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

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DEPARTMENT OF PLANT BREEDING AND GENETICS
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CERTIFICATE-I

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This is to certify that **Mr. Tulsi Ram Dhakar** has successfully completed the Comprehensive Examination held on / /2015 as required under the regulation for the degree of **Master of Science in Agriculture**.

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This is to certify that the 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 **Plant Breeding and Genetics,** embodies bonafide research work carried out by **Mr. Tulsi Ram Dhakar** 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 the thesis was also approved by the advisory committee on /08/2015.

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This is to certify that **Mr. Tulsi Ram Dhakar**, student of **Master of Science in Agriculture**, Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur has made all the 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 / /2015. The final copies of the thesis duly bound and corrected were submitted on / /2015, are enclosed here with for approval.

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ABSTRACT

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

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The present investigation entitled "Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)" was conducted with 93 genotypes (including three checks namely TG-37A, Pratap Mungphali-2 and Pratap Raj Mungphali) during *Kharif*- 2014 at the Instructional Farm, College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur (MPUAT). The genotypes were planted in augmented design in six blocks.

The observations were recorded for 15 characters viz., days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of matured pods per plant, dry pod yield per plant, kernel yield per plant, 100-kernel weight, sound mature kernel, shelling percentage, biological yield per plant, harvest index, dormancy, oil content and protein content on five randomly selected plants from each genotype in each rows, while days to 50 per cent flowering and days to maturity were recorded on plot basis and average value were subjected to analysis of genetic variance, correlation coefficients, path coefficients and genetic divergence.

The estimates of genotypic parameters revealed that differences between the estimates of GCV and PCV were found least for most of the characters. Higher estimates of GCV were observed for number of mature pods per plant, dry pod yield per plant, kernel yield per plant and dormancy. Maximum heritability was found for protein content followed by oil content, days to 50 per cent flowering, kernel yield per plant and dry pod yield per plant. While, maximum genetic gain was observed for dormancy followed by kernel yield per plant, dry pod yield per plant and number of mature pods per plant.

Present experimental findings revealed that characters viz ; number of mature pods per plant, dry pod yield per plant, kernel yield per plant showed high GCV,

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heritability and genetic gain. Hence, selection can be made for improvement of these characters.

Association estimates revealed that dry pod yield per plant was positively correlated at both genotypic as well as phenotypic levels with kernel yield per plant, 100-kernel weight, sound mature kernel and biological yield per plant. Similarly, kernel yield per plant also showed positive correlation with number of mature pods per plant, dry pod yield per plant, 100-kernel weight, sound mature kernels, shelling percentage and biological yield per plant, at both genotypic as well as phenotypic levels.

Path coefficient analysis revealed maximum direct effect by kernel yield per plant (2.28). While, high positive indirect effect on dry pod yield was exhibited by number of mature pods per plant through kernel yield per plant (2.07). Similarly, oil content through number of mature pods per plant (0.50) and number of branches per plant through kernel yield per plant (0.37) also showed high indirect effects.

Genotypes in cluster VIII possessed genotypes having high dry pod yield as well as number of mature pods per plant and kernel yield. Therefore, crosses among these genotypes are expected to give transgressive segregants.

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.) is a member of *Papilionaceae,* subfamily of the *Fabaceae* family which comprises important edible oil seed crops in the world. The cultivated groundnut or peanut (*Arachis hypogaea* L.) originated in South America. 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. The peanut was probably first domesticated and cultivated in the valleys of Paraguay. It is an annual herbaceous plant growing 30 to 50 cm tall.

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 2013)

Total groundnut oil production in India during the year 2014-15 was 1.4 million tones. In year 2013-14, India's share in global production of groundnut oil was 23.85 % (USDA). Owing to its high content of digestible proteins (22-30%), vitamins (E, K & B group), minerals (phosphorus, calcium, magnesium and potassium) and phytosterols, it has gained importance as a food crop in the recent years. The oil content of the seed ranges between 44% to 50%, depending upon the varieties and agronomic conditions. 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 and lubricants, olein, stearin and their salts. Raw, roasted or sweetened kernels are directly used for consumption which can provide a calorific value of 349 per 100 grams. Groundnut kernels are exported for confectionary purposes. The residual oilcake after extraction of oil, contains 7% to 8% of N, 1.5% of P_2O_5 and 1.2% of K_2O making it useful as a fertilizer. 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. Groundnut is a modulating legume with symbiotic nitrogen fixation in root nodules improving the soil fertility which makes it valuable for crop rotation.

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 4.19 million hectares area with a production of 6.68 million tones and productivity of about 1591 kg/ha (Annual Report of DGR Junagadh 2014-15). 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 5.00 lakh hectare with a production of 10.23 lakh tones and productivity of about 2044 kg/ha (Commissionerate of Agriculture, Rajasthan, Jaipur 2014-15).

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 ward analysis (1963) using euclidian distances. This technique is intensively used in plant breeding and genetics for the study of genetic divergence in various breeding materials. This is one of the potent technique of measuring genetic divergence.

Keeping this in view, 90 diverse genotype with 3 checks of groundnut were planted during *kharif*, 2014 with following objectives.

1. To estimate the nature and magnitude of variability present in groundnut with respect to yield and its component characters.
2. To estimate genotypic and phenotypic correlations among different economic characters.
3. To determine the direct and indirect influences of various yield attributing characters through path coefficient analysis.
4. To determine the genetic divergence among groundnut genotypes.

2. REVIEW OF LITERATURE

A thorough understanding of the nature of variation, character association and genetic diversity helps in development of sound plant improvement programmes. Availability of literature on groundnut is quite large hence, a brief review of available information on above aspects in groundnut is presented in this section under the following sub-headings.

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

1. Variability parameters

Patil and Bhapkar (1987) studied 21 genotypes for genetic variability and reported wide range of variation for height of main stem, pods per plant, pod yield, 100-kernel weight, days to maturity and seed dormancy. Phenotypic and genotypic variance were the highest for seed dormancy and lowest for pod breadth. Phenotypic and genotypic coefficient of variation ranged from 2.16 to 29.97 and 1.17 to 29.75, respectively. Broad sense heritability was >60% for almost all characters. Expected genetic advance (as percentage of the mean) was highest for secondary branches number and lowest for pod length.

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 weight.

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 and 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.

Venkataramana *et al.* (2001) studied genetic variability in 144 groundnut germplasm lines. High genotypic and phenotypic coefficients of variation were observed for plant height, oil percentage, 100 kernel weight and kernel yield per plant. They noticed high heritability coupled with high genetic advance as per cent of mean for plant height, pod yield per plant, 100 kernel weight and oil percentage. They suggested that characters like pod yield per plant, 100 kernel weight, plant height and oil percentage can be improved effectively through simple selection.

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

Nath and Alam (2002) found that estimates of PCV were in accordance with those of GCV for days to flowering, plant height, pods per plant, 100 pod weight, shelling per cent and harvest index. However, the heritability estimates were higher for all the characters studied, accordingly GA as per cent of mean was high for all the characters except days to flowering. Therefore, direct selection would be effective for improvement of all the characters except days to flowering.

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 weight. 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.

Makhan Lal *et al.* (2003) studied genetic variation and selection response for twelve attributes using 67 groundnut lines and cultivars. They reported high values of PCV than GCV for all the characters studied except days to maturity; however, the

estimates of GCV were low to moderate for all the characters. The heritability estimates were high along with GA as per cent of mean for plant height and 100 pod weight.

Kumar and Rajamani (2004) observed highly significant differences among 12 genotypes for seed yield and other characters. For plant height, pod yield, 100 kernel weight and percentage of sound mature kernels, GCV and PCV values were high. Where, moderate PCV and GCV values were observed for shelling percentage. The values of PCV were higher than GCV indicating an influence of environment in the expression of all the characters studied.

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 weight, 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.

Parmeshwarappa *et al.* (2004) reported that characters, pod yield per plant, kernel yield per plant, shelling out turn and sound mature kernels showed high value of genetic coefficient of variation. An extent of heritability was moderate for days to maturity and high for days to 50 per cent flowering as well as 100 kernel weight. High heritability coupled with high genetic advance as per cent of mean was expressed by pod yield, kernel yield and shelling out turn; hence, improvement in these traits could be brought by applying selection on per se performance of genotypes.

Sarker *et al.* (2004) observed that number of secondary branches per plant and pod setting percentage showed high genotypic and phenotypic coefficient of variations and broad sense heritability coupled with high genetic advance in percentage of mean.

Mahalakshmi *et al.* (2005) evaluated fifty seven groundnut genotypes for genetic parameters. High heritability estimates combined with genetic advance were observed for number of secondary branches, number of unproductive pegs, number of

immature pods, number of mature pods, total number of pods, total number of gynophores, maturity index, shelling percentage and 100-kernel weight.

Kadam *et al.* (2007) concluded 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 late leaf spot disease, severity, reducing sugar, kernel yield per plant and pod yield per plant.

Cholin *et al.* (2010) evaluated two spanish bunch groundnut genotypes for variability parameters and results revealed that magnitude of variation (PCV, GCV) was low to moderate. For the protein content, genetic advance as per cent of mean was moderate with high heritability indicating the role of additive gene action in controlling these traits and for oil content, lower magnitude of variation with higher heritability and lower genetic advance was reported.

