Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)

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VIKRAM SINGH MEENA

Thesis

Master of Science in Agriculture

(Genetics and Plant Breeding)

2021

DEPARTMENT OF GENETICS AND PLANT BREEDING
RAJASTHAN COLLEGE OF AGRICULTURE
MAHARANA PRATAP UNIVERSITY OF AGRICULTURE AND TECHNOLOGY
UDAIPUR – 313 001 (RAJASTHAN)

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Thesis

Submitted to the

Maharana Pratap University of Agriculture and Technology, Udaipur

In partial fulfillment of the requirement for the Degree of

Master of Science in Agriculture

(Genetics and Plant Breeding)

BY

VIKRAM SINGH MEENA

2021

CERTIFICATE-I

CERTIFICATE OF ORIGINALITY

The research work embodied in this thesis titled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** submitted for the award of degree of Master of Science in Agriculture in the subject of Genetics and Plant Breeding to Maharana Pratap University of Agriculture and Technology, Udaipur (Raj.), is original and bona fide record of research work carried out by me under the supervision of **Dr. P. B. Singh**, Assistant Professor, Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, Udaipur. The contents of the thesis, either partially or fully, have not been submitted or will not be submitted to any other Institute or University for the award of any degree or diploma.

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This is to certify that this thesis entitled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** submitted for the degree of Master of Science in Agriculture in the subject of Genetics and Plant Breeding, embodies bonafide research work carried out by **Mr. Vikram Singh Meena** under my guidance and supervision and that no part of this thesis has been submitted for any other degree. The assistance and help received during the course of investigation have been fully acknowledged. The draft of this thesis was also approved by the advisory committee on 25/07/2020.

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This is to certify that **Mr. Vikram Singh Meena** student of **M.Sc. (Ag.)**, **Department of Genetics and Plant Breeding,** has made all corrections/ modifications in the thesis entitled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** which were suggested by the external examiner and the advisory committee in the oral examination held on 23/03/2021. The final copies of the thesis duly bound and corrected were submitted on /04/2021.

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Date: **(VIKRAM SINGH MEENA)**

Place: Udaipur

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ABBREVIATIONS

%	Per cent
*	Significant at 5% level
**	Significant at 1% level
ANOVA	Analysis of variance
C. D.	Critical difference
G. C.V.	Genotype coefficient of variation
P. C. V.	Phenotypic coefficient of variation
MS	Mean square
S. Em.	Standard error of mean
S. Ed.	Standard error of difference
d. f.	Degree of freedom
et al.,	And others
Kg	Kilogram
G	Gram
M	Metre
Cm	Centimetre
Mm	Millimetre
°C	Degree Celsius
S. No.	Serial number
viz.,	Namely
i.e.,	That is
b_i	Regression coefficient
S^2_d	Mean square deviation from linear regression
μ_i	Mean
S	Significant
NS	Non-significant

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.), is the 'king' of oilseeds. It is very important oil seed crop for India as well as in world and this crop is a member of *Papilionaceae* family. The term *Arachis* is derived from the Greek word "arachos", meaning a weed and *hypogaea*, meaning underground chamber *i.e.,* in botanical terms, a weed with fruits produced below the soil surface. Groundnut was originated from Brazil and it was popularly known as peanut / monkey-nut /African nut /Chinese nut/ Manila nut/ Kipper nut/ Hawks nut/ Jar nut/ Earth chestnut/ Goober pea/ Ground pea and Ground bean (Johnson,1964). Groundnut is an annual legume crop which is responsible to supply edible oil for human consumption and recognized as peanut in America and several other names such as it is well known as Mungphali in India.

Groundnut is an autotetraploid legume crop with basic chromosome number of 2n = 4x = 40. The flowers of groundnut are characterized as cleistogamy, therefore, crop is highly self-pollinated in nature. After pollination overy becomes stalk like structure known as Gynophore. Groundnut’s fruit known as Pods.

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); and sub-species *fastigiata* into var. *fastigiata* (Valencia); and var. *vulgaris* (spanish). In trade, bold seeded types are referred to as Virginia and the small seeded as Spanish (Ramanathan, 2001).

Peanut is grown for its high amount of edible oil (45-50%) and a reasonable amount of digestible protein (25-30%). It is the richest source of thiamine and also rich in niacin, which is low in cereals. Peanut is also valuable source of vitamins E, K and B. Groundnut oil is extensively used as a cooking medium both as refined oil and vanaspati ghee in addition to its use in manufacturing cosmetics, soap making, lubricants, olein, stearin and their salts.

Groundnut kernels are consumed as raw, boiled, roasted or fried products and also used in a variety of culinary preparations like peanut candies, butter, peanut milk and chocolates (Desai *et al*., 1999). It is an important protein supplement in cattle and poultry feeds as well. The oil-cake can also be used for manufacturing artificial fiber. The haulms are used as fodder for livestock. The shell is used as fuel and in manufacturing coarse boards, cork substitutes etc. Vegetative parts of groundnut like leaf and stem are also good source of nutritionally high quality fodder for farm animals. The residual oil cake contains 7% to 8% of N, 1.5% of P_2O_5 and 1.2% of K_2O making it useful as a fertilizer. Groundnut is a modulating legume with symbiotic nitrogen fixation root nodules improving the soil fertility and makes it valuable for crop rotation.

Major groundnut producers in the world are China, India, Nigeria, USA, Indonesia and Sudan. It is grown in an area of 25.44 million hectares worldwide with a total production of 45.22 million tones and productivity of 1777.33 kg/ha (FAOSTAT, 2019-20).

Total groundnut oil production in India during the year 2019-20 was 63.11 lakh tonnes. In year 2019-20, India's share in global production of groundnut oil was 15% (USDA).

India ranks the first in area and second largest producer next to China. India accounts for about 40 per cent of the world area and 30 per cent of the world production of groundnut. In India, it is grown on about 48.537 lakhs hectares area with a production of 69.696 lakhs tones and productivity of about 1436 kg/ha (Annual Report of ICAR-DGR, Junagarh *Kharif*, 2019). In India, about 91 per cent of total groundnut area is mostly confined to the States of Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, Maharashtra and Orissa. The rest of the area and production is scattered mainly in the States of Rajasthan, Uttar Pradesh, Madhya Pradesh and Punjab.

In Rajasthan it is mainly grown in the districts of Chittorgarh, Jaipur, Dausa, Swai Madhopur, Tonk, Bhilwara, Nagaur, Sikar and Karauli covering an area of 7.34 lakhs hectare with a production of 16.122 lakhs tonnes and productivity of about 2195 kg/ha (Commissionerate of Agriculture, Jaipur, Rajasthan, 2019-20).

To increase production of groundnut, there is need of developing high yielding varieties which requires a systematic breeding approach to be adopted. Assessment of variability is a first step in any breeding programme. Greater the diversity in the material better are the chances of improvement, provided the heritability is high and genetic advance is more. Further, the selection is more effective when it is practiced simultaneously for the characters which have desired nature of association with the traits of ultimate interest.

In plant breeding, genetic diversity plays an important role and it arises due to geographical separation or due to genetic barriers to crossability. The evaluation of diversity is important to know the source of genes for particular trait within the available germplasm. So, it is essential to know the genetic diversity of the existing genotypes before undertaking any crop improvement programme. It can be studied by Mahalanobis generalized distance as described by Rao (1952). This technique is intensively used for the study of genetic divergence in various breeding materials. This is one of the potent techniques of measuring genetic divergence.

Keeping this in view, the present study was carried out with following objectives:

(i) To estimate the variability parameters for seed yield and its contributing traits.

(ii) To estimate the correlation coefficient for seed yield and its contributing traits.

(iii) To determine direct and indirect effects of various characters on seed yield using path analysis.

(iv) To estimate genetic divergence in different genotypes.

2. REVIEW OF LITERATURE

The literature related to different aspects of the present investigation entitled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** has been reviewed under the following titles:

1. Variability parameters
2. Correlation and path coefficients
3. Genetic divergence

1. VARIABILITY PARAMETERS

The magnitude of genetic variability present in base population of any crop species is pivotal to crop improvement which must be exploited by plant breeders for yield improvement. Collection of information about genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability estimates and genetic advance is absolutely necessary to start an efficient breeding programme.

Prakash *et al.* (2000) studied 91 groundnut genotypes and observed that genotypic coefficient of variation was the highest for pod yield per plant and it was the lowest for oil content. Heritability in broad sense was high for pod yield per plant, oil content and 100 kernel weight. High genetic advance as per cent of mean was observed for pod yield per plant, pods per plant and 100 kernel weights.

Venkatramana (2001) evaluated thirty groundnut genotypes including 20 Spanish bunch and 10 Virginia bunch for genetic variability parameters 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, heritability in broad sense were high for oil content, 100-kernel weight and sound mature kernel percentage. Moderate heritability coupled with high genetic advance as per cent of mean was observed for kernel yield and oil yield. Additive gene effect could be preponderant for 100-kernel weight as it had high heritability estimates along with high genetic advance.

Prasad *et al.* (2002) reported that PCV and GCV estimates were high for harvest index, while magnitude of these parameters was moderate for pod yield per plant, primary branches per plant, height of main axis, pods per plant and 100 kernel weights. High estimates of heritability and genetic advance as per cent of mean were observed for harvest index, pod yield per plant, height of main axis and pods per plant, indicating prime role of additive gene effects for the inheritance of these characters.

Mothilal *et al.* (2004) studied components of variation, heritability and genetic advance in 65 confectionery groundnut genotypes. They reported that values of GCV and PCV were high for mature pods per plant and pod yield per plant and those were moderate to low for plant height, branches per plant, shelling out turn, 100 pod weights, 100-kernel weight and sound mature kernels. These characters also exhibited high magnitude of heritability. However, genetic advance as per cent of mean was high for pods per plant and it was moderate for branches per plant, plant height and 100 kernels weight, thus indicating that due weightage should be given to these characters to improve yield potential of groundnut.

Kadam *et al.* (2007) concluded the results on the study of 40 groundnut genotypes that genotypic coefficient of variation was high for kernel yield, pod yield, number of pods, number of branches, plant height and harvest index. High heritability coupled with high genetic advance was also observed for pod yield and kernel yield.

Giri *et al.* (2009) observed high PCV, GCV, heritability and genetic advance as per cent of mean for kernel yield per plant and pod yield per plant.

Vishnuvardhan *et al.* (2012) recorded observations on sixteen characters. 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. High GCV accompanied by high heritability were obtained for number of immature pods per plant indicating predominant role of additive gene action and amenability for phenotypic selection in early generations. Moderate GCV and heritability were registered for plant height at harvest, number of primary branches per plant, number of leaves per plant at harvest, number of mature pods per plant, kernel weight per plant indicating that additive and non-additive gene actions have a role in their inheritance and phenotypic selection would be effective to some extent. For days to 50 per cent flowering and days to maturity, GCV was low and heritability was high. For sound mature kernel percentage and shelling out-turn all the genetic parameters were low indicating larger role of non-additive gene action and selection would be effective in later segregating generations.

John *et al*. (2013) observed high genetic coefficient of variation for days to 50 per cent flowering. High heritability of 97.33 per cent was observed for pod yield per plant. High heritability and high genetic advance as percent of mean was recorded for plant height, haulm yield per plant, pod yield per plant and kernel 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 primary branches per plant, number of secondary branches per plant, number of mature pods per plant and 100 pod weight indicating the importance of both additive and non additive gene action in the inheritance of these characters.

Rao *et al.* (2014) recorded that magnitude of PCV and GCV was moderate to high for number of pods per plant and plant height, kernel yield, dry pod yield, hundred kernel weights and dry haulm yield. High heritability coupled with high genetic advance as per cent of mean was observed for hundred kernel weight, dry pod yield, kernel yield, plant height and number of pods per plant indicating the role of additive genes in the expression of these traits.

Yadav *et al*. (2014) reported that magnitude of GCV, PCV, heritability and genetic advance as percentage of mean were recorded high for various characters like pod yield per plant, hundred seed mass, harvest index, plant height and shelling per cent. High broad sense heritability estimates were recorded for hundred seed mass, days to maturity, shelling per cent, pod yield per plant, harvest index, protein per cent indicating that these traits were less influenced by the environment.

2. CORRELATION COEFFICIENTS AND PATH COEFFICIENTS

The statistics which measure the relationship between two or more variable is known as correlation coefficient. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for improvement in yield. Path analysis is simply standardized partial regression coefficient which splits the correlation into measures of direct and indirect effects of a set of independent variable on dependent variable. Path analysis was initially suggested by Sewall wright (1921) but applied for the first time in plant breeding by Dewey and Lu (1959).

Mathews *et al*. (2001) studied path analysis with 55 genotypes of groundnut and they reported that pod yield per plant had significant and positive genotypic correlation with days to flowering, days to 75 per cent maturity, kernel yield per plant, plant height, haulm yield and 100 kernel weight. Dry pod yield showed positive and significant direct effect for kernel yield per plant.

Nagda *et al*. (2001) reported that number of mature pods per plant and kernel yield per plant had positive and significant association with dry pod yield in both parents and hybrids. Days to 50 per cent flowering as well as shelling per cent 100-kernel weight as well as harvest index had positive and significant association with dry pod yield in parents and hybrids, respectively. Path analysis revealed that kernel yield per plant had highest positive and significant direct effect on pod yield followed by 100-kernel weight and number of mature pods per plant in parents.

Venkatramana (2001) evaluated 30 groundnut genotypes and found that genotypic correlation coefficients were in general marginally higher than the phenotypic correlation coefficients for all the five characters *i.e.* 100 kernel weight, SMK per cent, kernel yield, oil yield and oil content. Oil content was significantly and positively correlated with 100 kernel weight, sound mature kernel per cent, kernel yield and oil yield.

Prasad *et al*. (2002) reported that pod yield per plant was significantly and negatively correlated with the height of the main axis; while, significantly positive correlation of pod yield per plant was observed with harvest index at both phenotypic and genotypic levels. Path analysis revealed that pod yield per plant had positive direct effect on harvest index; while, percentage of sound mature kernel and 100-kernel weight showed negative direct effect on harvest index.

Sumathi and Muralidharan (2007) reported that pod yield per plant had significant positive association with kernel yield, sound mature kernel weight and 100 seed weight both at genotypic and phenotypic levels. The characters shelling percentage and oil content had negative association with pod yield per plant both at genotypic and phenotypic level. The inter correlation of kernel yield with sound mature kernel weight and 100 seed weight were also positive and significant. The number of mature pods per plant exhibited positive and significant correlation with total number of kernels per plant and sound mature kernel number. Path analysis indicated that among eleven characters kernel yield per plant exerted the maximum positive direct effect on pod yield per plant. The direct effects of all the other traits were also positive except number of mature pods per plant, sound mature kernel weight and shelling percentage, these characters showed negative direct effects on pod yield per plant.

Giri *et al.* (2009) concluded that pod yield showed positive significant associations with days to 50 per cent flowering, days to maturity, kernel yield, test weight and oil content. The path analysis revealed that high positive direct effect of kernel yield exerted on pod yield as well as indirect effect of oil content, strong mature kernel, days to 50 per cent flowering, test weight and days to maturity through kernel yield. Therefore, it would be rewarding to lay due emphasis on the selection of these characters for rapid improvement in pod yield.

John *et al.* (2009) evaluated 60 genotypes of groundnut to study character association and they reported that pod and kernel yields per plant showed significant and positive association with days to 50 per cent flowering, plant height, number of secondary branches per plant, number of mature pods per plant, SMK weight, sound mature kernel number as well as weight and 100 kernel weight. So, these characters were considered as selection indices for the improvement of kernel and pod yield per plant.

Awatade *et al.* (2010) reported that genotypic correlation coefficients were slightly higher than phenotypic correlation coefficients. The characters, number of pods per plant, number of primary branches per plant, number of kernel per plant and kernel yield per plant showed significant positive correlation with dry pod yield per plant. Path analysis revealed that the number of pods per plant, shelling percentage, pod length, 100 seed weight and kernel yield per plant had positive direct effect on dry pod yield per plant.

Raut *et al.* (2010) investigated in F_2 generation for six crosses of groundnut. The correlation coefficients of pod yield per plant were found positive and highly significant with kernel yield per plant, number of mature pods per plant and shelling out-turn. Kernel yield per plant had the highest positive direct effect on pod yield per plant followed by mature pods per plant. While, shelling out-turn showed high negative direct effect towards pod yield per plant but it expressed high indirect effect via kernel yield per plant. Thus, on the basis of correlations and direct and indirect effects, kernel yield per plant, number of mature pods per plant and shelling out-turn were proved to be the outstanding characters influencing pod yield in groundnut and need to be given importance in selection to achieve higher pod yield.

Shinde *et al.* (2010) studied the correlation coefficients among ten yield contributing traits with their path effects towards pod yield. The correlation of pod yield per plant was associated significantly and positively with number of mature pods per plant, 100-kernel weight and number of primary branches per plant, but was negative with days to 50 per cent flowering and days to maturity. 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 and other characters had high indirect effects through number of mature pods per plant.

