GENETIC VARIABILITY FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SUMMER GROUNDNUT (*Arachis hypogaea L.*)

by

Mr. DHAGE MANOJKUMAR DATTATRAYA

(Reg. No. 11/042)

A Thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH,

RAHURI – 413 722 ; DIST. AHMEDNAGAR,

MAHARASHTRA (INDIA)

In partial fulfillment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE,

MAHATMA PHULE KRISHI VIDYAPEETH,

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2013

CANDIDATE'S DECLARATION

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

Place : M.P.K.V., Rahuri **(M. D. Dhage)**

Date : / / **2013**

Dr. C.B. Salunke,
Seed Production Officer,
Seed Cell,
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Rahuri – 413 722; Dist. Ahmednagar,
Maharashtra State (India).

CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC VARIABILITY FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SUMMER GROUNDNUT (*Arachis hypogaea L.*)",** submitted to the faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra State) in partial fulfillment 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 carried out by **Mr. DHAGE MANOJKUMAR DATTATRAYA,** under my guidance and supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation and sources of reference have been duly acknowledged.

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Place : M.P.K.V; Rahuri (**S.G. Borkar**)

Date : / /2013

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I place on record my sincere thanks to all those who helped me directly or indirectly in making of this work success.

Place : M.P.K.V., Rahuri. ***(M.D. Dhage)***

Date : / /2013

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LIST OF ABBREVIATIONS

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

ABSTRACT

GENETIC VARIABILITY FOR QUANTITATIVE AND QUALITATIVE TRAITS IN SUMMER GROUNDNUT (*Arachis hypogaea* L.)

by

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A candidate for the degree

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MAHATMA PHULE KRISHI VIDYAPEETH,

RAHURI – 413 722

2013

Research Guide : Dr. C.B. Salunke

Major discipline : Genetics and Plant Breeding

The present investigation entitled "Genetic variability for quantitative and qualitative traits in summer groundnut (*Arachis hypogaea* L.)" was undertaken to estimate the genetic variability, path analysis, correlation between dry pod yield and other yield contributing characters and genetic divergence on fifty germplasm lines and five checks of summer groundnut. Total 55 genotypes were evaluated during summer, 2012 season in a randomized block design with two

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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% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant, number of mature pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred kernel weight, oil percentage, protein content and sugar content.

The treatment differences were statistically significant for majority of the characters indicated the presence of good amount of variability. The character per cent oil content showed the highest heritability followed by per cent protein content, dry pod yield per plant, fresh pod yield per plant, number of mature pods per plant, days to maturity and days to 50% flowering. Other characters recorded moderate to low heritability. The fresh pod yield per plant showed the highest genetic advance followed by number of mature pods per plant, dry pod yield per plant, days to maturity and days to 50% flowering. Other characters showed moderate to low genetic advance.

The genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients. The characters, fresh pod yield per plant and number of mature pods per plant recorded highly significant and positive correlation with dry pod yield per plant. Whereas,

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number of mature pods per plant and per cent protein content exhibited significant and positive association with dry pod yield per plant. The path coefficient analysis revealed that the fresh pod yield per plant, hundred kernel weight, protein content, number of mature pods per plant and sugar content had highest positive direct effect on dry pod yield indicating the true and perfect association between these characters and dry pod yield. The correlation and path analysis studies revealed fresh pod yield per plant, number of mature pods per plant and hundred kernel weight as good indications of dry pod yield in groundnut.

The range of D^2 values indicated adequate diversity between the studied genotypes. On the basis of D^2 values, all the fifty five genotypes were grouped into eight clusters with substantial genetic divergence between them. Cluster I with 27 genotypes emerged as the largest cluster followed by cluster II with 15 genotypes, cluster IV with 6 genotypes and cluster III with 3 genotypes. Remaining four clusters were monogenotypic. The maximum inter cluster distance was found between cluster IV and cluster VI, while the minimum inter cluster distance was found between cluster I and cluster V.

Abstract contd..... ***M. D. DHAGE***

On the basis of cluster means, inter cluster distance, correlation studies and *per se* performance, following six genotypes of summer groundnut have been suggested for future hybridization programmes for crop improvement.

ICG-3266, ICG-4323, ICG-1971, ICG-3688, ICG-1954 and SB-XI.

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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 5.31 million hectares in the year 2011-12 with production of 7.07 million tonnes and productivity of 1323 kilogram per hectare (Source: Ministry of agriculture, Govt. of India, 2012).

In Maharashtra, total area under groundnut cultivation was 0.32 million hectare with production 0.35 million tonnes and productivity of 1158 kg per hectare during year 2011-12. (Source: Department of Economics and Statistics, Dept. of Agriculture and Cooperation, 2012).

Table No.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	2.72	1612
Andhra Pradesh	1.28	0.84	650
Tamil Nadu	0.46	1.06	2751
Rajasthan	0.41	0.81	1931
Karnataka	0.69	0.49	716
Maharashtra	0.32	0.35	1158
Madhya Pradesh	0.20	0.34	1618
Orissa	0.07	0.08	1147
Uttar Pradesh	0.09	0.09	1000
Others	0.25	0.11	---
All India	5.31	7.07	1323

(Source: Ministry of agriculture, Govt. of India, 2012 and Department of Economics and Statistics, Dept. of Agriculture and Cooperation, 2012).

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 hypogaea* Linn.
2. *Arachis hypogaea hirsuta* Kohler.
3. *Arachis hypogaea fastigiata* Waldron.
4. *Arachis hypogaea 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 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 than *Kharif* season. In summer, bud necrosis disease is the major cause of poor yield.

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

i) Optimum sowing time is not followed.
ii) Use of uncertified seeds.
iii) Recommended dose of fertilizer is not applied at proper time.
iv) Irrigation schedule is not followed properly.
v) 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. Summer is therefore, the ideal season for the cultivation of groundnut wherever irrigation facilities are available and soil is suitable. 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, associations, path coefficients and genetic diversity in a set of groundnut genotypes irrespective of their growth habit for yield and other component characters.

Keeping in view, in the above important aspects, the present investigation was carried out with the following objectives.

1. To study the amount and nature of variability and association among dry pod yield and yield contributing characters.
2. To study the direct and indirect contribution of component characters to the dry pod yield.
3. To study the nature and magnitude of divergence among different genotypes.

2. REVIEW OF LITERATURE

Attempts have been made to review the published literature on variability, path analysis 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 Character associations and path analysis in groundnut

2.3 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 seeds 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 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. Total 102 genotypes were evaluated during summer 2009, in a randomized block design with two replications at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, District - Ahmednagar (M.S).

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.

2.2 Character associations and path analysis

Vaddoria and Patel (1992) estimated character association and path analysis from data on ten yield related characters recorded on 50 Virginia runner groundnut genotypes grown during *Kharif* 1986 at Junagadh, Gujarat. Pod yield was significantly correlated with harvest index, shelling percentage, number of mature pods/plant, 100-seed weight and number of primary branches/plant at both the genotypic and phenotypic levels. Path analysis revealed that harvest index exerted the highest positive direct effect on yield followed by number of primary branches/plant. These two traits should thus be used in selection programmes for improving pod yield.

