pods per plant, pod yield per plant, harvest index and oil content; Patil *et al.* (2015) for oil content.

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

The genetic advance expressed as percentage of mean was the high for plant height followed by number of matured pods per plant, pod yield per plant, number of immature pods per plant, biological yield per plant, number of pods per plant, harvest index, days to 50% flowering, shelling out-turn, 100-kernel weight. Similar results have also been reported by Nath and Alam (2002) Maurya *et al.* (2014) and Patil *et al.* (2015) for plant height, pod yield per plant, 100-kernel weight and shelling out-turn; Mukesh and Lal (2017) and Mahesh *et al.* (2018) for plant height and 100-kernel

weight; Patil *et al.* (2015) and Mahesh *et al.* (2018) for number of matured pods per plant and number of immature pods per plant; for days to 50% flowering Maurya *et al.* (2014) and Patil *et al.* (2015); Nath and Alam (2002), Rao (2016) and Omima *et al.* (2018) for number of pods per plant; for biological yield per plant Gupta *et al*. (2015a); for harvest index Nath and Alam (2002), Vishnuvardhan *et al.* (2012) and Gupta *et al.* (2015a). Sound mature kernel (10.14) expressed moderate values of genetic advance expressed as percentage of mean. Similar results were reported by Maurya *et al.* (2014) and Mukesh and Lal (2017).

The value of genetic advance expressed as percent of mean were low for number of branches per plant, days to maturity and oil content. Low estimates of genetic advance expressed as percentage of mean for days to maturity have been reported by Maurya *et al*. (2014), Gupta *et al*. (2015a), Patil *et al.* (2015) and Mukesh and Lal (2017).

Johnson *et al*. (1955) suggested that the heritability and genetic advance when considered together would be more useful in predicting the resultant effects of selection.

In the present study, high estimates of heritability coupled with high genetic advance expressed as percentage of mean was observed for days to 50% flowering, plant height, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant, 100-kernel weight, shelling out-turn, biological yield and harvest index. Which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these characters for their rationale improvement (Panse *et al*. 1957). Similar results in same have been reported for days to 50% flowering Maurya *et al.* (2014) and Patil *et al.* (2015); for plant height Nath and Alam (2002), Maurya *et al.* (2014), Patil *et al.* (2015) and Mukesh and Lal (2017); for number of matured pods per plant Patil *et al.* (2015) and Mahesh *et al.* (2018); for number of immature pods per plant Mahesh *et al.* (2018); for number of pods per plant Nath and Alam (2002) and Omima *et al.* (2018); for pod yield per plant Nath and Alam (2002), Gupta *et al*. (2015a), Mukesh and Lal (2017) and Omima *et al.* (2018); for 100-kernel weight Nath and Alam (2002), Patil *et al.* (2015), Mukesh and Lal (2017) and Mahesh *et al.* (2018); for shelling out-turn Nath and Alam (2002) and Patil *et al.* (2015); for biological yield per plant Gupta *et al*. (2015a); for harvest index Nath and Alam (2002), Vishnuvardhan *et al.* (2012) and Gupta *et al*. (2015a).

High estimate of heritability with moderate genetic advance expressed as percentage of mean was observed for sound mature kernel which revealed the presence of non-additive gene action and influence of environment in the expression of these characters and thus, the selection would be less effective. Similar results in same have been reported by Maurya *et al.* (2014), Gupta *et al*. (2015a) and Mukesh and Lal (2017)**.**

## 5.2 CORRELATION COEFFICIENTS

The knowledge of association among the pod yield and yield contributing characters would be of great help in constructing a suitable plant type and in planning breeding programme. However, the correlation coefficient does not give any indication about comparative magnitude of contribution made by various component characters. Therefore, genotypic as well as phenotypic path coefficient analysis was carried out to find the direct and indirect effects of yield components and their correlation with pod yield per plant.

Correlation among traits may result from pleiotropy, 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 correlations were higher than their corresponding phenotypic correlations. 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 Zaman *et al*. (2011).

Pod yield per plant in groundnut is a complex and depends upon the interplay of number of component attributes. Correlation co-efficient explains nature and extent of association between different characters influencing yield. This helps in formulation of selection criteria for improvement of pod yield in groundnut. In order to achieve the goal of increased production by increasing the yield potential of groundnut crop, a knowledge of direction and magnitude of association between pod yield per plant and various traits is essential for plant breeders accordingly, the present investigation of pod yield and its component traits in elite groundnut genotypes.

In the present study, pod yield per plant had strong positively correlated at both genotypic and phenotypic level with number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, biological yield per plant and harvest index. So these characters should be given more weightage in selection process. These results indicated the importance of the characters towards contribution of pod yield per plant. Such positive inter-relationship between pod yield per plant and these attributes has also been reported in groundnut by several researchers. The result of present study is in conformity with Babariya and Dobariya (2012), Choudhary *et al.* (2016) and Tulsi *et al.* (2017) for number of matured pods per plant, biological yield per plant and harvest index; Kumar *et al.* (2014), Tulsi *et al.* (2017) and Mahesh *et al.* (2018) for sound mature kernel and Babariya and Dobariya (2012), Ashutosh *et al.* (2016) and Tulsi *et al.* (2017) for 100-kernel weight.

The pod yield per plant had non-significant and positive correlation both at genotypic and phenotypic levels with days to 50% flowering and days to maturity. This character showed non-significant and negative correlation both at genotypic and phenotypic levels with plant height, number of branches per plant and oil content.

Thus, for improving pod yield per plant outstanding characters are number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, biological yield per plant and harvest index. They can serve as indicator character for improvement in pod yield per plant and need to be given more emphasis in selection to achieve higher pod yield.

In the present finding days to 50% flowering had strongly high significant and positive association with days to maturity at both genotypic as well as phenotypic levels, while positive significant correlation only at phenotypic level with number of immature pods per plant and strongly high significant and positive association at

genotypic level. The characters *viz*., number of branches per plant and oil content reported to have negative correlation with days to 50% flowering. Choudhary *et al.* (2016) and Tulsi *et al.* (2017) had revealed negative correlation of days to 50% flowering with number of branches per plant and oil content respectively.

Days to maturity was strongly high significant and positive association with days to 50% flowering at both genotypic as well as phenotypic level. Mahesh *et al.* (2018) revealed similar result for correlation between days to maturity and days to 50% flowering.

Plant height had positive genotypic and phenotypic associations with days to 50% flowering, days to maturity, number of branches per plant, number of immature pods per plant. Choudhary *et al.* (2016) and Tulsi *et al.* (2017) had revealed similar correlation for days to maturity and number of branches per plant with plant height respectively.

In the present study, number of branches per plant registered positive genotypic and phenotypic associations with plant height, sound mature kernel, shelling out-turn, biological yield per plant and oil content. Choudhary *et al.* (2016) and Tulsi *et al.* (2017); Ashutosh *et al.* (2016) and Trivikrama *et al.* (2017); Tulsi *et al.* (2017) had revealed similar correlation for plant height, sound mature kernel, shelling out-turn and biological yield per plant respectively.

