Variability Assessment at Morphological and Molecular Level in Groundnut (*Arachis hypogaea* L.)

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VADODARIYA GOPAL DHIRAJ BHAI

Thesis

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CERTIFICATE-I

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This is to certify that **Mr. Vadodariya Gopal D.** has successfully completed the Comprehensive Examination held on 23/03/2013 as required under the regulation for the degree of **Master of Science in Agriculture**.

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Dated:16 /06 /2013

This is to certify that the thesis entitled "**Variability Assessment at Morphologocal and Molecular Level 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. Vadodariya Gopal D.** 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 15/06/2013.

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Dated: 19 /07/2013

This is to certify that the thesis entitled **"Variability Assessment at Morphologocal and Molecular Level in Groundnut (*Arachis hypogaea* L.)"** submitted by **Mr. Vadodariya Gopal D.** to the Maharana Pratap University of Agriculture and Technology, Udaipur in partial fulfilment of the requirements for the degree of **Master of Science in Agriculture** in the subject of **Plant Breeding and Genetics** after recommendation by the external examiner was defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination on his thesis has been found satisfactory; we therefore, recommend that the thesis be approved.

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This is to certify that **Mr. Vadodariya Gopal D,** 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 **"Variability Assessment at Morphologocal and Molecular Level in groundnut (Arachis hypogaea L.)"** which were suggested by the external examiner and the advisory committee in the oral examination held on 19/07/2013. The final copies of the thesis duly bound and corrected were submitted on 27/07/2013, are enclosed herewith for approval.

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Enclose: One original and three copies of bound thesis forwarded to the Director Resident Instructions, Maharana Pratap University of Agriculture and Technology, Udaipur through the Dean, Rajasthan College of Agriculture, Udaipur.

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ABSTRACT

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The present investigation entitled "Variability Assessment at Morphological and Molecular level in Groundnut (*Arachis hypogaea* L.)" was conducted with 25 genotypes (including National and State released varieties) during *Kharif*- 2012 at the Instructional Farm, College of Technology and Agricultural Engineering, Maharana Pratap University of Agricultural and Technology, Udaipur. The genotypes were planted in a randomized block design with three replications.

The observations were recorded for 13 characters viz., days to 50% 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 out turn, biological yield per plant, harvest index and seed oil content on five randomly selected plants from each genotype under all replications for all the above characters except days to flowering and days to maturity which were recorded on plot basis and average value was subjected to analysis of variance, estimation of variability parameters, correlation.

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 plant height, number of mature pods per plant, dry pods yield per plant, Kernel yield per plant, Biological yield per plant, 100 Kernel weight and oil content. Maximum heritability was found for 100 kernel weight followed by oil content and sound mature kernels. While, maximum genetic gain was observed for biological yield per plant followed by dry pods yield per plant and number of mature pods per plant.

Association study revealed that dry pod yield per plant was positively and significantly correlated at both genotypic and phenotypic level with number of branches per plant, number of mature pods per plant and biological yield per plant. Kernel yield per plant was positively and significantly correlated at both genotypic and phenotypic level with number of branches per plant, number of mature pods per plant and biological yield per plant.

Present experimental findings revealed that number of branches per plant, number of mature pods per plant and biological yield per plant sound mature kernel and shelling

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percentage are important yield contributing traits because they showed high magnitude of positive correlation. Hence, these traits can be used for selection of both high dry pod yield as well as high kernel yield.

Fifteen markers were used for RAPD analysis and 13 markers showed amplification. A dendrogram was constructed from similarity coefficients obtained for DNA banding pattern. The groups/ clusters obtained by dendrogram could also be distinguished by similarity for the morphological characteristics within each group. Such an association may used for more effective breeding programmes.

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1. INTRODUCTION

The cultivated Groundnut (*Arachis hypogaea* L.) is a self pollinated, annual, herbaceous legume, growing upright and has indeterminate growth habits. Groundnut is believed to be originated from South America (Southern Bolivia/North West America region). It has a wide range of adaptability in varying agro-climatic conditions and soils, which has made its cultivation possible in most of the tropical and sub-tropical countries in the world. It is a major oil seed crop of the world with oil content around 40-54% and extensively used for cooking purposes. Its oil is a rich source of vitamin A, B and E. Besides being an important source of vegetable oil, it is also used as an important source of food, feed, nutrition, and fodder. Groundnut is also known as the "King" of oilseeds or "Wonder nut" or "poor man's cashew nut".

Groundnut kernels are consumed as raw, boiled, roasted or fried products and also used in a variety of culinary preparations like peanut candies, butter, peanut milk and chocolates (Desai *et al.,* 1999). Cake left after extraction of the oil is an excellent feed for livestock. Vegetative parts of groundnut like leaf and stem are good source of nutritionally high quality fodder for farm animals.

In India, the area under Groundnut cultivation comprises marginal lands where the crop is grown under rainfed conditions. It is grown in an area of about 6.0 million ha with a production of 7.0 million tones of pods per annum (annual report of DGR Junagarh, kharif 2011). Currently, six states viz., Gujarat, Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra and Rajasthan accounts for more than 90% of the groundnut area and production of the country. It is a segmental amphidiploid (2n=4x=40) with basic chromosome number (x) of 10. The groundnut is characterized by cleistogamy and hence, it is highly self-pollinated in nature (Knauft *et al.,* 1995).

The cultivated groundnuts can be divided broadly into two groups i.e. the bunch and spreading or semi-spreading depending upon their branching pattern. The bunch groups consist of Spanish (*sub.sp. fastigiata var. vulgaris*) and Valencia (*sub.sp. fastigiata var. fastigiata*) where as the spreading and semi-spreading groups consist of sub sp. Virginia bunch and Virginia runner respectively (Rao, 1980).

In Rajasthan, it is mainly cultivated on an area of 4.15 lakh hectares with a production and productivity of 8.00 lakh tones and 1931 kg/ha, respectively (annual report of DGR Junagarh, kharif 2012). Under present scenario, the major area of groundnut in Rajasthan is represented by Jaipur, Chittorgarh, Tonk, Sawai Madhopur, Dausa, Bikaner and Bhilwara.

Genetic improvement for quantitative traits depends on the nature and amount of variability present in the genetic stock and the extent to which the desirable traits are heritable. Since, groundnut pods develop below the ground level hence, genotypes for yield cannot be screened or evaluated prior to harvest. Therefore, association studies are also very important.

Yield is the most important character for improvement of a crop and it has a complex inheritance governed by large number of genes and greatly affected by environmental factors. Therefore, selection made in field is not likely to reliable as characters are subjected to large non-genetic variability. DNA polymorphism can provide an opportunity to measure genetic variability more precisely because DNA markers are potentially unlimited in number and not affected by the environment. DNA analysis technique can add in assessment of variability that can be linked to phenotypic traits. Genotypic selection at the DNA level can be exploited in marker assisted selection to identify desirable genotypes.

The use of molecular marker technique which is independent of environmental factors like RAPD etc; using gel electrophoresis techniques offers significant advantage for species identification in that they are rapid, relatively cheap and eliminate the need to grow plants up to maturity.Therefore, attempts will be made to study molecular techniques for varietal identification of groundnut.

Keeping in view the above, the present investigation was carried out to fulfill the following objectives in ground nut (*Arachis hypogaea* L.) :

1. To estimate the genetic variability, heritability and genetic advance for yield and other yield attributing characters in groundnut.

2. To find out the genotypic and phenotypic correlation between yield and other yield contributing characters in groundnut.
3. To characterize groundnut genotypes through RAPD markers.

2. REVIEW OF LITERATURE

In the present investigation genetic variability, correlation and molecular characterization for yield and its component characters have been studied in groundnut. The literature pertaining to objectives of this investigation have been reviewed briefly under the following sub-heads:

2.1 Variability parameters

2.2 Correlation coefficients

2.3 Molecular characterization

2.1 VARIABILITY PARAMETERS

The existence of genetic variability is prerequisite for any crop improvement programme; however, loss of locally adapted variable material has been rapid which, need to be maintained. The variability existing among homozygous genotypes/ population is generally considered as free variability, which can be exploited for genetic advancement through selection. This together with information on heritability and genetic advance would be rewarding in designing an effective breeding programme. The genetic variability is determined with the help of certain genetic parameters *viz.* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and heritability estimates.

Heritability is the heritable portion of phenotypic variance and it is a good index of extent of transmission of a character from parents to their off-springs. Heritability in broad sense is the ratio of genotypic variance to phenotypic variance. Its estimation is important because it determines the expressivity of genes being carried by a genotype. If the heritability of a character is high, the phenotypic value provides a fairly close measure of the genotypic value and thus breeder can base his selection on the phenotypic performance. There by the knowledge of heritability helps the plant breeder in pre-assessing the results of selection for a particular character. However, for predicting the effect of selection, heritability estimates along with genetic advance are more useful than the heritability estimates alone. The review of literature pertaining to variability parameters in groundnut is presented in the subsequent paragraphs.

Chauhan and Shukla (1985) studied 20 groundnut varieties and revealed high genotypic coefficient of variation for pod yield per plant in both the groups, for primary

branches in spanish group and mature pods per plant in virginia group. The genotypic coefficient of variation value was low for shelling out-turn, oil content and days to maturity in both groups. High heritability along with high genetic advance as per cent of mean was observed for shelling out-turn, oil content and days to maturity in spanish group and for primary branches in virginia group. These results indicated the influence of additive gene effect; hence, selection for these characters would prove to be quite effective. Oil content and shelling out-turn showed low genetic gain in both the groups.

Bhagat *et al.* (1986) reported in groundnut that phenotypic coefficient of variation was greater than genotypic coefficient of variation for number of mature pods, pod weight and fodder yield. For oil content, the variability was low. Heritability and genetic advance as per cent of mean was high for pod yield per plant, shelling out-turn and 100-seed weight, suggested that selection based on phenotypic performance would be fruitful for improvement in these characters.

Deshmukh *et al.* (1986) reported more or less equal estimates of PCV and GCV for plant height, 100 pod weight, 100 kernel weight, shelling out-turn and oil percentage while studying 22 varieties of virginia bunch groundnut. High heritability estimates for plant height, 100-pod weight, 100-kernel weight, shelling out-turn and oil content. 100- pod weight and 100-kernel weight also expressed high genetic advance as per cent of mean indicating the role of additive gene action in controlling these traits. They reported the possibilities of selection response based on phenotypic expression of these characters.

Kuriakose and Josheph (1986) concluded that the magnitude of genotypic and phenotypic coefficients of variation was high for pods per plant and 100-kernel weight. The magnitude of heritability was high for branches per plant, days to flowering, pods per plant, 100-pod weight, 100-kernel weight and shelling out-turn. High heritability coupled with high genetic advance as per cent of mean and high genotypic coefficient of variation for pods per plant and 100-pod weight suggested that these traits would be the most expected to express maximum response to selection.

Nadaf and Habib (1987) observed high genotypic variability for pods per plant and 100-pod weight; for pod yield per plant and other important characters variability estimates were moderate; while, oil content and shelling out-turn had low variability estimates. However, high heritability estimates were observed for days to 50% flowering, 100-pod weight and 100-kernel weight, and those were low for oil content and shelling out-turn. The

expected genetic gain was high for 100-pod weight and moderate for pod yield and 100-kernel weight. Thus, indirect selection for pod yield through pods per plant and 100-pod weight would be more rewarding.

Kale and Dhoble (1988) studied variability parameters with 7 genotypes of groundnut for 6 characters and revealed that genotypic and phenotypic coefficients of variation were high for pod yield per plant. They also observed high heritability with high genetic advance as per cent of mean for pod yield per plant and plant height. Pods per plant and 100-kernel weight had moderate value of heritability. They suggested that selection for pods per plant and plant height on the basis of *per se* performance would be effective way for improvement of these traits.

Manoharan *et al*. (1990) observed low estimates of GCV and PCV for all the characters except dry matter production and pod yield. Heritability, in broad sense, was high for all the characters except number of primary branches and pod number. Accordingly genetic advance as per cent of mean was high for all the characters except number of primary branches. The characters plant height, dry matter yield, pod weight and pod yield were preponderant by additive gene effects.

Manoharan and Ramlingam (1990) studied association of oil content with 100-kernel weight and kernel yield in virginia groundnut and reported high genotypic coefficient of variation for kernel yield followed by 100-kernel weight; while, oil content showed very low genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was observed for 100-kernel weight, while, oil content showed high heritability with low genetic advance as per cent of mean.

Reddi *et al.* (1991) studied 32 genotypes belonging to two group's virginia bunch and virginia runner groundnut in three dates of sowing. They observed that genotypic coefficient of variation and phenotypic coefficient of variation had narrow difference in magnitude for most of the characters. The sound mature kernels, 100 pod weight, 100 kernel weight and pod yield per plant had high heritability and genetic advance as per cent of mean. These traits could be relied upon for further improvement through selection.

Reddy and Gupta (1992) studied genetic variability for yield and its components using 46 diverse genotypes in three environments and reported that in all three environments the estimates of GCV and PCV had close correspondence for all the characters. The extent of variability was high for secondary branches per plant, number of mature pods, pod yield,

kernel yield and harvest index; whereas, those were low for number of primaries, 100 kernel weight and shelling out-turn. The broad sense heritability estimates were high for all the characters in all the three environments. The genetic advance as per cent of mean was high for mature pods, pod yield and harvest index in all the three environments. Thus, results indicated that due weightage should be given to mature pods per plant, pod yield, kernel yield and harvest index in groundnut improvement programme.

Manoharan and Ramlingam (1993a) reported high genotypic coefficient of variation for pod yield, plant height, kernel yield, number of mature pods and 100 pod weight. Whereas, heritability estimates were high with high genetic advance as per cent of mean for plant height, number of mature pods, 100 pod weight, 100 kernel weight and kernel yield; these characters likely to preponded by additive gene effect; hence selection would be remunerative for their improvement.

Manoharan (1993) studied heritability and genetic advance as per cent of mean with 50 genotypes of spanish bunch groundnut and found high genotypic coefficient of variation for number of immature pods and moderate for plant height, number of mature pods, 100 pod weight, pod yield, 100 kernel weight and kernel yield; while, low genotypic coefficient of variation was observed for oil content, days to 50% flowering and shelling percentage. High heritability was observed for 100 pod weight, 100 kernel weight, oil content, plant height, shelling percentage and number of mature as well as immature pods. The genetic variance as per cent of mean was high for all the above characters except shelling per cent and oil content.

Manoharan and Ramlingam (1993b) studied associations of oil content with 100 kernel weight and kernel yield in virginia groundnut and reported high genotypic coefficient of variation for kernel yield followed by 100 kernel weight; while, oil content showed very low genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was observed for 100 kernel weight; whereas, oil content showed high heritability with low genetic advance as per cent of mean.

Reddy (1994) studied variability parameters for pod yield and its eleven components in 48 genotypes of spanish groundnut. He concluded that values of phenotypic coefficient of variation were higher than corresponding genotypic coefficient of variation for all the characters. However, high GCV and PCV were recorded for pod yield, 100 pod weight and 100 seed weight. The heritability estimates were high for 100 pod weight, harvest index, 100

seed weight, plant height and shelling out-turn suggesting the possibility of selection response based on phenotypic expression. The 100 pod weight also had high magnitude of genetic advance as per cent of mean, indicating an importance of the said character in enhancing the pod yield through selection.

Ganesan and Sudhakar (1995) studied variability parameters in 28 genotypes of spanish bunch groundnut for seven characters. They reported equality of PCV and GCV for days to initial flowering, days to 50% flowering, plant height and pod yield per plant; whereas, for rest of the characters PCV estimates were higher than those of GCV. The broad sense heritability estimates were high for all the characters except number of mature and immature pods. However, only primary branches per plant and pod yield per plant had high GA as percentage of mean, thereby suggesting effectiveness of selection through these characters.

Sharma and Varshney (1995) evaluated 18 varieties of groundnut as seven bunch type growth habit, two semi-spreading and nine spreading and found high values of PCV than GCV estimates for pod yield per plant, biological yield per plant and harvest index. However, heritability estimates were high along with high GA (%) for these characters.

Uddin *et al.*(1995) evaluated 23 diverse groundnut genotypes and observed high GCV for seed yield per plant, seeds per plant, primary branches per plant, plant height and 100 seed weight. Heritability estimates were high for all the above traits. All the characters, except days to maturity and shelling percentage had moderate to high genetic advance as per cent of mean.

Vindhiyavarman and Raveendran (1996) studied genetic variability in groundnut and observed higher values of PCV in comparison to corresponding GCV for all the characters under study viz. plant height, number of branches, number of mature pods, pod weight, kernel weight, pod yield, shelling out-turn and oil content. However, broad sense heritability estimates were high for all the above characters except shelling out-turn. Whereas, estimates of GA as per cent of mean was high only for plant height.

Singh (1998) studied genetic variability in groundnut and reported that there was close correspondence between GCV and PCV values for days to first flowering, primary branches per plant, kernels per plant and immature pods per plant. The character days to first flowering expressed high heritability. Matured pods per plant, kernels per plant, pod yield per plant and test weight showed high estimates of genetic advance as per cent of mean coupled

with moderate heritability and high GCV suggesting predominant role of additive gene effect for the expression of these characters.

Vasanthi *et al*. (1998) reported greater magnitude of PCV than GCV for 100 pod weight, shelling per cent, mature kernel weight (%), haulm weight as well as pod weight per plant in groundnut. While, for the characters 100 kernel weight, days to 50% flowering and days to maturity, PCV and GCV estimates were at par. They reported high heritability estimates for all characters except pod weight per plant, while GA as per cent of mean was high for 100 pod as well as kernel weight and haulm weight.

Yadav *et al.* (1998) studied variability parameters for yield and six yield and quality attributes in 34 lines of spanish bunch groundnut. They reported that GCV and PCV estimates were high for pod yield per plant and 100 pod weight. They also observed high heritability for all the characters under study. High heritability coupled with high genetic advance as per cent of mean was observed for pod yield per plant, 100 pod weight and 100 kernel weight, indicating that selection in existing variability would be effective for improvement of these traits.

Singh and Singh (1999) studied variability parameters for pod yield and yield component characters in groundnut. They reported that days to maturity, plant height, primary branches per plant, pods per plant, pod weight per plant, shelling percentage and 100 kernel weight exhibited high heritability.

Azad and Hamid (2000) observed very close estimation of GCV and PCV for all the characters under study except primary branches per plant. High values of GCV and PCV together with high heritability and genetic advance as per cent of mean were observed for plant height, pods number and kernel as well as pod yield.

Chishti *et al.* (2000) evaluated 16 early maturing genotypes of groundnut to estimate variability parameters. They observed significant variation for all the characters expect 100 kernel weight. The estimates of PCV were higher than those of GCV for all the characters except days taken to flowering as well as maturity; for these characters those were at par with high heritability estimates.

Naazar-Ali *et al.* (2000) studied genetic variability, heritability, genetic advance and correlation coefficients with 16 groundnut varieties, high values of GCV and PCV were observed for kernel weight, pod length and pod yield. High heritability coupled with high genetic advance as per cent of mean was observed for kernel weight and pod length revealing

an importance of additive gene effect for these traits and selection pressure on these attributes would be effective for their improvement.

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

Venkatramana (2001) evaluated thirty groundnut genotypes including 20 spanish bunch and 10 virginia bunch for genetic variability parameters and reported that estimates of PCV were higher than corresponding GCV for all the characters under study. However, both PCV and GCV estimates were high for 100 kernel weight and kernel yield as well as oil yield. Whereas, heritability in broad sense was 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 preponded 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 would 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% flowering, days to maturity, shelling per cent, 100 kernel weight and oil content revealing preponderance of non-additive gene effect.

Nath and Alam (2002) evaluated 15 exotic groundnut genotypes procured from ICRISAT along with a local check (Dhaka-1)and genetic variability parameters were studied for yield and yield contributing characters. The 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, heritability estimates were higher for all the characters studied and GA as per cent of mean was also 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) evaluated 30 spanish bunch groundnut genotypes to estimate the variability parameters, they 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 effect 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 higher values of PCV than GCV for all the characters studied except days to maturity; however, estimates of GCV were low to moderate for all the characters. The heritability estimates were high along with high GA as per cent of mean for plant height and 100 pod weights.

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 estimates were high whereas, those were moderate for shelling percentage. The values of PCV were higher than GCV indicating an influence of environment in expression of all the characters.

Parmeshwarappa *et al.* (2004) studied nature and magnitude of genetic variability in 44 released varieties of groundnut. The characters pod yield per plant, kernel yield per plant, shelling out-turn and sound mature kernels showed high values of genetic coefficient of variation. An extent of heritability was moderate for days to maturity and high for days to 50% 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 pressure on *per se* performance of genotypes.

Mothilal *et al.* (2004) reported that values of GCV and PCV were high for mature pods per plant and pod yield per plant and moderate to low for plant height, branches per

plant, shelling out-turn, 100-pod weight, 100-kernel weight and sound mature kernels in groundnut. 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, indicating that weightage should be given to these characters to improve yield potential of groundnut.

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

Golakia *et al.* (2005) evaluated 24 spanish bunch groundnut genotypes to study variability parameters. They noticed close correspondence between PCV and GCV estimates for all the eleven characters studied suggesting that characters studied were less influenced by environmental factors. They also estimated high GCV and PCV for all the characters, except shelling out-turn and oil content. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, pods per plant, 100 kernel weight and kernels as well as pods yield per plant. High heritability along with low genetic advance as per cent of mean was observed for shelling out-turn. For oil content heritability was moderate. All these indicated that large portion of non-additive gene action was responsible for expressions of shelling out-turn and oil content.

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

John *et al.* (2006b) studied variability parameters in groundnut and reported that estimates of PCV were in accordance with estimates of GCV for plant height and number of primary as well as secondary branches; whereas, PCV estimates were high than those of

GCV for number of mature as well as immature pods, pod length, pod width, pod weight, shelling out-turn and kernel yield. However, both the estimates were high for number of secondary branches and number of immature pods. The broad sense heritability was high for all characters except number of mature pods, pod length, pod weight and shelling out-turn, for these traits it was moderate; most of the studied characters had moderate to high estimates of GA as per cent of mean except pod width and shelling out-turn.

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

John *et al.* (2008) reported close correspondence between GCV and PCV values for days to maturity, pod yield per plant, shelling per cent and 100-kernel weight; whereas, value of PCV was higher than corresponding GCV for days to initial flowering, number of primary branches and kernel yield per plant. All the characters had high estimates of broad sense heritability, but GA as per cent of mean was high for shelling per cent and kernel yield per plant, hence improvement in these characters would be effective on the *per se* performance of the individual.

John *et al.* (2009) evaluated 60 genotypes of groundnut to study variability parameters for seventeen characters and they reported high GCV and PCV values for all the characters except for plant height, shelling percentage and 100 kernel weight. However, low GCV and PCV values were observed for days to initiation of flowering, days to 50% flowering and number of primary branches. In general estimates of PCV were high than those of GCV for respective character. The broad sense heritability estimates were high for all the characters and estimates of GA as per cent of mean were also high for all the characters except growth attributes, days to initiation of flowering as well as 50% flowering, plant height and number of primary branches per plant.

Korat *et al.* (2009) evaluated 80 diverse genotypes of bunch groundnut for variability parameters. The estimates of PCV and GCV were high for number of secondary branches per plant and number of aerial pegs per plant; whereas, for rest of the characters those were low to moderate. The broad sense heritability estimates were high for all the characters, but

genetic advance as per cent of mean was high for pod yield per plant, number of primary branches, number of secondary branches per plant, plant height and 100 kernel weight indicating that these traits predominantly governed by additive gene action and responsive to selection for their further improvement.

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.

