GENETIC DIVERSITY IN F4 GENERATION LINES OF GROUNDNUT (*Arachis hypogaea L.*)

by

Mr. Atak Sanjay Madan
(Reg. No. 12/036)

A Thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
MAHARASHTRA (INDIA)

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE
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DEPARTMENT OF AGRICULTURAL BOTANY
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MAHATMA PHULE KRISHI VIDYAPEETH,
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2014

CANDIDATE'S DECLARATION

I hereby declare that this thesis or a part

There of has not been submitted

by me or any other person

to any other University

or Institute for

a Degree or

Diploma.

Place : MPKV, Rahuri

Date : / / 2014 **(Atak S.M)**

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Groundnut Breeder
AICRP on Groundnut,
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CERTIFICATE

This is to certify that the thesis entitled, "**GENETIC DIVERSITY IN F4 GENERATION LINES OF GROUNDNUT (*Arachis hypogaea* L.)**", submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr. ATAK SANJAY MADAN,** under my guidance and supervision and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : MPKV, Rahuri **(V.L. Amolic)**

Date : / /2014.

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Post Graduate Institute,
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Rahuri - 413 722, Dist. Ahmednagar,
Maharashtra State (India).

CERTIFICATE

This is to certify that the thesis entitled, "**GENETIC DIVERSITY IN F4 GENERATION LINES OF GROUNDNUT (*Arachis hypogaea L.*)",** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the results of a piece of *bona fide* research work carried out by **Mr. ATAK SANJAY MADAN,** under the guidance and supervision of **Dr. V.L AMOLIC,** Groundnut Breeder, AICRP on Groundnut, M.P.K.V., Rahuri, and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : MPKV, Rahuri **(B.R. Ulmek)**

Date : / /2014.

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Place : M.P.K.V., Rahuri (Sanjay Atak)

Date : / /2014

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LIST OF ABBREVIATIONS

BS	:	Broad sense
cm	:	Centimeter
C.D.	:	Critical difference
C.V.	:	Coefficient of variation
Cov.	:	Covaraince
d.f.	:	Degree 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)
$\sum$	:	Summation
σ^2	:	Variance
σ	:	Standard deviation
/	:	Per
%	:	Per cent

ABSTRACT

GENETIC DIVERSITY IN F4 GENERATION LINES OF GROUNDNUT (*Arachis hypogaea* L.)

by

Mr. ATAK SANJAY MADAN

A candidate for the degree
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2014

Research Guide	: Dr. V.L. Amolic
Major discipline	: Genetics and Plant Breeding

The present investigation entitled “Genetic diversity in F4 generation lines of groundnut (*Arachis hypogaea* L.)” was undertaken to estimate the genetic variability and genetic divergence in thirty lines and one check of summer groundnut. Total 31 genotypes were evaluated during summer, 2013 season 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.). Observations were recorded on the traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of pegs per plants, number of mature pods per plant, peg to pod ratio, dry haulm yield per plant, number of immature pods per plant, dry pod yield per plant, hundred kernel weight, shelling percentage, harvest index,

oil content, protein content, sound mature kernel, photosynthetic rate, leaf temperature, total chlorophyll percentage, specific leaf area.

It was observed that the estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the characters.

Number of immature pods per plant recorded the highest estimate for GCV followed by number of mature pods per plant, number of pegs per plant, dry haulm yield per plant, dry pod yield per plant, plant height. The highest value of PCV were observed for number of immature pods per plant followed by number of mature pods per plant, number of pegs per plant, dry pod yield per plant, dry haulm yield per plant, plant height, harvest index. Low GCV and PCV value were recorded by character shelling percentage, sound of mature kernel and leaf temperature. Looking to the difference between GCV and PCV magnitudes, it was observed that all the characters except peg to pod ratio and no. of branches per plant showed low magnitudal difference between GCV and PCV estimates.

The treatment differences were statistically significant for majority of the characters indicated the presence of good amount of variability. The character number of pegs per plant showed 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 kernal weight, total chlorophyll, 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.

The range of D^2 values indicated adequate diversity between genotypes. On the basis of D values, all the thirty one genotypes were grouped into six clusters with substantial genetic divergence between them. Cluster I with 14 genotypes emerged as the largest cluster followed by cluster III with 8 genotypes, cluster II with 5 genotypes and cluster IV with 2 genotypes. Remaining four clusters were solitary. The maximum inter cluster distance was found between cluster II and cluster VI, while the minimum inter cluster distance was found between cluster I and cluster IV. On the basis of cluster means, inter cluster distances, and *per se* performance, eight genotypes viz., Phule Unnati, RHRG-1130, RHRG-1137, RHRG-1127, RHRG-1106, RHRG-1110, RHRG-1128 and RHRG-1118 have been suggested for future hybridization programme.

1. INTRODUCTION

Groundnut (*Arachis hypogaea L.*) is a major oilseed crop in India. The crop accounts for near about 45.00 per cent of total area under oilseed and 55.00 per cent of the oilseed produced in the country. Groundnut seeds contain about 50.00 per cent edible oil and 25.00 per cent protein. The haulms are used as valuable nutritious fodder. Groundnut oil cake is an important cattle feed and a good soil amendment.

Major groundnut producing countries of the world are China, USA, India, Senegal, Brazil and West Africa. The India is second in production of groundnut after China. The total area in India under groundnut cultivation was 5.19 million hectares in the year 2012-13 with production of 6.96 million tonnes and productivity of 1341 kilogram per hectare (Anonymous, 2012).

In Maharashtra, total area under groundnut cultivation was 0.32 million hectare with production 0.35 million tonnes and productivity of 1188 kg per hectare during year 2012-13 (Table 1.)

Table 1.1. Area, Production and Productivity of Groundnut in major producing states (2011-12)

State	Area (M.ha.)	Production (M.T.)	Productivity (kg/ha.)
Gujarat	1.54	2.71	1563
Andhra Pradesh	1.28	0.84	361
Tamil Nadu	0.46	1.06	2202
Rajasthan	0.41	0.80	1931

Karnataka	0.68	0.48	650
Maharashtra	0.30	0.35	1080
Madhya Pradesh	0.19	0.34	1618
Orissa	0.071	0.07	830
Uttar Pradesh	0.09	0.09	1000
Others	0.11	0.12	---
All India	5.19	6.96	1188

(Source : Ministry of agriculture, Govt. of India, 2013 and Department of Economics and Statistics, Dept. of Agriculture and Cooperation, 2013).

The word groundnut (*Arachis hypogaea* Linn.) is derived from the Greek word "Arachis" meaning legume and "hypogaea" meaning below ground. It is commonly known as peanut, monkeynut and goobernut. Groundnut is self pollinated, tetraploid with chromosome number 2n=40. The genus *Arachis* is a member of family Fabaceae (synonym: Leguminoseae), subfamily papillionoidae, tribe Aeschynomeneae and subtribe stylosanthinae. It belongs to the section *Arachis* and series amphiploidies and the family Fabaceae (Gregory *et al.,* 1980). The species *Arachis hypogaea* consists of two subspecies, *Hypogaea* sp. and *Fastigiata* sp. Each subspecies has two botanical varieties. Four cultivated types of groundnut according to Krapovickas and Rigoni (1957) are;

1. *Arachis hypogaea* Linn.
2. *Arachis hirsute* Kohler.
3. *Arachis fastigiata* Waldron.
4. *Arachis fastigiata vulgaris* Harz

Cultivated groundnut can be botanically classified into two subspecies differing in branching pattern viz., subspecies *hypogaea* with alternate branching and subspecies

fastigiata with sequential branching. Each subspecies is again divided into two botanical varieties, *subsp. Hypogaea* into variety *hypogaea* (Virginia) and *var. hirsuta*; and subsp. *Fastigiata* into *var. fastigiata* (Valencia), *var. vulgaris* (Spanish), *var.* peruviana, and *var.* aequatoriana in trade. The bold seeded types are referred as *Virginia*, the small seeded as Spanish and a third type runner is also recognized.

Groundnut belongs to C3 plant, it needs good sunshine and high temperature to produce more pods.

Therefore summer is the ideal season for groundnut cultivation wherever irrigation facilities are available. The average total dry matter produced per plant in bunch groundnut at harvest is 25.7 g in summer season (Ong, 1986).

Diseases are major constraints to groundnut production throughout the country during *kharif.* However, during *Summer* attack of diseases and pests are very less. In summer, bud necrosis disease is the major threat.

Some of the reasons for low productivity of groundnut in the country are,

1. Optimum sowing time is not followed.
2. Use of uncertified seeds.
3. Recommended dose of fertilizer is not applied at proper time.
4. Irrigation schedule is not followed properly.
5. Foliar diseases.

The use of uncertified seed and local types is one of the causes of poor groundnut yield in India. Groundnut needs

good sunshine and high temperature to produce more pods (Cox, 1979 and Ong, 1986) leading to higher productivity. Now, looking to the most favourable condition and high productivity of summer crop, it is essential to develop a genotype with fairly high yield potential than the existing ones to boost up productivity of groundnut substantially. The primary aim of plant breeder is to evolve the variety which will be superior to the existing one in respect of yield and quality. This may be achieved by selecting the promising types from naturally existing variation or by hybridization followed by selection of the good recombinants.

In formulating any hybridization programme, it is prerequisite to have genotype with higher yield potential i.e. high *per se* performance. In groundnut with this it is also important to have divergent parents with good performance for yield as well as other quantitative characters for hybridization, to obtain desirable segregants through selection in advanced generations. It is already proved in many crops that by using divergent parents, heterotic hybrids can be obtained than those between closely related. The Mahalanobis D^2 statistics is powerful tool to assess genetic diversity in large number of lines and helps in identification of genetic divergent parents for their exploitation in hybridization programme.

The magnitude of variability and the knowledge of extent to which desirable characters are heritable is a pre-requisite for crop improvement. The inbuilt variability in the breeding material is very important for 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 amounts of heritable and non-heritable variability exhibited by yield contributing characters.

The present study was undertaken to access variability and genetic diversity in a set of F_4 generation groundnut genotypes irrespective of their growth habit for yield and other component characters.

Keeping these things in view the present investigation was planned and executed with the following objectives.

