

**GENETIC VARIABILITY AND G x E INTERACTION STUDIES IN
GROUNDNUT (*Arachis hypogaea* L.)**

By

Mr. Shinde Hemant Nivrutti

(Reg. No. Ph.D./011/18)

A Thesis submitted to the
**MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI – 413 722, DIST. AHMEDNAGAR
MAHARASHTRA, INDIA**

in partial fulfillment of the requirements for the degree

Of

DOCTOR OF PHILOSOPHY (AGRICULTURE)

in

**AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**



DEPARTMENT OF AGRICULTURAL BOTANY

**POST GRADUATE INSTITUTE
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RAHURI – 413 722, DIST. AHMEDNAGAR
MAHARASHTRA, INDIA.**

2019

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
there of has not been submitted
by me or other person to any
other University or Institution
for a Degree or
Diploma

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Date : / /2019

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CERTIFICATE

This is to certify that the thesis entitled, “**GENETIC VARIABILITY AND G x E INTERACTION STUDIES IN GROUNDNUT (*Arachis hypogaea* L.)**” submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.) in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr. SHINDE HEMANT NIVRUTTI**, under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

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LIST OF ABBREVIATIONS

BS	:	Broad sense
cm	:	Centimeter
C.D.	:	Critical difference
C.V.	:	Coefficient of variation
Cov.	:	Covariance
d.f.	:	Degrees of freedom
EMP	:	Environment mean sum of products
et al.	:	And others (et alia)
Fig.	:	Figure
g	:	Gram (s)
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
h^2	:	Heritability
i.e.	:	That is (id est)
kg	:	Kilogram (s)
MSS	:	Mean sum of squares
PCV	:	Phenotypic coefficient of variation
S.E.	:	Standard error
S.S.	:	Sum of squares
SMK	:	Sound mature kernel
viz.,	:	Namely (Videlicet)
Σ	:	Summation
σ^2	:	Variance
σ	:	Standard deviation
/	:	Per
%	:	Per cent

ABSTRACT

**GENETIC VARIABILITY AND G X E INTERACTION STUDIES IN
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A candidate for the degree
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in
**DEPARTMENT OF AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI – 413 722
2019

Research Guide : Dr. V.L. Amolic

Major discipline : Genetics and Plant Breeding

The present investigation “Genetic Variability and G x E interaction studies in Groundnut (*Arachis hypogaea* L.)” conducted during summer 2018 to study variability, heritability and genetic advance, correlation, path analysis, diversity among eight crosses of groundnut. Each cross had five progenies. The experiment was laid in compact family block design with two replications and fourteen genotypes involved research work on stability studies during summer and *kharif* season 2018, at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.).

The observations were recorded on twelve characters *viz.*, days to 50 per cent flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg).

Analysis of variance revealed highly significant differences among the progenies of eight crosses for the characters studied, indicating appreciable amount of variability among the progenies for the characters studied. The estimation for phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters.

In present investigation, the characters number of branches per plant, number of immature pods per plant, number of mature pods per plant, hundred kernel weight and dry pod yield per plot expressed high estimates of heritability (broad sense) accompanied with high genetic advance and percent of mean indicating that these traits were predominantly governed by additive gene action and could be improved through simple selection only.

In correlation study, it was observed that dry pod yield per plot recorded significant positive correlation with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling per cent, sound mature kernel and protein content at both genotypic and phenotypic levels, while characters immature pods per plant and oil content were negatively associated with dry pod yield per plot.

Path analysis based on genotypic correlation revealed that number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling per cent and sound mature kernel showed moderate to high positive direct effects on dry pod yield, while days to 50% flowering, number of mature pods per plant, haulm yield per plot and protein content had negligible and negative direct effect on dry pod yield per plot.

Total forty genotypes were grouped in seven clusters. Cluster I with 12 genotypes emerged as the largest cluster followed by cluster V with 10 genotypes and cluster II and IV with 6 genotypes, cluster VI with 4 genotypes. Remaining two clusters (III and VII) were monogenotypic.

On the basis on per performance, inter cluster distance and cluster mean, the six F₅ progenies of crosses *viz.*, C1-P3, C2-P4, C3-P4, C4-P3, C6-P3 and C8-P2 were identified for further advancement of generation and will be used in crossing program.

The genotypes Phule Bharati, TAG-24, JL-501 and RHRG-1308 were found average stable for dry pod yield and other yield contributing traits. Phule Unnati was found stable in favourable environments for dry pod yield per plot and its stability for pod yield was because of average stability for number of branches per plant, number of mature pods per plant, haulm yield per plot, shelling per cent and oil content.

The present study indicated that summer sowing date E₁ (15th February) was most favourable followed by E₃ *kharif* (15th July) for expression of pod yield and yield contributing traits in groundnut.

1. INTRODUCTION

Groundnut (*Arachis hypogaea* L.), is an allotetraploid ($2n=4x=40$) species which likely evolved from two diploids (Kochert *et al.*, 1996). It belongs to the family *Leguminosae*, subfamily *Papilionoidae*, tribe *Aeschnomeneae*, sub-tribe *Stylosanthinae*, genus *Arachis* and species *hypogaea* (Isleib *et al.*, 1994). It is self-pollinated, annual, herbaceous legume growing upright or prostrate and has an indeterminate growth habit. Natural cross pollination occurs at rates of less than 1 to 6 per cent due to a typical flowers or action of bees (Duke, 1981 and Coffelt, 1989). The groundnut plant is sparsely hairy and generally grows 12 to 65 cm. It has a central, upright stem and many lateral branches. In runner types, the laterals are prostrate and in bunch types they are more or less erect in the young plants but tend to become prostrate at a later stage. The fruit is a pod with one to five seeds that develops underground within a needle like structure called a peg, an elongated ovarian structure.

Groundnut (*Arachis hypogaea* L.) also known as peanut is one of the world's most popular crops cultivated throughout the tropical, sub-tropical and warm temperate areas where annual precipitation is between 1000-1200 mm for optimum growth of the crop. The crop is native to South America, Mexico and Central America. Dissemination of groundnut to the old world most probably occurred in the sixteen and seventeen centuries with the discovery voyages of Spanish, Portuguese, British and dutch (Krapovickas, 1969; Hammons, 1994; Isleib *et al.*, 1994). Groundnut has high economic and nutritional value and is an important cash crop for peasants in poor tropical countries. Groundnut is ranked fifth among oilseed crops in the world after oil palm, soybean, rapeseed and sunflower in terms of volume of production and is widely grown in more than 100 countries of tropical, subtropical and warm temperate regions of the globe (FAOSTAT, 2016). It contains 48-50 per cent oil and 26-28 per cent protein and a rich source of dietary fiber, minerals and vitamins (Janila *et al.*, 2013). FAOSTAT (2016) estimated that, annual unshelled groundnut production was around 60.5 million tons from about 31.2 million hectares

of land and productivity of 1.9 tons per hectare in 2014 cropping season under rainfed conditions.

Groundnut is an important crop from the perspective of food and nutrition security of poor small holder farmers in developing countries, where it is grown widely. It is grown extensively in the developing countries of Asia, Africa and Latin America. About 62 per cent of the production comes from South, East and Central Asia. Africa and Asia produced 91 per cent of the world's total groundnut production (Nedumaran *et al.*, 2015).

However, in Maharashtra the area under groundnut was 1.92 lakh ha in *kharif* season (2018-19) and production was 2.24 lakh tonnes with an average productivity of 1167 kg/ha, while in *summer* season (2017-18) the area under groundnut was 0.513 lakh ha and production was 0.746 lakh tonnes with an average productivity of 1454.8 kg/ha, while in *kharif* and summer season (2017-18) the total area under groundnut was 2.642 lakh ha and production was 3.315 lakh tonnes with an average productivity of 1255 kg/ha (Anonymus, 2018). The major groundnut growing districts in Maharashtra are Satara, Kolhapur, Pune, Nashik, Ahmednagar, Parbhani, Jalgaon and Dhule.

To meet the demand of increasing population and maintaining self sufficiency, there is need to increase the groundnut production. Successful establishment of germplasm collection and plant introduction for crop improvement as well as germplasm conservations requires studies in genetic variability within plant populations. Genetic variability and heterozygosity existed within population in both natural and cultivated populations.

The magnitude of variability and the knowledge of extent to which desirable characters are heritable is a pre-requisite for crop improvement. The variability available in the breeding material is very important in the selection of superior plant types, where selection of superior plant is based not only on yield alone but also on the yield contributing characters. For the reliable field selection, it becomes necessary to partition the relative amount of heritable and non-heritable variability exhibited by yield contributing characters. Pod yield in groundnut is

quantitative in nature and polygenically controlled. Selection on the basis of yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable. Knowledge of the associations between yield and its component characters and among the component characters themselves can improve the efficiency of selection in plant breeding. Correlation studies taken alone are often misleading and the actual dependence of pod yield on the correlated yield, component characters needs confirmation, which can easily and untangled and unravelled by path coefficient analysis.

Further, majority of the economically important characters including dry pod yield and its components are amenable for genetic improvement through intense breeding among genetically diverse parent. The Mahalanobis's D^2 statistics is powerful tool for calculating the divergence between the population based on which genotype can be grouped into suitable clusters.

The new concept of selecting varieties through evaluation of variety within the poor and difficult environments where the farmer operates is an important issue among plant breeders and agronomists. The various environments would influence yield and make selection for a variety difficult due to genotypes and environments interaction.

To combat the changing environment, breeding of two season variety is important and similar effects were undertaken previously. The groundnut varieties like TAG-24, JL-501, Phule Unnati and Phule Bharati were released and recommended for cultivation in both *kharif* and summer season.

It is generally agreed that the more stable genotypes adjust their phenotypic response to provide some measure of uniformity in spite of environmental fluctuations. With this point of view, the present study entitled "Genetic variability and G x E interaction studies in Groundnut (*Arachis hypogaea* L.)" was undertaken with following objectives.

1. To study the genetic variability parameters in F_5 progenies of groundnut.
2. To study the association, cause and effect of yield contributing characters with dry pod yield in groundnut.

3. To study the effect of Genotype \times Environment on yield and yield contributing characters.
4. To identify stable genotypes suitable for summer and *kharif* cultivation in the changing environment.

2. REVIEW OF LITERATURE

The available literature and information pertaining to present investigation is briefly reviewed and presented in this chapter under the following sub headings.

2.1 Variability

2.2 Correlation and path analysis

2.3 Genetic diversity

2.4 G x E interaction and Stability

2.1 Variability in groundnut

Uddin *et al.* (1995) studied variability, correlation and path coefficient analysis for seven yield components in 23 divergent groundnut genotypes during 1988-89. High genotypic coefficients of variation were observed for seed yield/plant, seeds/plant, primary branches/plant, plant height and 100 seed weight. Heritability estimates were high for all of the traits studied. All the characters, except days to maturity and shelling percentage had moderate to high genetic advance.

Jayalakshmi and Lakshmikantha Reddy (2003) reported that twenty-one groundnut hybrids substantial genetic variability was observed for shoot biomass, harvest index and immature pod number per plant. High heritability and high genetic advance were also observed for these attributes. Harvest index, mature pod number per plant and specific leaf area were associated with each other and also with kernel yield, indicating that selection for these attributes will be helpful in improving the productivity of groundnut.

Suneetha *et al.* (2004) studied 23 diverse groundnut genotypes for characters 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.

Variability parameters were studied by John *et al.* (2008) with six F₂ population. They reported close correspondence between GCV and PCV values for days to maturity, pod yield per plant, shelling out-turn (%) and 100 kernel weight; whereas, values of PCV were 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 only for shelling out-turn (%) and kernels yield per plant, hence improvement in these characters would be effective on the per se performance of an individual.

John *et al.* (2009) studied that high heritability along with high GAM was observed for number of secondary branches per plant, number of immature pods per plant, shelling percentage, 100-kernel weight, SMK weight, total number of pods, total number of gynophores, maturity index, reproductive efficiency and pod yield. This showed additive type of gene action plays an important role. It indicates that phenotypic selection for these characters will be effective. Pod and kernel yields per plant showed significant and positive association with number of secondary branches per plant, number of mature pods per plant, SMK weight, SMK number, 100-kernel weight. So these characters have been considered as selection indices for the improvement of kernel and pod yields per plant.

Aghav (2010) evaluated fifty five genotypes of summer groundnut for variability, path analysis and genetic diversity. Appreciable amount of variability was observed for all characters studied. The magnitudes of genotypic and phenotypic coefficient of variation indicated the presence of good amount of variability. The number of mature pods per plant showed highest heritability followed by harvest index, oil content, dry pod yield and fresh pod yield per plant. The number of mature pods per plant showed highest genetic advance, while other characters recorded moderate genetic advance.

Sonawane (2010) estimated the genetic variability and genetic divergence in sixty six genotypes of summer groundnut. The genotypes were

evaluated during 2008 in a Randomized Block Design with two replications at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.). Appreciable amount of variability was observed for all the characters studied. The magnitude of genotypic and phenotypic coefficient of variation indicated the presence of good amount of variability for different characters.

In a study involving 460 genotypes of groundnut in four different seasons Pradhan and Patra (2011) estimated of correlation coefficients among pod yield and its components. They observed consistently positive association of unfilled pods per plant with number of branches per plant and hundred pod weight with hundred kernel weight in all the seasons. Further, they revealed that in rabi and kharif yield and yield contributing characters were positively correlated except unfilled pods per plant and plant height. They concluded that selection for high yield in groundnut could be based on pod weight, shelling percentage and hundred kernel weight as selection criteria along with plant height.

Thakur *et al.* (2011) reported low heritability with low genetic advance in percentage of mean for days to maturity, number of pod per plant, number of kernel per pod, pod length, 12 pod width, kernel length, kernel width, 100 kernel weight, selling per cent and haulm weight per hectare.

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

Narasimhulu *et al.* (2012) evaluated 18 selected groundnut genotypes for yield and yield components namely pod yield per plant, kernel yield per plant, hundred kernel weight, shelling percentage and SMK percent and observed that PCV

was generally higher than GCV for most of the characters studied but in some cases, the two values differed slightly. They reported low values of PCV and GCV for SMK per cent and shelling percentage, whereas high values for pod yield per plant, kernel yield per plant and test weight. They observed high heritability and high GAM for pod yield per plant, kernel yield per plant, test weight and shelling percentage indicating the importance of additive gene action and the ample scope for improvement of these traits through simple selection.

Kamble (2013) estimated the amount and nature of variability and association among dry pod yield and yield contributing characters and direct and indirect contribution of component characters to the dry pod yield and nature and magnitude of divergence on 55 germplasm lines. The character per cent oil content showed the highest heritability followed by per cent protein content, number of mature pods per plant, fresh pod yield per plant, dry pod yield per plant, days to maturity and days to 50 % flowering. Other characters recorded moderate to low heritability. The number of mature pods per plant showed the highest genetic advance followed by dry pod yield per plant, fresh pod yield per plant and days to 50 % flowering. Other characters showed moderate to low genetic advance. The genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients. The characters, fresh pod yield per plant and number of mature pods per plant recorded highly significant and positive correlation with dry pod yield per plant.

Atak (2014) studied variability for twenty different characters among 31 genotypes, genetic divergence among all genotypes in F₄ generation of groundnut (*Arachis hypogaea* L.). The treatment differences were statistically significant for majority of the characters and also the magnitude of genotypic and phenotypic coefficients of variations indicated the presence of good amount of variability. The character number of pegs per plant showed the highest heritability followed by dry haulm yield per plant, number of immature pods per plant, number of mature pods per plant, plant height, specific leaf area, oil content, dry pod yield per plant, days to 50 % flowering, photosynthetic rate, shelling percentage, harvest index, protein content,

days to maturity, 100 kernel weight, total chlorophyll and leaf temperature. Other characters recorded moderate to low heritability. The number of pegs per plant showed the highest genetic advance followed by dry haulm yield per plant, number of mature pods per plant, plant height and dry pod yield. Other characters showed moderate to low genetic advance.

Rao *et al.* (2014) studied analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for number of pods per plant, plant height, kernel yield, dry pod yield, 100 kernel weight and dry haulm yield.

Devasena *et al.* (2015) reported high estimates of PCV and GCV for pod yield per plant, kernel yield per plant and oil yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for 100 kernel weight, 100 pod weight and pod yield per plant.

Gupta *et al.* (2015) observed wide range of variation for plant height, number of mature pods per plant, 100-pod weight, 100-kernel weight, plant height, kernel yield per plant, pod yield per plant, biological yield per plant and harvest index in sixty genotypes of groundnut studied. They also found high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for plant height, number of primary branches per plant, number of mature pods per plant, 100 pod weight, 100-kernel weight, biological yield per plant, kernel yield per plant and harvest index. Narrow differences observed between the PCV and GCV in certain cases like days to 50 % flowering, days to maturity, sound mature kernels, biological yield per plant, oil content and protein content in their experiment.

Padmaja *et al.* (2015) studied variability in F₂ population of crosses JL 24 x ICG 11337 and JL 24 x ICG 13919 in groundnut. Among these F₂ populations both the crosses showed high variability in the form of PCV, GCV, heritability and genetic advance as per cent of mean for mature pods per plant, total pods per plant, mature seeds per plant, haulm weight per plant, LLS disease score at 75 DAS and pod yield per plant. High heritability coupled with moderate GAM for DS-90 in both the

crosses. The cross JL 24 x ICG 11337 recorded high heritability and genetic advance as per cent of mean for DS-102.

Kadam *et al.* (2016) reported considerable amount of variability for all the fifteen characters of groundnut genotypes studied (*viz.*, Days to 50 % flowering, plant height, plant spread, fresh biomass, dry biomass, fresh fodder yield, dry fodder yield, pegs per plant, mature pods per plant, immature pods per plant, shelling percentage, hundred kernel weight (g), oil content (%), fresh pod yield per plant and dry pod. He observed high magnitude of GCV and PCV for number of mature pods per plant, dry pod yield per plant and fresh pod yield per plant. The characters days to 50 percent flowering, shelling percentage and oil content had low GCV and PCV estimates in their experiment.

Rao (2016) studied genetic variability, for yield and its contributing traits in 30 groundnut genotypes under drought. Analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for number of pods per plant, dry haulm yield, kernel yield, plant height and dry pod yield. High heritability coupled with high genetic advance as per cent of mean was observed for kernel yield, plant height, dry pod yield and hundred kernel weight indicating the role of additive gene in expressing these traits.

Bhakal and Lal (2017) conducted research on variability, correlation and path coefficient analysis for yield and its contributing traits in groundnut germplasm. The highest genotypic coefficient of variation was observed for plant height at 20 DAS (32.72 %) and high heritability coupled with high genetic advance was observed for plant height at 60 DAS (99.50 and 27.48) and kernel uniformity (98.96 and 19.24).

Gouranga (2017) observed high GCV, high heritability coupled with high genetic advances as per cent of mean in case of kernel yield plant, number of pod plant, number of kernel plant and 100 kernel weight indicating the role of additive gene in expressing these traits and effectiveness of selection.

Mandal *et al.* (2017) revealed the highly significant differences and adequate variability among the genotypes for all the characters studied. High GCV, high heritability coupled with high genetic advance as per cent of mean were observed in case of kernel yield plant, number of pod plant, number of kernel plant and 100 kernel weight indicating the role of additive gene in expressing these traits and effectiveness of selection. Correlation studies and path coefficient analysis revealed the importance of plant height, number of pod plant, number of kernel plant, shelling (%), sound mature kernel and harvest index as they had positive direct effects on pod yield and kernel yield and should be considered for improvement in yield.

Rajarithnam *et al.* (2017) studied genetic variability, correlation and path coefficient analysis for nine quantitative characters in four F₃ population *viz.*, CO 7 x VRI Gn 6, TMV 2 x VRI Gn 6, TMV Gn 13 x VRI Gn 6 and VRI 2 x VRI Gn 6. High percentage of PCV, GCV and heritability coupled with high genetic advance as per cent of mean values were recorded by number of pods per plant, pod yield per plant (g), kernel yield per plant (g), late leaf spot score and rust score in varied crosses.

Sardar *et al.* (2017) evaluated thirty two F₆ progenies along with 4 released varieties as parents in R.B.D for yield and its component traits. The genotypic source of variations were highly significant (at 1% level) for all the traits. The PCV and GCV estimates were high for haulm yield per plant and low for harvest index and shelling percent. The rest of the characters exhibited medium PCV and GCV. However, low values of GCV were observed in shelling percentage and harvest index indicated that they were controlled largely by non-additive gene action and selection would be less effective, so there is need to create variability either by hybridization or mutation followed by selection. High heritability and high genetic advance indicated that these traits are mainly governed by additive gene action. Hence, improvement of these traits would be more effective through the phenotypic selection. Moderate heritability and genetic advance (GAM) as percent of mean for plant height, pod number per plant, kernel number per plant, kernel yield and pod

yield indicated the additive and non additive gene actions for these traits and phenotypic selection would be effective to some extent.

Wadikar *et al.* (2018) evaluated forty diverse genotype of groundnut to measure genetic variability and character association for thirteen different characters. Analysis of variances revealed significant differences among genotypes for all the characters indicating the presence of considerable amount of variability. Higher PCV and GCV values observed for kernel yield per plant followed by pod yield per plant, number of pods per plant indicating good amount of variation for these characters. High heritability coupled with high genetic advance as per cent of mean has been noticed for kernel yield per plant, number of pods per plant and pod yield per plant.

2.2 Correlation and path analysis

Venkataramana *et al.* (2000a) evaluated 144 germplasm accessions of groundnut for pod yield and 14 component characters and reported the positive direct effect of plant height, number of branches, total number of pods, number of mature pods, shelling percentage, sound mature kernel percentage, harvest index and kernel yield on pod yield indicating the importance of selection based on these traits for rapid improvement of pod yield.

Correlation analysis in Spanish bunch groundnut was carried out by Prasad *et al.* (2001) and concluded that pod yield per plant was significantly and negatively correlated with height of the main axis; while, significantly and positively correlation of pod yield per plant was observed with harvest index at both phenotypic and genotypic levels. Path analysis revealed that pod yield per plant had positive direct effect on harvest index; while, percentage of sound mature kernels and 100 kernel weight showed negative direct effect on harvest index.

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

Patil *et al.* (2006) studied that the correlation study revealed that pod yield per plant had significant positive association with number of pods per plant, shelling per cent and sound mature kernel per cent at minimum three locations. Path analysis also indicated that three traits *viz.*, number of pods per plant, shelling per cent and sound mature kernel per cent had the maximum direct effect on pod yield per plant at minimum three locations.

In their study with 48 diverse genotypes of groundnut, Sumathi and Muralidharan (2007) reported that pod yield per plant had significant and positive association with kernel yield, sound mature kernel weight and 100 kernel weight both at genotypic and phenotypic levels. The characters shelling percentage and oil content had negative association with pod yield per plant both at genotypic and phenotypic levels. The inter correlation of kernel yield with sound mature kernel weight and 100 seed weight were also positive and significant. The number of mature pods per plant exhibited positive and significant correlation with total number of kernels per plant and sound mature kernels number. Path analysis indicated that among eleven characters, kernel yield per plant exerted the maximum positive direct effect on pod yield per plant. The direct effects of all the other characters were also positive except number of mature pods per plant, sound mature kernels weight and shelling percentage, these characters showed negative direct effects on pod yield per plant.

Korat *et al.* (2009) reported that the estimate of genotypic correlation coefficients in general higher than their corresponding phenotypic correlations indicating strong inherent association among the traits. Yield contributing characters like biological yield per plant, 100-kernel weight and harvest index had positive and significant association with pod yield per plant at phenotypic level. Based on correlation and path analysis, biological yield per plant, 100-kernel weight and harvest index were identified as the most important yield contributing characters.

Babariya and Dobariya (2012) revealed that pod yield per plant was significantly and positively correlated with days to maturity, plant height, number of pods per plant, kernel yield per plant, number of mature pods per plant, 100 kernel weight, biological yield per plant and harvest index. Biological yield per plant and

harvest index exhibited high and positive direct effects on pod yield per plant. Whereas, kernel yield per plant, number of pods per plant and days to maturity showed moderate and positive effects on pod yield per plant.

Fikre *et al.* (2012) found positive and highly significant correlation of kernel yield (kg/ha) with pod yield (kg/ha) and number of mature pods per plant while non-significant correlation with number of seeds per pod. They also reported that kernel yield was negatively and significantly associated with days to 50 % flowering and days to maturity.

Ravi Kumar and Reddi (2012) observed that genotypic correlation coefficient was relatively higher magnitude than the corresponding phenotypic correlation coefficient, indicating strong inherent association between the characters. Pod yield per plant displayed significant positive association with kernel yield per plant, mature pods per plant, total pods per plant, harvest index, 100 seed weight, root weight, plant height and shoot weight. Path coefficient analysis revealed high direct effects of kernel yield per plant and harvest index on pod yield per plant.

Thakur *et al.* (2013) reported that the pod yield per hectare showed highly significant and positive association with days to maturity, sound matured kernel (SMK) per cent, pod length, pod width and kernel length but the highly significant and negative association was shown with days to flowering, number of pods per plant, shoots length, shelling (%) and specific leaf area. Days to flowering, shoot length, shelling (%), SMK (%) and 100 kernel weight had direct negative contribution with pod yield per hectare. Therefore, days to maturity, root length, pod width, pod length and kernel length were identified to be the important traits while selection for improvement of yield in groundnut.

Alam (2014) studied genetic correlation and path coefficient analysis in 45 genotypes of groundnut (*Arachis hypogaea* L.) for pod yield and its components. The genotypic correlation coefficients were found to be of relatively higher magnitude than the corresponding phenotypic correlation coefficient, indicated strong inherent association between the characters. Pod yield showed significant positive association with secondary branches per plant, harvest index, 100 pod weight, 100

kernel weight, pod size, diseases incidence and canopy temperature. Path coefficient analysis revealed high direct effects of primary branches per plant and harvest index. Hence, it would be rewarding to give due importance on the selection of these characters for rapid improvement in pod yield of groundnut.