Shinde *et al*. (2010) evaluated 50 elite genotypes of virginia bunch groundnut for variability parameters and observed that GCV and PCV estimates were higher for pod yield per plant, number of immature pods per plant, number of mature pods per plant and biological yield per plant. High heritability was associated with high genetic advance for pod yield per plant and number of mature pods per plant. These characters were mainly under the influence of additive gene action and there is ample scope for improvement in these traits through simple selection.

Madhura *et al.* (2012) conducted an using groundnut minicoreset, comprised of 182 accessions representing hypogaea bunch (42), hypogaea runner (39), Spanish bunch (63) and fastigiata (38) obtained from NRCG, Junagad with nine cultivars (GPBD-4, JL-24, Mutant-III, TGLPS-3, DSG-1, Gangapuri, ICGS-44, GAUG-10 and Kadiri-3) during Kharif 2005. High genetic advance was observed for test weight pod yield per plant, moderate for shelling per cent, sound mature kernel and oil content and for days 50 per cent flowering and days to maturity it was low.

2.2 CORRELATION COEFFICIENTS

The knowledge of association between yield and its component characters is of immense value for breeder, because it forms a basis for selection. It is well known phenomenon that different components of yield very often exhibit considerable degree of association in both positive and negative directions among themselves and with yield as well. Therefore, understanding of correlation between characters would helpful to accumulate optimum combination of yield contributing characters in a single genotype.

The concept of correlation was given by Galton (1889), which was further elaborated by Fisher (1918) in order to initiate effective selection programme aimed at genetic improvement in economic yield of a crop. It is an index of cause in the genesis of two variables and not to causes themselves. The degree of association between yield and component characters might vary with genetic make of the material under study. Hence, it is essential to measure the correlations at genotypic and phenotypic levels.

Some of the important research results obtained on correlation coefficients studies on various characters of groundnut are presented here.

Nadaf and Habib (1989) revealed that pod yield was positively correlated with number of primary branches and number of mature pods; whereas, it was negatively associated with 100-pod weight and shelling out-turn.

Manoharan and Ramlingam (1990) evaluated 50 virginia bunch and virginia runner genotypes to study characters association of oil content with related characters. Oil content was positively correlated with seed size and seed yield. Seed size and seed yield had also positive correlation.

Manoharan *et al*. (1990) revealed that pod yield was positively correlated with number of pods, 100-pod weight, plant height and number of primary branches. Among the component characters, number of pods and 100-pod weight were positively associated with plant height, number of primary branches, dry matter yield, and harvest index. Plant height and number of primary branches were also positively associated with dry matter yield, pod number and 100-pod weight had high positive direct effect on pod yield.

Reddi *et al*. (1991) evaluated 32 diverse genotypes of groundnut under three environments. They observed positive and significant association of pod yield with kernel yield per plant, sound mature kernels, 100-kernel weight and 100-pod weight. Besides this, kernel yield per plant exhibited significant and positive correlation with all the characters studied. They suggested that direct selection for 100-kernel weight and 100-pod weight may be effective in improving the yield in groundnut.

Reddy and Gupta (1992) indicated that pod yield was significantly and positively correlated with mature pods per plant, kernel yield per plant, shelling out-turn and harvest index. Pods per plant and kernel yield per plant were significantly and positively correlated with branches per plant, 100-kernel weight and shelling out-turn.

Mishra and Yadav (1993) studied correlation in groundnut and revealed that pod yield was significantly and positively correlated with number of secondary branches, dry matter production, harvest index and number of pods per plant. Positive and significant association of dry matter production with number of primary branches and number of secondary branches was also observed.

Sharma and Varshney (1995) reported that pod yield had significant and positive association with harvest index, pods per plant, shelling percentage and 100-kernel weight; whereas, pods per plant had also significant and positive association with harvest index and shelling percentage.

Sumathi and Ramanathan (1995) observed that pod yield had significant and positive genotypic correlation with pods per plant, 100-kernel weight and kernel yield in both the generations. Number of mature pods, kernel yield, 100-pod weight, 100-kernel weight and plant height had direct positive effect on pod yield. These characters had also indirect positive effect on pod yield.

Uddin *et al.* (1995) found that kernel yield was significantly and positively correlated with days to maturity, kernels per plant, plant height and primary branches per plant; but it was negatively associated with shelling percentage and 100-seed weight. Path analysis revealed that days to maturity, primary branches per plant and nuts per plant had large direct effects on kernel yield per plant.

Sarala and Gowda (1998) studied correlation in segregating generation of inter-sub-specific cross of groundnut was carried out and they observed that number of pods per plant and 100-kernel weight were significantly and positively correlated with pod yield.

Vasanthi *et al.* (1998) reported that pod weight per plant had significant and positive correlation with sound mature kernel; whereas, it had significant negative association with days to 50% flowering. Significant and positive association between 100 pod weight and 100-kernel weight, shelling percentage and sound mature kernel percentage was also observed.

Singh and Singh (1999) revealed that positive phenotypic and genotypic correlation for all the characters as results indicated that pod weight per plant exhibited significant and positive association with days to flowering, pods per plant, plant height and primary branches per plant. The 100-kernel weight had significant and positive correlation with days to first flower, days to maturity, and number and weight of pods per plant. Primary branches per plant and days to maturity showed significant positive correlation with days to 50%

flowering, while pods per plant exhibited highly significant and positive association with plant height.

Naazar-Ali *et al.* (2000) reported that pod yield was significantly and positively correlated with kernel weight and oil content. Positive and highly significant correlation between pod length and kernel weight indicated that selection for larger kernel size could result in heavier kernel, which had close positive correlation with yield.

Chishti *et al.* (2000) evaluated 16 spanish groundnut genotypes and reported that at genotypic level all the characters *viz.*, days taken to flowering, number of pods per plant, shelling percentage, 100-kernel weight, number as well as weight of sound mature kernel and oil per cent showed positive association with pod yield; whereas, pod yield depicted negative and significant association with days taken to maturity. However, sound mature kernel per cent by weight, shelling percentage, days taken to flowering and number of pods per plant showed high positive direct effects on pod yield, while sound mature kernel per cent by number, days taken to maturity contributed high negative effects on pod yield.

Jayalakshmi *et al.* (2000) 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.

Mathews *et al*. (2001) reported that pod yield per plant had significant and positive genotypic correlation with days to flowering, days to 75% 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.

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 5 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.

Kavani *et al.* (2004) evaluated 15 genotypes of groundnut and reported that pod yield expressed significant and positive association with pods per plant, kernel yield per plant, 100-kernel weight and biomass yield. Kernel yield per plant had significant and positive

association with pods per plant, 100-kernel weight and biomass yield per plant. Strong association between biomass and pod yield per plant indicated possibilities for simultaneous improvement in both the traits.

Nagda and Joshi (2004) evaluated 52 genotypes of groundnut and observed significant and positive association between pod yield per plant and harvest index. Harvest index expressed high positive direct effect towards pod yield per plant. While 100-kernel weight influenced indirectly *via* harvest index, suggested that harvest index and 100-kernel weight should be considered as important traits in selection programme.

Suneetha *et al.* (2004) studied 23 diverse genotypes for their character association 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% flowering with days to maturity and 100-pod weight with 100-kernel weight showed significant and positive correlations between themselves. Days to 50% flowering and plant height expressed negative direct contribution. They also concluded that days to 50% flowering, plant height and mature pods per plant should be considered as selection criteria for improving pod yield in groundnut.

Golakia *et al.* (2005) observed strong association of pod yield per plant in both groups with mature pods per plant, kernel yield per plant, developed pods per plant, biomass yield per plant and harvest index, indicating that simultaneous selection for these characters might bring an improvement in pod yield.

Kotzamanidis *et al.* (2006) observed that pod yield per plant had significant and positive correlation with seed length, 100-pod weight, 100-seed weight, pod length, pod width and seed width. However, significant and positive correlation was found between 100-seed weight and 100-pod weight.

Mane *et al.* (2008) performed correlation analyses to assess 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.

John *et al.* (2009) reported that pod and kernel yields per plant showed significant and positive association with days to 50% 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 yields per plant.

Awatade *et al.* (2010) carried out correlation analysis to assess the relationship among different characters in groundnut and reported that the phenotypic correlation coefficient was slightly higher than phenotypic correlation coefficient. The characters *viz.*, number of pods per plant, number of primary branches per plant, number of kernels per plant, and kernel yield per plant showed significant and positive correlation with dry pod yield per plant.

Shinde *et al.* (2010) recorded that 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% 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.

Vekariya, H.B. *et al.* (2011) evaluated fifty diverse genotypes of bunch groundnut during *Kharif* 2009 for genetic parameter *viz.*, correlation and path analysis. The magnitudes of genotypic correlation coefficients were higher as compared to the corresponding phenotypic correlation coefficients. The 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

Babariya, C.A. and Dobariya, K.L. (2012) estimated correlation coefficients for pod yield per plant and its components by using 100 genotypes of Spanish bunch groundnut. The 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. 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.

2.3 MOLECULAR CHARACTERIZATION THROUGH RAPD

Until recent advances in molecular genetics, breeders have been improving both qualitative and quantitative inherited traits by conventional breeding methods based on phenotypic evaluation and selection, which are resource and time consuming.

The RAPD markers (Williams *et al.*, 1990) have been increasingly employed for population studies and for analysing of molecular diversity (Hogbin*et al*., 1998; Fischer *et al*., 2000). RAPD technique has the advantage of assessing a greater number of potential polymorphic loci distributed randomly in the genome than allozymes. In addition, when compared to other DNA-based markers, the procedure is technically simple, economic and also does not require any prior knowledge of the target DNA sequence in the genome. However, most RAPD loci show dominant segregation and are assumed to possess only two alleles per locus, which may bias some population genetic parameters.

The standard RAPD technology utilized short synthetic oligonucleotides (10 bases long) of random sequences as a primer to amplify nanogram amounts of total genomic DNA under low annealing temperature by PCR. During annealing at appropriate temperature in the thermal cycler, oligonucleotide primers of random sequence bind several priming sites on the complementary sequences in the template genomic DNA and produced discrete DNA products. The profile of amplified DNA primarily depends on nucleotide sequence homology between the template DNA and oligonucleotide primer at the end of each amplified product. Welsh and McClelland (1990) independently developed a similar methodology using primers about 15 nucleotides long and different amplification and electrophoresis conditions than RAPD and called it arbitrarily primed polymerase chain reaction (AP-PCR) technique.

Lanham *et al.* (1992) studied the detection of polymorphic loci in *Arachis* germplasm using RAPDs. From a total of 60 decamer oligonucleotide primers, 49 polymorphic loci were identified between A. *hypogaea* type and a synthetic amphidiploids (B x C)$_2$ created from A. *batizocoi* and *A. chacoense* cross

Bhagwat *et al*. (1997) used RAPD analysis for radiation induced mutants of groundnut. It showed distinct morphological and biochemical characteristics. The analysis revealed characteristic band differences among the 12 mutants and their parents. The polymorphic bands were dominant in the F1 generation and segregated in a Mendelian fashion in F2.

Subramanian *et al*. (2000) selected 70 genotypes representing variability for several morphological, physiological and other characters. They studied polymorphism employing

random amplified polymorphic DNA (RAPD) assay with 48 oligonucleotide primers. In all 48 oligonucleotide primers only 7 (14.6%) yielded polymorphic amplification products. These 7 primers produced 408 bands, of which 27 were polymorphic. Detection of polymorphism in cultivated groundnut opens up the possibility of development of its molecular map by judicious selection of genotypes that show DNA polymorphism. This approach will be useful for developing marker assisted selection tools for genetic enhancement of groundnut for desirable traits.

Amadou *et al.* (2001) assessed genetic diversity in 25 bambara groundnut (*Vigna subterranean* L.) germplasm. Fifty random decamer primers were screened to assess their ability to detect polymorphism in bambara; 17 of them were selected for further study. The 17 primers produced a total of 63 bands, 25 of which (approximately 40%) were monomorphic, while the remaining 60% showed at least one polymorphic band. The lowest value of Jaccard's similarity coefficient observed was 0.63 ZM80-699 (Zambia) and FB85-3 (Nigeria), while the highest similarity coefficient (0.97) was found between ZM-2452B and ZM-2452C, both originating in Zambia.

Raina *et al.*(2001)used twenty-one random and 29 SSR primers to assess genetic variation and interrelationships among subspecies and botanical varieties of cultivated peanut, *Arachis hypogaea* (2n = 4x = 40). In contrast with the previous generalization that peanut accessions lack genetic variation, both random and SSR primers revealed 42.7 and 54.4% polymorphism, respectively, among 220 and 124 genetic loci amplified from 13 accessions. Moreover, the dendrograms based on RAPD, ISSR and RAPD + ISSR data precisely organized the five botanical varieties of the two subspecies into five clusters. One SSR primer was identified that could distinguish all the accessions analysed within a variety.

Bhagwat *et al.* (2001) revealed that random amplified polymorphic DNA (RAPD) analysis with a single random primer, OPX-10 (5'-CCCTAGACTG-3') expressed distinct polymorphism among closely related groundnut (*Arachis hypogaea*) varieties. The primer appeared very specific to groundnut as it did not reveal polymorphism in other crops. Considering the narrow genetic base of groundnut in general and that of the varieties analysed, all having been derived from a single variety (Spanish Improved), OPX-10 primer appears to have amplified a fast evolving region of the genome.

Dwivedi *et al.* (2001) selected twenty-six accessions and eight primers for random amplified polymorphic DNA assay to determine the genetic diversity. The genetic similarity

(Sij) ranged from 59.0 per cent to 98.8 per cent with an average of 86.2 per cent. Both multidimensional scaling and UPGMA dendrogram revealed the existence of five distinct clusters. However, this classification could not be related to known biological information about the accessions falling into different clusters. Some accessions with diverse DNA profile (ICG 1448, 7101, 1471, ICGV 99006 and 99014) were identified for mapping and genetic enhancement in groundnut.

Massawe *et al.* (2003) evaluated genetic diversity in 12 landraces of bambara groundnut (*Vigna subterranea*), an indigenous African legume, using RAPD markers. RAPDs revealed high levels of polymorphism among landraces. The percentage polymorphism ranged from 63.2 per cent to 88.2 per cent with the 16 RAPD primers evaluated. The construction of genetic relationships using cluster analysis groups the 12 landraces in two clusters.

Garcia *et al.* (2005) studied the RAPD-based linkage map of peanut based on a backcross population between the two diploid species *Arachis stenosperma* and *A. cardenasii*. Total 428 decamer primers were screened, from which 156 primers were selected based on the size and intensity of the RAPD polymorphisms amplified. One hundred sixty-seven RAPD loci were mapped to 11 linkage groups, covering a total genetic length of 800 cM. Clusters of 2 to18 markers were observed in most linkage groups. Twenty seven per cent of the markers showed segregation distortion and mapped to four regions. Six RAPD markers were used to establish correspondence between maps and to compare recombination frequencies between common markers. A generalized reduction in the recombination fraction was observed in the backcross map compared to the F2 map. All common markers mapped to the same linkage groups and mostly in the same order in both maps.

Mallikarjuna *et al.* (2005) studied genetic diversity among *Arachis* species using RAPDs. Thirty-two accessions of wild species of *Arachis* belonging to twenty-five species and grouped under six sections were used in this study for genetic relationship using RAPDs. Twenty-nine primers were used to study. All the primers showed polymorphic bands and the number of bands varied from five to thirty-three. Similarity values (Sij) for 464 pair wise comparisons among 32 accessions ranged from a minimum of 0% to a maximum of 49%, with an average of 15%.

Mondal *et al.* (2005) investigated the RAPD polymorphism among groundnut genotypes differing in disease reaction to late leaf spot and rust. Fifty primers were screened,

out of which 11 primers exhibited polymorphism among the 19 genotypes. The extent of polymorphism ranged from 12.5% to 76.9% with an average of 37.5%. Genetic distance among the genotypes ranged from 1.41 to 6.40.

Nelson *et al.* (2006) studied assessment of genetic diversity and sectional boundaries in tetraploid peanuts (*Arachis hypogaea*) using RAPD methods. Forty 10-base oligonucleotide primers were initially evaluated; 16 were polymorphic and utilized for analyses and 156 loci were identified for a mean of 9.75 loci per primer. Ninety-two percent of the loci were polymorphic. Forty-three RAPD markers were observed exclusively in *A. glabrata*, none in A. *hypogaea*, one in *A. monticola*, and 15 in *A. pseudovillosa*. Four populations of *A. Glabrata* showed high levels of genetic diversity and were genetically different from *A. pseudovillosa* even though they occur in the same section. These data provided the first evidence of high genetic diversity within wild, perennial, tetraploid peanuts, and for possible multiple origins of tetraploids in the section *rhizomatosae*.

Azzam *et al*. (2007) studied the molecular markers associated with resistance to pod rot diseases and aflatoxin contamination by RAPD in which ten peanut mutants and their parent variety were evaluated using 13 arbitrary primers; ten of which successfully amplified DNA fragments of all genotypes. Number of bands ranged from 6 to 14 across all genotypes. The level of polymorphism ranged from 57.1% to 83.3% while the genetic similarity ranged from 0.58 to 0.93.

Gagliardi *et al.* (2007) studied genetic stability among in vitro plants of *Arachis retusa*using RAPD markers for germplasm preservation. Total 10 primers were screened and five primers were selected which showed the highest number of RAPD loci and reproducibility. Ninety genomic regions (loci) generated from RAPD analyses were evaluated. All amplified fragments detected in plants derived from the two explants types were monomorphic. The results indicated that the recovered shoots are genetically stable at the assessed genomic regions.

Lang *et al.* (2007) demonstrated the utility of RAPD marker to analyses genetic divergence of groundnut genotype in the South Vietnam. They selected 29 groundnut cultivars and were amplified with 5 random decamer primers by PCR. The distinctive RAPD patterns generated from these cultivars could be used as genomic fingerprint to establish the identity of a given genotype. 29 groundnuts were clearly separated in distinct sub clusters in a phyllogram obtained by UPGMA of genetic distances.

Lang and Hang (2007) demonstrated utility of RAPDs to analyze genetic divergence in peanut genotypes. Nucleic acid extracts from 29 *Arachishypogaea* L. cultivars were amplified using five random decamers by PCR. The distinctive RAPD patterns generated from these cultivars could be used as genomic fingerprint to establish the identity of a given genotype.

Mondal *et al.* (2007) studied F_2 mapping population comprising 117 individuals, which were developed from a cross between the rust resistant parent VG 9514 and rust susceptible parent TAG 24. They identified 11 (out of 160) RAPD primers that exhibited polymorphism between these two parents. Using a modified bulk segregate analysis, primer J7 (5′CCTCTCGACA3′) produced a single coupling phase marker (J7 1350) and a repulsion phase marker (J7 1300) linked to rust resistance. Screening of the entire F_2 population using primer J7 revealed that both J7 1300 ($P = 0.00075$) and J7 1350 ($P < 0.00001$) were significantly associated with the rust resistance.

Vasanthi *et al.* (2008) analyzed genetic diversity among 12 genotypes using RAPD markers consisting of 6 released cultivars (Tirupati 4, Narayani, Tirupati 3, Kalahasti, Prasuna and Abhaya), 2 pre-release cultivars (TCGS 888 and 913) and 4 advanced breeding lines (TCGS 653, 750,645 and TG 47) with known pedigrees to know the extent of relationship and to correlate it with pedigree information. Seven RAPD primers detected 48 polymorphic bands. Jaccards similarity coefficients ranged from 32.6 per cent (Tirupati 4 and TCGS 645) to 92.9 per cent (Kalahasti and Narayani). Tirupati 4 and Tirupati 3 exhibited least similarity with other genotypes. The extent of similarity did not correlate with pedigree information.

Kumari *et al.* (2009) studied 21 mutants belonging to different botanical types of groundnut and used to assess molecular diversity using RAPD analysis. All twenty-seven random primers showed polymorphic bands. The polymorphism per primer ranged from 9.09 to 71.42 per cent with an average of 30.16 per cent. Although the cluster analysis grouped genotypes into five different clusters, most of the genotypes (17 of 21) were grouped in a single cluster, indicating narrow genetic diversity among the genotypes.

Varshakumari *et al.* (2009) studied the molecular characterization of induced mutants in groundnut using random amplified polymorphic DNA markers. All twenty-seven random primers showed polymorphic bands. The polymorphism per primer ranged from 9.09 to 71.42 per cent with an average of 30.16 per cent. High genetic similarity values (Sij) of

0.88 to 0.98 were obtained for the genotypes, indicating limited genetic diversity. The cluster analysis grouped genotypes into five different clusters; most of the genotypes (17 of 21) were grouped in a single cluster, indicating narrow genetic diversity among the genotypes.

Gowda *et al.* (2010) studied the mutational origin of genetic diversity in groundnut (*Arachis hypogaea* L.) where 271 fragments were amplified by 21 decamer primers in 30 genotypes, 104 were polymorphic (38.38%). On an average, 13 bands per primer were amplified and 4.95 bands per primer were polymorphic. The polymorphism per primer ranged from 7.69% to 75%. The PIC values for primers ranged from 0.06 to 0.42 with an average of 0.23. The dendogram revealed three distinct clusters at similarity coefficient (Sij) of 0.87, 0.92 and 0.94, respectively.

Sharaf *et al*. (2011) tested genetic similarity of four mutants of groundnut and their control using random amplified polymorphic DNA (RAPD) approach. Although natural polymorphism among peanut cultivars was very low, RAPD patterns showed high polymorphism percentage of DNA fragments (37.13%).

3. MATERIALS AND METHODS

The present investigation was carried out to elicit the information on "Variability Assessment at Morphological and Molecular level in Groundnut (*Arachis hypogaea* L.)" during *kharif*, 2012 at the Instructional Farm, College of Technology and Agricultural 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 observation during crop period

Weather Details		**Month**				
		July, 2012	Aug, 2012	Sept., 2012	Oct., 2012	Nov., 2012
Rainfall (mm)		65.7	236.4	323.5	000.0	000.0
Max. Temp. º C		31.6	29.3	29.9	32.1	28.3
Min. Temp. º C		24.4	23.2	21.6	13.4	8.4
Relative Humidity (%)	Morning	82	91	93	89	88
	Evening	65	70	70	33	35
Wind (km/hr)		5.1	2.4	2.0	1.0	0.8
Sunshine (hr.)		3.4	3.0	4.2	8.3	8.0
Evaporation (mm)		5.1	2.1	2.6	3.3	2.3

1. Experimental materials:

The experimental material comprised of 25 promising genotypes (including National and State level released varieties) of groundnut, which were obtained from the All India Coordinated Research Improvement Project on Groundnut, MPUAT, Udaipur. Details of selected germplasm lines are given in Table 3.2.

2. Experimental details:

Afield experiment was carried out with 25 (including National and State level released varieties) in a Randomized Block Design with three replications during *kharif*, 2012. In each replication, genotypes sown in a plot of 5 m x 0.9 m accommodating 3 rows of 5 m length spaced 30 cm apart with a plant to plant spacing of 10 cm. Recommended agronomic practices followed to raise a healthy crop.