1. To study genetic variability for morpho-physiological traits in F_4 generation groundnut genotypes.
2. To group different genotypes on the basis of their genetic divergence.

2. REVIEW OF LITERATURE

Attempts have been made to review the published literature on variability and diversity for important economic characters related to yield in groundnut. The review of literature is presented below under different subheadings.

2.1 Variability in groundnut

2.2 Genetic divergence in groundnut

2.1 Variability in groundnut

Reddy (1995) reported genetic variation and heritability derived from data on 12 yield-related traits in 48 spanish bunch groundnut (*Arachis hypogaea*) genotypes grown at Tirupati during *kharif* 1990.

Reddy *et al.* (1995) estimated heritability values for 12 yield components using F_3 and F_5 progenies, involving parents. Heritability values varied between generations, but were consistently high for secondary branches per plant, plant height and shelling percentage. The influence of environment was evident for number of pods, number of mature pods and pod yield per plant in the F_3 and F_4 generations, as these characters recorded negligible heritability estimates.

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.

Gowda *et al.* (1996) studied variability available for all selection, the nature and magnitude of the association with productivity and pod morphology. High levels of variability were recorded for leaf area affected by the disease, pod yield and pod number. High productivity was associated with larger pods and thick shells and low disease resistance. The frequency of desirable recombinants for pod yield, shelling percentage, sound mature kernel percentage and shell thickness was very low.

Singh *et al.* (1996) in seven selections of F_4 generation lines derived from three crosses in HPS groundnut observed an exploitable amount of genetic variability for days to first flowering, length of main axis, mature pods, 100 seed weight, shelling percentage and dry pod yield.

Khader and Gowda (1997) studied three-way back and double crosses of Virginia and Valencia bunch type varieties of groundnut with RMPL and P-1393516 and they were evaluated in the S_1 during *kharif* 1991 for yield components. Variability was greater between families than within families for most of the characters. Family selection in S_1 was recommended.

Naik and Nadaf (1997) generated variability for various quantitative characters in *A. hypogaea*. Dharwad Early Runner (DER), a growth habit variant, was treated with ethyl methane sulphonate (EMS) and resulting six mutant lines were further treated with EMS (0.5 %). Seed of treated plants were grown for 2 generations during 1993-95 and evaluated for five

yield components. Out of seven genotypes treated, DER, 124-5 and 225-1 were the most sensitive to treatment. Number of pods per plant and 100 seed weight were the most sensitive yield components to mutagenic treatment.

Chandran *et al.* (1998) collected 23 samples of *Arachis hypogaea* cv. TMV-2, released in 1940, from Karnataka, Andhra Pradesh, Tamil Nadu and Kerala and evaluated at Junagadh during 1994-95. Variations were found mainly in branching pattern, stem hairiness and leaflet hairiness, while most other characters, including seed storage proteins, had maintained their homogeneity.

Jayalakshmi *et al.* (1998) studied genotypic and phenotypic coefficients of variation, heritability and genetic advance to specific leaf area, total dry matter, pod weight per plant and harvest index in seven F_4 progenies in each of eight groundnut crosses grown during *rabi* 1996-97 at Tirupati. ICGV 86031 x JL-24 was the best for harvest index.

In twenty-seven M_7 groundnut mutants along with parent (AK-12-24) and two checks, Ramesh Kumar *et al.* (1998) observed high genotypic and phenotypic coefficient of variation for length of main axis, number of kernels per pod, kernel yield per plant and oil yield per plant. However, Islam and Rasul (1998) reported high magnitude of GCV for pods per plant and seed yield.

Khurram *et al.* (1998) studied 12 elite genotypes of groundnut in 1993-94. Estimates of variability were worked out for ten characters. The differences among the genotypes were

significant for all the characters studied except for oil content where the differences were non-significant.

Salara and Gowda (1998) studied sufficient variability existed in the crosses for selection to be effective for various characters. Pod yield and pod number exhibited high coefficient of variation values and genetic advance compared to test weight, shelling percentage and sound mature kernel percentage. Germination percentage exhibited the maximum variability.

Vasanthi *et al.* (1998) studied interrelationships among yield and its attributes and late leaf spot sensitivity in 11 elite lines and three varieties. A significant and positive association of shelling percentage and haulm weight per plant was reported.

Yadav *et al.* (1998) derived information on genetic variability, heritability and genetic advance from the data on seven yield and quality related traits in 34 strains/varieties of Spanish bunch groundnut (*Arachis hypogaea*) grown at Kanpur. High genotypic and phenotypic coefficients of variability were observed for pod yield and 100 pod weight. Heritability was high for all the characters under study. Genetic advance was highest for pod yield per plot followed by 100 pod weight and 100 kernel weight.

Rudraswamy *et al.* (1999) derived information on genetic variability, heritability and inbreeding depression from data on parental, F_1, F_2 and F_3 generations of six crosses of groundnut, grown at Banglore during *kharif* 1989. For number of secondary branches, number of immature pods, pod yield per

plant and shelling percentage, the genetic advance was moderate because of high heritability and variability in some of the crosses. None of the other characters in any cross showed substantial genetic advance, pod yield and other characters showed moderate to high genetic advance.

Singh and Singh (1999) derived information on heritability and genetic advance from data on high yield components in 44 lines grown during *kharif* 1994, 1995 and 1996. High values for heritability (7.80 %) were shown by days to maturity, plant height, primary branches per plant, pods per plant, pod weight per plant, shelling percentage and 100 kernel weight.

Gimenes *et al.* (2000) studied genetic variation and phylogenetic relationship based on RAPD analysis in section caulorrhizae, genus, Arachis (Leguminoseae). They studied many new accessions of the two species (*Arachis repens* and *A. pintoi*) and found that these accessions harbour significant genetic variability beyond that available in the few older accessions, previously available. Therefore, these new accession need to be conserved, documented and considered in terms of their potential for crop improvement and direct commercial use.

Kale and Murty (2000) by crossing a selection TG-19 having large pods low yield and dormancy with high yielding cultivars TAG-24 and TG-26, true breeding selection with large kernels, designated as TGLPS-1-8 were established in F_5 generation. For four seasons, they showed superior yield over the large kernel checks, TKG-19A and BAU-13. Among the eight

selections, TGRPS-2, 3 and 7 were found to have desirable traits such as early maturity, high yield and large kernels (> 80 g 100-kernel weight) and lacked dormancy. Due to lower oil content, they may suit for table purpose.

The findings of Prakash *et al.* (2000) in 91 genotypes of spreading groundnut for eight characters revealed a broad range of phenotypic variability for all characters except for days to 50 per cent flowering. GCV ranged from 3.68 (oil percentage) to 18.72 (pods per plant). The highest PCV (31.13) and GCV (29.20) were noticed for yield per plant followed by pods per plant, while Ganeshan and Sudhakar (1995) reported high PCV and GCV for pods per plant followed by primary branches. This difference between PCV and GCV was minimum (0.08) for oil percentage, suggesting that this trait was least affected by the environment. This was supported by very high value of heritability (95.77 %) for the character. The plant height, on the other hand, exhibited high gap (6.04) between PCV and GCV indicating role of high environmental influence on the character expression.

Shoba *et al.* (2009) made crosses to develop a foliar disease resistant groundnut lines with acceptable pod and kernel traits using TMV 2 and three foliar disease resistant parents. Three F_2 cross derivatives and their four parents were used to study their mean performance, genetic variability, heritability and genetic advance as percentage of mean for yield and contributing characters. Among the crosses, TMV2 x COG0437 had higher mean performance for all the characters followed by

TMV2 x COG 438. Higher PCV and GCV values were also recorded by this cross. The cross TMV2 x COG0437 had high heritability and high to moderate GAM for most of characters followed by TMV2 x COG0438. Hence, based on mean and variability parameters, TMV2 x COG437 is adjudged as best cross combination for further selection programme to evolve a promising progeny.

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.

Korat *et al.* (2009) evaluated eighty diverse genotypes of bunch groundnut during summer 2006 for genetic parameters *viz.*, variability, heritability and genetic advance. The estimates of PCV and GCV were high for number of secondary branches per plant and number of aerial pegs per plant. High heritability along with high genetic advance as per cent of mean was observed for number of secondary branches per plant and number of aerial

pegs per plant indicating that these traits are mainly governed by additive gene action and responsive to selection for further improvement of these traits.

Malave (2009) estimated the genetic variability, correlation between dry pod yield and other yield contributing characters and genetic divergence on one hundred germplasm lines and two checks of summer groundnut.

Cholin *et al. (*2010) studied that the groundnut (*Arachis hypogaea* L.) is the world's third most important source of oil and fourth most important source of vegetable protein. Oil content, protein content and fatty acid composition (O/L ratio) are the most important quality attributes of groundnut. A mapping population segregating for these traits was evaluated for genetic variability and correlation among the traits. The population exhibited significant variation among the genotypes, seasons and G x E interaction. Moderate magnitude of variability followed by higher heritability was observed for most of the quality traits. Negative correlation between oil and protein content, oleic and linoleic acid indicated their antagonistic nature. All the eight fatty acids were correlated with each other either positively or negatively. Superior RILs were identified for higher protein content, oil content, oleic acid and O/L ratio from the population.

Aghav (2010) evaluated fifty five genotypes of summer groundnut for variability, path analysis and genetic diversity during summer 2010, at Rahuri. 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 showed highest heritability followed by harvest index, oil content, dry pod yield and fresh pod yield per plant. The number of mature pods showed highest genetic advance, while other characters recorded moderate genetic advance.

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 offer an opportunity to further evolve the promising groundnut varieties to boost both the seed and oil production in the country.

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 and five checks of summer groundnut.

Dhage (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 and one checks(phule Unnati) of summer groundnut.

2.2 Genetic divergence in groundnut

Bansal and Satija (1992) analysed the data on seven yield related traits in 90 exotic and indigenous genotypes of groundnut, including 30 each of bunch, spreading and semi-spreading growth habits, grown in four environments at Ludhiana. Significant genetic diversity was observed among these genotypes and it was suggested that genotypes with different growth habits had different constitutions.

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 Nadaf *et 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.

Mane (1997) evaluated twenty seven genotypes each of Spanish and Virginia bunch types from different sources for genetic divergence in groundnut. He reported highly significant differences among the genotypes for individual characters and the range of D^2 value indicated considerable amount of genetic diversity among the strains studied.