Kahate *et al.* (2014) studied correlation and path analysis for morphological and biochemical traits in groundnut (*Arachis hypogaea* L.). They observed that kernel yield per plant, harvest index, phenol content, non-reducing sugar, test weight and oil content exhibiting significant positive association with pod yield. The path analysis study revealed that kernel yield per plant had positive direct effect on pod yield. Harvest index, non-reducing sugar, phenol content, test weight showed positive indirect effect on pod yield through kernel yield per plant.

Jeyaramraja and Fantahun (2014) reported positive correlation of days to maturity with 100-seed weight and negatively correlated with oil content and seeds per pod.

Rao *et al.* (2014) observed high heritability coupled with high genetic advance as per cent of mean for 100 kernel weight, dry pod yield per plant, kernel yield per plant, plant height and number of pods per plant indicating the role of additive gene in expressing these traits. Dry pod yield was significantly and positively correlated with kernel yield per plant, number of pods per plant, 100 kernel weight and dry haulm yield. Path coefficient analysis indicated that number of pods per plant and 100 kernel weight was important traits to be considered for realizing the improvement in yield.

Bhargavi *et al.* (2015) studied character association and path coefficient analysis of pod yield and yield components in 20 Spanish bunch groundnut (*Arachis hypogaea* L.) genotypes. They found that days to maturity, number of mature pods per plant, biological yield per plant, biological yield per hectare, harvest index, 100 kernel weight, kernel yield per plant, kernel yield per hectare, oil yield per hectare and pod yield per hectare showed significant positive association with pod yield per plant at both phenotypic and genotypic levels. Path analysis studies revealed that 100 kernel

weight, kernel yield per plant and biological yield per hectare exerted maximum positive direct effect on pod yield per plant.

Bilawal *et al.* (2015) reported that the current finding from experiment exhibited that sound mature kernel (%) had a positive and significant correlation with pod yield, however, plant height, pods per plant and shelling (%) revealed positive and non-significant correlation with pod yield per plant, 100 kernel weight and 20 pods length displayed negative and non-significant association with pod yield. Path analysis showed that the contribution of character *viz.*, sound mature kernel (%), pods per plant, 100 kernel weight and 20 pods length was in positive direction, therefore, these character were identified to be the important characters which could be used in selection for yield.

Gupta *et al.* (2015) evaluated sixty diverse genotypes of groundnut during *Kharif* 2013 for genetic parameters *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 level with number of mature pods per plant, 100 pod weight, shelling out turn, kernel yield per plant, biological yield per plant and harvest index. Path analysis revealed that the biological yield per plant and harvest index had high and positive direct effects on pod yield per plant.

John and Reddy (2015) reported that the estimate of genotypic correlation coefficients in general higher than their corresponding phenotypic correlations indicating strong inherent association among the traits. Pod yield per plant has significant positive association with days to 50 % flowering, days to maturity, number of well-filled and mature pods per plant, shelling per cent, sound mature kernel per cent, 100 kernel weight, proein per cent and kernel yield per plant. The high direct effect of pods per plant was appeared to be the main factor for its strong positive correlation with pod yield. Hence, a direct selection for this trait would be effective.

Nirmala and Jayalakshmi (2015) reported that the characters pod yield per plant, shelling out turn, harvest index, number of mature pods per plant, number

of sound mature kernel, plant height, specific leaf area, crop growth rate at 75 DAS to harvest and relative growth rate at 75 DAS to harvest were significantly and positively inter-related among themselves and also with kernel yield per plant. Hence the improvement of any of these attributes would simultaneously improve the kernel yield per plant.

Prabhu *et al.* (2015) carried out correlation analysis between yield and other yield components to identify the selection indices in BC₂F₁ generation of two crosses *viz.*, CO7 x GPBD 4 and CO 7 x COG 0437. From the upshot of correlation coefficient analysis, selection could be exercised on number of pods per plant, 100 pod weight, 100 kernel weight and shell weight for improving the pod yield and kernel yield per plant in groundnut. Hence, these characters may be considered as the important yield attributing characters and due emphasis should be placed while breeding for high pod and kernel yield per plant in groundnut.

Rathod *et al.* (2015) reported that the pod yield per plant exhibited significant positive association with number of pods per plant, total sugar, kernel yield, non reducing sugar, test weight, SCMR, harvest index, oil content and shelling per cent, whereas LLS severity, reducing sugar, stomata frequency and size showed significant negative association. Total sugar, kernel yield, stomata length, LLS severity, test weight, days to maturity and oil content extract the positive direct effect on pod yield per plant.

Rao (2016) studied character association and path analysis between yield and its contributing traits in 30 groundnut genotypes under drought. He found that dry pod yield was significant and positively correlated with kernel yield, number of pods per plant, 100 kernel weight and SPAD chlorophyll meter reading (SCMR). Path coefficient analysis indicated that number of pods per plant and 100 kernel weight were essential traits to be considered for realizing the improvement in yield.

Bagathariya and Patel (2017) observed that pod yield per plant was significantly and positively correlated with days to 50 % flowering, plant height, number of pods per plant, number of mature pods per plant, 100 kernel weight, kernel yield per plant, biological yield per plant and harvest index. Path analysis revealed that

the maximum direct effects as well as appreciable indirect influences on pod yield per plant were exerted by number of mature pods per plant and appreciable indirect influences were exerted by kernel yield per plant, plant height, number of mature pods per plant, biological yield per plant, days to 50 % flowering and 100 kernel weight.

Bhakal and Lal (2017) reported that, the results of phenotypic and genotypic correlation analysis revealed that plant height at 40 DAS (0.9215 and 0.8915), was significantly and positively correlated with pod yield q/ha (0.2897 and 0.2637) and hundred kernel weight (0.8981 and 0.4804) was positively correlated with pod yield/plant. Path analysis indicated that highest positive direct effect on pod yield per plant followed by kernel yield q/ha and kernel uniformity (0.0128).

Dhakar *et al.* (2017) studied correlation and path analysis for yield and its contributing traits in groundnut (*Arachis hypogaea* L.). They revealed that dry pod yield per plant showed positive and significant correlation at both genotypic and phenotypic levels with kernel yield per plant, 100 kernel weight, sound mature kernels and biological yield per plant. Correlation for dry pod yield per plant was divided into direct and indirect effects of different characters. Highest positive direct effect on dry pod yield per plant was exhibited by kernel yield per plant (2.28) followed by days to maturity (0.57), oil content (0.31) and days to 50 % flowering (0.22). This indicates that increase in kernel yield per plant, 100 kernel weight and sound mature kernels would improve the dry pod yield per plant of groundnut.

Gouranga (2017) studied correlation and path coefficient analysis revealed the importance of plant height, number of pod plant, number of kernels plant, shelling (%), sound mature kernel and harvest index as they had positive direct effects on pod yield and kernel yield and should be considered for improvement in yield.

Rajarathinam *et al.* (2017) reported that the traits number of pods per plant, 100 pod weight (g), 100 kernel weight (g), shelling (%) and pod yield per plant (g) were positively associated with kernel yield per plant (g). Inter correlation among these traits also recorded significantly positive association in most of the crosses

studied. So, these characters may be considered as the important yield attributing characters and due importance should be given while breeding for high pod and kernel yield per plant (g) in groundnut. Moreover in path analysis, the trait pod yield per plant (g) exhibited high positive direct effect on kernel yield per plant (g). It also possessed significant and positive association with kernel yield per plant (g). The pod yield per plant (g) plays a major role in determining the kernel yield per plant (g).

Reddy *et al.* (2017) studied character association and path analysis for kernel yield and its component characters in six parents and their 15 F₁ crosses in groundnut. The genotypic correlation coefficients were observed to be relatively of higher magnitude than the corresponding genotypic and phenotypic correlation coefficients indicating strong inherent association between the characters. Kernel yield per plant possessed significant positive association with pod yield per plant, number of mature pods per plant, 100-kernel weight, pods per plant, harvest index and shelling percentage at both genotypic and phenotypic levels. Path analysis also revealed the importance of these traits as they had direct effects on kernel yield. Therefore, selection based on these characters will lead to simultaneous improvement in kernel yield in groundnut.

Sardar *et al.* (2017) reported that kernel yield per plant had the highest positive direct effects on pod yield per plant followed by number of kernels per plant and 100 kernel weight. Plant height, number of branches per plant and number of pods per plant exhibited greater influence on pod yield per plant *via* number of kernel per plant and kernel yield per plant. Haulm yield and harvest index influenced indirectly on pod yield through kernel weight and number of kernel per plant, respectively. Present study thus indicated that kernel yield per plant, number of kernels per plant, 100 kernel weight followed by plant height and number of branches per plant were considered 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.

Aliyi *et al.* (2018) based on correlation and path coefficient analysis study suggested that the dry pod yield per hectare showed strong positive correlation

with grain yield. The trait will be useful for direct selection to increase grain yield. These indicated that there is a good opportunity to improve grain yield using the tested genotypes in groundnut breeding programs. Therefore, emphasis should be given for dry pod yield per hectare, primary branches per plant, pods per plant and 100-seed weight to enhance yield.

Shankar *et al.* (2018) reported that pod yield per plant had a significant positive association with kernel yield per plant, number of pods per plant, number of mature pods per plant, pod yield per plot, plant height at 90 days after sowing, plant height at 60 days after sowing, number of immature pods per plant, harvest index, test weight, number of primary branches per plant and plant height at 30 days after sowing.

Wadikar *et al.* (2018) studied the character association and indicated that highly significant positive association of kernel yield per plant with pod yield per plant followed by harvest index, number of pods per plant and test weight with pod yield at both genotypic and phenotypic level.

2.3 Genetic diversity in groundnut

In any crop improvement programme, genetic diversity has been considered as an essential pre-requisite for hybridization programme for obtaining high yielding progenies. If parents are identified on the basis of divergence analysis the resulting recombinants through hybridization would be more promising. The progeny originating from diverse parents exhibit greater heterosis and provide broad spectrum of variability in segregating generations through the production of transgressive segregants. Mahalanobis D^2 analysis is a powerful tool in quantifying the degree of divergence between biological populations at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance.

Nadaf *et al.* (1986) studied multivariate analysis using Mahalanobis D^2 statistic to group 83 genotypes from 18 countries on the basis of yield per plot and other six agronomic characters and the genotypes were grouped into nine clusters. Pod yield accounted for 88 percent of the total variation followed by number of

developed pods, days to 50 percent flowering and 1000- seed weight.

Golakia and Makne (1992) studied genetic diversity and clustering based on 16 characters in 35 genotypes of Virginia runner groundnut including 25 from ICRISAT and 10 from advance generation fixed genotypes derived through hybridization at Parbhani. The genotypes were grouped into seven clusters, three of which comprised of a single genotype. The largest cluster contained 25 genotypes of wide geographic origins and they recommended four genotypes as the promising parents for the hybridization programme.

Katule (1992) in genetic diversity of 18 genotypes reported eight clusters. Among these clusters maximum genotypes were grouped to cluster I (11.00). They reported genotypes from different eco-geographical region in different clusters showing no relation between genetic diversity and geographical diversity. The intra-cluster values ranged from 0.00 (cluster II and VIII) to 10.17 (cluster I) while maximum inter-cluster distance was observed between cluster VII and VIII (26.83) followed by cluster III and VIII (25.50) suggesting wide diversity between them. They reported maximum mean value for 100 kernel weight in cluster VII and for pod yield in cluster II. The height of main stem was the most important character (19.61) as its contribution was highest, followed by shelling percentage (16.99), number of mature pods (14.38) and 100 kernel weight (13.72). The findings of Sandhu and Sangha (1974) and Nadafet *al.* (1986) were also similar.

Reddy and Reddy (1993) studied genetic divergence in 48 genotypes (43 Spanish and five Virginia) from different geographical locations. An analysis of variance indicated significant difference between the genotypes for all 12 characters studied confirming the existence of genetic variability. The genotypes were grouped into 11 clusters, cluster I was the largest with 23 genotypes, followed by cluster VI and III with 9 and 7 genotypes, respectively. Geographical diversity was not related to genetic diversity. The analysis for estimating contribution of different characters to genetic diversity indicated that 100-pod weight (36 %), number of secondary branches per plant (31 %) and harvest index (15 %) accounted for more than 80 per

cent of the total divergence. Hence, these three characters deserve consideration in the breeding programmes.

Johan Joel and Mysamy (1998) using D^2 statistics of 26 groundnut genotypes of diverse origin revealed existence of moderate genetic diversity among the types of formation of three clusters where about 22 rust resistance genotypes with diverse origin congregating in cluster I and the rust susceptible, high yielding adopted varieties in cluster II and III and this clustering pattern showed that absence of parallelism between geographical and genetic diversities. The least intra-cluster I and high in cluster II. The intra-cluster distance was least in cluster I between ICG 10030A and ICG 10978 might be due to the common origin. They reported the highest inter-cluster distance between cluster I and III and the least between II and III. They finally concluded to use cluster I and III in crossing to create a wide spectrum of variability and to select segregants with high pod yield and rust resistance.

Ramesh Kumar *et al.* (1999) studied 21 M_7 generation mutant cultures of groundnut along with parent AK-12-24 and checks Chico and Kuber. They grouped 21 mutants in 16 clusters in which cluster I had five mutant cultures. Highest inter-cluster distance (61.12) was observed between cluster VI and XVI. The force of differentiation appeared different at inter and intra-cluster levels. The earlier results of Sandhu and Sangha (1974) and Nadaf *et al.* (1986) were similar.

Vijayasekhar (2002) grouped 65 genotypes into 10 clusters using Mahalanobis's D^2 analysis. The mode of distribution of genotypes into various clusters was at random suggesting that there was no correlation between geographical distribution and genetic diversity. The characters, harvest index, 100-seed weight and shelling percentage contributed maximum towards genetic divergence in both D^2 analysis and canonical root analysis.

Kumar (2004) studied divergence among 54 groundnut genotypes through D^2 statistic. He had formulated 11 clusters based on physiological characters. The mode of distribution of genotypes into different clusters for morphological and biochemical characters was at random and independent of each other suggesting that there was no relationship between geographical origin and genetic diversity.

Garjappa *et al.* (2005) studied two hundred genotypes of groundnut through D^2 analysis and principal component analysis and reported that number of secondary branches per plant contributed maximum towards divergence followed by days to maturity and total dry matter per plant.

Ravikumar (2005) studied genetic divergence among fifty groundnut genotypes through D^2 and Metroglyph analysis and reported that there was no relationship between geographic diversity and genetic diversity.

Laxmidevamma *et al.* (2006) evaluated 81 groundnut genotypes using Mahalanobis's D^2 analysis and grouped them into 16 clusters. They found that test weight, days to maturity and oil content were the most potential traits contributing to the total divergence.

Suneetha (2007) studied genetic divergence among 29 released and pre release groundnut cultivars and grouped them into 9 clusters. Grouping of genotypes in different clusters was not related to their geographical origin. The characters harvest index, days to emergence, length of main axis, leaflet length, 100 kernel weight and pod yield per plant were important in accounting for divergence.

Mane *et al.* (2008) evaluated forty bunch groundnut genotypes for genetic divergence. The D^2 values ranged between 3.85 and 1279.488 suggested presence of considerable amount of genetic diversity. All the forty genotypes were grouped into three clusters in which cluster-I had maximum number of genotypes followed by cluster-II with two genotypes and cluster-III was monogenotypic in nature indicating its wide divergence from other clusters. The clustering pattern showed absence of parallelism between geographical and genetic diversities.

Sonone and Thaware (2009) studied the forty genotypes of groundnut (*Arachis hypogaea* L.) selected from different geographical origins to assess the genetic diversity by using Mahalanobis's D^2 statistics.

Singh *et al.* (2010) evaluated thirty two groundnut genotypes of both spreading and bunch types for their yield, yield attributes, seed protein and oil content to analyse the degree of genetic variability in quantitative and qualitative traits. This degree of variation in seed yield and quality traits 16 offer an opportunity to further

evolve the promising groundnut varieties to boost both the seed and oil production in the country.

Zaman *et al.* (2010) assessed thirty four groundnut genotypes were for genetic divergence through D^2 analysis. They reported that the characters days to flowering, days to maturity, branches per plant, mature nuts per plant and 100 kernel weight contributed maximum towards divergence and also opined that there was no relationship between geographic diversity and genetic diversity.

Venkateswarlu *et al.* (2011) studied genetic divergence through Mahalanobis's D^2 analysis and grouped 74 groundnut genotypes into 12 clusters and reported that the characters 100-kernel weight, shelling percentage and harvest index contributed maximum towards genetic divergence.

Ravikumar and Reddi Sekhar (2012) evaluated 50 groundnut genotypes using D^2 and metroglyph analysis and grouped them into five and seven clusters, respectively. They reported that there was no relationship between geographic diversity and genetic diversity and D^2 analysis was more effective as compared to metroglyph analysis.

Makinde and Ariyo (2013) studied 22 genotypes of groundnut for 11 characters and reported higher GCV than PCV for all the traits viz., days to 50% flowering, number of leaves at flowering, days to maturity, final plant height, number of branches at flowering, nodes on main stem at maturity, stem girth at maturity, number of pods per plant, weight of 100 seeds. Hence there is less environmental effect on these traits.

Nirmala *et al.* (2013) evaluated thirty one genotypes of groundnut for genetic divergence and grouped into 14 clusters. They reported that the characters number of secondary branches per plant, 100-seed weight and harvest index contributed maximum towards genetic divergence.

Bhakal and Lal (2015) performed D^2 analysis of 40 genotypes of groundnut (*Arachis hypogaea* L.) of different geographical origins and revealed existence of considerable diversity for eleven quantitative and qualitative characters. The genotypes were grouped into 7 clusters. The clusters VI was the largest

containing 12 genotypes each followed by cluster V consisted 7 genotypes, cluster I and cluster VII consisted 6 genotypes, cluster III consisted 4 genotypes, cluster II consisted 3 genotypes and cluster IV consisted 2 genotypes. The diversity among the genotypes measured by intra-cluster and inter cluster distance was adequate for improvement of groundnut by hybridization and selection. The genotype included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in groundnut.

2.4 Effect of Genotype \times Environment and stability analysis of yield and yield contributing characters in groundnut

G \times E interactions are of major importance to plant breeder for developing improved varieties. A low level of interactions is useful for some characters so as to maximize the stability of performance over the number of environments. Environment is the sum of total of physical, chemical and biological factors.

Finlay and Wilkinson (1963) utilized technique to compare the performance of a set of cultivars grown at many sites for each variety. Varietal mean yield over environments and regression coefficients were used to classify the cultivars specially adapted to poor, better yielding environments and for general adaptability. They have indicated average phenotypic stability by a regression coefficient of unity ($b_i = 1.0$). A cultivar with $b_i < 1.0$ has above average stability, $b_i > 1.0$ has below average stability and $b_i = 1$ has absolute phenotypic stability which means a constant grain yield in all the environments. The ideal cultivar is one that possesses genetic potential in the highest yielding environment and maximum phenotypic stability.

Eberhart and Russell (1966) observed that the corn hybrids with a regression coefficient less than 1.0 usually means yields that were below average. Accordingly they suggested that a desired variety should have high mean, regression coefficient equal to 1.00 and variance due to regression as small as possible. Thus they modified the regression techniques, which enables partitioning of genotype \times environment interaction of each variety into two parts (b_i), the variation due to response of variety to varying environmental indices (sum of squares due to

regression) and the unexplainable deviation from the regression on the environmental index. They defined both the linear (bi) and non-linear (S^2_{di}) component as stability parameters. They compared two types of crosses in maize. They reported that hybrid \times year interactions were significantly greater for single crosses than for three way or double crosses. They further stated that some single crosses may show as much or more phenotypic stability than most stable three way or double crosses.

Bhole *et al.* (1987) studied phenotypic stability for pod yield in summer groundnut in a set of eight promising varieties at seven locations. The environment plus genotype \times environment interactions were significant which revealed that genotypes were interacted with environment. While among the cultivars, TG-17 and EC-21103 had low regression value and comparatively stable performance as the values of deviation around the regression line (S^2_{di}) were low. The variety JL-12 was the most stable for pod yield having regression value near to unity and the least mean square deviation (S^2_{di}).

Senapati and Roy (1991) evaluated 60 groundnut genotypes in five environments for stability analysis. The genotypes NG-5-9 and MCAC-2664 attained wider adaptability for seed yield, while genotypes JL-53, MC-434, ICGPRS-225, Guyabita Bunch, ICES-44-1, EC-259704 and MCAC-765 showed adaptability specifically to favorable environments in West Bengal.

Wu (1993) evaluated 10 promising lines and two standard varieties at nine locations in spring and four locations in autumn for two years. The analysis of variance over environments for pod and seed yield revealed that mean squares due to genotypes, environments and genotypes \times environments interaction were significant. Lines Nan-kai-si-133 and 134 showed the best pod and seed yield stability over all environments in the spring, and Nan-kai-si-133 also had the best yield performance over all environments in autumn. Whereas, line Nan-kai-si-132 showed high yields, but was lower in stability in autumn.

Varman and Manoharan (1993) derived stability parameters for dry pod yield and three related traits in ten genotypes of groundnut over four locations. They reported non significant. $G \times E$ interaction for pod yield and VG-77 exhibited high

mean performance for all the traits. JL-24, VG -55 and J-11 were stable for shelling percentage, 100 pod weight and seed weight, respectively.

Patra (1995) studied phenotypic stability for pod yield and quality factors in 10 varieties of Spanish bunch groundnut for pod yield, kernel yield, shelling percentage, sound mature kernels and 100 kernel weight. The difference between the varieties was significant for shelling percentage, sound mature kernel per cent and 100 kernel weight. On the basis of 5 characters, varieties Kisan, Jawan, Girnar and OG52-11 were found superior to the other by 26 per cent. ICGS-11 was found stable for four characters (pod yield, 100 kernel weight, kernel yield and sound mature kernel per cent) and Kisan and Jawan and ICGS 44 for three characters (pod and kernel yield and sound mature kernel per cent).

Chunilal and Ranvir (1998) studied stability analysis for pod and kernel yield in ten genotypes of Spanish groundnut including three released varieties at ten locations. Significant mean squares due to $G \times E$ interaction indicated that the genotypes interacted significantly with the environments. The magnitude of linear component was however higher than non linear component suggested the possibility of prediction across the environments.

Sojitra and Pethani (1998) evaluated 29 diverse bunch groundnut genotypes in four environments to assess stability parameters for 100 pod weight and shelling percentage. $G \times E$ (linear) and $G \times E$ (non-linear) interactions were significant against pooled error indicating existence of only non-linear portion of $G \times E$ interaction. Out of 29 genotypes, four genotypes for 100 seed weight and 14 genotypes for shelling per cent did not interact with the environments. A simultaneous consideration of three adaptation parameters (x , b_i and S^2d_i) suggested that bold pooled cultivars GG-2 and Girnar-1 were insensitive to changing environments for high 100 pod mass; whereas, higher shelling percentage cultivar J-11 exhibited low rate of changes to environmental differences, and it was well adapted to adverse environmental conditions.

Dabholkar (1999) had given applicability of stability models. He suggested that the genotype is having the general adaptability if the 'bi' value (linear

component) is at unity with pooled mean above the grand mean. Further, he also suggested that the performance of the particular genotype is predictable, if that genotype is having S^2_{di} value (non-linear component) non-significant.

Mahto and Mahto (2000) studied carried out analysis in nine promising varieties of groundnut under different environments. $G \times E$ interaction were significant for all the five quantitative traits *i.e.* days to 50 % flowering, days to maturity, shelling percentage, 100 kernel weight and pod yield (kg/plot). All the characters were controlled by non linear component of environment. The variety JL-24 and BG-3 were highly stable for pod yield and most of the other characters and suitable for cultivation in wide range of environmental conditions.

Venkataramana *et al.* (2000b) conducted experiment on stability analysis for pod yield with thirty genotypes of groundnut and observed that environment-1 was significant for plant height, days to 50 % flowering, days to maturity, number of mature pods per plant, pod yield per plant, shelling per cent, 100 kernel weight and oil yield per plant. The variance due to genotype \times environment (linear) was significant for plant height. The non linear component was significant for all the characters except for plant height.

Aroglu *et al.* (2001) tested against Virginia type ground genotypes for $G \times E$ interaction and stability for pod yield and seed weight. The genotypes 75/1073, PI 355276, PI 315633 and PI 346385 had high adaptability to all environments with respect to pod yield with regression coefficients close to 1.0 and yield values above general mean.

Kadam *et al.* (2001) studied stability for dry pod yield and days to maturity in eleven groundnut genotypes. Eleven genotypes were grown for three years at Karad. Both linear and non-linear effects of genotype \times environment interaction were highly significant for both the traits. Among all genotypes, BAU-18 and C-587 were shown above average stability for dry pod yield and days to maturity, respectively.

Naazar *et al.* (2001) performed stability analysis for pod yield in 10 groundnut genotypes and observed that $G \times E$ interaction was highly significant. The

regression coefficient (b) ranged from 0.76 to 1.17 and deviations from regression (s^2d) ranged from 0.06 to 0.82. BM-28 and ICGV-86550 were regarded as suitable genotypes for wide range of environments.

Singh and Singh (2001) studied 44 genotypes of groundnut during rainy season of 1995, 1996 and 1997 at research station of the university, Ujhani, Badaam and reported that $G \times E$ interactions were highly significant for days to maturity, height of central axis, number of pods per plant, pod yield per plant, shelling percentage and 100 kernel weight.

Viswanathan *et al.* (2001) worked out phenotypic stability in ten groundnut genotypes and observed that $G \times E$ interaction was significant for number of mature pods and pod yield per plant. VGN 24 recorded high mean value, average responsiveness and stability for both the traits based on Eberhart and Russell model and genotype grouping methods.

Nageswara Rao (2002) studied stability analysis in Spanish groundnut genotypes in rice fallows under scarce water regimes of K.G. zone in Andhra Pradesh and reported that land race TMV-2 exhibited stable for pod yield over all the environment.

Senapati and Sarkar (2002) estimated phenotypic stability of 34 groundnut genotypes over four environments for yield and seven yield related traits. The mean squares due to genotypes, environments and genotypes \times environment and the linear and non-linear component of genotype \times environment interactions were also significant for all the characters. TCF-1717 had very high pod yield and was stable for yield, number of primary branches per plant, shelling percentage and seeds per pod. ICGPRS-221 also had high pod yield and was stable for yield, maturity days, 100 seed weight and seeds per pod.