Meta and Monpara (2010) observed high GCV and PCV for pods per plant, kernel yield per plant and pod yield per plant indicated large extent of genetic variability for these traits in the material. High heritability was accompanied by high genetic advance for plant height and 100-pod weight, whereas, moderate heritability was associated with high genetic advance and high GCV for pods per plant and kernel yield per plant, indicating involvement of additive gene action for these traits. Pod yield per plant expressed high genetic advance with low heritability, however, its high magnitude of GCV suggested the scope of pod yield improvement.

Pod yield per plant was associated strongly and positively with kernel yield per plant, pods per plant, shelling outturn and oil content but its correlation was significantly negative with 100 pod weight, days to 50 per cent flowering and days to maturity. Pods per plant manifested maximum direct effects towards pod yield per plant followed by 100 pod weight and 100 kernel weights. Pods per plant and kernel yield per plant also contributed major share to pod yield per plant indirectly through other traits. Thus, pods per plant and kernel yield per plant would be the important component traits of pod yield and should be considered as selection criteria for enhancing yield in summer groundnut.

Nandini *et al.* (2011) studied variability parameters through 196 F_8 recombinant inbred lines and reported that PCV was higher than GCV for all the characters. Pod yield per plant recorded maximum GCV followed by kernel yield per plant, number of pods per plant, sound mature kernel percentage, specific leaf area, number of branches per plant, shelling percentage, plant height, SCMR and days to fifty per cent flowering. A moderate to high degree of heritability and genetic advance was observed for pod yield per plant, kernel yield per plant, pods per plant, sound mature kernel percentage, plant height, number of branches per plant and SLA.

Zaman *et al* (2011) observed high genetic coefficient of variation for kernel yield per hectare, followed by kernel yield per plant, branches per plant, immature and mature nuts per plant, 100 kernel weight and plant height. The highest heritability was observed in kernel yield per pant (95.08%), followed by kernel yield per hectare (94.38%), 100 kernel weight (87.01%), immature and mature nuts per plant (82.24%, 80.32%), branches per plant (79.54%) and 100 nut weight (78.98%), while high values of genetic advance were obtained in all the characters except days to maturity and days to 50 per cent flowering.

Upadhyaya *et al*. (2012) carried out variability analysis for nutritional traits in the mini core collection of peanut, 184 mini core accessions and four control cultivars were evaluated for nutritional traits for two seasons at two locations and for agronomic traits at one location. Significant genotypic and genotype x environment interactions were observed for all the nutritional and agronomic traits in the entire mini core collection.

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.

Vishnuvardhan *et al*. (2013) evaluated 8 parent and 28 crosses and observed high GCV accompanied by high heritability and high GAM were obtained for number of secondary branches per plant, percentage of leaves affected by foliar diseases per plant and number of immature pods per plant. Rust severity, number of mature pods per plant and pod yield per plant recorded high GCV and moderate heritability and GAM. Moderate GCV, moderate to low heritability and GAM were registered for number of primary branches per plant, kernel weight per plant, shelling out-turn, late leaf spot and harvest index.

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 weight 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.

Terkimbi and Terkula (2014) observed variability for basal stem diameter, biological yield, days to first and 50 per cent flowering, plant height, number of leaves per plant, branches per plant and 100-seed weight showing a wide scope for improvement through selection. Coefficient of variation at phenotypic and genotypic levels were close in magnitude for number of branches per plant, plant height, days to first flowering and grain yield suggesting the presence of additive gene effects. High

heritability estimates coupled with genetic advance were noted for number of branches per plant, plant height, days to first flowering and grain yield.

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

Bera and Das (2000) evaluated 44 genotypes of groundnut and concluded that path coefficient analysis indicated positive direct contribution of pods per plant and harvest index to the seed yield irrespective of locations and years effect. Their correlations with seed yield were also significantly positive. So pod yield per plant and harvest index can be used directly as selection criteria for improvement of seed yield in groundnut.

Jayalakshmi *et al.* (2000) studied correlation for twelve different characters with seven parents and their 21 F_1s of groundnut. They observed significant and positive association between kernel yield and mature pods per plant, but significant and negative association between kernel yield and oil content was also reported.

Khan *et al*. (2000) studied 13 geographically diverse peanut genotypes and concluded that 100 kernel weight showed the highest but non significant correlation with pod yield. Path coefficient analysis revealed that 100 kernel weight had the highest direct effect on pod yield followed by pods per plant, kernels per pod and sound mature kernel percentage, Kernel weight affected pod yield negatively *via* indirect influence of pods per plant, seeds per pod, sound mature kernel percentage and shelling percentage.

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.

Dashora and Nagda (2002) reported that dry pod yield exhibited significant and positive association with shelling percentage and kernel yield. Path analysis revealed that shelling percentage and kernel yield were major components of dry pod 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.

Sarker *et al*. (2004) concluded that pod yield was significantly and positively associated with 100-pod weight and plant height. Path coefficient analysis revealed that the pod yield was mainly governed by 100-pod weight, plant height and shelling percentage. Correlation coefficient and path coefficient analysis suggested that 100-pod weight and plant height were the most important yield contributing characters in groundnut.

Suneetha *et al*. (2004) studied 23 diverse genotypes of groundnut and reported significant and positive correlation of pod yield per plant with mature pods per plant and harvest index. The character combinations of days to 50 per cent flowering with

days to maturity and 100-pod weight with 100-kernel weight showed significant and positive correlations among themselves. Whereas days 50 per cent flowering and plant height were negatively correlated with pod yield per plant. The analysis indicated that harvest index expressed high direct effect towards pod yield followed by sound mature kernels. Days to 50 per cent flowering and plant height expressed negative direct contribution. They concluded that day to 50 per cent flowering, plant height and mature pods per plant should be considered as selection criteria for improving pod yield in groundnut.

Gomes and Lopes (2005) studied genotypic correlation coefficients between seed yield and the primary components of the yield apportioned into direct and indirect effects. The highest estimates of the coefficient of genotypic determination were obtained for weight of 100 seeds, number of pods per plot, seed yield, number of seeds per pod and pod yield. The splitting of the genotypic correlations into seed yield and the primary components, in direct and indirect effects, showed that the seed yield was positively influenced by the number of pods per plot and weight of 100 seeds and negatively by the number of seeds per pod. Thus, the number of pods per plot had the maximum direct influence on the seed yield.

Kalmeshwer *et al.* (2005) evaluated 13 genotypes along with four check and observed that pod yield per plant had significant positive association with number of pods per plant, shelling per cent and SMK per cent at minimum three locations. Path analysis also indicated that three traits viz., number of pods per plant, shelling per cent and sound mature kernel per cent had the maximum direct effect on pod yield per plant at minimum three locations. This indicates that increase in pod number per plant, shelling per cent and DMA per cent would improve the pod yield of groundnut.

Mahalakshmi *et al.* (2005) observed that kernel yield per plant showed significant and positive association with days to 50 per cent flowering, plant height, number of secondary branches, number of unproductive pegs, number of immature pods, number of mature pods, SMK weight, SMK number, total number of pods, total number of gynophores, shelling percentage, 100-kernel weight and pod yield. The association of kernel yield with other characters was non-significant.

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.

Mane *et al.* (2008) assessed the relationship among different characters in summer bunch groundnut and reported that pod yield per plant exhibited significant and positive correlation with per cent sound mature kernel, number of pegs per plant, number of pods per plant and shelling percentage. However, it showed negative and non-significant correlation with hundred kernel weight and days to 50 per cent flowering.

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, where as negative significant association with late leaf spot disease severity and reducing sugar indicated that they could be used as selection criteria for developing high yielding late leaf spot disease resistance varieties. 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, days to maturity and non reducing sugar 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 which 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.

Vaithiyalingan *et al.* (2010) observed that dry pod yield exhibited significant positive association with pods per plant, dry matter production, kernel weight and harvest index. Path analysis revealed maximum direct effect of pods per plant followed by dry matter production and kernel weight on pod yield.

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.

Dhaliwal *et al*. (2010) observed that dry pod yield had significant positive association with days to flowering, days to maturity, haulm yield per plant and kernel yield per plant. At genotypic level too these traits had high positive correlation with dry pod yield. Path analysis indicated high positive direct contribution of kernel yield per plant. Days to flowering, days to maturity and haulm yield per plant made indirect contribution to dry pod yield via kernel yield per plant. It was concluded that these traits must be given weightage during selection in the segregating generations for the improvement of dry pod yield in groundnut.

John *et al*. (2011) carried out correlation analysis to assess the relationship among different characters in F_2 population of groundnut and reported that SCMR had significant negative association with specific leaf area. Positive significant association of transpiration rate with photosynthetic rate and pod yield per plant, dry haulm yield per plant with harvest index. The high direct effect of pods per plant was appeared to be the main factor for its strong positive correlation with pod yield.

Lucas *et al*. (2011) revealed that the most relevant traits for selection for peanut pod yield were identified among the following: total number of pegs, number of pegs in the lower third of the plant, number of mature pods, main stem height and reproductive efficiency. The lines with best reproductive efficiency were L_8 and L_{11}. Path analysis detected a strong direct effect of the number of pegs in the lower third of the plant on the number of mature pods. This finding justifies the use of the number of pegs in the lower plant third in selection of peanut populations for number of mature pods.