Nayak and Patra (1997) recorded data on 18 characters in 128 *Arachis hypogaea* genotypes belonging to Spanish, Valencia and Virginia bunch. Analysis of variance indicated significant differences among genotypes for most characters except root nodules per plant. D^2 clustering pattern produced 15 clusters irrespective of geographic origin and botanical types.

Johan Joel and Mylsamy (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.

Bera and Das (1999) grouped 28 genotypes of groundnut into five clusters. Based on clustering pattern, they reported that genetic diversity among the genotypes was not always related with their place of acclimatization. They also reported maximum genetic divergence between cluster III and IV

at Midnapur and between cluster II and V at Purulia confirming that environment plays a major role in shifting a genotype from one cluster to another. The genotype PI-314817 of cluster I was the most stable and diverse.

Ramesh Kumar *et al.* (1999) studied 21 M_7 generation mutant cultures of groundnut alongwith 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.

Chavan (2002) using D^2 statistics of 35 HPS genotypes revealed the presence of considerable amount of genetic diversity. All these 35 genotypes were grouped into nine clusters, in which cluster I was the largest consisting 13 genotypes. The maximum intra-cluster distance was observed for cluster VII followed by cluster VI and V, suggesting that genotypes present in these clusters might have different genetic architecture. Whereas, maximum inter-cluster distance was observed between cluster IX and VII, followed by cluster VIII and VI and cluster IX and VII, indicating wide divergence among these clusters. The result of present investigation did not show any relation between genetic diversity and geographical diversity.

Sheikh (2002) observed considerable amount of genetic diversity while studying fifty groundnut germplams during summer 2002 at Rahuri. The D^2 values ranged between

63.52 and 1331.96 exhibiting good amount of diversity. Fifty genotypes were grouped into twelve clusters. Cluster I was the largest cluster while cluster IX, X, XI, and XII were mono-genotypic. The following genotypes were suggested for tentative breeding programme based on diverse studies, ICG-116, ICG-760, ICG-3417, ICG-42, ICG-3148 and ICG-1088.

Mane (2004) 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.

Lakshmidevamma *et al.* (2006) showed that Eighty-one genotypes of groundnut (*Arachis hypogaea* L.) representing different groundnut centres were studied for genetic divergence analysis utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 value) groundnut accessions were grouped into 16 clusters. Of the 16 clusters formed, cluster I was the largest with 47 accessions followed by cluster II with 10 accessions. Test weight, days to maturity and oil content were the most potential traits contributing to the total divergence. Cluster Xl and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII has

genotype with most favorable characters and hence can be involved as potential parent for development of superior genotypes.

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

Singh *et al.* (2010) evaluated thirty two groundnut genotypes of both spreading and bunch types were evaluated for their yield, yield attributes, seed protein and oil content to estimate the degree of genetic variability in quantitative and qualitative traits and to use as pedigree for further development of varieties with greater yield potential and seed quality. The genotypes showed the extent of variation from 550-1125 g/m^2 in biomass, 142-277 g/m^2 in pod weight, 91-216 g/m^2 in seed yield, 4-23 pods/plant, 1-3 seeds per pod, 53-87 per cent in shelling percent, 11-27 per cent in harvest index, 20.8-28.9 per cent in protein and 39.6-49.1 per cent in oil contents of seeds. This degree of variation in seed yield and quality traits offer an opportunity for evolving varieties to boost both the seed and oil production in the country.

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

Sadeghi *et al.* (2011) studied genetic diversity of the genotypes of peanut, an experiment was carried out with 23 genotypes of peanut by using randomized complete block design with three replications in the city Astaneh Ashrafieh, North of Iran at 2010 and showed that there was significant difference between different genotypes in term of the plant height, total number of pods, total weight of pods, 100 pods weight, 100 seed weight, biomass ($p<0.05$) total number of seeds and seed yield ($p<0.01$).

Venkateswarlu (2011) studied during kharif, 2007 genetic divergence, character association, path analysis and genetic parameters in 74 genotypes of groundnut (*Arachis hypogaea L.*) during kharif, 2007.

3. MATERIAL AND METHODS

The field experiment related to the present investigation entitled "Genetic diversity in f4 generation lines of 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 summer, 2013. The details of material used and methods adopted during the course of the investigation are given below.

3.1 Material

The material used in the present study consisted of thirty F_4 generation lines of groundnut and one check (Phule Unnati) (Table 3.1). The lines were obtained from the Groundnut Breeder, All India Co-ordinated Research Project, on Groundnut, M.P.K.V., Rahuri.

3.2 Methods

3.2.1 Experimental design

The experiment was conducted in a randomized block design with two replications. Each plot consisted of a single row of 3 m length with a spacing of 30 cm between rows and 10 cm between plants. One border row was sown at both the sides of block to reduce the border effect.

3.2.2 Sowing and cultural practices

The land was prepared by ploughing followed by two cross harrowings. The seeds were sown on 28th February 2013 by dibbling single seed per hill at 30 × 10 cm^2 distance (between

rows and between plants). During the growth period the usual cultural practices like weeding, irrigation and plant protection measures were followed as and when required.

Table 3.1 The genotype and their source

Sr. No.	Name of F_4 generation	Source	Pedigree
1.	RHRG-1106	MPKV, RAHURI	JL-24 x TAG-24
2.	RHRG-1109	MPKV, RAHURI	JL-24 x SB-XI
3.	RHRG-1110	MPKV, RAHURI	JL-24 x SB-XI
4.	RHRG-1111	MPKV, RAHURI	JL-24 x SB-XI
5.	RHRG-1112	MPKV, RAHURI	JL-24 x 6021
6.	RHRG-1114	MPKV, RAHURI	JL-24 x 6021
7.	RHRG-1115	MPKV, RAHURI	JL-24 x 6021
8.	RHRG-1116	MPKV, RAHURI	JL-24 x 6021
9.	RHRG-1117	MPKV, RAHURI	JL-24 x 6097
10.	RHRG-1118	MPKV, RAHURI	JL-24 x 6097
11.	RHRG-1119	MPKV, RAHURI	JL-24 x 6097
12.	RHRG-1120	MPKV, RAHURI	JL-24 x 6097
13.	RHRG-1121	MPKV, RAHURI	JL-24 x 6097
14.	RHRG-1122	MPKV, RAHURI	JL-24 x Ghungari
15.	RHRG-1123	MPKV, RAHURI	JL-24 x Ghungari
16.	RHRG-1124	MPKV, RAHURI	JL-24 x Ghungari
17.	RHRG-1126	MPKV, RAHURI	JL-24 x SB-XI
18.	RHRG-1127	MPKV, RAHURI	JL-24 x SB-XI
19.	RHRG-1128	MPKV, RAHURI	JL-24 x SB-XI
20.	RHRG-1129	MPKV, RAHURI	JL-24 x SB-XI
21.	RHRG-1130	MPKV, RAHURI	JL-24 x SB-XI
22.	RHRG-1131	MPKV, RAHURI	JL-24 x SB-XI
23.	RHRG-1132	MPKV, RAHURI	TAG-24 x JL-24
24.	RHRG-1135	MPKV, RAHURI	TAG-24 x JL-24
25.	RHRG-1137	MPKV, RAHURI	JL-24 x SB-XI
26.	RHRG-1138	MPKV, RAHURI	JL-24 x SB-XI
27.	RHRG-1140	MPKV, RAHURI	JL-24 x SB-XI
28.	RHRG-1142	MPKV, RAHURI	TAG-24 x 6021
29.	RHRG-1145	MPKV, RAHURI	TAG-24 x 6021
30.	RHRG-1149	MPKV, RAHURI	TAG-24 x 6097
31.	Phule Unnati (check)	MPKV, RAHURI	--

3.2.3 Manures and fertilizers

The chemical fertilizers were applied @ 25 kg N and 50 kg P_2O_5 per ha. at the time of sowing in the form of ammonium phosphate and single super phosphate, respectively.

3.2.4 Harvesting

The pods were picked after attaining their physiological maturity to avoid germination of kernels within pods in soil. The following symptoms were considered for the physiological maturity of groundnut.

a. Yellowing of foliage and dropping of older leaves.
b. The mature pod becomes hard and tough. The inside shell surface becomes rough with visible net venation with a dark brown colour.
c. The seed becomes smooth and testa develops colour typical of the variety.

3.2.5 Observations recorded

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

3.2.5.1 Days to 50 per cent flowering

Number of days required from sowing to day on which 50 per cent of the plants flowered was recorded as days to 50 per cent flowering.

3.2.5.2 Days to maturity

The number of days from the date of sowing till the date when at least eighty per cent plants were matured in each replication was recorded.

3.2.5.3 Plant height at maturity (cm)

Plant measured form ground level of uppermost tip of main branch of the plant in centimeters at physiological maturity on randomly height was selected plants

3.2.5.4 Number of branches per plant

The number of branches produced on the main stem of observational plants was counted as branches at the time of harvesting

3.2.5.5 Number of pegs per plant

The number of pegs per plant were counted at the time of harvest.

3.2.5.6 Number of immature pods per plant

The number of immature pods per plant was counted at the time of harvest.

3.2.5.7 Number of mature pods per plant

The number of mature pods per plant was counted at the time of harvest.

3.2.5.8 Pegs to pod ratio

The peg to pod ratio was calculated by comparing the number of pegs with number of mature pods

3.2.5.9 Dry haulm yield per plant (g)

The haulm of randomly selected plant was dried and the weigh was recorded.

3.2.5.10 Dry pod yield per plant (g)

The pods harvested from ten randomly selected experimental plants in each replication were cleaned and dried

under shade for one month after harvest. The weight of pods after drying was recorded and averaged.

3.2.5.11 Hundred kernel weight (g)

The weight of randomly selected hundred mature kernels taken from observational plants was considered as hundred kernel weight.

3.2.5.12 Shelling percentage (%)

Weight of mature pods of selected plants were recorded. After shelling, weight of kernel was also recorded. Shelling percentage was calculated using following formula.