Joshi *et al.* (2003) evaluated a set of 44 spreading groundnut types for pod yield and its components over five years for stability analysis. They reported that mean squares due to $G \times E$ interaction were significant for fodder yield, biological yield and harvest index. Whereas non-linear component is significant for all the traits,

indicating the presence of variability among the genotypes governed by various environmental conditions prevailing in different years.

Suneetha (2003) studied 23 diverse groundnut genotypes for characters 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.

Bentur *et al.* (2004) evaluated 13 confectionery groundnut genotypes for their genetic stability in terms of biochemical traits and reported that significant G x E interaction was recorded for protein content, total sugar content and oil content. Cultivar JGLPS 7 exhibited stability for oil and protein content, where as cultivars M 13 and TKG 19 A were the most stable for total sugar content.

Deshmukh (2004) evaluated 50 genotypes of groundnut for two seasons to estimate G x E interactions which were significant for number of mature pods per plant, shelling percentage and days to maturity. While the pooled deviation (non-linear) were non-significant for all the characters under studied.

Gitanjali and Sarma (2005) assessed yield stability in 67 genotypes of groundnut over three environments and observed that ICGV-87867 was the most stable genotype. Genotypes ICGV-86326, ICGV-88348, ICGV-88338 and ICGV-87415 performed well in favourable conditions. NRCG-1752 was good for unfavourable environment.

Venkateshmurthy (2005) carried out stability analysis in groundnut and reported that genotypes TMV-2, JL-24, K-134 and ICGS 44 were found to be stable over three environments.

Chunilal *et al.* (2006) conducted experiment with six groundnut genotypes under rainfed situations of Junagadh during *khariif* 1996-2000 to assess

stability for yield and quality characters. Cultivar B 95 registered highest pod yield, 100 pod weight and 100-kernel weight across the environments.

Olivera and Ignacio (2006) worked out of G x E interaction for 18 peanut lines in 10 field trials. They reported that genotypes L 127, L118, L123 line and runner IAC 886 accounted for the greatest part of G x E interaction. Lines L-132, L-149 and LI-50P presented the highest stability and pod yields above the overall mean.

Mekontchou *et al.* (2006) experimented with six advanced groundnut breeding lines grown at four locations, during three seasons and reported that significant line x environment interactions was detected for all the traits. Lines 82 D22P-466 and 82 D145-1809 registered mean yields and yield components higher than average and b values close to unity.

Masideni (2006) performed G x E interaction and yield stability for eight Bambara groundnut genotypes in three locations at two planting dates. Significant differences were found for genotype, environment and G x E interactions. The best genotype was SB4-4 across the locations.

Badigannavar *et al.* (2007) studied genotype x environment interaction by evaluating twelve genotypes over 16 environments during 2000 and 2001. Genotype, environment and interaction components were significant for seed yield per hectare. The genotype TG37A identified as highly productive and broadly adaptable genotype.

Hariprasanna *et al.* (2008) assessed G x E interaction and stability analysis in large seeded groundnut genotypes for three years and observed significant G x E interaction for pod and kernel yield. Two genotypes PBS 29010 and GG 20 had near unity regression coefficient (bi) for pod and kernel yield indicating adaptations.

Phakamas *et al.* (2008) evaluated 15 peanut lines varying in maturity duration, seed type and yield level grown in a field experiment at the Khon Khon University in Northeast Thailand during rainy season of 2002 and 2003 and dry season of 2003 and 2004. Seasonal effects were found for all the development and growth traits of the test peanut lines. Regression analysis identified pod growth as the

dominant physiological trait determining the genotype x seasonal interaction for pod yield.

Chavan *et al.* (2009) reported genotypes x environment interaction variances highly significant for all the characters studied. The genotypes LGN-107, LGN-110, LGN-121, LGN-125, LGN-126, LGN-128, LGN-129, LGN-130, LGN-117, LGN-162, LGN-1 and AK-159 were stable over the environments for pod yield per plant. Among them, LGN-110, GLN-112, LGN-115 and LGN-163 showed wider adaptability for shelling percentage. While LGN-111 and LGN-115 were adapted specifically to better environment and showed a high degree of stability for 100 kernel weight.

Iwo and Olorunjo (2009) assessed 23 advanced groundnut genotypes during 2001-2002 for yield stability and resistance to early leaf spot, late leaf spot and rosettr virus. They noticed that the groundnut line ICGV-IS-96805 combined very high yielding capacity and outstanding disease resistance, though not the highest yield stability.

Sreekala and Hemanth (2009) reported that among the three environments, the genotypes ICG-7332, ICG-3245, ICG-7633, ICG-11386, ICG-2184, JL-24, TPT-4 and K-134 were highly responsive to rabi inceptisols in terms of yield and yield contributing characters. Hence, they may be included as parents for developing a high protein and kernel yielding variety suitable for cultivation in all the environments studied.

Nawaz *et al.* (2009) experimented with eight groundnut genotypes for stability at ten locations. They reported that four entries produced more dry pod yield compared to overall mean. Genotype ICGV 92040 was stable over ten locations, it showed above average performance and bi value (1.09) nearer to unity.

Yogendra and Sunil (2009) studied yield stability in eight groundnut genotypes during the kharif season of 2002-2005. They noticed that six genotypes were stable for days to maturity, among which BAU-19 registered the lowest days to maturity.

Thaware (2009) evaluated 24 genotypes of groundnut for stability of dry pod yield. Linear component of genotype x environment interaction was higher than that of non linear. Out of 24, 12 genotypes had above average mean, average responsive and genotype number 123 was stable for dry pod yield.

Mothilal *et al.* (2010a) worked out the stability of 15 foliar disease resistant groundnut genotypes and one local variety (VRI 4) over four seasons in a single location and revealed that only one genotype (ICGV-92093) had near unity regression coefficient coupled with non-significant deviation from regression and high mean kernel yield.

Mothilal *et al.* (2010b) tested 16 groundnut genotype across four environment to study genotype x environment interaction for kernel yield. They found that G x E interaction was highly significant and both linear and non linear component are equally important for yield stability. The genotype ICGV 92004 was found to be stable genotype over four environments.

John and Raghava Reddy *et al.* (2011a) twenty eight F2 populations were evaluated for genetic parameters of 23 characters of morphological, physiological, yield and yield attributes during rabi 2009. TPT-4 x ICGV-91114 was distinct for its lowest mean value for days to maturity and highest mean values for number of well-filled and mature pods per plant, shelling per cent, 100- kernel weight. The F2 involving JL-220 as one of the parents viz., JL-220 x ICGV 99029 for SCMR, JL-220 x TCGS- 647 for SMK per cent, protein per cent, kernel yield per plant and pod yield per plant showed the highest per se performance High genotypic coefficient of variation was observed for number of secondary branches per plant. High heritability and high GAM was recorded for number of secondary branches per plant, high heritability and moderate GAM observed for days to 50% flowering. Moderate heritability and high GAM was showed for leaf area index, number of well filled and mature pods per plant, dry haulms yield per plant and harvest index. This indicates that these characters are under additive genetic control and selection for genetic improvement will be worthwhile and may rapidly contribute yield.

Patil *et al.* (2014) reported that mean squares due to genotype x environment (G x E) interactions were significant for the characters, days to 50 % flowering, number of primary branches per plant, days to maturity, plant height (cm), number of mature pods per plant, dry pod yield (g), kernel yield (g), haulm yield (g), dormancy (days), oil content (%) and protein content (%) except 100 pod weight (g), 100 kernel weight (g), sound mature kernel (%), shelling (%) and harvest index (%) indicating the influence of environmental conditions on the genotypes evaluated except for above 5 traits. The mean squares due to G x E (linear) were significant for days to 50 % flowering, days to maturity, dry pod yield (g), 100 kernel weight (g), sound mature kernel (%), shelling (%) and protein content (%). On further perusal of genotypes in relation to overall performance revealed that genotypes *viz.*, AG-2008-7, AG-2008-9, ICGV-99181 and J-68 were found stable for unfavourable environments.

Bhargavi and Rao (2016) revealed that the genotypes Tirupati 3, Abhaya, Greeshma, K 1535, JL 24 and K 1622 were stable over three environments for pod yield per hectare. These genotypes could be the most stable, since they had small and non significant deviations and had the highest yielding potentiality.

Minde *et al.* (2017) evaluated ten groundnut genotypes to know the role of G x E interaction and also to study stability performance over three environments. Analysis of variance revealed highly significant differences among the genotypes for all the characters studied. Genotypes x environment interactions were significant for all the characters under study indicating influence of environmental conditions. Stability analysis showed that both linear and non-linear components of G x E interactions were highly significant for all the characters. Environment (E₁) was observed to be most suitable for better expression of yield and its contributing characters. None of the genotype was found to be average stable for all the characters. Out of all the genotypes, JL-24 and Phule Unnati for fresh pod yield per plant and TPG-41 and JL-24 for dry pod yield per plant exhibited average stability across the environments

3. MATERIALS AND METHODS

The present investigation on “Genetic variability and G x E interaction studies in Groundnut (*Arachis hypogaea* L.)” was conducted at All India Co-ordinated Research Project on Groundnut, Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.), during 2018. The details of materials used and methods adopted during the course of the investigation are given below.

3.1 Materials

The materials used in the present study consisted of 40 F₅ progenies of eight crosses of groundnut received from Groundnut Breeder, All India Co-ordinated Research Project on Groundnut, Cotton Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (M.S.).

3.1.1 Experiment I :

Variability, correlation, path analysis and D² analysis study in F₅ generation in summer groundnut.

Number of genotypes : 40 F₅ progenies of eight crosses.

Sr. No	Name of cross	Number of progeny
1.	TAG-24 x Phule Unnati	5
2.	Phule Unnati x TPG-41	5
3.	WRGS-15 x RHRG-8808	5
4.	Phule 6021 x ICGV-00350	5
5.	Phule 6021 x Phule Unnati	5
6.	Phule Unnati x SB-XI	5
7.	Phule 6021 x RHRG-6110	5
8.	WRGS-15 x SB-XI	5
	Total	40

3.2 Methods

3.2.1 Experimental design :

- a. **Season** : Summer-2018
- b. **Design** : Compact Family Block Design
- c. **Replications** : 2

- d. **Spacing** : 30 × 10 cm
e. **Plot size** : Gross-5.00 × 1.80 m. Net- 4.80 ×1.20 m
f. **Fertilizers applied** : 25: 50 N: P kg/ha

3.2.2 Experiment II: List of fourteen genotypes involved in research work on stability studies during summer and *kharif* season are given as below:

Sr. No.	Genotype	Pedigree	Sr. No.	Genotype	Pedigree
1	JL-501	Selection from TAG-24	8	RHRG-1335	Ghungari x RHRG- 6097
2	TAG-24	TGS-2 x TTG-22	9	RHRG-1142	TAG-24 x Phule-6021
3	Phule-6021	Selection from ICG-3029	10	RHRG-1308	Phule Unnati x JL-501
4	TPG -41	TG 28A x TTG-22	11	RHRG-1189	RHRG-6021 x Phule Unnati
5	Phule Bharati	Selection from DTE-64	12	RHRG-1192	RHRG-6021 x RHRG-6097
6	Phule Unnati	(ICGV-92029 x ICGV-92184) x (ICGS-44 x ICGS-76)	13	RHRG-1130	JL-24 x SB-XI
7	SB-XI	Ah-4218 x Ah-4354	14	RHRG-1305	Phule Unnati x JL-501

- a. **Sowing Dates (4)** : **Summer** 1. 15.2.2018 2. 3.3.2018
Kharif 1. 15.7.2018 2. 30.7.2018
b. **Design** : Randomized Block Design
c. **Replications** : 3
d. **Spacing** : 30 × 10 cm
e. **Plot size** : Gross - 5.00 × 1.80 m. Net - 4.80 × 1.20 m
f. **Fertilizers applied** : 25: 50 N: P kg/ha

3.2.3 Observations recorded

Following observations were recorded on ten randomly selected plants from each treatment in each replication and averages were worked out.

1.	Days to 50% flowering (Nos.)	7.	Haulm yield per plot (Kg)
2.	Days to maturity (Nos.)	8.	Hundred kernel weight (g)
3.	Number of branches per plant (Nos.)	9.	Shelling (%)
4.	Number of mature pods per plant (Nos.)	10.	Sound Mature Kernel (%)
5.	Number of immature pods per plant (Nos.)	11.	Oil content (%)
6.	Pod yield per plot (Kg)	12.	Protein content (%)

3.3 Method of recording observations

3.3.1 Days to 50% flowering (Nos.)

To record days to 50 % flowering was observed the crop every day when flower initiation starts and record the days after emergence when 50 per cent of the plants have at least one flower completely open.

3.3.2 Days to maturity (Nos.)

The number of days taken from the date of sowing to the date on which more than 90 per cent of plant showed drying up confirmed by hardness of seed to bite was taken as days to maturity.

3.3.3 Number of branches per plant (Nos.)

The branches directly emerging from the base of the main shoot counted on five consecutive plants at the time of harvesting.

3.3.4 Number of mature pods per plant (Nos.)

The mature pods on five consecutive plants counted at the time of harvesting and calculated the mean number of mature pods per plant.

3.3.5 Number of immature pods per plant (Nos.)

The immature pods on five consecutive plants counted at the time of harvesting and calculated the mean number of immature pods per plant.

3.3.6 Pod yield per plot (kg)

The dry pods taken out after harvesting from each plot and weighted in kilograms (kg).

3.3.7 Haulm yield per plot (kg)

The dried plant is taken out from each consecutive plot after harvesting and count the weight of dry plant and calculate the mean of haulm yield per plot in kilograms (kg).

3.3.8 Hundred kernel weight (g)

A representative random sample of hundred kernel per treatment weighed in grams.

3.3.9 Shelling (%)

The developed pods from five randomly selected plant were shelled and the kernels were weighed in gram. The shelling percentage was estimated by using the following formula

$$\text{Shelling (\%)} = \frac{\text{Kernel yield per plant (g)}}{\text{Pod yield per plant (g)}} \times 100$$

3.3.10 Sound mature kernel (%)

The sample of hundred kernels taken from each variety and replication wise and counted only the sound mature kernels. The number of kernels matured sound is determined as sound mature kernel percentage. SMK (%) was calculated as follows.

$$\text{SMK (\%)} = \frac{\text{No. of fully matured, wrinkle free kernels}}{\text{Total number of kernels}} \times 100$$

3.3.11 Oil content (%)

The oil percentage was estimated by NIR Spectro Photo Analyzer machine.

3.3.12 Protein content (%)

Percent crude protein content of the groundnut sample was estimated by NIR Spectro-Photo Analyzer machine.

3.4 Statistical Analysis

The mean values of five randomly selected observational plants for 12 different traits were used for statistical analysis. The following statistical measures

/parameters were worked out for presentation of the data in different quantitative attributes.

3.4.1 Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in the following form

Source of variation	DF	MSS	Expected mean square
Replication	(r-1)	RMS	$\sigma^2_e + t \sigma^2_r$
Treatment	(t-1)	TMS	$\sigma^2_e + r \sigma^2_r$
Error	(r-1) (t-1)	EMS	σ^2_e
Total	(rt-1)		

Where,

r = Number of replications,

t = Number of treatments,

e = Error

3.4.2 Estimation of mean and range

The mean values for each character were worked out by the following formula:

$$\bar{X} = \frac{1}{N} \sum_{i=1}^n X_i$$

Where,

\bar{X} = Mean of character

X_i = Sum total of characters

N = Number of observations

The difference between the highest and the lowest values from mean of each character were recorded as range.

3.4.3 Estimation of standard error of mean, standard error of difference and critical difference

- i. The S.E. of mean difference was calculated as S.E. of mean [SEm]= $\sqrt{\sigma^2_e/r}$
- ii. The standard error of difference between two means was calculated as

S.E. of difference [SE (d)] = $SEm \times \sqrt{2}$

iii. The critical difference between any two means was calculated as C.D. = SE (d) x 't' at error d.f.

3.4.4 Estimation of components of variation

The phenotypic and genotypic variances were calculated by using the respective mean squares from variance table (Johnson *et al.* 1955) as below.

Environmental variance (σ^2_e) = EMS

Genotypic variance (σ^2_g) = $\frac{GMS-EMS}{r}$

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications.

3.4.5 Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated by the formulae as suggested by Burton and Vane (1953).

i. Genotypic coefficient of variation (GCV)

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

Where,

σ^2_g = Genotypic variance and

\bar{X} = Mean of character

ii) Phenotypic coefficient of variation (PCV)

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

Where,

σ^2_p = Phenotypic variance and

\bar{X} = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

- Low : 10 per cent
- Medium : 10 to 20 per cent
- High : > 20 per cent

d. Estimation of coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated by using the following formulae given by Burton (1952).

i. Genotypic Coefficient of Variation (GCV)

It was estimated by the formula suggested by Burton (1952).

$$GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100$$

Where,

$$\sigma^2_g = Vg = \text{Genotypic variance}$$
$$\bar{X} = \text{General mean of the character}$$

ii. Phenotypic Coefficient of variation (PCV)

It was estimated by the formula suggested by Burton (1952).

$$PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100$$

Where,

$$\sigma^2_p = Vp = \text{Phenotypic variance and}$$
$$\bar{X} = \text{General mean of the character}$$

e. Heritability percentage

Heritability percentage(broad sense) was calculated as per Burton (1952).

$$h^2 \text{ (b.s.)} = (Vg/Vp) \times 100$$

or

$$h^2 \text{ (b.s.)} = (\sigma^2_g / \sigma^2_p) \times 100$$

Where,

- $h^2 \text{ (b.s.)}$ = Heritability in broad sense
- $\sigma^2_g = Vg$ = Genotypic variance
- $\sigma^2_p = Vp$ = Phenotypic variance

Heritability estimates were classified as high, medium and low on the basis of values given by Robinson (1966):

- Low Heritability = < 30 per cent
- Medium Heritability = 30.1 to 60 per cent
- High Heritability = > 60 per cent

f. Genetic advance

Genetic advance was calculated as given by Johnson *et al.* (1955).

$$G.A. = K \times \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \text{ or } GA = k \times h^2 \times \sigma^2 p$$

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity

$\sigma^2 g = Vg =$ Genotypic variance

$\sigma^2 p = Vp =$ Phenotypic variance

$\sigma p =$ Phenotypic standard deviation

G.A. as percentage of mean (GAM)

$$GAM = \frac{G.A.}{\bar{X}} \times 100$$

Where,

G.A. = Genetic advance

\bar{X} = Character mean

Low : 10 per cent

Medium : 10.1 to 20 per cent

High : > 20 per cent

3.4.6 Correlations

To understand the association among the characters, genotypic and phenotypic correlation coefficient were worked out as given by Singh and Chaudhary (1977).

i. Phenotypic correlation coefficient (rp)

It is derived by

$$r_{p1.2} = \frac{(\text{COV. } p_{1.2})}{\sqrt{(\sigma^2 p_1) \cdot (\sigma^2 p_2)}}$$

Where,

- $r_{p1.2}$ = Phenotypic correlation between character 1 and 2
 $\text{COV. } p_{1.2}$ = Phenotypic covariance between character 1 and 2
 $\sigma^2 p_1$ and $\sigma^2 p_2$ = Phenotypic variance of character 1 and 2, respectively.

ii. Genotypic correlation coefficient (rg)

It is derived by

$$r_{g1.2} = \frac{(\text{COV. } g_{1.2})}{\sqrt{(\sigma^2 g_1) \cdot (\sigma^2 g_2)}}$$

Where,

- $r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2
 $\text{COV. } g_{1.2}$ = Genotypic covariance between character 1 and 2
 $\sigma^2 g_1$ and $\sigma^2 g_2$ = Genotypic variance of character 1 and 2, respectively.

The significance of genotypic and phenotypic correlation coefficient were tested by 't' test (Panse and Sukhatme, 1985).

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

Where,

- r = Correlation coefficient
 n = Total number of observations

The calculated 't' value was tested with table 't' value for respective (n-2) degrees of freedom for significance.

3.5 Path analysis

Path coefficient analysis was done according to procedure suggested by Dewey and Lu (1959). If 'y' is the effect 'x1' is the cause, path coefficient for the path from cause x1 to the effect y is $\delta x_1 / \delta y$. Direct and indirect effects were worked out by using genotypic correlation as given below.

Direct effect of x_1 on $y = P_{x_1.y}$

Where,

$P_{x_1} =$ Path coefficient of x_1 on y . Similarly, direct effects of other attributes on yield were calculated.

Indirect effect of x_1 via x_2 on $y = p_{x_2.y} \times r_{x_1.x_2}$

Where

$p_{x_2.y} =$ Path coefficient of the component character x_2 on y .

$r_{x_1.x_2} =$ Genotypic correlation between x_1 and x_2

Similarly, indirect effects in all possible combinations were calculated for all component characters. The residual effect (R) was calculated below.

$$R = [1 - (P_{x_1.y} \cdot r_{x_1.y}) - (P_{x_2.y} \cdot r_{x_2.y}) \dots \dots \dots (P_{x_n.y} \cdot r_{x_n.y})]^{1/2}$$

Where,

$P_{x_1.y}, P_{x_2.y}, \dots, P_{x_n.y} =$ Direct effects of respective character on seed yield.

$r_{x_1.y}, r_{x_2.y}, \dots, r_{x_n.y} =$ Correlation coefficient between respective characters and seed yield.

3.6 Mahalanobis generalized distance (D^2)

The generalized distance between two populations was defined by Mahalanobis (1936) as :

$$D^2 = \sum \sum \lambda_{i,j} \cdot \delta_i \cdot \delta_j$$

Where,

$\lambda_{i,j} =$ Reciprocal matrix to the common dispersion matrix

$\delta_i =$ Difference between the mean values of the two populations for the i^{th} character.

Estimation of D^2 value from the above formula is very complicated in the present study. Since, it requires the inversion of thirteen order determinants and then the evaluation of $B(BH)/2$ terms whose sum is D^2 . It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variables reduces to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation elements.

3.6.1 Determination of gene constellations

Tochers method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for findings the clusters because a cluster is not a well defined term. The only criterion appears to be that any two groups belonging to the same cluster should be at least on an average shows a smaller D^2 than those belonging to two different clusters. A simple device suggested by K.D. Tocher is to start with two closely associated groups and find the third group which has the smallest D^2 from the first three and so on. If at the any stage the average D^2 of group from those already listed appears to be high, then these groups does not fit in with the former groups and is therefore taken outside the former cluster. The group of first cluster then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to the inclusion of an additional group. If the changes are appreciable then the newly added group has to be considered as outside the cluster.

3.6.2 Average intra and inter cluster D^2 and D value

3.6.2.1 Average intra cluster D^2

$$D^2 = \Sigma D_i / n$$

Where,

D_i is the sum of distance between all possible combinations (n) of the population included in a cluster.

3.6.2.2 Average inter cluster D^2

$$D^2 = \Sigma \text{Distance between the population of cluster 1 and } j/n_i \cdot n_j$$

Where,

n_i = Number of population in cluster i

n_j = Number of population in cluster j

3.6.2.3 Average intra and inter cluster distance

$$D^2 = \sqrt{D^2}$$

3.6.3 Cluster means

Cluster mean were calculated for individual characters on the basis of mean performance of the genotypes included in that cluster.

3.7 Statistical analysis

The data was collected on randomly selected Five plants of each genotype per replication in each plot for each character. The collected data was subjected for testing the genotypic differences.

Stability analysis was performed as per Eberhart and Russell (1966), by considering three stability parameters to describe the performance of genotypes over different environments. According to them the regression of each variety on an environmental index and a function of square deviation from this regression provide estimates of stability parameters.

For each genotype stability was described by three parameters viz., mean performance (\bar{X}), regression coefficient (b_i) and the squared deviation from the regression ($S^2 d_i$).

These parameters are defined by using the following model.

$$Y_{ij} = \mu + \beta_i I_j + \delta_{ij} \quad (I= 1, 2 \dots\dots, t \text{ and } j = 1, 2 \dots\dots S)$$

Where,

- Y_{ij} = Mean of i^{th} genotype in j^{th} environment
- μ = Mean of all genotypes over all environments
- β_i = The regression coefficient of i^{th} genotype on the environmental index, which measures response of genotype to varying environments
- I_j = The environmental index which is defined as deviation of the mean of all the genotypes at a given environment from the overall mean.

$$\frac{\sum_j Y_{ij}}{t} - \frac{\sum_j \sum_j Y_{ij}}{ts} \quad \text{with } \sum I_j = 0$$

\sum_{ij} = The deviation from regression of the i^{th} genotype of j^{th} environment.

3.7.1 The stability parameters

a. The regression coefficient (b_i) is described as under

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij} I_j$ is the sum of products

$\sum_j I_j^2$ is the sum of squares of environmental index

b. Mean square deviation (S^2_{di}) from linear regression is calculated as

$$S^2_{di} = \frac{\sum_j \delta^2_{ij}}{(S-2)} - \frac{S^2_e}{r}$$

Where,

$$\sum_j \delta^2_{ij} = \left(\begin{array}{c} \sum_j Y^2_{ij} - \frac{Y^2_i}{t} \\ \sum_j Y_{ij} \cdot I_j \end{array} \right) \frac{(\sum_j Y_{ij} \cdot I_j)^2}{\sum_j I_j}$$

and

$$\begin{aligned} S^2_e &= \text{The estimate of pooled error} \\ t &= \text{Number of genotypes} \\ S &= \text{Number of environments} \end{aligned}$$

1. Computation of environmental index (I_j)

I_j is defined as

$$I_j = \frac{\sum_j Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{ts}$$

$$= \frac{\text{Total of all genotypes at } j^{\text{th}} \text{ location}}{\text{Number of genotypes}} - \frac{\text{Grand total}}{\text{Total number of observations}}$$

2. Computation of regression coefficient (b_i) for each genotype

$$b_i = \frac{\sum_j Y_{ij} \cdot I_j}{\sum_j I_j^2}$$

i. For each value of regression coefficient $\sum I_j^2$ is common, equal to sum of squares of environmental indices.

$$\sum_j I_j^2 = (I_1^2 + I_2^2 + \dots + I_j^2)$$

ii. The $\sum_j Y_{ij} \cdot I_j$ for each genotype of environmental index (I_j) with corresponding mean (\bar{X}) of that genotype at each environment.