Uddin *et al.* (1995) studied variability, correlation and path coefficient analysis for seven yield components in 23 groundnut genotypes and found that at the genotypic level, seed yield/plant was significantly and positively correlated with days to maturity, seed/plant, plant height and primary branches/plant but was negatively associated with shelling percentage and 100-seed weight. Path analysis revealed that days to maturity, primary branches/plant and nuts/plant had large direct effects on seed yield/plant.

Ursal *et al.* (1995) studied correlation and path coefficients between yield components and pod yield for groundnut cv. JL-24 grown in pots with different sources, application rates and application data of Ca.

Khan *et al.* (1998) evaluated twenty exotic and indigenous peanut (*A. hypogaea*) genotypes to selected the

best ones. Cia has the highest harvest index (53.12 %) and pod yield. ICGS-2261 exhibited the highest haulm yield with lower harvest index (15.27 %). A positive and significant correlation (r = 0.553) existed between pod yield and harvest index, whereas a negative and significant correlation (r = -0.617) was observed between haulm yield and harvest index.

Salara and Gowda (1998) used F_2 progenies from crosses between three Spanish bunch cultivar (*A. hypogaea* sub sp. fastigiata) and four Virginia cultivars (*A. hypogaea* sub sp hypogaea) studied variability and correlation in 11 agronomic and yield related traits. Pod number and test weight were highly correlated with pod yield

Arjunan *et al.* (1999) studied genotypic correlations and path analysis for the six characters related to drought resistance and pod yield in 24 groundnut genotypes. Pod yield was negatively correlated with transpiration rate. Dry matter production had the highest positive direct effect on pod yield, while leaf area had the highest negative direct effect.

Antony *et al.* (2000) studied correlations in groundnut varieties. Plant height had a negative relationship with number of branches, total dry matter at harvest, net assimilation rate and nitrogenase activity; whereas it had positive relationship with leaf area index, crop growth rate, harvest index and leaf nitrogen content. Total dry matter at harvest had significant negative relationship with harvest index. Leaf area index was positively correlated with crop growth rate and negatively correlated with net assimilation

rate. Yield had positive correlation with total dry matter at 60 days after sowing, leaf area index, net assimilation rate, nitrogenase activity and leaf nitrogen. These parameters can be used as a tool in selecting varieties for better performance.

Santos *et al.* (2000) studied correlation and path coefficient analysis of five yield related traits in 11 groundnut genotypes with the objective of verifying their influence on seed production. The genotypes were cultivated under rainfed condition at Itabaiana, PB, Brazil in 1997 in a randomized block design with five replications. Path coefficient analysis revealed that pod yield had the highest positive effect on seed production. Direct effects of empty pod percentage, 100 pod weight and 100 seed weight were all negative and showed a tendency to reduce the correlation with seed yield.

Venkataravana *et al.* (2000) carried out correlation and path analysis for pod yield and some of its component characters, in 144 germplasm accession of groundnut. The genotypic correlation coefficients were observed to be relatively higher magnitude than the corresponding phenotypic correlation coefficient indicating strong inherent association between the characters. Pod yield had positive and significant association with plant height, number of branches, total number of pods, number of matured pods, shelling per cent, haulm yield, 100 kernel weight, SMK, harvest index, kernal yield and oil yield. Path analysis also revealed the importance of these traits as they had affected pod yield directly indicating the importance of selection based on these traits for rapid improvement of pod yield.

Sah *et al.* (2000) studied correlation and path analysis in 24 genotypes of mutant cultures of groundnut (*Arachis hypogaea* L.). Pod yield/plant was positively and significantly correlated with number of pods per plant, 100 seed weight, harvest index, seed yield/plant, oil yield/plant, whereas, it was negatively associated with shelling percentage. Oil yield per plant was positively associated with number of pods per plant, 100 seed weight, harvest index, seed yield/plant, number of primary branches/plant and number of seeds/pod. The seed yield/plant, an important character, had high direct effect on pod as well as oil yield/plant.

Bera and Das (2000) evaluated forty four genotypes of groundnut for path coefficient analysis for three years at two locations.

Sumathi and Muralidharan (2007) reported that in the yield improvement programme of groundnut, the knowledge on the phenotypic and genotypic inter-relationships between pod and kernel characteristics would help the breeder to formulate effective selection programme.

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**.**

Dhaliwal *et al.* (2010) estimated inter trait associations along with direct and indirect effects by path analysis for dry pod yield and its components in groundnut and showed that dry pod yield had significant positive association with days to flowering, days to maturity, haulm yield per plant and kernel yield per plant.

Babariya and Dobariya (2012) estimated correlation coefficients and direct and indirect effects by path analysis for pod yield per plant and its components by using 100 genotypes of Spanish bunch groundnut. The pod yield per plant was significantly and positively correlated with days to maturity, plant height, number of pods per plant, kernel yield per plant, number of mature pods per plant, 100-kernel weight, biological yield per plant and harvest index.

2.3 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 monogenotypic. 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 form different geographicalorigins to assess the genetic diversity by using Mahalanobis's D^2 statistics.

Singh *et al.* (2010) Thirty two groundnut genotypes of both spreading and bunch types were evaluated for their yield, yield attributes, seed protein and oil content to analyse 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% in shelling percent, 11-27% in harvest index, 20.8-28.9% in protein and 39.6-49.1% 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 .The genotypes were evaluated during 2008 in a Randomized Block Design with two replications at All India Co-ordinated Research Project on Groundnut, Mahatma Phule Krishi Vidyapeeth, Rahuri, District-Ahmednagar (M.S). Appreciable amount of variability was observed for all the characters studied. The magnitude of genotypic and

phenotypic coefficient of variation indicated the presence of good amount of variability for different characters.

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, charecter 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 variability for quantitative and qualitative traits in Summer 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, 2012. 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 fifty germplasm lines of groundnut received from ICRISAT, Hyderabad and five checks (TPG-41, TAG-24, JL-501, SB-XI, RHRG-6021) (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 45 cm between rows and 15 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 18th February

2012 by dibbling single seed per hill at 45 × 15 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 germplasm lines and their source

Sr. No.	Name of genotype	Source
1.	ICG-1954	ICRISAT Hyderabad
2.	ICG-1971	ICRISAT Hyderabad
3.	ICG-1984	ICRISAT Hyderabad
4.	ICG-1986	ICRISAT Hyderabad
5.	ICG-2151	ICRISAT Hyderabad
6.	ICG-2158	ICRISAT Hyderabad
7.	ICG-2162	ICRISAT Hyderabad
8.	ICG-2167	ICRISAT Hyderabad
9.	ICG-2171	ICRISAT Hyderabad
10.	ICG-2186	ICRISAT Hyderabad
11.	ICG-2252	ICRISAT Hyderabad
12.	ICG-2306	ICRISAT Hyderabad
13.	ICG-2318	ICRISAT Hyderabad
14.	ICG-2320	ICRISAT Hyderabad
15.	ICG-2367	ICRISAT Hyderabad
16.	ICG-2379	ICRISAT Hyderabad
17.	ICG-2381	ICRISAT Hyderabad
18.	ICG-2718	ICRISAT Hyderabad
19.	ICG-2951	ICRISAT Hyderabad
20.	ICG-3013	ICRISAT Hyderabad