Vekariya *et al.* (2011) evaluated 50 diverse genotypes and observed that pod yield per plant had highly significant and positive correlations at phenotypic levels 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.

Zaman *et al.* (2011) observed that seed yield per plant showed the highly significant and positive association with nut size, number of nuts per plant, karnel size and days to 50 per cent flowering. The number of mature nuts per plant had high positive direct effect on seed yield per hectare followed by nut size, shelling percentage, days to 50 per cent flowering and days to maturity. Therefore, branches per plant, plant height, nuts per plant, nut size, karnel size, days to 50 per cent flowering, shelling percentage and days to maturity were identified to be the important characters which could be used in selection for yield.

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.

Nandini and Savithramma (2012) studied phenotypic and genotypic correlation coefficients revealed that pod yield per plant had strong positive

correlation with pods per plant, kernel yield per plant, sound mature kernel percentage indicating that improvement in these characters will lead to improvement in yield. Whereas significant negative association was observed for pod yield per plant with days to fifty per cent flowering and shelling percentage. Among these characters kernel yield per plant recorded maximum direct effect on pod yield per plant whereas all other characters recorded low direct effects. Sound mature kernel percentage, pods per plant and SLA recorded maximum indirect effect on pod yield per plant through kernel yield per plant. The results of the study revealed that the character kernel yield per plant and specific leaf area could be given emphasis for selection of genotypes with high yield coupled with high water use efficiency.

Shobha *et al*. (2012) observed that kernel yield was significant and positively correlated with number of pods per plant, pod yield per plant, shelling per cent and hundred kernel weight for all the crosses. Among the nine traits studied, pod yield per plant exerted maximum positive direct effect on kernel yield per plant for all the three crosses. When both direct and indirect positive contributions were considered, number of pods per plant and pod yield per plant influenced kernel yield per plant. Thus, on the basis of correlations and direct and indirect effects, number of pods per plant, pod yield per plant, hundred kernel weight and shelling percentage were proved to be the outstanding characters influencing kernel yield in groundnut and need to be given importance in selection to achieve higher kernel yield.

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 plant-1, 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, SMK per cent and100 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, phenol content, non reducing sugar, 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, non reducing sugar, phenol content 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.

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, no. 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.

Terkimbi and Terkula (2014) observed that grain yield was correlated positively with all the character except the phenological traits. The path analysis implicated biological yield, failed pegs per plant, number of leaves per plant and basal stem diameter as having substantial influence on grain yield in groundnut. Thus, selection of breeding lines based on the biological yield, failed pegs, number of leaves per plant and basal stem diameter could give a better scope for maximum grain yield in groundnut.

4. 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.

Sarker *et al*. (2004) concluded that genotypes under study fell into six clusters. The intercluster distances were larger than the intracluster distance suggesting the presence of wider genetic diversity among the genotypes of different groups. Plant

height contributed maximum to the diversity. The genotypes 4595, ICGS-E-55 and DM-1 were found potential parents based on cluster distance.

Mahalakshmi *et al*. (2005) reported maximum divergence between clusters II and VII followed by clusters VI and VII. Days to first flowering followed by shelling percentage contributed maximum to the total divergence. The genotypes VHI 2 (cluster II) for shelling percentage and oil content ICG 3063 (cluster VI) for SMK number and pods and ICG 3254 (cluster VII) for maturity- index and reproductive efficiency were found as potential parents based on cluster mean and genetic diversity.

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

Siddiquey *et al*. (2006) studied genetic diversity in groundnut and reported that genotype fell into 7 groups, which indicated that there exists considerable diversity among the genotypes. In cluster analysis it was found that pod length, shelling percentage, mature pods per plant, seeds per plant, protein content and 100-pod weight contributed maximum towards genetic divergence in ground nut genotypes.

Sonone and Thaware (2009) studied genetic diversity for pod yield and other characters in groundnut, forty genotypes of groundnut were selected from different geographical origins to assess the genetic diversity by using Mahalanobis's D^2 statistics. These genotypes were grouped into fifteen clusters, the diversity among the genotypes, measured by inter cluster distances was adequate for improvement by hybridization and selection.

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 number 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 segregants 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 (DAS) to harvest, CGR at 30-75 DAS, 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.

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,* 2014 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 Table 3.1.

Table 3.1: Meteorological observations during crop period (*kharif* - 2014)

S. No	Month	Temperature		R.H. (%)		Evaporation (mm)	Total Rainfall (mm)
		Max°C	Min°C	Morning	Evening		
1.	June	39.5	25.3	60.9	34.3	11.3	0
2.	July	33.5	25	76.7	56.7	6.3	200.40
3.	August	31.5	23.3	85.6	69.8	3.8	125.60
4.	Sept.	30.9	21.1	86.5	65.7	6.0	316.70
5.	Oct.	33.7	15.4	75.9	31.9	4.1	0.00
6.	Nov.	31.5	11.6	75.8	30.1	9.20	3.5

Total rainfall = 646.20 mm

1. Experimental materials:

The experimental material consisted of 90 diverse genotypes along with 3 checks of groundnut received from different origins, which were obtained from the All India Coordinated Research Improvement Project on Groundnut, MPUAT, Udaipur. Details of selected genotypes are given in Table 3.2.

2. Experimental details:

Ninty genotypes with three checks of groundnut were sown in six blocks in a Augmented Design during *kharif* - 2014 at the Instructional Farm, College of Technology and Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur. Each genotype was accommodated in a one row plot of 5.0 m

length with a spacing of 30 cm between rows and 10 cm between plants. The fertilizer in the experimental area was applied at the rate of 20 kg N ha^{-1} and 60 kg P ha^{-1} as it is a recommended dose for *kharif* cultivation of groundnut in the region. All other recommended agronomical practices were followed for reaping good crop.

Table 3.2: List of genotypes used in the present study and their pedigree

S.No.	Name of Genotypes	Pedigree	Palace
1	UG-3	Selection from ICGV98281	ICRISAT, Hyderabad
2	UG-4	Selection from ICGV98221	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, Junagadh
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, Junagadh
18	UG-61	GG-20 X Chico2	DGR, Junagadh
19	UG-62	PBS20176 X NRCG48291	DGR, Junagadh
20	UG-64	(EDRGVT X ICGV03056)	ICRISAT, Hyderabad
21	UG-65	(EDRGVT X ICGV03206)	ICRISAT, Hyderabad
22	UG-67	B95 X Giri-1	DGR, Junagadh
23	UG-68	PBS20176 X NRCG4829-1	DGR, Junagadh
24	UG-69	P95 X GG-2	DGR, Junagadh

25	UG-71	GG-2 X JCA16	DGR, Junagadh
26	UG-85	ICGV86031 X TAG24	DGR, Junagadh
27	UG-86	(ICGS44 X CSMG84-1) X GG-2	DGR, Junagadh
28	UG-87	TAG-24 X ICGS75	DGR, Junagadh
29	UG-88	PBS20176 X Code26	DGR, Junagadh
30	UG-89	ICG X 000102	ICRISAT, Hyderabad
31	UG-90	ICGS76 X ICGV86031	DGR, Junagadh
32	UG-91	TAG-24 X ICGV76-1	DGR, Junagadh
33	UG-92	PBS29017 X NRCG4829	DGR, Junagadh
34	UG-93	(ICGS44 X CSMG84-1) X ICGV86031	DGR, Junagadh
35	UG-94	TAG-24 X ICGS76	DGR, Junagadh
36	UG-95	ICGS44 X CSMG84-1-2	DGR, Junagadh
37	UG-100	PBS20176 X Code26-1	DGR, Junagadh
38	UG-102	ICGS44 X CSMG84-1	DGR, Junagadh
39	UG-103	(ICGS44 X CSMG84-1) X GG-2	DGR, Junagadh
40	UG-104	PBS11039 X ICGV86031	DGR, Junagadh
41	UG-105	PBS11039 X TAG-24	DGR, Junagadh
42	UG-107	(ICGV86031 X TAG-24) X CGMS84-1	DGR, Junagadh
43	UG-108	ICGS76 X ICGV86031-1	DGR, Junagadh
44	UG-109	ICG X 000103	ICRISAT, Hyderabad
45	UG-110	ICGS44 X CSMG84-1	DGR, Junagadh
46	UG-111	PBS11039 X TAG24-1	DGR, Junagadh
47	UG-112	PBS29031 X ICGV86031	DGR, Junagadh
48	UG-113	ICGS44 X CSMG84-1	DGR, Junagadh
49	UG-114	ICGS76 X ICGV86031-2	DGR, Junagadh
50	UG-115	PBS11039 X NRCG4829	DGR, Junagadh
51	UG-116	ICGV03063	ICRISAT, Hyderabad
52	UG-117	Kadiri-3 X TKG19A	DGR, Junagadh
53	UG-118	ICGS-11 X SBX1-2	DGR, Junagadh
54	UG-119	ICG X 020153	ICRISAT, Hyderabad
55	UG-120	ICGS76 X ICGV86325	DGR, Junagadh