These values were obtained in the following manner

$$\overline{(X)} (I_j) = (\sum_j Y_{ij} \cdot I_j) = (S)$$

$$\overline{(X)} = \text{Matrix of means}$$

- (I_j) = Vector of environmental index
 (S) = Vector for sum of products *i.e.* $\sum_j Y_{ij} \cdot I_j$

iii. The b_i value for each genotype was thus calculated by dividing $\sum_j Y_{ij} \cdot I_j$ [as calculated above in (ii)] by $\sum_j I_j^2$ obtained above under (i)

Thus,

$$b_i = \frac{\sum_j Y_{ij} \cdot I_j}{\sum_j I_j^2}$$

3. Computation of S^2_{di}

In regression analysis it is possible to partition the variance of the dependent variable (Y) into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity.

Symbolically

$$\sigma^2_y = \sigma^2_{\text{regression}} + \sigma^2_{\text{deviation from regression}}$$

By subtracting the variance due to regression from σ^2_y one can get the variance due to deviation from regression which in turn can be used for estimating S^2_{di} values. The variance of means over different environments was obtained as follows.

$$\sigma^2_{V_i} = \sum_j Y_{ij}^2 - (Y_i^2 / s)$$

Where,

- $\sum_j Y_{ij}^2$ = Sum of squares of mean of i^{th} genotype over j^{th} environment
 Y_i = Sum of means of i^{th} genotype over environments.
 S = Number of environments

The variance due to deviations from regression $\sum_j \sigma^2_{ij}$ for a genotype being.

$$\text{Where, } \sum_j \sigma^2_{ij} = \left[\frac{\sum_j Y_{ij}^2}{S} - \frac{(Y_i^2 / S)}{S} \right] = \frac{(\sum_j Y_{ij} \cdot I_j)^2}{\sum_j I_j^2}$$

Where,

- $(\sum_j Y_{ij} - Y_i / S)^2$ = The variance due to dependent variable
 and $(\sum_j Y_{ij} \cdot I_j)^2 / \sum_j I_j^2$ = The variance due to regression

Because,

$$\frac{(\sum_j Y_{ij} \cdot I_j)^2}{\sum_j I_j^2} = \frac{(\sum_j Y_{ij} \cdot I_j) (\sum_j Y_{ij} \cdot I_j)}{\sum_j I_j^2} = b_i \sum_j Y_{ij} \cdot I_j$$

Where,

b_i values have been calculated in (2) and

$\sum_j Y_{ij} \cdot I_j$ value in 2 (ii)

The $\sum_j \sigma^2_{ij}$ values may be computed as

$$\sum_j \sigma^2_{ij} = \sigma^2 V_i - b_i \sum_j Y_{ij} \cdot I_j$$

From $\sum_j \sigma^2_{ij}$, the stability parameter S^2_{di} for each genotypes was computed as follows.

$$S^2_{di} = [\sum_j \sigma^2_{ij} / (S-2)] - (S^2 e / r)$$

3.7.2 Analysis of variance

The analysis of variance partitioned into three main parts.

- a. Sum of squares due to genotypes
- b. Sum of squares due to environment + (genotype x environment)
- c. Pooled error

The sum of squares due to genotype x environment is further partitioned into two parts.

- i. S.S. due to genotype x environment (linear) which is in fact S.S. due to regression.
- ii. S.S. due to deviation from linearity of response (*i.e.* S.S. due to pooled deviation).

The latter can be further partitioned into as many components as the number of genotypes with (s-2) degrees of freedom (s represents number of environments).

The analysis of variance table for stability parameter was constructed in tabulated form as

Sources	d.f.	S.S.	M.S.S.
Genotypes	(t-1)	$1/s \sum_i Y_i^2 - C.F.$	MS ₁
Environments	(s-1)	$1/t \sum_i Y_i^2 - C.F.$	MS ₂
Genotype x Environments	(t-1)(s-1)	$\sum_i \sum_j Y_{ij}^2 - C.F. - G.S.S. - E.S.S.$	MS ₃
Environment + Genotype x Environment)	t(s-1)	$\sum_i \sum_j Y_{ij}^2 - Y_i^2 / S$	MS ₄
Environment (linear)	1	$1/t [\sum_i Y_{ij} I_j]^2 / \sum_j I_j^2$	
Genotype x Environment (linear)	(t-1)	$\sum_i \sum_j Y_{ij} I_j^2 / \sum_j I_j^2 - E(1)S.S.$	MS ₅
Pooled deviation	t(s-1)	$\sum_i \sum_j \sigma^2_{ij}$	MS ₆
Pooled error	s(r-1)(t-1)		MS ₇

Where,

- t = Number of genotypes
- s = Number of environments
- r = Number of replications
- G.S.S. = S.S. due to genotypes
- E.S.S. = S.S. due to environments

S.S. due to genotypes, environments and genotype x environment were calculated as per the method of pooled analysis.

The M.S. pooled error was calculated as

$$\frac{(n_1 - 1) (\text{M.S. error } L_1) + \dots + (n_s - 1) (\text{M.S. errors})}{(n_1 - 1) + (n_2 - 1) + \dots + (n_s - 1)}$$

Where,

- M.S. error L_s = Mean sum of squares due to error for s^{th} environment
- $n_1 - 1$ = Error d.f. in environmental 1
- $n_2 - 1$ = Error d.f. in environment 2

The S.S. due to remaining sources were calculated as follows:

$$\text{S.S. due to environment (Gen. x Env.)} = \sum_{ij} \sum Y_{ij}^2 - \sum_i Y_i^2 / t \text{ in fact,}$$

$$\text{S.S. (E + G x E)} = \text{S.S.E.} + \text{S.S.G. x E}$$

Where,

$$\text{S.S.E.} = 1/t (\sum_j Y_j \cdot I_j)^2 / E_j \cdot I_j$$

The Y_j and I_j values are already computed and by putting appropriate values we can get S.S. environment (linear) which can also be checked as,

$$\begin{aligned} &\text{S.S. Environment (linear)} \\ &= t \times \sum_j I_j^2 \end{aligned}$$

In fact,

$$\begin{aligned} &\text{S.S.G. x E (linear)} \\ &= \sum_j [\sum_j (Y_{ij} I_j)^2 / (\sum_j I_j)^2] - \text{S.S.E. (linear)} \\ &= b_i \sum_j Y_{ij} I_j \text{ for each genotype} \end{aligned}$$

Thus by taking simply the sum of these values over all the genotypes, the first part of S.S., G x E (linear) can be obtained.

S.S. due to pooled deviation is simply the sum of S.S. due to deviation for individual genotype for (s-2) degrees of freedom each.

3.7.3 Test of significance

- The significance of difference among genotypes were tested against the M.S.S. due to G x E interaction (MS_3). The genotypic differences were also tested against pooled deviation (MS_6).
- The G x E interaction (MS_3) was tested against effective pooled error.
- The components, environment (linear), G x E (linear) was tested against pooled deviation (MS_6).
- Pooled deviation was tested against effective pooled error (PE/r). Individual deviation from linear regression was tested as follows.

$$F = \frac{[(\sum_j \sigma^2_{ij}) / (S - 2)]}{\text{Pooled error}}$$

- Stable genotype *i.e.* test of significance for regression coefficient.

A genotype with unit regression coefficient ($b_i \sim 1$) or not significantly deviating from unity) and deviation not significantly deviating from zero ($S^2 d_i = 0$) is said to be stable one.

$$T \text{ test } b_i = \frac{|b_i - 1|}{\text{S.E. } (b_i)}$$

Where,

$$SE \ b_i = \sqrt{\frac{\text{MSS due to pooled deviation}}{\sum_j I^2_j}}$$

The significance of b_i values were tested by 't' test as against unity.

$$'t' \text{ test } b_i = \frac{|b_i - 1|}{\text{S.E. } (b_i)}$$

$$\text{Mean of } b_i = \sum_i b_i/t$$

Population mean and standard error are calculated as,

$$\text{Population mean } (\mu) = \frac{\text{Grand total}}{\text{Number of observations}}$$

$$\text{S.E. (Mean)} = \frac{\text{M.S. due to pooled deviation}}{\text{Number of environments} - 1}$$

4. RESULTS AND DISCUSSION

The results obtained in the present investigation entitled “Genetic variability and G x E interaction studies in groundnut (*Arachis hypogaea* L.)” conducted at AICRP, on Groundnut, Cotton Improvement Project, MPKV, Rahuri are presented and discussed under following sub-heads.

4.1 Results

The results obtained in the present investigation are given below.

Experiment I : Variability, correlation, path analysis and D² analysis study in F₅ progenies of groundnut

4.1.1 Analysis of variance

Analysis of variance revealed highly significant differences among the families (crosses) and progenies within family for the characters studied, indicating appreciable amount of variability among the genotypes for the studied characters. Aghav (2010), Atak (2014), Kadam (2016), Rao (2016), Sardar (2017) and Wadikar (2018) also observed appreciable amount of variability among the genotypes.

4.2 Mean performance of 40 F₅ groundnut progenies of 8 crosses

Cross	Name of cross	Progeny	Cross	Name of cross	Progeny
C1	TAG-24 x Phule Unnati	5	C5	Phule-6021 x Phule Unnati	5
C2	Phule Unnati x TPG-41	5	C6	Phule Unnati x SB-XI	5
C3	WRGS-15 x RHRG-8808	5	C7	Phule-6021 x RHRG-6110	5
C4	Phule-6021 x ICGV-00350	5	C8	WRGS-15 x SB-XI	5

4.2.1 Days to 50% flowering

The variation for days to 50% flowering ranged between 40.50 (C4-P5), (C3-P4) to 54.50 (C5-P3) days. The population mean for this character was 48.18. The following progenies of crosses flowered significantly earlier than the population mean. In cross C3-P4 and C4-P5 (40.50 days), C8-P2 and C8-P3 (41.00 days), C3-P1, C3-P2, C8-P1 and C8-P5 (41.50 days), C4-P3 (42.00 days) C6-P5 (42.50 days), C1-P3 (43.00 days), C6-P4 (43.50 days), C1-P1 (44.00 days) and C6-P1 (45.00 days), followed by the progenies of crosses flowered non significantly late than the population mean *viz.*, C5-P4 and C5-P5 (53.00 days), C4-P2, C4-P4, C5-P1 and C5-P2 (53.50days) C6-P2 and C7-P2 (54.00 days and C5-P3 (54.50).

Table 4.1. Analysis of variance of compact family block design for dry pod yield and yield contributing characters of 40 F₅ progenies of groundnut tested in summer, 2018

Sr. No.	Characters	df	Days to 50% flowering	Days to maturity	Number of branches/plant	Number of mature pods/plant	Number of immature pods/plant	Haulm yield/plot (kg)
1.	Replications	1	3.20	12.80**	7.19**	12.01	0.45	0.09
2.	Families	7	124.99**	494.31**	97.91**	715.94**	39.74**	14.03**
3.	Error (A)	7	2.20	1.51	0.97	2.61	0.45	0.03
4.	Main plot	15	59.56**	232.24**	46.62**	336.13**	18.79**	6.563**
5.	Progenies' with in families	8	17.40**	23.17**	1.17**	12.19**	4.93**	1.20**
6.	Error (B)	32	0.37	0.23	0.08	0.61	0.23	0.01

Sr. No.	Characters	df	Hundred kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Oil content (%)	Protein content (%)	Pod yield / Plot (kg)
1.	Replications	1	3.61	0.02	2.45	0.41	0.028	0.0001
2.	Families	7	233.84**	9.14**	281.66**	32.68**	0.967**	1.169**
3.	Error (A)	7	2.18	0.10	1.59	0.26	0.020	0.003
4.	Main Plot	15	110.38**	4.32**	132.35**	15.40**	0.462**	0.547**
5.	Progenies' with in families	8	4.85**	0.51**	9.11**	0.97**	0.868**	0.010**
6.	Error (B)	32	0.30	0.01	0.15	0.030	0.005	0.001

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

Table 4.2a. Mean performance of 40 F₅ groundnut progenies (of 8 crosses) for days to 50 % flowering, days to maturity and number of branches per plant tested in Summer 2018

Cross Progenies	Days to 50 % flowering								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	44.00	50.50	41.50	52.50	53.50	45.00	51.50	41.50	
P2	50.00	50.50	41.50	53.50	53.50	54.00	54.00	41.00	
P3	43.00	47.50	50.00	42.00	54.50	52.50	51.00	41.00	
P4	50.00	51.00	40.50	53.50	53.00	43.50	52.50	49.50	
P5	48.50	50.00	48.50	40.50	53.00	42.50	49.50	41.50	
Mean	47.10	49.90	44.40	48.40	53.50	47.50	51.70	42.90	48.18
S.Em.±	1.08	0.82	0.76	0.34	0.69	0.96	0.98	1.04	
CD at 5%	3.62	NS	2.53	1.13	NS	3.22	NS	3.46	
CV (%)	3.25	2.32	2.41	0.99	1.81	2.87	2.68	3.41	
Family S.Em.±	0.469								
CD at 5%	1.568								

Cross Progenies	Days to maturity								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	119.00	135.00	124.00	134.50	139.00	117.00	128.00	120.50	
P2	130.50	133.00	124.50	135.00	136.50	125.50	125.00	115.00	
P3	123.00	136.50	130.50	121.00	138.50	126.50	122.50	113.50	
P4	120.00	139.00	121.00	133.50	137.00	116.50	123.00	122.50	
P5	129.00	135.50	132.00	119.00	138.00	117.50	123.50	115.00	
Mean	124.30	135.80	126.40	128.60	137.80	120.60	124.40	117.30	126.90
S.Em.±	0.51	0.57	0.49	0.69	0.49	1.30	0.27	0.62	
CD at 5%	1.70	1.92	1.65	2.30	NS	4.34	0.89	2.08	
CV (%)	0.58	0.60	0.55	0.76	0.51	1.52	0.30	0.75	
Family S.Em.±	0.39								
CD at 5%	1.30								

Cross Progenies	Number of branches/plant								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	9.50	7.00	4.50	13.50	4.00	9.50	4.50	5.00	
P2	9.00	6.50	4.50	10.50	6.50	8.50	4.00	5.50	
P3	7.50	7.50	4.00	15.00	5.50	7.50	5.50	5.00	
P4	8.50	6.00	6.00	16.00	5.50	7.50	5.00	5.50	
P5	8.50	5.50	5.00	14.50	4.50	8.50	4.50	5.00	
Mean	8.60	6.50	4.80	13.90	5.20	8.30	4.70	5.20	7.15
S.Em.±	0.38	0.32	0.43	0.57	0.34	0.41	0.27	0.32	
CD at 5%	NS	NS	NS	1.92	1.13	NS	NS	NS	
CV (%)	6.22	6.88	12.70	5.83	9.19	7.05	8.04	8.60	
Family S.Em.±	0.31								
CD at 5%	1.04								

4.2.2 Days to maturity

The mean of four families were significantly earlier in maturity when compared with the population mean 126.90 days. The variation for days to maturity ranged between 113.50 (C8-P3) to 139 (C2-P4) days. The progeny C8-P3 (113.50 days), C8-P2 and C8-P5 (115.00 days), C6-P4 (116.50 days), C6-P1 (117.00 days), C6-P5 (117.50 days), C1-P1, C4-P5 (119 days) and C1-P4 (120.00 days) were found early in maturity. The progenies *viz.*, C5-P1 (139.00 days), C5-P3 (138.50 days), C5-P5 (138.00 days), C5-P4 (137.00 days) and C5-P2 (136.50 days) were observed late for maturity.

4.2.3 Number of branches per plant

The number of branches per plant ranged between 4.00 (C5-P1) and (C7-P2) to 16.00 (C4-P4). The population mean for number of branches per plant was 7.15. The number of branches per plant was significantly higher in progeny of cross-4 *viz.*, C4-P4 (16.00), C4-P3 (15.00), C4-P5 (14.50), C4-P1 (13.50) and C4-P2 (10.50). The progenies *viz.*, C3-P3, C5-P1 and C7-P2 recorded minimum branches per plant (4.00).

4.2.4 Number of mature pods per plant

The number of mature pods per plant ranged between 12.50 (C8-P2) to 48.50 (C4-P3). The population mean for this character was 29.06. The progeny C4-P3 (48.50) recorded significantly higher number of mature pods per plant. This was followed by C4-P1 (47.50), C4-P2 (47.00), C4-P5 (40.50), C6-P3 (39.50), C6-P1 (38.50), C6-P5 (35.50), C6-P5 (35.50), C2-P4 (34.50), C5-P5 (34.00), C3-P4 (33.00), C6-P3 (32.50) and C1-P3 (31.00). The progeny C8-P2 (12.50) recorded minimum number of mature pods per plant.

4.2.5 Number of immature pods per plant

The number of immature pods per plant ranged between 1.50 (C1-P2, C2-P2, C3-P2) to 12.50 (C7-P3) with population means 6.15. The progeny C7-P3 (12.50) had significantly more number of immature pods per plant followed by C7-P2 and C3-P4 (11.00).

4.2.6 Haulm yield per plot (kg)

The range for this character was 4.35 (C1-P3) to 10.65 (C8-P1) with population mean 8.56. The progeny C8-P1 produced higher significant performance

Table 4.2b. Mean performance of 40 F₅ groundnut progenies (of 8 crosses) for Number of mature pods/plant, number of immature pods/plant and haulm yield /plot (kg) tested in summer 2018

Cross Progenies	Number of mature pods/plant								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	28.50	30.00	22.50	47.50	26.50	38.50	22.50	18.50	
P2	27.50	26.00	25.50	47.00	27.50	39.50	24.00	12.50	
P3	31.00	27.00	22.50	48.50	29.50	32.50	22.50	20.50	
P4	22.50	34.50	33.00	41.50	25.50	38.00	24.00	17.50	
P5	26.50	25.00	26.50	40.50	34.00	35.50	22.50	17.50	
Mean	27.20	28.50	26.00	45.00	28.60	36.80	23.10	17.30	29.06
S.Em.±	0.85	1.68	1.35	0.74	1.12	0.93	0.98	0.86	
CD at 5%	2.83	NS	4.52	2.46	3.75	3.10	NS	2.88	
CV (%)	4.39	8.35	7.36	2.32	5.54	3.56	5.99	7.05	
Family S.Em.±	0.51								
CD at 5%	1.71								

Cross Progenies	Number of immature pods/plant								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	5.50	5.50	5.50	5.00	2.50	4.50	8.50	8.50	
P2	1.50	1.50	1.50	5.50	9.00	5.50	11.00	8.00	
P3	5.00	6.00	8.00	2.50	5.00	5.50	12.50	8.50	
P4	3.50	9.50	11.00	4.50	6.00	4.50	9.00	8.00	
P5	2.50	5.00	7.00	5.00	6.50	6.50	8.00	7.50	
Mean	3.60	5.50	6.60	4.50	5.80	5.30	9.80	8.10	6.15
S.Em.±	0.76	0.46	0.69	0.62	0.69	0.86	0.71	0.62	
CD at 5%	NS	1.55	2.30	NS	2.30	NS	2.36	NS	
CV (%)	29.70	11.90	14.71	19.52	16.74	23.00	10.20	10.84	
Family S.Em.±	0.21								
CD at 5%	0.71								

Cross Progenies	Haulm yield /plot (kg)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	6.60	10.20	9.05	9.75	8.70	10.50	9.25	10.65	
P2	6.30	8.50	8.60	9.00	7.25	10.20	9.55	9.70	
P3	4.35	9.35	7.40	8.25	10.15	9.45	9.70	9.70	
P4	5.50	8.45	5.95	8.80	9.35	7.40	8.15	8.25	
P5	7.60	8.60	6.20	9.30	9.80	8.45	8.85	9.50	
Mean	6.07	9.02	7.44	9.02	9.05	9.20	9.10	9.56	8.56
S.Em.±	0.15	0.10	0.12	0.23	0.15	0.07	0.09	0.15	
CD at 5%	0.52	0.34	0.41	NS	0.51	0.24	0.30	0.50	
CV (%)	3.61	1.60	2.31	3.53	2.38	1.12	1.41	2.20	
Family S.Em.±	0.05								
CD at 5%	0.17								

of haulm yield per plot (10.65), followed by C6-P1 (10.50), C2-P1 and C6-P2 (10.20) and C5-P3 (10.15). The progeny C1-P3 recorded minimum haulm yield per plot was (4.35).

4.2.7 Hundred kernel weight (g)

The variation in mean performance for this character ranged between 27.50 to 48.50, with population mean 33.81. Ten progenies showed higher performance for hundred kernel weight over population mean. The progeny C2-P4 (48.50) recorded higher hundred kernel weight followed by C2-P1 (45.50), C2-P2 (44.00), C2-P5 (43.50), C2-P3 (41.00) and C6-P4 (37.50) which were non significant, significantly higher mean performance was shown by C3-P5 (37.50) and C3-P1 (37.00).

4.2.8 Shelling (%)

The variation in mean performance for this character ranged between 67.15 to 72.30 per cent, with population mean 68.77 per cent. The highest shelling percentage was recorded by C6-P3 (72.30) followed by C6-P2 (71.45), C6-P1 (71.15), C6-P4 (70.35), C5-P3 (70.20), C6-P5 (69.75), C5-P2 (69.70), C4-P1 (69.45), C2-P2, C4-P3 (69.35) and C1-P1 (69.20), while the lowest shelling percentage was observed in C1-P2 (67.15).

4.2.9 Sound mature kernel (%)

Fifteen progeny showed higher performance for sound mature kernel percentage. The variation in mean performance for this character ranged between 80.50 to 98.50, with average mean 89.80. The progeny C4-P3 (98.50) was recorded highest sound mature kernel percentage followed by C6-P1 (98.00), C6-P3 (97.50), C4-P2, C6-P2 and C6-P4 (97.00), C4-P4 (96.50), C4-P5 (96.00), C1-P1, C4-P1 and C5-P3 (95.50), C6-P5 (95.00), C3-P1 (94.00), C1-P2 (93.00) and C1-P3 (91.50), while the lowest sound mature kernel percentage was observed in C3-P2 (80.50).

4.2.10 Oil content (%)

The mean performance for this character was 47.45 per cent with range from 45.5 to 51.00. The progenies showed higher oil content percentage were C1-P3 and C5-P2 (51.00) followed by C5-P5 (50.85), C7-P2 (50.75), C5-P4 (50.30), C5-P1 (50.05), C5-P3 (49.75), C7-P5 (49.60), C1-P1 (49.40), C7-P3 (49.30), C3-P1 (48.95), C1-P5 (48.65), C7-P1 (48.35), C1-P2 (48.30) and C7-P4 (48.20).

Table 4.2c. Mean performance of 40 F₅ groundnut progenies (of 8 crosses) for 100 kernel weight (g), shelling (%) and sound mature kernel (%) tested in summer 2018

Cross Progenies	100 kernel weight (g)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	27.50	45.50	37.00	30.50	36.00	34.50	29.00	30.50	
P2	32.50	44.00	34.00	35.50	33.00	35.00	31.00	31.00	
P3	34.00	41.00	33.00	27.50	31.00	35.50	30.00	30.00	
P4	31.00	48.50	33.50	30.50	33.00	37.50	28.00	30.00	
P5	29.50	43.50	37.50	33.50	33.50	35.00	29.00	30.50	
Mean	30.90	44.50	35.00	31.50	33.30	35.50	29.40	30.40	33.81
S.Em.±	0.27	1.40	0.78	0.00	0.38	0.57	1.15	0.57	
CD at 5%	0.89	NS	2.62	1.10	1.26	NS	NS	NS	
CV (%)	1.22	4.45	3.17	0.00	1.61	2.28	5.51	2.67	
Family S.Em.±	0.47								
CD at 5%	1.53								

Cross Progenies	Shelling (%)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	69.20	68.10	68.25	69.45	68.30	71.15	68.20	68.05	
P2	67.15	69.35	68.40	68.25	69.70	71.45	68.50	67.45	
P3	68.10	69.30	68.00	69.35	70.20	72.30	67.80	68.65	
P4	68.45	68.60	68.15	68.65	67.70	70.35	68.25	68.00	
P5	68.45	68.50	68.05	68.15	68.45	69.75	68.55	68.00	
Mean	68.27	68.77	68.17	68.77	68.87	71.00	68.26	68.03	68.77
S.Em.±	0.19	0.16	0.13	0.11	0.10	0.13	0.17	0.20	
CD at 5%	0.64	0.54	NS	0.38	0.34	0.44	NS	NS	
CV (%)	0.40	0.33	0.27	0.24	0.21	0.26	0.35	0.41	
Family S.Em.±	0.10								
CD at 5%	0.34								

Cross Progenies	Sound mature kernel (%)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	95.50	81.00	94.00	95.50	88.00	98.00	91.00	86.00	
P2	93.00	84.00	80.50	97.00	89.00	97.00	90.50	80.50	
P3	91.50	86.50	86.50	98.50	95.50	97.50	86.00	83.50	
P4	89.00	86.00	81.00	96.50	89.50	97.00	90.00	82.00	
P5	92.50	81.50	88.00	96.00	88.00	95.00	89.50	84.50	
Mean	92.30	83.80	86.00	96.70	90.00	96.90	89.40	83.30	89.80
S.Em.±	0.21	0.43	0.69	0.57	0.57	0.34	0.82	0.49	
CD at 5%	0.69	1.44	2.30	NS	1.92	1.13	NS	1.65	
CV (%)	0.32	0.73	1.13	0.84	0.90	0.49	1.30	0.84	
Family S.Em.±	0.40								
CD at 5%	1.33								

Table 4.2d. Mean performance of 40 F₅ groundnut progenies (of 8 crosses) for oil content (%), protein content (%) and dry pod yield/plot (kg) tested in summer 2018

Cross Progenies	Oil content (%)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	49.40	45.80	48.95	45.80	50.05	44.20	48.35	45.65	
P2	48.30	46.75	46.30	46.90	51.00	45.70	50.75	46.15	
P3	51.00	45.80	46.50	46.10	49.75	45.20	49.30	45.55	
P4	46.70	47.90	46.25	46.55	50.30	46.05	48.20	46.15	
P5	48.65	46.25	47.15	46.30	50.85	45.05	49.60	46.75	
Mean	48.81	46.50	47.03	46.33	50.39	45.24	49.24	46.05	47.45
S.Em.±	0.19	0.10	0.14	0.31	0.37	0.42	0.07	0.06	
CD at 5%	0.63	0.32	0.48	NS	NS	NS	0.23	0.21	
CV (%)	0.55	0.29	0.43	0.96	1.05	1.30	0.20	0.19	
Family S.Em.±	0.16								
CD at 5%	0.54								

Cross Progenies	Protein content (%)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	21.75	21.95	21.70	23.30	22.75	22.75	21.80	23.20	
P2	21.85	22.75	23.10	21.70	21.00	23.95	22.75	22.25	
P3	23.30	22.50	22.40	22.05	23.10	22.10	20.05	20.75	
P4	21.85	22.55	21.50	21.55	23.55	23.20	21.15	22.70	
P5	22.30	21.85	21.40	23.15	22.25	20.95	22.35	21.55	
Mean	22.21	22.32	22.02	22.35	22.53	22.59	21.62	22.09	22.22
S.Em.±	0.06	0.20	0.08	0.06	0.03	0.08	0.05	0.08	
CD at 5%	0.21	NS	0.28	0.19	0.11	0.27	0.17	0.27	
CV (%)	0.40	1.29	0.53	0.36	0.20	0.51	0.33	0.52	
Family S.Em.±	0.04								
CD at 5%	0.15								

Cross Progenies	Dry pod yield/plot (kg)								General Mean
	C1	C2	C3	C4	C5	C6	C7	C8	
P1	1.50	1.46	1.15	1.94	1.24	1.77	1.18	0.96	
P2	1.42	1.66	1.17	1.84	1.47	1.59	1.12	0.82	
P3	1.43	1.56	1.24	1.95	1.33	1.85	1.02	0.94	
P4	1.41	1.70	1.08	1.85	1.22	1.66	1.02	0.87	
P5	1.45	1.50	1.07	1.83	1.17	1.97	1.20	0.89	
Mean	1.44	1.58	1.14	1.88	1.28	1.77	1.11	0.90	1.39
S.Em.±	0.04	0.01	0.02	0.01	0.08	0.04	0.01	0.03	
CD at 5%	NS	0.04	0.07	0.04	NS	0.12	0.04	NS	
CV (%)	3.79	1.17	2.75	0.97	8.43	2.89	1.70	4.25	
Family S.Em.±	0.02								
CD at 5%	0.06								

4.2.11 Protein content (%)

The protein content ranged from 20.05 to 23.95 with general mean 22.22 %. The higher protein content was recorded by progeny C6-P2 (23.95) followed by C5-P4 (23.55), C1-P3 and C4-P1 (23.30), C6-P4 and C8-P1 (23.20), C4-P5 (23.15), C3-P2 and C5-P3 (23.10), C2-P2, C5-P1, C6-P1 and C7-P2 (22.75), C8-P4 (22.70), C2-P4 (22.55), C2-P3 (22.50) and C3-P3 (22.40) whereas the lowest protein content percent was found in C7-P3 (20.05).