21.	ICG-3075	ICRISAT Hyderabad
22.	ICG-3136	ICRISAT Hyderabad
23.	ICG-3215	ICRISAT Hyderabad
24.	ICG-3243	ICRISAT Hyderabad
25.	ICG-3244	ICRISAT Hyderabad
26.	ICG-3249	ICRISAT Hyderabad
27.	ICG-3254	ICRISAT Hyderabad
28.	ICG-3266	ICRISAT Hyderabad
29.	ICG-3267	ICRISAT Hyderabad
30.	ICG-3285	ICRISAT Hyderabad
31.	ICG-3287	ICRISAT Hyderabad
32.	ICG-3297	ICRISAT Hyderabad
33.	ICG-3309	ICRISAT Hyderabad
34.	ICG-3382	ICRISAT Hyderabad
35.	ICG-3398	ICRISAT Hyderabad
36.	ICG-3413	ICRISAT Hyderabad
37.	ICG-3445	ICRISAT Hyderabad
38.	ICG-3518	ICRISAT Hyderabad
39.	ICG-3634	ICRISAT Hyderabad
40.	ICG-3656	ICRISAT Hyderabad
41.	ICG-3686	ICRISAT Hyderabad
42.	ICG-3688	ICRISAT Hyderabad
43.	ICG-3689	ICRISAT Hyderabad
44.	ICG-3740	ICRISAT Hyderabad
45.	ICG-3745	ICRISAT Hyderabad
46.	ICG-3772	ICRISAT Hyderabad
47.	ICG-3819	ICRISAT Hyderabad

48.	ICG-4323	ICRISAT Hyderabad
49.	ICG-4581	ICRISAT Hyderabad
50.	ICG-8321	ICRISAT Hyderabad
51.	RHRG-6021	MPKV, Rahuri
52.	JL-501	ARS, Jalgaon, MH
53.	SB-XI	ARS, Jalgaon, MH
54.	TAG-24	Trombay, MH
55.	TPG-41	Trombay, MH

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% flowering

Number of days required from sowing to day on which 50 per cent of the plants flowered was recorded as days to 50% 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 Number of primary branches per plant

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

3.2.5.4 Number of secondary branches per plant

The number of secondary branches per plant was counted at the time of harvest.

3.2.5.5 Number of immature pods per plant

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

3.2.5.6 Number of mature pods per plant

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

3.2.5.7 Fresh pod yield per plant (g)

The total weight of both mature and immature pods taken at the time of harvest was recorded as the fresh pod yield per plant (g).

3.2.5.8 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.

3.2.5.9 Hundred kernel weight (g)

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

3.2.5.10 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).

3.2.5.11 Oil content percentage

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

3.2.5.12 Sugar content percentage

The sugar percentage of the Groundnut sample was estimated by Phenol-sulphuric acid method.

3.3 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.

3.3.1 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 (1929, 1938) as described by Rao (1950).

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

3.3.2 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

$\bar{x}$ = 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,

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

3.3.3 Correlations

Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariances were calculated as per the formulae given by Singh and Chaudhari (1977) as below.

Environmental covariance

$(eCOV_{1.2})$ = EMP

Genotypic covariance $(gCOV_{1.2})$

$$= \frac{GMP - EMP}{r}$$

Phenotypic covariance $(pCOV_{1.2})$

$$= (gCOV_{1.2}) + (eCOV_{1.2})$$

Appropriate variance and covariances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955).

The phenotypic correlation coefficient (rp) was calculated as,

$$rp_{1.2} = \frac{pCOV_{1.2}}{\sqrt{(\sigma^2 p_1)\,(\sigma^2 p_1)}}$$

Where,

$rp_{1.2}$ = Phenotypic correlation coefficient between Characters 1 and 2

$pCOV_{1.2}$ = Phenotypic covariance between 1 and 2

$\sigma^2 p_1$ and $\sigma^2 p_2$ = Phenotypic variance of character 1 and 2, respectively.

The genotypic correlation coefficient (rg) was calculated as,

$$rg_{1.2} = \frac{gCOV_{1.2}}{\sqrt{(\sigma^2 g_1)\,(\sigma^2 g_1)}}$$

Where,

$rg_{1.2}$ = Genotypic correlation coefficient between character 1 and 2

$gCOV_{1.2}$ = Genotypic covariance between 1 and 2

$\sigma^2 g_1$ and $\sigma^2 g_2$ = Genotypic variance of character 1 and 2, respectively

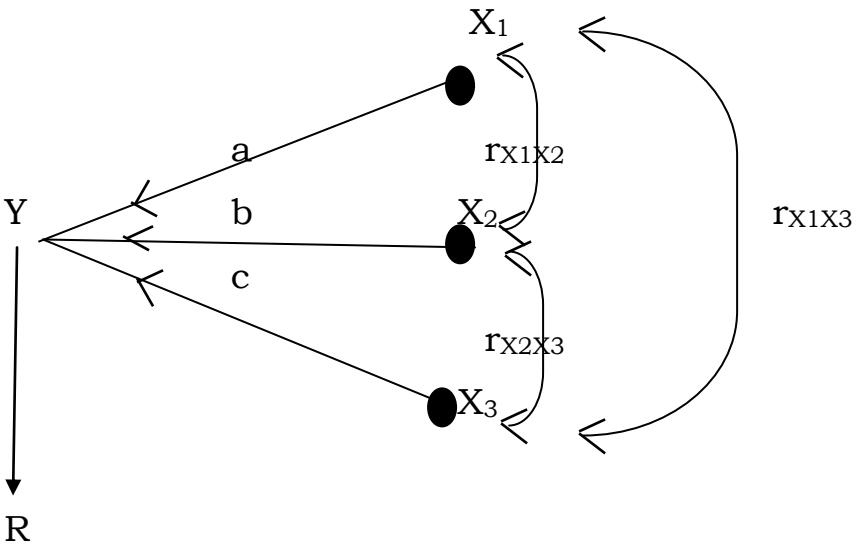
Significance of the various correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedecor and Cochran, 1967).

3.3.4 Path analysis

To establish a cause and effect relationship, the genotypic correlation were partitioned into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959). The first step in path analysis is to prepare a path diagram based on cause and effect.

The concept behind path analysis is that yield(Y) is the function of various components like X_1, X_2, X_3, etc.

Then these components show following type of association with one another.



From figure it is observed that yield is the result of X_1, X_2 and X_3 and other undefined factors designated by 'R'. The double arrowed lines indicates mutual association as a measured by correlation coefficient and the single arrowed lines represents direct influence as a measured by path coefficient Pij.

Path coefficients were obtained by solving a set of simultaneous equation of the form.

$$r_{ny} = P_{ny} + r_{n2}p_{2y} + r_{n3}p_{3y} + \ldots\ldots\ldots\ldots$$

Where,

r_{ny} represents correlation between one component and yield.

p_{ny} represent path coefficient between that character and yield.

r_{ny} represents correlation between that character and each of the other yield components in turn.

Matrix 'A'			Matrix 'B'
r_1y	1	$r_{1.2}$	$r_{1.3}$.....r_1n
r_2y	$r_{2.1}$	1	$r_{2.3}$.....r_2n
rny	rn_1	rn_2	rn3.....1

Where,

$r_{1.2}$ = $r_{2.1}$ and so on and rny

= Correlation between one component character and yield

The 'B' matrix was inverted (B^{-1}) and path coefficients (Pij) were obtained as (Pig) = A x (B^{-1}).

The indirect effects of a particular character through other characters were obtained by a multiplication of direct path effect and particular correlation coefficients between those characters separately.

