

**VARIABILITY, PATH ANALYSIS AND GENETIC
DIVERSITY IN SUMMER GROUNDNUT
(*Arachis hypogaea* L.)**

by

Mr. KAMBLE NITIN PANDIT

(Reg. No. 11/051)

A Thesis submitted to the

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

in partial fulfilment of the requirements for the degree
Of

MASTER OF SCIENCE (AGRICULTURE)

In

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

**DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE
MAHATMA PHULE KRISHI VIDYAPEETH,
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(GENETICS AND PLANT BREEDING)**

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CANDIDATE'S DECLARATION

I hereby declare that this thesis or a part

There of has not been submitted

by me or any other person

to any other University

or Institute for

a Degree or

Diploma.

Place : MPKV, Rahuri

Date : / / 2013

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CERTIFICATE

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

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Place : M.P.K.V., Rahuri

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Date : / /2013

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ABSTRACT

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A candidate for the degree

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MAHATMA PHULE KRISHI VIDYAPEETH,

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Research Guide : Dr. V.L. Amolic

Major discipline : Genetics and Plant Breeding

The present investigation entitled “Variability, path analysis and genetic diversity 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 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 all the characters and also the magnitude of genotypic and phenotypic coefficients of variations indicated the presence of good amount of variability. The character percent oil content showed the highest heritability followed by percent protein content, number of mature pods per plant, fresh pod yield per plant, dry pod yield per plant, days to maturity and days to 50% flowering. Other characters recorded moderate to low heritability. The number of mature pods per plant showed the highest genetic advance followed by dry pod yield per plant, fresh pod yield per plant, and days to 50% flowering. Other characters showed moderate to low genetic advance.

The genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients. The characters, fresh pod yield per plant and number of mature pods per plant recorded highly significant and positive correlation with dry pod yield per plant. Whereas, number of mature pod per plant exhibited significant and positive association with dry pod yield per plant. The path coefficient analysis revealed that fresh pod yield per plant, number of secondary branches per plant, days to 50 % flowering and number of mature pods per plant 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, number of secondary branches per plant, days to 50 % flowering 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 D2 values indicated adequate diversity between genotypes. On the basis of D values, all the fifty five genotypes were grouped into nine clusters with substantial genetic divergence between them. Cluster V with 14 genotypes emerged as the largest cluster followed by cluster II with 13 genotypes, cluster I with 11 genotypes and cluster III with 8 genotypes cluster IV with 5 genotypes. Remaining four clusters were monogenotypic. The maximum inter cluster distance was found between cluster V and cluster IX, while the minimum inter cluster distance was found between cluster II and cluster VI. On the basis of cluster means, inter cluster distances and per se performance, following seven genotypes of summer groundnut have been suggested for future hybridization programme.

ICG-6637, ICG-5721, ICG-4303, ICG-3814, ICG-8236, TAG-24 and RHRG-6021.

1. INTRODUCTION

Groundnut (*Arachis hypogaea L.*) is a major oilseed crop in India. Occupying 5.31 million ha. 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 (Source: Ministry of agriculture, Govt. of India, 2012). 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 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. (Source: Ministry of agriculture, Govt. of India, 2012).

Table No.1.1:- Area, Production and Productivity of major Groundnut producing states (2011).

State	Area (Million ha.)	Production (Million Tonnes)	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* L.) 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 $2n=4x=40$. The genus *Arachis* is a member of family Fabaceae (synonym: Leguminosae), subfamily papilionoidae, tribe Aeschynomeneae and subtribe stylosanthinae. It belongs to the section *Arachis* and series amphiploidies and the family Fabaceae (Gregory *et al.*, 1980). The species *Arachis hypogaea* consists of two subspecies, *Hypogaea* sp. and *Fastigiata* sp. Each subspecies has two botanical varieties. Four cultivated types of groundnut according to Krapovickas and Rigoni (1957) are;

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

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

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

Therefore summer is the ideal season for groundnut cultivation wherever irrigation facilities are available. The average total dry matter produced per plant in bunch groundnut at harvest is 25.7 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 cause 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 one 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 generation. 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 prerequisite 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, 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 character 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 F₄ 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 S₁ during *kharif* 1991 for yield components. Variability was greater between families than within families for most of the characters. Family selection in S₁ 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 F₄ progeny 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 M₇ groundnut mutant 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 Bangalore 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* (Leguminosae). They studied many new accessions of the two species (*Arachis repens* and *A. pinto*) 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 F₅ 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.

Aghav (2002) evaluated fifty five genotypes of summer groundnut for variability, path analysis and genetic diversity during summer 2000, 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.

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 F₂ 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.

Salara and Gowda (1998) used F₂ 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.

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.

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 M₇ 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 D² 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.

Lakshmiddevamma *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 XI and XVI had maximum inter-cluster distance suggesting wide diversity and by utilizing these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster XII has genotype with most favorable characters and hence can be involved as potential parent for development of superior genotypes.