4.2.12 Dry pod yield per plant (kg)

The variation in mean performance for this character ranged between 0.82 to 1.97, with general mean 1.39. The highest dry pod yield per plant was recorded by C6-P5 (1.97) followed by C4-P3 (1.95), C4-P1 (1.94), C4-P4 and C6-P3 (1.85), C4-P2 (1.84), C4-P5 (1.83), C6-P1 (1.77), C2-P4 (1.70), C2-P2 and C6-P4 (1.66), C6-P2 (1.59), C2-P3 (1.56), C1-P1 and C2-P5 (1.50), C5-P2 (1.47) and C2-P1 (1.46). The lowest dry pod yield was recorded by C8-P2 (0.82).

4.3 Parameters of genetic variability and heritability

Estimates mean, range of variation, phenotypic and genotypic variances and coefficients of variation, heritability (b.s.) and genetic advance expressed as per cent of mean for twelve characters in groundnut is given in Table 4.3.

4.3.1 Coefficient of genotypic and phenotypic variation

It was observed that the estimates of phenotypic coefficient of variation (PCV) were magnitudinally higher than the genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment of these traits. The highest estimate of GCV and PCV recorded by number of branches per plant (42.71, 44.09) followed by number of immature pods per plant (41.11, 45.46), number of mature pods per plant (29.0, 29.80) and dry pod yield per plant (23.90, 24.36), respectively. The moderate to low estimates of GCV and PCV was observed for the characters haulm yield per plant (16.88, 17.12), hundred kernel weight (14.31, 14.94). However, the low estimates of GCV and PCV were observed by characters *viz.*, days to 50% flowering (9.83, 10.37), sound mature kernel (6.22, 6.34), days to maturity (6.11, 6.19), oil content (3.95, 4.07), protein content (3.75, 3.83) and shelling

Table 4.3. Mean, range of variation, phenotypic and genotypic variances and coefficients of variation, heritability (bs.), genetic advance and genetic advance expressed as per cent of mean for twelve characters in groundnut genotypes

Sr. No.	Character	Mean	Range	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Genotypic coefficient of variation GCV (%)	Phenotypic coefficient of variation PCV (%)	Heritability (Broad sense) h^2 (bs) %	Genetic advance	GA expressed as per cent of mean (%)
1	Days to 50 % flowering	48.18	40.50-54.50	22.45	24.98	9.83	10.37	89.86	9.25	19.20
2	Days to maturity	126.90	113.5-139.0	60.21	61.80	6.11	6.19	97.42	15.78	12.43
3	Number of branches/ plant	7.15	4.00-16.00	9.33	9.94	42.71	44.09	93.86	6.09	85.24
4	Number of matured pods/plant	29.06	12.50-48.50	71.02	74.98	29.00	29.80	94.72	16.90	58.14
5	Number of immature pods/plant	6.15	1.50-12.50	6.39	7.82	41.11	45.46	81.78	4.71	76.59
6	Haulm yield/plot (kg)	8.56	4.35-10.65	2.09	2.15	16.88	17.12	97.13	2.93	34.26
7	100 kernel weight (g)	33.81	27.50-48.50	23.42	25.52	14.31	14.94	91.77	9.55	28.25
8	Shelling %	68.77	67.15-72.30	1.14	1.23	1.56	1.61	93.05	2.12	3.09
9	Sound mature kernel (%)	89.80	80.50-98.50	31.25	32.39	6.22	6.34	96.47	11.31	12.59
10	Oil content (%)	47.45	44.20-51.00	3.52	3.74	3.95	4.07	94.09	3.75	7.90
11	Protein Content (%)	22.22	20.05-23.95	0.70	0.72	3.75	3.83	95.94	1.68	7.57
12	Dry pod yield /plot (kg)	1.386	0.82-1.97	0.110	0.114	23.90	24.36	96.26	0.67	48.30

percentage (1.56, 1.61) respectively. Similar results were recorded by Korat (2009), Zaman *et al.* (2011).

4.3.2 Heritability (b.s.)

The heritability (b.s.) estimates were higher in case of characters, days to maturity (97.42), followed by haulm yield per plot (97.13), sound mature kernel (96.47), dry pod yield per plot (96.26), protein content (95.94), number of mature pods per plant (94.72), oil content (94.09), shelling per cent (93.05), hundred kernel weight (91.77), days to 50 % flowering (89.86) and number of immature pods per plant (81.78). Korat *et al.* (2009) and Zaman (2011) also observed higher estimates of heritability (b.s.) for these traits.

4.3.3 Genetic advance

The highest magnitude of genetic advance was observed for number of mature pods per plant (16.90) followed by days to maturity (15.78), sound mature kernel (11.31), hundred kernel weight (9.55), days to 50% flowering (9.25), number of branches per plant (6.09), number of immature pods per plant (4.71) and oil content (3.75). The lowest value of genetic advance was observed for dry pod yield per plot (0.67) Thakur *et al.* (2011) also reported higher estimates of genetic advance for above said characters.

Genetic advance as a percent of mean was the highest for number of branches per plant (85.24), number of immature pods per plant (76.59), number of mature pods per plant (58.14), dry pod yield per plant (48.30), haulm yield per plot (34.26) and hundred kernel weight (28.25) and moderate for sound mature kernel (12.59).

The characters number of branches per plant number of immature pods per plant, number of mature pods per plant, hundred kernel weight, dry pod yield and haulm yield per plot expressed high estimates of heritability (b.s.) accompanied with high genetic advance and percent of mean. Zaman *et al.* (2011), Narasimhulu *et al.* (2012) and Jayalaxmi and Laxmikantha (2003) recorded the similar findings.

4.4. Correlation studies

The genotypic and phenotypic correlations for twelve characters studied are given in Table 4.4, revealed that in general, the genotypic correlation coefficients were relatively higher than their corresponding phenotypic correlation coefficient.

4.4.1 Association of dry pod yield with its components

The dry pod yield had highly significant and positive correlation at both genotypic and phenotypic levels with number of mature pods per plant ($r_g = 0.865$, $r_p = 0.818$), number of branches per plant ($r_g = 0.785$, $r_p = 0.742$), sound mature kernel percent ($r_g = 0.678$, $r_p = 0.647$), shelling percent ($r_g = 0.576$, $r_p = 0.552$), hundred kernel weight ($r_g = 0.301$, $r_p = 0.288$) and significant positive with days to maturity ($r_g = 0.220$, $r_p = 0.209$) and protein content ($r_g = 0.178$, $r_p = 0.176$). Venkataramana *et al.* (2000a), Dhakar *et al.* (2017), Bhargavi *et al.* (2015), Babariya and Dobariya (2012) were observed significant and positive correlation for these characters. However number of immature pods per plant ($r_g = -0.523$, $r_p = -0.452$) and oil content ($r_g = -0.306$, $r_p = -0.296$) had highly significant and negative correlation with dry pod yield at both the levels. Similar results were also recorded by Sumathi and Muralidharan (2007) and Jeyaramraja and Fantahun (2014). Days to 50% flowering ($r_g = 0.142$, $r_p = 0.142$) had positive and non-significant correlation, whereas, haulm yield per plant ($r_g = -0.011$, $r_p = -0.018$) had negative and non significant correlation at both levels with dry pod yield per plant.

4.4.2 Days to 50 % flowering

Days to 50% flowering had highly significant and positive correlation at both genotypic and phenotypic levels with days to maturity ($r_g = 0.758$, $r_p = 0.717$) and oil content ($r_g = 0.389$, $r_p = 0.362$). But it showed positive non significant associations at both levels with number of mature pods per plant ($r_g = 0.129$, $r_p = 0.125$), number of immature pods per plant ($r_g = 0.022$, $r_p = 0.038$), haulm yield per plot ($r_g = 0.155$, $r_p = 0.144$), hundred kernel weight ($r_g = 0.125$, $r_p = 0.098$), shelling per cent ($r_g = 0.167$, $r_p = 0.143$), sound mature kernel ($r_g = 0.165$, $r_p = 0.145$) and protein content % ($r_g = 0.073$, $r_p = 0.055$). The results obtained in the present study

Table 4.4. Genotypic (Above diagonal) and phenotypic (Below diagonal) correlation coefficient among twelve characters in summer groundnut genotypes

Sr. No.	Character	Days to 50% flowering	Days to maturity	No. of branches /plant	No. of matured pods/ plant	No. of immature pods/ plant	Haulm yield/ plot (kg)	100 kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Oil content (%)	Protein Content (%)	Dry pod yield/ plot (kg)
1	Days to 50 % flowering	1.000	0.758**	-0.078	0.129	0.022	0.155	0.125	0.167	0.165	0.389**	0.073	0.142
2	Days to maturity	0.717**	1.000	-0.060	0.198*	-0.184*	0.079	0.476**	-0.043	-0.038	0.368**	0.169	0.220*
3	Number of branches/plant	-0.052	-0.047	1.000	0.788**	-0.451**	-0.043	-0.131	0.257*	0.642**	-0.350**	0.081	0.785**
4	Number of matured pods/ plant	0.125	0.199*	0.748**	1.000	-0.359**	0.024	0.127	0.471**	0.688**	-0.229*	0.212*	0.865**
5	Number of immature pods/ plant	0.038	-0.164	-0.388**	-0.307**	1.000	0.157	-0.168	-0.221*	-0.332**	0.165	-0.414**	-0.523**
6	Haulm yield/plot (kg)	0.144	0.071	-0.052	0.026	0.142	1.000	0.047	0.244*	0.013	-0.247*	0.163	-0.011
7	100 kernel weight (g)	0.098	0.440**	-0.144	0.122	-0.145	0.046	1.000	0.119	-0.277**	-0.202*	0.155	0.301**
8	Shelling percent	0.143	-0.032	0.230*	0.440**	-0.176*	0.235*	0.117	1.000	0.555**	-0.324**	0.232*	0.576**
9	Sound mature kernel (%)	0.145	-0.043	0.595**	0.663**	-0.304**	0.022	-0.253*	0.535**	1.000	0.016	0.171	0.678**
10	Oil content (%)	0.362**	0.363**	-0.324**	-0.208*	0.159	-0.228*	-0.194*	-0.305**	0.027	1.000	-0.027	-0.306**
11	Protein Content (%)	0.055	0.161	0.080	0.190*	-0.364**	0.162	0.140	0.227*	0.169	-0.023	1.000	0.178*
12	Dry pod yield /plot (kg)	0.142	0.209*	0.742**	0.818**	-0.452**	-0.018	0.288**	0.552**	0.647**	-0.296**	0.176*	1.000

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

was also supported by the findings of Mathews *et al.* (2001) and Dhakar *et al.* (2017). This trait had non significant and negative correlation at both genotype and phenotype levels with number of branches per plant ($r_g = -0.078$, $r_p = -0.052$). John *et al.* (2008), Ravikumar and Reddi (2012) was observed the same results as obtained in the present study.

4.4.3 Days to maturity

Days to maturity had positive and highly significant correlation at both genotypic and phenotypic levels with hundred kernel weight ($r_g = 0.476$, $r_p = 0.440$), and oil content ($r_g = 0.368$, $r_p = 0.363$) and positive significant correlation with number of mature pods per plant ($r_g = 0.198$, $r_p = 0.199$). The days to maturity showed positive but non-significant association at both levels with protein content ($r_g = 0.169$, $r_p = 0.161$) and haulm yield per plant ($r_g = 0.079$, $r_p = 0.071$). Similar finding were recorded by Pradhan and Patra (2011), Babariya and Dobariya (2012), Bhargavi *et al.* (2015) and Dhakar *et al.* (2017). The number of branches per plant ($r_g = -0.060$, $r_p = -0.047$), shelling % ($r_g = -0.043$, $r_p = -0.032$) and sound mature kernel ($r_g = -0.038$, $r_p = -0.043$) had non-significant and negative correlations at both genotypic and phenotypic levels for this trait. Venkataramana *et al.* (2000a), John *et al.* (2008) and Ravikumar and Reddi (2012) observed negative correlation which supports the earlier findings.

4.4.4 Number of branches per plant

The character number of branches per plant showed highly significant and positive correlation with number of mature pods per plant ($r_g = 0.788$, $r_p = 0.748$), followed by sound mature kernel percentage ($r_g = 0.642$, $r_p = 0.595$) and significant positive correlation with shelling percentage ($r_g = 0.257$, $r_p = 0.230$). Previously, Shankar *et al.* (2018) recorded positive and significant correlation for number of primary branches per plant. While the character showed highly significant negative correlation with number of immature pods per plant ($r_g = -0.451$, $r_p = -0.388$) and oil content ($r_g = -0.350$, $r_p = -0.324$) at both genotypic and phenotypic levels.

4.4.5 Number of mature pods per plant

Number of mature pods per plant recorded highly significant correlation at both genotypic and phenotypic levels with sound mature kernel percentage ($r_g = 0.688$, $r_p = 0.663$), shelling percentage ($r_g = 0.471$, $r_p = 0.440$) and significant positive correlation with protein content ($r_g = 0.212$, $r_p = 0.190$). This trait also had positive but non-significant association with hundred kernel weight ($r_g = 0.127$, $r_p = 0.122$) and haulm yield per plant ($r_g = 0.024$, $r_p = 0.026$). The character immature pods per plant ($r_g = -0.359$, $r_p = -0.307$) showed highly significant negative association, while oil content showed significant negative association ($r_g = -0.229$, $r_p = -0.208$) with number of matured pods per plant. Similar results for these traits were also recorded by Wu (1993), Venkaramana *et al.* (2000a), John *et al.* (2008, 2009), Babariya and Dobariya (2012), Bhargavi *et al.* (2015) and Gupta (2015).

4.4.6 Number of immature pod per plant

Number of immature pod per plant had positive but non-significant correlation at both genotypic and phenotypic levels with haulm yield per plant ($r_g = 0.157$, $r_p = 0.142$) and oil content ($r_g = 0.165$, $r_p = 0.159$). Shanker *et al.* (2018) recorded positive correlation with this trait. This trait showed highly significant and negative correlation with protein content ($r_g = -0.414$, $r_p = -0.364$), sound mature kernel ($r_g = -0.332$, $r_p = -0.304$), while significant and negative correlation with shelling percentage ($r_g = -0.221$, $r_p = -0.176$) at both the levels.

4.4.7 Haulm yield per plot

The character haulm yield per plot recorded positive significant correlation at both genotypic and phenotypic levels with shelling percentage ($r_g = 0.244$, $r_p = 0.235$) and non significant positive correlation with protein content ($r_g = 0.163$, $r_p = 0.162$), hundred kernel weight ($r_g = 0.047$, $r_p = 0.046$) and sound mature kernel ($r_g = 0.013$, $r_p = 0.022$). Oil content ($r_g = -0.247$, $r_p = -0.228$) exhibited significant but negative association with this trait at both the levels.

4.4.8 Hundred kernel weight

Hundred kernel weight had positive but non-significant correlation at both genotypic and phenotypic levels with protein content ($r_g = 0.155$, $r_p = 0.140$) and shelling percentage ($r_g = 0.119$, $r_p = 0.117$). Korat *et al.* (2009), John *et al.* (2009), Ravikumar and Reddi (2012), Bhargavi *et al.* (2015) and Dhakar *et al.* (2017) recorded positive correlation in the previous studies. However highly significant negative correlation at both levels was observed of this trait with sound mature kernel ($r_g = -0.277$, $r_p = -0.253$) and significant negative correlation with oil content ($r_g = -0.202$, $r_p = -0.194$). Uddin *et al.* (1995) was observed negative correlation previously.

4.4.9 Shelling percentage

The character shelling percentage recorded highly significant positive correlation at both genotypic and phenotypic levels with sound mature kernel ($r_g = 0.555$, $r_p = 0.535$) and significant positive with protein content ($r_g = 0.232$, $r_p = 0.227$). Similar results were also obtained by Venkataramana *et al.* (2000a) and Narasimhulu *et al.* (2012) for these traits. However, oil content ($r_g = -0.324$, $r_p = -0.305$) had highly significant and negative association at both genotypic and phenotypic levels with this traits. John *et al.* (2008) also observed negative correlation.

4.4.10 Sound mature kernel

Sound mature kernel showed non-significant positive correlation with with protein content ($r_g = 0.171$, $r_p = 0.169$) and oil content ($r_g = 0.016$, $r_p = 0.027$), at both genotypic and phenotypic levels. Dhakar *et al.* (2017), Bilawal *et al.* (2015), John *et al.* (2015) and Thakur *et al.* (2013) found out similar results, which supports the earlier findings.

4.4.11 Oil content

Oil content showed non-significant negative correlation with protein content ($r_g = -0.027$, $r_p = -0.023$), at both genotypic and phenotypic levels. Sumathi and Muralidharan (2007) and Jeyaramraja and Fantahun (2014) recorded same results.

4.5 Path coefficient Analysis

The genotypic correlation is due to common genotypic factor responsible for the inheritance of the traits in question, hence it indicates inherent relationship. The path coefficient analysis therefore was extended to genotypic correlations only to know the direct and indirect genotypic effect of each yield contributing character in dry pod yield per plot. The genotypic path coefficient were computed for twelve components on dry pod yield per plot and presented in Table 4.5 and shown through path diagram in Fig. 1.

Genotypic path coefficient analysis

4.5.1 Days to 50 % flowering vs. dry pod yield per plot

Days to 50 % flowering had positive association with dry pod yield per plot (0.142) and its direct effect was negligible and negative in magnitude (-0.002). Which supports the findings of Venkateshmurthy (2005) and John *et al.* (2008, 2009). This traits manifested negligible and positive indirect effects *via*, days to maturity (0.047), hundred kernel weight (0.044), shelling (%) (0.040), sound mature kernel (0.034), number of mature pods per plant (0.021) and oil content (0.010). Present findings are in agreement with Venkateshmurthy *et al.* (2005), John *et al.* (2009), Ravikumar and Reddi (2012), Makinde and Ariyo (2013), Korat *et al.* (2009). It also depicted negligible and negative indirect effects *via* number of branches per plant (-0.038), haulm yield per plot (-0.007), protein content (-0.006) and number of immature pods per plant (-0.002), which supports the earlier finding of Garjappa (2005), Suneetha (2003).

4.5.2 Days to maturity vs. dry pod yield per plot

Days to maturity had positive significant association with dry pod yield per plot (0.220) and its direct effect was negligible and positive (0.062). This trait had low positive indirect effect *via* hundred kernel weight (0.166), negligible *viz.*, number of mature pods per plant (0.032), number of immature pods per plant (0.015) and oil content (0.009), which supports the Babariya and Dobariya (2012), Suneetha *et al.* (2004), Ravikumar and Reddi (2012), while it also showed negative negligible indirect effect *via*, number of branches per plant (-0.029), protein content (-0.013),

shelling %

(-0.010), sound mature kernel (-0.008) and haulm yield per plot (-0.004). Ravikumar and Reddi (2012) and Garjappa (2005) had been reported similar findings.

4.5.3 Number of branches per plant vs. dry pod yield per plot

This character showed positive and highly significant association with dry pod yield per plot (0.785) and its direct effect was high and positive (0.488). This trait had low positive indirect effect *via* sound mature kernel (0.132), number of mature pods per plant (0.128) and negligible positive indirect effect *via*, shelling % (0.062), number of immature pods per plant (0.038) and haulm yield per plot (0.002). In the previous study this were reported by Nageswara Rao (2002), Garjappa (2005), John *et al.* (2008) and Ravikumar and Reddi (2012), while it showed negligible negative indirect effect *via* hundred kernel weight (-0.046), oil content (-0.009), protein content (-0.006) and days to maturity (-0.004).

4.5.4 Number of matured pods per plant vs. dry pod yield per plot

This character exhibited high and positive significant correlation with dry pod yield per plot (0.865) and its direct effect was low and positive (0.163). This trait had moderate positive indirect effect *via* number of branches per plant (0.384) and low *via*, sound mature kernel (0.141) and shelling % (0.113) and negligible *via* hundred kernel weight (0.044) and number of immature pods per plant (0.030) and days to maturity (0.012) which was confirmed by the earlier findings of Garjappa (2005), John *et al.* (2008) and Ravikumar and Reddi (2012) and Babariya and Dobariya (2012), while, it showed negligible negative indirect effect *via*, protein content (-0.017), oil content (-0.006) and haulm yield per plot (-0.001). Similar finding had been reported by Sumathi and Muralidharan (2007).

4.5.5 Number of immature pods per plant vs. dry pod yield per plot

This trait exhibited highly significant negative correlation with dry pod yield per plot (-0.523) and its direct effect was negligible and negative (-0.084). The traits had negative indirect effects *via* number of branches per plant (-0.220), number of mature pods per plant (-0.059), sound mature kernel (-0.068), hundred kernel

Table 4.5. Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on pod yield of groundnut genotypes

Sr. No.	Character	Days to 50% flowering	Days to maturity	No. of branches/plant	No. of mature pods/plant	No. of immature pods/plant	Haulm yield/plot (kg)	100 kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Oil content (%)	Protein Content (%)	Genotypic correlation with Dry pod yield/plot (kg)
1	Days to 50 % flowering	-0.002	0.047	-0.038	0.021	-0.002	-0.007	0.044	0.040	0.034	0.010	-0.006	0.142
2	Days to maturity	-0.001	0.062	-0.029	0.032	0.015	-0.004	0.166	-0.010	-0.008	0.009	-0.013	0.220*
3	No. of branches/plant	0.000	-0.004	0.488	0.128	0.038	0.002	-0.046	0.062	0.132	-0.009	-0.006	0.785**
4	No. of matured pods/plant	0.000	0.012	0.384	0.163	0.030	-0.001	0.044	0.113	0.141	-0.006	-0.017	0.865**
5	No. of immature pods/plant	0.000	-0.012	-0.220	-0.059	-0.084	-0.007	-0.058	-0.053	-0.068	0.004	0.033	-0.523**
6	Haulm yield/plot (kg)	0.000	0.005	-0.021	0.004	-0.013	-0.044	0.016	0.058	0.003	-0.006	-0.013	-0.011
7	100 kernel weight (g)	0.000	0.030	-0.064	0.021	0.014	-0.002	0.349	0.029	-0.057	-0.005	-0.012	0.301**
8	Shelling percent	0.000	-0.003	0.126	0.077	0.018	-0.011	0.042	0.240	0.114	-0.008	-0.018	0.576**
9	Sound mature kernel (%)	0.000	-0.002	0.313	0.112	0.028	-0.001	-0.097	0.133	0.205	0.000	-0.013	0.678**
10	Oil content (%)	-0.001	0.023	-0.171	-0.037	-0.014	0.011	-0.070	-0.078	0.003	0.025	0.002	-0.306**
11	Protein Content (%)	0.000	0.011	0.039	0.035	0.035	-0.007	0.054	0.056	0.035	-0.001	-0.079	0.178*

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

Residual effect, R = 0.240, **N.B. :** Values at diagonal indicate direct effects of respective character

weight (-0.058), shelling % (-0.053) and days to maturity (-0.012), while it had negligible positive indirect effect *via*, protein content (0.033) and oil content (0.004).