56	UG-122	J-83 X TG-41	DGR, Junagadh
57	UG-123	ICG X 020091	ICRISAT, Hyderabad
58	UG-124	CSMG84-1 X ICGV4747	DGR, Junagadh
59	UG-125	TAG-24 X ICGV4747	DGR, Junagadh
60	UG-126	CSMG84-1 X ICGV86031	DGR, Junagadh
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, Junagadh
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, Junagadh
80	UG-147	GG-20 X ICGV91114-1	DGR, Junagadh
81	UG-148	ICGV91114 X ICGV86564	DGR, Junagadh
82	UG-149	PBS28014 X NRCG1463	DGR, Junagadh
83	UG-150	PBS26002 X PBS29017	DGR, Junagadh
84	UG-151	AK159 X NRCG5001	DGR, Junagadh
85	UG-152	AK159 X NRCG5001-1	DGR, Junagadh
86	UG-153	AK159 X NRCG5001-2	DGR, Junagadh
87	UG-154	ICG X 020106	ICRISAT, Hyderabad
88	UG-155	(TKG19A X Kadiri-3) X TKG19A	DGR, Junagadh

89	UG-156	GG-20 X ICGV87250	DGR, Junagadh
90	UG-157	TKG19A X Kadiri-3	DGR, Junagadh
91	TG37A	TG25 X TG26	BARC, TROMBAY
92	PM-2	ICGV-86055 × ICG-(FDRs 10)	MPUAT, Udaipur
93	Pratap Raj Mungphali	Selection from ICGV 98223	MPUAT, Udaipur

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 % flowering, days to maturity and 100-kernel weight, which were recorded on plot basis. The methodology used for recording observations on different characters is described below:

(i) Days to 50% flowering

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

(ii) Days to maturity

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

(iii) Plant height (cm)

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.

(iv) Number of branches per plant

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

(v) Number of matured pods per plant

The numbers of fully developed seed bearing mature pods were counted for each randomly selected five plants at the time of harvesting.

(vi) Dry pod yield per plant (g)

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

(vii) Kernel yield per plant (g)

Kernel yield per plant was computed by multiplying the dry pod yield with shelling percentage and divided by hundred.

(viii) 100-kernel weight (g)

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

(ix) 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.

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

(x) Biological yield per plant (g)

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

(xi) Shelling percentage (%)

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

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

(xii) Harvest index (%)

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

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

(xiii) Dormancy

The groundnut genotypes were harvested at maturity as indicated by blackening of inner surface of shell. The pods were dried in partial shade for five days and shelled just before germination test. Three replicate samples of 25 seeds each was kept for germination in petriplate lined with filter paper and water added to a depth of 2 mm after moistening the filter paper. The petriplates were incubated at 27 ºC ± 3 ºC and germination count was made. The duration was observed by days taken by genotypes to attain 50 per cent germination.

(xiv) Oil content (%)

Two random samples of kernels were drawn from bulk harvest of five randomly selected plants under each replication and 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).

(xv) Protein content (%)

Two samples were drawn from bulk harvest of five randomly selected plants under each replication and nitrogen content of kernels was obtained by the standard Micro Kjeldahl method. Value of nitrogen so obtained was converted to crude protein per cent by multiplying with a factor of 6.25 and average protein per cent was worked out. (Detailed procedure is given in appendix III)

4. Statistical analysis:

The plot wise mean values of five randomly selected plants were used for the statistical analysis for 15 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.N.	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 ith Check in j^{th} block

X_i = Value of ith 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 $(1+\frac{1}{r}+\frac{1}{c}+\frac{1}{rc})$

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 $\sqrt{MSE\ (1+\frac{1}{r}+\frac{1}{s}+\frac{1}{rc})}$

For all L.S.D. the t value is two tail value at α level at (r-1) (c-1) degree of freedom. Howhere 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 (1940).

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

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)

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

Where,

$\overline{X}$ = Population mean

GA = Genetic advance = $\frac{K \sigma_g}{\sqrt{\sigma_p}}$

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 Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis. Phenotypic and genotypic covariances for pair of characters were calculated in the similar fashion as variance for individual character.

(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 9 characters on dry pod yield per plant (Y) were obtained as per procedure given below:

r_1Y	$r_{1\,1}\ r_{1\,2}$..... $r_{1\,9}$	P_1Y
r_2Y	$r_{2\,1}\ r_{2\,2}$..... $r_{2\,9}$	P_2Y
,,	,,	,,
,,	,,	,,
,,	,,	,,
,,	,,	,,
R_9Y	$r_{9\,1}\ r_{9\,2}$..... $r_{9\,9}$	P_9Y
A	B	C

Where,

r_1Y, r_2Y, r_3Y,…., r_9Y are the genotypic correlations of days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of mature pods per plant, kernel yield per plant, sound mature kernels, dormancy (days), oil content (%) and protein content (%) on dry pod yield per plant (Y), respectively.

P_1Y, P_2Y, P_3Y,…….., P_9Y are the direct effects of days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of mature pods per plant, kernel yield per plant sound mature kernels, dormancy, oil content (%) and protein content (%) on dry pod yield per plant (Y), 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:

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

Where, R is the residual effect.

4.5 Genetic divergence

Since, experimental design was augmented therefore, diversity analysis was carried out using ward (1963) method using euchlidian distances and calculated through SPSS version 19.

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 93 genotypes of groundnut (*Arachis hypogaea* L.) including three checks. These genotypes were studied to estimate genetic variability, correlation coefficients, path coefficients and genetic divergence among themselves.

Observations recorded for fifteen characters of 93 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 fifteen characters were subjected to statistical analysis. The mean sum of squares due to genotypes were highly significant for all the characters studied, except 100-kernel weight and biological yield per plant, indicating considerable differences among the genotypes used in the present study (Table 4.1).

4.2 MEAN VALUES AND RANGE

The mean performance of genotypes for different characters are presented in Appendix I. A perusal of the data revealed that the range was considerably high for most of the characters *viz*., days to 50% flowering (27 to 36 days), days to maturity (99 to 114 days), plant height (23.86 to 38.76 cm), number of branches per plant (4.60 to 8.40), number of mature pods per plant (7 to 15.80), dry pod yield per plant (8.80 to 18.60 g), shelling percentage (60 to 75 %), 100-kernel weight (30.28 to 52.43

g), sound mature kernel (75.28 to 93.24 %), biological yield per plant (24.26 to 42.35 g), kernel yield per plant (5.40 to 13.80 g), harvest index (25.41 to 46.72 %), dormancy (4 to 10 days), oil content (34.18 to 44.86 %) and protein content (18.42 to 26.87 %) indicating an adequate variability for exercising selection and use in the breeding programmes.

Table 4.1: Mean squares for various characters in Groundnut

SN	Character	Block	Treatment	Check	Germplasm	C v/s G	Error
1.	Days to 50 % flowering	1.26	5.66**	0.72	5.77**	6.23**	0.46
2.	Days to maturity	4.32	20.91*	2.39	21.04*	46.23*	6.72
3.	Plant height (cm)	2.08	8.43*	6.06	8.27*	27.97**	2.31
4.	Number of branches per plant	0.36	0.96**	0.01	0.97**	2.07*	0.22
5.	Number of mature pods per plant	4.22	6.99**	2.08	5.54*	145.91**	1.57
6.	Dry pod yield per plant (g)	1.21	6.11**	4.25*	6.03**	16.89**	1.03
7.	Kernel yield per plant (g)	0.46	3.31**	4.22**	3.21**	9.87**	0.53
8.	100-Kernel weight (g)	6.22	27.40	44.89	24.27	271.11**	11.57
9.	Sound mature kernel (SMK) %	10.92	22.77*	10.87	22.07*	109.14**	7.77
10.	Shelling percentage (%)	8.89	19.85*	22.39	19.95*	6.23	6.92
11.	Biological yield per plant (g)	5.74	16.05	10.72	15.27	96.33**	9.20
12.	Harvest index (%)	6.19	34.92*	5.39	27.94*	715.23**	10.46
13.	Dormancy	0.59	2.48**	3.56*	2.48**	0.31	0.56
14.	Oil content (%)	1.11	7.14**	5.38**	6.76**	44.71**	0.53
15.	Protein content (%)	0.84*	4.00**	0.21	3.30**	73.82**	0.24

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

4.2.1 Days to 50 % flowering

Among 93 genotypes, for mean days to 50 per cent flowering, genotype UG-17, UG-111, UG-117, UG-147 and UG-149 (27 days) were the earliest to flower

which were followed by UG-3, UG-9, UG-22, UG-65, UG-87, UG-93, UG-104, UG-115, UG-119, UG-125 and UG-137 (28 days). The overall mean recorded for the trait was 31.26 days.

4.2.2 Days to maturity

With respect to days to maturity, genotype UG-94, UG-95 and UG-120 were found earliest as they showed minimum 99 days to maturity followed by UG-109, UG-142 and UG-150 (100 days).

4.2.3 Plant height (cm)

For the trait plant height, maximum plant height was depicted by genotype UG-114 (38.76 cm) followed by UG-3 (37.93 cm) and UG-142 (37.46 cm). The mean for plant height was 30.13 cm.

4.2.4 Number of branches per plant

Maximum number of branches per plant were exhibited by the genotype UG-86 (8.40), followed by UG-120 (8.2), UG-132(8.1) and UG-114 (8). The mean for number of branches per plant was 6.35.