Korat *et al.* (2010) concluded that yield contributing characters like biological yield per plant, 100-kernel weight and harvest index had positive and significant association with pod yield per plant at phenotypic level. Phenotypic inter relationship between days to maturity and pod yield per plant was found negative and significant. Genotypic correlations of above said yield components with pod yield were also strong and in the same direction. The genotypic and phenotypic path analysis revealed the highest positive direct effects of biological yield per plant and harvest index towards pod yield. Hundred-kernel weight contributed indirectly via biological yield per plant and harvest index. Based on correlation and path analysis, biological yield per plant, 100-kernel weight and harvest index were identified as the most important yield contributing characters.

John *et al.* (2011) carried out correlation analysis to assess the relationship among different characters in F_2 population of groundnut and reported the high direct effect of pods per plant was appeared to be the main factor for its strong positive correlation with pod yield.

Vekariya *et al.* (2011) evaluated 50 diverse genotypes and observed that pod yield per plant had highly significant and positive correlations at phenotypic level with number of mature pods per plant, 100-pod weight, 100-kernel weight, kernel yield per plant, biological yield per plant and harvest index. Path analysis revealed that the kernel yield per plant, biological yield per plant and harvest index had high and positive direct effects on pod yield per plant.

Babariya and Dobariya (2012) studied 100 genotypes of Spanish bunch groundnut and concluded that pod yield per plant was significantly and positively correlated with days to maturity, plant height, number of pods per plant, kernel yield per plant, number of mature pods per plant, 100-kernel weight, biological yield per plant and harvest index. Biological yield per plant and harvest index exhibited high and positive direct effects on pod yield per plant. Whereas, kernel yield per plant, number of pods per plant and days to maturity showed moderate and positive direct effects on pod yield per plant. Thus, these characters were identified as the most important yield components and due emphasis should be placed on these characters while selecting for high yielding genotypes in Spanish bunch groundnut.

Kumar *et al.* (2012) observed that pod yield displayed significant positive association with kernel yield per plant, mature pods per plant, total pods per plant, harvest index, 100-seed weight, root weight, plant height and shoot weight. Path co-efficient analysis revealed high direct effects of kernel yield per plant and harvest index on pod yield. Hence, it would be rewarding to give due importance on the selection of these characters for rapid improvement in pod yield of groundnut.

Thakur *et al.* (2013) reported that pod yield ha-^{1} showed highly significant and positive association with days to maturity, sound mature kernel per cent, pod length, pod width and kernel length but the highly significant and negative association was shown with days to flowering, pod per plant, shoots length, shelling per cent and specific leaf area. Partitioning the total yield contributions into individual and combined effect showed that days to maturity, root length, pod width, pod length and kernel length made individual high positive direct contribution to pod yield ha-1.Days to flowering, shoot length, shelling per cent, sound mature kernels per cent and 100- kernel weights had direct negative contribution with pod yield ha-^{1}. Therefore, days to maturity, root length, pod width, pod length and kernel length were identified to be the important traits which could be used in selection for yield.

Kahate *et al.* (2014) observed that kernel yield per plant, harvest index, test weight and oil content exhibited significant positive association with pod yield. The path analysis study revealed that kernel yield per plant had positive direct effect on pod yield, harvest index, while test weight showed positive indirect effect on pod yield through kernel yield.

Rao *et al.* (2014) recorded that dry pod yield was significant positively correlated with kernel yield, number of pods per plant, hundred kernel weight and dry haulm yield. Path coefficient analysis indicated that number of pods per plant and hundred kernel weight was important trait to be considered for realizing the improvement in yield. Groundnut yield in rain fed areas has been limited by drought stress because pod yield and other growth parameters have been severely affected.

Yadlapalli (2014) observed that pod yield exhibited significant and positive genotypic correlations with all the characters except with plant height. 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 per cent flowering. Selection for characters showing high significant correlation and showing high direct effects will be helpful in the improvement of yield in the groundnut.

3. GENETIC DIVERGENCE

The assessment of genetic diversity using quantitative traits is very important for differentiating the well defined populations. Several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives of which Mahalanobis's generalized distance occupy a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

Korat *et al.* (2009) observed maximum inter cluster distances between clusters I and VIII followed by clusters IV and VIII, clusters III and VIII and clusters II and VIII. The cluster VII showed high mean in respect to pod yield per plant, number of secondary branches/plant, number of aerial pegs/plant, number of kernels per pod, 100-kernel weight and harvest index. The cluster I had desirable value for days to 50 per cent flowering and days to maturity. While higher numbers of primary branches were 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 be advisable to intercross among the genotypes from clusters I, II, III, IV and VIII for generation of transgressive segregates and wide spectrum genetic variability for improvement of pod yield in groundnut.

Dolma *et al.* (2010) studied genetic divergence in among 33 genotypes of groundnut and observed that 33 genotypes were grouped into six clusters, where a cluster I was the largest containing 18 genotypes followed by cluster II with 10 genotypes. The inter cluster distance was maximum between cluster IV and V followed by cluster III and V.

Khote *et al.* (2010) studied genetic divergence in 30 exotic genotypes of groundnut and observed that based on genetic distance, these genotypes were grouped into six different clusters. Cluster II and cluster V and cluster I and cluster VI were identified genetically diverse clusters could be used for hybridization programme in crop improvement in groundnut.

Kumar *et al*. (2010) studied of genetic divergence of sixty four genotype of groundnut revealed wide range of D^2 values ranging between 4.52 and 27.75 suggesting the presence of considerable amount of genetic diversity in the genotypes studied, which were grouped in to seven clusters where, cluster VII (28) was the largest followed by cluster I (24) and cluster VI (4). Maximum inter cluster distance was recorded between IV and VI representing wide divergence among these clusters. On the basis of inter cluster distance and cluster means the genotypes viz., ICGV-05033, ICGV-05052, PAFRGVT58, GG-20×ICGV- 91114, ICGX-020063-F-B-SSD-P20-B, ICGX-020055-F-SSD-P37-B were 21121 widely diverse therefore may be considered for future breeding programmes

Nirmala *et al.* (2013) studied 30 genotypes and grouped into 14 clusters. Among the various traits, the highest contribution towards divergence was found for number of secondary branches per plant, followed by crop growth rate (CGR) at 75 days after sowing (days) to harvest, CGR at 30-75 days, 100-seed weight, plant height, SPAD chlorophyll meter reading and harvest index.

Yadav *et al.* (2014) evaluated 60 genotypes for the study of genetic divergence. D^2 analysis indicated existence of wider genetic variability in the population of sixty genotypes which were grouped in twelve clusters, based on their inter clusters distance. The maximum inter-cluster distance (D = 7.044) was found between cluster III and X carrying one and two genotypes from each cluster, respectively followed by that between V and X (D = 6.447) and cluster III and XII (D = 5.943). The minimum inter cluster distance was observed between cluster VII and XI (D = 2.770). The intra-cluster distance (D) ranged from 1.909 to 2.863, the maximum being in cluster V (2.863). The minimum intra-cluster distance (D) was found in cluster II (1.909) which includes eight genotypes. Cluster III showed high genetic divergence with cluster X followed by cluster V.

Patil *et al. (2015)* studies forty genotypes were grouped into fourteen clusters. Cluster I contained the highest number of genotypes (21) and lowest number in clusters II, V, VII, VIII, IX, X, XI, XII and XIII were solitary with one genotype per cluster. The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity is present among the genotypes of distant grouped. The highest intra cluster distance was observed in cluster IV and lowest in cluster I, The highest inter cluster distance was observed between cluster VI and XII followed by cluster between III and VI, the minimum distance observed between cluster V and VII followed by between clusters VII and X. Pod yield per plant, days to 50 per cent flowering, 100 kernel weight, kernel weight per plant, number of pod bearing nodes were the most important contributors. But the highest cluster means for total number of kernels per plant, number of pod bearing nodes, number of matured pods per plant, kernel weight per plant and pod yield per plant was obtained from the cluster XIV. With moderate yield but early maturity varieties were found in cluster XII.

3. MATERIALS AND METHODS

The present investigation was carried out to elicit the information on **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** during *kharif,* 2017 at the Instructional Farm, College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur. Geographically, Udaipur is situated at an elevation of 582.17 meter above the mean sea level on latitude of 24º 34' North and longitude of 73º 42' East. The meteorological observations during crop period are given in Appendix-1.

1. EXPERIMENTAL MATERIALS

The experimental material consisted of 112 diverse genotypes along with 4 checks of groundnut received from different origins, which were obtained from the All India Coordinated Research Improvement Project on Groundnut, MPUAT at Udaipur. Details of selected genotypes are given in Table 3.1.

2. EXPERIMENTAL DETAILS

The 112 bunch genotypes along with 4 checks was evaluated in augmented design with seven blocks during *kharif*, 2017 at Instructional Farm College of Technology and Engineering, MPUAT, Udaipur. Each treatment were sown in a plot of 5 m length and 3 m width plot maintaining crop geometry of 30 cm row to row and 10 cm plant to plant spacing. All the recommended package of practices of zone IVA of Rajasthan was followed to raise a healthy crop. Observations were recorded on five randomly selected competitive plants from each treatment in each replication for all the characters except days to 50 per cent flowering, days to maturity, 100- kernel weight and oil content as they were recorded on plot basis in each replication for each genotype. Mean value of 5 plants was used for statistical analysis.

Table 3.1: List of genotypes used in the present study and their pedigree

S. No.	Name of Genotypes	Pedigree	Place
1.	Pratap Raj Mungphali	Selection from ICGV 98223	MPUAT, Udaipur
2.	UG-5	Selection from ICGV98281	ICRISAT, Hyderabad
3.	UG-6	ICGV93373 X ICGV92224	ICRISAT, Hyderabad
4.	UG-9	ICGV95322 X ICGV96398	ICRISAT, Hyderabad
5.	UG-10	ICGV93124 X (LI X ICGS44)	ICRISAT, Hyderabad
6.	UG-15	ICGV93134 X (LI X ICGS44)	ICRISAT, Hyderabad
7.	UG-16	ICGV93143 X (LI X ICGS44)	ICRISAT, Hyderabad
8.	UG-17	GAJAH X (NU X ICGS44) X (LI X ICGS44)	ICRISAT, Hyderabad
9.	UG-19	[{(ICGV86347 X ICGV8031) X JL-24} X Gajah X (NU X ICGV87883)]	ICRISAT, Hyderabad
10.	UG-20	(ICGV2411 X ICG7637) X Gajah x ICGV	ICRISAT, Hyderabad
11.	UG-21	(TAG-24 X ICG8666)	ICRISAT, Hyderabad
12.	UG-22	(ICGV87290 x ICGV87846)	ICRISAT, Hyderabad
13.	UG-24	(ICGV87290 X TAG-24)	ICRISAT, Hyderabad
14.	UG-56	B-95 X HPS20-2	DGR, Junagarh
15.	UG-57	BAU-13 X SEL12-2	ICRISAT, Hyderabad
16.	UG-59	GG-20 X Kadiri-3	ICRISAT, Hyderabad
17.	UG-60	ICGV86031 X TAG-24	DGR, Junagarh
18.	UG-61	GG-20 X Chico2	DGR, Junagarh
19.	UG-62	PBS20176 X NRCG48291	DGR, Junagarh
20.	UG-64	(EDRGVT X ICGV03056)	ICRISAT, Hyderabad
21.	UG-65	(EDRGVT X ICGV03206)	ICRISAT, Hyderabad
22.	UG-67	B95 X Giri-1	DGR, Junagarh
23.	UG-68	PBS20176 X NRCG4829-1	DGR, Junagarh
24.	UG-69	P95 X GG-2	DGR, Junagarh
25.	UG-71	GG-2 X JCA16	DGR, Junagarh
26.	UG-85	ICGV86031 X TAG24	DGR, Junagarh
27.	UG-86	(ICGS44 X CSMG84-1) X GG-2	DGR, Junagarh
28.	UG-87	TAG-24 X ICGS75	DGR, Junagarh
29.	UG-88	PBS20176 X Code26	DGR, Junagarh
30.	UG-89	ICG X 000102	ICRISAT, Hyderabad
31.	UG-90	ICGS76 X ICGV86031	DGR, Junagarh

S. No.	Name of Genotypes	Pedigree	Place
32.	UG-91	TAG-24 X ICGV76-1	DGR, Junagarh
33.	UG-92	PBS29017 X NRCG4829	DGR, Junagarh
34.	UG-93	(ICGS44 X CSMG84-1) X ICGV86031	DGR, Junagarh
35.	UG-94	TAG-24 X ICGS76	DGR, Junagarh
36.	UG-95	ICGS44 X CSMG84-1-2	DGR, Junagarh
37.	UG-100	PBS20176 X Code26-1	DGR, Junagarh
38.	UG-102	ICGS44 X CSMG84-1	DGR, Junagarh
39.	UG-103	(ICGS44 X CSMG84-1) X GG-2	DGR, Junagarh
40.	UG-104	PBS11039 X ICGV86031	DGR, Junagarh
41.	UG-105	PBS11039 X TAG-24	DGR, Junagarh
42.	UG-107	(ICGV86031 X TAG-24) X CGMS84-1	DGR, Junagarh
43.	UG-108	ICGS76 X ICGV86031-1	DGR, Junagarh
44.	UG-109	ICG X 000103	ICRISAT, Hyderabad
45.	UG-110	ICGS44 X CSMG84-1	DGR, Junagarh
46	UG-111	PBS11039 X TAG24-1	DGR, Junagarh
47.	UG-112	PBS29031 X ICGV86031	DGR, Junagarh
48.	UG-113	ICGS44 X CSMG84-1	DGR, Junagarh
49.	UG-114	ICGS76 X ICGV86031-2	DGR, Junagarh
50.	UG-115	PBS11039 X NRCG4829	DGR, Junagarh
51.	UG-116	ICGV03063	ICRISAT, Hyderabad
52.	UG-117	Kadiri-3 X TKG19A	DGR, Junagarh
53.	UG-118	ICGS-11 X SBX1-2	DGR, Junagarh
54.	UG-119	ICG X 020153	ICRISAT, Hyderabad
55.	UG-120	ICGS76 X ICGV86325	DGR, Junagarh
56.	UG-122	J-83 X TG-41	DGR, Junagarh
57.	UG-123	ICG X 020091	ICRISAT, Hyderabad
58.	UG-124	CSMG84-1 X ICGV4747	DGR, Junagarh
59.	UG-125	TAG-24 X ICGV4747	DGR, Junagarh
60.	UG-126	CSMG84-1 X ICGV86031	DGR, Junagarh
61.	UG-127	ICG X 020093	ICRISAT, Hyderabad
62.	UG-128	ICG X 020041	ICRISAT, Hyderabad
63.	UG-129	ICG X 990160	ICRISAT, Hyderabad
64.	UG-130	ICG X 010014	ICRISAT, Hyderabad
65.	UG-132	ICGS-11 X SBX1-1	DGR, Junagarh

S. No.	Name of Genotypes	Pedigree	Place
66.	UG-133	ICG X 040116	ICRISAT, Hyderabad
67.	UG-134	ICG X 040117	ICRISAT, Hyderabad
68.	UG-135	ICG X 040119	ICRISAT, Hyderabad
69	UG-136	ICG X 040120	ICRISAT, Hyderabad
70.	UG-137	ICG X 020048	ICRISAT, Hyderabad
71.	UG-138	ICG X 070064	ICRISAT, Hyderabad
72.	UG-139	ICG X 050061	ICRISAT, Hyderabad
73.	UG-140	ICG X 050062	ICRISAT, Hyderabad
74.	UG-141	ICG X 050064	ICRISAT, Hyderabad
75.	UG-142	ICG X 050066	ICRISAT, Hyderabad
76.	UG-143	ICG X 050069	ICRISAT, Hyderabad
77.	UG-144	ICG X 050072	ICRISAT, Hyderabad
78.	UG-145	ICG X 050075	ICRISAT, Hyderabad
79.	UG-146	GG-20 X ICGV91114	DGR, Junagarh
80.	UG-147	GG-20 X ICGV91114-1	DGR, Junagarh
81.	UG-148	ICGV91114 X ICGV86564	DGR, Junagarh
82.	UG-149	PBS28014 X NRCG1463	DGR, Junagarh
83.	UG-150	PBS26002 X PBS29017	DGR, Junagarh
84.	UG-151	AK159 X NRCG5001	DGR, Junagarh
85.	UG-152	AK159 X NRCG5001-1	DGR, Junagarh
86.	UG-153	AK159 X NRCG5001-2	DGR, Junagarh
87.	UG-154	ICG X 020106	ICRISAT, Hyderabad
88.	UG-155	(TKG19A X Kadiri-3) X TKG19A	DGR, Junagarh
89.	UG-156	GG-20 X ICGV87250	DGR, Junagarh
90.	UG-157	TKG19A X Kadiri-3	DGR, Junagarh
91.	UG-159	JSSP15 X JSSP-24	DGR, Junagarh
92.	UG-162	GG-2 X TIG-41	DGR, Junagarh
93.	UG-171	GG-7 X JL-502	DGR, Junagarh
94.	UG-174	TG-540 X ICGV86325	DGR, Junagarh
95.	UG-177	J-11 X TIG-41	DGR, Junagarh
96.	UG-180	TG37A X CS-19	DGR, Junagarh
97.	UG-182	UG-20 X ALR-3	DGR, Junagarh
98.	UG-184	GG-5 X TPG-41	DGR, Junagarh
99	UG-185	JAWL-43 X TG-26	DGR, Junagarh

S. No.	Name of Genotypes	Pedigree	Place
100.	UG-186	GG-12 X TG-26-2	DGR, Junagarh
101.	UG-187	GG-12 X GPBD-4	DGR, Junagarh
102.	UG-188	JAWL 43 X	DGR, Junagarh
103.	UG-189	ICU X 070062	ICRISAT, Hyderabad
104.	UG-192	GG-8 X B 95-4	JAU, Junagarh
105.	UG-195	GG-8 X JL-502	JAU, Junagarh
106.	UG-196	GG-8 X JL-501	JAU, Junagarh
107.	UG-197	VRI-2 X GG-21-2	JAU, Junagarh
108.	UG-199	VRI-2 X GG-21-3	JAU, Junagarh
109.	UG-200	TG37A X CS19-4	JAU, Junagarh
110.	UG-201	TKG19A x Kadiri X TKG19A-4	JAU, Junagarh
111.	UG-202	TG-40 X AGN-34	JAU, Junagarh
112.	UG-210	GG-5 X JSSP25-5	JAU, Junagarh
113.	UG-211	GPBD-4 X TG37A	JAU, Junagarh
114.	UG-213	VRI-2 X GG-21-4	JAU, Junagarh
115.	TG37A	TG25 X TG26	BARC, TROMBAY
116.	GBPD-4	KRG-1 X ICGV-8655	KARNATAK

3. CHARACTERS STUDIED

Observations were recorded on five randomly selected competitive plants of each genotype in each plot for various characters except days to 50 per cent flowering, days to maturity, 100-kernel weight and oil content which were recorded on plot basis. The methodology used for recording observations on different characters is described below:

(a) Quantitative Traits

(i) Days to 50 percent flowering

Number of days were counted from the date of sowing to date when at least 50 percent of the plants having at least one flower.