4.5.6 Haulm yield per plot vs. dry pod yield per plot

Haulm yield per plot had negligible and negative association with dry pod yield per plot (-0.011). Its direct effect was also negligible and negative in magnitude (-0.044). This trait had negligible and negative indirect effect *via* protein content (-0.013), number of immature pod per plant (-0.013), number of branches per plant (-0.021) and oil content (-0.006), while it showed negligible positive indirect effect *via* shelling % (0.058), hundred kernel weight (0.016), sound mature kernel (0.003) number of mature pods per plant (0.004) and days to maturity (0.005).

4.5.7 Hundred kernel weight vs. dry pod yield per plot

Hundred kernel weight had positive and significant association with dry pod yield per plot (0.301) and its direct effect was also high (0.349). The trait had negligible positive indirect effect *via* shelling (%) (0.029), days to maturity (0.030), number of matured pods per plant (0.021) and immature pods per plant (0.014), which supports the earlier findings of Garjappa (2005), John *et al.* (2008), Ravikumar and Reddi (2012), Singh and Singh (2001) and Sumathi and Muralidharan (2007). While, it showed negligible and negative indirect effect *via*, sound mature kernel (-0.057), number of branches per plant (-0.064), protein content (-0.012), oil content (-0.005) and haulm yield per plant (-0.002). Ravikumar and Reddi (2012), Garjappa (2005) and Babariya and Dobariya (2012) had been reported the similar findings.

4.5.8 Shelling (%) vs. dry pod yield per plot

Shelling per cent had positive and highly significant association with dry pod yield per plot (0.576) and its direct effect was also high (0.240). It had positive indirect effect *via* sound mature kernel (0.114), number of branches per plant (0.126), number of matured pods per plant (0.077), hundred kernel weight (0.042) and number of immature pods per plant (0.018), Garjappa (2005), Prasad *et al.* (2001), Mane *et al.* (2008) and Sumathi and Muralidharan (2007) observed the similar results. While it showed negative indirect effect on protein content (-0.018), oil content (-0.008), haulm yield per plot (-0.011) and days to maturity (-0.003). Garjappa

(2005), Ravikumar and Reddi (2012) and Sumathi and Muralidharan (2007) had been reported similar findings.

4.5.9 Sound mature kernel vs. dry pod yield per plot

Sound mature kernel had highly significant positive association with dry pod yield per plot (0.678) and it had high direct effect (0.205). This trait had positive indirect effect *via* number of branches per plant (0.313), shelling (%) (0.133), number of matured pods per plant (0.112) and number of immature pods per plant (0.028), while negative indirect effect on protein content (-0.013), hundred kernel weight (-0.097), days to maturity (-0.002) and haulm yield per plot (-0.001).

4.5.10 Oil content vs. dry pod yield per plot

Oil content had negative and highly significant association with dry pod yield per plot (-0.306) and its direct effect was positive (0.025) and negligible. This trait had negligible positive indirect effect *via* days to maturity (0.023), haulm yield per plot (0.011), sound mature kernel (0.003) and protein content (0.002), Garjappa (2005) and Suneetha (2003) reported positive association and direct positive effect for this trait. While it showed negative indirect effect *via* number of branches per plant (-0.171), number of matured pods per plant (-0.037), number of immature pods per plant (-0.014), shelling (%) (-0.078), hundred kernel weight (-0.070) and days to 50 % flowering (-0.001). Garjappa (2005), Sumathi and Muralidharan (2007) reported the similar findings earlier.

4.5.11 Protein content vs. dry pod yield per plot

Protein content had significant positive association with dry pod yield per plot (0.178) and its direct effect was negligible and negative (-0.079). This trait had negligible positive indirect effect *via* shelling (%) (0.056), hundred kernel weight (0.054), number of branches per plot (0.039), number of matured and immature pods per plant (0.035), sound mature kernel per cent (0.035) and days to maturity (0.011), were reported by Garjappa (2005), while it had negligible negative indirect effect *via* Haulm yield per plot (-0.007) and oil content (-0.001).

4.6 Genetic divergence

The significant mean squares due to genotypes suggested the preface of ample variability. The genetic divergence among forty genotypes of groundnut was estimated based upon observation of twelve characters. The D^2 values between all possible pairs, which indicated the presence of greater diversity among the genotypes for all the traits. The Mahalanobis D^2 statistics was computed for all possible pair of population under study.

4.6.1 Composition of cluster

The grouping of the genotypes was carried out by following Tocher's method as described by Rao (1952). The forty genotypes studied under present investigation were grouped into seven clusters. The composition of cluster is given in Table 4.6.

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

Cluster No.	No. of Genotypes	Name of Genotype	Pedigree	
I	12	32	C ₇ -P ₂	Phule -6021 x RHRG-6110
		35	C ₇ -P ₅	Phule -6021 x RHRG-6110
		31	C ₇ -P ₁	Phule -6021 x RHRG-6110
		34	C ₇ -P ₄	Phule -6021 x RHRG-6110
		11	C ₃ -P ₁	WRGS-15 x R-8808
		13	C ₃ -P ₃	WRGS-15 x R-8808
		5	C ₁ -P ₅	TAG 24 x Phule Unnati
		15	C ₃ -P ₅	WRGS-15 x R-8808
		22	C ₅ -P ₂	Phule -6021 x Phule Unnati
		2	C ₁ -P ₂	TAG 24 x Phule Unnati
		25	C ₅ -P ₅	Phule -6021 x Phule Unnati
		21	C ₅ -P ₁	Phule -6021 x Phule Unnati
II	6	38	C ₈ -P ₃	WRGS-15 x SB-XI
		40	C ₈ -P ₅	WRGS-15 x SB-XI
		37	C ₈ -P ₂	WRGS-15 x SB-XI
		39	C ₈ -P ₄	WRGS-15 x SB-XI
		36	C ₈ -P ₁	WRGS-15 x SB-XI
		12	C ₃ -P ₂	WRGS-15 x R-8808
III	1	24	C ₅ -P ₄	Phule -6021 x Phule Unnati

Table 4.6 contd...

Cluster No.	No. of Genotypes	Name of Genotype		Pedigree
IV	6	6	C ₂ - P ₁	Phule Unnati x TPG-41
		10	C ₂ - P ₅	Phule Unnati x TPG-41
		8	C ₂ - P ₃	Phule Unnati x TPG-41
		7	C ₂ - P ₂	Phule Unnati x TPG-41
		9	C ₂ - P ₄	Phule Unnati x TPG-41
		23	C ₅ - P ₃	Phule -6021 x Phule Unnati
V	10	17	C ₄ - P ₂	Phule 6021 x ICGV-00350
		19	C ₄ - P ₄	Phule 6021 x ICGV-00350
		16	C ₄ - P ₁	Phule 6021 x ICGV-00350
		20	C ₄ - P ₅	Phule 6021 x ICGV-00350
		18	C ₄ - P ₃	Phule 6021 x ICGV-00350
		26	C ₆ - P ₁	Phule Unnati x SB-XI
		30	C ₆ - P ₅	Phule Unnati x SB-XI
		28	C ₆ - P ₃	Phule Unnati x SB-XI
		27	C ₆ - P ₂	Phule Unnati x SB-XI
29	C ₆ - P ₄	Phule Unnati x SB-XI		
VI	4	1	C ₁ - P ₁	TAG 24 x Phule Unnati
		4	C ₁ - P ₄	TAG 24 x Phule Unnati
		3	C ₁ - P ₃	TAG 24 x Phule Unnati
		14	C ₃ - P ₄	WRGS-15 x R-8808
VII	1	33	C ₇ - P ₃	Phule -6021 x RHRG-6110

Cluster I was the largest having 12 genotypes followed by cluster V having 10 genotypes and cluster II and IV with 6 genotypes, cluster VI with 4 genotypes. Remaining two clusters viz., cluster III and VII were monogenotypic (Table 4.6). Similar findings were also reported by earlier workers Golakia and Makne (1992), Katule (1992), Reddy and Reddy (1993), Rameshkumar *et al.* (1999), Sonone and Thaware (2009) and Singh *et al.* (2010).

4.6.2 Percent contribution of various characters for divergence

The analysis of per cent contribution of twelve characters towards the expression of total genetic divergence (Table 4.7) indicated that dry pod yield per plot (23.85) followed by haulm yield per plot (17.18), protein content (13.08), days to maturity (12.82), sound mature kernel (9.23), shelling (%) (8.46), 100 kernel weight (6.28), oil content (4.23) and number of branches per plant (3.85) contributed maximum towards divergence. However, the contributions of number of mature pods

per plant (0.51), days to 50 % flowering (0.38) and number of immature pods per plant (0.13) were of low magnitude. The present results were also supported by earlier findings of Reddy and Reddy (1993) and Sonawane (2010).

Table 4.7. Percentage contribution of various characters towards total divergence

Sr. No.	Characters	Number of times appearing first	% contribution toward divergence
1	Days to 50 % flowering	3	0.38
2	Days to maturity	100	12.82
3	Number of branches/plant	30	3.85
4	Number of matured pods/plant	4	0.51
5	Number of immature pods/plant	1	0.13
6	Haulm yield/plot (kg)	134	17.18
7	100 kernel weight (g)	49	6.28
8	Shelling (%)	66	8.46
9	Sound mature kernel (%)	72	9.23
10	Oil content (%)	33	4.23
11	Protein content (%)	102	13.08
12	Dry pod yield /plot (kg)	186	23.85

4.6.3 Intra and inter cluster distance

The intra and inter cluster D values were worked out using Mahalanobis D^2 statistics. The mean D values of cluster elements were used as measure of intra and inter cluster distance and are presented in Table 4.8.

Cluster V exhibited maximum intra cluster distance *i.e.* (D=14.37), followed by cluster VI (D=13.2), cluster I (D=10.86), cluster II (D=10.63) and cluster IV (D=9.88). Being monogenotypic, remaining clusters showed no intra cluster distance.

The maximum inter cluster distance was observed between cluster II and cluster V (D=24.92) followed by cluster V and cluster VII (D=24.58), cluster V and cluster VI (D=23.78) and cluster IV and cluster VI (D=23.16). The lowest inter

cluster distance was observed between cluster III and cluster IV (D=11.94). The earlier workers Katule *et al.* (1992), Rameshkumar *et al.* (1999), Chavan *et al.* (2009), Johan Joel and Mysamy (1998) and Sonawane (2010) had been reported similar findings which supports to the above findings.

Table 4.8. Average inter and intra-cluster distance values for groundnut genotypes

Cluster No.	I	II	III	IV	V	VI	VII
I	10.86	15.45	12.5	14.93	21.1	16.39	14.62
II		10.63	18.37	19.64	24.92	18.24	14.16
III			0	11.94	22.77	21.52	20.25
IV				9.88	20.07	23.16	20.16
V					14.37	23.78	24.58
VI						13.2	19.84
VII							0

4.6.4 Cluster means

The cluster means for twelve characters studied are given in Table 4.9. It revealed wide range of variability for most of the characters. It was observed that cluster II had the lowest mean for early days to 50% flowering (42.67) and early maturity (118.50). Cluster V had the highest mean for number of branches per plant (11.10) and number of matured pods per plant (40.90) while lowest mean for number of immature pods per plant (4.90), highest shelling (%) (69.88 %), sound mature kernel per cent (96.80 %) and dry pod yield (1.82). Cluster VII had the highest mean for haulm yield per plot (9.70). Cluster IV had the highest mean for 100 kernel weight (42.25). Cluster III had the highest cluster mean for traits oil per cent (50.30) and protein content (23.55). The lowest dry pod yield mean was observed by cluster II (0.94). On the basis of per cent performance, inter cluster distance and cluster mean the six progenies of different crosses *viz.*, C1-P3, C2-P4, C3-P4, C4-P3, C6-P3 and C8-P2 were identified for advancing in F₆ and then will be selected for crossing programme for the genetic improvement in groundnut. Similar finding were also reported by Katule *et al.* (1992) and Nadaf *et al.* (1986).

Table 4.9. Cluster mean for twelve different characters in groundnut genotypes

Cluster	Days to 50% flowering	Days to maturity	No. of branches/ plant	No. of matured pods/ plant	No. of immature pods/ plant	Haulm yield/ plot (kg)	100 kernel weight (g)	Shelling (%)	Sound mature kernel (%)	Oil content (%)	Protein content (%)	Dry pod yield/ plot (kg)
I	50.50	129.92	5.33	25.54	6.58	8.18	32.42	68.32	90.00	49.03	21.98	1.22
II	42.67	118.50	5.08	18.67	7.00	9.40	31.00	68.09	82.83	46.09	22.26	0.94
III	53.00	137.00	5.50	25.50	6.00	9.35	33.00	67.70	89.50	50.30	23.55	1.22
IV	50.67	136.25	6.33	28.67	5.42	9.21	42.25	69.01	85.75	47.04	22.45	1.53
V	47.95	124.60	11.10	40.90	4.90	9.11	33.50	69.88	96.80	45.79	22.47	1.82
VI	44.38	120.75	7.88	28.75	6.25	5.60	31.50	68.48	89.25	48.34	22.10	1.35
VII	51.00	122.50	5.50	22.50	12.50	9.70	30.00	67.80	86.00	49.30	20.05	1.02

4.7 Stability analysis

4.7.1 Environment wise analysis of variance for twelve characters of 14 genotypes of groundnut tested in different environments

From the analysis of variance in individual environment, there were significant difference among the genotypes for all the characters, except days to 50 % flowering in E₂, E₃ and E₄. Days to maturity in E₄, number of mature pods per plant in E₁, E₂ and E₄, indicating the presence of substantial amount of variation in the material used for present investigation (Table 4.10).

4.8. Analysis of variance (Pooled)

The pooled analysis of variance presented in Table 4.11 revealed that mean variance due to genotypes and environments were found significant for all the characters.

Pooled analysis of variance over four different environments showed that genotypes and environments mean squares were found significant for all the characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and drypod yield per plot (kg), when tested against G x E interaction and pooled error indicating the presence of substantial variability among genotypes and environment.

The significant mean squares due to G x E interactions were observed for all characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and dry pod yield per plot (kg), indicating influence of environment on the evaluated genotypes.

Table 4.10. Environment wise analysis of variance for twelve characters of 14 genotypes of groundnut tested in different environments

Source	DF	Days to 50% flowering				Days to maturity				No. of branches/ plant				No. of mature pods/plant			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replication	2	23.023**	0.22	32.82**	17.05**	7.09**	0.99**	0.80**	2.44**	0.31	4.02	12.66*	16.09**	1.24	0.02	1.02	0.29
Genotypes	13	9.23**	3.18	1.58	2.36	2.86**	2.51**	2.44**	0.38	30.95**	65.58**	56.56**	114.00**	2.60	3.92	6.43	4.86
Error	26	1.68	1.71	1.15	1.81	0.57	0.24	0.25	0.35	2.98	4.15	3.33	3.68	0.78	0.59	0.54	0.59

Source	DF	No. of immature pods/plant				Haulm yield/ plot (kg)				100 kernel weight (g)				Shelling (%)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replication	2	0.01	3.42*	1.36	1.81	0.17	2.88	1.74	0.31	3.01	0.28	0.14	0.93	1.90	1.44	17.25	3.86
Genotypes	13	22.19**	14.30**	19.93**	12.04**	73.40**	70.60**	37.85**	35.17**	6.10**	3.02**	3.60**	3.32**	93.50**	103.02**	51.19**	53.05**
Error	26	0.72	0.66	0.90	0.84	1.17	1.03	2.17	0.92	0.39	0.47	0.50	0.39	6.29	6.28	8.14	3.12

Source	DF	Sound mature kernel (%)				Oil content (%)				Protein content (%)				Dry pod yield/ plot (kg)			
		E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄	E ₁	E ₂	E ₃	E ₄
Replication	2	1.24	2.00	1.74	1.14	0.19	0.13	0.03	0.46	0.04	0.08	0.02	0.13	0.001	0.04**	0.08**	0.12**
Genotypes	13	4.87*	4.52**	10.74**	9.30**	6.77**	3.59**	3.25**	4.18**	0.34**	1.24**	1.29**	1.04**	0.42**	0.40**	0.50**	0.33**
Error	26	2.14	1.23	1.22	1.17	0.14	0.09	0.06	0.22	0.12	0.04	0.06	0.07	0.01	0.01	0.01	0.02

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

Table 4.11. Pooled analysis of variance for twelve characters of 14 genotypes of groundnut over four environments

Sr. No.	Sources	df	Days to 50% flowering	Days to maturity	Number of branches/Plant	Number of mature pods/plant	Number of immature pods/plant	Haulm yield/plot (kg)
1	Genotypes	13	17.16**	65.32**	4.30**	73.22**	1.94**	1.37**
2	Environments	3	448.08**	548.51**	8.45**	235.75**	83.33**	10.39**
4	G x E	39	1.81**	2.25**	0.34*	9.16**	1.14**	0.45**
5	Pooled Error	104	0.26	1.33	0.14	1.99	0.54	0.12

Sr. No.	Sources	df	Shelling (%)	100 kernel weight (g)	Sound mature kernel (%)	Oil content (%)	Protein content (%)	Dry pod yield/plot (kg)
1	Genotypes	13	4.62**	75.48**	5.67**	4.85**	0.84**	0.517**
2	Environments	3	5.97**	117.13**	27.59**	2.16**	2.38**	0.396**
4	G x E	39	0.40*	4.07**	1.37**	0.36**	0.15**	0.013**
5	Pooled Error	104	0.21	1.19	0.48	0.04	0.02	0.004

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

4.9 Analysis of variance for stability

The analysis of variance representing the mean sum of square due to different source of variation as per Eberhart and Russell (1966) for the 12 characters is presented in Table 4.12.

The mean sum of squares due to genotypes were found significant for all the characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and dry pod yield per plot (kg), when tested against G x E interaction, pooled deviation and pooled error indicating substantial amount of variation in the material used for the present investigation.

Table 4.12. Analysis of variance (mean squares) for stability of dry pod yield and yield components in groundnut

Sr. No.	Sources	df	Days to 50% flowering	Days to maturity	Number of branches/plant	Number of mature pods/plant	Number of immature pods/plant	Haulm yield/plot (kg)
1.	Genotypes (G)	13	17.31 ^{@@+***}	65.49 ^{@+***}	4.34 ^{@+***}	72.74 ^{@+***}	1.88 ^{@+***}	1.38 ^{@+***}
2.	Environments (E)	3	446.80 ^{@+***}	546.90 ^{@+***}	8.48 ^{@+***}	233.45 ^{@+***}	83.37 ^{@+***}	10.37 ^{@+***}
3.	E + (G × E)	42	33.62 ^{@+***}	41.19 ^{@+***}	0.92 ^{@+***}	25.19 ^{@+***}	7.06 ^{@+***}	1.16 ^{@+***}
4.	G × E	39	1.84 ^{**}	2.28 ^{**}	0.34 [*]	9.17 ^{**}	1.19 ^{**}	0.45 ^{**}
5.	Environment (Linear)	1	1340.41 ⁺⁺⁺⁺	1640.70 ⁺⁺⁺⁺	25.45 ⁺⁺⁺⁺	700.36 ⁺⁺⁺⁺	250.10 ⁺⁺⁺⁺	31.10 ⁺⁺⁺⁺
6.	G × E (Linear)	13	2.21 ^{**}	4.11 ^{**}	0.35 ^{**}	11.80 ^{**}	1.75 ^{**}	0.76 ^{***}
7.	Pooled deviation	28	1.54 ^{**}	1.27 ^{**}	0.31 [*]	7.30 ^{**}	0.95 [*]	0.28 ^{**}
8.	Pooled error	104	0.26	0.44	0.15	1.99	0.53	0.12

Sr. No.	Sources	df	Shelling (%)	100 kernel weight (g)	Sound mature kernel (%)	Oil content (%)	Protein content (%)	Dry pod yield/plot (kg)
1.	Genotypes (G)	13	4.73 ^{@+***}	76.10 ^{@+***}	5.68 ^{@+***}	4.84 ^{@+***}	0.86 ^{@+***}	0.517 ^{@+***}
2.	Environments (E)	3	5.90 ^{@+***}	118.84 ^{@+***}	27.80 ^{@+***}	2.16 ^{@+***}	2.37 ^{@+***}	0.397 ^{@+***}
3.	E + (G × E)	42	0.79 ^{@+***}	12.49 ^{@+***}	3.26 ^{@+***}	0.49 ^{**}	0.31 ^{@+***}	0.041 ^{@+***}
4.	G × E	39	0.40 ^{**}	4.31 ^{**}	1.38 ^{**}	0.36 ^{**}	0.15 ^{**}	0.013 ^{**}
5.	Environment (Linear)	1	17.70 ⁺⁺⁺⁺	356.51 ⁺⁺⁺⁺	83.41 ⁺⁺⁺⁺	6.47 ⁺⁺⁺⁺	7.12 ⁺⁺⁺⁺	1.191 ⁺⁺⁺⁺
6.	G × E (Linear)	13	0.25 ^{**}	7.29 ^{**}	1.69 ^{**}	0.37 ^{**}	0.14 ^{**}	0.017 ^{**}
7.	Pooled deviation	28	0.44 [*]	2.62 ^{**}	1.13 ^{**}	0.33 ^{**}	0.14 ^{**}	0.011 ^{**}
8.	Pooled error	104	0.21	1.18	0.48	0.04	0.02	0.004

@,@@ significant at 5 and 1 % , respectively when tested against G x E

+ ,++ significant at 5 and 1 % , respectively when tested against pooled deviation

*, ** significant at 5 and 1 % , respectively when tested against pooled error

The mean sum of squares due to environments was significant for all characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%), pod yield per plot (kg), when tested against G x E interaction, pooled deviation and pooled error, indicating that environments were quite variable.

G x E interaction was also significant for all characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg), when tested against pooled error. This indicates that there was an influence of environments on the genotypes. The earlier workers Chunilal and Ranvir (1998), Joshi *et al.* (2003) had been also reported by Mahto and Mahto (2000), Viswanathan *et al.* (2001) and Naazar *et al.* (2001) had been reported similar results as observed in present study.

The mean squares due to environment plus G x E (E + G x E) were significant for all the characters except oil content when tested both against pooled deviation and pooled error suggesting that distinct nature of environments and genotype x environment interactions in phenotypic expression.

Partitioning of G x E interaction showed that, G x E (linear) effect was significant for all the characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg), when tested against pooled deviation and pooled error. Therefore, prediction of performance of genotypes over environment would be possible for all the characters.

Environment (linear) effects were significant for all the traits except number of branches per plant, number of immature pods per plant and shelling %, when tested against pooled deviation, indicating that environmental differences were present in all the four environments (15th February, 3rd March; 15th July and 30th July) studied. However, the magnitude of mean squares for environment (Linear) was

higher as compared to genotypes x environments (Linear) which indicated that linear response of environment account for major part of total variation for all the characters studied and which may be responsible for high adaption. Similar findings were also reported by Sojitra and Pethari (1998), Chunilal and Ranvir (1998) and Thaware (2009).

Pooled deviation effects were significant for the traits *viz.*, days to 50 % flowering, days to maturity, number of mature pods per plant, haulm yield per plot (kg), hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg), indicates the importance of non linear components in determining the interaction of genotypes with environments.

4.10 Mean performance of groundnut genotypes for twelve different characters over environments

The result obtained on the mean performance of groundnut genotypes over different sowing dates for characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg) are presented in Table 4.13 to 4.16.

4.10.1 Days to 50 % flowering

Among the 14 genotypes, the pooled mean for days to 50 % flowering ranged from 42.50 days (TAG-24 and SB-XI) to 48.42 days (Phule Unnati). Days to 50% flowering among the genotypes in different environments varied from 45.67 days (SB-XI) to 54.00 days (TPG-41) in E₁, 46.67 days (SB-XI) to 53.67 days (Phule Bharati) in E₂, 35.67 days (TAG-41) to 45.33 days (Phule Unnati) in E₃ and 37.67 days (RHRG-1335) to 44.00 days (RHRG-1189) in E₄. On the pooled basis, genotype TAG-24 and SB-XI (42.50 days) were the earliest to 50% flowering which was followed by RHRG-1305 (43.08 days) and Phule-6021 (43.33 days). The overall mean for days to 50% flowering was 45.23 days.

Table 4.13. Mean performance of groundnut genotypes for days to 50 % flowering, maturity and number of branches per plant over environments

Sr. No.	Genotypes	Days to 50 % Flowering					Days to Maturity					Number of branches/plant				
		E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean
1	JL-501	47.00	50.00	37.67	39.00	43.42	121.00	125.00	112.00	114.00	118.00	8.33	6.27	6.13	5.47	6.55
2	TAG-24	47.00	49.33	35.67	38.00	42.50	119.67	123.00	110.33	112.33	116.33	8.33	6.53	6.27	4.67	6.45
3	Phule-6021	46.33	48.67	38.33	40.00	43.33	121.67	126.67	113.33	117.33	119.75	6.33	4.67	5.20	6.00	5.55
4	TPG-41	53.67	52.33	42.67	43.33	48.00	136.00	139.00	121.67	125.00	130.42	8.00	6.20	6.13	5.67	6.50
5	Phule Bharati	52.00	54.00	43.33	41.00	47.58	130.67	138.00	122.33	122.67	128.42	10.27	8.13	7.73	8.00	8.53
6	Phule Unnati	53.33	52.33	45.33	42.67	48.42	132.00	135.33	121.00	123.67	128.00	9.80	7.27	8.20	7.60	8.22
7	SB-XI	45.67	46.67	38.33	39.33	42.50	120.67	125.00	115.00	117.67	119.58	5.67	6.00	5.47	4.80	5.48
8	RHRG-1335	51.00	51.33	39.67	37.67	44.92	131.00	131.00	117.33	120.00	124.83	7.53	7.33	6.33	5.80	6.75
9	RHRG-1142	49.33	53.33	41.00	39.00	45.67	126.33	132.67	115.67	118.33	123.25	5.73	5.33	3.87	4.53	4.87
10	RHRG-1308	50.33	52.67	40.67	42.33	46.50	127.33	129.67	117.67	119.00	123.42	7.87	6.93	7.00	5.87	6.92
11	RHRG-1189	51.00	53.00	41.33	44.00	47.33	127.00	132.33	118.00	120.33	124.42	6.20	5.60	5.47	4.60	5.47
12	RHRG-1192	47.33	50.00	41.00	41.67	45.00	123.33	129.00	116.33	118.33	121.75	7.00	4.60	6.73	5.33	5.92
13	RHRG-1130	47.00	52.00	39.33	41.33	44.92	124.00	128.33	114.00	117.67	121.00	6.13	5.73	5.33	4.80	5.50
14	RHRG-1305	47.00	48.33	37.67	39.33	43.08	123.00	127.67	117.67	120.33	122.17	7.13	6.13	5.87	5.60	6.18
	General mean	49.14	51.00	40.14	40.62	45.23	125.98	130.19	116.60	119.05	122.95	7.45	6.20	6.12	5.62	6.35
	S.E. \pm	0.69	0.66	0.77	0.75		0.88	0.83	1.20	0.79		0.51	0.56	0.58	0.51	
	CD at 5 %	1.42	1.36	1.59	1.53		1.81	1.71	2.48	1.61		1.05	1.15	1.19	1.04	
	CV (%)	1.72	1.59	2.36	2.25		0.86	0.78	1.27	0.81		8.39	11.05	11.53	11.06	

4.10.2 Days to maturity

With respect to days to maturity, on pooled basis mean values ranged from TAG-24 (116.33 days) to TPG-41 (130.42 days). Among the environments, mean days to maturity ranged in E₁ from TAG-24 (119.67 days) to TPG-41 (136.00 days), in E₂ from TAG-24 (123.00 days) to TPG-41 (139.00 days), in E₃ from TAG-24 (110.33 days) to Phule Bharati (122.33 days) and in E₄ from TAG-24 (112.33 days) to TPG-41 (125.00 days).