Correlation analysis revealed that number of matured pods per plant had strong positive and highly significant correlation with number of pods per plant, sound mature kernel, biological yield per plant and harvest index at both genotypic and phenotypic level, which indicated that the improvement in these characters will be improve results for number of matured pods per plant. The results are in conformity with findings of Babariya and Dobariya (2012); Tulsi *et al.* (2017) for sound mature kernel and biological yield per plant; Kumar *et al.* (2014), Trivikrama *et al.* (2017) and Tulsi *et al.* (2017) for harvest index; Mahesh *et al.* (2018) for sound mature kernel.

Number of immature pods per plant seemed to have strong positive and highly significant correlation with number of pods per plant and biological yield at both genotypic as well as phenotypic level.

The correlation of number of pods per plant with number of matured and immature pods per plant, sound mature kernel, biological yield per plant and harvest index was highly significant and strong positive which confirms that the improvement

in one character would results improvement in another character. The results are in conformity with findings of Babariya and Dobariya (2012); Babariya and Dobariya (2012) and Trivikrama *et al.* (2017) for biological yield per plant and number of matured pods per plant respectively.

Sound mature kernel was highly significant and positively correlated with number of matured pods per plant, number of pods per plant, biological yield per plant and harvest index at both levels. The results are in conformity with findings of Tulsi *et al.* (2017) for number of matured pods per plant, biological yield per plant and harvest index.

The character 100-kernel weight showed highly significant and strong positive correlation with shelling out-turn at both levels and negative significant correlation with plant height at both levels, which revealed that decrease in plant height will results in improvement in 100-kernel weight.

Shelling out-turn revealed highly significant and strong positive correlation with 100-kernel weight and negative highly significant correlation with plant height at both levels.

The character biological yield showed highly significant and strong positive correlation with number of matured pods per plant, number of immature pods per plant, number of pods per plant and sound mature kernel. The results are in conformity with findings of Tulsi *et al.* (2017) for number of matured pods per plant and sound mature kernel; Babariya and Dobariya (2012) and Choudhary *et al.* (2016) for number of matured pods per plant and Babariya and Dobariya (2012) for number of pods per plant.

Harvest index revealed highly significant and strong positive correlation with number of matured pods per plant, number of pods per plant and sound mature kernel. The results are in conformity with findings of Tulsi *et al.* (2017) for number of matured pods per plant and sound mature kernel; Kumar *et al.* (2014) and Choudhary *et al.* (2016) for number of matured pods per plant. The oil content showed highly significant and strong positive correlation with number of branches per plant only at genotypic level.

The present results on correlation coefficients revealed that number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight biological yield per plant and harvest index were the most important attributes and may contribute considerably towards higher pod yield. The inter-relationship among

yield components would help in increasing the yield levels and therefore more emphasis should be given to those components while selecting in groundnut breeding.

Generally, the value of correlation coefficients lies between -1.0 to 1.0. In present study most of the value of correlation coefficients ranged between -1.0 to 1.0. In 2 cases, the value of correlation coefficients were more than 1, it may be due to when covariance is over estimated whereas variance is under estimated (Roy, 2000).

## 5.3 PATH ANALYSIS

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 genotypes from the diverse breeding population. Pod yield is polygenic trait, which influenced by its various components directly as well as indirectly *via* other traits, which create a complex situation before a breeder for making selection. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship, as it considers direct as well as indirect effects of the variables by partitioning the correlation coefficient. When two or more variables are included in the correlation studies, it becomes difficult to determine which characters enhance the yield. The technique of path coefficient analysis overcomes this situation which partitions the forces of association and examines the relative contribution of direct and indirect effects of the independent variables on the dependent variables.

In the present study, number of pods per plant revealed the highly significant positive phenotypic correlation with pod yield per plant followed by number of matured pods per plant, sound mature kernel, harvest index, biological yield per plant and 100-kernel weight. It revealed true relationship between them and direct selection for these traits, it will be rewarding for yield improvement. The result of present study is in agreement with findings of Rathod *et al.* (2015) and Ashutosh *et al.* (2016) for number of pods per plant, harvest index and 100-kernel weight; Bhargavi *et al.* (2017) for 100-kernel weight and biological yield per plant; Vasanthi *et al.* (2015), Bhargavi *et al.* (2017) and Mahesh *et al.* (2018) for number of matured pods per plant; Mahesh *et al.* (2018) for sound mature kernel.

In the present study, the path analysis revealed that number of matured pods per plant, 100-kernel weight, biological yield and harvest index exhibited high and

positive direct effect on pod yield per plant. Thus, these characters turned-out to be the major components of pod yield. High and positive direct effect of number of matured pods per plant have also been reported by Patil *et al.* (2015) and Ashutosh *et al.* (2016) for harvest index.

In present study, positive direct effect towards pod yield observed for days to 50% flowering, days to maturity, plant height, number of immature pods per plant and shelling out-turn. Therefore it is suggested that these characters may be considered as the most important yield contributing character for selection. The result of present study is in agreement with findings of Vasanthi *et al.* (2015) and Ashutosh *et al.* (2016) for days to 50% flowering and shelling out-turn; Patil *et al.* (2015) and Vasanthi *et al.* (2015) for number of immature pods per plant; Bhargavi *et al.* (2017) and Mahesh *et al.* (2018) for days to 50% flowering.

Number pods per plant also showed high and negative direct effect on pod yield per plant, but its positive correlation with pod yield per plant was primarily formed through its indirect contribution through days to 50% flowering, number of branches per plant, number of matured pods per plant, number of immature pods per plant, 100-kernel weight, biological yield per plant and harvest index. Similarly, sound mature kernel exerted very low negative direct effect on pod yield per plant but, it contributed by exerting indirect positive effects *via* days to 50% flowering, number of matured pods per plant, number of immature pods per plant, 100-kernel weight, biological yield per plant and harvest index, which resulted in its positive phenotypic correlation with pod yield per plant. The character number of matured pods per plant had not only exerted high direct effect on pod yield per plant, but also contributed indirectly through the positive indirect effects *via* days to 50% flowering, days to maturity, number of branches per plant, number of immature pods per plant, biological yield per plant and harvest index, thereby giving significant association with pod yield per plant.

It was clear from the path analysis that the maximum direct effects as well as appreciable indirect influences were exerted by number of matured pods per plant and appreciable indirect influences were exerted by number of pods per plant, sound mature kernel, 100-kernel weight, biological yield and harvest index. These characters also exhibited highly significant and positive associations with pod yield per plant and hence, they may be considered as the most important yield contributing characters and due emphasis should be placed on these components while selecting for high yield.

## 5.4 GENETIC DIVERGENCE

Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. Genetic improvement mainly depends upon the amount of genetic variability present in the population. The use of Mahalanobis's $D^2$-statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population given in any group before effecting actual crosses.

Earlier, geographic diversity among the parents was generally taken as an index of genetic diversity. However, Korat *et al*. (2009b) 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).

In the present study, $D^2$-statistic estimated on 60 genotypes of groundnut for 14 characters. On the basis of $D^2$-values, 13 clusters were formed from 60 genotypes. The cluster I contained 29 genotypes from different origins. On the other hand, the clusters II, III, VI, VII, VIII, IX, XI and XIII possessed only one genotype in each cluster and therefore, their intra-cluster distance was zero.