Indirect effect =r_{ij} x P_{ij}

Where,

i = 1 to 12

j = 1 to 12 and

P_{ij} = P_1Y, P_2Y,.....,PnY

Path coefficient (Pij), correlation coefficient (rij) and residual factor (R) were diagrammatically presented. The residual factors i.e. variation in yield unaccounted for by these associations were calculated from the following formula.

$$\text{Residual factor (R)} = \sqrt{(1-R^2)}$$

Where,

$$R^2 = P_{1y}.r_{1y} + P_{2y}.r_{2y} + P_{3y}.r_{3y} + \ldots\ldots\ldots P_{ny}.r_{ny}$$

Where,

$P_{1y}, P_{2y}, \ldots\ldots, P_{ny}$ = Path values

$r_{1y}, r_{2y}, \ldots\ldots, r_{ny}$ = Correlation coefficients

3.3.5 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. $\sum (Y_i{}^1 - \overline{Y}_i{}^2)$. ¯

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 variability for quantitative and qualitative traits in summer 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 twelve characters of fifty-five 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 28.50 to 39.00 days. The population mean for this character was 33.80 days. 25 out of 55 genotypes flowered significantly earlier than the population mean. The genotype ICG-3689 (28.50) was the earliest followed by ICG-3740 (29.50), ICG-3445 and ICG-3309 (30.50 each). The genotypes TAG-24 (39.00), SB-XI, TPG-41 (38.00 each) and RHRG-6021, ICG-2379 (37.50 each) were comparatively late in days to 50% flowering.

4.1.2 Days to maturity

Twenty three out of fifty five genotypes showed significantly early maturity when compared with the population mean of 120.38 days. The variation for this character ranged between 107.50 (SB-XI) to 127.00 (ICG-3688) days. The genotype SB-XI recorded the lowest days to maturity (107.50) followed by JL-501 (113.00). The genotypes ICG-3688 (127.00), ICG-3285

(126.00) and ICG-2379 (125.50) were comparatively late in maturity.

4.1.3 Number of primary branches per plant

The variation for number of primary branches per plant ranged between 5.50 and 7.00. Looking to the population mean of 6.12 branches per plant, twenty five genotypes showed higher branches than population mean. ICG-2367, ICG-3398, ICG-1971, ICG-2306, JL-501, SB-XI and TPG-41 were the genotypes possessing high number of primary branches per plant. The treatment differences for this trait were non-significant.

4.1.4 Number of secondary branches per plant

Thirty three genotypes showed higher number of secondary branches when compared with the population mean of 10.47 branches per plant. The variation for number of secondary branches per plant ranged between 7.50 and 13.00. SB-XI (13.00), RHRG-6021, ICG-3689, ICG-3287 (12.50 each), ICG-4581, ICG-3634, ICG-3013 and ICG-2151 (12.00 each) were the genotypes possessing high number of secondary branches per plant.

4.1.5 Number of immature pods per plant

The number of immature pods per plant ranged between 3.00 (ICG-1954, RHRG-6021) and 6.00 (ICG-3243), while the population mean was 4.27. Thirty one genotypes showed lower number of immature pods per plant than population mean.

ICG-4581, ICG-4323, ICG-1971, ICG-2171, ICG-3244, ICG-3745 and RHRG-6021(3.00 each) produced lowest number of immature pods per plant. The treatment differences for this trait were non-significant.

4.1.6 Number of mature pods per plant

The variation for the character ranged between 14.00 (SB-XI, ICG-3634, ICG-3309) and 33.00 (ICG-4323). The population mean for this character was 18.47. Twenty five genotypes showed higher number of mature pods per plant over population mean of which ICG-4323 (33.00), ICG-3266 (28.00), ICG-2252 (24.00), ICG-1971 (23.50) produced the highest number of mature pods per plant.

4.1.7 Fresh pod yield per plant (g)

The range observed for fresh pod yield per plant was between 12.18 (ICG-3413) and 32.50 (ICG-3266). Twenty one genotypes recorded significantly more fresh pod yield per plant as compared to the population mean of 18.59 g. The genotype ICG-3266 (32.50) ranked first followed by ICG-4323 (30.43) and ICG-1971 (28.45). However, ICG-3413 (12.18), ICG-3249 (13.84) and ICG-3309 (14.68) showed less fresh pod yield per plant.

4.1.8 Dry pod yield per plant (g)

Population mean for dry pod yield per plant was 13.90 g. The genotype ICG-3266 (27.71) recorded the highest dry pod yield per plant followed by ICG-4323 (23.45), ICG-1971 (22.05) and ICG-3267 (19.25). The genotype ICG-3249 (8.44) alongwith ICG-3413 (9.92) recorded low yield. Eighteen out of 55 genotypes

showed higher mean values for this character than population mean.

4.1.9 Hundred kernel weight (g)

The variation for this character ranged between 31.12 (ICG-1986) and 41.39 (ICG-1954). Eighteen out of 55 genotypes showed numerically high hundred kernel weight when compared with population mean of 34.42 g. Genotypes ICG-1954(41.39), ICG-2151 (40.42), ICG-2320 (38.47) and ICG-3215 (37.76) showed higher hundred kernel weight.

4.1.10 Oil content (%)

The population mean for this character was 46.91 per cent. The genotype ICG-2252 (43.95) recorded the lowest oil content while the genotype ICG-3688 (50.05) recorded highest oil content followed by ICG-1971 (50.00), ICG-2951 (49.22) and ICG-3740 (49.05). Twenty nine genotypes recorded high value for oil content as compared to population mean.

4.1.11 Protein content (%)

The protein content in 55 summer genotypes ranged between 21.21 (ICG-3254) and 26.50 (ICG-2167) with a population mean of 24.19 per cent. The genotypes ICG-2167 (26.50), ICG-3445, ICG-3266 (26.37), and ICG-2151 (26.30) recorded the highest amount of per cent protein. In contrast the genotypes ICG-3254 (21.21), ICG-4323 (21.79), ICG-3285 (22.21) recorded lowest values for protein content.

4.1.12 Sugar content (%)

The population mean for sugar content was 12.34 per cent. The genotype ICG-2379 (10.45) recorded the lowest sugar

content while the genotype ICG-3215 (13.75) recorded highest sugar content followed by ICG-3249 (13.67), ICG-2381 (13.56) and RHRG-6021 (13.55). Twenty nine genotypes recorded high value for sugar content as compared to population mean.

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 primary branches per plant, no. of immature pods per plant and sugar content (%), indicating appreciable amount of diversity 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 coefficients of variation (GCV) were lower than the phenotypic coefficients of variation (PCV) for all the characters.

Number of primary branches per plant (24.20) recorded the highest estimate for GCV followed by dry pod yield per plant (21.75), no. of immature pods per plant (20.21), fresh pod yield per plant (18.26), no. of mature pods per plant (16.68) and sugar content (13.17). The highest value of PCV were observed for no. of immature pods per plant (31.06), followed by dry pod yield per plant (26.29), no. of primary branches per plant (26.26), fresh pod yield per plant (22.25), number of mature pods per plant (20.53), and per cent sugar content (16.84).