On the pooled basis, genotype TAG-24 (116.33 days) had early maturity period followed by JL-501 (118.00 days). The overall mean for days to maturity was 122.95 days.

4.10.3 Number of branches per plant

The pooled mean values over environment for number of branches per plant ranged from RHRG-1142 (4.87) to Phule Bharati (8.53). The range of number of branches per plant among the genotypes in E₁ varied from SB-XI (5.67) to Phule Bharati (10.27) in E₂, RHRG-1192 (4.60) to Phule Bharati (8.13); in E₃, RHRG-1142 (3.87) to Phule Unnati (8.20); in E₄, RHRG-1142 (4.53) to Phule Bharati (8.00). Genotype Phule Bharati (8.53) had maximum number of branches per plant on pooled basis followed by Phule Unnati (8.22). The overall mean for this character was 6.35 branches per plant.

4.10.4 Number of mature pods per plant

The pooled mean data for number of mature pods per plant revealed that among 14 genotypes Phule Unnati (40.05 pods) possessed maximum number of mature pods per plant followed by Phule Bharati (34.75 pods). The number of mature pods per plant ranged from 18.80 pods (SB-XI) to 41.00 pods (Phule Unnati) in E₁; 17.00 pods (RHRG-1130) to 41.00 pods (Phule Unnati) in E₂; 27.67 pods (TAG-24) to 41.00 pods (Phule Bharati) in E₃ and 23.07 pods (RHRG-1142) to 37.53 pods (Phule Unnati) in E₄. The overall mean for this character was 28.92 number of mature pods per plant.

Table 4.14. Mean performance of groundnut genotypes for number of mature, immature pods per plant and haulm yield per plot (kg) over environments

Sr. No.	Genotypes	Number of mature pods/plant					Number of immature pods/plant					Haulm yield/plot (kg)				
		E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean
1	JL-501	30.00	24.60	35.33	27.00	29.23	12.27	6.67	4.53	3.67	6.78	5.58	3.61	4.47	3.70	4.34
2	TAG-24	26.33	24.27	27.67	23.53	25.45	6.67	4.93	4.87	3.00	4.87	4.30	3.64	4.53	4.26	4.18
3	Phule-6021	29.33	23.00	36.33	24.67	28.33	10.67	4.87	3.40	3.33	5.57	4.53	4.16	4.20	3.65	4.14
4	TPG-41	25.00	19.40	29.00	28.33	25.43	9.33	5.67	3.93	3.73	5.67	5.16	4.20	5.33	4.01	4.67
5	Phule Bharati	36.67	26.33	41.00	35.00	34.75	9.33	6.60	5.33	4.80	6.52	5.17	6.15	6.43	4.30	5.51
6	Phule Unnati	41.00	41.00	40.67	37.53	40.05	11.27	6.40	5.20	4.93	6.95	6.60	6.35	6.27	4.82	6.01
7	SB-XI	18.80	19.67	30.13	28.67	24.32	6.67	7.20	3.53	3.67	5.27	6.60	4.32	6.60	4.18	5.43
8	RHRG-1335	27.40	18.67	32.33	26.47	26.22	10.47	4.80	4.40	5.67	6.33	6.70	3.57	6.33	3.79	5.10
9	RHRG-1142	24.27	25.00	29.33	23.07	25.42	8.00	7.07	2.93	4.13	5.53	7.10	3.96	5.23	3.56	4.96
10	RHRG-1308	31.93	21.67	34.67	28.13	29.10	10.73	7.73	4.47	4.00	6.73	6.53	3.79	5.93	3.79	5.01
11	RHRG-1189	26.13	20.00	34.53	28.67	27.33	8.20	7.00	4.27	3.67	5.78	6.27	4.35	5.53	3.97	5.03
12	RHRG-1192	31.93	24.67	37.00	30.53	31.03	10.87	6.67	3.73	4.53	6.45	6.50	3.46	4.40	3.72	4.52
13	RHRG-1130	27.13	17.00	31.40	33.80	27.33	7.60	5.00	3.67	3.93	5.05	5.40	3.46	4.37	3.66	4.22
14	RHRG-1305	33.60	27.33	33.00	29.33	30.82	9.60	5.00	5.00	6.13	6.43	4.20	4.45	4.30	3.57	4.13
	General mean	29.25	23.76	33.74	28.91	28.92	9.41	6.11	4.23	4.23	6.00	5.76	4.25	5.28	3.93	4.80
	S.E. \pm	2.05	2.05	2.33	1.44		1.06	1.07	0.87	1.10		0.62	0.40	0.41	0.48	
	CD at 5 %	4.21	4.21	4.79	2.97		2.173	2.197	1.797	-		1.27	0.83	0.84	-	
	CV (%)	8.57	10.55	8.46	6.11		13.77	21.41	25.29	31.82		13.12	11.64	9.46	15.05	

4.10.5 Number of immature pods per plant

The pooled mean data for number of immature pods per plant revealed that among 14 genotypes TAG-24 (4.87 pods) possessed minimum number of immature pods per plant followed by RHRG-1130 (5.05 pods). The number of immature pods per plant ranged from JL-501 (12.27 pods) to TAG-24 and SB-XI (6.67 pods) in E₁, RHRG-1308 (7.73 pods) to RHRG-1335 (4.80 pods) to in E₂, Phule Bharati (5.33) to Phule-6021 (3.40 pods) in E₃ and RHRG-1335 (5.67 pods) to TAG-24 (3.00 pods) in E₄ had minimum number of immature pods per plant. The overall mean for this character was 6.00 number of immature pods per plant.

4.10.6 Haulm yield per plot (kg)

With respect to haulm yield per plant, pooled mean values ranged from 4.13 (RHRG-1305) to 6.01 (Phule Unnati). Among the environments, haulm yield per plant ranged from RHRG-1142 (7.10 kg) to RHRG-1305 (4.20 kg) in E₁, Phule Unnati (6.35 kg) to RHRG-1192, RHRG-1130 (3.46 kg) in E₂, SB-XI (6.60 kg) to Phule-6021 (4.20 kg) in E₃ and Phule Unnati (4.82 kg) to RHRG-1142 (3.56 kg) in E₄ possessed maximum haulm yield per plant. The overall mean for this character was 4.80 kg haulm yield per plot.

4.10.7 Shelling percentage

Among the 14 genotypes, pooled mean values of shelling percentage ranged from TPG-41 (65.00 %) to SB-XI (69.92 %). Among genotypes of different environments ranged from SB-XI (70.67 %) to TPG-41 (67.33 %) in E₁, SB-XI (69.67 %) to RHRG-1189 (66.00 %) in E₂, Phule Unnati (70.00 %) to TPG-41 (63.67 %) in E₃ and in E₄ SB-XI (69.67 %) to RHRG-1335 (66.00 %) was observed with maximum shelling percentage. The overall mean for this character was 67.84 shelling percentage.

4.10.8 Hundred kernel weight (g)

The mean value of hundred kernel weight on pooled basis ranged from 28.00 g (RHRG-1335) to 45.17 g (TPG-41). Among the genotypes of different environments hundred kernel weight ranged from 44.33 g (TPG-41) to 31.67 g (TAG-24

Table 4.15. Mean performance of groundnut genotypes for shelling (%), 100 kernel weight (g) and sound mature kernel (%) over environments

Sr. No.	Genotypes	Shelling (%)					100 kernel weight (g)					Sound mature kernel (%)				
		E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean
1	JL-501	69.00	67.00	69.00	67.67	68.17	34.00	31.33	34.67	30.00	32.50	96.00	93.00	96.00	94.00	94.75
2	TAG-24	68.67	67.67	68.67	67.33	68.08	31.67	26.33	32.67	25.67	29.08	93.33	91.00	91.33	90.67	91.58
3	Phule-6021	68.33	67.67	68.33	66.33	67.67	35.33	26.67	35.33	24.00	30.33	93.00	91.33	94.67	91.00	92.50
4	TPG-41	67.33	64.67	63.67	64.33	65.00	44.33	42.33	48.33	45.67	45.17	94.00	90.00	89.33	87.67	90.25
5	Phule Bharati	69.00	67.33	68.67	67.67	68.17	36.00	31.33	36.00	31.67	33.75	95.67	92.67	95.00	93.00	94.08
6	Phule Unnati	70.00	68.67	70.00	68.33	69.25	34.67	35.00	34.00	35.00	34.67	94.00	94.33	95.00	95.00	94.58
7	SB-XI	70.67	69.67	69.67	69.67	69.92	33.00	22.67	32.00	26.67	28.58	94.00	91.67	93.67	92.00	92.83
8	RHRG-1335	67.67	67.33	68.33	66.00	67.33	31.67	26.00	30.67	23.67	28.00	93.67	92.67	92.00	90.33	92.17
9	RHRG-1142	68.00	67.67	67.67	67.67	67.75	34.00	27.67	32.67	25.33	29.92	95.67	92.00	94.33	91.00	93.25
10	RHRG-1308	68.67	67.33	68.67	67.33	68.00	33.67	30.67	34.33	30.67	32.33	96.00	93.00	93.33	91.33	93.42
11	RHRG-1189	67.67	66.00	68.33	67.00	67.25	33.00	28.67	30.33	23.67	28.92	93.00	92.67	94.33	92.67	93.17
12	RHRG-1192	68.33	67.67	67.67	67.33	67.75	32.33	28.67	32.67	25.33	29.75	95.33	93.33	95.00	91.67	93.83
13	RHRG-1130	68.33	68.00	68.33	65.67	67.58	31.67	30.33	33.00	23.00	29.50	97.00	90.67	92.00	90.67	92.58
14	RHRG-1305	67.67	67.67	68.33	67.67	67.83	33.33	29.67	34.00	32.00	32.25	94.67	90.67	95.67	92.00	93.25
	General mean	68.52	67.45	68.24	67.14	67.84	34.19	29.81	34.33	28.74	31.77	94.67	92.07	93.69	91.64	93.02
	S.E. \pm	0.72	0.63	0.60	0.63		1.41	1.66	1.49	1.57		1.19	0.91	0.90	0.88	
	CD at 5 %	1.48	1.29	1.23	1.29		2.90	3.42	3.06	3.22		2.45	1.86	1.86	1.81	
	CV (%)	1.29	1.14	1.07	1.15		5.05	6.84	5.32	6.68		1.54	1.21	1.18	1.18	

and RHRG-1335) in E₁, 42.33 g (TPG-41) to 22.67 g (SB-XI) in E₂, 48.33 g (TPG-41) to 30.33 g (RHRG-1189) in E₃ and 45.67 g (TPG-41) to 23.00 g (RHRG-1130) in E₄. The overall mean for this character was 31.77 g hundred kernel weight.

4.10.9 Sound mature kernel (%)

The pooled mean value for sound mature kernel percentage ranged from 90.25 % (TPG-41) to 94.75 % (JL-501). Whereas maximum sound mature kernel percentage ranged in E₁ 96 % (JL-501 and RHRG-1308) to 93.00 % (Phule-6021 and RHRG-1189), in E₂ 94.33 % (Phule Unnati) to 90.00 % (TPG-41), in E₃ 96 % (JL-501) to 91.33 % (TAG-24) and in E₄ 95.00 % (Phule Unnati) to 87.67 % (TPG-41). The overall mean for this character was 93.02 %.

4.10.10 Oil content (%)

The pooled mean value for oil content ranged from 46.03 % (TPG-41) to 50.21 % (Phule Unnati). Among the genotypes of different environments maximum oil content ranged was 50.70 % (Phule Unnati) to 45.27 % (TPG-41) in E₁, 50.43 % (Phule Unnati) to 46.55 % (TAG-24) in E₂, 50.32 % (Phule Unnati) to 46.18 % (TPG-41) in E₃ and 49.40 % (Phule Unnati) to 45.92 % (TPG-41) in E₄. The overall mean for this character was 48.40 %.

4.10.11 Protein content (%)

The pooled mean value for protein content ranged from 21.47 % (RHRG-1130) to 23.12 % (TAG-24). Among the genotypes of different environments protein content ranged was 23.35 % (TAG-24) to 22.19 % (RHRG-1130) in E₁, 23.05 % (TAG-24) to 20.71 % (RHRG-1305) in E₂, 23.39 % (TAG-24) to 21.43 % (RHRG-1130) in E₃ and 22.68 % (TAG-24) to 20.55 % (RHRG-1305) in E₄. The overall mean for this character was 22.22 %.

4.10.12 Dry pod yield per plot (Kg)

The pooled mean value for dry pod yield per plot ranged from 1.110 kg (SB-XI) to 2.319 (Phule Unnati). Among the genotypes of different environments highest dry pod yield per plot ranged was 2.687 kg (Phule Unnati) to 1.170 kg (SB-XI) in E₁, 2.157 kg (Phule Unnati) to 0.993 kg (RHRG-1189) in E₂, 2.483 kg (Phule Unnati) to 1.127 kg (RHRG-1130) in E₃ and 2.080 kg (Phule Bharati) to 1.020 kg (SB-XI) in E₄. The overall mean for this character was 1.429 kg.

Table 4.16. Mean performance of groundnut genotypes for oil content (%), protein content (%) and dry pod yield per plot (kg) over environments

Sr. No.	Genotypes	Oil content (%)					Protein content (%)					Dry pod yield/plot (Kg)				
		E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean
1	JL-501	48.87	48.97	48.79	48.17	48.70	22.96	22.41	22.74	22.13	22.56	1.637	1.337	1.527	1.280	1.445
2	TAG-24	48.55	46.55	47.51	48.52	47.78	23.35	23.05	23.39	22.68	23.12	1.653	1.350	1.580	1.350	1.483
3	Phule-6021	48.93	48.52	48.24	46.45	48.04	22.53	22.42	22.61	22.26	22.46	1.297	1.080	1.627	1.197	1.300
4	TPG-41	45.27	46.73	46.18	45.92	46.03	22.64	22.57	21.61	21.64	22.12	1.573	1.200	1.793	1.193	1.440
5	Phule Bharati	49.48	48.87	48.77	48.30	48.86	22.70	21.82	21.38	21.83	21.93	2.090	2.083	2.273	2.080	2.132
6	Phule Unnati	50.70	50.43	50.32	49.40	50.21	22.82	22.48	22.48	22.12	22.48	2.687	2.157	2.483	1.950	2.319
7	SB-XI	46.23	47.45	47.93	46.12	46.93	22.92	22.67	22.88	21.91	22.59	1.170	1.050	1.200	1.020	1.110
8	RHRG-1335	49.93	48.27	49.21	48.40	48.95	22.97	22.17	22.79	21.78	22.43	1.460	1.123	1.250	1.033	1.217
9	RHRG-1142	49.47	49.34	49.20	48.60	49.15	22.46	21.74	21.55	20.76	21.63	1.357	1.150	1.240	1.030	1.194
10	RHRG-1308	50.43	49.73	50.00	49.13	49.83	22.20	22.82	22.43	21.28	22.18	1.620	1.423	1.453	1.220	1.429
11	RHRG-1189	49.28	48.53	48.76	48.10	48.67	22.32	22.39	21.48	21.92	22.03	1.603	0.993	1.407	1.040	1.261
12	RHRG-1192	47.85	48.33	49.48	48.47	48.53	22.99	22.33	22.75	21.83	22.48	1.570	1.210	1.383	1.163	1.332
13	RHRG-1130	47.94	47.40	48.51	46.06	47.48	22.19	21.15	21.43	21.11	21.47	1.437	1.143	1.127	1.100	1.202
14	RHRG-1305	48.56	48.63	48.56	48.18	48.48	22.83	20.71	22.11	20.55	21.55	1.370	1.017	1.130	1.040	1.139
	General mean	48.68	48.41	48.68	47.85	48.40	22.71	22.20	22.26	21.70	22.22	1.609	1.308	1.534	1.264	1.429
	S.E. \pm	0.30	0.24	0.20	0.38	-	0.29	0.16	0.19	0.21	-	0.06	0.07	0.10	0.11	-
	CD at 5 %	0.62	0.50	0.41	0.79	-	0.59	0.34	0.39	0.44	-	0.12	0.14	0.20	0.23	-
	CV (%)	0.76	0.62	0.50	0.98	-	1.54	0.90	1.06	1.20	-	4.41	6.40	7.82	10.89	-

4.11 Estimates of environmental indices

Estimates of environmental indices (I_j) are presented in Table 4.17 which revealed that environment E₁ (15th February) was found favourable for the characters *viz.*, number of branches per plant, number of mature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%), pod yield per plot (kg), environment E₃ and E₄ was found favourable for days to 50 % flowering, days to maturity and number of immature pods per plant.

Environment E₃ (15th July) was also found favourable for other characters *viz.*, number of mature pods per plant, haulm yield per plot, shelling %, hundred kernel weight, sound mature kernel, oil content and dry pod yield per plot.

Table 4.17. Environmental Indices for twelve characters of 40 F₅ progenies of groundnut tested in four environments

Sr. No.	Character	E ₁ 15 th Feb.	E ₂ 3 rd March	E ₃ 15 th July	E ₄ 30 th July
1	Days to 50 % flowering	3.92	5.77	-5.08	-4.61
2	Days to maturity	3.02	7.24	-6.36	-3.91
3	Number of branches/plant	1.10	-0.15	-0.23	-0.73
4	Number of matured pods/plant	3.41	-5.16	4.83	-0.01
5	Number of immature pods/plant	0.34	0.12	-1.76	-1.77
6	Haulm yield/plot (kg)	0.956	-0.555	0.477	-0.878
7	Shelling percent	0.69	-0.39	0.40	-0.70
8	100 kernel weight (g)	2.42	-1.96	2.57	-3.03
9	Sound mature kernel (%)	1.65	-0.95	0.67	-1.38
10	Oil content (%)	0.28	0.01	0.27	-0.56
11	Protein content (%)	0.49	-0.02	0.05	-0.52
12	Dry pod yield/plot (kg)	0.180	-0.120	0.105	-0.165

In general environment E₁ (15th Feb.) was most favourable followed by E₃ (15th July) for yield and yield contributing characters in summer and *kharif* groundnut, respectively.

4.12 Stability parameters for individual characters

Since G x E interaction was detected for all the traits, stability parameters were estimated and are presented in Table 4.18 to 4.20. These points are considered for deciding stability of genotypes *i.e.* the genotypes with at least mean performance numerically greater than population mean and S^2_{di} low or non significant and (1) 'bi' approaching to unity or not significantly deviating from unity are regarded with general adaptability or average stability. (2) 'bi' significantly greater than unity is considered as better adaptable to rich or favourable environment (below average stability). (3) 'bi' significantly less than unity and or having lower magnitude than unity are considered as better adaptable to poor or unfavourable environment (above average stability). The genotypes with significant S^2_{di} components are considered as highly unpredictable. The non significant bi values were considered as round unity irrespective of their high or low numerical values.

4.12.1 Days to 50% flowering

For earliness, less number of days to 50 % flowering is desirable. Out of fourteen, four genotypes *viz.*, TAG-24, Phule-6021, JL-501 and RHRG-1305 exhibited less mean value than general mean, regression coefficient around unity, hence these genotypes can be considered as stable for earliness suggesting non significant deviation from regression. Whereas two genotypes SB-XI and RHRG-1192 showed less mean value than general mean regression coefficient significantly less than unity and non significant deviation from linear regression revealing that these genotypes would have above average stability and likely to be adopted to poor environment. The genotype *viz.*, TPG-41, Phule Bharati, Phule Unnati, RHRG-1335. While, none of the genotype was well adapted for favourable environment. The genotypes *viz.*, TPG-41, Phule Bharati, Phule Unnati, RHRG-1335, RHRG-1189 and RHRG-1130 were found to differ significantly from linear regression revealing their inconsistent performance across the environment and hence they would be unstable. Mahto and Mahto (2000) reported this is controlled by non linear component of environment. The earlier workers Venkataramana *et al.* (2000b) and Patil *et al.* (2014) had been reported similar findings.

Table 4.18. Stability parameters of different genotypes for twelve characters in groundnut

Sr. No.	Genotypes	Days to 50% flowering			Days to maturity			Number of branches/plant			Number of matured pods/plant		
		x	bi	S ² di	x	Bi	S ² di	x	bi	S ² di	x	bi	S ² di
1	JL-501	43.42	1.061	0.163	118.00	0.968	-0.400	6.55	1.590*	-0.156	29.23	1.072	1.401
2	TAG-24	42.50	1.176	0.514	116.30	0.956	-0.300	6.45	1.87*	0.044	25.45	0.342	0.466
3	Phule-6021	43.33	0.870	0.246	119.80	0.905	0.800	5.55	0.414	0.542*	28.33	1.329	7.269*
4	TPG-41	48.00	1.001	2.321**	130.40	1.329	1.40*	6.50	1.314*	-0.145	25.43	0.963	3.672
5	Phule Bharati	47.58	1.110	1.771**	128.40	1.172	2.60**	8.53	1.398	0.107	34.75	1.484	-0.246
6	Phule Unnati	48.42	0.878	3.881**	128.00	1.08	0.000	8.22	1.29	0.223	40.05	-0.032	2.244
7	SB-XI	42.50	0.754*	-0.137	119.60	0.675*	0.500	5.48	0.342	0.116	24.32	1.003	25.247**
8	RHRG-1335	44.92	1.263	2.457**	124.80	1.108	5.50**	6.75	0.857	0.187	26.22	1.377	-1.458
9	RHRG-1142	45.67	1.181	2.183**	123.30	1.236	-0.100	4.87	0.743	0.376*	25.42	0.413	4.913*
10	RHRG-1308	46.50	1.039	0.106	123.40	0.946	0.600	6.92	0.984	-0.035	29.10	1.323	1.841
11	RHRG-1189	47.33	0.971	0.947*	124.40	1.04	-0.200	5.47	0.78	-0.060	27.33	1.443	0.365
12	RHRG-1192	45.00	0.770*	0.133	121.80	0.896	0.500	5.92	0.901	1.059**	31.03	1.238*	-1.752
13	RHRG-1130	44.92	0.981	2.890**	121.00	1.021	-0.100	5.50	0.665	-0.076	27.33	1.456	27.584**
14	RHRG-1305	43.08	0.945	0.134	122.20	0.666	0.800	6.18	0.853	-0.149	30.82	0.589	2.762
	G. Mean	45.23			123.00			6.35			28.92		
	SE (bi)		0.72	0.13		0.70	0.10		0.32	0.41		1.56	0.38

4.12.2 Days to maturity

For days to maturity genotypes took less days to maturity in comparison to population mean were considered for interpretation of stability parameters. Out of fourteen genotypes only three genotypes depicted significant deviation from linear regression, hence rest of the genotypes were considered for their adaptation in different environments. Total five genotypes *viz.*, JL-501, TAG-24, Phule-6021, RHRG-1192 and RHRG-1130 had average stability. Whereas, the genotypes, SB-XI and RHRG-1305 had above average stability and would be well adapted to poor environment. The three genotypes *viz.*, TPG-41, Phule Bharti and RHRG-1335 significantly deviated from linear regression suggesting their inconsistency performance over environments. The genotypes Phule Unnati, RHRG-1142, RHRG-1308 and RHRG-1130 took more number of days to maturity, unit regression coefficient and non significant deviation from regression, also had genes for stability. The present results are in accordance with those of Mahto and Mahto (2000) and Yogendra *et al.* (2009).

4.12.3 Number of branches per plant

Total four genotypes *viz.*, Phule Bharati, Phule Unnati, RHRG-1335 and RHRG-1308 had average stability, while genotypes *viz.*, JL-501, TAG-24 and TPG-41 had below average stability and suitable for favourable environment. While three genotypes Phule-6021, RHRG-1142 and RHRG-1192 were significantly deviated from linear regression suggesting their inconsistency performance over environment and not adapted to any specific environment. The other genotypes *viz.*, SB-XI, RHRG-1189 and RHRG-1130 had depicted non significant regression coefficient and S^2_{di} , however they had low mean values for this trait and hence not considered as average stable. Previously Patil *et al.* (2014) observed similar findings.

4.12.4 Number of mature pods per plant

Among the fourteen genotypes, five genotypes *viz.*, JL-501, Phule Bharti, Phule Unnati, RHRG-1308 and RHRG-1305 had higher mean value than population mean, non significant regression coefficient and hence categorised as average stable. The genotype RHRG-1192 had higher mean than population mean, bi

>1 and significant and $S^2di=0$, non significant and hence grouped as below average stable and suitable for favourable environment. The four genotypes *viz.*, Phule-6021, SB-XI, RHRG-1142 and RHRG-1130 had significant deviation from regression and hence these genotypes were considered as unadaptable. Venkataramana *et al.* (2000b), Singh and Singh (2001), Vishwanathan *et al.* (2001), Chavan *et al.* (2009) and Patil *et al.* (2014) supports the findings of present study.