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

Sr. No.	Name of genotypes	Pedigree
1.	GG-2	J 11 × EC 16659
2.	GG-3	GAUG 1 × JL – 24
3.	GG-4	CGC-3 × Chico
4.	GG-5	27-5-1 × JL 24
5.	GG-7	S 206 × FESR 8 1-1-9-B-B
6.	GG-8	27-5-1 × JL 24 30-3-2-B-B
7.	JCG-88	J 11 × TG (E)-1
8.	R-2001-2	ICGS 11 × ICG-4728
9.	R-2001-3	ICGS 11 ×ICG-4728
10.	GAUG-10	G224-3 × G0343
11.	Kadiri-5	JL 24 × VG 55-7
12.	Kadiri-6	JL 24 × Ah 316/S
13.	Kadiri-9	Kadiri 4 × Vemana
14.	GPBD-4	KRG 1 × ICGV 86855
15.	ICGV-91114	(ICGV 86055 × ICGV 86533) F2-P8-B1-B1-B1-B1
16.	JAL-24	Selection from 'EC 94943'
17.	JAL-39	S206 x C-55-437-162-2
18.	TG-37-A	TG 25 × TG 26
19.	Chico	Germplasm accession
20.	Vemana	Kadiri 3 × JL 24
21.	TIR-46	An advance breeding line from RRS, Tirupati
22.	TAG-24	Selection from TGS 2 (TG 18A × M 13) × TGE
23.	Pratapmungphali -1	ICGV- 86033 × ICG- 2214
24.	Pratapmungphali -2	ICGV- 86055 × ICG- (FDRs 10)
25.	Pratap raj mungphali	Selection from ICGV 98223

3. Characters studied:

Observations were recorded on five randomly selected competitive plants of each genotype in each replication for various characters except days to 50 % flowering and days to maturity, which were recorded on plot basis. The methodology used for recording observation on different characters is described below:

1. 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.

2. 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.

3. 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.

4. Number of branches per plant

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

5. 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.

6. 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.

7. Kernel yield per plant (g)

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

8. 100-kernel weight (g)

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

9. 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.

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

10. Shelling Out Turn (%)

The shelling out-turn based on the weight of kernels recovered from the pods was calculated as under.

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

11. Biological yield per plant (g)

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

12. 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:

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

13. Seed 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 I).

4. Statistical analysis:

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

4.1 Analysis of variance for experimental design

The mean values for various characters were subjected to statistical analysis for various parameters *viz.*, variability, genotypic and phenotypic correlations as per details given below.

The analysis of variance for R.B.D. was based on following linear model.

$$Y_{ij} = \mu + r_i + g_j + \epsilon_{ij}$$

$i = 1,2,3,\ldots, r$

$j = 1,2,3,\ldots, g.$

Where, Y_{ij}= Response of j^{th} genotype in i^{th} replication

μ = General mean

r_i = Effect of i^{th} replication

g_j = Effect of j^{th} genotype

ϵ_{ij} = Uncontrolled variation associated with j^{th} genotype in i^{th} replication

To test the variation among the genotypes, analysis of variance was carried out as per method suggested by R. A. Fisher (1918).The general structure of ANOVA is given in Table 3.3.

Table 3.3: Analysis of variance and expected mean squares

Source	**df**	**Mean sum of squares**	**Expected mean sum of squares**
Replications	(r-1)	M_r	$\sigma^2_e + g\sigma^2_r$
Genotypes	(g-1)	M_g	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (g-1)	M_e	σ^2_e
Total	(rg-1)		

Where,

r = Number of replications

g = Number of genotypes

M_r= Mean sum of squares due to replications

M_g= Mean sum of squares due to genotypes

M_e= Mean sum of squares due to error

Significance of mean sum of squares due to replications (M_r) and genotypes (M_g) were tested against error mean sum of squares (M_e).

The standard error of mean (S.Em.) was calculated using following formula:

S.Em. = $\sqrt{M_e / r}$

The critical difference (C.D.) to compare the mean of any two genotypes was calculated using following formula:

C.D. = S.Em. X $\sqrt{2}$ X 't'

Where,

t' = Table value of 't' at 5 % level of significance at error degree of freedom.

The coefficient of variation (C.V.) was determined according to the following formula:

$$CV \quad \% \quad = \quad \frac{\sqrt{M_e}}{\overline{X}} \quad \times 100$$

Where,

$\overline{X}$ = General mean of a character.

4.2 Estimation of variability parameters

Total variation was partitioned into phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variance based on expected mean sum of square for respective source of variation described in ANOVA (Table 3.3).

$\sigma^2_e = M_e$

$\sigma^2_g = \frac{Mg-Me}{r}$

$\sigma^2_p = \sigma_g + \sigma_e$

Genotypic and phenotypic coefficients of variation were estimated as under.

(a) Genotypic coefficient of variation (GCV):

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

(b) Phenotypic coefficient of variation (PCV):

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

(c) Heritability (h^2):

In broad sense heritability is the ratio of genotypic variance to the phenotypic variance and was calculated according to formula suggested by Brton and Devane (1953).

$$h^2(\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

(d) Genetic advance (GA):

The expected genetic advance under selection (Gs) was estimated as per the formula described Brton and Devane (1953).

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

Where,

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

σ_p = Estimated phenotypic standard deviation.

(e) Genetic gain (GG):

The genetic gain was calculated by using the following formula suggested by Johnson *et al* (1955).

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

Where,

Gs = Expected genetic advance under selection

$\bar{X}$ = General mean of a character.

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 in Table 3.4.

Table 3.4: Analysis of covariance between two characters

Source sum of products	df	Mean of sum sum of products	Expected mean of
Replication	(r-1)	Mr_1	—
Genotypes	(g-1)	Mg_1	$Cov_{exy} + Cov_{gxy}$
Error	(r-1) (g-1)	Me_1	Cov_{exy}

Where,

r = Number of replications

g = Number of genotypes

Cov = Covariance

1. Genotypic covariance ($Cov_{(xy)g}$)

The formula for calculating genotypic covariance is described as below:

$$Cov_{(xy)g} = (M_{g1} - M_{e1}) /r$$

Where,

M_{g1} = Mean sum of products due to genotypes between variables x and y

M_{e1} = Mean sum of products due to error between variables x and y

r = Number of replications

2. Phenotypic covariance ($Cov_{(xy)p}$)

The formula for calculating phenotypic covariance is explained as under:

$$Cov_{(xy)p} = Cov_{(xy)g} + M_{e1}/r$$

Where,

M_{e1} = Mean sum of products due to error between variables x and y

r = Number of replication

(a) Genotypic correlation coefficient (r_{gxy})

$$rgxy = \frac{Cov(xy)g}{\sqrt{\sigma^2 gx . \sigma^2 gy}}$$

Where,

Cov(xy)g = Genotypic covariance between two characters x and y.

σ^2_{gx} = Genotypic variance for character x

σ^2_{gy} = Genotypic variance for character y

(b) Phenotypic correlation coefficient (r_{pxy})

$$rpxy - \frac{Cov(xy)p}{\sqrt{\sigma^2 px.\sigma^2 py}}$$

Where,

Cov (xy)p = Phenotypic covariance between two characters x and y.

σ^2_{px} = Phenotypic variance for character x

σ^2_{py} = Phenotypic variance for character y

(c) Test of significance

The significance of the correlation coefficient values for (n-2) degrees of freedom was done by calculating the 't' value using following formula described by Panse and Sukhatme (1985).

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

Where,

't' = Calculated value of 't'

r = Correlation coefficient between two variables

n = Total number of observations

5. Molecular Analysis

DNA extracted from different groundnut cultivars were compared using RAPD methodology. In this DNA was extracted from young leaves (3 weeks old) using CTAB method. DNA was amplified by using decamer random oligonucleotide primer in a thermo cycler (Sigma). The amplified samples were separated on agarose gel electrophoresis (1.5 %). The bands were scored for their presence or absence. The details of the technique of DNA isolation and RAPD are as given below:

5.1 Chemicals and Glassware's

All chemicals used in DNA isolation and PCR (Polymerase Chain Reaction) were of analytical grade. All the chemicals used in the experiments were of molecular and analytical grade and were obtained from standard manufacturers' *viz.*, Himedia Laboratory, Aldrich, SRL and Bangalore Genei. *etc*. These chemicals were procured through local dealers.

5.2 Preparation of stock solutions for reagents and buffers for DNA extraction

The reagents and buffers for DNA isolation were prepared as per Sambrook *et al.* (1989).The composition and procedure for preparation of various stock solutions and buffers are given in Table 3.5 and 3.6.

Table 3.5: Preparation of stock solutions for DNA extraction and electrophoresis

Sr. No	Solution	Method of preparation
1	1M TrisHCl (pH 8.0), 100 ml	12.11g Tris base was dissolved in 80 ml distilled water. The pH was adjusted to 8.0 by adding concentrated HCl. A total volume was adjusted to 100 ml. It was dispensed to reagent bottle and sterilized by autoclaving.
2	0.5M EDTA (pH 8.0), 100 ml	18.60 g EDTA di Sodium salt was Dissolved in 80 ml distilled water. The pH was Adjusted to 8.0 by adding NaOH pellets. A total volume was adjusted to 100 ml. It was dispensed to reagent bottle and sterilized by autoclaving.
3	5M NaCl 100 ml	29.22 g NaCl was taken in to beaker; 50 ml of distilled water was added and mixed well. When the salts get completely dissolved, the final volume was adjusted to 100 ml. It was dispensed to reagent bottle and sterilized by autoclaving.
4	70% Ethanol, 100 ml	70 ml of ethanol and 30 ml of distilled water was mixed well and dispensed to reagent bottle and stored at 4^0C.
5	Chloroform: Isoamyl alcohol (24:1), 100 ml	96 ml of chloroform and 4 ml of isoamyl alcohol were measured, mixed well and stored in reagent bottle at room temperature.
6	Ethidium Bromide (10 mg/ml), 1.0 ml	10 mg Ethidium Bromide was added to 1.0 ml of distilled water and it was kept on magnetic stirrer to ensure that the dye has dissolved completely. It was dispensed into amber colored eppendorf tube and stored at 4^0C.

7	1X TE buffer 100 ml 10mM TrisHCl, (pH 8.0) 0.1mM EDTA, (pH 8.0)	1.0 ml of TrisHCl (1M), 200 µl of EDTA (0.5M) were taken and distilled water was added to adjust the final volume of 100 ml, mixed thoroughly, autoclaved and stored at room temperature.
8	10% CTAB, 100 ml	10 g of CTAB powder was taken and it was added into boiling water to dissolve completely and the final volume was made up to 100 ml.
9	3M Sodium acetate (pH 7.0), 20 ml	8.16 g Sodium acetate trihydrate salt was dissolvedin distilled water and the final volume was made up to 20 ml. The pH was adjusted up to 7.0.

Table 3.6: Preparation of extraction buffer for DNA extraction

Buffer	Method of preparation
CTAB Extraction buffer (3%), 10 ml	1.0 ml of 1M TrisHCl (pH 8.0), 3.0 ml of 5M NaCl, 0.8 ml of 0.5 M EDTA (pH 8.0) and 3.0 ml of 10% CTAB and 2.1 ml of distilled water were taken in to a flask and mixed well. 0.1 ml (1%) β- mercaptoethanolwas addedinto a mixture just before use.

5.3 DNA Isolation (Doyle and Doyle, 1990)

Total genomic DNA was extracted from the 3 weeks old leaves by Cetyl Trimethyl Ammonium Bromide (CTAB) method (Doyle and Doyle, 1990) with some modifications.

1. 0.5 to 1 g of leaf tissue material was ground well using liquid nitrogen in a pestle and mortal. 750 µl pre-warmed (65^0C) DNA isolation buffer (CTAB DNA extraction Buffer) was added in homogenized leaf material. Homogenized material was transferred in capped polypropylene tubes. Incubated for 30 min. at 65^0C in water bath with gentle swirling.
2. Tubes were removed from water bath and equal volume of chloroform: isoamyl alcohol in the ratio of 24:1 (w/v) was added. The contents were mixed gently by inverting the tubes so as to form emulsion.
3. The tubes were centrifuged at 12000 rpm for 10 minutes . Contents were separated into 3 phases and the aqueous phase was taken and transferred to another clean tube. DNA was precipitated by the addition of 100 per cent chilled alcohol.
4. DNA-CTAB complex was precipitated as a fibrous network, which was lifted by using cut tips and transferred to another tube containing 750 µl TE buffer.

5. 750 µl solution of phenol : chloroform : isoamyl alcohol(25:24:1)was added and shaked for 10 min. and spin at 12000 rpm for 10 min.

6. Suppernatant is taken and added 1 ml ethanol, spinned at 5000 rpm for 5 min.

7. Supernatant discarded , the pellet was washed with 0.2M sodium acetate 500 µl and spinned at 5000 rpm for 5 min.

8. The pellet was rewashed by keeping it in 500 µl solution of 10 Mm ammonium acetate 70 per cent alcohol for 2 minutes followed by centrifugation.DNA was washed with 70 per cent alcohol. The pellet was collected by centrifugation at 5,000 rpm for 5 minutes.

9. The pellet was re dissolved in 100 µl of TE buffer by keeping overnight at -20^{o}C without agitation

5.4 Purification of DNA

An impurity of RNA was removed by treating the sample with DNase free RNase. An impurity of protein including RNase was removed by treating with chloroform: isoamyl alcohol (24:1). The purification was carried out in following steps.

1. 2.5 µl of RNase was added to 0.5 ml of crude DNA preparation.

2. It was gently mixed and incubated at 37^{0}C for 1 hour.

3. After 1 hour 0.3-0.4 ml mixture of chloroform: isoamyl alcohol (24:1) was added and mixed thoroughly for 15 minutes, till an emulsion was formed.

4. Spun for 15 minutes at 15,000 rpm.

5. Supernatant was taken, avoiding the whitish layer at interface.

6. The DNA was re-precipitated by adding double the quantity of absolute alcohol.

7. To pellet the DNA, the tubes were centrifuged for 5 minutes at 5,000-10,000 rpm.

8. The pellet was washed with 70 per cent alcohol and dried over night.

9. The DNA was re-dissolved in 250 µl of TE buffer.

5.5 Gel Analysis

Electrophoresis was carried out on solid matrix, the agarose gel containing ethidium bromide and DNA was visualized under transilluminated UV light.

5.5.1 Casting of Gel

1. Prepared 1.5 per cent agarose gel in 1X TAE buffer. The mixture was heated for few minutes till the agarose dissolved and then allowed to cool.
2. To the cooled solution, 50 µl ethidium bromide per 100 ml solution was added and mixed well.
3. The solution was poured into the gel castor using desired comb and allowed to set. The comb was removed after the gel was set and the gel was kept in the gel unit.

5.5.2 Preparation of Sample

DNA (15 µl) solution was mixed with 2 µl of 6X loading dye and spun for few second in order to mix well.

5.5.3 Electrophoresis

The gel tray was filled with 1X TAE buffer and 15 µl DNA sample was loaded using micropipette. The gel was run at 50 volt till the dye traveled 2/3 rd of the length of the gel. Gel was removed, visualized under UV light and photographed with the help of gel documentation system.

5.5.4 Quantification of DNA

The quantification of DNA was done by measuring optical density (OD) at 260 nm and 280 nm wavelengths by using a spectrophotometer (UV visible from UNICAM). The steps involves are as follow:

1. Take 3 ml of TE buffer in a cuvette and calibrate the spectrophotometer at 260 nm as well as 280 nm wavelengths.
2. Transfer 3 ml of DNA mix (2990 µl of TE buffer and 10 µl of DNA) to a cuvette and record the OD at 260 and 280 nm.
3. Estimate the DNA concentration employing the following formula

$$\text{Amount of DNA } (\mu g/\mu l) = \frac{A260 \times 50 \times \text{dilution factor}}{1000}$$

4. Quality of DNA was assessed by ratio of OD value recorded at 260 nm and 280 nm using spectrophotometer.

5.6 List of the Primers

A set of decanucleotide RAPD primers were used for PCR amplification. The sequences of these primers were selected from literature and obtained from Bangalore Genei Pvt. Ltd., Bangalore. The details of primer code sequence of the primer and GC contents are given in Table 3.7.

Table 3.7: Detail of RAPD primers used in molecular analysis of groundnut cultivars

S. No.	Primer*	Sequence 5' to 3'	G: C Content (%)
1.	OPA-1	CAGGCCCTTC	70
2.	OPA-5	AGGGGTCTTG	60
3.	OPA-8	GTGACGTAGG	60
4.	OPA-9	GGGTAACGCC	70
5.	OPA-10	GTGATCGCAG	60
6.	OPA-12	TCGGCGATAG	60
7.	OPA-15	TTCCGAACCC	60
8.	OPC-4	CCGCATCTAC	60
9.	OPC-5	GATGACCGCC	70
10.	OPC-6	GAACGGACTC	60
11.	OPC-11	AAAGCTGCGG	60
12.	OPC-12	TGTCATCCCC	60
13.	OPC-13	AAGCCTCGTC	60
14.	OPC-15	GACGGATCAG	60
15.	OPJ-6	TCGTTCCGCA	60

***** Operon series code

5.7 Dilution of DNA for PCR

Quantity of DNA was diluted to final concentration of 50 ng/µl using TE buffer (10 mM Tris HCl, 1 mM EDTA, pH 8.0). The details of PCR reaction mixture is as given below (Table 3.8):

Table 3.8: PCR reaction mixture content

S. No.	Components	Final Concentration	Single tube (20µl)
1.	DNA template 50 ng/µl	50 ng	2.00µl
2.	Master mixture		
	1.dNTP mix	200 µM	2.5µl
	2.*Taq* DNA polymerase	3U	0.60µl

	3. Reaction buffer (10X)	1X	2.5µl
	4. Primer	0.5 µM	2.00µl
	5. dd H_2O		15.4µl

5.8 RAPD Analysis (Williams *et al.* 1990)

Random amplification of polymorphic DNA was done by using 15 primers obtained from Bangalore Genei Pvt. Ltd., Bangalore. PCR reaction was performed in final volume of 25 µl containing 10X Reaction Buffer, 3 unit of *Taq* DNA polymerase, 200 µM each of dNTPs mix, 0.5 µM/reaction of random primer's (OPERON TECHNOLOGIES) and 50 ng of template DNA. The Polymerase Chain Reaction (PCR) was performed in PCR machine (Thermo cycler) using the following cycling parameters:

Table 3.9: Different cycles of PCR amplification

Cycle	Denaturation		Annealing		Extension	
First cycle	94°C	4 min	-	-	-	-
2-44 cycles	94°C	30 sec.	35°C	30 sec.	72°C	5 min
Last cycle	-	-	-	-	72°C	5 min

5.9 Agarose Gel Electrophoresis

Submerged gel electrophoresis unit was used for fractionating amplified PCR products on 1.5 per cent agarose gel. The gel was prepared in 1X TAE buffer (Sambrook *et al*. 1989) containing (50µl/100ml) of ethidium bromide. The samples and loading dye were mixed in 4:1 ratio and loaded with micropipette. Electrophoresis was carried out at 50 V for 3 hours in 1X TAE buffer. After separation the gel was viewed under UV transilluminator and photographed with the help of gel documentation system (Alpha DG DOC).

5.10 Scoring of the RAPD Products

In order to score and preserve banding patterns, photographs of the gel were taken by a Gel Documentation System, under UV transilluminator. DNA ladders were loaded as reference as well as PCR product. Molecular size of PCR products was estimated by referencing to the DNA ladder. The presence of each band was scored as (1) and its absence

as (0). Faintly visible bands were not scored, but a major band corresponding to faint bands was considered for scoring

5.11 Statistical Analysis for Similarity Coefficient

The scores (0 or 1) for each band obtained from photograph were entered in the form of a rectangular data matrix (qualitative data matrix). The pair-wise association coefficients were calculated from qualitative data matrix using Jaccard's similarity coefficient (Jaccard, 1908). The equation for calculating Jaccard's similarity coefficients 'F' between two samples A and B is:

$f = n_{xy} / (n_1 - n_z)$

n_{xy} = Number of bands common to sample A and sample B.

n_1 = Total number of bands present in all samples.

n_z = Number of bands not present in sample A or B but found in other samples.

Cluster analysis for the genetic distance was then carried out using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) clustering method (Sneath and Sokal, 1973). The genetic distances obtained from cluster analysis through UPGMA were used to construct the dendrogram, depicting the relationships of the genotypes using computer program NTSYSpc version 2.02 (Rohlf, 2004).

4. RESULTS AND DISCUSSION

The present study entitled "Variability Assessment at Morphological & Molecular level in Groundnut (*Arachis hypogaea* L.)" was carried out at the instructional Farm, CTAE, MPUAT, Udaipur.

The experimental material of present investigation was comprised of 25 genotypes including national & the state released varieties of bunchtype groundnut (*Arachis hypogaea* L.) Thirteen characters were studied for variability and correlation among themselves. The same material was also used for molecular characterization.

The results obtained for thirteen characters of 25 genotypes are discussed under following heads:

4.1. Analysis of variance

4.2. Mean values and Range

4.3 Variability parameters

4.4. Correlation analyses

4.5. Molecular characterization

4.1 ANALYSIS OF VARIANCE

The data recorded on thirteen characters were subjected to statistical analyses. The mean sum of squares due to genotypes were highly significant for all the characters studied, indicating considerable differences among the genotypes used in the study (Table 4.1).

4.2 MEAN VALUES AND RANGE

The mean performance of genotypes for different characters are presented in Appendix II. A perusal of the data revealed that the range was considerably high for most of the characters *viz*., days to 50% flowering (23 to 29), days to maturity (91 to 95), plant height (20.67 to 36 cm), number of branches per plant (4 to 7), number of mature pods per plant (8 to 20), dry pod yield per plant(7.6 to 17.23 g), shelling percentage (58 to 72), 100-kernel weight (21.2 to 43.53 g), sound mature kernel (59 to 87 %), biological yield per plant (19.2 to 47.47 g), kernel yield per plant(5.1 to 11.03 g) , harvest index (33 to 48 %), seed oil content (24 to 43 %) indicating an adequate variability for exercising selection and use in the breeding programmes.

4.2.1 Days to 50 % flowering

Among 25 genotypes, mean days to 50% flowering ranged from 23 days (Pratap Mungphali-2) to 29 days (JCG-88). Genotype Pratap Mungphali-2 (23 days) was the earliest to flower which was followed by GG7 (23.3 days) and GG2 (24.3 days). The overall mean recorded for the trait was 26 days.

4.2.2 Days to maturity (Days)

With respect to days to maturity, mean values ranged from 91 days (Vemana) to 95 days (GAUG-10). Genotype Vemana was found earliest as it showed minimum 91.3 days to maturity followed by GG2.GG-3, GG-4,Kadiri-5, ICGV-911141 (91.7 days) and GG-8, TG-37-A, Pratap Raj. Mungphali (92 days)

4.2.3 Plant height (cm)

The mean plant height ranged from 20.67 cm (TAG-24) to 36 cm (Kadiri-6). The mean for plant height was 27.54 cm.

4.2.4 Number of branches per plant

The mean number of branches per plant ranged from 4 (GG-4) to 7 (R-2001-3). Maximum number of branches per plant was exhibited by the genotype R-2001-3 (7.13), followed by GAUG-10 (7) and JCG-88 (6.07).

4.2.5 Number of mature pods per plant

Mean data for number of mature pods per plants revealed that among 25 genotype GPBD-4 (19.87 pods) possessed maximum number of mature pods per plant followed by R-2001-3 (16.87 pods) and GG-2 (16.8 pods). The numbers of mature pods per plant ranged from 8 pods (Kadiri-6) to 20 pods (GPBD-4). The overall mean for this character was 13 mature pods per plant.

4.2.6 Dry pod yield per plant (g)

The mean dry pod yield per plant of 25 genotypes exhibited wide range of variation. The mean dry pod yield per plant ranged from 7.6 g (ICGV-91114) to 17.23 g (GAUG-10). Maximum dry pod yield was exhibited by genotype GAUG-10 (17.2 g), followed by TIR-46 (17.2 g) and GPBD-4 (15.03 g). The overall mean for this character was 11.82 g

4.2.7 Kernel yield per plant (g)

Wide range of variation was found for kernel yield per plant among the 25 genotypes. The mean values ranged from 5.1 g (ICGV-91114) to 11.03 g (TIR-46). The genotype TIR-46 (11.03 g) gave maximum kernel yield followed by GAUG-10 (10.63 g) and R-2001-3 (10.27 g). The overall mean for this character was 7.79 g.