(ii) Duration between flowering to pegging

Number of days was counted from the days of flowering to days to pegging.

(iii) Initiation of flowering

Numbers of days were counted from the date of sowing to date of initiation of pegging.

(iv) Plant height

Plant height was measured in centimeter from ground level to the tip of main axis at the time of maturity on each randomly selected five plants.

(v) Number of branches per plant

The branches arising on main axis were counted on each randomly selected five plants at the time of maturity.

(vi) Days to maturity

The total numbers of days were calculated from the date of sowing to date when all the plants attained complete physiological maturity.

(vii) Dry pod yield per plant

The fully developed dry pods were weighed in gram from each randomly selected five plant at the time of maturity and average weight per plant was calculated.

(viii) Sound mature kernel

Fully matured kernels were counted from representative sample of 100 kernels obtained from each plot and was expressed as per cent sound mature kernels.

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

(ix) 100-kernel weight

Hundred kernels were counted from random sample from each plot and weighed in gram.

(x) Shelling per cent

The 100 g pods were weighed from each plot and shelled. The shelling per cent was calculated as:

$$\text{Shelling Percentage } (\%) = \frac{\text{Weight of kernels } (\text{g})}{\text{Weight of pods } (\text{g})} \times 100$$

(xi) Biological yield per plant

After harvesting and sun drying, all the randomly selected five plants were weighed in gram and average was calculated.

(xii) Harvest index

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

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

(b) Qualitative Traits

(i) Oil content

Two random samples of kernels were drawn from bulk harvest of five randomly selected plants under each replication. Oil content of kernels was determined by the Soxhlet's Method and average oil content in per cent was worked out. (Detailed procedure is given in Appendix II).

4. STATISTICAL ANALYSIS

The plot wise mean values of five randomly selected plants were used for the statistical analysis for 13 characters studied.

4.1 ANALYSIS OF VARIANCE FOR EXPERIMENTAL DESIGN

The analysis of variance for different characters in augmented RBD was done following Federer (1956). The skeleton of ANOVA was as follows.

Table 3.3: ANOVA

S. No.	Source	d. f.	SS	MS	F	EMS
1.	Block	r-1	$\sum_{j=1}^{r}(\sum_{i=1}^{c} X_{ij})^2/c - (\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij})^2/rc$			
2.	Check	c-1	$\sum_{i=1}^{c}(\sum_{j=1}^{r} X_{ij})^2/r - (\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij})^2/rc$			
3.	Germplasm lines	g-1	$\sum_{j=1}^{g} X_i^2 - (\sum_{i=1}^{g} X_i)^2/g$			
4.	Check v/s Germplasm lines	1	$(\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij})^2/rc + (\sum_{i=1}^{g} X_i)^2_g - (\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij} + \sum_{i=1}^{g} X_i)^2/(c.r+g)$			
5.	Error	(r-1)(c-1)	Total SS – Block SS – Check SS			
	Total		$\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij}^2 - (\sum_{i=1}^{c}\sum_{j=1}^{r} X_{ij})^2/cr$			

Where

X_{ij} = Value of i^{th} Check in j^{th} block

X_i = Value of i^{th} germplasm

r = Number of blocks

c = Number of checks

g = Number of germplasm

Variances for different pair wise comparison:

1. Difference between two check means = 2 MSE/r

2. Difference between adjusted mean of two germplasm in the same blocks = 2 MSE

3. Difference between adjusted means of two germplasm in different blocks = 2 MSE $\left[1+\frac{1}{c}\right]$

4. Difference between adjusted yield of germplasm and check mean =

$$MSE\left(1+\frac{1}{r}+\frac{1}{c}+\frac{1}{rc}\right)$$

Least significant difference values:

Comparison of different critical differences can be calculated as follows:

1. For two check means = t α $\sqrt{2MSE/r}$

2. For two adjusted germplasm in same block = t α $\sqrt{2MSE}$

3. For two adjusted germplasm in different block = t α $\sqrt{2MSE\,(c+1)/c}$

4. For an adjusted germplasm against check mean = t α $\sqrt{MSE\left(1+\frac{1}{r}+\frac{1}{c}+\frac{1}{rc}\right)}$

For all L.S.D. the t value is two tail values at α level at (r-1) (c-1) degree of freedom. How here these critical values were not calculated in the present investigation except no. 1.

4.2 Estimation of variability parameters

The following genetic parameters were estimated for the character exhibiting significant mean squares due to the genotypes.

(a) Genotypic variance: It was calculated using following formula.

$$Vg = \frac{MSG - MSE}{r}$$

Where,

Vg = Genotypic variance, MSG = Mean square due to germplasm

MSE = Error mean square, and r = Number of blocks

(b) Phenotypic variance: It was calculated as follows:

$$V_p = V_g + V_e$$

Where,

V_p = Phenotypic variance, V_g = Genotypic variance, and

V_e = Error variance *i.e.* MSE

(c) **Genotypic coefficient of variation (GCV):** It was calculated using the following formula as suggested by the Burton (1952).

$$GCV = \frac{\sqrt{V_g}}{\overline{X}} \times 100$$

Where,

V_g = Genotypic variance, and $\overline{X}$ = Population mean

(d) **Phenotypic coefficient of variation (PCV):** It was calculated using the following formula as suggested by Burton (1952).

$$PCV = \frac{\sqrt{V_p}}{\overline{X}} \times 100$$

Where,

V_p = Phenotypic variance, and $\overline{X}$ = Population mean

(e) **Heritability (h^2):** It was estimated in broad sense by using following formula as suggested by Lush (1949).

$$h^2 = \frac{V_g}{V_p} \times 100$$

Where,

h^2 = Heritability in broad sense

Vg = Genotypic variance

V_p = Phenotypic variance

(f) **Genetic gain**

It is percent expected genetic advance over the population mean. It was computed as follows using the formula of Johnson *et al.* (1955).

$$GG = \frac{GA}{\overline{X}} \times 100$$

Where,

$\overline{X}$ = Population mean

GA = Genetic advance = $\frac{K.v_g}{\sqrt{v_p}}$

Where,

Vg = Genotypic variance V_p = Phenotypic variance

K = Selection differential at 5 per cent selection pressure *i.e.*, 2.06

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 characters were worked-out as per Fisher (1954) Al-Jibouri *et al.* (1958) and Singh and Choudhary (1979). 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.

(a) Genotypic correlation coefficient

$$r_{xy}(g) = \frac{Covxy\ (g)}{\sqrt{Vx\ (g).Vy\ (g)}}$$

(b) Phenotypic correlation coefficient

$$r_{xy}(p) = \frac{Covxy(p)}{\sqrt{Vx\,(p).Vy\,(p)}}$$

Where,

r_{xy} (g) = Genotypic correlation coefficient between X and Y traits

r_{xy} (p) = Phenotypic correlation coefficient between X and Y traits

Cov_{xy} (g) = Genotypic covariance of X and Y traits

Cov_{xy} (p) = Phenotypic covariance of X and Y traits

V_x (g) = Genotypic variance for X trait

V_y (g) = Genotypic variance for Y trait

V_x (p) = Phenotypic variance for X trait

V_y (p) = Phenotypic variance for Y trait

The significance of correlation was tested by using the procedure of ‘t’ test given by William Sealy Gosset (1908).

4.4 PATH COEFFICIENT ANALYSIS

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influences of one variable upon another thereby permitting the separation of the correlation coefficient into the component of direct and indirect effects.

Path coefficient is the ratio of the standard deviation of the effect due to a given cause of the total standard deviation of the effects. The path coefficient analysis was carried out as per the method suggested by Dewey and Lu (1959).

Path coefficients were analyzed at genotypic level for dry pod yield per plant.

The direct and indirect effects of 12 characters on dry pod yield per plant (Y) were obtained as per procedure given below:

r_1Y	$r_{1\,1}\ r_{1\,2} \ldots\ldots\ldots\ r_{1\,12}$	P_1Y
r_2Y	$r_{2\,1}\ r_{2\,2} \ldots\ldots\ldots\ r_{2\,12}$	P_2Y
,,	,,	,,
,,	,,	,,
,,	,,	,,
,,	,,	,,
$R_{12}Y$	$r_{12\,1}\ r_{12\,2} \ldots\ldots\ldots\ r_{12\,12}$	$P_{12}Y$
A	B	C

Where,

r_1Y, r_2Y, r_3Y,…., $r_{12}Y$ are the genotypic correlations of days to 50 per cent flowering, duration between flowering to pegging, initiation of pegging, plant height (cm), number of branches per plant, days to maturity, sound mature kernels (%), 100-kernel weight (g), shelling percentage (%), biological yield per plant (g), harvest index (%), oil content (%) and dry pod yield per plant (g) respectively.

(i) P_1Y, P_2Y, P_3Y,………………….., P_9Y are the direct effects of days to 50 per cent flowering, duration between flowering to pegging, initiation of pegging, plant height (cm), number of branches per plant, days to maturity, dry pods yield per plant (g), sound mature kernels (%), 100-kernel weight (g), shelling percentage (%), biological yield per plant (g), harvest index (%), oil content (%) respectively.

Or A = BC

Values of 'C' vector were obtained as:

$$C = B^{-1}A$$

Where,

A is the vector of direct correlations of nine characters with yield Y.

B^{-1} is the inverse of mutual correlation matrix of characters.

C is the vector of direct effects.

The inverse of this matrix was carried out by Pivotal Condensation Method (Singh and Chaudhary, 1979).

To obtain indirect effect, B matrix was multiplied with vector C as follows:

$$D = C \times B$$

Where,

D is the matrix of direct and indirect effect

B is the matrix of correlation among nine characters.

The residual effect was computed as follows:

$$R = \sqrt{1 - (r_1 YP_1 Y + r_2 YP_2 Y + r_3 YP_3 Y + \ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_9 YP_9 Y}$$

Where, R is the residual effect.

4.5 GENETIC DIVERGENCE

4.5.1 Mahalanobis D^2 -statistics

In the present investigation genetic divergence was estimated based on Mahalanobis generalized distance as described by Rao (1952). Original variable means were transformed to un-correlated variables by the pivotal condensation method of inversion matrix. The D^2 values between the genotypes were obtained as the sum of squares of differences of the values of the corresponding transformed variables. For each pair of combinations the mean deviation *i.e.* di = $Y_i^1 - Y_i^2$, where

Y_i denotes the transformed variables (i = 1, 2, 3, 4, 5……….p) were calculated and the D^2 was then calculated as sum of the squares of those deviations, *i.e.*

$$D^2 = \Sigma\ (Y_i^1 - Y_i^2)^2$$

Where, p = Number of characters.

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degrees of freedom where p is the number of characters considered.

4.5.2 Grouping of genotypes by Tocher’s method

After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher’s method described by Rao (1952). The criterion used in this method was that any two varieties belonging to the same cluster, at least on an average, show a smaller D^2 value than those belonging to two different clusters. Then inter and intra-cluster distances were calculated and their relationships were diagrammatically represented.

4. RESULTS AND DISCUSSION

The present study entitled **“Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)”** was carried out at the instructional farm, CTAE, MPUAT, Udaipur.

The experimental material of present investigation was comprised of 112 genotypes of groundnut (*Arachis hypogaea* L.) including four checks. These genotypes were studied to estimate genetic variability, correlation coefficients, path coefficients and genetic divergence among themselves.

Observations recorded for thirteen characters of 112 genotypes were used for analysis of following parameters.

4.1 Analysis of variance

4.2 Mean values and Range

4.3 Variability parameters

4.4 Correlation coefficients

4.5 Path coefficients

4.6 Genetic divergence

4.1 ANALYSIS OF VARIANCE

The data recorded on thirteen characters were subjected to statistical analysis. The mean sum of squares due to genotypes were significant for the characters *viz.,* number of branches per plant, sound mature kernels (%), 100-kernel weight (g), biological yield per plant (g), harvesting index, dry pod yield per plant (g), oil content (%) and non- significant for the characters days to 50% flowering, days to maturity, initiation of pegging, duration between flowering to pegging (day), plant height (cm) and shelling per cent (%) that show considerable difference among the genotypes used in this research (Table 4.1).

4.2 MEAN VALUES AND RANGE

Weekly meteorological data are presented in Appendix-I. The mean performance of genotypes for different characters is presented in Table 4.2.1 and 4.2.2. These data show that the range was considerably high for most of the characters *viz*., days to 50 per cent flowering (29 to 36 days), days to maturity (99 to 114 days), Initiation of pegging (33 to 40 days), duration between flowering to pegging (days) (2 to 7 days), plant height (30.40 to 48.60 cm), number of primary branches per plant (4 to 8.40), sound mature kernels (75.33 to 92.84%), 100-kernel weight (30.28g to 48.80 g), shelling percent (60% to 76%), biological yield per plant (g) (26.3 to 39.55), harvesting index (27.31% to 63.55%), dry pod yield per plant (g) (10.20 to 18.40) and oil content (%) (30.50 to 48.49) indicating an adequate variability for exercising selection and use in the breeding programmes (Table 4.2.1 and Table 4.2.2).