4.12.5 Number of immature pods per plant

The genotypes with less number of immature pods per plant were considered as better performing genotypes. The five genotypes TAG-24, SB-XI, RHRG-1142, RHRG-1130 and RHRG-1189 had mean lower than population mean, non significant regression coefficient (bi) and non significant deviation from regression (S^2di) and hence they were grouped as average stable. While three genotypes *viz.*, TAG-24, TPG-41 and RHRG-1130 were grouped as above average stability and favourable for poor environment and only one genotype Phule-6021 was grouped as below average stable. However, three genotypes *viz.*, RHRG-1135, RHRG-1142 and RHRG-1305 were found unstable.

4.12.6 Haulm yield per plot (kg)

Among the fourteen genotype, two genotypes *viz.*, Phule Unnati and SB-XI had higher mean than population mean, non significant regression coefficient (bi) and non significant deviation from regression ($S^2di=0$) suggesting that these genotypes can be considered as average stable. Four genotype *viz.*, RHRG-1335, RHRG-1142, RHRG-1308 and RHRG-1189 had below average stability, while two genotypes Phule Bharti and RHRG-1192 were found unpredictable for haulm yield. Similar findings were reported by Joshi *et al.* (2003) and Patil *et al.* (2014).

4.12.7 Hundred kernel weight (g)

The results revealed that among the fourteen genotypes for hundred kernel weight (g) three genotypes *viz.*, RHRG-1308, RHRG-1305 and Phule Bharati were grouped as average stable. Two genotypes, JL-501 and Phule Unnati were grouped as above average stable and therefore suitable for poor environment. However four genotypes *viz.*, TPG-41, SB-XI, RHRG-1189 and RHRG-1130 were

Table 4.19. Stability parameters of different genotypes for twelve characters in groundnut

Sr. No.	Genotypes	Number of immature pods/plant			Haulm yield/ plot(kg)			100 kernel weight (g)			Shelling (%)		
		x	bi	S ² di	x	Bi	S ² di	x	bi	S ² di	x	bi	S ² di
1	JL-501	6.78	1.576*	-0.680	4.34	0.998	-0.032	32.50	0.748*	-1.140	68.17	1.350	0.142
2	TAG-24	4.87	0.529*	-0.058	4.18	0.231	-0.020	29.08	1.225	-1.015	68.08	1.043	-0.187
3	Phule-6021	5.57	1.403*	-0.424	4.14	0.369*	-0.130	30.33	2.01*	-1.205	67.67	1.309	0.044
4	TPG-41	5.67	1.062*	-0.906	4.67	0.734	-0.103	45.17	0.398	6.190**	65.00	1.315	2.589**
5	Phule Bharati	6.52	0.825	-0.856	5.51	0.368	1.097**	33.75	0.874	-0.875	68.17	1.142	-0.088
6	Phule Unnati	6.95	1.192	-0.590	6.01	0.695	0.265	34.67	-.0.13*	-1.182	69.25	1.329	-0.171
7	SB-XI	5.27	0.609	1.389	5.43	1.526	0.001	28.58	1.447	6.960**	69.92	0.544	-0.020
8	RHRG-1335	6.33	1.035	1.309	5.10	1.854*	0.072	28.00	1.287	-0.710	67.33	1.234	0.276
9	RHRG-1142	5.53	0.876	0.799	4.96	1.784*	0.097	29.92	1.384	-0.522	67.75	0.182*	-0.188
10	RHRG-1308	6.73	1.264	-0.392	5.01	1.641*	-0.094	32.33	0.655	-1.084	68.00	1.146	-0.148
11	RHRG-1189	5.78	0.828	-0.003	5.03	1.203*	-0.172	28.92	1.175	4.280*	67.25	1.091	0.527*
12	RHRG-1192	6.45	1.302	-0.761	4.52	1.409	0.469*	29.75	1.148	-0.153	67.75	0.547	-0.133
13	RHRG-1130	5.05	0.733*	-0.896	4.22	0.953	-0.029	29.50	1.268	8.180**	67.58	1.575	0.712*
14	RHRG-1305	6.43	0.766	0.948	4.13	0.208	-0.003	32.25	0.508	0.912	67.83	0.212*	-0.070
	G. Mean	6.00			4.80			31.77			67.84		
	SE (bi)		0.53	0.22		4.34	-0.032		0.94	0.32		0.38	0.59

found to differ significantly from linear regression and hence they would be unstable. Varama and Manoharan (1993), Patra (1995), Sojitra and Pethni (1998) and Mahto and Mahto (2000) reported similar results as observed in present investigation.

4.12.8 Shelling (%)

For the shelling per cent six genotype *viz.*, Phule bharati, SB-XI, Phule Unnati, JL-501, TAG-24 and RHRG-1308 had high mean, non significant regression coefficient (bi) and non significant $S^2_{di} = 0$ and hence they were average stable and found suitable for wide range of environments. While the genotype RHRG-11305 shown above average stability and suitable for poor environments. However three genotypes *viz.*, TPG-41, RHRG-1189 and RHRG-1130 were found unstable as these genotypes deviated significantly from linear regression. Similar findings were recorded by Verma and Manoharan (1993), Patra (1995), Mahto and Mahto (2000), Venkataramana *et al.* (2000b) and Singh and Singh (2001).

4.12.9 Sound mature kernel

For the sound mature kernel the genotypes *viz.*, JL-501, Phule Bharati, RHRG-1308 and RHRG-1192 were grouped as average stable. The genotype Phule Unnati and RHRG-1189 were grouped as above average stable, while genotype RHRG-1142 shown below average stability. The genotypes *viz.*, Phule-6021, TPG-41 and RHRG-1130 were found unstable for sound mature kernel. Patra (1995), Chavan *et al.* (2009) and Patil *et al.* (2014) supported the above findings.

4.12.10 Oil content (%)

The results revealed that among the fourteen genotypes, six genotypes *viz.*, JL-501, Phule Bharati, Phule Unnati, RHRG-1189, RHRG-1142 and RHRG-1308 were grouped as average stable for oil content. While single genotype RHRG-1305 was grouped as above average stable and suitable for poor environment. However five genotypes *viz.*, TAG-41, Phule-6021, TPG-41, SB-XI and RHRG-1135 were found to be unstable. Present results are in accordance with those of Venkataramana *et al.* (2000b), Bentur *et al.* (2004), Patil *et al.* (2014) and Minde *et al.* (2017).

Table 4.20. Stability parameters of different genotypes for twelve characters in groundnut

Sr. No.	Genotypes	Sound mature kernel (%)			Oil content (%)			Protein content (%)			Pod yield/ plot(kg)		
		x	bi	S ² di	x	Bi	S ² di	x	bi	S ² di	x	bi	S ² di
1	JL-501	94.75	0.938	0.271	48.70	0.799	0.003	22.56	0.850	-0.005	1.445	0.979	-0.005
2	TAG-24	91.58	0.760	-0.052	47.78	-0.616	1.230**	23.12	0.695	0.016	1.483	0.926	-0.005
3	Phule-6021	92.50	0.915	1.30*	48.04	2.575	0.220**	22.46	0.28*	-0.010	1.300	0.908	0.043**
4	TPG-41	90.25	1.570	2.990**	46.03	-0.222	0.500**	22.12	0.927	0.241**	1.440	1.536	0.025**
5	Phule Bharati	94.08	1.017	-0.298	48.86	0.993	0.084	21.93	0.803	0.270**	2.132	0.255	0.006
6	Phule Unnati	94.58	-0.17*	-0.194	50.21	1.341	0.020	22.48	0.69*	-0.023	2.319	1.925*	0.000
7	SB-XI	92.83	0.795	-0.308	46.93	1.164	0.850**	22.59	1.030	0.037	1.110	0.497	-0.004
8	RHRG-1335	92.17	0.740	0.831	48.95	1.394	0.400**	22.43	1.216	0.053*	1.217	1.043	0.000
9	RHRG-1142	93.25	1.500*	-0.447	49.15	0.888	-0.005	21.63	1.667	-0.001	1.194	0.781	-0.002
10	RHRG-1308	93.42	1.253	0.441	49.83	1.299	0.009	22.18	0.924	0.398**	1.429	0.847	0.005
11	RHRG-1189	93.17	0.281*	0.228	48.67	1.103	0.039	22.03	0.331	0.213**	1.261	1.711	0.000
12	RHRG-1192	93.83	1.126	0.016	48.53	0.228	0.650**	22.48	1.181	0.011	1.332	1.066	-0.002
13	RHRG-1130	92.58	1.903	2.320**	47.48	2.595	0.046	21.47	1.069	0.059*	1.202	0.684	0.012*
14	RHRG-1305	93.25	1.364	2.020**	48.48	0.458*	-0.030	21.55	2.335	0.426**	1.139	0.842	0.004
	G. Mean	93.02			48.40			22.22			1.429		
	SE (bi)		0.61	0.44		0.33	0.85		0.22	0.532	0.059		0.35

4.12.11 Protein content (%)

Among the fourteen genotypes, four genotypes *viz.*, JL-501, TAG-24, SB-XI and RHRG-1192 were found to be average stable while two genotype *viz.*, Phule-6021 and Phule Unnati were suitable for poor environments. Seven genotypes *viz.*, TPG-41, Phule Bharati, RHRG-1335, RHRG-1308, RHRG-1189, RHRG-1130 and RHRG-1305 were found unadaptable for protein content. Bentur *et al.* (2004), Sreekala and Hemant Kumar (2009), Patil *et al.* (2014) and Minde *et al.* (2017) recorded the similar findings for protein per cent.

4.12.12 Pod yield per plot (g)

Total four genotype *viz.*, JL-501, TAG-24, Phule Bharti and RHRG-1308 were showed average stability for pod yield per plant, while the genotype Phule Unnati was showed as below average stable and well adapted to favourable environment. The three genotypes *viz.*, Phule-6021, TPG-41 and RHRG-1130 were found unstable while the genotypes *viz.*, SB-XI, RHRG-1335, RHRG-1142, RHRG-1189, RHRG-1192 and RHRG-1305 had non significant regression coefficient (bi) and non significant deviation from regression (S^2_{di}), however these genotypes produced low pod yield than population means. Therefore, these are not grouped as average stable. These genotypes had genes for stability and hence these genotypes may further use for hybridization. Previously Senapati and Roy (1991), Patra (1995), Mahto and Manto (2000), Viswanthan *et al.* (2001), Nazar *et al.* (2001), Aroglu *et al.* (2001), Gitanjali and Sharma (2005), Venkateshmurthy (2005), Nawaz (2009) and Chavan *et al.* (2009) reported the similar findings.

4.13 Classification of genotypes on the basis of their stability parameters for various characters

The genotypes found to be average stable for pod yield and yield contributing characters were JL-501, TAG-24, Phule-6021 and RHRG-1308 for days to 50 % flowering. For days to maturity (JL-501, TAG-24, Phule-6021), number of mature pods per plant (JL-501, Phule Bharati, Phule Unnati, RHRG-1308 and RHRG-1305), hundred kernel weight (Phule Bharati, RHRG-1308 and RHRG-1305). Shelling percent JL-501, TAG-24, Phule Bharati, Phule Unnati, SB-XI and RHRG-1308),

sound mature kernel (JL-501, Phule Bharati, RHRG-1308 and RHRG-1192), oil content percent (JL-501, Phule Bharati, Phule Unnati, RHRG-1142 and RHRG-1308, RHRG-1189), protein content (JL-501, TAG-24, SB-XI and RHRG-1192), dry pod yield per plot (JL-501, TAG-24, Phule Bharati and RHRG-1308). Senapati and Roy (1991), Verma and Manoharan (1993), Patra (1995), Mahto and Mahto (2000), Aroglu *et al.* (2001), Naazar *et al.* (2001), Viswanathan (2001), Nageswara Rao (2002), Gitanjali and Sharma (2005), Venkateshmurthy (2005), Nawaz *et al.* (2009), Chavan *et al.* (2009) and Minde *et al.* (2017) recorded the supportive finding.

The genotypes grouped as below average stability and suitable for favourable environments were RHRG-1130 for days to maturity, JL-501, TAG-24 and TPG-41 for number of branches per plant, RHRG-1192 for number of matured pods per plant, RHRG-1135, RHRG-1142, RHRG-1308, RHRG-1189 for haulm yield per plot, Phule-6021 for hundred kernel weight, RHRG-1142 for sound mature kernel and Phule Unnati for dry pod yield per plot. Mothilal *et al.* (2000a,b), Gitanjali and Sharma (2005), Chavan *et al.* (2009), Thaware (2009) and Minde *et al.* (2017) had also been reported the similar findings as above.

The genotypes grouped as above average stability and suitable for unfavourable (poor) environment were SB-XI and RHRG-1192 for days to 50% flowering, SB-XI for days to maturity, JL-501 and Phule Unnati for hundred kernel weight, RHRG-1142, RHRG-1305 for shelling percentage, Phule Unnati, RHRG-1189 for sound mature kernel, RHRG-1305 for oil content and Phule-6021 and Phule Unnati for protein content, which was confirmed by the earlier findings of Mothilal *et al.* (2000a,b), Gitanjali and Sharma (2005), Thaware (2009), Patil *et al.* (2014) and Minde *et al.* (2017).

Table 4.21. Classification of genotypes on the basis of their stability parameters for various characters

Sr. No.	Characters	Group-I Ideal genotypes with general adaptability	Group-II		Group-III Unstable or unpredictable behaviour	Group-IV Stable but mean is low for traits other than flowering and maturity
			Specific adaptability for			
			Favourable (better) environment	Unfavourable (poor) environment.		
1	Days to 50 % flowering	JL-501, TAG-24, Phule-6021	-	SB-XI, RHRG-1192	TPG-41, Phule Bharati, Phule Unnati, RHRG-1335, RHRG-1142, RHRG-1189, RHRG-1130	RHRG-1308
2	Days to maturity	JL-501, TAG-24, Phule-6021	RHRG-1130	SB-XI,	TPG-41, Phule Bharati, RHRG-1335	Phule Unnati, RHRG-1142, RHRG-1308, RHRG-1130
3	Number of branches/plant	Phule Unnati, RHRG-1335, Phule Bharati	JL-501, TAG-24, TPG-41	-	Phule-6021, RHRG-1142, RHRG-1192	SB-XI, RHRG1189, RHRG-1130
4	Number of mature pods/plant	JL-501, Phule Bharati, Phule Unnati, RHRG-1308, RHRG-1305	RHRG-1192	-	Phule-6021, SB-XI, RHRG-1142, RHRG-1130	TAG-24, TPG-41, RHRG-1335, RHRG-1189
5	Number of immature pods/plant	SB-XI, RHRG-1189, RHRG-1142	Phule-6021, TPG-41	TAG-24	RHRG-1335, RHRG-1142, RHRG-1305,	TPG-41, Phule Bharati, Phule Unnati, RHRG-1335, RHRG-1308, RHRG-1192
6	Haulm yield/plot (kg)	Phule Unnati, SB-XI	RHRG-1335, RHRG-1142, RHRG-1308, RHRG-1189	-	Phule Bharati, RHRG-1192	JL-501, TAG-24, Phule-6021, TPG-41, RHRG-1130, RHRG-1305
7	100 kernel weight (g)	Phule Bharati, RHRG-1308, RHRG-1305	Phule-6021	JL-501, Phule Unnati	TPG-41, SB-XI, RHRG-1189, RHRG-1130	TPG-41, RHRG-1335, RHRG-1142, RHRG-1192.

Table 4.22. Classification of genotypes on the basis of their stability parameters for various characters

Sr. No.	Characters	Group-I	Group-II		Group-III and Group-IV	Stable but mean is low for traits other than flowering and maturity
		Ideal genotypes with general adaptability	Specific adaptability for		Unstable or unpredictable behaviour	
			Favourable (better) environment	Unfavourable (poor) environment.		
8	Shelling percent	JL-501TAG-24, Phule Bharati, Phule Unnati, SB-XI, RHRG-1308	-	RHRG-1142, RHRG-1305	TPG-41, RHRG-1189, RHRG-1130	Phule-6021, RHRG-1335, RHRG-1142, RHRG-1192
9	Sound mature kernel (%)	JL-501, Phule Bharati, RHRG-1308, RHRG-1192	RHRG-1142	Phule Unnati, RHRG-1189	Phule-6021, TPG-41, RHRG-1130, RHRG-1305	SB-XI,
10	Oil content (%)	JL-501, Phule Bharati, Phule Unnati, RHRG-1142, RHRG-1308, RHRG-1189,	-	RHRG-1305	TAG-24, Phule-6021, TPG-41, SB-XI, RHRG-1135	RHRG-1192, RHRG-1130
11	Protein content (%)	JL-501, TAG-24, SB-XI, RHRG-1192	-	Phule-6021, Phule Unnati	TPG-41, Phule Bharati, RHRG-1335, RHRG-1308, RHRG-1189, RHRG-1130, RHRG-1305	RHRG-1142
12	Dry pod yield/plot(kg)	JL-501, TAG-24, Phule Bharati, RHRG-1308	Phule Unnati	-	Phule-6021, TPG-41, RHRG-1130	SB-XI, RHRG-1335, RHRG-1142, RHRG-1189, RHRG-1192, RHRG-1305

5. SUMMARY AND CONCLUSION

The present investigation on “Genetic variability and G x E interaction studies in groundnut (*Arachis hypogaea* L.)” conducted during summer 2018 to study variability, heritability and genetic advance, correlation, path analysis, diversity among eight crosses of groundnut. Each cross had five progenies. The experiment was laid out in compact family block design with two replications.

The observations were recorded on twelve characters *viz.*, days to 50 % flowering, days to maturity, number of branches per plant, number of mature pods per plant, number of immature pods per plant, haulm yield per plot (kg), shelling %, hundred kernel weight (g), sound mature kernel (%), oil content (%), protein content (%) and pod yield per plot (kg).

Analysis of variance

Analysis of variance revealed highly significant differences among the progenies of eight crosses for the characters studied, indicating appreciable amount of variability among the progenies for the characters studied.

5.1 Variability parameters

Adequate variability was observed among the genotypes under study. Further, wide range was observed for number of mature pods per plant, dry pod yield per plant and number of branches per plant.

The estimation for phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. The number of branches per plant recorded the highest estimate of GCV and PCV followed by number of immature pods per plant, number of mature pods per plant and dry pod yield per plant. The moderate estimates of GCV and PCV were observed for haulm yield per plot and hundred kernel weight.

In present investigation, the characters, number of branches per plant, number of immature pods per plant, number of mature pods per plant, hundred kernel weight and dry pod yield per plot expressed high estimates of heritability (broad sense) accompanied with high genetic advance and per cent of mean indicating that

these traits were predominantly governed by additive gene action and could be improved through simple selection only.

5.2 Correlation coefficient

In present study, it was observed that dry pod yield per plot recorded significant positive correlation with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling %, sound mature kernel and protein content at both genotypic and phenotypic levels, while characters immature pods per plant and oil content were negatively associated with dry pod yield per plot.

5.3 Path coefficient analysis

Path analysis based on genotypic correlation revealed that number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling %, sound mature kernel showed moderate to high positive direct effects on dry pod yield per plot, while days to 50 % flowering, number of immature pods per plant, halum yield per plot and protein content had negligible and negative direct effect on dry pod yield per plot.

5.4 Genetic diversity analysis

Total forty genotypes were grouped in seven clusters. Cluster I with 12 genotypes emerged as the largest cluster followed by cluster V with 10 genotypes and cluster II and IV with 6 genotypes, cluster VI with 4 genotypes. Remaining two clusters (III and VII) were monogenotypic.

5.5 Intra and inter cluster distance

Cluster V exhibited maximum intra cluster distance *i.e.* ($D=14.37$), followed by cluster VI, cluster I, cluster II and cluster IV. Being monogenotypic, remaining clusters showed no intra cluster distance. Maximum inter cluster distance was found between cluster II and V, followed by V and VII and IV and VI.

The cluster means revealed wide range of variability for most of the characters. It was observed that cluster II had the lowest cluster mean for days to 50% flowering and maturity. Cluster V had the highest cluster mean for number of branches per plant, number of mature pods per plant and recorded also lowest mean

for number of immature pods per plant, highest shelling %, sound mature kernel (%) and dry pod yield per plant. Cluster VII had the highest mean for haulm yield per plot. Cluster IV had the highest mean for hundred kernel weight. Cluster III had the highest mean for traits oil and protein content.

5.6 Percent contribution of various characters for divergence

The character dry pod yield per plot contributed the highest for divergence and was followed by haulm yield per plot, protein content, days to maturity, sound mature kernel, shelling %, hundred kernel weight, oil content, number of branches per plant, However, the contributions of number of matured pods per plant, days to 50 % flowering and number of immature pods per plant were of very low magnitude.

On the basis of *per se* performance, inter cluster distance and cluster mean, the six progenies of different crosses *viz.*, C1-P3 (TAG-24 x Phule Unnati), C2-P4 (Phule Unnati x TPG-41), C3-P-4 (WRGS-15 x RHRG-8808), C4-P3 (Phule-6021 x ICGV-00350), C6-P3 (Phule Unnati x SB-XI) and C8-P2 (WRGS-15 x SB-XI) were indentified for further advancement of generation and use in crossing program.

5.7 G x E interaction and stability parameters

- i. The values of mean squares due to genotypes were found significant for all the characters indicating existence of considerable differences among genotypes in each individual environment and pooled over the environments. Similarly, mean sum of squares due to environments were also significant for all the characters which indicated that the predictable environment had difference.
- ii. The mean squares due to genotype x environmental interaction were significant for all characters which revealed differential performance of genotype to the array of environments for all the characters.
- iii. The value of mean squares due to E + (G x E) were significant for all the characters which suggested that genotypes behaved differentially for their performance with the change of environment and thus satisfy the requirement of stability analysis.
- iv. The higher magnitude of mean squares due to environment (linear) as

compared to genotypes x environments (linear) interaction indicated that linear response of environments accounted for the major part of total variation for all the characters. The significance and preponderance of linear component of G x E interaction in comparison to non linear component (pooled deviation) for all the characters revealed that performance of the genotypes may be predicted in varied environment.

- v. Non linear component of G x E interaction was also significant for all the characters indicating the importance of non linear component in determination of interaction of genotypes with environments. The genotypes JL-501, TAG-24, Phule Bharati and RHRG-1308 were found average stable for dry pod yield per plot and their stability for dry pod yield was because of stability for yield contributing characters (Table 4.17). JL-501 was found average stable for days to 50 % flowering, days to maturity, number of mature pods per plant, shelling percentage, sound mature kernel (%), oil content and protein content; TAG-24 for days to maturity, days to 50% flowering, shelling percent and protein content. Similarly, Phule Bharati was average stable for the characters number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling per cent, sound mature kernel (%) and oil content and RHRG-1308, besides dry pod yield per plot was also found average stable for number of mature pods per plant, hundred kernel weight, shelling per cent, sound mature kernel (%) and oil content (%).

Phule Unnati was found stable in favourable environments for dry pod yield per plot and its stability for pod yield was because of average stability for number of branches per plant, number of mature pods per plant, halum yield per plot, shelling per cent and oil content.

5.8 Stability analysis estimation of environmental index

The present study indicated that summer sowing date E₁ (15th February) was most favourable followed by E₃ *kharif* (15th July) for expression of yield and yield contributing traits in groundnut.

Conclusions

1. Analysis of variance revealed highly significant differences among the F₅ progenies of eight crosses for all the characters studied, indicating appreciable amount of variability among the genotypes for the characters studied.
2. The characters number of branches per plant, number of immature pods per plant, number of mature pods per plant, hundred kernel weight and dry pod yield per plot expressed high estimates of heritability (b.s.) accompanied with high genetic advance and percent of mean can be improved through simple selection.
3. The dry pod yield per plot had significant positive association with days to maturity, number of branches per plant, number of mature pods per plant, hundred kernel weight, shelling per cent, sound mature kernel and protein content at both genotypic and phenotypic levels.
4. Path analysis revealed that number of branches per plant, hundred kernel weight, shelling per cent and sound mature kernel had moderate to high possible direct effect on dry pod yield. Hence, more emphasizes given on these characters while selection for improvement of pod yield in groundnut.
5. The total forty genotypes were grouped into seven clusters. Maximum inter cluster distance was found between cluster II and V and V and VII. Cluster V had the highest cluster mean for majority of characters including dry pod yield per plot. The dry pod yield was contributed highest for genetic divergence followed by haulm yield, protein content, days to maturity, sound mature kernel and shelling per cent.
6. On the basis of *per se* performance, inter cluster distance and cluster mean the progenies *viz.*, C1-P3 (TAG-24 x Phule Unnati), C2-P4 (Phule Unnati x TPG-41), C3-P4 (WRGS-15 x RHRG-8808), C4-P3 (Phule-6021 x ICGV-00350), C6-P3 (Phule Unnati x SB-XI) and C8-P2 (WRGS-15 x SB-XI) are suggested for used further in breeding programme for genetic improvement in groundnut.

7. Stability analysis indicated that the environment E₁ (15th February) for summer and E₃ (15th July) for *kharif* season found to be the most suitable for better expression of yield and yield contributing characters in groundnut.
8. The significance of both linear and non-linear components for various characters suggested importance of both the components for the G x E interaction, however greater magnitude of linear component was observed, therefore performance of genotypes would be predictable in varied environments.
9. The different genotypes behaved differently across the environments for various characters.
10. None of the genotypes was found stable for all the characters in any specific environment. However the genotypes Phule Bharati, TAG-24, JL-501 and RHRG-1308 were found average stable for dry pod yield and yield contributing traits.

Future Plan

1. Regorrou selection could be effected to have good genotype for both season in F₆ progenies of groundnut.
2. After multilocation testing over the years and seasons, the genotypes Phule Bharati, TAG-24, JL-501 and RHRH-1308 could be recommended for commercial cultivation in both *kharif* and summer season.

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7. VITAE

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DOCTOR OF PHILOSOPHY (AGRICULTURE)

**IN
AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**

2019

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