Table 4.2 Analysis of variance for twelve characters in summer groundnut

Sr. No	Characters	MSS	
		Treatment	Error
1	Days to 50% flowering	10.92**	3.14
2	Days to maturity	18.68**	3.91
3	Number of primary branches per plant	0.38	4.77
4	Number of secondary branches per plant	3.36**	1.52
5	Number of immature pods per plant	1.02	2.51
6	Number of mature pods per plant	23.88**	4.88
7	Fresh pod yield per plant (g)	28.63**	5.58
8	Dry pod yield per plant (g)	22.49**	4.21
9	Hundred kernel weight	9.93**	4.43
10	Oil content (%)	4.08**	0.08
11	Protein content (%)	4.18**	0.10
12	Sugar content (%)	1.68	6.93

Low GCV and PCV value were recorded by characters days to maturity (2.26 and 2.79), oil content percentage (3.02 and 3.08), protein content percentage (5.91 and 6.05), and hundred kernel weight (4.82 and 7.79 g).

4.3.2 Heritability (b.s.)

The heritability (b.s.) estimates were high in case of characters *viz.*, per cent oil content (96.10%), per cent protein content (95.20%), dry pod yield per plant (68.50%), fresh pod yield per plant (67.40%), no. of mature pods per plant (66.10%), days to maturity (65.40%), days to 50% flowering (55.30%). It was medium for hundred kernel weight (38.30%) and no. of secondary branches per plant (37.60%). The characters, no. of primary branches per plant (-85.00%), percent sugar content (-61.20%) and no. of immature pods per plant (-42.40%).

4.3.3 Genetic advance

The highest magnitude of genetic advance was observed for fresh pod yield per plant (5.74) followed by no. of mature pods per plant (5.16), dry pod yield per plant (5.15), days to maturity (4.53) and days to 50% flowering (3.02). The lowest value of genetic advance was observed for number of primary branches per plant (-2.81) followed by per cent sugar content (-2.62) and number of immature pods per plant (-1.16).

Genetic advance as a per cent of mean was the highest for dry pod yield per plant (37.09) followed by fresh pod yield per plant (30.87) and number of mature pods per plant (27.94). In contrast, number of primary branches per plant (-45.95) recorded lowest value followed by number of immature

pods per plant (-27.11) and sugar content (-21.22).

4.4 Correlation

The simple genetic correlation coefficients among the twelve characters are provided in Table 4.4.

4.4.1 Association of dry pod yield with other characters

The characters, fresh pod yield per plant (0.93) and number of mature pods per plant (0.93) showed highly significant and positive association with dry pod yield per plant. The character per cent protein content (0.22) showed significant and positive correlation with dry pod yield per plant.

The characters, days to 50% flowering (0.01), days to maturity (0.07), number of primary branches per plant (0.2), hundred kernel weight (0.18) and per cent oil content (0.16), percent sugar content (0.07) showed positive and non-significant correlation with dry pod yield per plant. Whereas, character number of secondary branches per plant (-0.30), number of immature pods per plant (-0.22) and per cent oil content (-0.16) showed negative and non-significant correlation with dry pod yield per plant.

4.4.2 Association between remaining characters

The correlation between other characters at genotypic level are presented below,

Days to 50% flowering recorded significant positive correlation with number of mature pods per plant.

Days to maturity recorded highly significant positive correlation with hundred kernel weight.

Number of primary branches per plant showed highly significant and positive correlation with hundred kernel weight and significant and positive correlation with sugar content.

Number of secondary branches per plant exhibited highly significant and positive correlation with percent oil content.

Number of mature pods per plant recorded highly significant and positive correlation with fresh pod yield per plant. It showed significant and positive correlation with hundred kernel weight.

4.5 Path coefficient analysis

The genotypic correlation is due to common genotypic factors responsible for the inheritance of the traits in question, hence it indicates inherent relationship. The path coefficient analysis therefore was extended to genotypic correlations only to know the direct and indirect genotypic effects of each yield contributing character on dry pod yield per plant. The path coefficients computed for twelve components on dry pod yield per plant are presented in Table 4.5 and depicted in Fig. 3.

4.5.1 Direct effects

In present investigation it was found that fresh pod yield per plant (1.3074) exerted maximum direct effects toward dry pod yield per plant, followed by number of mature pods per plant (0.5725), hundred kernel weight (0.3609), protein content (0.1423) and sugar content (0.0575). However, six traits *viz.,* number of secondary branches per plant (-0.4010), number of primary branches per plant (-0.2946), days to maturity (-0.2159), oil content (-0.1495), number of immature pods per plant

(-0.0916) and days to 50% flowering (-0.0857) had negative direct effect on dry pod yield per plant.

4.5.2 Indirect effect

All the independent characters except fresh pod yield per plant, hundred kernel weight, protein content, number of mature pods per plant and sugar content exhibited very low indirect effects. Fresh pod yield had positive indirect effect via number of mature pod per plant (1.0045) followed by number of immature pod per plant (0.2003), days to 50% flowering (0.1420), protein content (0.1361), hundred kernel weight (0.1310) and sugar content (0.1252), while it had negative indirect effect via number of secondary branches per plant (-0.2959) and oil content (-0.0386).

Hundred kernel weight had positive indirect effect via days to maturity (0.1210), number of primary branches per plant (0.0918), number of mature pods per plant (0.0808) and fresh pod yield per plant (0.0361), while it had negative indirect effect via protein content (-0.0870), number of immature pods per plant (-0.0637), sugar content (-0.0263) and oil content (-0.0258).

Protein content had positive indirect effect via days to 50% flowering (0.0158), fresh pod yield per plant (0.0104) and number of primary branches per plant (0.0085), while it had negative indirect effect via hundred kernel weight (-0.0278), oil content (-0.0267), days to maturity (-0.0127), number of secondary branches per plant (-0.0156) and sugar content (-0.0104).

Number of mature pods per plant showed positive indirect effects via number of secondary branches per plant

(0.2431) followed by hundred kernel weight (0.1283), oil content (0.1128), protein content (0.0681) and sugar content (0.0378), while it showed negative indirect effects via number of immature pods per plant (-0.1784), days to 50% flowering (-0.1113) and days to maturity (-0.0718).

Sugar content exhibited positive indirect effect via number of immature pods per plant (0.0280), number of primary branches per plant (0.0138), number of secondary branches per plant (0.0042), oil content (0.0019) and fresh pod yield per plant (0.0018), while it had negative indirect effect via protein content hundred kernel weight (-0.0088), days to 50% flowering (-0.0062) and days to maturity (-0.0052).

4.6 Divergence analysis

Genetic divergence in fifty five genotypes of summer groundnut was estimated using D^2 statistics (Mahalanobis, 1936). The D^2 values corresponding to pair of comparison between fifty five genotypes ranged between 4.36 and 396.81.

4.6.1 Cluster formation

The cluster formation was done by following Tocher's method, as described by Rao (1952). All the 55 genotypes studied under investigation were grouped into eight clusters as presented in Table 4.6.

Cluster I with 27 genotypes emerged as the largest cluster followed by cluster II with 15 genotypes, cluster IV with 6 genotypes and cluster III with 3 genotypes. Cluster V, VI, VII and VIII included one genotype each (monogenotypic).

4.5.2 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 4.7.

Cluster IV exhibited maximum intra cluster distance i.e. (D=7.81), followed by cluster II (D=6.11), cluster I (D=5.90) and cluster III (D=4.70).

Being monogenotypic, remaining clusters showed no intra cluster distance.