4.2.5 Number of mature pods per plant

Mean data for number of mature pods per plants revealed that among 93 genotypes UG-120 (15.80 pods) possessed maximum number of mature pods per plant followed by UG-116 (15.60 pods) and UG-93 (15.40 pods). The overall mean for this trait was 10.82 mature pods per plant.

4.2.6 Dry pod yield per plant (g)

The mean dry pod yield per plant of 93 genotypes exhibited wide range of variation. Maximum dry pod yield was exhibited by genotype UG-108 (18.60 g), followed by UG-109 (18.20 g) and UG-67, UG-120 (17.40 g). The overall mean for this character was 12.78 g.

4.2.7 Kernel yield per plant (g)

Wide range of variation was found for kernel yield per plant among the 93 genotypes. The genotype UG-108 (13.80 g) gave maximum kernel yield followed by UG-87(12.30 g) and UG-103, UG-120 (12 g). The overall mean for this character was 8.82 g.

4.2.8 100 Kernel weight (g)

The data for 100 kernel weight depicted that genotype UG-126 (52.43 g) had maximum 100 kernel weight followed by UG-141 (51.78 g) and UG-122 (51.47 g). The mean 100 kernel weight was 41.73 g.

4.2.9 Sound mature kernel (%)

Maximum sound mature kernel percentage was exhibited by the genotype UG-93 (93.24 %) followed by UG-122 (92.76 %) and UG-126 (92.43 %).

4.2.10 Shelling percentage (%)

The mean values for shelling percentage revealed that genotype UG-9, UG-19, UG-105, UG-117, UG-119, UG-124, UG-129, UG-150 showed maximum shelling percentage (75 %) followed by UG-3, UG-21, UG-68, UG-107, UG-108, UG-122, UG-127, UG-139, UG-143, UG-147, UG-148 (74 %). The general mean for this trait was 68.91%.

4.2.11 Biological Yield per plant (g)

Among 93 genotypes, maximum mean biological yield per plant was exhibited by genotype UG-108 (42.35 g) followed by UG-109 (40.24 g) and UG-90 (39.24 g). The overall mean observed for this trait was 32.99 g.

4.2.12 Harvest index (%)

Mean values among the 93 genotypes for harvest index expressed that genotype UG-120 (46.72 %) had highest harvest index followed by UG-152 (46.29%) and UG-95 (46.05 %). The general mean for this trait was 38.71.

4.2.13 Dormancy

Genotype UG-65 (10 days) had maximum dormancy whereas genotype UG-19, UG-69, UG-92, UG-109, UG-114, UG-118, UG-125, UG-150 and UG-154 (4 days) had lowest dormancy. The mean for dormancy was 6.87 days.

4.2.14 Oil content (%)

With respect to oil content, genotype UG-62 had maximum oil content (44.86 %) followed by UG-9 (44.74 %), UG-128 (44.62 %) and UG-145 (44.57 %) whereas the genotype UG-120 (34.18 %) had minimum oil content. The overall mean for oil content was 39.76 %.

4.2.15 Protein content (%)

With respect to protein content, genotype UG-157 (26.87 %) had maximum protein content, followed by UG-69 (25.64 %), and UG-148 (25.41 %) whereas the genotype UG-150 (18.42 %) had minimum protein content. The overall mean for protein content was 21.90 %.

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 (GCV) coefficients of variation, heritability and genetic gain were estimated and character wise results are presented in table 4.2 and discussed as follows.

4.3.1 Days to 50 % flowering

A perusal of the data showed low values of both GCV (7.37 %) and PCV (7.68 %) 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.

High value of heritability (92.10 %) and low genetic gain (14.57 %) indicated presence of non additive gene action. High heritability being exhibited was may be due to favourable influence of environment rather than genotype. Selection of such trait may not be fruitful. The findings of these results obtained are in accordance with the finding of Dashora and Nagda (2002), Nath and Alam (2002), Parmeshwarappa *et al.* (2004) and Vishnuvardhan *et al.* (2012).

4.3.2 Days to maturity

Partitioning of total variance into its components revealed that the genotypic (3.54 %) and phenotypic (4.29 %) coefficients of variation were low in magnitude for days to maturity. However, narrow difference between these two parameters indicated

less influence of environment in the expression of this trait. Present findings are in accordance with the findings of Vishnuvardhan *et al.* (2012).

However, low value of heritability (68.06 %) and low genetic gain (6.01 %) indicated presence of non additive gene action.

Table 4.2: Variability parameters for various characters in Groundnut (*Arachis hypogaea* L.)

SN	Character	GCV %	PCV%	H^2%	GG%
1	Days to 50 % flowering	7.37	7.68	92.10	14.57
2	Days to maturity	3.54	4.29	68.06	6.01
3	Plant height (cm)	8.10	9.54	72.12	14.18
4	Number of branches per plant	13.61	15.47	77.43	24.67
5	Number of mature pods per plant	18.40	21.74	71.59	32.07
6	Dry Pod yield per plant (g)	17.50	19.21	82.94	32.82
7	Kernel yield per plant (g)	18.58	20.33	83.54	34.99
8	100-Kernel weight (g)	8.54	11.80	52.32	12.72
9	Sound mature kernel (SMK) (%)	4.42	5.50	64.79	7.34
10	Shelling percentage (%)	5.24	6.48	65.30	8.72
11	Biological yield per plant (g)	7.47	11.85	39.76	9.70
12	Harvest index (%)	10.80	13.66	62.57	17.60
13	Dormancy	20.18	22.92	77.57	36.62
14	Oil content (%)	6.28	6.54	92.17	12.41
15	Protein content (%)	7.99	8.30	92.74	15.85

4.3.3 Plant height (cm)

Estimates of genetic parameters indicated that plant height exhibited low value of GCV (8.10 %) and PCV (9.54 %). The GCV and PCV values for plant height were more or less equal. 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 Venkatramana *et al*. (2001).

The magnitude of heritability in broad sense (72.12 %) was high, with low genetic gain (14.18 %) for plant height. High 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.

High heritability was also reported by Venkatramana *et al*. (2001), Prasad *et al*. (2002), Makhan *et al*. (2003), Mothilal *et al.* (2004), Meta and Monpara (2010), John *et al.* (2013), Rao *et al.* (2014), Terkimbi and Terkula (2014) and Yadav *et al.(*2014).

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 (13.61 %) and PCV (15.47 %) were moderate for this trait. The moderate estimates of genotypic and phenotypic coefficients have also been reported by Prasad *et al*. (2002), Mothilal *et al.* (2004) and Kadam *et al.* (2007) for this trait.

The trait number of primary branches per plant exhibited high heritability (77.43%) coupled with moderate genetic gain (24.67 %). These results were in accordance with the findings of Mothilal *et al.* (2004), Kadam *et al*. (2007), Nandini *et al*. (2011), John *et al*. (2013) and Terkimbi and Terkula (2014). Moderate to high magnitude of heritability and moderate genetic gain, as observed in the present study suggested that branches per plant was 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 Number of mature pods per plant

The magnitude of genotypic coefficient of variation (18.40 %) and phenotypic coefficient of variation (21.74 %) was found high for number of mature pods per plant. Mothilal *et al*. (2004) and John *et al*. (2013) also reported high magnitude of both GCV and PCV for number of mature pods per plant in groundnut.

On the other hand, heritability (71.59 %) was high in magnitude, in conjunction with high estimates of genetic gain (32.82 %). It revealed that the

character is governed by additive gene effects and hence, selection would be effective for improvement of this trait.

4.3.6 Dry pod yield per plant

The estimates of genotypic (17.50 %) and phenotypic (19.21 %) coefficients of variation indicated that both the parameters were high in magnitude for dry pod yield per plant. The higher estimates of GCV and PCV have been earlier reported by Prakash *et al*. (2000), Kumar and Rajamani (2004), Mothilal *et al*. (2004), Parmeshwarappa *et al*. (2004), Kadam *et al*. (2007), Giri *et al*. (2009), Meta and Monpara (2010), Nandini *et al.* (2011), Rao *et al*. (2014) and Yadav *et al.* (2014).

The heritability in broad sense (82.94 %) was high and genetic gain (32.82 %) was also high for this trait. Prakash *et al.* (2000), Venkataramana *et al*. (2001), Dashora and Nagda (2002), Prasad *et al.* (2002), Mothilal *et al*. (2004), Parmeshwarappa *et al*. (2004), Kadam *et al*. (2007), Giri *et al*. (2009), Meta and Monpara (2010), Nandini *et al.* (2011), John *et al.* (2013), 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.

4.3.7 Kernel yield per plant

A perusal of the data for kernel yield per plant indicated that genotypic coefficient of variation (18.58 %) and phenotypic coefficient of variation (20.33 %) were high in magnitude for this character. These findings are in accordance with the results reported by Venkatramana (2001), Parmeshwarapa *et al.* (2004), John *et al*. (2007), Kadam *et al.* (2007), Giri *et al*. (2009), Meta and Monpara (2010) and Zaman *et al.* (2011).

The estimates of heritability for kernel yield per plant were high (83.54%) and genetic gain (34.99) was also high for this trait These results are in accordance with the Venkatramana (2001), Dashora and Nagda (2002), Parmeshwarapa *et al.* (2004), John *et al*. (2007), Kadam *et al.* (2007), Giri *et al*. (2009), Meta and Monpara (2010), Nandini *et al.* (2011), Zaman *et al.* (2011), John *et al*. (2013) and Rao *et al*. (2014). This indicated that the trait was under the control of additive gene action.