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

3.2.5.13 Harvest index on dry weight basis

The ratio economic yield i.e. pod yield to the biological yield was taken as harvest index

3.2.5.14 Sound of mature kernel percentage

Form the total pods harvested form ten experimental plants in each replication, fully matured pods were counted and SMK (%) was calculated as follows.

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

3.2.5.15 Protein percentage

Percent crude protein content of the groundnut sample was estimated by determining N from kernels adopting Macro Kjeldhal method (A.O.A.C., 1975). Total N content was

multiplied by factor values 5.46 which gave protein contents of that sample (Thimmaiah, 1982).

3.2.5.16 Oil content percentage

The oil percentage was estimated on NMR (Nuclear magnetic resonance) in each plot from each replication.

3.3.6 Physiological observation

3.3.6.1 Photosynthetic rate (μ mol per m^2s)

For measuring the rate of photosynthetic in field condition a portable IRGA (Infra Red Gas Analyser) has been developed in the recent year. This can be used for measuring the rate of photosynthesis (Co2 fixation)

Procedure:-

An intact leaf of plant was clamped into the chamber and 2 to 10 observation measurable parameter was logged. The time between observation fixed to 20 sec (second observation upto 10 sec total 10 observation) during measurement photosynthetic rate were logged computed and stored in the memory.

Computation and storage

The data on the photosynthetic rate for each part observation were logged also summary statistics were computed on all the variable. After examining the data on the system, the data was concerned and stored in internal memory and next observation were taken following same procedure.

3.3.6.2 Leaf temperature (^0C)

Leaf temperature observation was recorded with the help of IRGA (Infra Red Gas Analyser).

3.3.6.3 Specific Leaf Area (gm/m²)

Leaf area of each sample plant was recorded using automated leaf area meter (model LIE 3000 A^0).

3.3.6.4 Total chlorophyll (mg/g)-SPAD meter

The chlorophyll content of the leaves was estimated with the help of SPAD meter.

3.4 Statistical analysis

The mean values of ten randomly selected observational plants for twelve different characters were used for statistical analysis.

The following statistical parameters were calculated for presentation of data on different quantitative attributes.

3.4.1 Analysis of variance (ANOVA)

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1967). Statistical analysis will be performed by using the methods proposed by Dewey and Lu (1959) and Mahalnobis (1936) as described by Rao (1952).

The genotypic mean squares (GMS) were tested for their significance against error mean squares (EMS) by 'F' test for n_1 = (g-1) and n_2 = (r-1) (g-1) degrees of freedom

Where,

g = Number of genotypes

r = Number of replications

The characters showing significant differences were only subjected to further analysis

3.4.2 Estimates of components of variability

a. Mean

The mean values for all the characters were worked out by dividing total corresponding number of observations.

$$\bar{X} = \frac{\sum xi}{n}$$

Where,

$\bar{X}$ = Mean

$\sum xi$ = Total of all observations

n = Number of observations

b. Range

The lowest and the highest values of mean for each character represented the range.

c. Estimation of coefficient of variation

The genotypic and phenotypic coefficient of variation was calculated by using the following formula given by Burton (1952).

i. Genotypic coefficient of variation (PCV)

$$GCV = \frac{\sigma^2 g}{\bar{x}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sigma^2 p}{\bar{x}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\overline{x}$ = Mean of character

The high, medium and low estimates of coefficient of variation were classified as

Low = 0 to 10 %

Medium = 10 to 20 %

High = 20 % and above

d. Heritability (b.s.)

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al*. (1956).

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

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The high, medium and low heritability estimates were classified as;

Low = 0 to 30 %

Medium = 30 to 60 %

High = 60 % and above

e. Genetic advance (GA)

Genetic advance (at 5 % selection intensity) was calculated using formula cited by Allard (1960).

$$GA = K \times \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

K = Selection differential

(At 5 % selection intensity the value of K = 2.60)

ii. GA as percentage of mean

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

Where,

GA = Genetic advance

$\overline{X}$ = Character mean

The estimates of genetic advance as percentage of mean were classified as below;

Low = 0 to 10 %

Medium = 10 to 20 %

High = 20 % and above

3.4.3 D^2 analysis

The analysis of divergence was carried out by D^2 statistics of Mahalanobis (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per RBD to test the significances of differences among the genotypes. The characters exhibiting significant differences were only used for further analysis of D^2 statistics.

a. Wilk's criterion

After testing differences from population, a simultaneous test of significance of difference in the mean values of a number of correlated variables with regard to the pooled

effect of eleven characters considered together was carried out using Wilk's criterion, which was estimated using the relationship,

$$\Delta = \frac{|E|}{|E + V|}$$

Where, |E| is the determinant of experimental error sum of squares and sum of products matrix and E + V|, the determinant of experimental error sum of squares and sum of products, plus the population sum of squares and product matrix. Significance of Δ estimated by X^2 as,

$$X^2_{pq} = V = -m.10\ ge^{\wedge}$$

Where,

n = N_1 +……+ NK-1=Total number of observations-1

p = Number of characters

q = K-1

K = Number of varieties

b. Mahalanobis's generalized distance (D^2)

The generalized distance between any two populations in defined as:

$$\Delta^2 = \sum\sum\lambda_{ij}\delta_i\delta_j$$

Where,

λ_{ij} = Reciprocal matrix to the common depression matrix

δ_I = Difference between the mean values of the two populations for I^{th} character

This quality is estimated by the D^2 statistic as

$$D^2 = \sum\sum S_{ij}\, d_i\, d_j$$

Where,

S_{ij} is the sample estimate of λ_{ij} and S_i and δ_j. Since this formula for computation requires the inversion of tenth order determinant fifteen evaluation of 15 (15 + ½) terms whose sum is D^2.

c. Computation of D^2 values

For each combination, mean deviation i.e. $\overline{Y}_i^2 - \overline{Y}_i^2$ with I = 1,2 …. P was computed and the d^2 was calculated as sum of squares of these deviations i.e. $\sum (\overline{Y}_i^1 - \overline{Y}_i^2)$.

d. Determination of population constellations

No rules can be laid down for finding the clusters because the cluster is not a well defined term. The only way appears to be that any two groups belonging to the same cluster should be at least, on an average show a smaller D^2 values than those belonging to two different clusters.

A simple device suggested by Tocher (Rao, 1952) for cluster formation is to start with closely related groups and find a third group which had smaller average D^2 from the first two. Similarly, the fourth group is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further for the cluster formation, if at any stage of average D^2 value of a group appears to be higher than those already listed, then this group does not enter in that former group and taken to be outside of that cluster. Varieties included in the first cluster are

then omitted and the rest are treated similarly to form next cluster.

e. Average intra cluster distance

The intra cluster distances were calculated as $\sum Di^2/n$, where $\sum Di^2$ is the sum of distance between all possible combinations (n) of genotypes included in a cluster.

n = Number of genotypes included in a cluster

f. Average inter-cluster distances

The procedure followed for calculating the inter cluster distances was first to measure the distance between cluster I and II, between I and III, between I and IV and so on, likewise the clusters were taken one by one and the distance from other cluster were calculated. The average inter cluster distance were then calculated as,

$$\sum Di^2 / (n_i n_j)$$

Where,

n_i = Number of genotypes in cluster 'i'

n_j = Number of population in cluster 'j'

The intra and inter cluster distance (n) values were obtained by taking square root of average D^2 values of the respective genotypes.

g. Cluster diagram

With the help of D values between the clusters, a diagram showing the relationship between different genotypes was drawn.

4. EXPERIMENTAL RESULTS

The results obtained in the present investigation entitled “Genetic diversity in F4 generation lines of groundnut (*Arachis hypogaea L.*)” conducted at AICRP, Groundnut, Cotton Improvement Project, MPKV, Rahuri are presented in this chapter under different sub-headings.

4.1 Range and mean performance

The data on mean performance for twenty characters of thirty one genotypes of summer groundnut is presented in Table 4.1.

4.1.1 Days to 50 % flowering

The variation for days to 50 % flowering ranged between 39.50 to 49.20 days. The population mean for this character was 45.04 days. Seventeen out of 31 genotypes flowered significantly earlier than the population mean. The genotype RHRG-1116 (39.50) was the earliest followed by RHRG-1129 (40.00), RHRG-1128 (40.20). The genotypes RHRG-1138 (49.20), RHRG-1124 (48.00) RHRG-1106 (47.90) were comparatively late in days to 50 % flowering.

4.1.2 Days to maturity

Nineteen out of thirty one genotypes showed significantly early maturity when compared with the population mean of 127.20 days. The variation for this character ranged between 117.35 (RHRG-1116) to 131.15 (RHRG-1138) days. The genotype RHRG-1116 recorded the lowest days to maturity (117.35) followed by RHRG-1128 (121.45). The genotypes RHRG-1138 (131.15), RHRG-1132 (130.90) were comparatively late in maturity.