Table 4.6 Distribution of 55 genotypes of summer groundnut into different clusters

Clusters No.	Total number of genotypes included	Genotypes
I	27	ICG-03113,ICG-03634,ICG-03686, ICG-02186, ICG-02158, ICG-03243, ICG-04581, ICG-03309, ICG-03297, ICG-02320, ICG-03413, ICG-03244, ICG-03136, ICG-03287, ICG-03285, ICG-03745, ICG-02171, TAG-24, ICG-08321, ICG-02162, ICG-03772, ICG-01954, ICG-03398, ICG-02306, ICG-03249, ICG-03267, ICG-03518
II	15	ICG-02718, ICG-03382, ICG-03656, ICG-03445, ICG-01986, ICG-02167, TPG-41, ICG-03819, ICG-02381, ICG-02367, ICG-03215, ICG-01984, ICG-02318, ICG-03266, ICG-02151
III	3	ICG-02252,ICG-03075,RHRG-6021
IV	6	ICG-02951, ICG-03740, JL-501, ICG-01971, ICG-03688, ICG-03689
V	1	ICG-03254
VI	1	ICG-02379
VII	1	SB-XI
VIII	1	ICG-04323

Table 4.7 Average intra and inter cluster D values

Clusters	I	II	III	IV	V	VI	VII	VIII
I	5.90	9.04	9.99	10.46	7.20	9.63	10.85	9.93
II		6.11	8.25	11.43	13.30	13.02	11.84	14.83
III			4.70	15.67	13.39	9.16	13.60	15.47
IV				7.81	12.43	17.50	10.14	12.32
V					0.00	8.94	12.55	7.77
VI						0.00	16.41	12.61
VII							0.00	13.57
VIII								0.00

The maximum inter cluster distance was observed between cluster IV and cluster VI (D=17.50), followed by cluster VI and cluster VII (D=16.41), cluster III and cluster IV (D=15.67), cluster III and cluster VIII (D=15.47) and cluster III and cluster VII (D=13.60). The lowest inter cluster distance was observed between cluster I and cluster V (D=7.20).

4.6 Cluster means

The cluster means for twelve characters studied are given in Table 4.8. It revealed wide range of variability for most of the characters. On perusal of Table 4.8, it was observed that cluster II had highest cluster means for protein content (25.78) and sugar content (12.53%). Cluster III had the lowest cluster mean for oil content (44.31%). Cluster IV had the highest cluster mean for oil content (49.36%). In contrast, it showed lowest cluster mean for days to 50% flowering (32.75).

Cluster V had the highest cluster mean for hundred kernel weight (37.57g) and number of immature pods per plant (5.00), while the lowest cluster mean for fresh pod yield per plant (15.31g), dry pod yield per plant (10.70g) and protein content (21.21).

Cluster VI had the lowest cluster mean for traits no. of primary branches per plant (5.50), no. of secondary branches per plant (8.50) and sugar content (10.46%), while the highest cluster mean for days to maturity (125.50) and no. of immature pods per plant (5.00).

Clusters VII ranked the highest in respect of days to 50% maturity (38.00), no. of primary branches per plant (6.50), no. of secondary branches per plant (13.00). Cluster VII had the

Table 4.8 Cluster means for twelve characters in summer groundnut

lowest cluster mean for traits, days to maturity (107.50), no. of mature pods per plant (14.00) and hundred kernel weight (31.67g).

Cluster VIII had the lowest cluster mean for no. of immature pods per plant (3.00), while the highest cluster mean for traits, number of mature pods per plant (33.00), fresh pod yield per plant (30.44g) and dry pod yield per plant (23.45g).

4.9 Per cent contribution of various characters for divergence

All the 55 genotypes of summer groundnut were studied for twelve different characters and the data collected was used to determine genetic divergence. Out of twelve characters studied, the character per cent oil content (43.57%) contributed the highest for divergence and was followed by percent protein content (42.49%), days to maturity (4.98%), dry pod yield per plant (3.37%), number of mature pods per plant (2.42%), days to 50% flowering (1.08%), fresh pod yield per plant (1.01%) and hundred kernel weight (0.94%). However, the traits number of primary branches per plant, number of immature pods per plant and percent sugar content had no contribution towards divergence. (Table 4.9)

Table 4.9 Contribution of various characters to divergence

Sr. No.	Characters	Times ranked Ist	Contribution (%)
1.	Days to 50% flowering	16	1.08
2.	Days to maturity	74	4.98
3.	No. of primary branches per plant	0	0.00
4.	No. of secondary branches per plant	2	0.13
5.	No. of immature pods per plant	0	0.00
6.	No. of mature pods per plant	36	2.42
7.	Fresh pod yield per plant (g)	15	1.01
8.	Dry pod yield per plant (g)	50	3.37
9.	Hundred kernel weight (g)	14	0.94
10.	Oil content (%)	647	43.57
11.	Protein content (%)	631	42.49
12.	Sugar content (%)	0	0.00

5. DISCUSSION

Success of any plant breeding programme depends on selection of elite genotypes which ultimately depends on knowledge of variability and genetic diversity of the germplasm. Therefore, to assess the extent of variability present in the population for particular characters, 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 correlation study provides the interrelationships among the quantitative characters which facilitates the choice of suitable parents for the improvement in the crop. 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 variability for quantitative and qualitative traits in summer groundnut (*Arachis hypogaea L.*)" attempts were made to study the variability for twelve different characters among 55 genotypes, the correlation between the dependant and independent variables and 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 Correlation

5.5 Genetic divergence

5.1 Genetic variability

A wide range of variability was observed in respect of days to 50% flowering (28.50-39.00 days), days to maturity (107.50-127.00 days), no. of secondary branches per plant (7.50-13.00), number of mature pods per plant (14.00-33.00), fresh pod yield per plant (12.18-32.50 g), dry pod yield per plant (8.45-27.71 g), hundred kernel weight (31.12-41.39 g) and oil content (43.95-50.05%).

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 estimates 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 these traits.

The PCV estimates were higher for number of immature pods per plant, dry pod yield per plant, number of primary branches per plant, fresh pod yield per plant, number of mature pods per plant, per cent sugar content and number of primary branches per plants. 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 primary branches per plant, dry pod yield per plant, number of immature pods per plant, fresh pod yield per plant, number of mature pods per plant and percent sugar content. 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 days to 50% flowering, hundred kernel weight, percent protein content, per cent oil content and days to maturity, 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.