4.2.8 Sound mature kernel (%)

The sound mature kernel percentage ranged from 59 % (TAG-24) to 87 % (Kadiri-9, ICGV-91114). Maximum sound mature kernel percentage was exhibited by the genotype Kadiri-9, ICGV-91114 (86.67 %) followed by Vemana (86%) and GG-7, GG-8 (85 %).

4.2.9 Shelling percentage (%)

The means for shelling percentage ranged from 58 % (JAL-24) to 72 % (GG-3) with a general mean of 67 %. The genotype GG-3 (72 %) showed maximum shelling percentage followed by GG-5 (71.67 %) and GG-8, Pratap Mungphali-1(70.67 %).

4.2.10 Biological Yield per plant (g)

Among 25 genotypes, mean biological Yield per plant ranged from 19.2 g (GG-4) to 47.47 g (GAUG-10). Genotype GAUG-10 (47.47 g) was exhibited maximum biological Yield per plant which was followed by GPBD-4 (40.2 g) and TIR-46 (39.63 g). The overall mean recorded for the trait was 29.56 g.

4.2.11 Harvest index (%)

Mean values among the 25 genotypes for harvest index ranged from 33 % (JAL-39) to 48 % (Pratap Mungphali-2). Genotype Pratap Mungphali-2 (48.3 %) had highest harvest index followed by GG-7 (43.87 %) and TG-37-A (43.73 %).

4.2.12 100 Kernel weight (g)

Genotype TIR-46 (43.53 g) had maximum100 kernel weight, whereas Chico (21.2 g) had lowest 100 kernel weight. The data for 100 kernel weight ranged from 21.2 g (Chico) to 43.53 g (TIR-46). The mean 100 kernel weight was 34.21 g.

4.2.13 Oil content (%)

With respect to oil content genotype Pratap Raj. Mungphali (42.67 %) had maximum oil content, followed by Kadiri-5, Pratap Mungphali-1(42 %) and JCG-88, Chico (41.33 %) whereas the genotype ICGV-91114 (23.67 %) had minimum oil content. The overall mean for oil content was 34 %.

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, genetic gain and genetic advance were estimated and character wise results are presented in table 4.2 and discussed as follows.

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

SN	Characters	GCV	PCV	h^2	GA	GG
1	Days to 50% flowering	5.45	6.34	74.02	2.50	9.66
2	Days to maturity	0.83	1.20	47.55*	1.09	1.18
3	Plant height (cm)	14.94	15.21	96.56	8.33	30.25
4	Number of branches per plant	19.00	23.03	68.07	1.56	32.29
5	Number of mature pods per plant	21.86	22.99	90.43	5.36	42.83
6	Dry pods yield per plant (g)	23.05	24.46	88.80	5.29	44.75
7	Kernel yield per plant (g)	19.50	24.62	62.76	2.48	31.83
8	Sound mature kernels (%)	8.96	9.02	98.75	14.32	18.34
9	Shelling percentage	5.19	5.38	93.01	6.88	10.31
10	Biological yield per plant	24.88	25.12	98.14	15.01	50.78
11	Harvest index (%)	8.16	8.53	91.56	6.47	16.08
12	100 KERNEL Wt. (g)	14.50	14.53	99.58	10.20	29.81
13	Oil content (%)	18.62	18.72	98.98	12.95	38.17

4.3.1 Days to 50 % flowering

A perusal of the data showed low values of both GCV (5.45 %) and PCV (6.34 %) for days to 50 % 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. Ganeshan and Sudhakar (1995); Vasanthi *et al.* (1998), Chisthi *et al.* (2000) and Nath and Alam (2002) also reported low magnitude of both GCV and PCV for days to 50 % flowering.

However, high value of heritability (74.02 %) and moderate genetic gain (9.66 %) and low genetic advance (2.50), indicated presence of additive gene action . Selection of such trait may be rewarded. The findings of these results obtained are in accordance with the finding of Nadaf and Habib *et al.* (1987); Vaddoria and Patel (1990), Parmeshwarrapa *et al.* (2004), and Mahalaxmi *et al.* (2005).

4.3.2 Days to maturity

Partitioning of total variance into its components revealed that the genotypic (0.83 %) and phenotypic (1.20 %) coefficients of variation were low in magnitude for days to maturity. However, narrow difference between these two parameters indicated less influence of environment in expression of this trait. Present findings are in accordance with the findings of Chauhan and Shukla (1985), Vasanthi *et al.* (1998) and Chisthi *et al.* (2000).

4.3.3 Plant height

Estimates of genetic parameters indicated that plant height exhibited moderate value of GCV (14.94 %) and PCV (15.2 %). The GCV and PCV values for plant height were more or less equal. The present findings are in accordance with the findings of Deshmukh *et al.* (1986) and John *et al.* (2006b). Higher magnitude of phenotypic coefficient of variation than genotypic coefficient of variation suggested that appreciable portion of variability has been accounted by environmental effect. Vindhiyavarman and Raveendran (1996), Prasad *et al.* (2002), Kumar and Rajamani (2004) and Mothilal *et al.* (2004) also reported moderate magnitude of GCV and high magnitude of PCV for plant height in groundnut.

The magnitude of heritability in broad sense (96.56 %) was high, with moderate genetic gain (30.25 %) and low genetic advance (8.33 %) for plant height. High heritability accompanied with high genetic gain indicates that most likely the heritability was due to the additive gene effects and selection may be effective.

High heritability along with high genetic gain, was also reported by Deshmukh *et al.* (1986), Azad and Hamid (1987), Kale and Dhole (1988), Manoharan *et al.* (1990), Manohran and Ramlingam (1990), Manohran and Ramlingam (1993), Reddy (1994), Vindhiyavarman and Raveendran (1996), Kumar and Patel (1998), Singh and Singh (1999), , Venkatramana *et al.* (2001), Nath and Alam (2002), Prasad *et al.* (2002), Makhan Lal *et al.*

(2003), Mothilal *et al.* (2004), Golakia *et al.* (2005), Mahalaxmi *et al*. (2005), John *et al.* (2006b) and Korat *et al.* (2009) and suggested the involvement of additive gene action for the inheritance of plant height in bunch groundnut.

4.3.4 Numbers of branches per plant

The values of GCV and PCV for branches per plant revealed that the magnitudes of GCV (19.00 %) and PCV (23.03 %) were moderate for this trait. The larger difference between these two parameters indicated that environmental factors accounted for total variability for this trait. The moderate estimates of genotypic and phenotypic coefficients have also been reported by Chauhan and Shukla (1985), Prasad *et al*. (2002) and Mothilal *et al.* (2004) for branches per plant.

The trait number of primary branches per plant exhibited moderate heritability (68.07%) coupled with moderate genetic gain (32.29 %). These results are in accordance with the findings of Kuriakose and Joseph (1986a) and Singh and Singh (1999). Moderate to high magnitude of heritability and low 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 (21.8 %) and phenotypic coefficient of variation (22.99 %) was found high for number of mature pods per plant. Bhagat *et al.* (1986); Kale and Dhoble (1988), Vindhiyavarman and Raveendram (1996) and Mothilal *et al*. (2004), Wani *et al.* (2004), Mahalaxmi *et al*. (2005), John *et al.* (2006b) and Kadam *et al.* (2007) also reported high magnitude of both GCV and PCV for number of mature pods per plant in groundnut.

On the other hand, heritability (90.43 %) was high in magnitude, in conjunction with high estimates of genetic gain (42.83 %) and low estimates of genetic advance (5.36 %). 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 (23.05 %) and phenotypic (24.46 %) coefficient 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 Chauhan and Shukla (1985); Kale and Dhoble (1988), Reddy (1994), Saxena *et al.* (1995), Sharma and Varshney (1995), Vasanthi *et al.* (1998), Yadahv *et al.* (1998), Nazar-Ali *et al.* (2000), Kumar and Rajamani (2004), Mothilal *et al.* (2004), Parameshwarappa *et al.* (2004), and Kadam *et al.* (2007).

The heritability in broad sense (88.80 %) was high and genetic gain (44.75 %) was also high for this trait. The high value of heritability as well as genetic gain indicated role of additive gene action. Selection may reward for such traits.

4.3.7 Kernel yield per plant

A perusal of the data for kernel yield per plant indicated that genotypic coefficient of variation (19.50 %) and phenotypic coefficient of variation (24.62 %) were high in magnitude for this character. Wide difference between these two parameters indicated the role of environmental factors on the expression of kernel yield per plant. These findings are in accordance with the results reported by Uddin *et al.* (1995), Venkatramana (2001), Venkatramana *et al.* (2001), Parmeshwarapa *et al.* (2004), John *et al.* (2006b) and Kadam *et al.* (2007).

The estimates of heritability for kernel yield per plant were moderate (62.76%). These results are in accordance with the Dashora and Nagda (2002); Golakia *et al.* (2005) and Mahalaxmi (2005). Likewise, genetic gain was also moderate (31.83 %). This indicated that the trait was under the control of additive gene action.

4.3.8 Sound mature kernel percentage

Sound mature kernels showed low estimates of genotypic coefficient of variation (8.96%) and phenotypic coefficient of variation (9.02 %). Such a low amount of variation for sound mature kernels in groundnut was also reported by Mothilal *et al.* (2004).

The estimates of heritability (98.75 %) were high, which suggested that larger portion of variation for this character in the material was due to additive gene action. Moderate estimates of genetic gain (18.34 %) further suggested that prediction of performance for this character would be easier. Similar findings has already been reported by Venkatramana (2001), Kumar and Rajamani (2004), Parmeshwarappa et al. (2004).

4.3.9 Shelling percentage

Magnitude of genetic parameters for shelling percentage indicated that estimates of genotypic coefficient of variation (5.19 %) and phenotypic coefficient of variation (5.38 %) 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 Chauhan and Shukla (1985), Deshmukh *et al.* (1986), Reddy and Gupta (1993), Nath and Alam (2002), Mothilal *et al*. (2004), Golakia *et al.* (2005) and Mahalaxmi *et al.* (2005).

The high heritability (93.01 %), with moderate genetic gain (10.31 %) and moderate genetic advance (6.88 %) was revealed for shelling percentage. High heritability coupled with moderate genetic gain was also reported by Deshmukh *et al.* (1986) and Bhagat *et al*. (1986), whereas, moderate to high heritability was recorded by Chauhan and Shukla (1985); Vaddorai and Patel (1990), Reddy (1994), Singh and Singh (1999), Nath and Alam (2002), Parmeshwarrappa *et al.* (2004) and John *et al.* (2009).

4.3.10 Biological Yield per plant

The estimates of genotypic (24.88 %) and phenotypic (25.12 %) coefficient 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 Vasanthi et al. (1998), Sharma and Varshney (1995).

The heritability in broad sense (98.14 %) was high and genetic gain (50.78 %) was also high for this trait. The high value of heritability as well as genetic gain indicated role of additive gene action. Selection would be effective for this trait. These results are in accordance with the findings of Sharma and Varshney (1995).

4.3.11 Harvest Index

The genotypic coefficient of variation (8.16 %) and phenotypic coefficient of variation (8.53 %) for harvest index were low in magnitude. While high amount of genetic variability for harvest index in groundnut was reported by Sharma and Varshney (1995).

The estimates of heritability (91.56 %) and genetic gain (16.08 %) were high with moderate genetic advance (6.47 %) for this trait. Moderate to high heritability, coupled with high genetic gain was also earlier reported by Reddy (1994), Sharma and Varshney (1995), Nath and Alam (2002) and Prasad *et al.* (2002). The magnitude of heritability and genetic gain in the present material indicated that harvest index was under the control of additive gene action and there is tremendous scope of improvement through selection in this character.

4.3.12 100 kernel weight

The results pertaining to genetic variability for 100- kernel weight indicated that genotypic coefficient of variation (14.50 %) and phenotypic coefficient of variation (14.53 %) were moderate for this trait. The present findings are in accordance with the findings of Deshmukh *et al.* (1986), Nadaf and Habib (1987), Prasad *et al.* (2002), Mothilal *et al.* (2004) and Kumar and Rajamani (2004).

100-kernel weight expressed high heritability (99.58 %), high genetic gain (29.81 %) and high genetic advance (10.20 %) suggested the involvement of additive gene action for governing this character. The selection may be effective for improvement in 100- kernel weight. Similar results for 100- kernel weight were reported by; Bhagat *et al.* (1986), Deshmukh *et al.* (1986), Reddi (1986a), Azad and Hamid (1987), Manohran and Ramlingam (1990), Reddi *et al.* (1991), Manoharan (1993), Manohran and Ramlingam (1993), Ventakramana (2001), Reddy (1994), Singh (1998), Vasanthi *et al.* (1998), Yadav *et al.* (1998), Singh and Singh (1999), Nazar-Ali *et al.* (2000), Prakash *et al.* (2000), Venkatramana *et al.* (2001), Dashora and Nagda (2002), Mothilal *et al.* (2004), Wani *et al.* (2004), Golakia *et al.* (2005), John *et al*. (2009) and Korat *et al.* (2009).

4.3.13 Oil content

Estimates of oil content revealed that genotypic coefficient of variation (18.62 %) and phenotypic coefficient of variation (18.72 %) were moderate in magnitude for this character. Similar findings for moderate amount of genetic variability for oil content in groundnut were also reported by Chauhan and Shukla (1985) Deshmukh *et al.* (1986), Manoharan (1993), Prakash *et al.* (2000) and Golakia *et al.* (2005).

The estimates of heritability (98.98 %) and genetic gain (38.17 %) for oil content were high. High heritability coupled with high genetic gain were also earlier reported by Manohran and Ramlingam (1993), Manoharan (1993), Prakash *et al.* (2000), Venkatramana *et al.* (2000*)*, Dashora and Nagda (2002).

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 plant height (14.19 %), number of mature pods per plant (21.86 %), dry pods yield per plant (23.05 %), Kernel yield per plant (19.50 %), Biological yield per plant (24.88 %), 100 Kernel weight (14.50 %) and oil content (18.62 %).

Whereas, moderate estimates were found for sound mature kernels (8.96 %), harvest index (8.16 %). For days to 50% flowering (5.45 %), days to maturity (0.83 %) and shelling percentage (5.19 %) both GCV and PCV estimates were found low.

The estimates of heritability were moderate to high for all the characters. However, maximum heritability was found for 100 kernel weight (99.58 %) followed by oil content (98.98 %) and sound mature kernels (98.75 %). While, maximum genetic gain was observed for biologocal yield per plant (50.78 %) followed by dry pods yield per plant (42.75 %) and number of mature pods per plant (42.83 %).

The maximum genetic advance was found for biological yield per plant (15.01 %) followed by sound mature kernel (14.32 %) and oil content (12.95 %). In general, moderate to high heritability coupled with moderate to high genetic gain and genetic advance for 100 kenel weight (99.58 % , 29.81% and 10.20), oil content (98.98 %, 38.17% and 12.95%) and sound mature kernels (98.75 %, 18.34 % and 14.32 %) indicated involvement of additive gene action and scope of improvement for these characters through selection.

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 character like yield for which direct selection is not very effective, 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).

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	0.47*	0.37
2.	Days to maturity	0.46*	0.36
3.	Plant height (cm)	-0.52**	-0.49*
4.	Number of branches per plant	0.78*	0.66**
5.	Number of mature pods per plant	0.74*	0.71**

7.	Kernel yield per plant (g)		0.88**
8.	Sound mature kernels (%)	-0.43*	-0.40*
9.	Shelling percentage	-0.53*	-0.49*
10.	Biological yield per plant (g)	0.95**	0.90**
11.	Harvest index	0.00	0.01
12.	100-kernel Wt. (g)	0.38	0.36
13.	Oil content (%)	-0.05	-0.05

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

In the present investigation, correlation coefficients were estimated among 13 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 are in accordance with Reddy and Gupta (1992) and Sumathi and Ramnathan (1995).

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 and phenotypic level with number of branches per plant (rg =0.78**, rp =0.66**), number of mature pods per plant (rg =0.74*, rp =0.71**) and biological yield per plant (rg =0.95**, rp =0.90**) . These findings are in accordance with Nadaf and Habib (1989), Manoharan et al. (1990), Mishra and Yadav (1993) and Kavani et al. (2004).

4.4.2 Correlation between kernel yield per plant and other characters:

Kernel yield per plant was positively and significantly correlated at both genotypic and phenotypic level with number of branches per plant (rg =0.67**, rp =0.57**), number of mature pods per plant (rg =0.81**, rp =0.69**) and biological yield per plant (rg =0.96*, rp =0.79**). These findings are in accordance with Uddin et al. (1995), Kavani et al. (2004) and John et al. (2009) [Table 4.4].

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	0.37	0.24
2.	Days to maturity	0.36	0.26
3.	Plant height (cm)	-0.45*	-0.36
4.	Number of branches per plant	0.67**	0.57**
5.	Number of mature pods per plant	0.81**	0.69**
7.	Dry pod yield per plant (g)	1.04	0.88**
8.	Sound mature kernels (%)	-0.37	-0.30
9.	Shelling percentage	-0.35	-0.26
10.	Biological yield per plant (g)	0.96**	0.79**
11.	Harvest index (%)	0.06	0.11
12.	100-kernel Wt. (g)	0.33	0.26
13.	Oil content (%)	-0.00	-0.01

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

4.4.3 Correlation among different characters:

A perusal of table 4.5 revealed existence of positive correlation between days to 50% flowering and days to maturity (rg =0.55**, rp =0.32) at both genotypic as well as phenotypic level. Further, days to 50% flowering exhibited significant positive correlation with number of branches per plant (rg = 0.69**, rp=0.52*) and biological yield per plant (rg =0.54**, rp =0.45*) at both genotypic as well as phenotypic level. Similarly, days to maturity also exhibited significant positive correlation with number of branches per plant (rg =0.71**, rp =0.43*) at phenotypic and genotypic levels (Table 4.5). Similar findings have already been reported by Suneetha et al. (2004) and Singh and Singh (1999).

Likewise, number of branches per plant showed significant positive correlation at genotypic as well as phenotypic levels with number of mature pods per plant (rg =0.57**, rp =0.53**) and biological yield per plant. Character sound mature kernel and shelling percentage showed significant positive correlation with each other at both genotypic as well as phenotypic level(rg =0.53**, rp =0.50*). Manoharan et al.1990) and Vasanthi et al. (1998).

Whereas number of mature pods per plant exhibited significant positive correlation with biological yield only (rg =0.70**, rp =0.67**) at both the levels. Manoharan et al. (1990), also reported the correlation among above traits.

While, harvest index, 100 kernel weight and oil content didn't show positive significant correlation with any character under study.

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

4.5 Molecular Observations

The RAPD markers (Williams *et al.*, 1990) have been increasingly employed for population studies and for analyzing the molecular diversity (Hogbin *et al.*, 1998; Fischer *et al.*, 2000). RAPD technique has the advantage of assessing a greater number of potential polymorphic loci distributed randomly in the genome than allozymes.

Since, varieties of groundnut under study were procured from different centers on AICRIP on Groundnut of the country, it was expected that this pool of germplasm would exhibit considerable diversity for morphological traits, therefore, it was thought justified to find out its diversity with respect to their DNA profile.

Table 4.6: Concentration of DNA in groundnut cultivars

S. No.	Genotypes Name	Code No.	Ratio of A260/A280	Conc. of DNA (ng/µl)
1	GG-2	G1	1.86	826.7
2	GG-3	G2	1.80	466.7
3	GG-4	G3	1.79	212.6
4	GG-5	G4	1.82	455.5
5	GG-7	G5	1.82	569.3
6	GG-8	G6	1.87	842.9
7	JCG-88	G7	1.87	497.0
8	R-2001-2	G8	1.76	481.4
9	R-2001-3	G9	1.79	509.8
10	GAUG-10	G10	1.85	306.0

11	Kadiri-5	G11	1.87	737.0
12	Kadiri-6	G12	1.85	872.1
13	Kadiri-9	G13	1.90	911.9
14	GPBD-4	G14	2.00	466.0
15	ICGV-91114	G15	1.84	558.2
16	JAL-24	G16	1.79	297.3
17	JAL-39	G17	1.88	742.4
18	TG-37-A	G18	1.81	522.6
19	Chico	G19	1.79	370.5
20	Vemana	G20	1.84	930.5
21	TIR-46	G21	1.77	496.5
22	TAG-24	G22	1.82	371.6
23	Pratap Mungphali-1	G23	1.87	538.2
24	Pratap Mungphali-2	G24	1.82	531.7
25	Pratap Raj. Mungphali	G25	1.81	930.0

Characterization of genotypes based on RAPD profile is well documented in groundnut by Bhagwat, *et al*. (2001), Massawe *et al.* (2003), Azzam *et al*. (2007), Vasanthi *et al.* (2008) and Sharaf *et al.* (2011).

Technique of RAPD is simple therefore, can be used in laboratories with limited resources, but requires optimization of the reaction for reproducible results. Once the reaction conditions have been optimized the technique is reliable, reproducible and informative.

Twenty five genotypes of groundnut were examined for DNA polymorphism using 15 decamer primers (OPERON) showing high (G+C) content. Out of 15 primers used, amplification could be obtained with 13 primers, whereas 2 primers *viz.* OPA-5 and OPA-6 failed to show any amplification. Out of 13 primers, 12 primers showed variable degree of polymorphism ranging from 60 per cent (OPA -10) to 100 per cent (OPA -1, OPA -8, OPA -12, OPA -15, OPC -4, OPC-6, OPC- 12 and OPC-13). The primer OPA-9 was monomorphic. Overall polymorphism was found to be 91.02 per cent. Similar results were reported by Reddy, (2004). They reported that 10 primers produced polymorphic bands ranging from 16.6 per cent to 100 per cent and overall polymorphism was 71.4 per cent. The DNA amplification and polymorphism generated among various genotypes of groundnut using random primers are presented in Table 4.7.

Electrophoretic pattern of RAPD profile was studied on 1.5 per cent agarose gel. Only those fragments, which amplified consistently, were considered for analysis. Each RAPD band was assumed to represent a single locus and data were scored as presence of bands (1) and its absence as (0). Results are illustrated in Table 4.7. This table combines the comparative information about total number of fragments with base pairs obtained by all the primers in all groundnut genotypes.

The representative photographs of electrophoresis gels showing RAPD profiles after amplification with different random primers are depicted in plate I, plate II, plate III and plate IV.

Thirteen primers on twenty five groundnut genotypes generated 78 total bands out of which 71 were polymorphic (Table 4.8). The average number of bands per primer was found to be 6.0. Similar results were also reported by Subramanian *et al.* (2000), Amadou *et al.* (2001), Mondal*et. al.* (2005) , and Varsha Kumari *et al.* (2009) in groundnut.

Table 4.8: Polymorphism information of RAPD primers used

S.No.	Primers	Sequences (5'→3')	Total No of bands(a)	Total No of polymorphic bands (b)	Polymorphism %(b/a × 100)
1	OPA-1	CAGGCCCTTC	8	8	100
2	OPA-8	GTGACGTAGG	5	5	100
3	OPA-10	GTGATCGCAG	5	3	60
4	OPA-12	TCGGCGATAG	4	4	100
5	OPA-15	TTCCGAACCC	6	6	100
6	OPC-4	CCGCATCTAC	6	6	100
7	OPC-5	GATGACCGCC	6	4	67
8	OPC-6	GAACGGACTC	9	9	100
9	OPC-11	AAAGCTGCGG	9	7	77
10	OPC-12	TGTCATCCCC	11	11	100
11	OPC-13	AAGCCTCGTC	6	6	100
12	OPC-15	GACGGATCAG	3	2	66

13	OPA-9	GGGTAACGCC	A		
14	OPA-5	AGGGGTCTTG	NA		
15	OPJ-6	TCGTTCCGCA	NA		
		Total	78	71	91.02

The maximum number of amplicons were produced by the primers OPC-11 (156) followed by OPC-12 (143), respectively. The minimum number of amplicons were produced by the primer OPC-6 (50). Among all the primers tested, OPC-12 proved to be the best primer as it produced 143 amplicons and11 scorable bands of which 11 were polymorphic. Average polymorphism was 100 per cent. Primer OPC-6 produced 9 scorable bands of which 9 were polymorphic which amount to 100 per cent polymorphism. Primer OPA-1 produced 8 scorable bands of which 8 bands were polymorphic which amount to 100 per cent polymorphism. While Primer OPA-15, OPC-4 and OPC-13 produced 6 scorable bands of which all 6 were polymorphic which amount to 10 per cent polymorphism.