Table 4.1. Mean performance of thirty one genotypes for twenty characters in F4 generation lines of groundnut

Sr . No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No.of Branches/ plant	No.of pegs/ plant	No of Mature pods / plant	Peg to pod ratio	Dry haulm yield/ plant (g)	No.of immature pods/ plant	Dry pod yield/ plant (g)	Hundred kernel wt.(g)	Shelling %	Harvest Index (dry wt. basis)	Oil %	Protein (%)	Sound of mature kernel (%)	Photosynthetic rate	Leaf temperature	Total chlorophyll (mg/g)	Specific leaf area (g/m^2)
1	RHRG-1106	47.9	128.4	20.4	5.4	24	12.5	1.91	18.4	6.5	11.5	33.1	70.33	29	45.88	23.4	85.6	14.71	38.04	44.14	15.29
2	RHRG-1109	43.7	124.9	29.0	4.4	33.4	16.9	1.97	12.8	3.0	13.6	35.3	67.75	27.9	48.75	23.2	84.7	15.79	35.68	48.52	16.84
3	RHRG-1110	42.4	122.4	35.4	4.2	23.7	15.5	1.53	33	3.6	15.0	31.9	70.16	27.4	46.21	23.4	85.6	14.53	36.01	41.91	16.34
4	RHRG-1111	44.3	128.3	33.9	5.0	33.1	20.1	1.66	34	5.5	18.5	37.2	68.22	29.4	48.02	23.7	86.3	15.69	36.09	39.84	15.60
5	RHRG-1112	46.9	129.1	30.8	4.2	25.1	16.9	1.50	20.6	4.7	12.9	32.7	69.30	27.8	49.97	24.0	87.0	13.45	37.47	41.13	15.01
6	RHRG-1114	43.5	121.8	39.8	4.3	31.1	16	2.05	21.2	4.8	15.5	36.9	68.26	27	47.19	23.4	86.7	14.41	36.89	44.91	15.99
7	RHRG-1115	43.5	128.9	32.8	4.2	32.4	20.2	1.62	16	4.85	17.8	32.7	68.59	30.1	47.85	23.6	84.9	14.79	36.29	41.07	17.38
8	RHRG-1116	39.5	117.3	35.3	4.6	23.8	10.4	2.32	14.7	4.75	10.8	37.1	69.09	27.5	47.64	24.2	84.6	14.54	36.66	42.3	15.73
9	RHRG-1117	44.6	128.5	30.0	4.4	24.7	14.1	1.78	26.2	5.15	12.8	32	68.51	28.9	48.1	24.0	85.9	15.33	35.11	47.74	18.05
10	RHRG-1118	46.3	129.5	29.3	4.6	44.5	19.9	2.34	17.6	12.40	19.8	31.5	68.78	30.8	45.46	23.7	84.5	13.18	34.73	41.50	15.39
11	RHRG-1119	46.1	129.4	34.2	4.6	15.7	11.0	1.45	24.2	3.0	13.5	34.0	68.09	29.3	48.51	23.6	88.6	15.84	36.17	44.39	15.31
12	RHRG-1120	45.9	128.0	32.0	4.9	24.1	13.0	1.87	17	3.8	12.4	33.5	68.25	32.4	49.15	24.0	89.2	15.09	36.45	40.81	16.76
13	RHRG-1121	45.3	126.5	24.4	4.7	25.4	14.3	1.79	21.2	3.5	16	33.6	68.43	39.9	49.72	23.5	86.2	15.82	36.21	45.06	16.24
14	RHRG-1122	47.2	130.9	30.3	4.7	28.5	15.2	1.88	17	4.2	12.8	31.3	67.27	29.4	47.12	24.4	85.0	14.84	36.26	45.35	13.99
15	RHRG-1123	47.2	129.6	31.1	4.6	11.7	8.6	1.37	14.6	2.8	10.6	35.3	67.08	22.8	46.87	23.5	87.2	14.31	36.44	38.24	15.69
16	RHRG-1124	48.0	130.4	25.8	5.3	14.9	8.6	1.72	15.6	4.0	9.5	31.9	68.52	25.1	47.24	23.9	84.5	14.2	36.16	44.99	15.73
17	RHRG-1126	43.3	124.1	24.9	5.3	39.5	21.6	1.82	17.9	7.5	20.6	35.3	69.11	36.9	48.32	23.7	90.8	14.76	37.11	44.16	16.16

Table 4.1 contd...

Sr . No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No.of Branches/ plant	No.of pegs/ plant	No of Mature pods / plant	Peg to pod ratio	Dry haulm yield/ plant (g)	No.of immature pods/ plant	Dry pod yield/ plant (g)	Hundred kernel wt.(g)	Shelling %	Harvest Index (dry wt. basis)	Oil %	Protein (%)	Sound of mature kernel (%)	Photosynthetic rate	Leaf temperature	Total chlorophyll (mg/g)	Specific leaf area (g/m^2)
18	RHRG-1127	42.8	125.8	31.4	6.2	43.0	27.5	1.56	29.51	6.1	21.4	32.4	67.9	38.2	45.81	22.8	85.0	13.45	36.58	41.89	14.92
19	RHRG-1128	40.2	121.4	32.1	5.7	29	16.8	1.73	20	5.7	14.9	31.3	68.81	31.2	46.02	24.6	84.1	13.93	36.71	41.66	18.05
20	RHRG-1129	40.00	122.6	30.5	4.8	24.7	11.9	2.08	35.4	5.7	13	33.0	66.77	30.2	48.67	23.5	85.5	14.54	37.22	38.49	17.31
21	RHRG-1130	42.00	126.3	19.9	5.4	50.2	36.7	1.37	33.9	12.3	29.2	35.7	67.01	40.7	46.82	23.9	86.4	15.25	36.42	41.86	17.46
22	RHRG-1131	45.50	127.8	23.2	5.5	33.9	18.5	1.83	20.7	6.0	14.8	31.8	68.77	29.9	47.83	23.2	86.4	15.07	36.41	44.93	16.69
23	RHRG-1132	47.90	130.9	25.8	6.8	40	20.0	2.0	35.8	7.1	22	32.7	69.36	35	45.13	22.7	85.4	15.29	36.44	44.13	17.7
24	RHRG-1135	47.20	129.4	22.9	4.9	40.5	27.5	1.47	17	11.8	18.4	34.1	66.74	33.6	49.64	23.0	85.3	13.67	35.27	41.33	18.1
25	RHRG-1137	46.70	127.1	21.3	6.2	41.9	23.7	1.76	34	9.8	22.9	34.9	69.12	35.5	48.01	22.7	85.8	15.62	35.75	46.16	16.1
26	RHRG-1138	49.20	131.1	21.8	5.4	46.8	26.6	1.77	29.5	7.1	11.6	34.4	66.91	35.5	45.26	24.7	84.1	15.27	35.59	47.39	14.65
27	RHRG-1140	47.90	130	17.6	6.6	50.3	23.8	2.12	24.9	11.8	18	31.6	69.44	34.2	45.83	22.8	85.3	15.84	36.25	48.62	17.19
28	RHRG-1142	46.70	129	16.9	5.0	32	19.2	1.66	22	5.3	16.1	32	67.56	34.2	44.86	23.0	87.1	14.98	37.13	47.56	19.05
29	RHRG-1145	43.50	126.9	26.7	4.9	33.9	19.3	1.76	23.2	5.4	16.2	33.9	69.09	31	46.43	22.4	88.4	14.98	35.41	42.75	16.35
30	RHRG-1149	45.40	127.3	20.3	4.3	35.7	21.6	1.64	16	5.2	16.0	31.9	67.73	32.9	46.29	23.6	86.8	15.73	35.26	42.07	14.13
31	Phule Unnati	45.90	128.8	20.2	6.9	68.4	47.4	1.44	30.8	7.8	33.9	35.8	66.85	40.2	46.68	23.5	88.1	15.90	36.04	44.83	17.52
	Mean	45.04	127.2	27.41	5.09	33.1	19.20	1.76	23.1	6.32	16.8	33.6	68.31	31.4	47.30	23.6	86.16	14.86	36.28	43.54	16.34
	S.E.	0.85	1.47	1.36	0.44	0.95	1.61	0.16	1.43	0.61	1.79	0.81	0.39	1.71	0.44	0.23	1.08	0.26	0.41	1.54	0.29
	C.D.at 5%	2.45	4.25	3.92	1.27	2.74	4.65	0.47	4.13	1.78	5.18	2.36	1.13	4.96	1.29	0.68	3.12	0.77	1.19	4.46	0.85
	C.V.%	2.67	1.63	7.01	12.2	4.06	11.87	13.0	8.78	13.84	15.0	3.44	0.81	7.74	1.33	1.41	1.77	2.55	1.61	5.01	2.56

4.1.3 Plant height (cm)

The variation for plant height ranged between 16.90 and 39.80. The line RHRG-1114 was the tallest genotype having maximum plant height of 39.80 cm followed by RHRG-1110 (35.40) and RHRG-1116 (35.30). The genotype RHRG-1142 (16.90) was dwarfest followed by RHRG-1140 (17.60) and RHRG-1130 (19.90).

4.1.4 Number of branches per plant

The variation for number branches per plant ranged between 4.20 and 6.90. Looking to the population mean of 5.09 branches per plant, twelve genotypes showed higher branches than population mean. RHRG-1132(6.80), RHRG-1140(6.60), RHRG-1137(6.20), RHRG-1128(5.70) were the genotypes possessing high number of branches per plant.

4.1.5 Number of pegs per plant

The range observed for number of pegs per plant was between 11.70 (RHRG-1123) and 68.40 (Phule Unnati). Fifteen genotypes recorded significantly more pegs per plant as compared to the population mean (33.09). The genotype Phule Unnati (68.40) ranked first followed by RHRG-1140 (50.35), RHRG-1130 (50.26), RHRG-1138 (46.80) and RHRG-1118 (44.50). In contrast the genotypes viz., RHRG-1123 (11.70), RHRG-1124 (14.90) and RHRG-1119 (15.70) recorded lower values for number of pegs per plant.

4.1.6 Number of mature pods per plant

The variation for the character ranged between 8.60 (RHRG-1123) and 47.40 (Phule Unnati). The population mean for

this character was 19.20. Fifteen genotypes showed higher number of mature pods per plant over population mean of which Phule Unnati (47.40), RHRG-1130 (36.70) and RHRG-1135 (27.50 each) produced the high number of mature pods per plant.

4.1.7 Peg to pod ratio

The range observed for peg to pod ratio was between 1.37 (RHRG-1130) and 2.34 (RHRG-1118). Seventeen genotypes recorded significantly more peg to pod ratio as compared to population mean (1.76). The genotype RHRG-1118 (2.34) ranked first followed by RHRG-1116 (2.32), RHRG-1138 (2.12) and RHRG-1114 (2.05). In contrast the genotypes RHRG-1130 (1.37), RHRG-1119 (1.45) and RHRG-1135 (1.47) recorded lower values for peg to pod ratio.

4.1.8 Dry haulm yield per plant (g)

The genotype RHRG-1132 produced the higher dry haulm yield per plant (35.80) followed by RHRG-1129 (35.40), RHRG-1111 (34.00) and RHRG-1130 (33.90). The genotype RHRG-1109 (12.80) produced the lowest dry haulm yield per plant followed by RHRG-1123 (14.60) and RHRG-1116 (14.70). The population mean was 23.05.

4.1.9 Number of immature pods per plant

The number of immature pods per plant ranged between 2.80 (RHRG-1123) and 12.40 (RHRG-1118), while the population mean was 6.32. Twenty two genotypes showed lower number of immature pods per plant than population mean. The

genotypes RHRG-1123 and RHRG-1119 (3.00 each) produced lowest number of immature pods per plant.