4.3.8 100 kernel weight

The results pertaining to genetic variability for 100- kernel weight indicated that genotypic coefficient of variation (8.54 %) and phenotypic coefficient of variation (11.80 %) were moderate for this trait. Similar results were obtained by Prasad *et al.* (2002) and Mothilal *et al.* (2004).

100-kernel weight expressed moderate heritability (52.32 %) and low genetic gain (12.72 %).

4.3.9 Sound mature kernel (%)

Sound mature kernels showed low estimates of genotypic coefficient of variation (4.42 %) and phenotypic coefficient of variation (5.50 %). 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 (64.79 %) were moderate and genetic gain (7.34 %) was also low. This indicated the impact of non additive gene effect.

4.3.10 Shelling percentage (%)

Magnitude of genetic parameters for shelling percentage indicated that estimates of genotypic coefficient of variation (5.24 %) and phenotypic coefficient of variation (6.48 %) were low for this character, indicating narrow base of variability for shelling out-turn in the material studied. These results are in close agreement with the earlier reports of Nath and Alam (2002), Mothilal *et al.* (2004) and Vishnuvardhan *et al.* (2012).

The moderate heritability (65.30 %), with low genetic gain (8.72 %) was revealed for shelling percentage. While moderate heritability coupled with moderate genetic gain was reported by Dashora and Nagda (2002) and John *et al.* (2013).

4.3.11 Biological Yield per plant

The estimates of genotypic (7.47 %) and phenotypic (11.85 %) 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 in broad sense (39.76 %) was low and genetic gain (9.70 %) was also low for this trait. The low value of heritability as well as genetic gain

indicated role of non additive gene action. Selection would not be effective for this trait.

4.3.12 Harvest Index

The genotypic coefficient of variation (10.80 %) and phenotypic coefficient of variation (13.66 %) for harvest index were moderate in magnitude. On the contrary, the higher estimates of GCV & PCV for harvest index were reported by Prasad *et al*. (2002), Makhan *et al*. (2003), Kadam *et al.* (2007) and Yadav *et al.* (2014).

The estimates of heritability (62.57 %) were moderate and genetic gain (17.60 %) were low to moderate for this trait. Moderate heritability, coupled with low to moderate genetic gain was also earlier reported by Prasad *et al*. (2002) and *John et al.* (2013).

4.3.13 Dormancy

Dormancy showed high estimates of genotypic coefficient of variation (20.18 %) and phenotypic coefficient of variation (22.92 %).

The estimates of heritability (77.57 %) were high and genetic gain (36.62 %) were very high. The high heritability coupled with high genetic gain indicated that the character is governed by additive gene effects and selection for this character will help in improvement. Similar result were also reported by Patil and Bhapkar (1987).

4.3.14 Oil content (%)

Estimates of oil content revealed that genotypic coefficient of variation (6.28%) and phenotypic coefficient of variation (6.54 %) were low in magnitude for this character. Similar findings for low amount of genetic variability for oil content in groundnut were also reported by Prakash *et al*. (2000) and Cholin *et al.* (2010).

The estimates of heritability (92.17 %) were high and genetic gain (12.41 %) for oil content were low. High heritability coupled with low genetic gain were also earlier reported by Prakash *et al.* (2000), Venkatramana et al. (2001) Dashora and Nagda (2002), and Cholin *et al.* (2010).

4.3.15 Protein content (%)

Estimates of protein content revealed that genotypic coefficient of variation (7.99 %) and phenotypic coefficient of variation (8.30 %) were low in magnitude for

this character. Similar findings for low amount of genetic variability for seed protein content in groundnut were also reported by Cholin *et al.* (2010).

The estimates of heritability (92.74 %) were high and genetic gain (15.85 %) for seed protein content were low. High heritability coupled with low genetic gain were also earlier reported by Cholin *et al.* (2010) and Yadav *et al.* (2014).

Thus, estimates of genotypic parameters revealed that differences between the estimates of GCV and PCV were found high for most of the characters. Higher estimates of GCV were observed for number of mature pods per plant (18.40 %), dry pods yield per plant (17.50 %), kernel yield per plant (18.58 %) and dormancy (20.18 %). Whereas, moderate estimates were found for number of branches per plant (13.61 %) and harvest index (10.18 %). For days to 50 per cent flowering (7.37 %), days to maturity (3.54 %), plant height (8.10 %), sound mature kernels (4.42 %), shelling percentage (5.24 %), oil content (6.28 %) and protein content (7.99 %) both GCV and PCV estimates were found low. For biological yield per plant (7.47 %) and 100-kernel weight (8.54 %) estimates of GCV were found low but PCV were found moderate.

The estimates of heritability were moderate to high for all the characters. However, maximum heritability was found for protein content (92.74 %) followed by oil content (92.17 %), days to 50 per cent flowering (92.10 %), kernel yield per plant (83.54 %) and dry pod yield per plant (82.94 %). While, maximum genetic gain was observed for dormancy (36.62 %) followed by kernel yield per plant (34.99 %), dry pod yield per plant (32.82 %) and number of matured pods per plant (32.07 %).

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 4.3 and 4.4).

In the present investigation, correlation coefficients were estimated among 15 characters to find out association of dry pod yield per plant with its components at genotypic (r_g) as well as phenotypic (r_p) levels. The perusal of table revealed that, genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlations for all the characters studied indicating negligible effect of environment. These findings were in accordance with Venkatramana (2001).

4.4.1 Correlation between dry pod yield per plant and other characters:

A perusal of Table 4.3 revealed that dry pod yield per plant was positively and significantly correlated at both genotypic as well as phenotypic level with kernel yield per plant (rg =0.96**, rp =0.95**), 100-kernel weight (rg =0.75**, rp =0.39**), Sound mature kernels (rg =0.62**, rp =0.50**) and biological yield per plant (rg =0.81**, rp =0.69**) . These findings are in accordance with Dashora and Nagda (2002), Sumathi and Muralidharan (2007), Mane *et al.* (2008), Giri *et al.* (2009), John *et al.* (2009), Raut *et al.* (2010), Korat *et al.* (2010), Shinde *et al.* (2010), Awatade *et al.* (2010), Vaithiyalingan *et al.* (2010), Dhaliwal *et al*. (2010), Vekariya *et al.* (2011), Babariya and Dobariya (2012), Kumar *et al.* (2012), Kahate *et al.* (2014) and Rao *et al.* (2014).

4.4.2 Correlation between kernel yield per plant and other characters:

A perusal of Table 4.4 revealed that kernel yield per plant was positively and significantly correlated at both genotypic as well as phenotypic level with number of mature pods per plant (rg =0.91**, rp =0.68**), dry pod yield per plant (rg =0.96**, rp =0.95**), 100-kernel weight. (rg =0.73**, rp =0.38**), sound mature kernels (rg =0.60**, rp =0.50**), shelling percentage (rg =0.38**, rp =0.35**) and biological yield per plant (rg =0.72**, rp =0.65**). These findings are in accordance with Jayalakshmi *et al*. (2000), Mahalakshmi *et al.* (2005), Sumathi and Muralidharan (2007), Awatade *et al.* (2010) and Shobha *et al*. (2012).

4.4.3 Correlation among different characters:

A perusal of table 4.5 revealed existence of significant positive correlation of days to 50 % flowering with number of branches per plant (rg =0.29**) at genotypic level while positive correlation at phenotypic level (rp =0.15) and dormancy (rg =0.25*) at genotypic level while positive correlation at phenotypic level (rp =0.15). However negative correlation between days to 50 per cent flowering and 100-kernel

weight was also reported by Mane *et al.* (2008). Days to maturity exhibited significant positive correlation with dormancy (rg =0.27**) at genotypic level while positive correlation at phenotypic level (rp =0.12). Further, plant height exhibited significant positive correlation with protein content (rg = 0.22**) at genotypic level while positive correlation at phenotypic level (rp=0.15). Number of branches per plant showed significant positive correlation with sound mature kernel (rg = 0.32**, rp=0.36**) and biological yield per plant (rg =0.89**, rp =0.42**) at both genotypic as well as phenotypic level. Similarly, 100- kernel weight also exhibited positive correlation with number of branches per plant (rg =0.30**, rp =0.18), sound mature kernel (rg = 1.13, rp=0.76**), biological yield per plant (rg =1.37, rp =0.35**) and harvest index (rg = 0.17, rp=0.24**) at genotypic and phenotypic levels (Table 4.5).