A wide range of variation for several characters among single as well as multi-genotype clusters was observed. However, the differences were clearer for harvest index followed by number of immature pods per plant, number of pods per plant, pod yield per plant and plant height. 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 values of any cluster can be used in hybridization programme for further selection and improvement.

The maximum inter-cluster distance varied from 6.71 (clusters IV and II) to 16.79 (clusters XIII and V), which indicates considerable diversity among the genotypes evaluated, whereas the lowest inter cluster distance (D=6.46) found between clusters VI and V (Table 4.8). The lowest intra-cluster distance were found

in cluster X (D=5.90), whereas the highest intra-cluster distance was in cluster XIII (D=9.34).

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. The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster, whereas the genotypes belonging to same country or origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity. The results obtained in the present study are in accordance to the findings of Korat *et al*. (2009b) who reported that there was no parallelism between geographic distribution and genetic diversity. The earlier findings of Murty and Arunachalam (1966) also stated that genetic drift and selection in different environments could cause greater diversity than geographic distance. Further, the free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality.

The lowest intra-cluster distance were in cluster X (D=5.90) (Table 4.7), whereas the highest intra-cluster distance was in cluster XIII (D=9.34). The maximum inter-cluster distance was observed between clusters XIII and V (D=16.79) followed by that between clusters VI and XII (D=15.03), X and XII (D=15.01), XIII and VII (D=14.79), III and XIII (D=14.74). The closest proximity was observed between clusters VI and V (D=6.46). The genotypes belonging to different 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 XIII (ICGV-86564), V (ICGS-05, GG 21, HNG-57-A, and ICGV-00350), XII (BAV-18 and CSMG-2005-18), X (ICGV-86590 and ICGV-87846), VII (KDG-128), III (GJG 22) could be selected as parents in hybridization programme using appropriate mating design.

In the present study, the cluster II was the best for number of branches per plant; cluster III for number of pods per plant, 100-kernel weight and biological yield; cluster V for number of matured pods per plant, sound mature kernel and harvest index; cluster VII for days to maturity, pod yield per plant and shelling out-turn; cluster VIII for number of branches per plant; cluster IX for number of immature pods per plant. The cluster X had best value for days to 50% flowering and oil content. The cluster XI had desirable value for plant height because it showed the longer plant

height. Therefore, intercrossing of genotypes involved in these clusters would be useful for inducing variability in the respective characters and their rational improvement for increasing the pod yield in groundnut.

The analysis of percent contribution of various characters towards the expression of total genetic divergence (Table 4.8) indicated that pod yield per plant followed by days to 50% flowering, biological yield per plant, shelling out-turn, plant height and number of matured pods per plant contributed maximum towards divergence in the present study. These six characters accounted for more than 85% of 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 (Arunachalm, 1981). It has also been observed that the most productive hybrids result 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 XIII with the genotypes of cluster V as well as XII, VII, X which may lead to broad spectrum of favorable genetic variability for yield improvement in groundnut.

## 5.5 SELECTION INDICES

The use of discriminant function was a better way of exploiting genetic correlation with several traits having high heritability is to construct an index which combines information on all the characters associated with yield. The best known selection indices involve discriminant function based on the relative economics importance of various clusters. The selection based on such an index is more efficient than selecting indices has been proved by Hazel (1943), Hazel and Lush (1943) and Robinson *et. al.* (1951).

Hazel and Lush (1943) stated that the superiority of selection based on number of characters under selection. In the present study also, the genetic advance and relative efficiency assessed for different indices increase considerably when selection was based on two or more characters.

The maximum genetic gain advance (Gs) and relative efficiency in a single character discriminant function was 17.30g and 315.65%, respectively which

however, increased to 21.27g and 388.12%, respectively in two character combinations, 26.13g and 476.79%, respectively in three character combinations and 29.29g and 534.49%, respectively in four character combinations. Thus, there was an increase in the genetic gain as well as relative efficiency with inclusion of an addition of trait in the character combinations. The index based on five component characters *viz*., pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_2+X_3+X_4+X_5$) possessed the highest genetic advance and relative efficiency (31.49g and 574.67%) as compared to straight selection for pod yield per plant. Dobariya *et al*., 2008 were also with the same opinion that an increase in character 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 pod yield per plant was not that much rewarding (Gs=5.48g, RI=100%) as it was through its components like number of matured pods per plant (Gs=4.82g, RI=87.90%), 100-kernel weight (Gs=8.55g, RI=156.03%), biological yield per plant (Gs=17.30g, RI=315.65%) and harvest index (Gs=6.26g, RI=114.23%) or in their combinations. The maximum efficiency in selection for pod yield per plant was exhibited by discriminant function involving pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_2+X_3+X_4+X_5$) exerted highest genetic advance 31.49g and relative efficiency 574.67%, pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant ($X_1+X_2+X_3+X_4$) exerted 29.29g genetic advance and 534.49% relative efficiency followed by pod yield per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_3+X_4+X_5$) 27.65g genetic advance and 504.54% relative efficiency.

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, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_2+X_3+X_4+X_5$) followed by a selection index involving pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant ($X_1+X_2+X_3+X_4$) could be advantageously exploited in the groundnut breeding.

# CHAPTER-VI

## SUMMARY AND CONCLUSIONS

The present investigation was carried out to assess the genetic variability, correlation, path analysis, genetic divergence and selection indices in 60 genotypes of virginia groundnut. The experiment was laid-out in a Randomized Block Design with three replications at Instructional farm, College of Agriculture, J.A.U., Junagadh during *kharif* 2018.

The observations were recorded on five randomly selected plants from each genotype and average values were used for statistical analysis. Except, days to 50% flowering and days to maturity, all the characters studies were recorded on five randomly selected plants per plot. For days to 50% flowering and days to maturity, the observations were recorded from the whole plot. The characters studied were days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant (g), sound mature kernel (%), 100-kernel weight (g), shelling out-turn (%), biological yield per plant (g), harvest index (%) and oil content (%).

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

Mean performance of genotypes indicated that genotypes ICGS-05, ALG-05-253 and K-1577 were found to be superior in respect of pod yield per plant. The genotype JVR-HPS-2289 recorded the lowest plant height, while genotype AK-143, CSMG-9101 and NRCG-8 exhibited high number of branches per plant. Among the experimental materials, the genotypes JVB-49 recorded high oil content and ICGS-05 possessed maximum number of pods per plant followed by 48-11 and JVR- HOC- 3.

The highest genotypic coefficient of variation was observed for plant height. The results indicated the presence of wide variation for this character under study which allows further improvement by selection of this trait. Matured pods per plant, pod yield per plant, number of immature pods per plant, number of pods per plant, biological yield per plant, harvest index, 100-kernel weight, days to 50% flowering and shelling out-turn showed moderate genotypic coefficients of variation.