The results obtained were in conformity with the earlier findings by Bhagwat *et al.* (1997), Massawe *et al.* (2003) and Reddy, (2004). Thus, it is opined that RAPD assays can be efficient in identifying DNA polymorphism provided suitable primers are used.

Table 4.9: Details of the random primers used for amplification of genomic DNA of groundnut

Total number of primers	15
Number of primers which showed amplification	13
Number of primer which did not show amplification	2
Number of primers which showed polymorphism	12
Number of primers which did not showed polymorphism	1
Total number of bands	78
Total number of polymorphic bands	71
Total number of monomorphic bands	4
Total number of amplicons produce	1181
Total number of polymorphic amplicons	263

Assessment of Relationship between Groundnut Genotypes based on Morphological Characters and Cluster Analysis based on RAPD

Genetic similarity estimates based on RAPD banding patterns were calculated using method of Jaccard's coefficient analysis (Jaccard, 1908). The similarity coefficient matrix generated was subjected to algorithm UPGMA (Unweighted Pair Group Method with Arithmetic Mean) and dendrogram was generated using NTSYSpc 2.02 program (Rohlf, 2004).

The Jaccard's similarity co-efficient between different varieties ranged from 0.22 to 0.88 with a mean of 0.58 (Table 4.10). The maximum similarity coefficient (0.88) was observed between G5 and G4, G6 and G4 and G12 and G11 followed by G6 and G5, G8 and G6 showed similarity of 0.86 percent. The minimum similarity coefficient 0.22 (maximum diversity) was observed between G14 and G2, G14 and G10. Similar results were obtained by Dwivedi *et al*. (2001) and Vasanthi *et al.* (2008).

Dendrogram

A dendrogram was constructed using Jaccard's similarity coefficients obtained for DNA banding pattern observed on the 25 genotypes of groundnut employing NTSYSpc programme (Fig. 4.1). The cluster analysis on the genotypes revealed 7 distinct clusters. The salient finding of the clustering are described as follows:

(1) The genotype G14 (GPBD-4) was entirely separated from all other genotypes and had scored values of lower order with all the genotypes (average similarity coefficiency being 0.35 over rest of the genotypes and hence, maximum diverse from the rest).

(2) The genotypes G11 (Kadiri 5) and G12 (Kadiri 6) were in same cluster with very high confidence limit and showed similarity for days to 50% flowering and number of branches per plant [subcluster within cluster 7].

(3) Another sub cluster within cluster 7 had two genotypes viz., G3 (GG-4) and G5 (GG-7) which also showed similarity for number of branches per plant and sound mature kernel percentage.

(4) Similarly, genotypes G2 (GG-3) and G4 (GG-5) had similar number of mature pods per plant [sub cluster within Cluster 5].

(5) Two genotypes viz., G3 (GG-4) and G5 (GG-7) had similarity for 100 kernel weight, dry pod yield, kernel yield per plant, number of branches per plant and number of mature pods per plant [sub cluster within Cluster 3]. Lang *et al*.(2007) also reported formation of distinct clusters and sub clusters from RAPD pattern among 29 groundnut genotypes.

On the basis of present study, it may be concluded that RAPD profile of the genotypes, on account of its easy detection and dependability, can be used for the diversity studies. Further, the groups/ clusters obtained by dendrogram could also be distinguished by similarity for the morphological characteristics within each group. Such an association may be used for more effective breeding programmes.

Table 4.5: Correlation matrix

SN	Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of mature pods per plant	Dry pods yield per plant (g)	Kernel yield per plant (g)	Sound mature kernels (%)	Shelling percentage	Biological yield per plant	Harvest index (%)	100 KERNEL Wt. (g)	Oil content (%)
1	Days to 50% flowering		0.55**	-0.72**	0.69**	0.27	0.47*	0.37	-0.64**	-0.69**	0.54**	-0.31	0.24	-0.11
2	Days to maturity	0.32		-0.44*	0.71**	0.09	0.46*	0.36	-0.62**	-0.61**	0.57**	-0.28	0.13	0.06
3	Plant height (cm)	-0.61**	-0.31		-0.65**	-0.54**	-0.52**	-0.45*	0.62**	0.64**	-0.51**	0.11	-0.03	0.13
4	Number of branches per plant	0.52**	0.43*	-0.54**		0.57**	0.78**	0.67**	-0.50*	-0.70**	0.79**	-0.25	0.21	-0.08
5	Number of mature pods per plant	0.25	0.04	-0.50*	0.53**		0.74**	0.81**	-0.28	-0.26	0.70**	-0.07	-0.02	0.19
6	Dry pods yield per plant (g)	0.37	0.36	-0.49*	0.66**	0.71**			-0.43*	-0.53**	0.95**	0.00	0.38	-0.05
7	Kernel yield per plant (g)	0.24	0.26	-0.36	0.57**	0.69**	0.88**		-0.37	-0.35	0.96**	0.06	0.33	-0.00
8	Sound mature kernels (%)	-0.56**	-0.42*	0.60**	-0.40*	-0.26	-0.40*	-0.30		0.53**	-0.45*	0.09	-0.10	-0.03
9	Shelling percentage	-0.58**	-0.45*	0.62**	-0.58**	-0.24	-0.49*	-0.26	0.50*		-0.57**	0.29	-0.42*	0.12
10	Biological yield per plant	0.45*	0.39	-0.50*	0.69**	0.67**	0.90**	0.79**	-0.44*	-0.55**		-0.35	0.35	-0.02
11	Harvest index (%)	-0.28	-0.20	0.11	-0.21	-0.04	0.01	0.11	0.09	0.28	-0.33		-0.01	-0.02
12	100 KERNEL Wt. (g)	0.21	0.09	-0.03	0.17	-0.02	0.36	0.26	-0.10	-0.41*	0.35	-0.01		-0.24
13	Oil content (%)	-0.09	0.04	0.13	-0.08	0.18	-0.05	-0.01	-0.03	0.12	-0.02	-0.02	-0.24	

IV. EXPERIMENTAL RESULTS

The present investigation entitled “Heterosis and Combining Ability Analysis for Yield and its Contributing Traits in Early Maturing Maize (*Zea mays* L.) Genotypes” consisted of 50 genotypes (9 lines,36 single cross hybridsand 5 standard checks *viz.*,Bio-9637, Pratap Hybrid Maize-1, EI-116, EI-364 and Vivek Hybrid-9). Crosses were developed using diallel mating design without reciprocals. The experiment was conducted at Instructional Farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur during *kharif* 2012. The results obtained after statistical analysis are presented under the following sub-heads:

4.1 Analysis of variance and mean performance

4.2 Heterosis

4.3 Combining ability analysis

4.1 ANALYSIS OF VARIANCE AND MEANPERFORMANCE

The analysis of variance for all the 16 characters is presented in Table 4.1. The character wisemean performance of parents, hybrids and checksis presented in Appendix-I and II.

The mean squares due to genotypes were significant for all the traits under study except number of cobs per plant. The mean squares due to parents were significant for all the characters except for cob leaf area, number of cobs per plant and ear length.Mean squares due to hybrids were significant forall the charactersexcept for days to 50 per cent silking, number of cobs per plant and shelling percentage

Mean squares due to parents v/s hybrids were also significant for all the characters except for days to 50 per cent silking, number of leaves per plant, number of cobs per plant, 100 grain weight, harvest index and shelling percentage.

Table 4.1: Analysis of variance for characters under study

SN	Characters	Source					
		Rep	Genotype	Parent	F1	P vs F1	Error
		[2]	[44]	[8]	[35]	[1]	[88]
1	Days to 50% tasselling	67.05**	19.03**	41.83**	13.01**	47.40**	6.85
2	Days to 50% silking	53.25**	16.05**	29.64**	12.85	19.26	8.88
3	Days to maturity	43.88**	18.87**	44.37**	12.47*	38.93*	6.85
4	Plant height (cm)	4104.62**	868.59**	1226.17**	746.84**	2269.35**	258.86
5	No. of leaves/plant	2.007*	1.52**	2**	1.46**	0.029	0.62
6	Tassel length (cm)	4.45	19.007**	5.23*	7.89**	518.22**	2.48
7	No. of primary branches/tassel	3.16	15.59**	4.06*	11.69**	244.01**	1.50
8	Cob leaf area (cm^2)	293.52	1333**	614.06	1269.45**	9308.45**	318.97
9	No. of cobs/plant	0.051	0.027	0	0.033	0.029	0.029
10	Ear length (cm)	1.69	7.80**	2.5	6.53**	94.58**	2.29
11	No. of grain rows/ear	3.05*	3.59**	5.25**	2.47**	29.4**	0.99
12	100 grain wt. (g)	29.54	38.62**	73.33**	31.59**	6.89	10.09
13	Grain yield/plant (g)	1051.59*	978.01**	2359.63**	589.17**	3534.34**	200
14	Harvest index (%)	15.68	13.25**	22.49**	11.41**	3.73	5.85
15	Shelling percentage	58.88*	37.57**	95.68**	24.13	43.19	16.38
16	Protein content (%)	0.15**	3.96**	2.08**	4.34**	6.05**	0.011

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

The character wise mean values were as follows:

4.1.1 Days to 50 per cent tasselling (Appendix-I)

The days to50 per cent tasselling varied from 52.33 (P3 x P5) to 64.67 days (P6). The best check for this trait was Vivek Hybrid-9 (50.67 days). No genotypes were found significantly superior from the best check.

4.1.2 Days to 50 per cent silking (Appendix-I)

The days to 50 per cent silking varied from 53.33 (P3 x P5 and P6 x P9) to 63.33 days (P8 x P9). The best check for this trait was Vivek Hybrid-9 (52.33 days). No genotypes were found significantly superior from the best check.

4.1.3 Days to maturity (Appendix-I)

The days to maturity varied from 81.33 (P6 x P9) to 93.67 days (P6). For this trait also, the best check was Vivek Hybrid-9 (80.33 days). No genotypes were found significantly superior from the best check.

4.1.4 Plant height (cm) (Appendix-I)

The mean values for plant height varied from 140.00 (P2) to 228.33 cm (P2 x P9). The best checks for this trait are EI-116 and EI-364 (170.00 cm). From best check, 3 genotypes were found significantly superior viz., P2 (140.00 cm), P8 (165.00 cm) and P8 x P9 (153.33 cm).

4.1.5 Number of leaves per plant (Appendix-I)

The number of leaves per plant varied from 12.33 (P2) to 15.33 (P2 x P9). Best checks for this character are Pratap Hybrid Maize-1 and EI-116 (15.00). One genotype P2 x P9 was found significantly superior than these best checks. 12 genotypes (2 parents and 10 hybrids) were at par to the best genotype P2 x P9.

4.1.6 Tassel length (cm) (Appendix-I)

The tassel length varied from 26.33 (P5) to 37.00 cm (P6 x P9). Best check for the trait is EI-364 (35.33 cm). From best check, 4 genotypes viz., P6 x P9 (37.00), P2 x P5 (36.00), P3 x P8 and P7 x P8 (35.67 cm) were significantly superior.

4.1.7 Number of primary branches per tassel (Appendix-I)

The mean values for number of primary branches per tassel ranged from 12.33 (P4) to 23.00 (P5 x P6).The best check was EI-116 (19.33). 4 genotypes viz., P2 x P3 (20.00), P4 x P7 (20.33), P4 x P9 (21.00) and P5 x P6 (23.00) were significantly superior from the best check.

4.1.8 Cob leaf area (cm^2) (Appendix-I)

Cob leaf area varied from 76.03 (P8 x P9) to 174.03 cm^2 (P2 x P9).The best check was Pratap Hybrid Maize-1 (139.27 cm^2). Twelve genotypes were found significantly superior from the best check.

4.1.9 Ear length (cm) (Appendix-II)

The ear length varied from 11.67 (P8) to 17.67 cm (P2 x P7 and P2 x P9). Best check for this trait was Pratap Hybrid Maize-1 (15.00 cm). Twenty genotypes were found significantly superior from the best check. Out of these, four were at par to the best genotypes P2 x P7 and P2 x P9.

4.1.10 Number of grain rows per ear (Appendix-II)

The number of grain rows per ear ranged from 10.00 (P6) to 16.00 (P1 x P4 and P3 x P4).The best check for this character was Vivek Hybrid-9 (15.33). From this check, only two genotypes were significantly superior viz., P1 x P4 and P3 x P4 (16.00).

4.1.11 100 grain weight (g) (Appendix-II)

100 grain weight ranged from 17.33 (P5) to 31.67 g (P3 and P1 x P4). The best check was Pratap Hybrid Maize-1 (29.67 g). Five genotypes i.e. two inbreds viz., P3 (31.67) and P4 (30.67 g) and three hybridsviz., P1 x P4 (31.67) and P1 x P8 and P2 x P7 (30.00 g) were significantly superior from this check.

4.1.12 Grain yield per plant (g) (Appendix-II)

The range of grain yield per plant varied from 51.73 (P1) to 126.10 g (P9). Best check for this character was Bio-9637 (117.03 g). Parent P9 (126.10 g) and hybrids P2 x P9 (118.40) and P3 x P7 (122.70 g) were significantly superior from the best check.

4.1.13 Harvest index (%) (Appendix-II)

The harvest index ranged from 31.62 (P6) to 39.91% (P3). The best check was Vivek Hybrid-9 (38.37%). From best check, five genotypes viz., P3 (39.91), P7 (38.79), P3 x P6 (38.45), P3 x P9 (38.77) and P5 x P8 (38.42%)were significantly superior.

4.1.14 Shelling percentage (Appendix-II)

The range of shelling percentage varied from 69.89 (P8) to 88.29% (P3 x P9). The best check was Vivek Hybrid-9 (85.89%). One parent P4 (85.93) and two hybrids P3 x P9 (88.29) and P4 x P8 (86.41%) were significantly superior from this check.

4.1.15 Protein content (%) (Appendix-II)

The protein content ranged from 8.00 (P2 x P4) to 12.77% (P2 x P3).Best check was Bio-9637 (11.37%) for this trait. Six hybrids were significantly superior from this check and out of these, two genotypes P1 x P6 (12.17) and P2 x P6 (12.57%) were at par to the best genotype.

4.2 MAGNITUDE OF HETEROSIS

In present investigation, heterosis, heterobeltiosis and economic heterosis was estimated. For all the characters, positive values were considered desirable whereas for days to 50 per cent tasselling, days to 50 per cent silking, days to maturity and plant height negative values were desirable. The character wise results were as follows:

4.2.1 Days to 50 per cent tasselling

The heterosis ranged from -14.36 (P6 x P9) to 12.24 per cent (P8 x P9). Ten crosses exhibited negative significant heterosis and two crosses positive significant heterosis. Heterobeltiosis varied significantly from -10.61 (P1 x P2) to -8.20 per cent (P1 x P6). None of the hybrid showed economic heterosis for this trait.

4.2.2 Days to 50 per cent silking

The relative heterosis ranged from -12.33 (P6 x P9) to 11.76 per cent (P8 x P9). Five hybrids exhibited negative significant heterosis while one showed positive significant heterosis. Four hybrids exhibited negative significant heterobeltiosis with magnitude varied from -10.99 (P1 x P2) to -8.06 per cent (P1 x P6). None of the hybrid exhibited significant negative economic heterosis.

Table 4.2 Extent of heterosis for Days to 50% tasselling and silking

SN.	Crosses	Days to 50% tasselling			Days to 50% silking		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-11.60**	-10.61**		-11.96**	-10.99**	
2.	P1 x P3	-1.97			-2.49		
3.	P1 x P4	-2.05			-3.15		
4.	P1 x P5	-4.13	-3.33		-4.04	-3.78	
5.	P1 x P6	-10.88**	-8.20*		-8.56*	-8.06*	
6.	P1 x P7	-2.26			-0.56		
7.	P1 x P8	-2.62			-2.58		
8.	P1 x P9	-6.70*	-4.57		-5.79	-3.39	
9.	P2 x P3	-1.99			-1.40		
10.	P2 x P4	-3.26			-2.61		
11.	P2 x P5	-9.75**	-9.50**		-8.45*	-7.69	
12.	P2 x P6	-8.31**	-4.47		-5.41	-3.85	
13.	P2 x P7	-1.14			0.56		
14.	P2 x P8	0.88			0.87		
15.	P2 x P9	-6.78*	-5.71		-5.85	-4.52	
16.	P3 x P4	-0.61			0.00		
17.	P3 x P5	-10.80**	-8.72*		-11.11**	-8.57*	
18.	P3 x P6	-4.37			-3.03		
19.	P3 x P7	-1.46	-1.17		-0.29		
20.	P3 x P8	3.01			4.14		
21.	P3 x P9	-3.17	-2.33		-3.41	-2.86	
22.	P4 x P5	3.55			2.87		
23.	P4 x P6	-7.39*			-3.13		
24.	P4 x P7	5.78			5.67		
25.	P4 x P8	8.18*			6.75		
26.	P4 x P9	6.31			6.47		
27.	P5 x P6	-5.88*	-2.22		-2.95	-2.16	
28.	P5 x P7	0.28			0.84		
29.	P5 x P8	-0.59			0.57		
30.	P5 x P9	0.28			0.55		
31.	P6 x P7	-5.21			-1.67		
32.	P6 x P8	-3.39			-0.85		
33.	P6 x P9	-14.36**	-9.71**		-12.33**	-9.60*	
34.	P7 x P8	2.72			4.48		
35.	P7 x P9	2.31			3.15		
36.	P8 x P9	12.24**			11.76**		

*,** Significant at 5 and 1 percent respectively

4.2.3 Days to maturity

The heterosis for days to maturity varied from -10.29(P6 x P9) to 7.24 per cent (P8 x P9). Out of these, 7 crosses showed significant negative heterosis, while, 4 crosses exhibited positive significant heterosis. The estimates of hetero beltiosis ranged from -7.84(P1 x P2) to

-5.73 per cent (P3 x P5) for this trait.None of the hybrid exhibited economic heterosis for this trait.

4.2.4 Plant height (cm)

Estimates of mid-parent heterosis for plant height ranged from -13.21 (P8 x P9) to 39.09 per cent (P2 x P9). Only one hybrid expressed significant negative heterosis, whereas, 8 crosses exhibited significant positive heterosis. None of the hybrid showed significant negative heterobeltiosis and economic heterosis for this trait.

Table 4.3: Extent of heterosis for Days to maturity and Plant height (cm)

SN	Crosses	Days to maturity			Plant height (cm)		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-8.52**	-7.84**		27.08**	12.96	3.39
2.	P1 x P3	-2.62	-0.76		7.76	6.31	
3.	P1 x P4	-0.97			-10.43		
4.	P1 x P5	-2.95	-2.59		-11.28		
5.	P1 x P6	-7.78**	-6.25**		3.93		0.85
6.	P1 x P7	-1.32			4.39		0.85
7.	P1 x P8	-2.31			10.14	5.56	
8.	P1 x P9	-3.93	-2.28		1.36		
9.	P2 x P3	-1.51	-0.38		33.33**	17.12*	10.17
10.	P2 x P4	-0.97			8.74		
11.	P2 x P5	-6.32**	-5.97*		19.54**	6.09	
12.	P2 x P6	-4.92*	-2.61		2.44		
13.	P2 x P7	0.95			25.49**	6.67	8.47
14.	P2 x P8	0.39			30.05**	20.20*	0.85
15.	P2 x P9	-4.71*	-3.80		39.09**	21.24**	16.10*
16.	P3 x P4	-0.20			16.74**	11.48	15.25*
17.	P3 x P5	-7.14**	-5.73*		0.27		
18.	P3 x P6	-3.13			10.34	5.79	8.47
19.	P3 x P7	0.19			3.03		0.85
20.	P3 x P8	2.75			20.00**	13.51	6.78
21.	P3 x P9	-2.86	-2.67		8.04	7.08	2.54
22.	P4 x P5	2.52			-1.04		
23.	P4 x P6	-2.28			-7.00		
24.	P4 x P7	4.78*			-9.09		
25.	P4 x P8	4.67*			7.69		0.85
26.	P4 x P9	4.72*			-5.53		
27.	P5 x P6	-3.81	-1.85		2.88		
28.	P5 x P7	0.19			-1.05		
29.	P5 x P8	-0.00			4.15		
30.	P5 x P9	0.19			4.79	2.65	
31.	P6 x P7	-1.86			-6.22		
32.	P6 x P8	-1.70			4.55		
33.	P6 x P9	-10.29**	-7.22**		0.85		
34.	P7 x P8	3.37			0.46		
35.	P7 x P9	-1.92	-0.78		-7.30		
36.	P8 x P9	7.24**			-13.21*		

*,** Significant at 5 and 1 percent respectively

4.2.5 Number of leaves per plant

The heterosis over mid parent for number of leaves per plant ranged from -11.63 (P1 x P6) to 15.38per cent (P2 x P7). 6 crosses exhibited significant positive heterosis and 2 hybrids showed negativesignificantheterosis. Heterobeltiosisexhibited by only one cross P2 x P7 (9.76 per cent). Whereas, none of the hybrid showed significant positive economic heterosis.

Table 4.4 Extent of heterosis for No. of leaves/plant and Tassel length (cm)

SN.	Crosses	No. of leaves/plant			Tassel length (cm)		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	12.82**	7.32		4.00		
2.	P1 x P3	-2.44			21.21**	19.05**	
3.	P1 x P4	2.33			24.26**	23.53**	
4.	P1 x P5	-7.14			16.56**	13.10**	
5.	P1 x P6	-11.63**			23.35**	22.62**	
6.	P1 x P7	-2.44			22.54**	19.10**	0.00
7.	P1 x P8	-1.20			6.36	3.37	
8.	P1 x P9	-2.38			15.29**	13.95**	
9.	P2 x P3	10.26*	4.88		10.47**	4.40	
10.	P2 x P4	-7.32			15.91**	12.09**	
11.	P2 x P5	5.00			27.06**	18.68**	1.89
12.	P2 x P6	-2.44			10.34**	5.49	
13.	P2 x P7	15.38**	9.76*	0.00	13.33**	12.09**	
14.	P2 x P8	11.39**	4.76		16.67**	15.38**	
15.	P2 x P9	15.00**	6.98	2.22	8.47*	5.49	
16.	P3 x P4	-4.65			18.07**	15.29**	
17.	P3 x P5	-2.38			26.25**	24.69**	
18.	P3 x P6	4.65	0.00	0.00	24.39**	22.89**	
19.	P3 x P7	0.00			15.29**	10.11*	
20.	P3 x P8	8.43*	7.14	0.00	25.88**	20.22**	0.94
21.	P3 x P9	4.76	2.33		13.77**	10.47*	
22.	P4 x P5	-4.55			23.17**	18.82**	
23.	P4 x P6	-4.44			20.24**	18.82**	
24.	P4 x P7	-2.33			14.94**	12.36**	
25.	P4 x P8	3.45	0.00	0.00	18.39**	15.73**	
26.	P4 x P9	-2.27			20.47**	19.77**	
27.	P5 x P6	-4.55			27.16**	24.10**	
28.	P5 x P7	-2.38			11.90**	5.62	
29.	P5 x P8	-8.24*			16.67**	10.11*	
30.	P5 x P9	2.33	2.33		18.79**	13.95**	
31.	P6 x P7	0.00			9.30*	5.62	
32.	P6 x P8	-1.15			11.63**	7.87	
33.	P6 x P9	-0.00			31.36**	29.07**	4.72
34.	P7 x P8	1.20	0.00		20.22**	20.22**	0.94
35.	P7 x P9	-4.76			14.29**	12.36**	
36.	P8 x P9	-3.53			6.29	4.49	

*,** Significant at 5 and 1 percent respectively

4.2.6 Tassel length (cm)

The range of relative heterosis observed from8.47 (P2 x P9) to 31.36 per cent (P6 x P9) for this trait. 33 hybrids exhibited significant positive heterotic effects out of 36 hybrids. The minimum and maximum estimates for heterobeltiosis were 10.11 (P3 x P7 and P5 x P8)and29.07 per cent (P6 x P9) for this character, respectively. 27F_1 hybrids showed positive estimate in desirable direction of heterobeltiosis for tassel length. None of the hybrids showed significant positive economic heterosis for this trait.