Table 4.3: Genotypic and phenotypic correlation coefficients between dry pod yield per plant and other characters in groundnut

S. No.	Characters	Genotypic Correlation Coefficient (r_g).	Phenotypic Correlation Coefficient (r_p).
1.	Days to 50% flowering	0.08	0.06
2.	Days to maturity	-0.47**	-0.20
3.	Plant height (cm)	-0.08**	-0.03*
4.	Number of branches per plant	0.21	0.21*
5.	Number of mature pods per plant	1.02	0.75*
6.	Kernel yield per plant (g)	0.96**	0.95**
7.	100-kernel weight (g)	0.75**	0.39**
8.	Sound mature kernels (%)	0.62**	0.50**
9.	Shelling percentage	0.11	0.04
10.	Biological yield per plant (g)	0.81**	0.69**
11.	Harvest index	1.03	0.77**
12.	Dormancy (days)	0.08	0.10
13.	Oil content (%)	-0.77**	-0.65**
14.	Protein content (%)	-0.34**	-0.30**

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

Table 4.4: Genotypic and phenotypic correlation coefficients between kernel yield per plant and other characters in groundnut

S. No.	Characters	Genotypic Correlation Coefficient (r_g).	Phenotypic Correlation Coefficient (r_p).
1.	Days to 50% flowering	0.02	-0.00
2.	Days to maturity	-0.49**	-0.21**
3.	Plant height (cm)	-0.04	0.06
4.	Number of branches per plant	0.16	0.13
5.	Number of mature pods per plant	0.91**	0.68**
6.	Dry pod yield per plant (g)	0.96**	0.95**
7.	100-kernel Weight. (g)	0.73**	0.38**
8.	Sound mature kernels (%)	0.60**	0.50**
9.	Shelling percentage (%)	0.38**	0.35**
10.	Biological yield per plant (g)	0.72**	0.65**
11.	Harvest index (%)	1.04	0.73**
12.	Dormancy	0.09	0.06
13.	Oil content (%)	-0.74**	-0.64**
14.	Protein content (%)	-0.33**	-0.30**

** Significant at 1% level of significance.

Likewise, sound mature kernel showed significant positive correlation at genotypic as well as phenotypic levels with number of mature pods per plant (rg =0.32**, rp =0.36**) Sumathi and Muralidharan (2007) also reported positive and significant correlation between number of mature pods per plant with sound mature kernel, 100- kernel weight (rg =1.13, rp=0.76**), biological yield per plant (rg =0.67**, rp =0.40**) and harvest index (rg = 0.48**, rp=0.33**). Character shelling percentage showed positive correlation with plant height (rg =0.20, rp =0.31**), and harvest index (rg =0.33**, rp =0.05) at both genotypic as well as phenotypic level.

Whereas, biological yield per plant exhibited significant positive correlation with number of branches per plant (rg =0.51**, rp =0.33**), number of mature pods

per plant (rg =0.89**, rp =0.42**), 100- kernel weight (rg = 1.37, rp=0.35**), sound mature kernel (rg = 0.67**, rp=0.40**), harvest index (rg = 0.75**, rp=0.08) and dormancy (rg =0.39**, rp =0.15) either at genotypic or at both the level.

Harvest index showed positive correlation with number of mature pods per plant (rg =1.01, rp =0.66**), 100- kernel weight (rg = 0.17, rp=0.24*), sound mature kernel (rg = 0.48**, rp=0.33**), shelling percentage (rg =0.33**, rp =0.05**) and biological yield per plant (rg = 0.75**, rp=0.08) at both phenotypic and genotypic levels.

Dormancy exhibited positive correlation with days to 50 per cent flowering (rg =0.25*, rp =0.15), days to maturity (rg =0.27*, rp =0.66**), and biological yield per plant (rg =0.39**, rp =0.15) at both phenotypic and genotypic level. Oil content showed negative correlation with days to 50 per cent flowering (rg = -0.05, rp = -0.04), number of branches per plant (rg = -0.15, rp = -0.14), number of mature pods per plant (rg = -0.67**, rp = -0.57**), 100- kernel weight (rg = -0.28**, rp= -0.26*), sound mature kernel (rg = -0.44**, rp= -0.27**), shelling percentage (rg = -0.12, rp = -0.11), biological yield per plant (rg = -0.94**, rp= -0.50**) harvest index (rg = -0.60**, rp= -0.48**) and dormancy (rg = -0.14, rp = -0.15). Protein content showed negative correlation with days to maturity (rg = -0.05, rp= -0.04), number of mature pods per plant (rg = -0.38**, rp = -0.32**), 100- kernel weight (rg = -0.31**, rp= -0.28**), sound mature kernel (rg = -0.37**, rp= -0.29**), shelling percentage (rg = -0.03, rp = -0.05), biological yield per plant (rg = -0.43**, rp= -0.20) harvest index (rg = -0.24*, rp= -0.25*) and dormancy (rg = -0.01, rp = -0.01) at both genotypic as well as phenotypic level.

Present experimental findings revealed that 100-kernel weight, sound mature kernel and biological yield per plant are important contributing traits for dry pod yield per plant because these showed high magnitude of significant positive correlation with dry pod yield. Similarly number of mature pods per plant, 100-kernel weight, sound mature kernel, shelling percentage and biological yield per plant are important traits for kernel yield because they showed significant positive correlation with kernel yield. Hence, these traits can be used for selection of both high dry pod yield as well as high kernel yield.

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

s.no.	Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of mature pods per plant	Dry pod yield per plant (g)	Kernel yield per plant (g)	100-Kernel weight (g)	Sound mature k ernel (SMK) %	Shelling percentage (%)	Biological yield per plant (g)	Harvest index (%)	Dormancy	Oil content (%)	Protein content (%)
1	Days to 50 percent flowering		0.05	-0.02	0.29**	0.03	0.08	-0.02	-0.09	-0.19	-0.30**	-0.03	0.15	0.25*	-0.05	0.17
2	Days to maturity	0.02		-0.24*	0.01	-0.07	-0.47**	-0.49**	0.21	-0.31**	-0.13	-0.49**	-0.35**	0.27*	0.04	-0.05
3	Plant height (cm)	0.05	-0.06		-0.18	-0.19	-0.08	-0.04	0.02	-0.15	0.20	-0.26*	0.09	-0.18	0.17	0.22*
4	Number of branches per plant	0.15	0.03	-0.13		0.10	0.21	0.16	0.30**	0.20	-0.12	0.51**	0.01	-0.11	-0.15	0.07
5	Number of mature pods per plant	-0.02	-0.13	-0.07	0.17		1.02	0.91**	0.15	0.32**	-0.11	0.89**	1.01	0.07	-0.67**	-0.38**
6	Dry pod yield per plant (g)	0.06	-0.20	-0.03	0.21*	0.75**		0.96**	0.75**	0.62**	0.11	0.81**	1.03	0.08	-0.77**	-0.34**
7	Kernel yield per plant (g)	-0.00	-0.21*	0.06	0.13	0.68**	0.95**		0.73**	0.60**	0.38**	0.72**	1.04	0.09	-0.74**	-0.33**
8	100-Kernel weight (g)	-0.10	-0.12	-0.11	0.18	0.18	0.39**	0.38**		1.13	0.10	1.37	0.17	-0.42**	-0.28**	-0.31**
9	Sound mature kernel (SMK)(%)	-0.17	-0.17	-0.10	0.17	0.36**	0.50**	0.50**	0.76**		0.12	0.67**	0.48**	0.06	-0.44**	-0.37**
10	Shelling percentage (%)	-0.17	-0.09	0.31**	-0.20	-0.03	0.04	0.35**	0.06	0.13		-0.17	0.33**	0.05	-0.12	-0.03
11	Biological yield per plant (g)	0.04	-0.01	-0.02	0.33**	0.42**	0.69**	0.65**	0.35**	0.40**	0.00		0.75**	0.39**	-0.94**	-0.43**
12	Harvest index (%)	0.05	-0.24*	-0.02	0.01	0.66**	0.77**	0.73**	0.24*	0.33**	0.05	0.08		-0.14	-0.60**	-0.24*
13	Dormancy	0.15	0.12	-0.25*	-0.00	0.13	0.10	0.06	-0.13	0.03	-0.10	0.15	0.03		-0.14	-0.01
14	Oil content (%)	-0.04	0.04	0.09	-0.14	-0.57**	-0.65**	-0.64**	-0.26*	-0.27**	-0.11	-0.50**	-0.48**	-0.15		0.24*
15	Protein content (%)	0.19	-0.04	0.15	0.02	-0.32**	-0.30**	-0.30**	-0.28**	-0.29**	-0.05	-0.20	-0.25*	-0.01	0.25*	

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

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 fourteen characters. Out of these fourteen characters only two i.e. kernel yield per plant and sound mature kernel 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.

(i) Kernel yield per plant

A perusal of Table-4.6 indicated that the highly significant positive correlation of kernel yield per plant with dry pod yield per plant (0.96**) was mainly due to its high direct effect (2.28). These results are in accordance with the findings of Nagda *et al*. (2001), Dashora and Nagda (2002), Sumathi and Muralidharan (2007), Giri *et al.* (2009), Awatade *et al.* (2010), Raut *et al*. (2010), Dhaliwal *et al*. (2010), Vekariya *et al.* (2011), Kumar *et al*. (2012), Nandini and Savithramma (2012) and Kahate *et al.* (2014).

(ii) Sound mature kernel

A perusal of Table-4.6 indicated that the significant positive correlation of sound mature kernel with dry pod yield per plant (0.62**) was mainly due to its indirect effect through kernel yield per plant (1.37). While direct effect of sound mature kernel with dry pod yield per plant was negative in magnitude (-0.11). Similar results were also reported by Sumathi and Muralidharan (2007).

Table 4.6: Direct (diagonal) and indirect effects of different correlated characters towards dry pod yield per plant in Groundnut (*Arachis hypogaea* L.)