Table 4.1: Mean squares for various characters in Groundnut

S. No.	Characters	Block	Treatment	Check	Germplasm	C v/s G	Error
		[6]	[115]	[3]	[111]	[1]	[18]
1.	Days to 50% flowering	1.45	2.73	7.85*	2.53	8.75*	1.60
2.	Days to maturity (day)	6.24	18.84	27.95	18.70	7.54	23.17
3.	Initiation of pegging (day)	2.62	3.04	8.70*	2.86	5.80	2.62
4.	Duration b/w flowering to pegging(days)	0.56	0.97	0.52	0.99	0.22	1.05
5.	Plant height (cm)	27.97	17.88	17.05	18.04	2.63	11.93
6.	No. of branches per plant	0.01	0.96**	0.03	0.96	4.59**	0.02
7.	Sound mature kernels (%)	1.06	19.69**	6.04	19.37**	96.60**	1.97
8.	100-kernel weight (g)	0.54	22.81**	43.04**	19.66**	312.01**	1.05
9.	Shelling (%)	30.39	16.01	26.04	15.74	16.54	20.77
10.	Biological yield per plant (g)	0.86	13.28**	16.86**	12.30**	110.30**	0.99
11.	Harvesting index (%)	2.91	55.15**	32.20**	51.82**	493.31**	3.55
12.	Dry pod yield per plant (g)	0.09	4.25**	3.36**	4.23**	9.48**	0.06
13.	Oil content (%)	0.09**	18.28**	31.89**	17.38**	78.19**	0.00

*, ** Significant at 5% and 1% level of significance, respectively

Table 4.2.1: Mean values for Days to 50% flowering, Days to maturity, Initiation of pegging, Duration between flowering to pegging (DAS), Plant height (cm), Number of branches per plant, Sound mature kernels (%)

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
1	G1	33.00	32.96	113.00	112.39	37.00	37.54	4.00	4.57	32.60	33.46	5.40	5.44	83.30	82.90
2	G2	32.00	31.96	103.00	102.39	37.00	37.54	5.00	5.57	34.00	34.86	6.20	6.24	78.52	78.12
3	G3	32.00	31.96	110.00	109.39	35.00	35.54	3.00	3.57	35.00	35.86	5.50	5.54	82.43	82.03
4	G4	31.00	30.96	110.00	109.39	35.00	35.54	4.00	4.57	34.20	35.06	6.50	6.54	88.56	88.16
5	G5	33.00	32.96	104.00	103.39	37.00	37.54	4.00	4.57	40.40	41.26	6.80	6.84	90.45	90.05
6	G6	31.00	30.96	111.00	110.39	34.00	34.54	3.00	3.57	38.00	38.86	5.40	5.44	78.54	78.14
7	G7	32.00	31.96	108.00	107.39	35.00	35.54	3.00	3.57	33.20	34.06	4.80	4.84	78.52	78.12
8	G8	32.00	31.96	102.00	101.39	36.00	36.54	4.00	4.57	31.60	32.46	6.70	6.74	82.50	82.10
9	G9	30.00	29.96	114.00	113.39	35.00	35.54	5.00	5.57	34.80	35.66	5.10	5.14	82.40	82.00
10	G10	33.00	32.96	107.00	106.39	37.00	37.54	4.00	4.57	43.00	43.86	6.60	6.64	86.34	85.94
11	G11	34.00	33.96	101.00	100.39	39.00	39.54	5.00	5.57	42.00	42.86	8.20	8.24	84.32	83.92
12	G12	34.00	33.96	109.00	108.39	39.00	39.54	5.00	5.57	38.60	39.46	6.10	6.14	82.64	82.24
13	G13	33.00	32.96	102.00	101.39	38.00	38.54	5.00	5.57	48.60	49.46	5.10	5.14	82.65	82.25
14	G14	30.00	29.96	110.00	109.39	34.00	34.54	4.00	4.57	35.40	36.26	6.02	6.06	82.40	82.00
15	G15	36.00	35.96	99.00	98.39	39.00	39.54	3.00	3.57	31.60	32.46	4.70	4.74	88.24	87.84
16	G16	34.00	33.96	112.00	111.39	38.00	38.54	4.00	4.57	36.80	37.66	8.20	8.24	91.80	91.40
17	G17	29.00	29.46	103.00	104.39	33.00	33.54	4.00	4.07	37.00	36.54	6.90	6.87	90.12	91.10
18	G18	31.00	31.46	111.00	112.39	36.00	36.54	5.00	5.07	34.40	33.94	5.90	5.87	92.58	93.56
19	G19	33.00	33.46	109.00	110.39	37.00	37.54	4.00	4.07	38.60	38.14	7.20	7.17	78.54	79.52
20	G20	34.00	34.46	104.00	105.39	37.00	37.54	3.00	3.07	37.80	37.34	6.80	6.77	85.24	86.22
21	G21	31.00	31.46	109.00	110.39	35.00	35.54	4.00	4.07	32.40	31.94	5.00	4.97	91.80	92.78
22	G22	35.00	35.46	105.00	106.39	37.00	37.54	2.00	2.07	39.20	38.74	4.00	3.97	78.64	79.62
23	G23	36.00	36.46	112.00	113.39	39.00	39.54	3.00	3.07	43.90	43.44	5.60	5.57	84.27	85.25
24	G24	34.00	34.46	101.00	102.39	38.00	38.54	4.00	4.07	33.40	32.94	6.20	6.17	86.63	87.61

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**
25	G25	34.00	34.46	108.00	109.39	37.00	37.54	3.00	3.07	41.20	40.74	5.20	5.17	90.25	91.23
26	G26	35.00	35.46	108.00	109.39	38.00	38.54	3.00	3.07	33.20	32.74	7.80	7.77	89.23	90.21
27	G27	35.00	35.46	109.00	110.39	39.00	39.54	4.00	4.07	47.20	46.74	6.40	6.37	85.65	86.63
28	G28	32.00	32.46	105.00	106.39	36.00	36.54	4.00	4.07	47.20	46.74	7.40	7.37	84.27	85.25
29	G29	34.00	34.46	101.00	102.39	38.00	38.54	4.00	4.07	35.60	35.14	7.90	7.87	82.27	83.25
30	G30	33.00	33.46	101.00	102.39	36.00	36.54	3.00	3.07	31.00	30.54	7.50	7.47	89.56	90.54
31	G31	33.00	33.46	109.00	110.39	36.00	36.54	3.00	3.07	34.80	34.34	7.30	7.27	81.24	82.22
32	G32	34.00	34.46	111.00	112.39	38.00	38.54	4.00	4.07	36.60	36.14	5.30	5.27	76.54	77.52
33	G33	34.00	33.71	106.00	106.64	37.00	36.79	3.00	3.07	39.60	42.81	6.80	6.81	85.45	85.34
34	G34	33.00	32.71	102.00	102.64	38.00	37.79	5.00	5.07	30.40	33.61	5.40	5.41	78.65	78.54
35	G35	31.00	30.71	109.00	109.64	34.00	33.79	3.00	3.07	38.80	42.01	6.80	6.81	89.56	89.45
36	G36	35.00	34.71	110.00	110.64	39.00	38.79	4.00	4.07	42.40	45.61	4.40	4.41	85.24	85.13
37	G37	34.00	33.71	103.00	103.64	39.00	38.79	6.00	6.07	33.60	36.81	7.20	7.21	80.50	80.39
38	G38	34.00	33.71	99.00	99.64	37.00	36.79	3.00	3.07	36.40	39.61	6.80	6.81	86.27	86.16
39	G39	33.00	32.71	114.00	114.64	37.00	36.79	4.00	4.07	34.40	37.61	6.30	6.31	88.25	88.14
40	G40	33.00	32.71	101.00	101.64	39.00	38.79	6.00	6.07	31.40	34.61	5.80	5.81	82.34	82.23
41	G41	35.00	34.71	99.00	99.64	38.00	37.79	3.00	3.07	46.90	50.11	4.90	4.91	86.24	86.13
42	G42	33.00	32.71	101.00	101.64	38.00	37.79	5.00	5.07	45.60	48.81	7.20	7.21	87.34	87.23
43	G43	32.00	31.71	109.00	109.64	35.00	34.79	3.00	3.07	34.20	37.41	5.80	5.81	86.24	86.13
44	G44	32.00	31.71	105.00	105.64	37.00	36.79	5.00	5.07	31.40	34.61	6.30	6.31	88.20	88.09
45	G45	36.00	35.71	103.00	103.64	40.00	39.79	4.00	4.07	32.20	35.41	7.10	7.11	88.66	88.55
46	G46	32.00	31.71	100.00	100.64	35.00	34.79	3.00	3.07	32.20	35.41	5.40	5.41	90.54	90.43
47	G47	32.00	31.71	107.00	107.64	36.00	35.79	4.00	4.07	38.80	42.01	6.30	6.31	82.43	82.32
48	G48	34.00	33.71	110.00	110.64	37.00	36.79	3.00	3.07	33.80	37.01	7.40	7.41	78.44	78.33
49	G49	32.00	30.96	106.00	104.39	36.00	34.79	3.00	2.82	32.80	31.51	6.50	6.53	87.65	87.76
50	G50	31.00	29.96	109.00	107.39	35.00	33.79	4.00	3.82	34.00	32.71	6.10	6.13	90.56	90.67

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**
51	G51	31.00	29.96	102.00	100.39	36.00	34.79	5.00	4.82	34.80	33.51	6.50	6.53	85.24	85.35
52	G52	35.00	33.96	103.00	101.39	40.00	38.79	5.00	4.82	36.80	35.51	8.10	8.13	87.25	87.36
53	G53	31.00	29.96	104.00	102.39	36.00	34.79	5.00	4.82	31.00	29.71	8.20	8.23	82.36	82.47
54	G54	32.00	30.96	101.00	99.39	37.00	35.79	5.00	4.82	37.20	35.91	7.20	7.23	86.43	86.54
55	G55	32.00	30.96	105.00	103.39	36.00	34.79	4.00	3.82	33.40	32.11	6.20	6.23	81.58	81.69
56	G56	33.00	31.96	110.00	108.39	39.00	37.79	6.00	5.82	32.20	30.91	7.40	7.43	85.15	85.26
57	G57	32.00	30.96	108.00	106.39	37.00	35.79	5.00	4.82	39.80	38.51	5.70	5.73	78.25	78.36
58	G58	30.00	28.96	110.00	108.39	35.00	33.79	5.00	4.82	31.20	29.91	5.80	5.83	85.65	85.76
59	G59	32.00	30.96	107.00	105.39	38.00	36.79	6.00	5.82	45.60	44.31	6.40	6.43	85.96	86.07
60	G60	32.00	30.96	110.00	108.39	35.00	33.79	3.00	2.82	40.20	38.91	7.80	7.83	86.25	86.36
61	G61	31.00	29.96	99.00	97.39	35.00	33.79	4.00	3.82	36.40	35.11	6.10	6.13	85.84	85.95
62	G62	32.00	30.96	100.00	98.39	38.00	36.79	5.00	4.82	40.80	39.51	5.90	5.93	81.38	81.49
63	G63	30.00	28.96	102.00	100.39	35.00	33.79	5.00	4.82	37.60	36.31	6.80	6.83	81.84	81.95
64	G64	31.00	29.96	106.00	104.39	35.00	33.79	4.00	3.82	33.80	32.51	7.90	7.93	91.36	91.47
65	G65	32.00	32.71	101.00	102.64	36.00	36.79	4.00	4.07	32.80	28.16	7.80	7.76	78.65	78.04
66	G66	31.00	31.71	110.00	111.64	36.00	36.79	5.00	5.07	31.60	26.96	5.20	5.16	81.38	80.77
67	G67	33.00	33.71	102.00	103.64	38.00	38.79	3.00	3.07	35.40	30.76	5.20	5.16	87.34	86.73
68	G68	30.00	30.71	110.00	111.64	34.00	34.79	4.00	4.07	38.00	33.36	6.50	6.46	79.52	78.91
69	G69	33.00	33.71	99.00	100.64	37.00	37.79	4.00	4.07	43.40	38.76	7.00	6.96	92.25	91.64
70	G70	33.00	33.71	99.00	100.64	37.00	37.79	4.00	4.07	33.00	28.36	8.00	7.96	75.33	74.72
71	G71	32.00	32.71	109.00	110.64	36.00	36.79	4.00	4.07	36.00	31.36	8.10	8.06	78.25	77.64
72	G72	32.00	32.71	114.00	115.64	35.00	35.79	3.00	3.07	34.80	30.16	7.20	7.16	86.24	85.63
73	G73	32.00	32.71	103.00	104.64	38.00	38.79	6.00	6.07	38.20	33.56	6.40	6.36	92.25	91.64
74	G74	31.00	31.71	100.00	101.64	35.00	35.79	4.00	4.07	35.20	30.56	6.90	6.86	87.65	87.04
75	G75	31.00	31.71	103.00	104.64	38.00	38.79	7.00	7.07	41.40	36.76	5.20	5.16	78.26	77.65
76	G76	32.00	32.71	101.00	102.64	36.00	36.79	4.00	4.07	35.00	30.36	6.80	6.76	89.24	88.63

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
77	G77	31.00	31.71	107.00	108.64	35.00	35.79	4.00	4.07	32.60	27.96	4.90	4.86	88.34	87.73
78	G78	32.00	32.71	110.00	111.64	37.00	37.79	5.00	5.07	37.60	32.96	6.60	6.56	82.64	82.03
79	G79	30.00	30.71	109.00	110.64	34.00	34.79	4.00	4.07	39.60	34.96	6.30	6.26	78.44	77.83
80	G80	33.00	33.71	101.00	102.64	37.00	37.79	4.00	4.07	41.00	36.36	6.90	6.86	89.24	88.63
81	G81	32.00	31.71	101.00	99.89	38.00	37.04	6.00	5.32	32.60	35.31	5.10	5.01	85.15	84.96
82	G82	30.00	29.71	112.00	110.89	36.00	35.04	6.00	5.32	31.60	34.31	6.40	6.31	78.85	78.66
83	G83	34.00	33.71	110.00	108.89	39.00	38.04	5.00	4.32	32.40	35.11	5.70	5.61	88.35	88.16
84	G84	34.00	33.71	104.00	102.89	39.00	38.04	5.00	4.32	33.80	36.51	6.60	6.51	92.34	92.15
85	G85	31.00	30.71	112.00	110.89	34.00	33.04	3.00	2.32	34.40	37.11	5.80	5.71	86.54	86.35
86	G86	31.00	30.71	110.00	108.89	34.00	33.04	3.00	2.32	33.70	36.41	4.90	4.81	82.27	82.08
87	G87	31.00	30.71	111.00	109.89	36.00	35.04	5.00	4.32	36.60	39.31	7.30	7.21	88.35	88.16
88	G88	30.00	29.71	112.00	110.89	33.00	32.04	3.00	2.32	33.40	36.11	6.50	6.41	81.84	81.65
89	G89	32.00	31.71	114.00	112.89	36.00	35.04	4.00	3.32	32.20	34.91	7.10	7.01	88.67	88.48
90	G90	35.00	34.71	104.00	102.89	38.00	37.04	3.00	2.32	40.60	43.31	7.10	7.01	88.31	88.12
91	G91	33.00	32.71	101.00	99.89	37.00	36.04	4.00	3.32	33.60	36.31	6.20	6.11	86.63	86.44
92	G92	30.00	29.71	110.00	108.89	34.00	33.04	4.00	3.32	31.30	34.01	6.40	6.31	89.61	89.42
93	G93	30.00	29.71	104.00	102.89	35.00	34.04	5.00	4.32	32.40	35.11	5.20	5.11	92.55	92.36
94	G94	32.00	31.71	112.00	110.89	38.00	37.04	6.00	5.32	38.80	41.51	8.40	8.31	88.31	88.12
95	G95	31.00	30.71	108.00	106.89	37.00	36.04	6.00	5.32	33.80	36.51	5.80	5.71	75.33	75.14
96	G96	33.00	32.71	103.00	101.89	38.00	37.04	5.00	4.32	40.40	43.11	6.20	6.11	82.69	82.50
97	G97	31.00	31.46	107.00	106.64	35.00	35.54	4.00	4.07	35.40	35.01	7.60	7.69	92.84	93.06
98	G98	30.00	30.46	99.00	98.64	33.00	33.54	3.00	3.07	31.00	30.61	7.40	7.49	81.24	81.46
99	G99	34.00	34.46	102.00	101.64	38.00	38.54	4.00	4.07	39.60	39.21	6.50	6.59	82.75	82.97
100	G100	32.00	32.46	107.00	106.64	36.00	36.54	4.00	4.07	40.80	40.41	5.00	5.09	88.46	88.68
101	G101	35.00	35.46	106.00	105.64	39.00	39.54	4.00	4.07	36.40	36.01	7.50	7.59	92.84	93.06
102	G102	32.00	32.46	112.00	111.64	39.00	39.54	7.00	7.07	40.80	40.41	6.30	6.39	88.34	88.56