4.2.7 Number of primary branches per tassel

The minimum and maximum values of heterotic effects over mid parent were 14.94 (P6 x P8) and 62.35per cent (P5 x P6) respectively. 26 crosses showed positive significant relative heterosis. The significant positive estimate of heterobeltiosis was observed in 25 hybrids, with range varied from 12.24 (P5 x P7) to 56.82 per cent (P5 x P6). In case of standard heterosis, only one hybrid (P5 x P6) showed significant positive value of 18.97 per cent.

4.2.8 Cob leaf area (cm^2)

For cob leaf area, the estimates of heterosis over mid parent depicted 12 crosses showing significant positive value having the range from20.91 (P6 x P9) to 65.46per cent (P2 x P9). 8 hybrids exhibited positive significant heterobeltiosis with the magnitude varied from 24.39 (P4 x P7) to 64.92 per cent (P2 x P7). Only one hybrid (P2 x P9) showed significant positive standard heterosis (24.96 per cent).

Table 4.5 Extent of heterosis for No. of primary branches/tassel and cob leaf area (cm^2)

SN	Crosses	No. of primary branches/tassel			Cob leaf area		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	18.60**	13.33*		5.12	1.89	
2.	P1 x P3	40.74**	39.02**		16.42	6.69	
3.	P1 x P4	41.03**	34.15**		-20.36		
4.	P1 x P5	4.88	4.88		7.36	6.48	
5.	P1 x P6	1.18			27.56*	17.21	6.29
6.	P1 x P7	4.44			17.81	13.89	
7.	P1 x P8	16.67**	13.95*		53.43**	41.81**	7.73
8.	P1 x P9	32.56**	26.67**		7.01	4.47	
9.	P2 x P3	41.18**	33.33**	3.45	4.95		
10.	P2 x P4	39.02**	26.67**		26.59*	11.54	4.33
11.	P2 x P5	27.91**	22.22**		7.83	3.69	
12.	P2 x P6	10.11	8.89		-5.11		
13.	P2 x P7	-10.64			65.37**	64.92**	17.59
14.	P2 x P8	18.18**	15.56*		57.40**	49.85**	6.85

SN	Crosses	No. of primary branches/tassel			Cob leaf area		
		Het	Hb	EH	Het	Hb	EH
15.	P2 x P9	15.56**	15.56*		65.46**	56.69**	24.96*
16.	P3 x P4	42.86**	37.50**		6.52	5.19	
17.	P3 x P5	35.80**	34.15**		3.81		
18.	P3 x P6	33.33**	27.27**		5.42	5.12	
19.	P3 x P7	3.37			20.05	6.69	
20.	P3 x P8	18.07**	13.95*		8.89		
21.	P3 x P9	27.06**	20.00**		36.72**	28.13*	16.87
22.	P4 x P5	35.90**	29.27**		12.52	2.71	
23.	P4 x P6	40.74**	29.55**		-1.34		
24.	P4 x P7	41.86**	24.49**	5.17	41.49**	24.39*	16.35
25.	P4 x P8	42.50**	32.56**		17.29		
26.	P4 x P9	53.66**	40.00**	8.62	4.64		
27.	P5 x P6	62.35**	56.82**	18.97**	18.67	9.87	
28.	P5 x P7	22.22**	12.24*		53.41**	47.13**	13.64
29.	P5 x P8	2.38	0.00		51.55**	39.01**	7.37
30.	P5 x P9	9.30	4.44		20.54	18.64	
31.	P6 x P7	7.53	2.04		16.88	4.14	
32.	P6 x P8	14.94*	13.64*		11.54		
33.	P6 x P9	28.09**	26.67**		20.91*	13.62	3.04
34.	P7 x P8	15.22**	8.16		31.05*	25.08	
35.	P7 x P9	4.26			9.90	3.81	
36.	P8 x P9	25.00**	22.22**		-24.28		

*,** Significant at 5 and 1 percent respectively

4.2.9 Ear length (cm)

Relative heterosis for this trait varied from 16.67 (P6 x P9) to 41.33 per cent (P2 x P7). 16 crosses exhibited significant positive heterosis. The significant positive estimate of heterobeltiosis was observed in 9 hybrids, with range varied from 21.05 (P2 x P5) to 39.47 per cent (P2 x P7). Two hybrids (P2 x P7 and P2 x P9) showed positive significant economic heterosis with the magnitude of 17.78 per cent.

4.2.10 Number of grain rows per ear

The range of heterotic effects over mid parent observed from -12.20 (P1 x P5) to 33.33 (P2 x P6) for number of grain rows per ear. 12 crosses exhibited significant positive heterosis and 1 cross showed negative significant heterosis.5 hybrids exhibited significant positive heterobeltiosis with range from 16.67 (P4 x P8) to 26.32 (P1 x P4 and P3 x P4). None of the hybrid showed positive significant economic heterosis for this character.

Table 4.6: Extent of heterosis for ear length (cm) and No. of grain rows/ear

SN	Crosses	Ear length			No. of grain rows/ear		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	14.67	13.16		2.70		
2.	P1 x P3	15.00	9.52	2.22	10.53	10.53	
3.	P1 x P4	-10.00			29.73**	26.32**	4.35
4.	P1 x P5	2.63	2.63		-12.20*		
5.	P1 x P6	20.99**	13.95	8.89	17.65**	5.26	
6.	P1 x P7	10.53	10.53		5.26	5.26	
7.	P1 x P8	39.73**	34.21**	13.33	2.70		
8.	P1 x P9	6.33	2.44		5.00	0.00	
9.	P2 x P3	8.86	2.38		-2.70		
10.	P2 x P4	18.99*	11.90	4.44	22.22**	22.22**	
11.	P2 x P5	22.67**	21.05*	2.22	5.00		
12.	P2 x P6	0.00			33.33**	22.22**	
13.	P2 x P7	41.33**	39.47**	17.78*	13.51*	10.53	
14.	P2 x P8	33.33**	29.73**	6.67	11.11	11.11	
15.	P2 x P9	35.90**	29.27**	17.78*	7.69	0.00	
16.	P3 x P4	14.29	14.29	6.67	29.73**	26.32**	4.35
17.	P3 x P5	17.50*	11.90	4.44	2.44		
18.	P3 x P6	12.94	11.63	6.67	23.53**	10.53	
19.	P3 x P7	12.50	7.14	0.00	0.00		
20.	P3 x P8	22.08**	11.90	4.44	13.51*	10.53	
21.	P3 x P9	25.30**	23.81**	15.56	5.00	0.00	
22.	P4 x P5	17.50*	11.90	4.44	10.00		
23.	P4 x P6	8.24	6.98	2.22	21.21**	11.11	
24.	P4 x P7	27.50**	21.43*	13.33	8.11	5.26	
25.	P4 x P8	14.29	4.76		16.67**	16.67*	
26.	P4 x P9	1.20	0.00		2.56		
27.	P5 x P6	13.58	6.98	2.22	2.70		
28.	P5 x P7	34.21**	34.21**	13.33	-7.32		
29.	P5 x P8	28.77**	23.68*	4.44	0.00		
30.	P5 x P9	13.92	9.76	0.00	-2.33		
31.	P6 x P7	11.11	4.65	0.00	11.76		
32.	P6 x P8	15.38	4.65	0.00	21.21**	11.11	
33.	P6 x P9	16.67*	13.95	8.89	22.22**	4.76	
34.	P7 x P8	20.55*	15.79		8.11	5.26	
35.	P7 x P9	6.33	2.44		5.00	0.00	
36.	P8 x P9	-13.16			7.69	0.00	

*,** Significant at 5 and 1 percent respectively

4.2.11 100 grain weight (g)

The heterosis for 100 grain weight varied from -26.58 (P6 x P8) to 37.40 g (P1 x P8).9 crosses exhibited positive significant heterosis and 4 crosses exhibited negative significant heterosis. Heterotic response over better parent was depicted by one hybrid, P2 x P7 (30.43 g). None of the hybrid showed positive heterotic response for economic heterosis.

4.2.12 Grain yield/plant (g)

The heterosis ranged from -31.06 (P8 x P9) to 109.13 g (P1 x P6). 14 crosses showed significant positive heterosis and 2 hybrids showed negative significant heterosis.

Heterobeltiosis ranged significantly positive from 29.01 (P1 x P8) to 99.42 g (P1 x P6). None of the hybrid showed estimates of economic heterosis in positive direction.

Table 4.7 Extent of heterosis for 100 grain wt. (g) and Grain yield/plant (g)

SN	Crosses	100 grain wt.			Grain yield/plant		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	31.20**	18.84		33.84	21.49	
2.	P1 x P3	11.26			27.73*		
3.	P1 x P4	28.38**	3.26	6.74	-21.77		
4.	P1 x P5	1.85			92.70**	91.42**	
5.	P1 x P6	19.42*	0.00		109.13**	99.42**	
6.	P1 x P7	18.03	9.09		6.92		
7.	P1 x P8	37.40**	20.00	1.12	63.67**	29.01*	
8.	P1 x P9	20.00	8.70		-5.87		
9.	P2 x P3	-8.54			5.67		
10.	P2 x P4	-20.50*			9.10		
11.	P2 x P5	9.09			51.44**	38.31*	
12.	P2 x P6	-1.32			53.90**	46.14*	
13.	P2 x P7	33.33**	30.43**	1.12	39.29**	22.83	
14.	P2 x P8	18.06	13.33		-2.85		
15.	P2 x P9	21.74*	21.74		24.94*		1.17
16.	P3 x P4	-15.51*			-0.14		
17.	P3 x P5	-7.48			43.06**	6.57	
18.	P3 x P6	-14.61			33.77**	2.52	
19.	P3 x P7	-0.62			29.09**	14.64	4.84
20.	P3 x P8	-10.59			-1.30		
21.	P3 x P9	3.66			-1.29		
22.	P4 x P5	-5.56			21.62		
23.	P4 x P6	-18.86*			6.17		
24.	P4 x P7	-15.19			-13.12		
25.	P4 x P8	-13.77			-2.81		
26.	P4 x P9	-4.35			-21.29*		
27.	P5 x P6	27.41**	3.61		88.31**	80.71**	
28.	P5 x P7	35.59**	21.21		49.18**	21.67	
29.	P5 x P8	-2.36			21.55		
30.	P5 x P9	23.97*	8.70		0.56		
31.	P6 x P7	-8.72			31.43*	10.83	
32.	P6 x P8	-26.58**			16.83		
33.	P6 x P9	-0.00			-6.73		
34.	P7 x P8	0.71			4.24	0.37	
35.	P7 x P9	-12.59			-4.96		
36.	P8 x P9	-16.67			-31.06**		

*,** Significant at 5 and 1 percent respectively

4.2.13 Harvest index (%)

The mid-parent heterosis varied from -13.37 (P4 x P7) to 17.23% (P5 x P6). 2 hybrids showed significant positive heterosis, whereas, 2 hybrids showed significant negative heterosis. Significant positive heterosis over better parent was depicted by only one hybrid having the magnitude of 13.78 per cent (P5 x P6). None of the hybrid showed significant positive standard heterosis.

4.2.14 Shelling percentage

The relative heterosis for shelling percentage varied from -8.09 (P4 x P7) to 13.22 per cent (P2 x P6). Two crosses exhibited significant negative heterosis and nine crosses exhibited significant positive heterosis. Only one hybrid (P2 x P6) showed significant positive better parent heterosis having the magnitude of 10.62 per cent. None of the hybrid showed significant positive economic heterosis.

Table 4.8 Extent of heterosis for Harvest index (%) and Shelling percentage

SN	Crosses	Harvest index			Shelling percentage		
		Het	Hb	EH	Het	Hb	EH
1.	P1 x P2	-5.50			-4.30		
2.	P1 x P3	3.04			1.15	1.11	
3.	P1 x P4	-2.98			-6.08		
4.	P1 x P5	9.94	9.53		-6.08		
5.	P1 x P6	14.37*	11.42		4.96		
6.	P1 x P7	-5.41			-1.72		
7.	P1 x P8	9.30	4.26		7.79*		
8.	P1 x P9	-1.22			-4.62		
9.	P2 x P3	-4.80			3.78		
10.	P2 x P4	-12.81*			2.29		
11.	P2 x P5	-5.15			-0.58		
12.	P2 x P6	-0.70			13.22**	10.62*	
13.	P2 x P7	-8.09			0.64		
14.	P2 x P8	-8.90			11.65**	7.06	
15.	P2 x P9	2.51	0.36		-4.51		
16.	P3 x P4	-9.19			-3.82		
17.	P3 x P5	1.18			-4.38		
18.	P3 x P6	7.51		0.19	8.02*	1.40	
19.	P3 x P7	-7.31			-3.90		
20.	P3 x P8	-6.07			5.75		
21.	P3 x P9	0.24		1.03	8.55*	6.63	2.79
22.	P4 x P5	3.10			-0.71		
23.	P4 x P6	4.74			3.38		
24.	P4 x P7	-13.37**			-8.09*		
25.	P4 x P8	-5.93			10.91**	0.56	0.61
26.	P4 x P9	-3.22			-1.38		
27.	P5 x P6	17.23**	13.78*		8.48*	2.90	
28.	P5 x P7	1.12			-7.00*		
29.	P5 x P8	9.29	4.62	0.13	8.39*	0.97	
30.	P5 x P9	-3.14			3.41	2.70	
31.	P6 x P7	5.79			3.36		
32.	P6 x P8	-1.80			9.24*	7.17	
33.	P6 x P9	-5.91			6.55	1.73	
34.	P7 x P8	-1.80			4.65		
35.	P7 x P9	-3.71			-4.41		
36.	P8 x P9	-6.11			6.95	0.27	

*,** Significant at 5 and 1 percent respectively

4.2.15 Protein content (%)

The range of heterosis varied from -19.33 (P2 x P4) to 40.93 per cent (P2 x P6). Eleven hybrids showed negative significant heterosis and twenty one crosses exhibited positive significant heterosis. The estimates of significant positive heterobeltiosis were

observed in 16 hybrids with range between 1.83 (P4 x P7) to 29.55 per cent (P2 x P6).The estimates of significant standard heterosis in positive direction were found in 6 hybrids having the range varied from 3.52 (P2 x P7 and P8 x P9) to 12.32 per cent (P2 x P3).

Table 4.9: Extent of heterosis for Protein content (%)

SN	Crosses	Protein content		
		Het	Hb	EH
1.	P1 x P2	-6.73**		
2.	P1 x P3	-4.43**		
3.	P1 x P4	2.14**	1.97*	
4.	P1 x P5	0.34		
5.	P1 x P6	33.46**	20.46**	7.04**
6.	P1 x P7	12.38**	8.26**	3.81**
7.	P1 x P8	5.28**	1.98*	
8.	P1 x P9	-3.19**		
9.	P2 x P3	28.31**	25.16**	12.32**
10.	P2 x P4	-19.33**		
11.	P2 x P5	-5.54**		
12.	P2 x P6	40.93**	29.55**	10.56**
13.	P2 x P7	14.24**	7.95**	3.52**
14.	P2 x P8	5.39**	4.12**	
15.	P2 x P9	1.09		
16.	P3 x P4	-16.72**		
17.	P3 x P5	3.88**	0.65	
18.	P3 x P6	20.36**	8.17**	
19.	P3 x P7	2.37**		
20.	P3 x P8	8.47**	4.58**	
21.	P3 x P9	0.88		
22.	P4 x P5	-7.61**		
23.	P4 x P6	10.95**	0.00	
24.	P4 x P7	5.55**	1.83*	
25.	P4 x P8	7.48**	3.95**	
26.	P4 x P9	12.57**	4.61**	
27.	P5 x P6	20.53**	11.50**	
28.	P5 x P7	-1.95**		
29.	P5 x P8	-9.98**		
30.	P5 x P9	-8.03**		
31.	P6 x P7	8.93**		
32.	P6 x P8	17.42**	9.15**	
33.	P6 x P9	-0.20		
34.	P7 x P8	-9.98**		
35.	P7 x P9	8.50**		
36.	P8 x P9	29.54**	24.30**	3.52**

*,** Significant at 5 and 1 percent respectively

4.2 COMBINING ABILITY ANALYSIS

The analysis of variance for combining ability was carried out as per procedure given by Griffing (1956, Method 2-Model I).

Analysis of variance components

Table 4.10 Combining ability mean square and expected mean square for sixteen characters

SN	Characters	Source			Var Model I		
		GCA [8]	SCA [36]	Error [88]	GCA	SCA	Error
1	Days to 50% tasselling	5.22*	6.59**	2.28	2.13	155.09	2.28
2	Days to 50% silking	3.87	5.67**	2.96	0.66	97.77	2.96
3	Days to maturity	4.47	6.69**	2.28	1.59	158.83	2.28
4	Plant height (cm)	302.49**	286.65**	86.28	157.23	213.13	86.28
5	No. of leaves/plant	0.49*	0.51**	0.20	0.208	11.004	0.20
6	Tassel length (cm)	1.11	7.49**	0.82	0.209	240.06	0.82
7	No. of primary branches/tassel	2.30**	5.83**	0.50	1.31	192.18	0.50
8	Cob leaf area (cm^2)	198.48	498.96**	106.32	67.02	14135.1	106.32
9	No. of cobs/plant	0.0061	0.0098	0.0097	-0.0025	0.0060	0.0097
10	Ear length (cm)	1.30	2.89**	0.76	0.38	76.53	0.76
11	No. of grain rows/ear	1.29**	1.17**	0.33	0.69	30.48	0.33
12	100 grain wt. (g)	17.63**	11.81**	3.36	10.37	304.30	3.36
13	Grain yield/plant (g)	529.88	280.69**	66.66	336.88	7705.12	66.66
14	Harvest index (%)	7.44**	3.74**	1.95	3.99	64.49	1.95
15	Shelling percentage	14.26*	12.13**	5.46	6.40	240.40	5.46
16	Protein content (%)	1.46**	1.29**	0.0037	1.06	46.34	0.0037

*,** Significant at 5 % and 1 %, respectively (Model).

The mean squares for combining abilityand $\sum^2$ GCA and $\sum^2$ SCAfordifferent characters are presented in Table 4.10.The mean square due toGCA was significant for days to 50 per cent tasselling, plant height, number of leaves per plant, number of primary branches per tassel, number of grain rows per ear,100 grain weight, harvest index, shelling percentage and protein content. Whereas, mean square due to SCA was significant for all the characters except number of cobs per plant.The ratio of $\sum^2$SCA/$\sum^2$ GCA was greater than one for all the traits, where ever it was estimated.

The effects were calculated only where mean square due to GCA/SCA were significant. The character wise results were as follows. (Table 4.11, 4.12 and 4.13):

4.4.1 Days to 50% tasselling

GCA effects for days to 50% tasselling was significant negative for P4 (-1.22) only, whereas, SCA was significant negative for 4 hybrids viz; P1 x P2 (-3.36), P2 x P5 (-3.03), P3 x P5 (-4.67) and P6 x P9 (-5.85).

4.4.2 Days to 50% silking

SCA effect for days to 50% silking was negatively significant for P1 x P2 (-3.89), P3 x P5 (-5.10) and P6 x P9 (-5.65).

4.4.3 Days to maturity

Four hybrids showed significant negative SCA effects viz; P1 x P2 (-3.97), P2 x P5 (-3.03), P3 x P5 (-4.61) and P6 x P9 (-6.27).

4.4.4 Plant height (cm)

Only two inbred lines exhibited significant negative GCA effects with magnitude varied from -6.70 (P8) to -5.82 (P5). Among the hybrids, only four hybrids showed the negative significant SCA effects with the magnitude ranged from -17.78 (P1 x P4) to -30.20 (P8 x P9).

4.4.5 Number of leaves per plant

Estimates of data for number of leaves per plant revealed that the GCA effects were non-significant for parents. SCA effects were positive significant for P1 x P2 (1.15), P2 x P7 (1.27), P2 x P9 (1.21) and P3 x P8 (0.84).

4.4.6 Tassel length (cm)

Out of 36 hybrids, only 13 hybrids depicted positive significant SCA effects with the magnitude varied from 1.72 (P1 x P3 and P4 x P9) to 4.72 (P6 x P9).

Table 4.11: Estimates of general and specific combining ability effects for Days to 50% tasselling, Days to 50% silking, Days to maturity, Plant height (cm), No. of leaves/plant and Tassel length (cm)

SN	Genotype	Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	No. of leaves/plant	Tassel length (cm)
1	P1	0.15			-3.97	-0.36**	
2	P2	-0.49			-1.39	-0.15	
3	P3	-0.52			9.82**	0.03	
4	P4	-1.22**			2.55	0.22	
5	P5	0.48			-5.82*	-0.15	
6	P6	0.97*			3.91	0.22	
7	P7	0.48			2.24	-0.15	
8	P8	-0.37			-6.70*	0.09	
9	P9	0.51			-0.64	0.25	
10	P2 x P1	-3.36*	-3.89*	-3.97**	17.83*	1.15**	-1.85*
11	P3 x P1	1.33	1.02	0.45	-0.05	-0.37	1.72*
12	P4 x P1	-0.30	-0.92	-0.15	-17.78*	0.78	2.63**
13	P5 x P1	0.33	0.26	0.36	-21.08*	-0.52	0.12
14	P6 x P1	-2.15	-1.68	-2.61	7.53	-1.22**	2.30**
15	P7 x P1	0.00	0.59	0.12	9.19	-0.19	3.08**
16	P8 x P1	-1.15	-1.22	-1.48	9.80	-0.10	-1.58
17	P9 x P1	-2.03	-1.59	-0.91	0.41	-0.25	0.81
18	P3 x P2	1.30	1.41	1.06	17.38*	0.42	-0.52
19	P4 x P2	-1.00	-0.86	-0.55	-5.35	-1.43**	1.05
20	P5 x P2	-3.03*	-2.68	-3.03*	8.01	0.27	3.87**
21	P6 x P2	-0.52	0.05	-0.33	-18.38*	-0.76	-0.61
22	P7 x P2	0.64	0.99	1.73	21.62*	1.27**	1.18
23	P8 x P2	0.82	0.50	0.45	15.56	0.69	2.18*
24	P9 x P2	-2.06	-1.86	-1.97	39.50**	1.21**	-0.43
25	P4 x P3	-0.64	-0.28	-0.79	23.44**	-0.61	0.30
26	P5 x P3	-4.67**	-5.10**	-4.61**	-11.53	-0.25	2.12*
27	P6 x P3	0.85	0.62	0.42	8.74	0.72	1.96*
28	P7 x P3	-0.67	-0.44	0.15	-4.59	-0.25	0.42
29	P8 x P3	0.85	1.41	1.55	16.01	0.84*	3.42**
30	P9 x P3	-1.03	-1.28	-1.21	1.62	0.36	-0.19
31	P5 x P4	2.03	1.62	1.79	2.41	-0.10	1.36
32	P6 x P4	-2.45	-0.98	-0.85	-8.99	-0.13	0.87
33	P7 x P4	1.70	1.29	1.88	-12.32	-0.10	0.33
34	P8 x P4	1.88	1.14	0.94	11.62	0.66	1.33
35	P9 x P4	2.67	2.78	3.18*	-7.78	-0.16	1.72*
36	P6 x P5	0.18	0.87	0.00	7.71	-0.10	2.36**
37	P7 x P5	0.67	0.47	0.39	1.04	-0.07	-0.85
38	P8 x P5	-0.82	-0.35	-0.55	1.65	-0.98*	0.48
39	P9 x P5	1.30	1.29	1.70	8.92	0.54	0.87
40	P7 x P6	-0.82	-0.13	0.09	-8.68	0.24	-1.34
41	P8 x P6	-0.64	-0.28	-0.52	3.59	-0.01	-0.67
42	P9 x P6	-5.85**	-5.65**	-6.27**	2.53	0.18	4.72**
43	P8 x P7	-0.48	-0.01	0.55	-3.08	0.02	2.78**
44	P9 x P7	0.97	0.96	-1.88	-12.47	-0.79	0.84
45	P9 x P8	5.48**	5.14**	5.18**	-30.20**	-0.70	-1.49
	Standard error						
	Gi	0.43	0.49	0.43	2.64	0.13	0.26
	Gi-Gj	0.64	0.73	0.64	3.96	0.19	0.39
	Sii	1.22	1.39	1.22	7.52	0.37	0.74
	Sij	1.38	1.57	1.38	8.50	0.42	0.83
	Sij-ik	2.04	2.32	2.04	12.53	0.61	1.23
	Sij-Skl	1.93	2.20	1.93	11.88	0.58	1.16

*,** Significant at 5 and 1 percent respectively

4.4.7 Number of primary branches per tassel

The data for number of primary branches per tassel revealed that only two parents viz, P4 and P9 depicted positive significant GCA effects with the magnitude of 0.71 and 0.47, respectively. Whereas, 15 hybrids exhibited positive significant SCA effects with the magnitude ranged from 1.29 (P3 x P6) to 5.93 (P5 x P6).