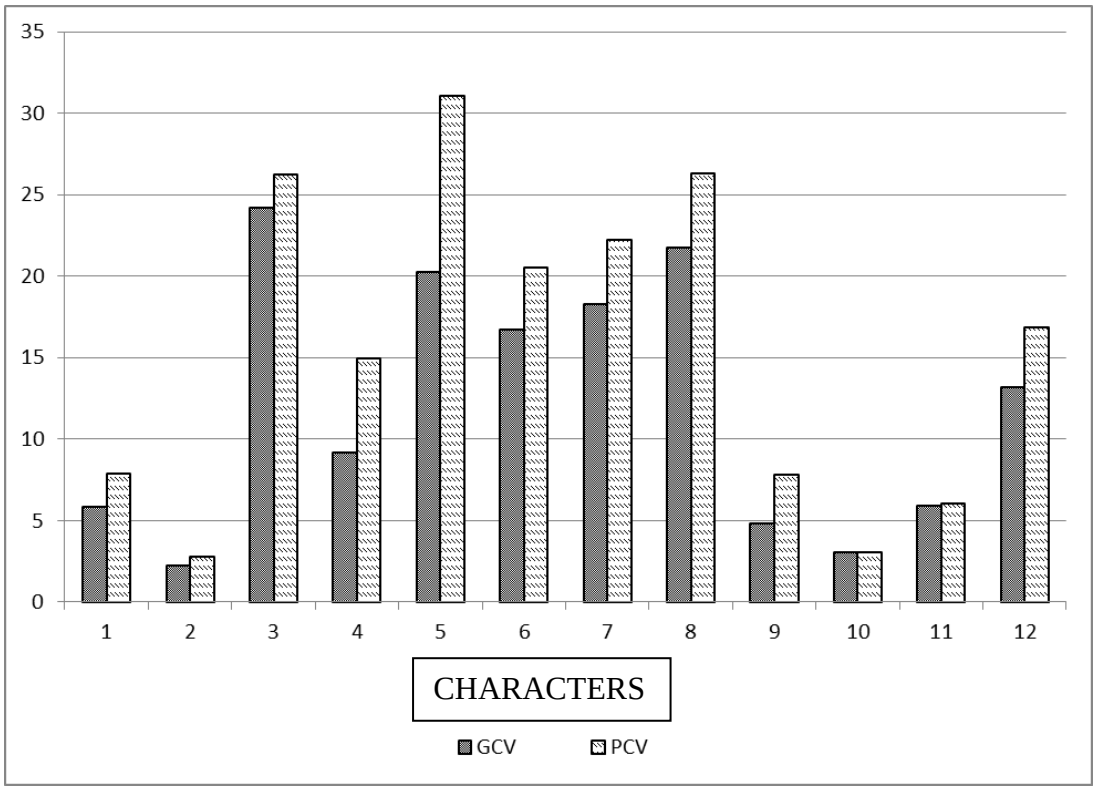


Fig.1. GCV and PCV

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, days to 50% flowering, days to maturity, number of mature pods per plant, fresh pod yield per plant, hundred kernel weight and dry pod yield 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.

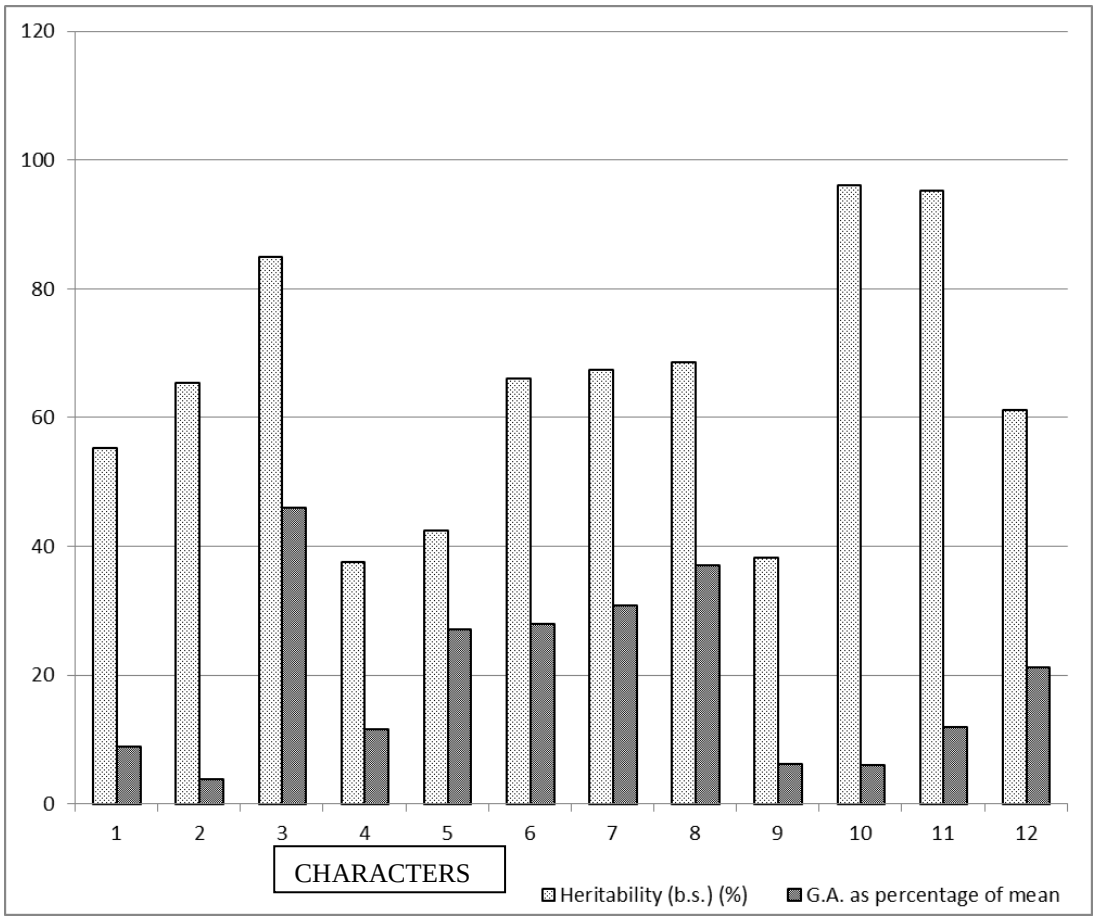


Fig.2. Heritabilty and GA as a percentage of mean.

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.*, number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant, percent oil content, percent protein content and per cent sugar 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 Correlation

Yield improvement is the main objective in most of the crop improvement programmes. It is believed that yield is determined by the action of several independent yield determining component characters. A positive correlation between yield and a component character is desirable as it could help in simultaneous improvement of both the traits.

The knowledge about the inter-relationship between yield and yield contributing characters facilitates the choice of a suitable breeding method to be applied and selecting the parents for crop improvement. Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables. The phenotypic correlation coefficient helps in determining selection index, whereas genotypic correlation coefficient provides a close measure of association between characters which may be useful for overall improvement of crop.

In the present investigation, dry pod yield per plant showed positive and highly significant correlation with fresh pod yield per plant, number of mature pods per plant and per cent protein content.

Similar results were obtained by Vaddoria and Patel (1992), Salara and Gowda (1998), Antony *et al.* (2000),

Sah *et al.* (2000) and Venkataravana *et al.* (2000), John *et al.* (2009), Singh *et al.* (2010).

The characters days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, hundred kernel weight, oil content and sugar content showed positive and non-significant correlation with dry pod yield per plant. Contrasting results i.e. negative and significant were observed for days to 50% flowering and days to maturity by Venkataravana *et al.* (2000).

Likewise number of secondary branches per plant was negatively and non-significantly associated with dry pod yield per plant.

Fresh pod yield per plant showed highly positive and significant association with number of mature pods per plant and number of immature pods per plant. This result confirmed earlier findings of Salara and Gowda (1998) for pod number and of Sah *et al.* (2000) for pod number and harvest index.

Number of mature pods per plant recorded highly significant and positive correlation with fresh pod yield per plant. It showed significant and positive correlation with hundred kernel weight. Similar results were obtained by Vaddoria and Patel (1992) and Venkataravana *et al.* (2000), John *et al.* (2009) for pod yield.