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**
103	G103	34.00	34.46	107.00	106.64	37.00	37.54	4.00	4.07	40.80	40.41	7.40	7.49	88.56	88.78
104	G104	33.00	33.46	103.00	102.64	37.00	37.54	4.00	4.07	33.40	33.01	6.30	6.39	86.43	86.65
105	G105	32.00	32.46	106.00	105.64	35.00	35.54	3.00	3.07	36.40	36.01	8.10	8.19	86.27	86.49
106	G106	32.00	32.46	109.00	108.64	36.00	36.54	4.00	4.07	32.20	31.81	7.50	7.59	91.55	91.77
107	G107	32.00	32.46	111.00	110.64	35.00	35.54	3.00	3.07	34.20	33.81	6.20	6.29	87.68	87.90
108	G108	31.00	31.46	103.00	102.64	36.00	36.54	5.00	5.07	45.20	44.81	4.80	4.89	86.43	86.65
109	G109	31.00	31.46	112.00	111.64	36.00	36.54	5.00	5.07	35.60	35.21	6.20	6.29	92.34	92.56
110	G110	29.00	29.46	110.00	109.64	33.00	33.54	4.00	4.07	37.60	37.21	6.00	6.09	85.61	85.83
111	G111	30.00	30.46	106.00	105.64	33.00	33.54	3.00	3.07	31.20	30.81	5.90	5.99	84.75	84.97
112	G112	34.00	34.46	110.00	109.64	38.00	38.54	4.00	4.07	32.40	32.01	6.20	6.29	88.66	88.88
	GP Mean	32.34	-	106.22	-	36.53	-	4.17	-	36.37	-	6.42	-	85.38	-
	Min	29.00	-	99.00	-	33.00	-	2.00	-	30.40	-	4.00	-	75.33	-
	Max	36.00	-	114.00	-	40.00	-	7.00	-	48.60	-	8.40	-	92.84	-
1	Check1	31.57	31.57	105.43	105.43	35.43	35.43	3.86	3.86	38.87	38.87	5.89	5.89	82.46	82.46
2	Check2	33.14	33.14	106.00	106.00	37.29	37.29	4.14	4.14	36.46	36.46	5.93	5.93	83.29	83.29
3	Check3	34.14	34.14	103.14	103.14	38.00	38.00	3.86	3.86	35.14	35.14	6.03	6.03	84.61	84.61
4	Check4	33.00	33.00	108.00	108.00	37.43	37.43	4.43	4.43	36.37	36.37	6.02	6.02	82.87	82.87
	Check Mean	32.96	-	105.64	-	37.04	-	4.07	-	36.71	-	5.97	-	83.31	-
	Min	31.57	-	103.14	-	35.43	-	3.86	-	35.14	-	5.89	-	82.46	-
	Max	34.14	-	108.00	-	38.00	-	4.43	-	38.87	-	6.03	-	84.61	-
	GM	32.46	-	106.11	-	36.63	-	4.15	-	36.44	-	6.33	-	84.97	-
	SEd Check	0.68	0.68	2.57	2.57	0.87	0.87	0.55	0.55	1.85	1.85	0.08	0.08	0.75	0.75
	CD5	-	-	-	-	-	-	-	-	-	-	0.16	0.16	1.57	1.57
	CD1	-	-	-	-	-	-	-	-	-	-	0.23	0.23	2.16	2.16
	SEd AdM WB	1.79	1.79	6.81	6.81	2.29	2.29	1.45	1.45	4.89	4.89	0.21	0.21	1.98	1.98
	CD5	-	-	-	-	-	-	-	-	-	-	0.44	0.44	4.17	4.17

S. No.	Genotype	Days to 50% flowering		Days to maturity		Initiation of pegging		Duration b/w flowering to pegging(DAS)		Plant height(cm)		No. of branches per plant		Sound mature kernels (%)	
		Mean	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**	**Mean**	**AdM**
	CD1	-	-	-	-	-	-	-	-	-	-	0.60	0.60	5.71	5.71
	SEd AdM DB	2.00	2.00	7.61	7.61	2.56	2.56	1.62	1.62	5.46	5.46	0.23	0.23	2.22	2.22
	CD5	-	-	-	-	-	-	-	-	-	-	0.49	0.49	4.66	4.66
	CD1	-	-	-	-	-	-	-	-	-	-	0.67	0.67	6.39	6.39
	SEd C & AdM	1.51	1.51	5.75	5.75	1.93	1.93	1.23	1.23	4.13	4.13	0.18	0.18	1.68	1.68
	CD5	-	-	-	-	-	-	-	-	-	-	0.37	0.37	3.52	3.52
	CD1	-	-	-	-	-	-	-	-	-	-	0.50	0.50	4.83	4.83
	SEd Avg	1.89	1.89	7.22	7.22	2.43	2.43	1.54	1.54	5.18	5.18	0.22	0.22	2.10	2.10
	CD5	-	-	-	-	-	-	-	-	-	-	0.46	0.46	4.42	4.42
	CD1	-	-	-	-	-	-	-	-	-	-	0.63	0.63	6.06	6.06
	CV	3.83	3.83	4.56	4.56	4.37	4.37	25.19	25.19	9.41	9.41	2.46	2.46	1.68	1.68

4.2.1 days to 50% flowering

Among 112 genotypes, for mean days to 50 per cent flowering, genotype G-17 and G-110 (29 days) were the earliest to flower which were followed by G-9, G-14, G-58, G-63, G-68, G-79, G-82, G-88, G-92, G-93, G-98 and G-111 (30 days). The overall mean recorded for the trait was 32.34 days (Table 4.2.1).

4.2.2 Days to maturity

With respect to days to maturity, genotype G-98, G-70, G-61, G-41, G-38 and G-15 were found earliest as they showed minimum 99 days to maturity followed by G-74 and G-46 (100 days). The overall mean recorded for the trait was 106.22 days (Table 4.2.1).

4.2.3 Initiation of pegging (days)

Among 112 genotypes, for mean days to initiation of pegging**,** genotype G-17, G-110, G-111, G-98 and G-88 (33 days) were the earliest to initiation of pegging which were followed by G-85, G-86, G-14, G-6, G-68, G-79 and G-35 (34 days). The mean for initiation of pegging were 36.53 days (Table 4.2.1).

4.2.4 Duration between flowerings to pegging (days)

Among 112 genotypes, for mean days to flowering to pegging genotype G-22 (2 days) was the earliest to flowering to pegging which were followed by G-111, G-107, G-105, G-98, G-88, G-90, G-86, G-85, G- 72, G-67, G-60 and G-26 (3 days). The mean days to flowering to pegging were 4.17 days (Table 4.2.1).

4.2.5 Plant height (cm)

Maximum plant height (cm) were exhibited by the genotype G-13 (48.60 cm), followed by G-28 and G-17 (47.20 cm). The mean plant height was 36.37cm, (Table 4.2.1).

4.2.6 Number of branches per plant

Maximum number of branches per plant were exhibited by the genotype G-94 (8.40), followed by G-11, G-16, G-53 (8.20) and G-71 (8.10). The mean for number of branches per plant was 6.42 (Table 4.2.1).

4.2.7 Sound mature kernel (%)

Maximum sound mature kernel percentage was exhibited by the genotype G-101 (92.84 %) and G-97 (92.84 %) followed by G-18 (92.58 %) and G-93 (92.55 %). The mean sound mature kernel percentage was 85.38 % (Table 4.2.1).

4.2.8 100-kernel weight (g)

The data for 100-kernel weight depicted that genotype G-11 (48.80g) had maximum 100-kernel weight followed by G-104 (48.25g) and G-50 (48.25g). The mean 100-kernel weight was 41.60g (Table 4.2.2).

4.2.9 Shelling percentage (%)

The mean values for shelling percentage revealed that genotype G-112 (76%) showed maximum shelling percentage followed by G-98 (75.30 %). The general mean for this trait was 70.41 % (Table 4.2.2).

4.2.10 Biological yield per plant (g)

Maximum mean biological yield per plant was exhibited by genotype G-51 (39.55g) followed by G-544 (38.85g) and G-18 (38.46g). The overall mean observed for this trait was 32.98g (Table 4.2.2).

4.2.11 Harvest index (%)

Harvest index expressed that genotype G-20 (63.55%) had highest harvest index followed by G-93 (60.29%). The general mean for this trait was 40.08 % (Table 4.2.2).

4.2.12 Dry pod yield per plant (g)

The mean dry pod yield per plant of 112 genotypes exhibited wide range of variation. Maximum dry pod yield was exhibited by genotype G-10 (18.40 g), followed by G-20 (18.20 g) and G-17 (18.20 g). The overall mean for this character was 13.09 g (Table 4.2.2).

4.2.13 Oil content (%)

With respect to oil content, genotype G-49 had maximum oil content (48.49%) followed by G-55 (46.77%) and G-83 (46.72%). The overall mean for oil content was 39.99 per cent (Table 4.2.2).

Table 4.2.2: Mean values for 100-kernel weight (g), Shelling %, Biological yield per plant (g), harvesting index, Dry pod yield per plant (g), Oil content %

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
1	G1	34.32	34.43	60.00	57.05	27.80	27.90	38.13	38.02	10.60	10.60	33.86	34.20
2	G2	43.87	43.98	73.00	70.05	34.23	34.33	41.19	41.08	14.10	14.10	44.86	45.20
3	G3	35.42	35.53	73.00	70.05	34.67	34.77	41.25	41.14	14.30	14.30	39.40	39.74
4	G4	44.87	44.98	64.00	61.05	34.28	34.38	40.26	40.15	13.80	13.80	43.03	43.37
5	G5	43.85	43.96	72.00	69.05	34.25	34.35	36.20	36.09	12.40	12.40	37.60	37.94
6	G6	48.11	48.22	74.10	71.15	27.26	27.36	56.49	56.38	15.40	15.40	33.50	33.84
7	G7	46.57	46.68	73.51	70.56	27.80	27.90	44.96	44.85	12.50	12.50	35.10	35.44
8	G8	40.25	40.36	64.00	61.05	31.52	31.62	36.17	36.06	11.40	11.40	44.74	45.08
9	G9	39.42	39.53	62.00	59.05	32.56	32.66	32.25	32.14	10.50	10.50	39.24	39.58
10	G10	42.53	42.64	65.00	62.05	38.40	38.50	47.92	47.81	18.40	18.40	46.50	46.84
11	G11	39.27	39.38	68.00	65.05	31.31	31.41	33.85	33.74	10.60	10.60	41.62	41.96
12	G12	40.86	40.97	70.00	67.05	32.26	32.36	41.54	41.43	13.40	13.40	39.50	39.84
13	G13	43.56	43.67	72.00	69.05	34.42	34.52	42.13	42.02	14.50	14.50	46.29	46.63
14	G14	41.25	41.36	72.10	69.15	31.52	31.62	33.31	33.20	10.50	10.50	41.43	41.77
15	G15	42.61	42.72	67.00	64.05	28.56	28.66	44.12	44.01	12.60	12.60	42.84	43.18
16	G16	36.64	36.75	66.00	63.05	35.62	35.72	41.27	41.16	14.70	14.70	40.08	40.42
17	G17	46.84	47.01	68.00	70.30	37.60	38.15	48.40	47.58	18.20	18.21	43.76	43.70
18	G18	48.80	48.97	63.00	65.30	38.46	39.01	42.12	41.30	16.20	16.21	42.85	42.79
19	G19	30.28	30.45	65.00	67.30	30.48	31.03	37.07	36.25	11.30	11.31	34.24	34.18
20	G20	38.46	38.63	74.50	76.80	28.64	29.19	63.55	62.73	18.20	18.21	36.30	36.24
21	G21	45.74	45.91	70.60	72.90	28.56	29.11	46.92	46.10	13.40	13.41	45.25	45.19
22	G22	36.74	36.91	70.00	72.30	28.35	28.90	46.21	45.39	13.10	13.11	44.24	44.18
23	G23	42.53	42.70	73.00	75.30	31.54	32.09	52.63	51.81	16.60	16.61	37.64	37.58

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
24	G24	40.25	40.42	70.00	72.30	33.54	34.09	31.31	30.49	10.50	10.51	37.30	37.24
25	G25	45.27	45.44	67.00	69.30	36.26	36.81	40.26	39.44	14.60	14.61	43.83	43.77
26	G26	48.67	48.84	73.00	75.30	35.47	36.02	29.60	28.78	10.50	10.51	40.33	40.27
27	G27	30.87	31.04	75.00	77.30	27.23	27.78	47.37	46.55	12.90	12.91	34.30	34.24
28	G28	42.52	42.69	72.00	74.30	28.35	28.90	36.68	35.86	10.40	10.41	38.40	38.34
29	G29	38.27	38.44	75.00	77.30	27.26	27.81	53.19	52.37	14.50	14.51	40.07	40.01
30	G30	42.31	42.48	65.00	67.30	30.25	30.80	50.25	49.43	15.20	15.21	43.17	43.11
31	G31	44.50	44.67	72.00	74.30	36.85	37.40	41.25	40.43	15.20	15.21	44.94	44.88
32	G32	40.17	40.34	64.00	66.30	28.94	29.49	39.74	38.92	11.50	11.51	44.20	44.14
33	G33	46.34	46.19	73.20	74.50	29.51	29.90	34.56	34.16	10.20	10.22	37.50	37.44
34	G34	33.52	33.37	73.50	74.80	37.42	37.81	28.06	27.66	10.50	10.52	42.50	42.44
35	G35	44.62	44.47	74.00	75.30	27.26	27.65	43.65	43.25	11.90	11.92	36.30	36.24
36	G36	40.85	40.70	62.00	63.30	34.42	34.81	29.92	29.52	10.30	10.32	38.82	38.76
37	G37	38.24	38.09	62.00	63.30	29.35	29.74	55.54	55.14	16.30	16.32	41.09	41.03
38	G38	43.57	43.42	75.00	76.30	35.82	36.21	41.32	40.92	14.80	14.82	33.58	33.52
39	G39	48.23	48.08	74.00	75.30	33.46	33.85	38.25	37.85	12.80	12.82	38.96	38.90
40	G40	34.27	34.12	71.02	72.32	26.43	26.82	54.11	53.71	14.30	14.32	31.40	31.34
41	G41	45.28	45.13	73.20	74.50	38.43	38.82	30.44	30.04	11.70	11.72	38.50	38.44
42	G42	43.57	43.42	74.00	75.30	34.42	34.81	41.26	40.86	14.20	14.22	40.30	40.24
43	G43	43.21	43.06	74.00	75.30	28.64	29.03	42.95	42.55	12.30	12.32	44.24	44.18
44	G44	36.57	36.42	68.00	69.30	34.25	34.64	39.42	39.02	13.50	13.52	32.30	32.24
45	G45	45.67	45.52	73.00	74.30	33.43	33.82	38.59	38.19	12.90	12.92	38.50	38.44
46	G46	48.57	48.42	70.00	71.30	30.27	30.66	40.30	39.90	12.20	12.22	36.95	36.89
47	G47	37.46	37.31	72.00	73.30	35.14	35.53	32.44	32.04	11.40	11.42	37.90	37.84
48	G48	44.86	44.71	75.00	76.30	36.52	36.91	43.26	42.86	15.80	15.82	37.80	37.74

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
49	G49	45.67	45.79	70.60	73.40	28.64	28.24	46.79	46.51	13.40	13.14	48.49	48.43
50	G50	48.25	48.37	73.00	75.80	27.23	26.83	44.44	44.16	12.10	11.84	38.30	38.24
51	G51	32.56	32.68	62.00	64.80	39.55	39.15	27.31	27.03	10.80	10.54	39.84	39.78
52	G52	41.27	41.39	75.00	77.80	31.54	31.14	43.12	42.84	13.60	13.34	40.38	40.32
53	G53	41.25	41.37	69.00	71.80	35.42	35.02	43.76	43.48	15.50	15.24	40.20	40.14
54	G54	45.37	45.49	74.00	76.80	38.85	38.45	30.63	30.35	11.90	11.64	32.54	32.48
55	G55	43.25	43.37	71.20	74.00	27.63	27.23	40.54	40.26	11.20	10.94	46.77	46.71
56	G56	41.27	41.39	74.30	77.10	27.23	26.83	47.37	47.09	12.90	12.64	37.46	37.40
57	G57	41.27	41.39	71.00	73.80	37.42	37.02	30.73	30.45	11.50	11.24	43.21	43.15
58	G58	48.11	48.23	69.00	71.80	32.51	32.11	50.75	50.47	16.50	16.24	45.15	45.09
59	G59	38.57	38.69	69.00	71.80	35.24	34.84	42.00	41.72	14.80	14.54	43.92	43.86
60	G60	45.74	45.86	68.30	71.10	31.85	31.45	37.68	37.40	12.00	11.74	30.50	30.44
61	G61	48.29	48.41	74.00	76.80	28.54	28.14	43.80	43.52	12.50	12.24	32.60	32.54
62	G62	40.25	40.37	70.80	73.60	31.84	31.44	42.71	42.43	13.60	13.34	44.45	44.39
63	G63	38.57	38.69	74.00	76.80	37.42	37.02	30.46	30.18	11.40	11.14	34.30	34.24
64	G64	46.24	46.36	70.00	72.80	38.43	38.03	39.81	39.53	15.30	15.04	38.40	38.34
65	G65	43.56	43.29	67.00	69.30	34.41	33.61	41.27	43.10	14.20	14.46	44.27	44.21
66	G66	40.14	39.87	74.00	76.30	37.58	36.78	40.98	42.81	15.40	15.66	45.23	45.17
67	G67	42.52	42.25	67.50	69.80	26.34	25.54	39.48	41.31	10.40	10.66	44.70	44.64
68	G68	40.28	40.01	69.00	71.30	31.42	30.62	33.10	34.93	10.40	10.66	35.65	35.59
69	G69	42.61	42.34	72.90	75.20	34.23	33.43	37.10	38.93	12.70	12.96	45.98	45.92
70	G70	40.14	39.87	75.00	77.30	38.43	37.63	36.95	38.78	14.20	14.46	46.30	46.24
71	G71	37.42	37.15	68.00	70.30	36.52	35.72	28.48	30.31	10.40	10.66	38.76	38.70
72	G72	38.46	38.19	62.00	64.30	38.27	37.47	38.15	39.98	14.60	14.86	44.97	44.91
73	G73	43.27	43.00	73.00	75.30	34.12	33.32	42.50	44.33	14.50	14.76	32.65	32.59