The values of phenotypic coefficient of variation were the maximum for plant height, number of matured pods per plant, pod yield per plant. In case of number of immature pods per plant, harvest index, biological yield per plant, 100-kernel weight, days to 50% flowering and shelling out-turn moderate values of phenotypic coefficients of variation was observed, while, the characters *viz*., number of branches per plant, sound mature kernel, oil content and days to maturity exhibited low phenotypic coefficients of variation. The narrow differences between GCV and PCV estimates of respective characters indicated that environmental factors had little role for the expression of the characters.

The estimates of heritability were observed to be high for days to 50% flowering followed by biological yield per plant, number of matured pods per plant, shelling out-turn, plant height, pod yield per plant, number of pods per plant, number of immature pods per plant, 100-kernel weight, sound mature kernel, harvest index, days to maturity, number of branches per plant indicating that these characters are less influenced by the environmental fluctuations. Moderate heritability value was observed for oil content.

Genetic advance was moderate for biological yield per plant and shelling out-turn. It was low for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of matured pods per plant, number of immature pods per plant, number of pods per plant, pod yield per plant, sound mature kernel, 100-kernel weight, harvest index and oil content. Genetic advance gives an indication of expected progress for a particular trait under selection.

Genetic advance expressed as percentage of mean was found high for plant height followed by number of matured pods per plant, pod yield per plant, number of immature pods per plant, biological yield per plant, number of pods per plant, harvest index, days to 50% flowering, shelling out-turn and 100-kernel weight. The value was moderate for sound mature kernel. The values were low for number of branches per plant, days to maturity and oil content.

The magnitudes of genotypic correlations were higher as compared to the corresponding phenotypic correlations indicating that there was an inherent association between the characters at genotypic level. Pod yield per plant was significantly and positively correlated at both genotypic and phenotypic levels with number of matured pods per plant, number of pods per plant, sound mature kernel,

100-kernel weight, biological yield per plant and harvest index. The interrelationship among these yield components would help in increasing the yield levels in groundnut.

It was clear from the path analysis that the maximum direct effects as well as appreciable indirect influences were exerted by number of matured pods per plant and appreciable indirect influences were exerted by number of pods per plant, sound mature kernel, 100-kernel weight, biological yield and harvest index. These characters also exhibited highly significant and positive associations with pod yield per plant. These characters would be considered as the most important yield contributing characters and due emphasis would be placed on these components while selecting for high yielding types in groundnut.

Among all the 31 selection indices, the index based on five component characters *viz*., pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_2+X_3+X_4+X_5$) possessed the highest genetic gain and relative efficiency (31.49g and 574.67%) as compared to straight selection for pod yield per plant. Other two important index based on four characters *viz.*, pod yield per plant, number of matured pods per plant, 100-kernel weight and biological yield per plant ($X_1+X_2+X_3+X_4$) possessed the highest genetic gain and relative efficiency (29.29g and 534.49%), while the other possessing, pod yield per plant, 100-kernel weight, biological yield per plant and harvest index ($X_1+X_3+X_4+X_5$) exerted genetic gain of 27.65g and relative efficiency of 504.54% as compared to straight selection for pod yield per plant.

The $D^2$ analysis indicated ample genetic diversity among the 60 genotypes, which were grouped in as many as 13 clusters. The clustering pattern did not show any relationship between geographic distribution and genetic divergence as genotypes from the same area scattered in different clusters and the genotypes of different areas were grouped in the same cluster. The lowest intra-cluster distance were found in cluster X (D=5.90), whereas the highest intra-cluster distance was in cluster XIII (D=9.34). On the other hand, the clusters II, III, VI, VII, VIII, IX, XI and XIII possessed only one genotype in each cluster and therefore, their intra-cluster distance was zero. The maximum inter-cluster distance (D=16.79) found between cluster XIII and V followed by that between clusters VI and XII (D=15.03), X and XII (D=15.01), XIII and VII (D=14.79), III and XIII (D=14.74). The minimum inter-cluster distance (D=6.46) found between cluster VI and V. Based on percent contribution of characters towards divergence the character pod yield per plant followed by days to

50% flowering, biological yield per plant, sound mature kernel, plant height and number of matured pods per plant contributed maximum towards divergence. The cluster II was the best for number of branches per plant; cluster III for number of pods per plant, 100-kernel weight and biological yield; cluster V for number of matured pods per plant, sound mature kernel and harvest index; cluster VII for days to maturity, pod yield per plant and shelling out-turn; cluster VIII for number of branches per plant; cluster IX for number of immature pods per plant. The cluster X had best value for days to 50% flowering and oil content. The cluster XI had desirable value for plant height because it showed the longer plant height. The genotypes from cluster XIII (ICGV-86564), V (ICGS-05, GG 21, HNG-57-A, and ICGV-00350), XII (BAV-18 and CSMG-2005-18), X (ICGV-86590 and ICGV-87846), VII (KDG-128), III (GJG 22) could be selected as parents in hybridization programme using appropriate mating design.

The conclusions drawn from the present investigation are as under:

1. The analysis of variance revealed the presence of sufficient variability among the genotypes for different characters.
2. The highest genotypic coefficient of variation was observed for the plant height. High magnitude of GCV indicated the presence of wide variation for the characters under studied.
3. Highest phenotypic coefficient of variation was observed for the plant height, number of matured pods per plant, pod yield per plant.
4. High estimates of heritability were observed for the days to 50% flowering followed by biological yield per plant, number of matured pods per plant, shelling out-turn, plant height, pod yield per plant, number of pods per plant, number of immature pods per plant, 100-kernel weight, sound mature kernel, harvest index, days to maturity, number of branches per plant suggesting the existence of sufficient heritable variation and selection based on phenotypic value could be effective for isolating better types also indicating that these characters had less influenced by environment.
5. The expected genetic advance was the moderate for the biological yield per plant and shelling out-turn.
6. The genetic advance expressed as percentage of mean was found maximum for the plant height followed by number of matured pods per plant, pod yield per

plant, number of immature pods per plant, biological yield per plant, number of pods per plant, harvest index, days to 50% flowering, shelling out-turn and 100-kernel weight.

7. Estimates of heritability coupled with moderate genetic advance expressed as percentage of mean was observed for the biological yield per plant and shelling out-turn which.
8. The magnitudes of genotypic correlation were higher as compared to the corresponding phenotypic correlations thereby indicating the presence of an inherent relationship between the variables.
9. Pod yield per plant had strong positively correlated at both genotypic and phenotypic level with characters *viz.*, number of matured pods per plant, number of pods per plant, sound mature kernel, 100-kernel weight, biological yield per plant and harvest index. So these characters should be given more weightage in selection process.
10. Path coefficient analysis showed that number pods per plant also showed high and negative direct effect on pod yield per plant, but its positive correlation with pod yield per plant was primarily formed through its indirect contribution through plant height, number of branches per plant and shelling out-tern.
11. The genetic diversity analysis revealed the formation of thirteen clusters suggested the presence of genetic diversity among the 60 genotypes studied.
12. The geographic diversity was not associated with genetic diversity. Thus, clustering pattern showed no parallelism between geographic distribution and genetic diversity.
13. Pod yield per plant followed by days to 50% flowering, biological yield per plant, shelling out-turn, plant height and number of matured pods per plant contributed maximum towards the total genetic divergence.
14. Based on inclusion of large inter-cluster distances, it would be advantageous to attempt crossing of the genotypes from cluster XIII with the genotypes of cluster V as well as XII, VII, X which may lead to favourable genetic variability for yield improvement in groundnut.
15. The discriminant selection had higher genetic advance and relative efficiency over straight selection for pod yield per plant alone. There was an increase in genetic advance and relative efficiency with inclusion of an additional trait in the character combination.