4.1.10 Dry pod yield per plant (g)

Population mean for dry pod yield per plant was 16.83 g. The genotype Phule Unnati (33.90) recorded the highest dry pod yield per plant followed by RHRG-1130 (29.20), RHRG-1137 (22.90) and RHRG-1132 (22.00). The genotype RHRG-1124 (9.50) along with RHRG-1116 (10.80) recorded low yield. Twelve out of 31 genotypes showed higher mean values for this character than population mean.

4.1.11 100 kernel weight (g)

The variation for this character ranged between 31.30 (RHRG-1128) and 37.20 (RHRG-1111). Fourteen out of 31 genotypes showed numerically high hundred kernel weight when compared with population mean of 33.57 g. Genotypes RHRG-1111 (37.20), RHRG-1116 (37.10) and RHRG-1114 (36.90) showed higher hundred kernel weight.

4.1.12 Shelling percentage

The population mean for this trait was 68.31. The variation ranged between 66.74 (RHRG-1135) and 70.33 (RHRG-1106). The highest shelling percentage was recorded by RHRG-1106 (70.33) followed by RHRG-1110 (70.16), RHRG-1140 (69.44), RHRG-1126 (69.11). The lowest value for shelling percentage was recorded by RHRG-1135 (66.74) followed by RHRG-1129 (66.77), Phule Unnati (66.85) and RHRG-1138 (66.91).

4.1.13 Harvest index (%)

Twelve genotypes recorded significantly higher harvest index over the population mean of 31.41. The range observed for this character was between 22.80 (RHRG-1123) and 40.70 (RHRG-1130). The genotype RHRG-1130 had the highest harvest index (40.70) followed by Phule Unnati (40.20), RHRG-1127 (38.20) and RHRG-1126 (36.90). The lowest value for harvest index was recorded by RHRG-1123 (22.80) followed by RHRG-1124 (25.10).

4.1.14 Oil content (%)

The population mean for this character was 47.26 per cent. The genotype RHRG-1142 (44.86) recorded the lowest oil content while the genotype RHRG-1112 (49.97) recorded highest oil content followed by RHRG-1135 (49.64), RHRG-1121 (49.72) and RHRG-1120 (49.15). Fifteen genotypes recorded high value for oil content as compared to population mean.

4.1.15 Protein content (%)

The protein content in 31 summer genotypes ranged between 22.48 (RHRG-1145) and 24.78 (RHRG-1138) with a population mean of 22.57 per cent. The genotypes RHRG-1138 (24.78), RHRG-1128 (24.68), RHRG-1122 (24.39), and RHRG-1116 (24.19) recorded the highest amount of percent protein. In contrast the genotypes RHRG-1145 (22.48), RHRG-1137 (22.70) and RHRG-1132 (22.78) recorded lowest values for protein content.

4.1.16 Sound mature kernel (%)

The range observed for sound mature kernel percentage was between 84.10 (RHRG-1128) and 90.80 (RHRG-

1126). The population mean for this character was 86.16. The highest sound mature kernel percentage was observed for genotype RHRG-1126 (90.80) followed by RHRG-1120 (89.20) and RHRG-1119 (86.60).

4.1.17 Photosynthetic rate

The variation for photosynthetic rate ranged between 13.18 to 15.90. The population mean for this character was 14.86. Sixteen out of 31 genotypes having higher photosynthetic rate than the population mean. The genotype Phule Unnati (15.90) was the highest followed by RHRG-1119 and RHRG-1140 (15.84). The genotype RHRG-1118 (13.18) was the lowest photosynthetic rate followed by RHRG-1127 (13.45) and RHRG-1124 (14.20).

4.1.18 Leaf temperature (^{0}C)

Fifteen out of thirty one genotypes showed higher leaf temperature when compared with the population mean of 36.28. The variation for this character ranged between 34.73 (RHRG-1118) to 38.04 (RHRG-1106). The genotype RHRG-1106 recorded the highest leaf temperature (38.04) followed by RHRG-1112 (37.47). The genotypes RHRG-1118 (34.73) and RHRG-1117 (35.11) were comparatively low leaf temperature.

4.1.19 Total chlorophyll

The variation for total chlorophyll ranged between 38.24 and 48.62. The genotype RHRG-1140 having maximum total chlorophyll recorded 48.62 followed by RHRG-1109 (48.52) and RHRG-1117 (47.74). The genotype RHRG-1123 (38.24) was

recorded minimum total chlorophyll followed by RHRG-1129 (38.49) and RHRG-1111 (39.84).

4.1.20 Specific leaf area

The variation for specific leaf area ranged between 13.99 and 19.05. Looking to the population mean of 16.34 specific leaf area, sixteen genotypes showed higher specific leaf area than population mean. The genotypes RHRG-1142 (19.05), RHRG-1135 (18.10), RHRG-1128 (18.05) and RHRG-1132 (17.70) recorded high specific leaf area.

4.2 Analysis of variance

Analysis of variance (Table 4.2) revealed highly significant differences among the genotypes for the characters studied except no. of branches per plant, no. of immature pods per plant, dry pod yield, 100 kernel weight, oil content and specific leaf area, indicating appreciable amount of variability among the genotypes.

4.3 Parameters of genetic variability and heritability

Estimates of range, variability heritability (b.s.) and genetic advance are presented in Table 4.3.

4.3.1 Coefficient of genotypic and phenotypic variation

It was observed that the estimates for genotypic coefficient of variation (GCV) were lower than the phenotypic coefficient of variation (PCV) for all the characters.

Number of immature pods per plant (48.20) recorded the highest estimate of GCV followed by no. of mature pods per plant (41.27), number of pegs per plant (35.72), dry haulm yield

Table 4.2. Analysis of variance for twenty characters in F4 generation lines of groundnut

Sr. No.	Characters	MSS	
		Treatments	Error
1	Days to 50 % flowering	12.77**	1.44
2	Days to maturity	21.39**	4.34
3	Plant height (cm)	70.29**	3.70
4	No.of Branches /plant	1.19*	0.39
5	No.of pegs/plant	281.38**	1.81
6	No of Mature pods / plant	130.85**	5.20
7	Peg to pod ratio	0.12	0.05
8	Dry haulm yield/plant(g)	103.14**	4.09
9	No.of immature pods/plant	19.37*	0.76
10	dry pod yield/plant	57.23*	6.44
11	Hundred kernel wt.(g)	6.48*	1.33
12	shelling %	1.92	0.30
13	Harvest Index(dry wt.basis)	35.52**	5.91
14	Oil%	4.05*	0.39
15	Protein (%)	0.62	0.11
16	Sound of mature kernel (%)	5.01**	2.34
17	Photosynthetic rate	1.20	0.14
18	Leaf temperature	1.00	0.34
19	Total chlorophyll %	15.52**	4.77
20	Specific leaf area	3.07*	0.17

Table 4.3. Estimates of variability and heritability for 20 characters in F4 generation lines of groundnut

Sr. No.	Characters	Range	General mean	GCV	PCV	Heritability (b.s.) %	GA	GA at percentage of mean
1	Days to 50 % flowering	39.50-49.20	45.04	5.28	5.91	79.6	4.37	9.71
2	Days to maturity	117.35-131.15	127.20	2.29	2.82	66.2	4.89	3.84
3	Plant height (cm)	16.90-39.80	27.41	21.04	22.18	90	11.27	41.12
4	No.of Branches /plant	4.20-6.90	5.09	12.43	17.46	50.7	0.93	18.24
5	No.of pegs/plant	11.70-68.40	33.09	35.72	35.95	98.7	24.19	73.12
6	No of Mature pods/plant	8.60-47.40	19.20	41.27	42.95	92.4	15.69	81.71
7	Peg to pod ratio	1.37-2.34	1.76	10.99	17.05	41.5	0.25	14.59
8	Dry haulm yield/plant(g)	12.80-35.80	23.05	30.52	31.76	92.4	19.93	60.43
9	No.of immature pods/ plant	2.80-16.30	6.32	48.20	50.15	92.4	6.03	95.43
10	Dry pod yield/plant	9.50-33.90	16.83	29.92	33.51	79.7	9.27	55.05
11	Hundred kernel wt.(g)	31.30-37.20	33.57	4.78	5.89	65.8	2.68	7.98
12	shelling %	66.74-70.33	68.31	1.31	1.54	72.3	1.57	2.30
13	Harvest Index (dry wt. basis)	22.80-40.70	31.41	12.24	14.48	71.5	6.70	21.32
14	Oil (%)	44.86-49.97	47.26	2.85	3.15	82.1	2.52	5.33
15	Protein (%)	22.48-24.78	23.57	2.14	2.57	69.5	0.86	3.68
16	Sound of mature kernel (%)	84.10-90.80	86.16	1.34	2.22	36.2	1.43	1.66
17	Photosynthetic rate	13.18-15.90	14.86	4.89	5.52	78.6	1.32	8.93
18	Leaf temperature	34.73-38.04	36.28	1.58	2.26	49.1	0.83	2.29
19	Total chlorophyll (%)	38.24-48.62	43.54	5.32	7.13	53	3.47	7.98
20	Specific leaf area	13.99-19.05	16.34	7.36	7.79	89.2	2.34	14.32

per plant (30.52), dry pod yield per plant (29.92), plant height (21.04). The highest value of PCV were observed for no. of immature pods per plant (50.15) followed by number of mature pods per plant (42.95), no. of pegs per plant (35.95), dry pod yield per plant (33.51), dry haulm yield per plant (31.76), plant height (22.18), harvest index (14.48).Low GCV and PCV were recorded by character shelling percentage (1.31 and 1.54), sound of mature kernel (1.34 and 2.22), leaf temperature (1.58 and 2.26).Looking to the difference between GCV and PCV magnitudes, it was observed that all the characters except peg to pod ratio and no. of branches per plant showed low magnitudal difference between GCV and PCV estimates.