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
74	G74	44.62	44.35	63.00	65.30	34.22	33.42	33.31	35.14	11.40	11.66	40.15	40.09
75	G75	36.28	36.01	74.00	76.30	28.95	28.15	46.29	48.12	13.40	13.66	42.77	42.71
76	G76	36.74	36.47	68.90	71.20	32.84	32.04	31.97	33.80	10.50	10.76	38.70	38.64
77	G77	43.27	43.00	71.50	73.80	36.52	35.72	28.75	30.58	10.50	10.76	41.40	41.34
78	G78	34.26	33.99	70.00	72.30	27.63	26.83	41.62	43.45	11.50	11.76	35.27	35.21
79	G79	30.87	30.60	67.00	69.30	35.86	35.06	34.86	36.69	12.50	12.76	45.52	45.46
80	G80	42.36	42.09	75.00	77.30	36.41	35.61	43.39	45.22	15.80	16.06	41.80	41.74
81	G81	42.34	42.92	67.00	63.90	29.34	29.30	42.60	42.64	12.50	12.46	40.40	40.34
82	G82	38.28	38.86	74.30	71.20	34.83	34.79	29.86	29.90	10.40	10.36	41.75	41.69
83	G83	38.27	38.85	72.50	69.40	32.42	32.38	37.94	37.98	12.30	12.26	46.72	46.66
84	G84	42.36	42.94	75.00	71.90	36.85	36.81	36.36	36.40	13.40	13.36	37.20	37.14
85	G85	36.87	37.45	69.00	65.90	31.84	31.80	35.49	35.53	11.30	11.26	38.84	38.78
86	G86	33.52	34.10	65.00	61.90	32.84	32.80	36.54	36.58	12.00	11.96	41.70	41.64
87	G87	40.28	40.86	72.00	68.90	33.83	33.79	45.52	45.56	15.40	15.36	40.29	40.23
88	G88	43.36	43.94	73.00	69.90	27.46	27.42	48.07	48.11	13.20	13.16	37.60	37.54
89	G89	45.25	45.83	74.00	70.90	37.52	37.48	31.72	31.76	11.90	11.86	37.20	37.14
90	G90	40.85	41.43	75.00	71.90	35.42	35.38	38.40	38.44	13.60	13.56	41.30	41.24
91	G91	40.28	40.86	72.50	69.40	35.82	35.78	34.62	34.66	12.40	12.36	34.80	34.74
92	G92	39.42	40.00	67.00	63.90	34.23	34.19	43.24	43.28	14.80	14.76	39.16	39.10
93	G93	45.28	45.86	72.00	68.90	28.53	28.49	60.29	60.33	17.20	17.16	42.19	42.13
94	G94	46.49	47.07	65.00	61.90	37.24	37.20	44.04	44.08	16.40	16.36	40.30	40.24
95	G95	32.48	33.06	74.00	70.90	32.45	32.41	33.28	33.32	10.80	10.76	40.30	40.24
96	G96	41.37	41.95	71.30	68.20	34.62	34.58	41.02	41.06	14.20	14.16	34.21	34.15
97	G97	43.21	42.65	72.00	69.33	31.85	32.05	49.29	49.03	15.70	15.71	38.60	38.54
98	G98	46.49	45.93	75.30	72.63	33.43	33.63	43.37	43.11	14.50	14.51	45.50	45.44

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
99	G99	36.34	35.78	67.00	64.33	32.57	32.77	53.42	53.16	17.40	17.41	42.23	42.17
100	G100	44.86	44.30	70.00	67.33	32.41	32.61	31.78	31.52	10.30	10.31	31.39	31.33
101	G101	48.40	47.84	71.00	68.33	36.45	36.65	38.96	38.70	14.20	14.21	39.45	39.39
102	G102	44.46	43.90	74.00	71.33	31.46	31.66	33.06	32.80	10.40	10.41	34.30	34.24
103	G103	43.67	43.11	70.80	68.13	36.48	36.68	39.47	39.21	14.40	14.41	33.60	33.54
104	G104	48.25	47.69	74.20	71.53	29.34	29.54	50.78	50.52	14.90	14.91	40.44	40.38
105	G105	44.60	44.04	74.00	71.33	31.54	31.74	34.56	34.30	10.90	10.91	42.83	42.77
106	G106	35.64	35.08	62.00	59.33	32.42	32.62	36.71	36.45	11.90	11.91	37.16	37.10
107	G107	43.25	42.69	64.00	61.33	36.72	36.92	37.31	37.05	13.70	13.71	44.97	44.91
108	G108	36.46	35.90	74.00	71.33	32.48	32.68	37.56	37.30	12.20	12.21	41.43	41.37
109	G109	47.90	47.34	73.00	70.33	36.27	36.47	32.53	32.27	11.80	11.81	45.46	45.40
110	G110	38.64	38.08	72.00	69.33	33.27	33.47	37.27	37.01	12.40	12.41	45.50	45.44
111	G111	41.27	40.71	68.60	65.93	34.22	34.42	32.14	31.88	11.00	11.01	36.65	36.59
112	G112	46.20	45.64	76.00	73.33	35.24	35.44	30.08	29.82	10.60	10.61	37.40	37.34
	GP Mean	41.60	-	70.41	-	32.98	-	40.08	-	13.09	-	39.99	-
	Min	30.28	-	60.00	-	26.34	-	27.31	-	10.20	-	30.50	-
	Max	48.80	-	76.00	-	39.55	-	63.55	-	18.40	-	48.49	-
1	Check1	36.93	36.93	72.37	72.37	28.83	28.83	44.80	44.80	12.91	12.91	41.17	41.17
2	Check2	35.00	35.00	68.00	68.00	31.85	31.85	45.31	45.31	14.42	14.42	42.46	42.46
3	Check3	38.76	38.76	68.86	68.86	32.17	32.17	41.91	41.91	13.46	13.46	44.43	44.43
4	Check4	40.79	40.79	68.99	68.99	30.18	30.18	47.08	47.08	14.19	14.19	39.36	39.36
	Check Mean	37.87	-	69.55	-	30.76	-	44.77	-	13.75	-	41.86	-
	Min	35.00	-	68.00	-	28.83	-	41.91	-	12.91	-	39.36	-
	Max	40.79	-	72.37	-	32.17	-	47.08	-	14.42	-	44.43	-
	GM	40.86	-	70.24	-	32.53	-	41.02	-	13.22	-	40.36	-

S. No.	Genotype	100-kernel weight(g)		Shelling %		Biological yield per plant(g)		Harvesting index		Dry pod yield per plant (g)		Oil content %	
		Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM	Mean	AdM
	SEd Check	0.55	0.55	2.44	2.44	0.53	0.53	1.01	1.01	0.13	0.13	0.03	0.03
	CD5	1.15	1.15	-	-	1.12	1.12	2.12	2.12	0.28	0.28	0.06	0.06
	CD1	1.58	1.58	-	-	1.54	1.54	2.90	2.90	0.38	0.38	0.08	0.08
	SEd AdM WB	1.45	1.45	6.44	6.44	1.41	1.41	2.67	2.67	0.35	0.35	0.08	0.08
	CD5	3.04	3.04	-	-	2.96	2.96	5.60	5.60	0.73	0.73	0.16	0.16
	CD1	4.17	4.17	-	-	4.06	4.06	7.68	7.68	1.00	1.00	0.22	0.22
	SEd AdM DB	1.62	1.62	7.21	7.21	1.58	1.58	2.98	2.98	0.39	0.39	0.08	0.08
	CD5	3.40	3.40	-	-	3.31	3.31	6.26	6.26	0.82	0.82	0.18	0.18
	CD1	4.66	4.66	-	-	4.54	4.54	8.58	8.58	1.12	1.12	0.24	0.24
	SEd C & AdM	1.22	1.22	5.45	5.45	1.19	1.19	2.25	2.25	0.29	0.29	0.06	0.06
	CD5	2.57	2.57	-	-	2.50	2.50	4.73	4.73	0.62	0.62	0.13	0.13
	CD1	3.52	3.52	-	-	3.43	3.43	6.49	6.49	0.85	0.85	0.18	0.18
	SEd Avg	1.53	1.53	6.84	6.84	1.50	1.50	2.83	2.83	0.37	0.37	0.08	0.08
	CD5	3.22	3.22	-	-	3.14	3.14	5.94	5.94	0.77	0.77	0.17	0.17
	CD1	4.42	4.42	-	-	4.31	4.31	8.14	8.14	1.06	1.06	0.23	0.23
	CV	2.70	2.70	6.55	6.55	3.24	3.24	4.21	4.21	1.79	1.79	0.13	0.13

4.3 VARIABILITY PARAMETERS

Genetic variability is a pre-requisite for any crop improvement programme as it provides scope for selection. Phenotypic coefficient of variation measures the amount of variation present for a particular character. However, it does not determine the proportion of heritable variation of the total variation present for particular character. Johanson *et al.* (1955) suggested that heritability and genetic gain together would be more useful in predicting the effect of selection. Therefore, in the present investigation, phenotypic (PCV) and genotypic coefficients of variation (GCV), heritability and genetic gain were estimated and character wise results are presented in Table 4.3 and discussed as follows.

4.3.1 Days to 50 per cent flowering

A perusal of the data showed low values of both GCV (2.99%) and PCV (4.92%) for days to 50 per cent flowering. However, the value of PCV was higher than that of GCV, suggested the involvement of non-genetic factors contributing to total variation for this trait.

Low value of heritability (37.01%) and low genetic gain (3.75%) indicated presence of non additive gene action, (Table 4.3).

Table 4.3: Variability parameters for various characters in groundnut *(Arachis hypogaea* L.)

S. No.	Characters	GCV %	PCV%	H^2%	GA	GG%
1.	Days to 50% flowering	2.99	4.92	37.01	1.21	3.75
2.	Days to maturity (days)	-	-	-	-	-
3.	Initiation of pegging	1.36	4.63	8.56	0.30	0.82
4.	Duration between flowering to pegging (days)	-	-	-	-	-
5.	Plant height (cm)	6.79	11.68	33.84	2.96	8.14
6.	Number of branches per plant	15.05	15.23	97.75	1.97	30.66
7.	Sound mature kernels (%)	4.89	5.15	89.84	8.14	9.54
8.	100-kernel weight (g)	10.37	10.66	94.68	8.65	20.78
9.	Shelling %	-	-	-	-	-
10.	Biological yield per plant (g)	10.20	10.64	91.92	6.64	20.14
11.	Harvesting index	17.33	17.96	93.15	13.81	34.46
12.	Dry pod yield per plant (g)	15.59	15.71	98.57	4.18	31.89
13.	Oil content (%)	10.42	10.42	99.98	8.59	21.47

4.3.2 Initiation of pegging

A perusal of the data showed low values of both GCV (1.36%) and PCV (4.63%) for initiation of pegging. However, the value of PCV was higher than that of GCV. Suggested the involvement of non-genetic factors contributing to total variation for this trait.

Low value of heritability (8.56%) and low genetic gain (0.82%) indicated presence of non-additive gene action (Table 4.3).

4.3.3 Plant height

Estimates of genetic parameters indicated that plant height exhibited low value of GCV (6.79%) and PCV (11.78%). The present findings are in accordance with the findings of Mothilal *et al.* (2004). Higher magnitude of phenotypic coefficient of variation than genotypic coefficient of variation suggested that appreciable portion of variability has been accounted by environmental effects. These finding are in accordance with the findings of Mothilal *et al.* (2004).

The magnitude of heritability in broad sense (33.84%) was low, with low genetic gain (8.14%) for plant height. low heritability accompanied with low genetic gain indicates that most likely the heritability was due to the non additive gene effects and selection may not be effective (Table 4.3).

4.3.4 Numbers of branches per plant

The values of GCV and PCV for number of branches per plant revealed that the magnitudes of GCV (15.05%) and PCV (15.23%) were moderate for this trait. The moderate estimates of genotypic and phenotypic coefficients have also been reported by Prasad *et al*. (2002) for this trait.

The trait number of primary branches per plant exhibited high heritability (97.75%) coupled with moderate genetic gain (30.66%). These results were in accordance with the findings of Mothilal *et al.* (2004). High magnitude of heritability and moderate genetic gain, as observed in the present study suggested that branches per plant were under the control of non-additive gene action which is not fixable one. Hence, improvement would not be possible for this character through selection.

4.3.5 Sound mature kernel

Sound mature kernels showed low estimates of genotypic coefficient of variation (4.89%) and phenotypic coefficient of variation (5.15%). Such a low amount of variation for sound mature kernels in groundnut was also reported by Mothilal *et al.* (2004), Vishnuvardhan *et al*. (2012).

The estimates of heritability (89.84%) were high and genetic gain (9.54%) was low. This indicated the impact of non-additive gene effect (Table 4.3).

4.3.6 100-kernel weight

The results pertaining to genetic variability for 100- kernel weight indicated that genotypic coefficient of variation (10.37%) and phenotypic coefficient of variation (10.66%) were moderate for this trait. Similar results were obtained by Prasad *et al.* (2002) and Mothilal *et al*. (2004).

100-kernel weight expressed high heritability (94.68%) and moderate genetic gain (20.78%) (Table 4.3).

4.3.7 Biological yield per plant

The estimates of genotypic (10.20%) and phenotypic (10.64 %) coefficients of variation were low for biological yield per plant. However, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation.

The heritability (91.92 %) was high and genetic gain (20.14%) was moderate for this trait. The high value of heritability and moderate genetic gain indicated role of non-additive and additive gene action. Selection would be effective for this trait (Table 4.3).

4.3.8 Harvest index

The genotypic coefficient of variation (17.33%) and phenotypic coefficient of variation (17.96%) for harvest index were moderate in magnitude.

The estimates of heritability (93.15%) were high and genetic gain (34.46%) was also high for this trait. High heritability coupled with high genetic gain was also earlier reported by yadav *et al.* (2014) (Table 4.3).

4.3.9 Dry pod yield per plant

The estimates of genotypic (15.59 %) and phenotypic (15.71 %) coefficients of variation indicated that both the parameters were moderate in magnitude for dry pod yield per plant. The higher estimates of GCV and PCV have been earlier reported by Rao *et al.* (2014) and Yadav *et al.* (2014).

The heritability (98.57%) was high and genetic gain (31.89%) was also high for this trait. Kadam *et al*. (2007), Giri *et al*. (2009), Rao *et al*. (2014) and Yadav *et al.* (2014) also reported high heritability and high genetic gain for dry pod yield per plant.

The high value of heritability as well as genetic gain indicated role of additive gene action. Selection may reward for such trait (Table 4.3).

4.3.10 Oil content

The data (Table 4.3) indicates that genotypic coefficient of variation (10.42%) and phenotypic coefficient of variation (10.42%) were moderate in magnitude for oil content in kernels of groundnut. The estimates of heritability (99.98%) were high and genetic gain (21.47%) for oil content was moderate. High heritability coupled with moderate genetic gain was reported by Prakash *et al.* (2000) and Venkatramana *et al.* (2001).

4.4 CORRELATION COEFFICIENTS

For selection of a suitable plant type, information regarding nature and extent of association of various morphological characters with the character of economic importance would be helpful in developing a suitable plant type. For the improvement of complex characters like dry yield for which direct selection is not very effective, while selection for associated characters would be effective. Keeping this in view, genotypic and phenotypic correlation coefficients among different characters and with dry pod yield per plant and kernel yield per plant were estimated through variance and covariance analysis (Table 4.4).