SN	Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches/ plant	Number of mature pods/ plant	Kernel yield/ plant (g)	Sound mature kernel (SMK) %	Dormancy	Oil content (%)	Protein content (%)	Genotypic Correlation Coefficient
1	Days to 50% flowering	**0.22**	0.03	0.00	-0.05	-0.02	-0.04	0.02	-0.07	-0.02	0.01	0.08
2	Days to maturity	0.01	**0.57**	0.04	-0.00	0.06	-1.11	0.03	-0.08	0.01	-0.00	-0.47**
3	Plant height (cm)	-0.01	-0.13	**-0.16**	0.03	0.14	-0.09	0.02	0.05	0.05	0.01	-0.08
4	Number of branches per plant	0.06	0.01	0.03	**-0.16**	-0.07	0.37	-0.02	0.03	-0.05	0.00	0.21
5	Number of mature pods per plant	0.01	-0.04	0.03	-0.02	**-0.75**	2.07	-0.04	-0.02	-0.21	-0.02	1.02
6	Kernel yield per plant (g)	-0.00	-0.28	0.01	-0.03	-0.68	**2.28**	-0.07	-0.03	-0.23	-0.01	0.96**
7	Sound mature kernel (SMK) %	-0.04	-0.18	0.02	-0.03	-0.24	1.37	**-0.11**	-0.02	-0.14	-0.02	0.62**
8	Dormancy	0.05	0.15	0.03	0.02	-0.05	0.21	-0.01	**-0.28**	-0.04	-0.00	0.08
9	Oil content (%)	-0.01	0.02	-0.03	0.02	0.50	-1.69	0.05	0.04	**0.31**	0.01	-0.77**
10	Protein content (%)	0.04	-0.03	-0.03	-0.01	0.28	-0.75	0.04	0.00	0.08	**0.04**	-0.34**

Residual effect = 0.4420

Residual effect

The value of residual effect of undefined factors (Table 4.6) was 44 %. This residual effect of path analysis indicated that 95 % variability for dry pod yield could be attributed to variation in 10 independent characters considered in this study and 5 % variation in yield was attributable to some undefined factors.

Highest positive direct effect on dry pod yield was exhibited by kernel yield per plant (2.28). Highest positive indirect effect on dry pod yield was exhibited by number of matured pods per plant through kernel yield per plant (2.07). Similarly, oil content through number of matured pods per plant (0.50) and number of branches per plant through kernel yield per plant (0.37) also showed high indirect effects.

However, as revealed from the Table-4.6 the traits like kernel yield per plant, sound mature kernel, number of matured pods per plant and number of branches per plant can be selected for further crop improvement in groundnut.

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.

(i) Composition of clusters:

Ninty three genotypes were grouped into VIII clusters on the basis of observed distance among genotypes within a cluster as compared to genotypes in other cluster in **Table 4.7**. Cluster VI contains maximum number of genotypes i.e. 18 followed by 16 in cluster VII, 15 in cluster I, 12 in cluster V and cluster VIII, 10 in cluster IV, 7 in cluster III and 3 in cluster II. 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 4.7: Groundnut genotypes included in each cluster

Clusters	Number of genotypes	Name of genotypes
I	15	UG-59, UG-69, UG-88, UG-90, UG-107, UG-112, UG-114, UG-115, UG-116, UG-119, UG-123, UG-143, UG-151, TG37A and UG-5
II	3	UG-85, UG-104 and UG-141
III	7	UG-10, UG-15, UG-20, UG-64, UG-132, UG-136 and UG-151
IV	10	UG-9, UG-16, UG-86, UG-94, UG-95, UG-113, UG-129, UG-130, UG-134 and UG-142
V	12	UG-62, UG-65, UG-91, UG-100, UG-128, UG-133, UG-135, UG-137, UG-138, UG-144, UG-152 and PM-2
VI	18	UG-3, UG-17, UG-19, UG-22, UG-24, UG-56, UG-61, UG-68, UG-105, UG-117, UG-124, UG-127, UG-140, UG-145, UG-146, UG-150, UG-154 and UG-156
VII	16	UG-4, UG-6, UG-21, UG-57, UG-60, UG-71, UG-92, UG-102, UG-110, UG-110, UG-125, UG-139, UG-147, UG-148, UG-149, UG-153 and UG-157
VIII	12	UG-67, UG-87, UG-89, UG-93, UG-103, UG-108, UG-109, UG-111, UG-118, UG-120, UG-122 and UG-126

(ii) Intra and inter cluster divergence:

As evident from **Table 4.8**, average inter cluster values were maximum between cluster III and VIII on the basis of analysis. At intra cluster level, maximum values were recorded for cluster V followed by cluster IV, cluster VI, cluster VII, cluster VIII, cluster I, cluster II and cluster III. 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. Sarker *et al.* (2004), Khote *et al.* (2010) and Kumar *et al.* (2010) also reported maximum and minimum inter and intra cluster distances in groundnut.

Table 4.8: Average intra and inter-cluster Euclidian distances in 93 genotypes of groundnut

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**8.99**	19.05	16.50	11.34	11.09	8.97	11.57	14.45
II		**8.12**	16.39	15.25	20.87	14.55	17.88	18.45
III			**7.62**	14.80	11.33	18.45	11.81	23.93
IV				**9.69**	12.13	10.19	14.93	11.98
V					**10.09**	14.93	12.72	20.93
VI						**9.25**	13.71	12.19
VII							**9.15**	22.50
VIII								**9.09**

Bold number = intra-cluster distance

Thus, cluster VIII displayed high inter cluster distances from cluster II, cluster VI, cluster VII, cluster V and cluster IV. Cluster VIII also possessed genotypes with high dry pod yield per plant, number of mature pods per plant, 100-kernel weight and sound mature kernel. Therefore, crosses between such genotypes are expected to give desirable transgressive segregants.

5. SUMMARY AND CONCLUSIONS

The present investigation entitled **"Character Association and Genetic Divergence in Groundnut (*Arachis hypogaea* L.)"** was carried out on 93 groundnut genotypes to elicit information on the genetic variability, correlation coefficients, path coefficients and genetic divergence for yield and its contributing characters.

The groundnut genotypes were evaluated in augmented design in 6 blocks during *kharif*- 2014 at the Instructional Farm, College of Technology and Engineering (CTAE), Maharana Pratap University of Agriculture and Technology, Udaipur. Observations were recorded on five competitive plants for plant height, number of branches per plant, number of mature pods per plant, dry pod yield, kernel yield, 100-kernel weight, sound mature kernel, shelling percentage, biological yield per plant, harvest index, dormancy, oil content and protein content**.** While observation for days to 50% flowering and days to maturity were recorded on plot basis.

- Mean squares due to genotypes for all the characters were significant except 100-kernel weight and biological yield per plant, 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 (27 to 36), days to maturity (99 to 114), plant height (23.86 to 38.76 cm), number of branches per plant (4.60 to 8.40), number of mature pods per plant (7 to 15.80), dry pod yield per plant(8.80 to 18.60 g), shelling percentage (60 to 75 %), sound mature kernel (75.28 to 93.24 %), kernel yield per plant(5.40 to 13.80 g), harvest index (25.41 to 46.72 %), dormancy (4 to 10 days), oil content (34.18 to 44.86 %) and protein content (18.42 to 26.87 %). Genotypes UG-108, UG-109, UG-67 and UG-120 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., oil content (GCV 6.28 % and PCV 6.54 %), days to 50% flowering (GCV 7.37 % and PCV 7.68 %), protein content (GCV 7.99 % and PCV 8.30 %), days to maturity (GCV 3.54 % and PCV 4.29 %), sound mature kernel (GCV 4.42 % and PCV 5.50 %), shelling percentage (GCV 5.24 % and PCV 6.48 %), plant height

(GCV 8.10 % and PCV 9.54 %) indicating that without much influence of environment, entire genetic determinants are translated into phenotype.

- Maximum heritability was observed for protein content followed by oil content, days to 50% flowering, kernel yield per plant, dry pod yield per plant, dormancy, number of branches per plant, plant height, number of mature pods per plant, days to maturity, shelling percentage, sound mature kernel and harvest index. While maximum genetic gain was observed for dormancy followed by kernel yield per plant, dry pod yield per plant, number of mature pod per plant, number of branches per plant and harvest index. 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 at both genotypic and phenotypic levels with kernel yield per plant, 100-kernel weight, sound mature kernels and biological yield per plant. Similarly, kernel yield per plant also showed positive and significant correlation with number of mature pod per plant, dry pod yield per plant, 100-kernel weight, sound mature kernel, shelling percentage and biological yield 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 kernel yield per plant (2.28) followed by days to maturity (0.57), oil content (0.31) and days to 50% flowering (0.22). While, high indirect effect on dry pod yield was exhibited by number of mature pods per plant (2.07), oil content (0.50), number of branches per plant (0.37) and protein content (0.28).
- As per cluster analysis 93 genotypes were divided into VIII clusters. Average inter cluster values were maximum between cluster III and cluster VIII. Cluster VIII possessed genotypes with high dry pod yield, number of mature pods per plant and 100-kernel weight.
- From, the present investigation it can be concluded that genotypes UG-67, UG-108, UG-109 and UG-120 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 uptill uprooting. Existence of diversity among genotypes in different clusters provided scope of getting transgressive segregants on making crosses among them.

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