4.3.2 Heritability (b.s.)

The heritability (b.s.) estimates were high in case of characters *viz.*, no. of pegs per plant (98.70), number of mature pods per plant, number of immature pods per plant, dry haulm yield per plant (92.40), plant height (90.00), specific leaf area (89.20), dry pod yield per plant (29.92), plant height (21.04), percent oil content (82.10), dry pod yield per plant (79.70), days to 50% flowering (79.60), photosynthetic rate (78.60), shelling percentage (72.30), harvest index (71.50), percent protein content (69.50), days to maturity (66.20), hundred kernel weight (65.80), total chlorophyll (53.00) and leaf temperature (49.10). It was medium for sound mature kernel (36.20).

4.3.3 Genetic advance

The highest magnitude of genetic advance was observed for no. of pegs per plant (24.19) followed by dry haulm

yield per plant (19.93), no. of mature pods per plant (15.69), plant height (11.27), dry pod yield per plant (9.27), harvest index (6.70), number of immature pods per plant (6.03). The lowest value of genetic advance was observed for peg to pod ratio (0.25), leaf temperature (0.83), per cent protein content (0.86), number of branches per plant (0.93).

Genetic advance as a percent of mean was the highest for number of immature pods per plant (95.43) followed by number of mature pods per plant (81.71), no. of pegs per plant (73.12) and In contrast, sound mature kernel (1.66) recorded lowest value followed by leaf temperature (2.29) and shelling percentage (2.30).

4.4 Divergence analysis

Genetic divergence in thirty F_4 generation genotypes of summer groundnut was estimated using D^2 statistics (Mahalanobis, 1936). The D^2 values corresponding to pair of comparison between thirty one genotypes ranged between 47.52 (RHRG-1126 and RHRG-1149) and 3669.17 (RHRG-1123 and Phule Unnati).

4.4.1 Cluster formation

The cluster formation was done by following Tocher's method, as described by Rao (1952). All the 31 genotypes studied under investigation were grouped into six clusters as presented in Table 4.4.

Cluster I with 14 genotypes emerged as the largest cluster followed by cluster III with 8 genotypes, cluster II with 5 genotypes and cluster IV with 2 genotypes. Cluster V and VI included one genotype each (monogenotypic).

Table. 4.4. Composition of 31 groundnut genotypes into different clusters by Tocher's method

Cluster No.	No.of strains	Genotypes included in the cluster
I	14	RHRG-1126, RHRG-1145, RHRG-1131, RHRG-1115, RHRG-1111, RHRG-1114, RHRG-1129, RHRG-1117, RHRG-1149, RHRG-1142, RHRG-1120, RHRG-1121, RHRG-1122, RHRG-1112
II	5	RHRG-1123, RHRG-1124, RHRG-1119, RHRG-1106, RHRG-1116
III	8	RHRG-1132, RHRG-1137, RHRG-1138, RHRG-1140, RHRG-1118, RHRG-1127, RHRG-1130, RHRG-1135
IV	2	RHRG-1110, RHRG-1128
V	1	RHRG-1109
VI	1	Phule Unnati

4.4.2 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 4.5.

Cluster III exhibited maximum intra cluster distance i.e. (D=16.93), followed by cluster I (D=12.97), cluster II (D=12.95) and cluster IV (D=10.44).

Being monogenotypic, remaining clusters showed no intra cluster distance.

The maximum inter cluster distance was observed between cluster II and cluster VI (D=56.13), followed by cluster IV and cluster VI (D=46.71), cluster I and cluster VI (D=41.63), cluster V and cluster VI (D=39.70). The lowest inter cluster distance was observed between cluster I and cluster V (D=15.82).

4.5 Cluster means

The cluster means for twenty characters studied are given in Table 4.6. It revealed wide range of variability for most of the characters. On perusal of Table 4.6, it was observed that cluster III had highest cluster means for days to 50 % flowering (46.25 %) and lowest in cluster IV (41.30 %), cluster VI had highest cluster means for days to maturity (128.80 %) and lowest in cluster IV (121.95 %), cluster IV had highest cluster means for plant height (33.75 %) and lowest in cluster VI (20.20 %), cluster VI had highest cluster means for no. of branches per plant (6.90 %) and lowest in cluster V (4.40 %), cluster VI had highest cluster means for no. of pegs per plant (68.40 %) and lowest in cluster II (18.02 %).

Table 4.5. Average intra and inter cluster distances (D) from genotypes in F4 generation lines of groundnut

Cluster	I	II	III	IV	V	IV
I	**12.97**	19.39	21.34	16.82	15.82	41.63
II		**12.95**	33.48	20.43	23.10	56.13
III			**16.93**	24.71	23.82	29.25
IV				**10.44**	25.89	46.71
V					**0.00**	39.70
VI						**0.00**

Table 4.6. Cluster means for 20 characters in F4 generation lines of groundnut

Sr. No.	Characters	Clusters						Overall mean
		1	2	3	4	5	6	
1	Days to 50% flowering	44.69	45.74	46.25	41.30	43.70	45.90	44.59
2	Days to maturity	127.15	127.06	128.79	121.95	124.90	128.80	126.44
3	Plant height (cm)	28.32	29.36	23.75	33.75	29	20.20	27.39
4	No. of Branches /plant	4.73	4.90	5.76	4.95	4.40	6.90	5.27
5	No. of pegs/plant	30.30	18.02	44.66	26.35	33.40	68.40	36.85
6	No of Mature pods / plant	17.28	10.22	25.71	16.15	16.90	47.40	22.27
7	Peg to pod ratio	1.78	1.76	1.80	1.63	1.98	1.45	1.73
8	Dry haulm yield/plant(g)	22.03	17.50	27.78	26.50	22.80	30.80	22.86
9	No.of immature pods/plant	5.19	4.21	10.30	4.65	3	7.80	5.85
10	dry pod yield/plant	15.39	11.18	21.66	14.95	13.60	33.90	18.44
11	Hundred kernel wt.(g)	33.41	34.28	33.41	31.60	35.30	35.80	33.86
12	shelling %	68.28	68.63	68.16	69.49	67.76	66.86	68.19
13	Harvest Index(dry wt.basis)	30.71	26.74	35.44	29.30	27.90	40.20	31.71
14	Oil%	47.83	47.23	46.50	46.12	48.76	46.69	47.18
15	Protein (%)	23.60	23.74	23.33	24.08	23.25	23.54	23.59
16	Sound of mature kernel (%)	86.87	86.10	85.22	84.50	84.70	88.10	85.97
17	Photosynthetic rate	14.97	14.72	14.70	14.23	15.80	15.91	15.55
18	Leaf temperature	36.41	36.70	35.88	36.57	35.69	36.04	36.18
19	Total chlorophyll %	43.28	42.81	44.11	41.79	48.52	44.83	44.22
20	Specific leaf area	16.34	15.55	16.44	17.20	16.85	17.53	16.65

Cluster VI had highest cluster means for no. of mature pods (47.40 %) and lowest in cluster II (10.22 %), cluster V had highest cluster means for peg to pod ratio (1.98 %) and lowest in cluster VI (1.45 %), cluster VI had highest cluster means for days to dry haulm yield per plant (30.80 %) and lowest in cluster V (12.80 %), cluster III had highest cluster means for no. of immature pods (10.30 %) and lowest in cluster V (3.00 %), Cluster VI had highest cluster means for dry pod yield per plant (33.90 %) and lowest in cluster II (11.18 %), Cluster VI had highest cluster means for 100 kernel weight (35.80 %) and lowest in cluster IV (31.60 %), cluster IV had highest cluster means for shelling percentage (69.49 %) and lowest in cluster VI (66.86 %), cluster VI had highest cluster means for harvest index (40.20 %) and lowest in cluster II (26.74 %), cluster V had highest cluster means for oil percentage (48.76 %) and lowest in cluster IV (46.12 %), cluster IV had highest cluster means for protein content (24.08 %) and lowest in cluster V (23.25 %), cluster VI had highest cluster means for sound mature kernel (88.10 %) and lowest in cluster V (84.70 %).

Cluster VI had highest cluster means for photosynthetic rate (15.91 %) and lowest in cluster III (14.70 %), Cluster II had highest cluster means for leaf temperature (36.70 %) and lowest in cluster V (35.69 %), Cluster V had highest cluster means for total chlorophyll (48.52 %) and lowest in cluster IV (41.79 %), Cluster VI had highest cluster means for specific leaf area (17.53 %) and lowest in cluster II (15.55 %).

4.6 Percent contribution of various characters for divergence

All the 31 genotypes of summer groundnut were studied for twenty different characters and the data collected was used to determine genetic divergence. Out of twenty characters studied, the character specific leaf area (36.43 %) contributed the highest for divergence and was followed by dry haulm yield per plant (14.51 %), total chlorophyll (13.34 %), number of pegs per plant (11.61 %), dry pod yield per plant (4.20 %), harvest index (3.87 %), photosynthetic rate (3.01 %), hundred kernel weight (3.00 %).However, the traits days to 50 % flowering, peg to pod ratio and no. of branches per plant had no contribution towards divergence (Table 4.7).

Table 4.7. Contribution of various characters to divergence

Sr. No.	Characters	Times Ranked 1st	Contribution (%)
1	Days to 50 % flowering	0	0.00
2	Days to maturity	1	0.22
3	Plant height (cm)	8	1.72
4	No.of Branches /plant	0	0.00
5	No.of pegs/plant	54	11.61
6	No of Mature pods / plant	1	0.22
7	Peg to pod ratio	0	0.00
8	Dry haulm yield/plant(g)	69	14.51
9	No.of immature pods/plant	5	1.08
10	dry pod yield/plant	20	4.20
11	Hundred kernel wt.(g)	14	3.00
12	shelling %	5	1.08
13	Harvest Index(dry wt.basis)	10	2.06
14	Oil%	18	3.87
15	Protein (%)	12	2.58
16	Sound of mature kernel (%)	3	0.65
17	Photosynthetic rate	14	3.01
18	Leaf temperature	2	0.43
19	Total chlorophyll %	63	13.34
20	Specific leaf area	168	36.43

5. DISCUSSION

Success of any plant breeding programme depends on selection of elite genotypes which ultimately depends on knowledge of variability and genetic diversity in the breeding material. Therefore, to assess the extent of variability present in the population for different character, genotypic and phenotypic coefficients of variation were studied. The heritability which gives the relative role of genetic factors in the expression of phenotypes and also acts as an index of inheritance of a particular character to its offspring was also studied. The genetic advance measures the expected genetic gain from the selection applied in a population. Heritability along with genetic advance will help to fix the possible genetic control for any particular characters. The genetic divergence enables the evaluation of genotypes without actual crossing and grouping the genetic material into distinct clusters in a significant pattern.