4.4.8 Cob leaf area (cm^2)

Nine hybrids showed significant positive SCA effects having the range from 24.87 (P1 x P6) to 46.93 (P2 x P9).

4.4.9 Ear length (cm)

SCA was significant positive for 6 hybrids having the range varying from 2.01 (P4 x P7) to 3.25(P1 x P8).

4.4.10 Number of grain rows per ear

GCA effects for number of grain rows per ear was positive significant for P4 (0.44) and P7 (0.50), whereas, SCA effects were significant positive for 4 hybridsviz; P1 x P4 (2.22), P2 x P6 (1.85), P3 x P4 (1.98) and P6 x P9 (1.25).

4.4.11 100 grain weight (g)

The GCA effects for 100 grain weight revealed that only one parent depicted positive significant GCA effects with the magnitude of 2.10 (P3). SCA effects for this trait was significantly positive for 6 hybrids with magnitude varying from 3.67 (P2 x P8) to 5.82(P5 x P6).

Table 4.12 Estimates of general and specific combining ability effects for No. of primary branches/tassel, Cob leaf area (cm^2), Ear length (cm), No. of grain rows/cob and 100 grain weight (g)

SN	Genotype	No. of primary branches/tassel	Cob leaf area (cm	Ear length (cm)	No. of grain rows/ear	100-grain weight (g)
1	P1	-0.74**			-0.11	0.13
2	P2	-0.01			-0.11	0.47
3	P3	0.11			0.13	2.10**
4	P4	0.71**			0.44**	1.01
5	P5	-0.20			0.20	-2.41**
6	P6	0.32			-0.53**	0.47
7	P7	-0.23			-0.29	-0.74
8	P8	-0.44*			-0.23	-0.59
9	P9	0.47			0.50**	-0.44
10	P2 x P1	0.81	-12.96	0.04	-0.57	1.95
11	P3 x P1	2.68**	11.01	0.64	0.52	0.98
12	P4 x P1	1.41*	-30.30**	-2.24**	2.22**	5.73**
13	P5 x P1	-1.68*	-6.18	-1.21	-1.54**	-4.18*

14	P6 x P1	-2.19**	24.87**	1.82*	0.52	2.28
15	P7 x P1	-0.32	-3.20	-0.36	0.28	-0.18
16	P8 x P1	0.56	36.60**	3.25**	-0.45	5.67**
17	P9 x P1	2.32**	-4.02	-0.08	0.16	0.52
18	P3 x P2	2.96**	-12.81	-1.05	-1.48**	-2.36
19	P4 x P2	1.35*	13.95	0.73	0.88	-4.93**
20	P5 x P2	1.59*	-16.23	0.43	0.46	-0.84
21	P6 x P2	-0.92	-23.18*	-1.87*	1.85**	-0.72
22	P7 x P2	-2.71**	33.01**	2.61**	0.95	5.49**
23	P8 x P2	0.84	28.32**	1.55	0.22	3.67*
24	P9 x P2	-0.07	46.93**	2.88**	0.16	3.19
25	P4 x P3	0.56	1.92	0.67	1.98**	-1.57
26	P5 x P3	1.47*	-9.76	0.37	0.22	-1.81
27	P6 x P3	1.29*	-0.45	0.40	0.95	-2.02
28	P7 x P3	-1.50*	1.02	-0.45	-0.63	0.52
29	P8 x P3	-0.28	-6.22	0.82	0.64	-0.96
30	P9 x P3	0.47	31.90**	2.16**	-0.08	1.88
31	P5 x P4	0.20	2.50	0.82	0.58	-0.72
32	P6 x P4	1.02	-7.19	0.19	-0.02	-2.60
33	P7 x P4	2.90**	27.74**	2.01*	-0.27	-2.72
34	P8 x P4	1.78**	5.01	0.28	0.34	-1.21
35	P9 x P4	2.87**	-4.38	-0.72	-1.05*	0.31
36	P6 x P5	5.93**	8.60	0.22	-0.45	5.82**
37	P7 x P5	1.81**	27.56**	2.04*	-0.69	5.04**
38	P8 x P5	-1.98**	29.10**	1.31	-0.08	-1.12
39	P9 x P5	-1.56*	4.71	0.31	-0.15	3.07
40	P7 x P6	-0.38	-1.62	-0.27	0.04	-1.84
41	P8 x P6	-0.16	-2.39	0.34	0.64	-5.33**
42	P9 x P6	1.26	13.99	1.34	1.25*	0.52
43	P8 x P7	1.38*	0.11	0.16	0.40	0.22
44	P9 x P7	-0.86	-14.75	-0.84	0.34	-3.93*
45	P9 x P8	1.35*	-43.74**	-3.24**	0.28	-3.75*
	Standard error					
	Gi	0.20	2.93	0.25	0.16	0.52
	Gi-Gj	0.30	4.40	0.37	0.25	0.78
	Sii	0.57	8.34	0.71	0.47	1.48
	Sij	0.65	9.43	0.80	0.53	1.68
	Sij-ik	0.95	13.90	1.18	0.78	2.47
	Sij-Skl	0.91	13.19	1.12	0.74	2.35

*,** Significant at 5 and 1 percent respectively

4.4.12 Grain yield/plant (g)

GCA effects for grain yield per plant was positive significant for P3 (13.28) and P9 (7.69), whereas, estimates of SCA effects for this character was significant positive for six hybrids with the magnitude ranging from 16.41 (P3 x P7) to 34.10 (P1 x P8).

4.4.13 Harvest index (%)

GCA effects for harvest index was significant positive for P3 (1.64) only, whereas, out of 36 hybrids, only three hybrids depicted positive significant SCA effects viz. P2 x P9 (2.76), P1 x P8 (2.78) and P5 x P6 (3.07).

4.4.14 Shelling percentage

The GCA effects for shelling percentage revealed that only two parents viz; P3 (1.59) and P4 (1.75) depicted positive significant GCA effects, whereas, only 3 hybrids exhibited positive significant SCA effects viz; P4 x P8 (5.33), P2 x P6 (5.34) andP3 x P9 (6.13).

4.4.15 Protein content (%)

GCA effects for protein content revealed that out of 9 parents, 5 parents showed positive significant GCA effects with the magnitude ranged from 0.10 (P6) to 0.61 (P7). Estimates of SCA effects revealed that out of 36 hybrids, 18 hybrids expressed positive significant SCA effects with the magnitude varied from 0.13 (P1 x P5) to 2.30 (P2 x P3).

Table 4.13 Estimates of general and specific combining ability effects for Grain yield/plant (g), Harvest index (%), Shelling percentage and Protein content (%)

SN	Genotype	Grain yield/plant (g)	Harvest index (%)	Shelling percentage	Protein content (%)
1	P1	-8.71**	-0.43	-0.14	0.17**
2	P2	-5.68*	-1.24**	-1.30	0.13**
3	P3	13.28**	1.64**	1.59*	0.26**
4	P4	2.93	-0.36	1.75*	-0.21**
5	P5	-3.65	0.08	-0.36	-0.51**
6	P6	-3.75	-0.68	-0.59	0.10**
7	P7	0.26	0.51	0.70	0.61**
8	P8	-2.37	0.19	-1.45*	-0.04*
9	P9	7.69**	0.30	-0.21	-0.51**
10	P2 x P1	-1.29	-1.38	-3.25	-1.15**
11	P3 x P1	4.08	0.77	1.57	-0.81**
12	P4 x P1	-22.90**	-0.59	-3.12	0.29**
13	P5 x P1	19.98**	1.39	-3.34	0.13*
14	P6 x P1	33.45**	2.51	1.56	1.81**
15	P7 x P1	-12.22	-1.72	1.51	0.94**
16	P8 x P1	34.10**	2.78*	3.14	0.09
17	P9 x P1	-8.02	-0.66	-2.82	-0.64**
18	P3 x P2	-10.28	-0.09	1.40	2.30**
19	P4 x P2	5.74	-2.17	1.66	-2.00**
20	P5 x P2	4.31	-1.65	-1.03	-0.60**
21	P6 x P2	9.38	-0.32	5.34*	2.25**
22	P7 x P2	14.71	-0.71	1.26	0.95**
23	P8 x P2	-10.30	-1.63	3.49	-0.07
24	P9 x P2	23.64**	2.76*	-4.79*	-0.40**
25	P4 x P3	0.44	-1.89	-2.98	-1.67**
26	P5 x P3	11.68	-0.29	-3.71	0.44**
27	P6 x P3	7.45	1.73	2.18	0.59**
28	P7 x P3	16.41*	-1.43	-2.09	-0.14*
29	P8 x P3	-6.56	-1.59	-0.19	0.37**
30	P9 x P3	1.35	1.07	6.13**	-0.29**
31	P5 x P4	8.00	1.18	0.68	-0.26**
32	P6 x P4	-2.16	1.49	0.03	0.16**
33	P7 x P4	-11.17	-2.86*	-4.35*	0.62**
34	P8 x P4	4.76	-0.67	5.33*	0.70**
35	P9 x P4	-9.63	0.57	-0.57	1.24**
36	P6 x P5	17.71*	3.07*	3.48	1.00**
37	P7 x P5	11.71	0.26	-3.62	-0.14*
38	P8 x P5	-0.33	2.41	2.78	-0.96**

SN	Genotype	Grain yield/plant (g)	Harvest index (%)	Shelling percentage	Protein content (%)
39	P9 x P5	-7.02	-1.73	2.95	-0.65**
40	P7 x P6	2.81	1.66	0.95	-0.42**
41	P8 x P6	-0.90	-1.70	-0.89	0.19**
42	P9 x P6	-11.29	-2.88*	1.26	-1.27**
43	P8 x P7	-0.57	0.63	1.39	-1.48**
44	P9 x P7	-1.29	0.14	-2.13	0.46**
45	P9 x P8	-23.67**	-1.42	0.96	2.24**
	Standard error				
	Gi	2.32	0.40	0.66	0.02
	Gi-Gj	3.48	0.60	1.00	0.03
	Sii	6.61	1.13	1.89	0.05
	Sij	7.47	1.28	2.14	0.06
	Sij-ik	11.01	1.88	3.15	0.08
	Sij-Skl	10.44	1.79	2.99	0.08

*,** Significant at 5 and 1 percent respectively

4. RESULTS AND DISCUSSION

The present study entitled "Variability Assessment at Morphological & Molecular level in Groundnut (*Arachis hypogaea* L.)" was carried out at the instructional Farm, CTAE, MPUAT, Udaipur.

The experimental material of present investigation was comprised of 25 genotypes including national & the state released varieties of bunchtype groundnut (*Arachis hypogaea* L.) Thirteen characters were studied for variability and correlation among themselves. The same material was also used for molecular characterization.

The results obtained for thirteen characters of 25 genotypes are discussed under following heads:

4.1. Analysis of variance

4.2. Mean values and Range

4.3 Variability parameters

4.4. Correlation analyses

4.5. Molecular characterization

4.1 ANALYSIS OF VARIANCE

The data recorded on thirteen characters were subjected to statistical analyses. The mean sum of squares due to genotypes were highly significant for all the characters studied, indicating considerable differences among the genotypes used in the study (Table 4.1).

4.2 MEAN VALUES AND RANGE

The mean performance of genotypes for different characters are presented in Appendix II. A perusal of the data revealed that the range was considerably high for most of the characters *viz*., days to 50% flowering (23 to 29), days to maturity (91 to 95), plant height (20.67 to 36 cm), number of branches per plant (4 to 7), number of mature pods per plant (8 to 20), dry pod yield per plant(7.6 to 17.23 g), shelling percentage (58 to 72), 100-kernel weight (21.2 to 43.53 g), sound mature kernel (59 to 87 %), biological yield per plant (19.2 to 47.47 g), kernel yield per plant(5.1 to 11.03 g) , harvest index (33 to 48 %), seed oil content (24 to 43 %) indicating an adequate variability for exercising selection and use in the breeding programmes.

4.2.1 Days to 50 % flowering

Among 25 genotypes, mean days to 50% flowering ranged from 23 days (Pratap Mungphali-2) to 29 days (JCG-88). Genotype Pratap Mungphali-2 (23 days) was the earliest to flower which was followed by GG7 (23.3 days) and GG2 (24.3 days). The overall mean recorded for the trait was 26 days.

4.2.2 Days to maturity (Days)

With respect to days to maturity, mean values ranged from 91 days (Vemana) to 95 days (GAUG-10). Genotype Vemana was found earliest as it showed minimum 91.3 days to maturity followed by GG2.GG-3, GG-4,Kadiri-5, ICGV-911141 (91.7 days) and GG-8, TG-37-A, Pratap Raj. Mungphali (92 days)

4.2.3 Plant height (cm)

The mean plant height ranged from 20.67 cm (TAG-24) to 36 cm (Kadiri-6). The mean for plant height was 27.54 cm.

4.2.4 Number of branches per plant

The mean number of branches per plant ranged from 4 (GG-4) to 7 (R-2001-3). Maximum number of branches per plant was exhibited by the genotype R-2001-3 (7.13), followed by GAUG-10 (7) and JCG-88 (6.07).

4.2.5 Number of mature pods per plant

Mean data for number of mature pods per plants revealed that among 25 genotype GPBD-4 (19.87 pods) possessed maximum number of mature pods per plant followed by R-2001-3 (16.87 pods) and GG-2 (16.8 pods). The numbers of mature pods per plant ranged from 8 pods (Kadiri-6) to 20 pods (GPBD-4). The overall mean for this character was 13 mature pods per plant.

4.2.6 Dry pod yield per plant (g)

The mean dry pod yield per plant of 25 genotypes exhibited wide range of variation. The mean dry pod yield per plant ranged from 7.6 g (ICGV-91114) to 17.23 g (GAUG-10). Maximum dry pod yield was exhibited by genotype GAUG-10 (17.2 g), followed by TIR-46 (17.2 g) and GPBD-4 (15.03 g). The overall mean for this character was 11.82 g

4.2.7 Kernel yield per plant (g)

Wide range of variation was found for kernel yield per plant among the 25 genotypes. The mean values ranged from 5.1 g (ICGV-91114) to 11.03 g (TIR-46). The genotype TIR-46 (11.03 g) gave maximum kernel yield followed by GAUG-10 (10.63 g) and R-2001-3 (10.27 g). The overall mean for this character was 7.79 g.

4.2.8 Sound mature kernel (%)

The sound mature kernel percentage ranged from 59 % (TAG-24) to 87 % (Kadiri-9, ICGV-91114). Maximum sound mature kernel percentage was exhibited by the genotype Kadiri-9, ICGV-91114 (86.67 %) followed by Vemana (86%) and GG-7, GG-8 (85 %).

4.2.9 Shelling percentage (%)

The means for shelling percentage ranged from 58 % (JAL-24) to 72 % (GG-3) with a general mean of 67 %. The genotype GG-3 (72 %) showed maximum shelling percentage followed by GG-5 (71.67 %) and GG-8, Pratap Mungphali-1(70.67 %).

4.2.10 Biological Yield per plant (g)

Among 25 genotypes, mean biological Yield per plant ranged from 19.2 g (GG-4) to 47.47 g (GAUG-10). Genotype GAUG-10 (47.47 g) was exhibited maximum biological Yield per plant which was followed by GPBD-4 (40.2 g) and TIR-46 (39.63 g). The overall mean recorded for the trait was 29.56 g.

4.2.11 Harvest index (%)

Mean values among the 25 genotypes for harvest index ranged from 33 % (JAL-39) to 48 % (Pratap Mungphali-2). Genotype Pratap Mungphali-2 (48.3 %) had highest harvest index followed by GG-7 (43.87 %) and TG-37-A (43.73 %).

4.2.12 100 Kernel weight (g)

Genotype TIR-46 (43.53 g) had maximum100 kernel weight, whereas Chico (21.2 g) had lowest 100 kernel weight. The data for 100 kernel weight ranged from 21.2 g (Chico) to 43.53 g (TIR-46). The mean 100 kernel weight was 34.21 g.

4.2.13 Oil content (%)

With respect to oil content genotype Pratap Raj. Mungphali (42.67 %) had maximum oil content, followed by Kadiri-5, Pratap Mungphali-1(42 %) and JCG-88, Chico (41.33 %) whereas the genotype ICGV-91114 (23.67 %) had minimum oil content. The overall mean for oil content was 34 %.

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, genetic gain and genetic advance were estimated and character wise results are presented in table 4.2 and discussed as follows.

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

SN	Characters	GCV	PCV	h^2	GA	GG
1	Days to 50% flowering	5.45	6.34	74.02	2.50	9.66
2	Days to maturity	0.83	1.20	47.55*	1.09	1.18
3	Plant height (cm)	14.94	15.21	96.56	8.33	30.25
4	Number of branches per plant	19.00	23.03	68.07	1.56	32.29
5	Number of mature pods per plant	21.86	22.99	90.43	5.36	42.83
6	Dry pods yield per plant (g)	23.05	24.46	88.80	5.29	44.75
7	Kernel yield per plant (g)	19.50	24.62	62.76	2.48	31.83
8	Sound mature kernels (%)	8.96	9.02	98.75	14.32	18.34
9	Shelling percentage	5.19	5.38	93.01	6.88	10.31
10	Biological yield per plant	24.88	25.12	98.14	15.01	50.78
11	Harvest index (%)	8.16	8.53	91.56	6.47	16.08
12	100 KERNEL Wt. (g)	14.50	14.53	99.58	10.20	29.81
13	Oil content (%)	18.62	18.72	98.98	12.95	38.17

4.3.1 Days to 50 % flowering

A perusal of the data showed low values of both GCV (5.45 %) and PCV (6.34 %) for days to 50 % 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. Ganeshan and Sudhakar (1995); Vasanthi *et al.* (1998), Chisthi *et al.* (2000) and Nath and Alam (2002) also reported low magnitude of both GCV and PCV for days to 50 % flowering.

However, high value of heritability (74.02 %) and moderate genetic gain (9.66 %) and low genetic advance (2.50), indicated presence of additive gene action . Selection of such trait may be rewarded. The findings of these results obtained are in accordance with the finding of Nadaf and Habib *et al.* (1987); Vaddoria and Patel (1990), Parmeshwarrapa *et al.* (2004), and Mahalaxmi *et al.* (2005).

4.3.2 Days to maturity

Partitioning of total variance into its components revealed that the genotypic (0.83 %) and phenotypic (1.20 %) coefficients of variation were low in magnitude for days to maturity. However, narrow difference between these two parameters indicated less influence of environment in expression of this trait. Present findings are in accordance with the findings of Chauhan and Shukla (1985), Vasanthi *et al.* (1998) and Chisthi *et al.* (2000).

4.3.3 Plant height

Estimates of genetic parameters indicated that plant height exhibited moderate value of GCV (14.94 %) and PCV (15.2 %). The GCV and PCV values for plant height were more or less equal. The present findings are in accordance with the findings of Deshmukh *et al.* (1986) and John *et al.* (2006b). Higher magnitude of phenotypic coefficient of variation than genotypic coefficient of variation suggested that appreciable portion of variability has been accounted by environmental effect. Vindhiyavarman and Raveendran (1996), Prasad *et al.* (2002), Kumar and Rajamani (2004) and Mothilal *et al.* (2004) also reported moderate magnitude of GCV and high magnitude of PCV for plant height in groundnut.

The magnitude of heritability in broad sense (96.56 %) was high, with moderate genetic gain (30.25 %) and low genetic advance (8.33 %) for plant height. High heritability accompanied with high genetic gain indicates that most likely the heritability was due to the additive gene effects and selection may be effective.

High heritability along with high genetic gain, was also reported by Deshmukh *et al.* (1986), Azad and Hamid (1987), Kale and Dhole (1988), Manoharan *et al.* (1990), Manohran and Ramlingam (1990), Manohran and Ramlingam (1993), Reddy (1994), Vindhiyavarman and Raveendran (1996), Kumar and Patel (1998), Singh and Singh (1999), , Venkatramana *et al.* (2001), Nath and Alam (2002), Prasad *et al.* (2002), Makhan Lal *et al.*

(2003), Mothilal *et al.* (2004), Golakia *et al.* (2005), Mahalaxmi *et al*. (2005), John *et al.* (2006b) and Korat *et al.* (2009) and suggested the involvement of additive gene action for the inheritance of plant height in bunch groundnut.

4.3.4 Numbers of branches per plant

The values of GCV and PCV for branches per plant revealed that the magnitudes of GCV (19.00 %) and PCV (23.03 %) were moderate for this trait. The larger difference between these two parameters indicated that environmental factors accounted for total variability for this trait. The moderate estimates of genotypic and phenotypic coefficients have also been reported by Chauhan and Shukla (1985), Prasad *et al*. (2002) and Mothilal *et al.* (2004) for branches per plant.

The trait number of primary branches per plant exhibited moderate heritability (68.07%) coupled with moderate genetic gain (32.29 %). These results are in accordance with the findings of Kuriakose and Joseph (1986a) and Singh and Singh (1999). Moderate to high magnitude of heritability and low 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 (21.8 %) and phenotypic coefficient of variation (22.99 %) was found high for number of mature pods per plant. Bhagat *et al.* (1986); Kale and Dhoble (1988), Vindhiyavarman and Raveendram (1996) and Mothilal *et al*. (2004), Wani *et al.* (2004), Mahalaxmi *et al*. (2005), John *et al.* (2006b) and Kadam *et al.* (2007) also reported high magnitude of both GCV and PCV for number of mature pods per plant in groundnut.

On the other hand, heritability (90.43 %) was high in magnitude, in conjunction with high estimates of genetic gain (42.83 %) and low estimates of genetic advance (5.36 %). 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 (23.05 %) and phenotypic (24.46 %) coefficient 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 Chauhan and Shukla (1985); Kale and Dhoble (1988), Reddy (1994), Saxena *et al.* (1995), Sharma and Varshney (1995), Vasanthi *et al.* (1998), Yadahv *et al.* (1998), Nazar-Ali *et al.* (2000), Kumar and Rajamani (2004), Mothilal *et al.* (2004), Parameshwarappa *et al.* (2004), and Kadam *et al.* (2007).