Table 4.4: **Genotypic path analysis for dry pod yield per plant (g)**

S. No.	Characters	Days to 50% flowering	Days to maturity	Initiation of pegging	Duration b/w flowering to pegging(DAS)	Plant height(cm)	No. of branches per plant	Sound mature kernels (%)	100-kernel weight (g)	Shelling %	Biological yield per plant (g)	Harvesting index	Oil content %	Rg
1.	Days to 50% flowering	**6.47**	-0.20	-1.10	-0.20	-4.55	-0.57	0.09	0.00	-0.20	0.11	0.14	0.06	0.08
2.	Days to maturity	58.19	**-0.02**	-7.58	-0.20	-45.77	-58.04	5.96	-1.31	-0.20	33.88	27.51	-3.43	9.00
3.	Initiation of pegging	8.44	-0.20	**-0.84**	-0.20	-6.44	-1.00	0.03	0.05	-0.20	-0.34	0.83	0.11	0.25**
4.	Duration between flowering to pegging (days)	58.19	-0.20	-7.58	**-0.02**	-45.77	-58.04	5.96	-1.31	-0.20	33.88	27.51	-3.43	9.00
5.	Plant height (cm)	5.78	-0.20	-1.07	-0.20	**-5.09**	0.71	0.05	0.01	-0.20	0.18	0.01	0.05	0.05
6.	No. of branches per plant	0.57	-0.20	-0.13	-0.20	0.56	**-6.45**	0.10	-0.01	-0.20	0.97	0.00	0.03	0.19*
7.	Sound mature kernels (%)	0.92	-0.20	-0.04	-0.20	-0.41	-1.02	**0.66**	-0.08	-0.20	0.50	0.16	0.04	0.16
8.	100-kernel weight(g)	-0.20	-0.20	0.29	-0.20	0.31	-0.45	0.34	**-0.15**	-0.20	0.33	0.31	-0.02	0.19*
9.	Shelling %	58.19	-0.20	-7.58	-0.20	-45.77	-58.04	5.96	-1.31	**-0.02**	33.88	27.51	-3.43	9.00
10.	Biological yield per plant(g)	0.20	-0.20	0.08	-0.20	-0.24	-1.67	0.09	-0.01	-0.20	**3.76**	-1.40	-0.06	0.17
11.	Harvesting index	0.29	-0.20	-0.23	-0.20	-0.01	-0.00	0.04	-0.01	-0.20	-1.72	**3.06**	-0.03	0.80**
12.	Oil content %	-1.01	-0.20	0.24	-0.20	0.68	0.56	-0.06	-0.01	-0.20	0.56	0.21	**-0.38**	0.20

Residual effect = .127

4.4.1 Correlation between dry pod yield per plant and other characters

A perusal of Table 4.5 revealed that dry pod yield per plant was positively and significantly correlated at both genotypic as well as phenotypic level with number of branches per plant (rg =0.19*, rp =0.19*), 100-kernel weight (rg =0.19*, rp =0.19**), harvesting index (rg =0.80**, rp =0.78**) and oil content (rg =0.20*, =0.20*). These findings are in accordance with Mathews *et al*. (2001), Nagda *et al*. (2001), Giri *et al.* (2009), Sumathi and Muralidharan (2007), John *et al.* (2009) Awatade *et al.* (2010), Shinde *et al.* (2010), Vekariya *et al.* (2011), Babariya and Dobariya (2012), Kumar *et al*. (2012), Rao *et al.* (2014), Yadlapalli (2014) and Kahate *et al.* (2014).

4.4.2 Correlation among different characters

A perusal of Table 4.5 revealed existence of significant positive correlation of days to 50 per cent flowering with plant height (rg =0.89**,rp= 0.25**) at both genotypic phenotypic level, initiation of pegging (0.82**), days to 75 % maturity (-0.21*), duration between flowering to pegging (-0.19*) shows significant correlation at phenotypic level. Days to 75 per cent maturity shows significant negative correlation with initiation of pegging (-0.23*) at phenotypic level only. Initiation of pegging shows significant negative correlation with 100-kernals weight (-0.34**), oil content (-0.28**) and shows significant positive correlation with harvesting index (0.27**) at genotypic level while shows significant positive correlation with duration between flowering to pegging (rp =0.39**) and plant height (0.27**) at phenotypic level. Duration between flowering to pegging (days) shows significant positive correlation with 100- kernels weight (-0.21*) at phenotypic only. The plant height shows significant positive correlation with days to 50 % flowering (0.89**) at genotypic level only. Number of branches per plant shows significant positive correlation with biological yield (rg=0.26**, rp=0.24*) and dry pod yield per plant (rg=0.19*, rp=0.19*) at both genotypic and phenotypic levels. Sound mature kernels shows significant positive correlation with 100-kernals weight (rg=0.52**, rp=0.43**) at both genotypic and phenotypic levels. 100-kernel weight shows significant positive correlation with dry pod yield per plant (rg=0.19*, rp=0.19*) both genotypic and phenotypic levels. While shelling percent (rp=0.24*), sound mature kernels (rg=0.52**), initiation of pegging (rg=-0.34**) shows significant positive correlation with 100-kernel weigh. Biological yield per plant shows significant negative correlation with harvesting index (rg=-0.46**, rp=-0.49**) at genotypic and phenotypic levels and number branches per plant showed positive correlation at genotypic level (rg=0.26**) with biological yield per plant. Harvesting index shows significant positive correlation with dry pod yield per plant (rg=0.80**,rp=0.78**) both genotypic as well as phenotypic levels while initiation of pegging (rg=0.27**) and biological yield per plant (rg=-0.46**) shows significant correlation with harvesting index at genotypic level only. Oil content per cent shows significant positive correlation with dry pod yield per plant (rg=0.20*, rp=0.20*) at both genotypic and phenotypic levels. While initiation of pegging shows significant negative genotypic correlation (rg=-0.28**) with oil content.

Present experimental findings revealed that number of branches per plant, 100-kernel weight, biological yield per plant and oil content are important contributing traits for dry pod yield per plant because these showed high magnitude of significant positive correlation with dry pod yield. Hence, these traits can be used for selection for high dry pod yield per plant.

4.5 PATH COEFFICIENT ANALYSIS

Correlation studies alone can’t provide a clear-cut picture of cause and effect of relationship between yield attributes and their extent of association. Path analysis devised by Wright (1921) provides measure of direct and indirect effects of traits on yield, splitting the correlation coefficients into direct and indirect effects. In present study path coefficient analysis was carried out for dry pod yield per plant at genotypic level.

4.5.1 Path coefficient analysis for dry pod yield per plant

Path coefficient analysis for dry pod yield per plant was carried out at genotypic level using thirteen characters. Out of these thirteen characters Initiation of pegging, number of branches per plant, 100-kernel weight, harvesting index and oil content exhibited positive significant association with dry pod yield per plant, hence only these characters were described for path analysis study. The description is as under.

Table 4.5: Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients among different characters in Groundnut (*Arachis hypogaea* L.)

S No.	Characters	Days to 50% flowering	Days to maturity	Initiation of pegging	Duration b/w flowering to pegging (days)	Plant height(cm)	No. of branches per plant	Sound mature kernels (%)	100-kernel weight (g)	Shelling %	Biological yield per plant(gm)	Harvesting index	Oil content %	Dry pod yield per plant (g)
1.	Days to 50% flowering		9.00	1.31	9.00	0.89**	0.09	0.14	-0.03	9.00	0.03	0.05	-0.16	0.08
2.	Days to maturity	-0.21*		9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00
3.	Initiation of pegging	0.82**	-0.23*		9.00	1.27	0.15	0.04	-0.34**	9.00	-0.09	0.27**	-0.28**	0.25**
4.	Duration b/w flowering to pegging (days)	-0.19*	-0.04	0.39**		9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00	9.00
5.	Plant height (cm)	0.25**	-0.09	0.27**	0.06		-0.11	0.08	-0.06	9.00	0.05	0.00	-0.13	0.05
6.	No. of branches per plant	0.07	-0.08	0.06	0.03	-0.04		0.16	0.07	9.00	0.26**	0.00	-0.09	0.19*
7.	Sound Mature kernels (%)	0.07	-0.00	0.03	-0.07	0.00	0.13		0.52**	9.00	0.13	0.05	-0.10	0.16
8.	100-kernel weight (g)	-0.01	-0.04	-0.12	-0.21*	-0.08	0.08	0.43**		9.00	0.09	0.10	0.04	0.19*
9.	Shelling %	0.09	-0.18	0.10	0.02	0.12	0.06	-0.03	0.24**		9.00	9.00	9.00	9.00
10.	Biological yield per plant(g)	-0.04	0.00	-0.02	0.08	0.05	0.24*	0.12	0.06	-0.07		-0.46**	0.15	0.17
11.	Harvesting index	0.08	-0.09	0.05	-0.03	-0.02	0.01	0.04	0.12	0.08	-0.49**		0.07	0.80**
12.	Oil content %	-0.09	-0.03	-0.08	-0.05	-0.08	-0.09	-0.09	0.04	-0.14	0.14	0.07		0.20*
13.	Dry pod yield per plant (g)	0.05	-0.08	0.04	0.01	0.03	0.19*	0.15	0.19*	0.02	0.14	0.78**	0.20*	

*, ** Significant at 5% and 1% level of significance, respectively

(i) Initiation of pegging

The result depict in Table-4.4 indicated that significant positive correlation of initiation of pegging with dry pod yield per plant (0.25**) was mainly due to its high direct effect (-0.84). Characters *viz.,* 100-kernel weight (0.29), biological yield per plant (0.08), oil content (0.24) also affects this association in positive direction but days to 50% flowering (-1.10), days to maturity (-7.58), duration between flowering to pegging (days) (-7.58), plant height (-1.07), number of branches per plant (-0.13), sound mature kernels (-0.04), shelling % (-7.58), harvesting index (-0.23) also affects this association in negative direction.

(ii) Number of branches per plant

The result depict in Table-4.4 indicated that the significant positive correlation of number of branches per plant with dry pod yield per plant (0.19*) was mainly due to its direct effect (-6.45). Characters *viz*., plant height (0.71) and oil content (0.56) also affects this association in positive direction but 100-kernel weight (-0.45), biological yield per plant (-1.67), days to 50% flowering (-0.57), days to maturity (-58.04), duration between flowering to pegging (days) (-58.04), sound mature kernels (-1.04), shelling percent (-58.04) and initiation of pegging (-1.0) also affects this association in negative direction.

(iii) 100-kernals weight

The result depict in Table-4.4 indicated that the significant positive correlation of 100-kernals weight with dry pod yield per plant (0.19*) was mainly due to its direct effect (-0.15). Characters *viz*., plant height (0.01) and initiation of pegging (0.05) also affects this association in positive direction but oil content (-0.01), biological yield per plant (-0.01), days to maturity (-1.31), duration between flowering to pegging (-1.31), number of branches per plant, (-0.01), sound mature kernels (-0.08), shelling percent (-1.31), harvesting index (-1.0) also affects this association in negative direction. Similar results were also reported by Mathews *et al*. (2001) and Awatade *et al.* (2010).

(iv) Harvesting index

The result depicts in Table-4.4 indicated that the significant positive correlation of harvesting index with dry pod yield per plant (0.80**) was mainly due to its direct effect (3.06). Characters *viz*., plant height (0.01), initiation of pegging

(0.83), days to 50% flowering (0.14), days to maturity (27.51), duration between flowering to pegging (27.51), sound mature kernels (0.16), shelling percent (27.51), initiation of pegging (0.83), oil content (0.21) and 100-kernels weight (0.31) affects this association in positive direction but biological yield per plant (-1.40) also affects this association in negative direction. Similar results were also reported by Korat *et al.* (2010), Vekariya *et al.* (2011), Babariya and Dobariya (2012) and Kumar *et al.* (2012).

(v) Oil content

The result depict in Table-4.4 indicated that the significant positive correlation of oil content with dry pod yield per plant (0.20*) was mainly due to its direct effect (-0.38). Characters *viz*., days to 50% flowering (0.06), initiation of pegging (0.11), plant height (0.05), number of branches per plant (0.03), sound mature kernel (0.04) affects this association in positive direction but days to maturity (-3.43), duration between flowering to pegging (-3.43), 100-kernel weight (-0.02), shelling per cent (-3.43), biological yield per plant (-0.06) and harvesting index (-0.03) also affects this association in negative direction. Similar results were also reported by Kahate *et al.* (2014) and Awatade *et al.* (2010).

Residual effect

The residual effect on dry pod yield per plant was 0.12 indicated that 99.88 percent of variability was governed by above said character and 0.12 per cent variability was due to environment effect.

4.6 GENETIC DIVERGENCE

Genetic diversity is an essential pre-requisite in selecting parents for hybridization and evolving high yielding genotyping in any crop breeding programme. The concept of D^2 was originally developed by P.C. Mahalanobis in 1928 but the application of this technique for the assessment of genetic diversity in plant breeding was suggested by Rao (1952). Higher the genetic diversity between the parents, greater are the chances of achieving transgressive segregants. Progenies derived from diverse crosses are expected to show broad spectrum of genetic variability, providing greater scope for isolating high yielding segregants in advance generation. D^2 statistics is a potential tool for obtaining quantitative estimates of divergence between biological populations and has extensively been applied to assess diversity.

4.6.1 Composition of clusters

One hundred sixteen genotypes were grouped into VII clusters on the basis of observed distance among genotypes within a cluster as compared to genotypes in other cluster in Table 4.6. Cluster VI contains maximum number of genotypes *i.e.* 25 followed by 22 in cluster II, 20 in cluster IV, 14 in cluster V and cluster III, 10 in cluster I and 11 in cluster VII. The clustering pattern revealed that, in general, genotypes from same origin showed no tendency to be in same cluster.

Looking to the pattern of genotypes distribution into different clusters in the present study, it appeared that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. These finding are in close agreement to earlier reported Dolma *et al.* (2010) and Yadav *et al.* (2014).

Table 4.6: Cluster compositions

Cluster	Number	Name of genotypes
I	10	G1, G9, G19, G32, G36, G44, G68, G85, G86 and G106
II	22	G2, G7, G8, G15, G31, G43, G45, G46, G48, G49, G52, G53, G55, G61, G62, G65, G66, G67, G70, G81, G98 and GPBD-4
III	14	G14, G24, G34, G47, G51, G57, G63, G71, G76, G77, G79, G82, G95 and G111
IV	20	G4, G10, G16, G17, G18, G21, G25, G39, G50, G64, G72, G83, G87, G89, G92, G94, G101, G107, G109 and G110
V	14	G3, G12, G22, G23, G27, G35, G56, G59, G75, G78, G88, PM-2, UG-5 and TG-37A
VI	25	G5, G11, G13, G26, G28, G33, G38, G41, G42, G54, G60, G69, G73, G74, G80, G84, G90, G91, G96, G100, G102, G103, G105, G108 and G112
VII	11	G6, G20, G29, G30, G37, G40, G58, G93, G97, G99 and G104

4.6.2 Intra and inter cluster divergence

As evident from Table 4.7 average inter cluster values were maximum between cluster III and VII on the basis of analysis. At intra cluster level, maximum values were recorded for cluster VII followed by cluster VI, cluster IV, cluster II, cluster I, cluster III and cluster V. The inter-cluster distances were greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes. Therefore, the genotypes falling in these clusters appeared to be divergent and might have different geographical/genetic origin hence could be gainfully utilized in groundnut improvement programme. Khote *et al.* (2010) and Kumar *et al.* (2010) also reported maximum and minimum inter and intra cluster distances in groundnut.

Table 4.7: Average intra and inter-cluster euclidian distances in 116 genotypes of groundnut

Cluster	I	II	III	IV	V	VI	VII
I	**9.20**	14.21	10.02	13.19	13.17	13.96	21.80
II		**9.54**	13.79	10.27	10.12	10.83	13.67
III			**9.07**	15.23	16.55	11.85	25.38
IV				**9.78**	12.41	11.12	16.90
V					**9.02**	12.99	11.84
VI						**9.82**	20.11
VII							**11.12**

Bold number = intra-cluster distance

Thus, cluster VII displayed highest inter cluster distances from cluster III, followed by cluster I, cluster VI, cluster IV and cluster II. Therefore, crosses between such genotypes are expected to give desirable transgressive segregates.

4.6.3 Clusters means

The cluster means (Table 4.8) indicated that cluster VII was having maximum dry pod yield per plant (15.96) and highest harvest index (54.33), cluster III maximum biological yield per plant (35.38), cluster VI shelling percent (72.45), cluster IV seed index (43.99) and sound mature kernels percent (89.45), cluster VI number of primary branches per plant (6.68) and maximum plant height (40.00), cluster II shows minimum duration between flowering to pegging (3.90), cluster III shows minimum days to pegging (35.79), cluster II shows minimum days to maturity (102.42), cluster III shows minimum days to flowering (31.26). Therefore, selection of genotypes for these characters may be made from these clusters. Higher mean values of different characters in different clusters were also reported by Kumar *et al*. (2010), Patil *et al.* (2015).

Table 4.8: Cluster Means

Cluster	DF	DM	IoP	DbFP	PHt	NB	SMK	SI	SP	BYPP	HI	DPYPP	OC
1	32.10	110.30	36.10	4.00	35.47	5.84	83.41	36.79	64.60	31.70	35.84	11.33	37.60
2	32.60	103.42	36.68	3.90	33.65	6.42	83.30	43.37	71.22	31.96	41.82	13.34	42.44
3	31.29	106.00	35.79	4.50	35.00	6.22	82.05	37.52	70.49	35.38	30.93	10.91	39.97
4	31.80	109.95	35.95	4.15	35.56	6.63	89.48	43.99	68.66	35.23	40.82	14.35	42.25
5	32.76	108.24	37.01	4.24	38.90	6.02	83.26	38.39	71.76	29.91	45.37	13.54	39.39
6	33.04	103.84	37.20	4.20	40.00	6.68	87.48	43.43	72.45	34.16	36.30	12.40	37.85
7	32.45	104.27	36.64	4.27	34.49	6.55	85.33	41.90	70.53	29.45	54.33	15.96	39.47

5. SUMMARY AND CONCLUSIONS

The present investigation entitled **“Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)”** was carried out on 112 groundnut genotypes along with 4 standard checks to elicit information on the genetic variability, correlation coefficients, path coefficients and genetic divergence for dry pod yield and its contributing characters.