16. The selection index consisting of pod yield per plant, number of matured pods per plant, 100-kernel weight, biological yield per plant and harvest index could be advantageously exploited in the groundnut breeding.

The final conclusion that can be reached from genetic variability, correlation, path analysis, genetic divergence and selection indices in virginia groundnut (*Arachis hypogaea* L.) is that the characters like number of matured pods per plant, number of pods per plant, pod yield per plant, 100-kerenl weight, biological yield per pant and harvest index are most important component characters hence, these traits should be considered as selection criteria for increasing yield level in groundnut.

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* Original not seen

# Appendix I

**Mean weekly meteorological data recorded during the crop growth period (July 2018 to November2018) at Meteorological Observatory, College of Agriculture, Junagadh Agricultural University, Junagadh**

| Standard Week No. | Temperature ($^{o}$C) | | Relative humidity (%) | | Rainfall (mm) | Rainy days |
|---|---|---|---|---|---|---|
| | Maximum | Minimum | Maximum | Minimum | | |
| **July 2018** | | | | | | |
| 28 | 30.0 | 25.5 | 95 | 87 | 447.8 | 6 |
| 29 | 27.8 | 25.1 | 98 | 93 | 166.7 | 6 |
| 30 | 30.2 | 26.1 | 90 | 76 | 1.8 | 0 |
| 31 | 32.1 | 26.1 | 88 | 63 | 4.5 | 1 |
| **August 2018** | | | | | | |
| 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 |
| 35 | 29.5 | 24.0 | 92 | 78 | 31.3 | 4 |
| **September 2018** | | | | | | |
| 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 |
| 39 | 34.7 | 23.1 | 76 | 38 | 0.0 | 0 |
| **October 2018** | | | | | | |
| 40 | 37.4 | 22.9 | 76 | 32 | 0.0 | 0 |
| 41 | 37.9 | 23.1 | 66 | 29 | 0.0 | 0 |
| 42 | 36.7 | 21.1 | 74 | 28 | 0.0 | 0 |
| 43 | 37.5 | 20.2 | 64 | 22 | 0.0 | 0 |
| 44 | 37.0 | 19.8 | 60 | 23 | 0.0 | 0 |
| **November 2018** | | | | | | |
| 45 | 36.7 | 18.0 | 68 | 22 | 0.0 | 0 |
| 46 | 35.4 | 18.7 | 75 | 27 | 0.0 | 0 |
| 47 | 35.9 | 18.0 | 67 | 21 | 0.0 | 0 |
| 48 | 34.0 | 16.6 | 67 | 30 | 0.0 | 0 |

## Appendix II

### Mean values of 14 characters in 60 genotypes of virginia groundnut

| Sr. No. | Genotypes | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of branches per plant | Number of matured pods per plant | Number of immature pods per plant | Number of pods per plant |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| 1 | **4343** | 41.06 | 128.67 | 24.67 | 3.10 | 10.67 | 4.78 | 15.55 |
| 2 | **4896** | 44.64 | 129.34 | 24.53 | 2.83 | 11.90 | 6.40 | 18.96 |
| 3 | **48-114** | 50.52 | 136.00 | 25.80 | 3.30 | 17.30 | 5.33 | 22.59 |
| 4 | **59-112** | 43.27 | 129.33 | 24.67 | 2.80 | 8.53 | 3.44 | 12.40 |
| 5 | **59-239** | 40.28 | 127.58 | 24.87 | 3.20 | 10.83 | 3.57 | 13.23 |
| 6 | **72-39** | 47.35 | 132.52 | 22.23 | 3.23 | 10.43 | 5.49 | 15.85 |
| 7 | **AK 143** | 42.65 | 126.00 | 19.33 | 3.63 | 10.93 | 5.77 | 16.56 |
| 8 | **ALG-05-253** | 46.95 | 131.00 | 19.97 | 3.10 | 15.33 | 4.80 | 19.74 |
| 9 | **AMR-174** | 44.22 | 127.58 | 17.30 | 2.80 | 2.70 | 3.87 | 16.90 |
| 10 | **BAV-18** | 47.99 | 131.00 | 19.80 | 3.17 | 8.43 | 8.03 | 15.76 |
| 11 | **C-156** | 43.57 | 127.21 | 20.50 | 3.10 | 12.00 | 5.57 | 17.04 |
| 12 | **CGC-07** | 34.80 | 124.88 | 14.97 | 3.00 | 11.27 | 3.88 | 15.47 |
| 13 | **CGC-1-19** | 46.12 | 130.00 | 33.30 | 3.17 | 12.23 | 4.55 | 16.94 |
| 14 | **CSMG-2005-18** | 49.51 | 135.68 | 25.83 | 2.93 | 11.10 | 7.08 | 16.43 |
| 15 | **CSMG-884** | 41.65 | 129.00 | 20.67 | 3.23 | 9.50 | 5.21 | 14.70 |
| 16 | **CSMG-9101** | 41.14 | 125.00 | 21.40 | 3.40 | 11.67 | 6.00 | 17.47 |
| 17 | **CSMG-9708** | 43.37 | 125.36 | 19.53 | 3.27 | 14.20 | 5.98 | 19.98 |
| 18 | **CSMG-9907** | 43.23 | 128.04 | 18.40 | 2.97 | 8.27 | 4.65 | 13.05 |
| 19 | **CSMG-HPS-9101** | 45.29 | 130.19 | 20.70 | 3.23 | 10.60 | 4.45 | 15.23 |
| 20 | **EC-146615** | 50.40 | 137.00 | 30.93 | 3.07 | 12.77 | 6.99 | 19.31 |
| 21 | **GG 11** | 43.23 | 129.26 | 22.37 | 2.37 | 10.27 | 5.76 | 15.88 |
| 22 | **GG 13** | 45.64 | 130.00 | 17.77 | 2.63 | 12.73 | 5.19 | 17.93 |
| 23 | **GG 20 (C)** | 40.48 | 127.52 | 21.53 | 2.73 | 12.73 | 5.18 | 17.92 |
| 24 | **GG 21** | 45.30 | 129.52 | 15.27 | 2.90 | 11.00 | 3.94 | 15.25 |
| 25 | **GG14** | 43.76 | 128.25 | 18.40 | 2.67 | 10.93 | 5.11 | 16.06 |
| 26 | **GJG 22 (C)** | 41.99 | 130.00 | 24.43 | 3.00 | 15.47 | 5.45 | 20.85 |
| 27 | **HNG-36** | 42.68 | 128.82 | 18.92 | 2.90 | 15.73 | 4.38 | 19.40 |
| 28 | **HNG-56 B** | 48.81 | 132.06 | 16.91 | 4.47 | 12.70 | 4.73 | 17.55 |
| 29 | **HNG-57(A)** | 48.83 | 133.69 | 18.45 | 3.07 | 15.53 | 5.40 | 20.61 |
| 30 | **HNG-HPS-2** | 42.12 | 129.32 | 21.80 | 2.97 | 8.83 | 4.04 | 11.87 |
| 31 | **ICGS-05** | 44.85 | 128.88 | 25.67 | 3.03 | 20.50 | 4.20 | 25.30 |
| 32 | **ICGV- 91026** | 42.11 | 127.43 | 17.08 | 2.93 | 13.00 | 5.87 | 18.70 |
| 33 | **ICGV-00350** | 52.33 | 139.20 | 19.40 | 2.70 | 11.97 | 4.76 | 16.84 |