In the present investigation, entitled "Genetic diversity in F_4 generation lines of groundnut (*Arachis hypogaea L.*)" attempts were made to study the variability parameters for twenty different characters among 31 genotypes, genetic divergence among all genotypes. The following sub-heads are taken into consideration, while discussing the results on various aspects.

5.1 Genetic variability

5.2 Genotypic and phenotypic coefficient of variation

5.3 Heritability (b.s.) and genetic advance

5.4 Genetic divergence

5.1 Genetic variability

A wide range of variability was observed in respect of number of pegs per plant (11.70-68.40), plant height (16.90-39.80), number of mature pods per plant (8.60-47.40), dry haulm yield per plant (12.80-35.80 g), dry pod yield per plant (9.50-29.20 g), harvest index (20.80-40.70), days to maturity (117.35-131.15 days) and number of immature pods per plant (2.80-16.30).

This indicated a great scope for exploitation of these traits. The findings of Reddy *et al.* (1995), Gowda *et al.* (1996), Singh *et al.* (1996), Khurram *et al.* (1998), Gimenes *et al.* (2000) were similar to the results of the present research. The rest of the characters (Table 4.3) exhibited comparatively less variability.

5.2 Genotypic and phenotypic coefficient of variation

The magnitudes of phenotypic coefficient of variation (PCV) were magnitudinally higher than the estimates of genotypic coefficient of variation (GCV) for all the characters studied (Fig. 1) indicating the influence of environment on all these traits.

The PCV estimates were higher for number of immature pods per plant, number of mature pods per plant, number of pegs per plant, dry pod yield per plant, dry haulm yield per plant, plant height, number of branches per plant, peg to pod ratio, harvest index. These results confirmed earlier findings of Ganeshan and Sudhakar (1995), Jayalakshmi *et al.*

(1998), Ramesh Kumar *et al.* (1998), Yadav *et al.* (1998), Prakash *et al.* (2000), Aghav (2010) and John *et al.* (2009).

The GCV estimates were higher for number of immature pods per plant, number of mature pods per plant, number of pegs per plant, dry haulm yield per plant, dry pod yield per plant, plant height, number of branches per plant, harvest index, peg to pod ratio. This confirmed the earlier results of Reddy *et al.* (1995), Jayalakshmi *et al.* (1998), Islam and Rasul (1998), Yadav *et al.* (1998), Ramesh Kumar *et al.* (1998) and John *et al.* (2009).

Low GCV and PCV values were observed for character shelling percentage, sound mature kernal, leaf temperature, indicating hardly any scope for improvement of these traits by selection. These results are in confirmity with the earlier findings of Korat *et al.* (2009).

5.3 Heritability and genetic advances

Heritability is used to predict the resemblance between parents and their progeny. Whereas, the genetic advance provides the knowledge about expected gain for a particular character after selection.

In general, in self-pollinated crops, characters with high heritability possess high genetic advance which is said to be governed by additive gene action suggesting direct selection for traits. In contrast, high heritability with low genetic advance or low heritability with high genetic advance are the results of non-additive gene action and selection for such traits may not be rewarding.

In the present investigation, number of pegs per plant, dry haulm yield per plant, number of mature pods per plant, plant height, dry pod yield per plant, harvest index and number of immature pods per plant had high heritability along with high genetic advance indicating that these traits were governed by additive gene action and simple selection would be effective.

Similar results were observed by Ganeshan and Sudhakar (1995), Jayalakshmi *et al.* (1998), Islam and Rasul (1998), Vasanthi *et al.* (1998), Yadav *et al.* (1998), Singh and Singh (1999), Prakash *et al.* (2000) and John *et al.* (2009).

The traits *viz.*, oil content, photosynthetic rate, days to 50 % flowering, day to maturity, percent oil content, percent protein content exhibited high heritability coupled with low genetic advance indicating importance of non-additive gene action in the inheritance of these traits. Heterosis breeding may be useful in such characters. Similar results were obtained by Rudraswamy *et al.* (1999), Uddin *et al.* (1995) and Korat *et al.* (2009).

5.4 Genetic divergence

Selection of elite genotypes with high *per se* performance for yield and component characters along with high genetic divergence is important for starting any hybridization programme.

D^2 statistics, a concept developed by Mahalanobis's (1936) is important tool for plant breeder. It is useful in quantifying degree of divergence between biological population at

genotypic level and to assess the relative contribution of different components to the total divergence at both intra and inter cluster levels. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding.

5.4.1 Cluster formation intra and inter cluster distance and mean performance

The cluster formation i.e. intra and inter cluster divergence provide a basis for selecting genetically diverse parents belonging to different clusters. The crosses between strains of widely separated clusters with high inter cluster diversity are generally effective. It is assumed that the statistical distance (D) is index of genetic diversity.

In the present investigation clustering of genotypes following the Tocher's method as described by Rao (1952) led to formation of six clusters. The distribution of genotypes into different clusters is presented in Table 4.5. Cluster I with 14 genotypes was the largest, followed by cluster III containing 8 genotypes, cluster II containing 5 genotypes and cluster IV with 2 genotypes. Remaining clusters were monogenotypic. Similar results were obtained by Bansal and Satija (1992), Golakia and Makne (1992), Katule *et al.* (1992), Reddy and Reddy (1993), Nayak and Patra (1997), Johan Joel and Mylsamy (1998), Bera and Das (1999) and Rameshkumar *et al.* (1999).

It was observed that the maximum intra cluster distance was found in cluster III (D=16.73) which was followed by cluster I (D=12.97), cluster II (D=12.95) and cluster IV

(D=10.44). Remaining cluster were monogenotypic, therefore had no intra cluster distance.

The maximum inter cluster distance was observed between cluster II and cluster VI (D=56.13), followed by cluster IV and cluster VI (D=46.71), cluster I and cluster VI (D=41.63), cluster V and cluster VI (D=39.70) indicating wide divergence among the genotypes of these clusters. This also suggested that the genetic architecture of the genotypes in one cluster differs substantially from those included in other cluster (Table 4.6).

The minimum inter cluster distance was observed between cluster III and cluster VI (D=29.25). The lower inter cluster D values between these clusters suggested that the genetic constitution of the genotypes in these clusters were in close proximity (Table 4.6).

Based on cluster means of twenty characters (Table 4.7), it was observed that the cluster VI recorded the highest cluster mean for number of mature pods per plant and dry pod yield per plant.

5.5.2 Relative contribution of various characters for divergence

In the present investigation, the character specific leaf area (36.43) contributed highest towards genetic divergence. This was followed by dry haulm yield per plant (14.51), total chlorophyll (13.34), number of pegs per plant (11.61), dry pod yield per plant (4.20), oil content (3.87).The characters days to maturity, number of mature pods per plant (0.22), leaf temperature (0.43), sound mature kernel (0.65) had low

contribution towards divergence. The characters days to 50% flowering (0.00), number of branches per plant (0.00) and peg to pod ratio (0.00) had no contribution towards divergence.

On the basis of inter cluster distances, cluster means in present study, genotypes Phule Unnati, RHRG-1130, RHRG-1137, RHRG-1118, RHRG-1128 , RHRG-1106 , RHRG-1127 and RHRG-1110 were found to be overall superior genotypes for further breeding programme.

Table 5.1. Suggested genotypes for future hybridization programme

Sr. No.	Characters	Source clusters	Number of genotypes	Name of genotypes
1.	Dry pod yield per plant	VI, III, III	3	Phule Unnati, RHRG-1130, RHRG-1137
2.	Number of mature pods per plant	VI, III, III	2	Phule Unnati, RHRG-1130, RHRG-1127
3.	Hundred kernel weight	I	1	RHRG-1110
4.	Shelling %	II	1	RHRG-1106
5.	Oil content percentage	I, I	2	RHRG-1128, RHRG-1118

6. SUMMARY AND CONCLUSION

The present investigation on "Genetic diversity in F_4 generation lines of groundnut (*Arachis hypogaea L.*)" was undertaken to study genetic advance, heritability, GCV, PCV for twenty characters and to assess the genetic divergence average thirty one genotypes of summer groundnut. The genotypes were evaluated during summer, 2013, in a randomized block design with two replications. Observations were recorded on days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pegs per plants, number of mature pods per plant, peg to pod ratio, dry haulm yield per plant, number of immature pods per plant, dry pod yield per plant, hundred kernel weight, shelling percentage, harvest index, oil content, protein content, sound mature kernel, photosynthetic rate, leaf temperature, total chlorophyll percentage, specific leaf area.

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 kernal weight, total chlorophyll,

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.

It was observed that the estimates for genotypic coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the characters.

Number of immature pods per plant recorded the highest estimate for GCV followed by number of mature pods per plant, number of pegs per plant, dry haulm yield per plant, dry pod yield per plant, plant height. The high value of PCV was observed for number of immature pods per plant followed by number of mature pods per plant, number of pegs per plant, dry pod yield per plant, dry haulm yield per plant, plant height, harvest index. Low GCV and PCV value were recorded by character shelling percentage, sound of mature kernel, leaf temperature. Looking to the difference between GCV and PCV magnitudes, it was observed that all the characters except peg to pod ratio and no. of branches per plant showed low magnitudal difference between GCV and PCV estimates.

The range of D^2 values indicated adequate diversity between genotypes. On the basis of D values, all the thirty one genotypes were grouped into six clusters with substantial genetic divergence between them. Cluster I with 14 genotypes emerged as the largest cluster followed by cluster III with 8 genotypes, cluster II with 5 genotypes and cluster IV with 2 genotypes.

Remaining four clusters were monogenotypic. The maximum inter cluster distance was found between cluster II and cluster IV, while the minimum inter cluster distance was found between cluster III and cluster IV. On the basis of cluster means, inter cluster distances, and *per se* performance, following eight genotypes viz., Phule Unnati, RHRG-1130, RHRG-1137, RHRG-1127, RHRG-1106, RHRG-1110, RHRG-1128, RHRG-1118 have been suggested for future hybridization programme.

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*** Originals not seen**

8. VITA

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