The groundnut genotypes were evaluated in augmented design in 4 blocks during *kharif,* 2017 at the Instructional Farm, College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur (Rajasthan). Observations were recorded on five competitive plants for plant height, number of branches per plant, initiation of pegging, duration between flowering to pegging, dry pod yield per plant, 100-kernel weight, sound mature kernel, shelling percentage, biological yield per plant, harvest index and oil content**.** While, observation for days to 50 per cent flowering and days to maturity were recorded on plot basis.

Mean squares due to genotypes for all the characters were significant except days to 50% flowering, days to maturity, initiation of pegging, duration between flowering to pegging, plant height and for shelling per cent as revealed from ANOVA indicating substantial amount of genetic variability among the genotypes under study. Genotypes exhibited wide range of variation for different characters *viz*., days to 50% flowering (29 to 36 days), days to maturity (99 to 114 days), Initiation of pegging (33 to 40 days), duration between flowering to pegging (days) (2 to 7 days), plant height (30.40 to 48.60 cm), number of primary branches per plant (4 to 8.40), sound mature kernels (75.33 to 92.84%), 100-kernel weight (30.28g to 48.80 g), shelling percentage (60 to76%), biological yield per plant (26.34 to 39.55 g), harvesting index (27.31 to 63.55%), dry pod yield per plant (10.20 to18.40 g), oil content (30.50 to 48.49%). genotypes G-10, G-17, G-20, G-93 and G-99 appeared promising with respect to dry pod yield.

- The estimates of genotypic parameters revealed that the phenotypic coefficient of variation along with least difference from genotypic coefficient of variation observed for characters *viz.*, number of branches per plant (GCV 15.05% and PCV 15.23%), 100-kernel weight (GCV 10.37% and PCV 10.66%), dry pod yield per plant (GCV 15.59% and PCV 15.71%), oil content (GCV 10.42% and PCV 10.42%), sound mature kernels (GCV 4.89 % and PCV 5.15%), harvesting index (GCV 17.33 and PCV 17.96%), biological yield per plant (GCV 10.20% and PCV 10.64%) indicating that without much influence of environment, entire genetic determinants are translated into phenotype.
- Maximum heritability was observed for oil content followed by dry pod yield per plant, number of branches per plant, 100-kernel weight, harvesting index, biological yield per plant and sound mature kernel percent. While maximum genetic gain was observed for harvesting index followed by dry pod yield per plant, number of branches per plant, 100-kernal weight, oil content, biological yield per plant, sound mature kernel, plant height, days to 50 per cent flowering and initiation of pegging. In general, moderate to high heritability coupled with moderate to high genetic gain indicated the involvement of additive gene action, indicating scope of improvement in these traits through selection.
- Association estimates revealed that dry pod yield per plant showed positive and significant correlation with number of branches per plant, 100-kernel weight, harvesting index and oil content at both genotypic and phenotypic levels.
- Correlation for dry pod yield per plant was divided into direct and indirect effects of different characters. Highest positive direct effect on dry pod yield was exhibited by days to 50 per cent flowering (6.47) followed by biological yield per plant (3.76), harvesting index (3.06) and sound mature kernels (%) (0.66). While, high indirect effect on dry pod yield was exhibited positive and negative through other characters.

- As per cluster analysis 116 genotypes were divided into VII clusters. Averages inter cluster values were maximum between cluster III and cluster VII. Cluster VII possessed genotypes with high dry pod yield and highest harvesting index.
- From, the present investigation it can be concluded that genotypes G-10, G-17, G-20, G-93 and G-6 appeared promising with respect to dry pod yield as well as other yield contributing trait. Least difference between GCV and PCV for different characters indicated the least effect of environment and total genetic potential was reflected in genotypes. Thus, selection of genotypes would be effective. Positive and significant correlation among dry pod yield and contributing characters would help in indirect selection for dry pod yield in the crop like groundnut where economic part remains underground up till uprooting. Existence of diversity among genotypes in different clusters provided scope of getting transgressive segregates on making crosses among them.

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Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)

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Abstract

The present investigation entitled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)''** was carried out with 116 genotypes (including four checks) during *Kharif*, 2017 at the Instructional Farm, College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur. The genotypes were planted in augmented randomized block design.

The observations were recorded for 13 characters *viz*., initiation of pegging, duration between flowering to pegging, plant height, number of primary branch per plant, sound mature kernel (%), shelling percentage (%), dry pod yield per plant, 100-kernels weight, biological yield per plant and harvest index on five randomly selected plants from each genotype in each rows, while days to 50 per cent flowering and days to maturity and oil content were recorded on plot basis and average values were subjected to analysis variability parameters, correlation coefficients, path coefficients and genetic divergence.

The estimates of genotypic parameters revealed that the phenotypic coefficient of variation along with least difference from genotypic coefficient of variation observed for characters *viz*., number of branches per plant (GCV 15.05% and PCV 15.23%), 100-kernel weight (GCV 10.37% and PCV 10.66%), dry pod yield per plant (GCV 15.59% and PCV 15.71%), oil content % (GCV 10.42% and PCV 10.42%), sound mature kernels (GCV 4.89% and PCV 5.15%), harvesting index (GCV 17.33% and PCV 17.96%), biological yield per plant (GCV 10.20% and PCV 10.64%) indicating that without much influence of environment, entire genetic determinants are translated into phenotype.

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Maximum heritability was observed for oil content followed by dry pod yield per plant, number of branches per plant, 100-kernel weight (g), harvesting index, biological yield per plant and sound mature kernel percent. While maximum genetic gain was observed for harvesting index followed by dry pod yield per plant, number of branches per plant, 100-kernal weight, oil content, biological yield per plant. In general, moderate to high heritability coupled with moderate to high genetic gain indicated the involvement of additive gene action, indicating scope of improvement in these traits through selection.

Association estimates revealed that dry pod yield per plant showed positive and significant correlation with number of branches per plant, 100-kernel weight, harvesting index and oil content at both genotypic and phenotypic levels.

Correlation for dry pod yield per plant was divided into direct and indirect effects of different characters. Highest positive direct effect on dry pod yield was exhibited by days to 50% flowering followed by biological yield per plant, harvesting index and sound mature kernels. While, high indirect effect on dry pod yield was exhibited positive and negative through other character.

On the basis of present study, the genotype Genotypes G-10, G-20, G-17, G-99 and G-93 were found to have considerably higher means values for the traits dry pod yield per plant. Hence emphasis should be given to utilize these genotypes in further breeding programme.

On the basis of divergence studies, it was concluded that there was no relationship between genotypes and geographical origin. All genotypes group into VII cluster having maximum inter- cluster distance with genotypes of cluster III. Hence genotypes of these clusters with per se performance could be utilized in breeding programmes. Genetically diverse and high yielding genotypes of groundnut G-10, G-17, G-93 and G-6 could be used for breeding programme so as to ameliorate the productivity of groundnut.

exQyh ¼,jfd l gkbikft;k ,y-½ e y{k.k l?k ,o vkuokf'kd fopyu

foØe flg eh.kk* — शोधकर्ता

Mk- ih-ch- flg** — मुख्य सलाहकार

vu{ki.k

exQyh ¼,jfd l gkbikft;k ,y-½ e y{k.k l?k ,o vkuokf'kd fopyu नामक वर्तमान परीक्षण खरीफ–2017 में उदयपुर के महाराणा प्रताप कृषि एवं प्रौद्योगिकी विश्वविद्यालय के संघटक प्रौद्योगिक एवं अभियांत्रिकी महाविद्यालय (सी.टी.ए.ई.) के अनुदेशात्मक कृषि क्षेत्र में 116 जीन प्रारूपों (चार मानक तुलनको सहित) के साथ किया गया। सभी जीन प्रारूप संवर्धित यादृच्छिक खण्ड अभिकल्पना में रोपित किये गये।

सभी निरीक्षण 13 लक्षणों के लिये जैसे :– अधिकिलन बनने की प्रारम्भिक अवस्था, पुष्प आने एवं अधिकिलन के मध्य समय अंतराल, पौधे की ऊँचाई, प्रत्येक पौधे पर प्राथमिक टहनियों की संख्या, पूर्ण परिपक्व दाना, छीलन प्रतिशत, प्रति पौधा सूखी फलियों की उपज, सौ दानों का वजन, प्रति पौधा जैविक उपज एवं प्रत्येक पंक्ति के प्रत्येक जीन प्रारूप से 5 यादृच्छिक रूप से चयनित पौधों का फसल सूचकांक जबकि 50 प्रतिशत पुष्प आने में लगा समय व पकने में लगा समय एवं तेल सामग्री भूखण्ड आधार पर दर्ज किये गये तथा सामान्य मान परिवर्तनशीलता प्राचल, सहसंबंध गुणांक, पथ गुणांक आनुवांशिक विचलन के आधार पर दर्ज किये गये।

जीनप्रारूपिक मापदण्ड का अनुमान बताता है कि भिन्नता के लक्षण प्रारूपिक गुणांक भिन्नता के जीनप्रारूपिक गुणांक से कम से कम अंतर के साथ प्रति पौधा टहनियों की (जी.सी.वी. 15.05%) एवं (पी.सी.वी. 15.23%), प्रति पौधा सूखी फलियों की उपज (जी.सी.वी. 15.59% एवं पी.सी.वी. 15.72%), तेल सामग्री प्रतिशत (जी.सी.वी. 10.42% एवं पी.सी.वी. 10.42%) पूर्ण परिपक्व दाना (जी.सी.वी. 4.89 एवं पी.सी.वी. 5.15%) फसल सूचकांक (जी.सी.वी 17.33% एवं पी.सी.वी. 17.96%), प्रति पौधा जैविक उपज (जी.सी.वी. 10.20% एवं पी.सी.वी. 10.64%) आदि लक्षणों में यह दर्शाता है कि पर्यावरण के बहुत सारे प्रभाव के बिना पूरे आनुवंशिक निर्धारक के रूप में लक्षण प्रारूप में अनुवादित किया गया है।

* स्नातकोत्तर (कृषि) शोधार्थी, आनुवंशिकी एवं पादप प्रजनन विभाग, राजस्थान कृषि महाविद्यालय, एमपीयूएटी, उदयपुर (राज.)

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अधिकतम आनुवंशिकता तेल सामग्री के बाद प्रति पौधा सूखी फली की उपज, प्रति पौधा टहनियों की संख्या, 100 दानों का वजन, फसल सूचकांक, प्रति पौधा जैविक उपज व पूर्ण परिपक्व दाना प्रतिशत आदि के लिये देखी गई जबकि आनुवंशिक लाभ फसल सूचकांक के बाद प्रति पौधा सूखी फलियों की उपज, प्रति पौधा टहनियों की संख्या, 100 दानों का वजन, तेल सामग्री, प्रति पौधा जैविक उपज में देखा गया।

सामान्यतः मध्यम से उच्च आनुवांशिकता लाभ के साथ जुडे हुए युगल कार्यवाही की भागीदारी का संकेत मिलता है, जो चयन के माध्यम से इन लक्षणों में सुधार की संभावना दर्शाता है।

संगति आंकलन यह बताता है कि प्रति पौधा सूखी फली की उपज, प्रति पौधा टहनियों की संख्या, 100 दानों का वजन एवं फसल सूचकांक और तेल सामग्री के साथ जीन प्रारूपिक व लक्षण प्रारूपिक दोनों ही प्रकार से सकारात्मक एवं महत्वपूर्ण सहसंबंध दर्शाता है। प्रति पौधा सूखी फली की उपज के लिये सहसंबंध विभिन्न लक्षणों के लिये प्रत्यक्ष एवं अप्रत्यक्ष तरीकों से बांटा गया है। सूखी फली की उपज पर अधिकतम सकारात्मक प्रत्यक्ष प्रभाव, 50 प्रतिशत पुष्पों की संख्या का प्रदर्शन किया गया था जिसके बाद प्रति पौधा जैविक उपज, फसल सूचकांक व पूर्ण परिपक्व दानें का प्रदर्शन किया गया था जबकि शुष्क फली उपज पर उच्च अप्रत्यक्ष प्रभाव अन्य लक्षणों के द्वारा सकारात्मक एवं नकारात्मक प्रभाव का प्रदर्शन किया गया।

जीन प्रारूप के वर्तमान अध्ययन के आधार पर जीन प्रारूप जी–10, जी–20, जी–17, जी–99 एवं जी–93 को शुष्क फली उपज के लिये काफी महत्व मिला। इसलिये इन प्रजनन कार्यक्रम में जीन प्रारूपों का उपयोग करने के लिये जोर दिया जाना चाहिये।

विचलन अध्ययन के आधार पर यह निष्कर्ष निकाला गया कि जीन प्रारूप व भौगोलिक मूल स्थान के बीच कोई संबंध नहीं था।

क्लस्टर VII के सभी जीन प्रारूप समूह क्लस्टर III के जीन प्रारूप के साथ अधिकतम अन्तःक्लस्टर दूरी पर है। इसलिये इन क्लस्टरों की जीन प्रारूप के प्रदर्शन का प्रजनन कार्यक्रमों में उपयोग किया जा सकता है।

आनुवांशिक रूप से विविध और उच्च उपज देने वाले मूंगफली के जीन प्रारूप जी–10, जी–17, जी–93 एवं जी–6 का प्रजनन कार्यक्रम के लिये उपयोग किया जा सकता है ताकि मूंगफली की उत्पादकता की उन्नति को समझा जा सके।

APPENDIX - I

Mean weekly meteorological parameters during crop growing season (*kharif* 2017)

Standard Week	Date	Temperature (°C)		R.H. (%)		Sunshine (hrs)	Total Rainfall (mm)	Evaporation (mm day^{-1})
		Max.	Min.	Max.	Min.			
27	2 July-8 July	30.7	22.7	95.5	83.5	2.6	32.8	4.2
28	9 July-15 July	28.7	23.2	98.7	86.0	2.1	35.0	3.7
29	16 July-22 July	31.1	24.8	90.1	83.0	2.8	32.6	4. 2
30	23 July-29 July	30.0	23.3	95.9	84	3.4	64.2	2.8
31	30 July-5 Aug	31.6	24.2	91.4	78.9	4.3	56.6	3.9
32	6 Aug-12 Aug	28.7	23.2	90.7	86.9	1.7	37.0	2.9
33	13 July-19 Aug	28.2	22.7	96.9	83.0	2.6	63.4	2.4
34	20 Aug-26 Aug	30.7	22.7	96.4	86.7	3.7	86.6	1.8
35	27 Aug-2 Sept	30.4	22.7	98.7	86.0	4.2	162.4	2.4
36	3 Sep-9 Sept	27.8	22.9	97.4	85.1	2.1	90.0	2.2
37	10 Sep-16 Sept	28.8	23.2	92.4	74.1	3.9	153.5	3.0
38	17 Sep-23 Sept	29.3	21.2	90.1	66.7	5.0	27.8	2.4
39	24 Sep-30 Sept	30.6	19.2	86.1	55.9	8.7	0.0	3.8
40	1 Oct-7 Oct	31.4	18.3	77.9	44.3	9.5	0.0	3.9
41	8 Oct-14 Oct	33.4	19.3	70.2	37.1	8.5	0.0	4.5
42	15 Oct-21Oct	33.5	17.3	66.4	29.7	8.2	0.0	4.3
43	22 Oct-28 Oct	32.4	15.2	66.3	28.1	7.8	0.0	3.4
44	29 Oct-4 Nov	30.7	14.8	72.3	29.7	7.2	0.0	2.8

Source: Meteorological Observatory, CTAE Farm, MPUAT, Udaipur.

APPENDIX - II

Estimation of seed oil content (Soxhlet's Ether Extraction Method A.O.A.C., 1984)

1. Grind 500 mg of pre dried seed material and transfer it in thimble, plug the mouth of the thimble with tallow free absorbent cotton.
2. Take the clean, dry receiver flask from the soxhlet assembly and weight it accurately.
3. Introduce the thimbles with sample into the soxhlet.
4. Assemble the apparatus and fill soxhlet with petroleum ether (boiling point 40-60^{o}C) by pouring it through the condenser at the top. The amount of solvent is taken about 1.5 times the capacity of the soxhlet.
5. Place the apparatus on a water bath at 60^{o}C and start cold water circulation in the condenser.
6. Extract for 8 hours.
7. After extraction is over, remove the thimble with the material from soxhlet.
8. Assemble the apparatus again and heat it on water bath to recover all the ether from the receiver flask. The flask now contains only the crude fat.
9. Disconnect the receiver flask, wipe the outside of the flask thoroughly with a clean dry cloth to remove the film of moisture and dust and dry it in a hot air oven at 100^{o}C for 1 hour.
10. Cool in a desicator and weight (W_1) per cent oil content (%) is determined by the following formula:

    Oil content (%) = (W_1-W)/M x 100

    Where W_1 = Weight of oil flask after extraction.

    W = Weight of empty flask

    M = Weight of dried material taken

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