## Appendix II. Contd…

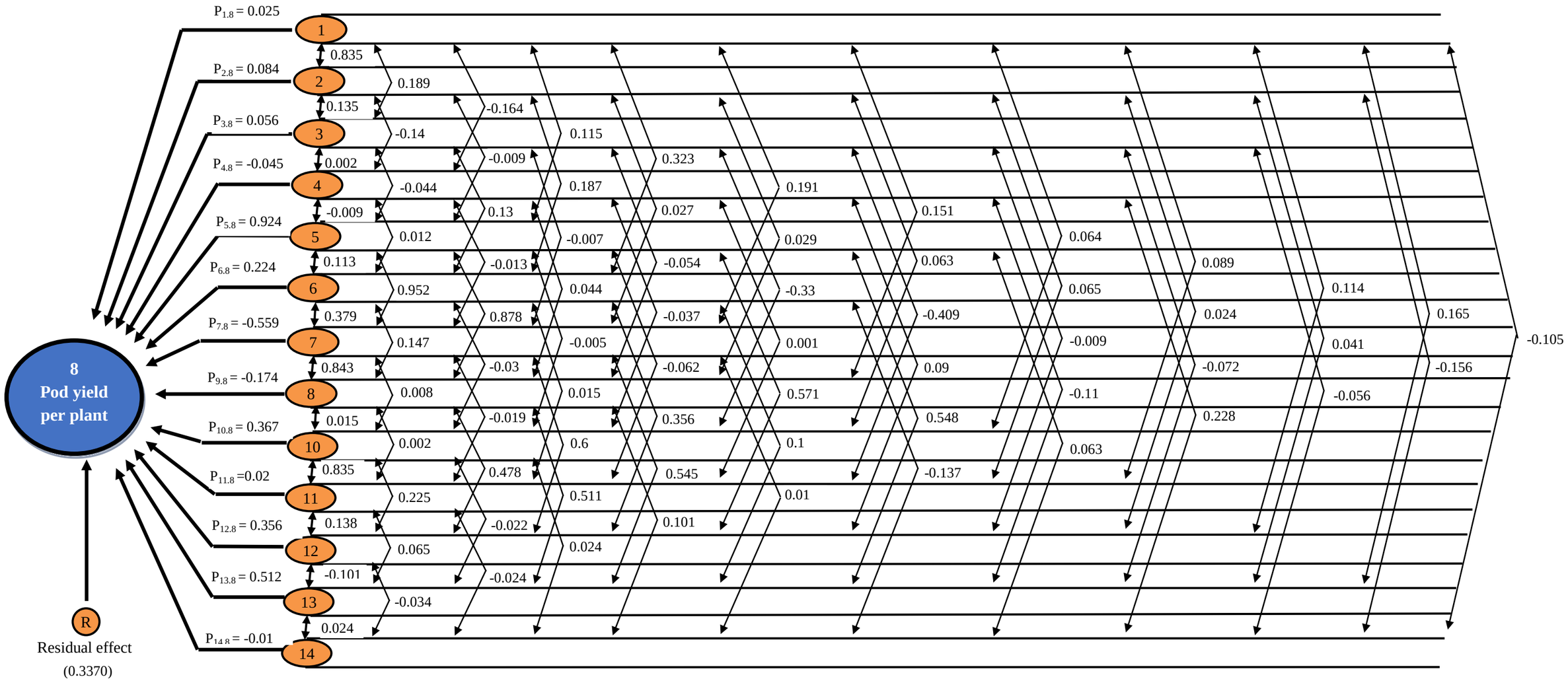
| Sr. No. | Genotypes | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of branches per plant | Number of matured pods per plant | Number of immature pods per plant | Number of pods per plant |
|---|---|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
| **34** | **ICGV-86325** | 37.98 | 126.63 | 23.57 | 2.90 | 11.73 | 4.27 | 15.84 |
| **35** | **ICGV-86564** | 35.00 | 124.07 | 29.35 | 3.10 | 6.07 | 3.63 | 10.08 |
| **36** | **ICGV-86590** | 32.66 | 122.95 | 22.47 | 3.23 | 14.93 | 3.71 | 19.01 |
| **37** | **ICGV-87846** | 31.01 | 120.00 | 17.95 | 3.30 | 11.53 | 5.23 | 16.75 |
| **38** | **ICGV-89955** | 44.64 | 131.00 | 15.84 | 2.73 | 12.17 | 4.60 | 16.91 |
| **39** | **ICGV-9001** | 40.06 | 126.52 | 13.22 | 3.27 | 13.23 | 5.10 | 18.36 |
| **40** | **JVB- 154** | 49.52 | 133.00 | 25.98 | 3.20 | 11.03 | 3.61 | 14.54 |
| **41** | **JVB-147** | 51.73 | 139.00 | 23.88 | 3.07 | 12.33 | 4.78 | 15.55 |
| **42** | **JVB-49** | 32.55 | 122.85 | 19.50 | 3.30 | 14.00 | 4.84 | 18.96 |
| **43** | **JVR- HOC- 3** | 49.66 | 134.55 | 24.02 | 3.30 | 10.87 | 4.11 | 22.59 |
| **44** | **JVR-308** | 46.54 | 129.00 | 24.46 | 2.83 | 15.57 | 5.39 | 12.40 |
| **45** | **JVR-309** | 40.38 | 129.92 | 15.60 | 3.37 | 9.90 | 4.29 | 13.23 |
| **46** | **JVR-HPS-2284** | 39.30 | 123.00 | 18.15 | 3.20 | 10.50 | 4.13 | 15.85 |
| **47** | **JVR-HPS-2289** | 40.26 | 129.98 | 12.71 | 3.27 | 12.80 | 4.39 | 16.56 |
| **48** | **K-1574** | 42.36 | 127.53 | 21.54 | 2.93 | 12.80 | 3.77 | 19.74 |
| **49** | **K-1577** | 45.68 | 130.00 | 19.41 | 3.00 | 19.00 | 4.60 | 16.90 |
| **50** | **K-1643** | 46.03 | 130.00 | 24.85 | 3.23 | 11.30 | 4.93 | 15.76 |
| **51** | **KADIRI-7** | 43.38 | 125.00 | 24.25 | 3.03 | 13.13 | 5.12 | 17.04 |
| **52** | **KAUSHAL** | 41.04 | 129.00 | 21.71 | 3.10 | 12.00 | 4.99 | 15.47 |
| **53** | **KDG-123** | 39.49 | 125.00 | 15.77 | 3.10 | 13.87 | 4.72 | 16.94 |
| **54** | **KDG-128** | 34.94 | 117.41 | 19.95 | 3.07 | 14.80 | 4.85 | 16.43 |
| **55** | **KDG-213** | 35.30 | 124.95 | 15.87 | 3.07 | 12.07 | 3.67 | 14.70 |
| **56** | **NRCG-8** | 41.28 | 130.20 | 16.00 | 3.40 | 14.63 | 4.76 | 17.47 |
| **57** | **RG-382** | 43.02 | 129.52 | 27.93 | 3.03 | 10.00 | 4.43 | 19.98 |
| **58** | **RG-438-2** | 48.32 | 136.79 | 13.27 | 3.23 | 9.43 | 4.72 | 13.05 |
| **59** | **RG-559-3** | 41.31 | 127.73 | 25.97 | 3.00 | 10.73 | 5.48 | 15.23 |
| **60** | **SOMNATH** | 38.27 | 122.00 | 26.53 | 3.07 | 12.57 | 5.28 | 19.31 |
| | | | | | | | | |
| **Mean** | | 43.28 | 128.88 | 21.13 | 3.05 | 12.25 | 4.91 | 17.10 |
| **S. Em.±** | | 1.16 | 2.37 | 1.27 | 0.15 | 0.71 | 0.40 | 1.07 |
| **C.D. at 5%** | | 3.25 | 6.63 | 3.55 | 0.41 | 1.97 | 1.11 | 2.99 |
| **C.D. at 1%** | | 4.30 | 8.77 | 4.69 | 0.54 | 2.61 | 1.47 | 3.95 |
| **C.V.%** | | 4.65 | 3.18 | 10.38 | 8.28 | 9.97 | 13.98 | 10.81 |