5.5 Path coefficient analysis

Path coefficient analysis is one of the efficient ways to understand the direct and indirect effects of different component characters on dependent variable i.e. yield. In the present investigation, path coefficient analysis was worked out by following Dewey and Lu (1959) to find out the magnitude and direction of direct and indirect effects of various yield contributing characters towards dry pod yield. Direct effect of any characters on yield gives an idea about how reliable selection can be made for a particular character to bring improvement in the yield. If the correlation between a casual factor and the direct effect is more or less of equal magnitude, it explains the true relationship between the characters and direct selection through such traits will be effective. However, if the final correlation coefficient is positive and the direct effect is negative or negligible, then the indirect casual factors are to be considered simultaneously for selection.

In the present investigation, fresh pod yield per plant, hundred kernel weight, number of mature pods per plant, protein content and sugar content showed positive direct effects. However, six traits *viz.,* oil content, number of immature pods per plant, days to maturity, number of primary branches per plant, number of secondary branches per plant and days to 50% flowering had negative direct effect on dry pod yield per plant had negative direct effect on dry

Genotypic Path Diagram

pod yield per plant. Similar results were obtained by Vaddoria and Patel (1992), Uddin *et al.* (1995), Ursal *et al.* (1995), Salara and Gowda (1998), Arjunan *et al.* (1999), Santos *et al.* (2000), Venkataravana *et al.* (2000) and Sah *et al.* (2000).

Fresh pod yield per plant, hundred kernel weight, number of mature pods per plant, protein content and sugar content exhibited high, positive direct effects on dry pod yield as well as these traits were also correlated positively and significantly with dry pod yield. Therefore, direct selection for these traits will be effective in improving dry pod yield in the genotypes studied and under the growing conditions adopted for the present investigation.

Indirect effects of fresh pod yield via number of mature pods per plant, hundred kernel weight, protein content, sugar content, oil content and number of secondary branches per plant were high and positive. Similarly, indirect effects of hundred kernel weight via fresh pod yield per plant and oil content were high and positive.

Indirect effects of number of mature pods per plant via fresh pod yield per plant, number of primary branches per plant, number of secondary branches per plant, oil content, protein content and sugar content were high and positive. Similarly, indirect effects of protein content via fresh pod yield per plant, number of mature pods per plant,

number of secondary branches per plant, oil content and days to maturity were high and positive.

Thus, it was apparent that fresh pod yield per plant, hundred kernel weight, number of mature pods per plant, protein content and sugar content had high direct effects as well as high and positive indirect effects through various component characters in the present studies. Similar results were obtained by Vaddoria and Patel (1992), Khan *et al.* (1998) and Santos *et al.* (2000).

The remaining component traits contributed insignificantly, directly as well as indirectly to dry pod yield in groundnut.

5.6 Genetic divergence

Selection of elite genotypes with high *per se* performance for yield and component characters with genetic divergence is important for starting any hybridization programme. It would be possible to identify desirable genotypes from the estimates of genetic variability.

D^2 statistics, a concept developed by Mahalanobis (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.

5.6.1 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 eight clusters. The distribution of genotypes into different clusters is presented in Table 4.5. Cluster I with 27 genotypes was the largest, followed by cluster II containing 15 genotypes, cluster IV containing 6 genotypes and cluster III with 3 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 IV (D=15.6) which was followed by cluster II (D=6.11), cluster I (D=5.90) and cluster III (D=4.70). Remaining cluster were monogenotypic, therefore had no intra cluster distance.

CLUSTER DIAGRAM

The maximum inter cluster distance was observed between cluster IV and cluster VI (D=17.50), followed by cluster VI and cluster VII (D=16.41), cluster III and cluster IV (D=15.67), cluster III and cluster VIII (D=15.47) and cluster III and cluster VII (D=13.60) indicating wide divergence among 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 I and cluster V (D=7.20). 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 twelve characters (Table 4.7), it was observed that the cluster VIII recorded the highest cluster mean for number of mature pods per plant, fresh pod yield per plant and dry pod yield per plant.

5.6.2 Relative contribution of various characters for divergence

In the present investigation, the character oil content (43.57) contributed the highest towards genetic divergence. This was followed by per cent protein content (42.49), days to maturity (4.98), dry pod yield per plant (3.37), number of mature pods per plant (2.42), days to 50% flowering (1.08), fresh pod yield per plant (1.01) and hundred kernel weight (0.94). The characters number of primary

branches per plant (0.00), number of immature pods per plant (0.00) and per cent sugar content (0.00) had no contribution towards divergence.

On the basis of inter cluster distances, cluster means, correlation studies and *per se* performance observed in present study, genotypes ICG-3266, ICG-4323, ICG-1971, ICG-3688, ICG-1954 and SB-XI 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	II, IV, VIII	3	ICG-3266, ICG-4323, ICG-1971
2.	Number of mature pods per plant	II,VIII	2	ICG-3266, ICG-4323
3.	Hundred kernel weight	I	1	ICG-1954
4.	Days to maturity	VII	1	SB-XI
5.	Oil content percentage	IV	2	ICG-3688, ICG-1971

6. SUMMARY AND CONCLUSION

The present investigation on “Genetic variability for quantitative and qualitative traits in summer groundnut (*Arachis hypogaea L.*)” was undertaken to study the association between the dependant and independent variables, genetic advance, heritability, GCV, PCV for twelve characters and to assess the genetic divergence in fifty five genotypes of summer groundnut. The genotypes were evaluated during summer, 2012, in a randomized block design with two replications. Observations were recorded on days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of immature pods per plant, number of mature pods per plant, fresh pod yield per plant, dry pod yield per plant, hundred kernel weight, oil percentage, protein percentage and sugar percentage.

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 per cent oil content showed the highest heritability followed by per cent protein content, dry pod yield per plant, fresh pod yield per plant, number of mature pods per plant, days to maturity and days to 50% flowering. Other characters recorded moderate to low heritability. The fresh pod yield per plant showed the highest genetic advance followed by number of mature pods per

plant, dry pod yield per plant, days to maturity and days to 50% flowering. Other characters showed moderate to low genetic advance.

The genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients. The characters, fresh pod yield per plant and number of mature pods per plant recorded highly significant and positive correlation with dry pod yield per plant. Whereas, per cent protein content exhibited significant and positive association with dry pod yield per plant. The path coefficient analysis revealed that fresh pod yield per plant, hundred kernel weight, protein content, number of mature pods per plant and sugar content had highest positive direct effect on dry pod yield indicating the true and perfect association between these characters and dry pod yield. The correlation and path analysis studies revealed 'fresh pod yield per plant, number of mature pods per plant and hundred kernel weight as good indications of dry pod yield in groundnut. Other characters such as sugar content and protein content may be considered while selecting genotypes for high yield.

The range of D^2 values indicated adequate diversity between genotypes. On the basis of D values, all the fifty five genotypes were grouped into eight clusters with substantial genetic divergence between them. Cluster I with 27 genotypes emerged as the largest cluster followed by cluster II with 15 genotypes, cluster IV with 6 genotypes and cluster III with 3 genotypes. Remaining four clusters were

monogenotypic. The maximum inter cluster distance was found between cluster IV and cluster VI, while the minimum inter cluster distance was found between cluster I and cluster V. On the basis of cluster means, inter cluster distances, correlation studies and *per se* performance, following six genotypes of summer groundnut have been suggested for future hybridization programme.

ICG-3266, ICG-4323, ICG-1971, ICG-3688, ICG-01954 and SB-XI.

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*** Originals not seen**

8. VITA

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in

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