The heritability in broad sense (88.80 %) was high and genetic gain (44.75 %) was also high for this trait. The high value of heritability as well as genetic gain indicated role of additive gene action. Selection may reward for such traits.

4.3.7 Kernel yield per plant

A perusal of the data for kernel yield per plant indicated that genotypic coefficient of variation (19.50 %) and phenotypic coefficient of variation (24.62 %) were high in magnitude for this character. Wide difference between these two parameters indicated the role of environmental factors on the expression of kernel yield per plant. These findings are in accordance with the results reported by Uddin *et al.* (1995), Venkatramana (2001), Venkatramana *et al.* (2001), Parmeshwarapa *et al.* (2004), John *et al.* (2006b) and Kadam *et al.* (2007).

The estimates of heritability for kernel yield per plant were moderate (62.76%). These results are in accordance with the Dashora and Nagda (2002); Golakia *et al.* (2005) and Mahalaxmi (2005). Likewise, genetic gain was also moderate (31.83 %). This indicated that the trait was under the control of additive gene action.

4.3.8 Sound mature kernel percentage

Sound mature kernels showed low estimates of genotypic coefficient of variation (8.96%) and phenotypic coefficient of variation (9.02 %). Such a low amount of variation for sound mature kernels in groundnut was also reported by Mothilal *et al.* (2004).

The estimates of heritability (98.75 %) were high, which suggested that larger portion of variation for this character in the material was due to additive gene action. Moderate estimates of genetic gain (18.34 %) further suggested that prediction of performance for this character would be easier. Similar findings has already been reported by Venkatramana (2001), Kumar and Rajamani (2004), Parmeshwarappa et al. (2004).

4.3.9 Shelling percentage

Magnitude of genetic parameters for shelling percentage indicated that estimates of genotypic coefficient of variation (5.19 %) and phenotypic coefficient of variation (5.38 %) 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 Chauhan and Shukla (1985), Deshmukh *et al.* (1986), Reddy and Gupta (1993), Nath and Alam (2002), Mothilal *et al*. (2004), Golakia *et al.* (2005) and Mahalaxmi *et al.* (2005).

The high heritability (93.01 %), with moderate genetic gain (10.31 %) and moderate genetic advance (6.88 %) was revealed for shelling percentage. High heritability coupled with moderate genetic gain was also reported by Deshmukh *et al.* (1986) and Bhagat *et al*. (1986), whereas, moderate to high heritability was recorded by Chauhan and Shukla (1985); Vaddorai and Patel (1990), Reddy (1994), Singh and Singh (1999), Nath and Alam (2002), Parmeshwarrappa *et al.* (2004) and John *et al.* (2009).

4.3.10 Biological Yield per plant

The estimates of genotypic (24.88 %) and phenotypic (25.12 %) coefficient 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 Vasanthi et al. (1998), Sharma and Varshney (1995).

The heritability in broad sense (98.14 %) was high and genetic gain (50.78 %) was also high for this trait. The high value of heritability as well as genetic gain indicated role of additive gene action. Selection would be effective for this trait. These results are in accordance with the findings of Sharma and Varshney (1995).

4.3.11 Harvest Index

The genotypic coefficient of variation (8.16 %) and phenotypic coefficient of variation (8.53 %) for harvest index were low in magnitude. While high amount of genetic variability for harvest index in groundnut was reported by Sharma and Varshney (1995).

The estimates of heritability (91.56 %) and genetic gain (16.08 %) were high with moderate genetic advance (6.47 %) for this trait. Moderate to high heritability, coupled with high genetic gain was also earlier reported by Reddy (1994), Sharma and Varshney (1995), Nath and Alam (2002) and Prasad *et al.* (2002). The magnitude of heritability and genetic gain in the present material indicated that harvest index was under the control of additive gene action and there is tremendous scope of improvement through selection in this character.

4.3.12 100 kernel weight

The results pertaining to genetic variability for 100- kernel weight indicated that genotypic coefficient of variation (14.50 %) and phenotypic coefficient of variation (14.53 %) were moderate for this trait. The present findings are in accordance with the findings of Deshmukh *et al.* (1986), Nadaf and Habib (1987), Prasad *et al.* (2002), Mothilal *et al.* (2004) and Kumar and Rajamani (2004).

100-kernel weight expressed high heritability (99.58 %), high genetic gain (29.81 %) and high genetic advance (10.20 %) suggested the involvement of additive gene action for governing this character. The selection may be effective for improvement in 100- kernel weight. Similar results for 100- kernel weight were reported by; Bhagat *et al.* (1986), Deshmukh *et al.* (1986), Reddi (1986a), Azad and Hamid (1987), Manohran and Ramlingam (1990), Reddi *et al.* (1991), Manoharan (1993), Manohran and Ramlingam (1993), Ventakramana (2001), Reddy (1994), Singh (1998), Vasanthi *et al.* (1998), Yadav *et al.* (1998), Singh and Singh (1999), Nazar-Ali *et al.* (2000), Prakash *et al.* (2000), Venkatramana *et al.* (2001), Dashora and Nagda (2002), Mothilal *et al.* (2004), Wani *et al.* (2004), Golakia *et al.* (2005), John *et al*. (2009) and Korat *et al.* (2009).

4.3.13 Oil content

Estimates of oil content revealed that genotypic coefficient of variation (18.62 %) and phenotypic coefficient of variation (18.72 %) were moderate in magnitude for this character. Similar findings for moderate amount of genetic variability for oil content in groundnut were also reported by Chauhan and Shukla (1985) Deshmukh *et al.* (1986), Manoharan (1993), Prakash *et al.* (2000) and Golakia *et al.* (2005).

The estimates of heritability (98.98 %) and genetic gain (38.17 %) for oil content were high. High heritability coupled with high genetic gain were also earlier reported by Manohran and Ramlingam (1993), Manoharan (1993), Prakash *et al.* (2000), Venkatramana *et al.* (2000*)*, Dashora and Nagda (2002).

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 plant height (14.19 %), number of mature pods per plant (21.86 %), dry pods yield per plant (23.05 %), Kernel yield per plant (19.50 %), Biological yield per plant (24.88 %), 100 Kernel weight (14.50 %) and oil content (18.62 %).

Whereas, moderate estimates were found for sound mature kernels (8.96 %), harvest index (8.16 %). For days to 50% flowering (5.45 %), days to maturity (0.83 %) and shelling percentage (5.19 %) both GCV and PCV estimates were found low.

The estimates of heritability were moderate to high for all the characters. However, maximum heritability was found for 100 kernel weight (99.58 %) followed by oil content (98.98 %) and sound mature kernels (98.75 %). While, maximum genetic gain was observed for biologocal yield per plant (50.78 %) followed by dry pods yield per plant (42.75 %) and number of mature pods per plant (42.83 %).

The maximum genetic advance was found for biological yield per plant (15.01 %) followed by sound mature kernel (14.32 %) and oil content (12.95 %). In general, moderate to high heritability coupled with moderate to high genetic gain and genetic advance for 100 kenel weight (99.58 % , 29.81% and 10.20), oil content (98.98 %, 38.17% and 12.95%) and sound mature kernels (98.75 %, 18.34 % and 14.32 %) indicated involvement of additive gene action and scope of improvement for these characters through selection.

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 character like yield for which direct selection is not very effective, 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).

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	0.47*	0.37
2.	Days to maturity	0.46*	0.36
3.	Plant height (cm)	-0.52**	-0.49*
4.	Number of branches per plant	0.78*	0.66**
5.	Number of mature pods per plant	0.74*	0.71**

7.	Kernel yield per plant (g)		0.88**
8.	Sound mature kernels (%)	-0.43*	-0.40*
9.	Shelling percentage	-0.53*	-0.49*
10.	Biological yield per plant (g)	0.95**	0.90**
11.	Harvest index	0.00	0.01
12.	100-kernel Wt. (g)	0.38	0.36
13.	Oil content (%)	-0.05	-0.05

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

In the present investigation, correlation coefficients were estimated among 13 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 are in accordance with Reddy and Gupta (1992) and Sumathi and Ramnathan (1995).

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 and phenotypic level with number of branches per plant (rg =0.78**, rp =0.66**), number of mature pods per plant (rg =0.74*, rp =0.71**) and biological yield per plant (rg =0.95**, rp =0.90**) . These findings are in accordance with Nadaf and Habib (1989), Manoharan et al. (1990), Mishra and Yadav (1993) and Kavani et al. (2004).

4.4.2 Correlation between kernel yield per plant and other characters:

Kernel yield per plant was positively and significantly correlated at both genotypic and phenotypic level with number of branches per plant (rg =0.67**, rp =0.57**), number of mature pods per plant (rg =0.81**, rp =0.69**) and biological yield per plant (rg =0.96*, rp =0.79**). These findings are in accordance with Uddin et al. (1995), Kavani et al. (2004) and John et al. (2009) [Table 4.4].

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	0.37	0.24
2.	Days to maturity	0.36	0.26
3.	Plant height (cm)	-0.45*	-0.36
4.	Number of branches per plant	0.67**	0.57**
5.	Number of mature pods per plant	0.81**	0.69**
7.	Dry pod yield per plant (g)	1.04	0.88**
8.	Sound mature kernels (%)	-0.37	-0.30
9.	Shelling percentage	-0.35	-0.26
10.	Biological yield per plant (g)	0.96**	0.79**
11.	Harvest index (%)	0.06	0.11
12.	100-kernel Wt. (g)	0.33	0.26
13.	Oil content (%)	-0.00	-0.01

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

4.4.3 Correlation among different characters:

A perusal of table 4.5 revealed existence of positive correlation between days to 50% flowering and days to maturity (rg =0.55**, rp =0.32) at both genotypic as well as phenotypic level. Further, days to 50% flowering exhibited significant positive correlation with number of branches per plant (rg = 0.69**, rp=0.52*) and biological yield per plant (rg =0.54**, rp =0.45*) at both genotypic as well as phenotypic level. Similarly, days to maturity also exhibited significant positive correlation with number of branches per plant (rg =0.71**, rp =0.43*) at phenotypic and genotypic levels (Table 4.5). Similar findings have already been reported by Suneetha et al. (2004) and Singh and Singh (1999).

Likewise, number of branches per plant showed significant positive correlation at genotypic as well as phenotypic levels with number of mature pods per plant (rg =0.57**, rp =0.53**) and biological yield per plant. Character sound mature kernel and shelling percentage showed significant positive correlation with each other at both genotypic as well as phenotypic level(rg =0.53**, rp =0.50*). Manoharan et al.1990) and Vasanthi et al. (1998).

Whereas number of mature pods per plant exhibited significant positive correlation with biological yield only (rg =0.70**, rp =0.67**) at both the levels. Manoharan et al. (1990), also reported the correlation among above traits.

While, harvest index, 100 kernel weight and oil content didn't show positive significant correlation with any character under study.

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

4.5 Molecular Observations

The RAPD markers (Williams *et al.*, 1990) have been increasingly employed for population studies and for analyzing the molecular diversity (Hogbin *et al.*, 1998; Fischer *et al.*, 2000). RAPD technique has the advantage of assessing a greater number of potential polymorphic loci distributed randomly in the genome than allozymes.

Since, varieties of groundnut under study were procured from different centers on AICRIP on Groundnut of the country, it was expected that this pool of germplasm would exhibit considerable diversity for morphological traits, therefore, it was thought justified to find out its diversity with respect to their DNA profile.

Table 4.6: Concentration of DNA in groundnut cultivars

S. No.	Genotypes Name	Code No.	Ratio of A260/A280	Conc. of DNA (ng/µl)
1	GG-2	G1	1.86	826.7
2	GG-3	G2	1.80	466.7
3	GG-4	G3	1.79	212.6
4	GG-5	G4	1.82	455.5
5	GG-7	G5	1.82	569.3
6	GG-8	G6	1.87	842.9
7	JCG-88	G7	1.87	497.0
8	R-2001-2	G8	1.76	481.4
9	R-2001-3	G9	1.79	509.8
10	GAUG-10	G10	1.85	306.0

11	Kadiri-5	G11	1.87	737.0
12	Kadiri-6	G12	1.85	872.1
13	Kadiri-9	G13	1.90	911.9
14	GPBD-4	G14	2.00	466.0
15	ICGV-91114	G15	1.84	558.2
16	JAL-24	G16	1.79	297.3
17	JAL-39	G17	1.88	742.4
18	TG-37-A	G18	1.81	522.6
19	Chico	G19	1.79	370.5
20	Vemana	G20	1.84	930.5
21	TIR-46	G21	1.77	496.5
22	TAG-24	G22	1.82	371.6
23	Pratap Mungphali-1	G23	1.87	538.2
24	Pratap Mungphali-2	G24	1.82	531.7
25	Pratap Raj. Mungphali	G25	1.81	930.0

Characterization of genotypes based on RAPD profile is well documented in groundnut by Bhagwat, *et al*. (2001), Massawe *et al.* (2003), Azzam *et al*. (2007), Vasanthi *et al.* (2008) and Sharaf *et al.* (2011).

Technique of RAPD is simple therefore, can be used in laboratories with limited resources, but requires optimization of the reaction for reproducible results. Once the reaction conditions have been optimized the technique is reliable, reproducible and informative.

Twenty five genotypes of groundnut were examined for DNA polymorphism using 15 decamer primers (OPERON) showing high (G+C) content. Out of 15 primers used, amplification could be obtained with 13 primers, whereas 2 primers *viz.* OPA-5 and OPA-6 failed to show any amplification. Out of 13 primers, 12 primers showed variable degree of polymorphism ranging from 60 per cent (OPA -10) to 100 per cent (OPA -1, OPA -8, OPA -12, OPA -15, OPC -4, OPC-6, OPC- 12 and OPC-13). The primer OPA-9 was monomorphic. Overall polymorphism was found to be 91.02 per cent. Similar results were reported by Reddy, (2004). They reported that 10 primers produced polymorphic bands ranging from 16.6 per cent to 100 per cent and overall polymorphism was 71.4 per cent. The DNA amplification and polymorphism generated among various genotypes of groundnut using random primers are presented in Table 4.7.

Electrophoretic pattern of RAPD profile was studied on 1.5 per cent agarose gel. Only those fragments, which amplified consistently, were considered for analysis. Each RAPD band was assumed to represent a single locus and data were scored as presence of bands (1) and its absence as (0). Results are illustrated in Table 4.7. This table combines the comparative information about total number of fragments with base pairs obtained by all the primers in all groundnut genotypes.

The representative photographs of electrophoresis gels showing RAPD profiles after amplification with different random primers are depicted in plate I, plate II, plate III and plate IV.

Thirteen primers on twenty five groundnut genotypes generated 78 total bands out of which 71 were polymorphic (Table 4.8). The average number of bands per primer was found to be 6.0. Similar results were also reported by Subramanian *et al.* (2000), Amadou *et al.* (2001), Mondal*et. al.* (2005) , and Varsha Kumari *et al.* (2009) in groundnut.

Table 4.8: Polymorphism information of RAPD primers used

S.No.	Primers	Sequences (5'→3')	Total No of bands(a)	Total No of polymorphic bands (b)	Polymorphism %(b/a × 100)
1	OPA-1	CAGGCCCTTC	8	8	100
2	OPA-8	GTGACGTAGG	5	5	100
3	OPA-10	GTGATCGCAG	5	3	60
4	OPA-12	TCGGCGATAG	4	4	100
5	OPA-15	TTCCGAACCC	6	6	100
6	OPC-4	CCGCATCTAC	6	6	100
7	OPC-5	GATGACCGCC	6	4	67
8	OPC-6	GAACGGACTC	9	9	100
9	OPC-11	AAAGCTGCGG	9	7	77
10	OPC-12	TGTCATCCCC	11	11	100
11	OPC-13	AAGCCTCGTC	6	6	100
12	OPC-15	GACGGATCAG	3	2	66

13	OPA-9	GGGTAACGCC	A		
14	OPA-5	AGGGGTCTTG	NA		
15	OPJ-6	TCGTTCCGCA	NA		
		Total	78	71	91.02

The maximum number of amplicons were produced by the primers OPC-11 (156) followed by OPC-12 (143), respectively. The minimum number of amplicons were produced by the primer OPC-6 (50). Among all the primers tested, OPC-12 proved to be the best primer as it produced 143 amplicons and11 scorable bands of which 11 were polymorphic. Average polymorphism was 100 per cent. Primer OPC-6 produced 9 scorable bands of which 9 were polymorphic which amount to 100 per cent polymorphism. Primer OPA-1 produced 8 scorable bands of which 8 bands were polymorphic which amount to 100 per cent polymorphism. While Primer OPA-15, OPC-4 and OPC-13 produced 6 scorable bands of which all 6 were polymorphic which amount to 10 per cent polymorphism.

The results obtained were in conformity with the earlier findings by Bhagwat *et al.* (1997), Massawe *et al.* (2003) and Reddy, (2004). Thus, it is opined that RAPD assays can be efficient in identifying DNA polymorphism provided suitable primers are used.

Table 4.9: Details of the random primers used for amplification of genomic DNA of groundnut

Total number of primers	15
Number of primers which showed amplification	13
Number of primer which did not show amplification	2
Number of primers which showed polymorphism	12
Number of primers which did not showed polymorphism	1
Total number of bands	78
Total number of polymorphic bands	71
Total number of monomorphic bands	4
Total number of amplicons produce	1181
Total number of polymorphic amplicons	263

Assessment of Relationship between Groundnut Genotypes based on Morphological Characters and Cluster Analysis based on RAPD

Genetic similarity estimates based on RAPD banding patterns were calculated using method of Jaccard's coefficient analysis (Jaccard, 1908). The similarity coefficient matrix generated was subjected to algorithm UPGMA (Unweighted Pair Group Method with Arithmetic Mean) and dendrogram was generated using NTSYSpc 2.02 program (Rohlf, 2004).

The Jaccard's similarity co-efficient between different varieties ranged from 0.22 to 0.88 with a mean of 0.58 (Table 4.10). The maximum similarity coefficient (0.88) was observed between G5 and G4, G6 and G4 and G12 and G11 followed by G6 and G5, G8 and G6 showed similarity of 0.86 percent. The minimum similarity coefficient 0.22 (maximum diversity) was observed between G14 and G2, G14 and G10. Similar results were obtained by Dwivedi *et al*. (2001) and Vasanthi *et al.* (2008).

Dendrogram

A dendrogram was constructed using Jaccard's similarity coefficients obtained for DNA banding pattern observed on the 25 genotypes of groundnut employing NTSYSpc programme (Fig. 4.1). The cluster analysis on the genotypes revealed 7 distinct clusters. The salient finding of the clustering are described as follows:

(1) The genotype G14 (GPBD-4) was entirely separated from all other genotypes and had scored values of lower order with all the genotypes (average similarity coefficiency being 0.35 over rest of the genotypes and hence, maximum diverse from the rest).

(2) The genotypes G11 (Kadiri 5) and G12 (Kadiri 6) were in same cluster with very high confidence limit and showed similarity for days to 50% flowering and number of branches per plant [subcluster within cluster 7].

(3) Another sub cluster within cluster 7 had two genotypes viz., G3 (GG-4) and G5 (GG-7) which also showed similarity for number of branches per plant and sound mature kernel percentage.

(4) Similarly, genotypes G2 (GG-3) and G4 (GG-5) had similar number of mature pods per plant [sub cluster within Cluster 5].

(5) Two genotypes viz., G3 (GG-4) and G5 (GG-7) had similarity for 100 kernel weight, dry pod yield, kernel yield per plant, number of branches per plant and number of mature pods per plant [sub cluster within Cluster 3]. Lang *et al*.(2007) also reported formation of distinct clusters and sub clusters from RAPD pattern among 29 groundnut genotypes.

On the basis of present study, it may be concluded that RAPD profile of the genotypes, on account of its easy detection and dependability, can be used for the diversity studies. Further, the groups/ clusters obtained by dendrogram could also be distinguished by similarity for the morphological characteristics within each group. Such an association may be used for more effective breeding programmes.

5. SUMMARY AND CONCLUSIONS

The present investigation was carried out on 25 groundnut genotypes to elicit information on the genetic variability, correlation coefficients and molecular characterization for yield and its component characters.

The groundnut genotypes were evaluated in randomized block design with 3 replications during *kharif*- 2012 at the Instructional farm, College of Technology and Agricultural Engineering, Maharana Pratap University of Agriculture and Technology, Udaipur. Observations were recorded on five competitive plants for 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, kernel yield,100-kernel weight, sound mature kernel, shelling out turn, biological yield per plant, harvest index and seed oil content**.** Further, DNA was isolated with CTAB extraction buffer method in laboratory. DNA concentration and purity was checked by spectrophotometer and agarose gel electrophoresis. Isolated DNA was used as template for random amplification of DNA using 15 randomly selected decamer primers. The results are summarized and concluded as below:

- Mean squares due to genotypes for all the characters were significant 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., plant height (21-36 cm), dry pod yield (7.60-17.23 g), 100-kernel weight (21.2-43.5 g) and kernel yield (5.1- 11.03 g). Genotypes G10, G21 and G9 appeared promising with respect to dry pod yield.

- The estimates of genotypic parameters revealed that differences between the values of GCV and PCV were least for most of the characters. High phenotypic coefficient of variation along with least difference from genotypic coefficient of variation for characters viz., biological yield per plant (GCV 24.88% and PCV 25.12%) followed by dry pod yield per plant (GCV 23.05 % and PCV 24.46%) , number of mature pods per plant (GCV 21.86% and PCV 22.99%), sound mature kernel (GCV 8.96% and PCV 9.02%), 100 kernel weight (GCV 14.50 and PCV 14.53%) and Oil content (GCV 18.62% and PCV 18.72%) indicating that entire genetic determinants are translated into phenotype.

- Maximum heritability was observed for 100 kernel weight followed by oil content, sound mature kernel, biological yield per plant, harvest index and number of mature pods per plant. While maximum genetic gain was observed for biological yield per plant followed by dry pod yield per plant and number of mature pods per plant. Similarly maximum genetic advance found for biological yield per plant followed by sound mature kernels and oil content. In general, moderate to high heritability coupled with moderate to high genetic gain indicated the involvement of additive gene action and scope of improvement in these traits through selection.

- Association estimate revealed that dry pod yield per plant was positively and significantly correlated at both genotypic and phenotypic level with number of branches per plant, number of mature pods per plant and biological yield per plant . The mutual correlation among most of the combinations was also positive and significant.

- For molecular characterization, 15 primers were screened, out of which 13 primers produced amplification. A total 78 scorable bands were produced, out of which 71 bands were polymorphic and the level of polymorphism was 71.4 per cent.

- Primers OPA-1, OPA-15, OPA-8, OPA-12, OPC-4, OPC-6, OPC-12 and OPC-13 proved to be the finest as they showed 100 % average polymorphism.

- Based on the banding pattern of RAPD markers, dendrogram was constructed using the UPGMA method. The similarity coefficient ranged from 0.22 to 0.88 with a mean of 0.58. The dendrogram clearly divided the 25 cultivars into seven main clusters. genotype G14 (GPBD-4) had scored average similarity coefficient being 0.35 over rest of the genotypes and hence, maximum diverse from the rest the genotypes

- The result showed that there was an association between dendrogram obtained by RAPD analysis and morphological characters. Pairs of cultivars *viz.* G11 (Kadiri 5) and G12 (Kadiri 6), G3 (GG-4) and G5 (GG-7), G2 (GG-3) and G4 (GG-5) and G3 (GG-4) and G5 (GG7) were genetically as well as morphologically related with each other.

On the basis of present study, it may be concluded that RAPD profile of the genotypes, on account of its easy detection and dependability, can be used for the diversity studies. Further, the groups/ clusters obtained by dendrogram could also be distinguished by

similarity for the morphological characteristics within each group. Such an association may used for more effective breeding programmes.

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