## Appendix II. Contd…

| Sr. No. | Genotypes | Pod yield per plant (g) | Sound mature kernel (%) | 100-kernel weight (g) | Shelling out-turn (%) | Biological yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| 1 | **4343** | 9.95 | 73.84 | 35.30 | 63.54 | 39.73 | 26.31 | 45.02 |
| 2 | **4896** | 12.60 | 78.66 | 37.46 | 67.43 | 50.00 | 27.01 | 45.52 |
| 3 | **48-114** | 16.20 | 87.16 | 36.55 | 65.78 | 56.23 | 33.03 | 46.27 |
| 4 | **59-112** | 9.80 | 70.88 | 39.63 | 71.34 | 41.22 | 22.86 | 49.30 |
| 5 | **59-239** | 11.00 | 77.07 | 32.20 | 57.96 | 47.30 | 23.26 | 44.99 |
| 6 | **72-39** | 14.90 | 77.76 | 46.16 | 83.09 | 55.00 | 30.24 | 45.57 |
| 7 | **AK 143** | 16.59 | 78.37 | 46.73 | 84.11 | 62.00 | 26.65 | 48.80 |
| 8 | **ALG-05-253** | 19.00 | 81.34 | 42.70 | 76.86 | 63.45 | 32.82 | 44.31 |
| 9 | **AMR-174** | 15.93 | 77.67 | 41.84 | 75.31 | 51.21 | 30.00 | 45.50 |
| 10 | **BAV-18** | 11.35 | 68.53 | 39.78 | 71.60 | 61.45 | 18.51 | 46.46 |
| 11 | **C-156** | 14.63 | 77.02 | 45.63 | 82.13 | 60.12 | 25.58 | 47.61 |
| 12 | **CGC-07** | 12.00 | 75.79 | 46.66 | 83.98 | 48.63 | 27.23 | 44.73 |
| 13 | **CGC-1-19** | 9.11 | 78.18 | 35.45 | 63.81 | 69.25 | 15.16 | 45.70 |
| 14 | **CSMG-2005-18** | 10.40 | 78.42 | 31.20 | 56.16 | 69.52 | 22.32 | 45.96 |
| 15 | **CSMG-884** | 11.00 | 77.62 | 43.99 | 79.19 | 52.66 | 20.89 | 46.53 |
| 16 | **CSMG-9101** | 13.54 | 80.02 | 45.20 | 81.36 | 64.52 | 20.99 | 46.97 |
| 17 | **CSMG-9708** | 17.99 | 79.90 | 40.52 | 72.94 | 70.00 | 31.65 | 46.38 |
| 18 | **CSMG-9907** | 10.86 | 66.23 | 42.63 | 76.73 | 45.06 | 21.72 | 45.77 |
| 19 | **CSMG-HPS-9101** | 10.70 | 78.27 | 34.53 | 62.16 | 57.68 | 23.24 | 44.06 |
| 20 | **EC-146615** | 18.50 | 79.11 | 50.00 | 86.40 | 71.00 | 24.84 | 44.53 |
| 21 | **GG 11** | 15.60 | 76.68 | 41.63 | 74.93 | 50.55 | 29.55 | 42.78 |
| 22 | **GG 13** | 13.52 | 77.17 | 50.00 | 73.96 | 65.85 | 21.11 | 45.00 |
| 23 | **GG 20 (C)** | 14.00 | 77.28 | 36.46 | 65.63 | 63.85 | 25.00 | 42.40 |
| 24 | **GG 21** | 11.45 | 74.20 | 42.83 | 77.10 | 42.33 | 29.26 | 42.87 |
| 25 | **GG14** | 12.68 | 75.51 | 47.65 | 85.77 | 63.65 | 19.84 | 41.58 |
| 26 | **GJG 22 (C)** | 18.52 | 80.87 | 51.80 | 73.22 | 70.95 | 26.87 | 47.77 |
| 27 | **HNG-36** | 17.60 | 80.98 | 41.23 | 74.21 | 69.87 | 29.04 | 47.60 |
| 28 | **HNG-56 B** | 16.80 | 79.05 | 42.52 | 76.54 | 55.52 | 27.88 | 47.00 |
| 29 | **HNG-57(A)** | 16.00 | 82.91 | 40.23 | 72.41 | 70.00 | 27.03 | 47.68 |
| 30 | **HNG-HPS-2** | 10.00 | 71.64 | 37.52 | 67.54 | 50.22 | 19.91 | 45.90 |
| 31 | **ICGS-05** | 20.76 | 89.99 | 40.00 | 72.00 | 72.00 | 33.94 | 45.62 |
| 32 | **ICGV- 91026** | 14.50 | 77.90 | 42.00 | 75.60 | 67.85 | 23.52 | 44.98 |
| 33 | **ICGV-00350** | 15.70 | 77.85 | 50.63 | 88.20 | 64.52 | 21.11 | 46.28 |

## Appendix II. Contd...

| Sr. No. | Genotypes | Pod yield per plant (g) | Sound mature kernel (%) | 100-kernel weight (g) | Shelling out-turn (%) | Biological yield per plant (g) | Harvest index (%) | Oil content (%) |
|---|---|---|---|---|---|---|---|---|
| | | 8 | 9 | 10 | 11 | 12 | 13 | 14 |
| 34 | ICGV-86325 | 14.60 | 75.29 | 50.23 | 72.73 | 52.12 | 21.91 | 46.66 |
| 35 | ICGV-86564 | 9.00 | 56.05 | 35.00 | 63.00 | 54.09 | 17.41 | 47.20 |
| 36 | ICGV-86590 | 10.00 | 85.18 | 32.52 | 58.54 | 62.56 | 20.82 | 48.78 |
| 37 | ICGV-87846 | 12.97 | 76.98 | 36.80 | 66.24 | 48.36 | 26.02 | 48.73 |
| 38 | ICGV-89955 | 15.87 | 81.10 | 49.03 | 88.26 | 55.32 | 28.69 | 48.31 |
| 39 | ICGV-9001 | 16.00 | 77.52 | 48.00 | 86.40 | 70.00 | 22.86 | 46.57 |
| 40 | JVB- 154 | 15.00 | 76.00 | 50.00 | 74.18 | 65.24 | 19.61 | 45.00 |
| 41 | JVB-147 | 15.04 | 76.44 | 43.52 | 78.34 | 57.52 | 28.48 | 46.32 |
| 42 | JVB-49 | 14.66 | 82.14 | 34.52 | 74.16 | 57.40 | 26.86 | 50.18 |
| 43 | JVR- HOC- 3 | 12.51 | 75.35 | 47.83 | 86.10 | 50.78 | 25.58 | 47.66 |
| 44 | JVR-308 | 16.85 | 82.96 | 38.23 | 68.82 | 55.65 | 30.29 | 46.66 |
| 45 | JVR-309 | 11.47 | 72.76 | 43.37 | 78.06 | 40.15 | 28.56 | 44.96 |
| 46 | JVR-HPS-2284 | 12.01 | 76.53 | 48.63 | 81.00 | 59.85 | 21.55 | 46.87 |
| 47 | JVR-HPS-2289 | 16.90 | 79.20 | 52.56 | 75.76 | 62.85 | 23.10 | 48.36 |
| 48 | K-1574 | 12.37 | 78.86 | 50.52 | 75.60 | 57.52 | 25.51 | 47.97 |
| 49 | K-1577 | 18.95 | 86.63 | 38.03 | 68.46 | 71.00 | 26.69 | 44.35 |
| 50 | K-1643 | 12.26 | 76.55 | 36.23 | 65.22 | 53.18 | 22.59 | 43.49 |
| 51 | KADIRI-7 | 17.63 | 78.80 | 51.97 | 76.69 | 69.84 | 25.24 | 44.87 |
| 52 | KAUSHAL | 15.20 | 76.55 | 43.85 | 78.93 | 67.00 | 23.34 | 45.08 |
| 53 | KDG-123 | 15.63 | 78.03 | 44.52 | 80.14 | 70.52 | 22.89 | 46.28 |
| 54 | KDG-128 | 18.80 | 82.00 | 48.77 | 87.79 | 70.00 | 25.70 | 45.35 |
| 55 | KDG-213 | 14.11 | 80.10 | 45.52 | 81.94 | 66.85 | 21.53 | 47.27 |
| 56 | NRCG-8 | 16.77 | 81.74 | 43.63 | 78.54 | 70.52 | 23.78 | 43.43 |
| 57 | RG-382 | 12.33 | 76.87 | 46.40 | 83.52 | 49.61 | 25.45 | 46.52 |
| 58 | RG-438-2 | 9.85 | 71.84 | 48.73 | 87.72 | 58.74 | 17.46 | 43.46 |
| 59 | RG-559-3 | 15.04 | 75.22 | 43.52 | 78.34 | 63.45 | 23.71 | 41.40 |
| 60 | SOMNATH | 15.00 | 76.77 | 42.77 | 76.98 | 56.42 | 27.12 | 43.93 |
| | | | | | | | | |
| Mean | | 14.17 | 77.62 | 42.72 | 75.17 | 59.33 | 24.85 | 45.88 |
| S. Em.± | | 0.86 | 2.37 | 2.41 | 2.29 | 2.40 | 2.03 | 1.40 |
| C.D. at 5% | | 2.42 | 6.65 | 6.76 | 6.40 | 6.71 | 5.68 | 3.92 |
| C.D. at 1% | | 3.20 | 8.79 | 8.93 | 8.46 | 8.87 | 7.51 | 5.19 |
| C.V.% | | 10.57 | 5.30 | 9.78 | 5.27 | 6.99 | 14.14 | 5.29 |




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

**1)** Days to 50% flowering, **2)** Days to maturity, **3)** Plant height (cm), **4)** Number of branches per plant **5)** Number of matured pods per plant, **6)** Number of immature pods per plant**, 7)** Number of pods per plant**, 8)** Pod yield per plant (g), **9)** Sound mature kernel (%), **10)** 100-kernel weight (g), **11)** Shelling out-turn (%), **12)** Biological yield per plant (g), **13)** Harvest index (%) and **14)** Oil content (%)

**Figure 4.2 Diagrammatic representation of phenotypic path analysis in Virginia groundnut**

(HNG-56 B)
**Small**

(ICGV-00350)
**Medium**

**Leaflet size**

(AK 143)
**Green**

(C-156)
**Dark green**

(HNG-57-A)
**Simple**

**Leaflet color**

**Inflorescence**

(CSMG-2005-18)
**Sparse**

(CGC-1-19)
**Medium**

(HNG-36)
**Dense**

**Stem pubescence**

**Plate 4.1 Photographs of leaflet size, leaflet color, inflorescence and stem pubescence in virginia groundnut**

(C-156)
**Absent**

(ICGV- 91026)
**Shallow**

(59-112)
**Medium**

(ICGV-00350)
**Deep**

(CSMG-2005-18)
**Very deep**

**Pod constriction**

(ICGS-05)
**Slight**

(AMR-174)
**Medium**

(HNG-57-A)
**Prominent**

**Pod reticulation**

**Plate 4.2 Photographs of pod constriction and pod reticulation in virginia groundnut**

(JVR-HPS-2289)
**Absent**

(JVB- 154)
**Slight**

(JVR-HPS-2284)
**Medium**

(AK 143)
**Prominent**

**Prominence of beak**

(KDG-128)
**Curved**

(ICGV-87846)
**Straight**

**Shape of beak**

(BAV-18)
**One seeded**

(CSMG-9907)
**Two seeded**

**Number of kernels**

**Plate 4.3 Photographs of prominence of beak, shape of beak and number of kernels in virginia groundnut**

(AMR-174)
**Off-white**

(59-112)
**Tan**

(HNG-56 B)
**Salmon**

(CSMG-9101)
**Red**

(JVR- HOC- 3)
**Dark red**

(JVR-HPS-2284)
**Dark purple**

**Kernel: color of testa**

**Plate 4.4 Photographs of color of testa in virginia groundnut**

(BAV-18)
**Monochrome**

(CSMG-2005-18)
**Variegated**

**Kernel color**

(59-112)
**Spheroidal**

(ALG-05-253)
**Cylindrical**

(KDG-123**)**
**Fusiform**

**Kernel shape**

**Plate 4.5 Photographs of kernel color and kernel shape in virginia groundnut**