Sonone and Thaware (2009) studied the forty genotypes of groundnut (*Arachis hypogaea* L.) selected from different geographical origins 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/m² in biomass, 142-277 g/ m² in pod weight, 91-216 g /m² 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 ($p < 0.01$).

3. MATERIAL AND METHODS

The field experiment related to the present investigation entitled “Variability, path analysis and genetic diversity 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 and five checks (TPG-41, TAG-24, JL-501, SB-XI, RHRG-6021) (Table 3.1). The above genotypes 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 $45 \times 15 \text{ cm}^2$ distance (between rows and between plants within rows). 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 Groundnut germplasm lines used for the present investigation and their source

Sr. No.	Name of genotype	Source
1.	ICG-3814	ICRISAT Hyderabad
2.	ICG-3806	ICRISAT Hyderabad
3.	ICG-3785	ICRISAT Hyderabad
4.	ICG-3829	ICRISAT Hyderabad
5.	ICG-3891	ICRISAT Hyderabad
6.	ICG-3899	ICRISAT Hyderabad
7.	ICG-3953	ICRISAT Hyderabad
8.	ICG-4049	ICRISAT Hyderabad
9.	ICG-4057	ICRISAT Hyderabad
10.	ICG-4082	ICRISAT Hyderabad
11.	ICG-4087	ICRISAT Hyderabad
12.	ICG-4109	ICRISAT Hyderabad
13.	ICG-4230	ICRISAT Hyderabad
14.	ICG-4303	ICRISAT Hyderabad
15.	ICG-4452	ICRISAT Hyderabad
16.	ICG-4487	ICRISAT Hyderabad
17.	ICG-4490	ICRISAT Hyderabad
18.	ICG-4492	ICRISAT Hyderabad
19.	ICG-4507	ICRISAT Hyderabad

Sr. No.	Genotype	Source
20.	ICG-4508	ICRISAT Hyderabad
21.	ICG-4540	ICRISAT Hyderabad
22.	ICG-5721	ICRISAT Hyderabad
23.	ICG-6080	ICRISAT Hyderabad
24.	ICG-6096	ICRISAT Hyderabad
25.	ICG-6141	ICRISAT Hyderabad
26.	ICG-6357	ICRISAT Hyderabad
27.	ICG-6381	ICRISAT Hyderabad
28.	ICG-6499	ICRISAT Hyderabad
29.	ICG-6637	ICRISAT Hyderabad
30.	ICG-7195	ICRISAT Hyderabad
31.	ICG-7315	ICRISAT Hyderabad
32.	ICG-7358	ICRISAT Hyderabad
33.	ICG-7367	ICRISAT Hyderabad
34.	ICG-7406	ICRISAT Hyderabad
35.	ICG-7620	ICRISAT Hyderabad
36.	ICG-7681	ICRISAT Hyderabad
37.	ICG-7706	ICRISAT Hyderabad
38.	ICG-7815	ICRISAT Hyderabad
39.	ICG-7834	ICRISAT Hyderabad
40.	ICG-8033	ICRISAT Hyderabad
41.	ICG-8235	ICRISAT Hyderabad
42.	ICG-8236	ICRISAT Hyderabad
43.	ICG-8264	ICRISAT Hyderabad
44.	ICG-8286	ICRISAT Hyderabad
45.	ICG-8308	ICRISAT Hyderabad

Sr. No.	Genotype	Source
46.	ICG-8328	ICRISAT Hyderabad
47.	ICG-8341	ICRISAT Hyderabad
48.	ICG-8442	ICRISAT Hyderabad
49.	ICG-8827	ICRISAT Hyderabad
50.	ICG-9064	ICRISAT Hyderabad
51.	RHRG-6021	MPKV, Rahuri (MS)
52.	JL-501	ARS, Jalgaon, (MS)
53.	SB-XI	ARS, Jalgaon, (MS)
54.	TAG-24	Trombay, (MS)
55.	TPG-41	Trombay, (MS)

3.2.3 Manures and fertilizers

The chemical fertilizers were applied @ 25 kg N and 50 kg P₂O₅ 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 (Nos.)

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 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 mature pods per plant

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

3.2.5.6 Number of immature pods per plant

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

3.2.5.7 Fresh pod yield per plant (g)

The total weight of both filled and unfilled 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 Mahalanobis (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.

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

Where,

$\bar{X}$ = Mean

$\sum x_i$ = 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 (GCV)

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

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Mean of character

ii. Phenotypic coefficient of variation (PCV)

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

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).

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

Where,

σ^2g = Genotypic variance

σ^2p = 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).

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

Where,

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

K = Selection differential

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

ii. GA as percentage of mean

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

Where,

GA = Genetic advance

$\bar{X}$ = 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,

$$rp_{1.2} = \frac{pCOV_{1.2}}{(\sigma^2 p_1) (\sigma^2 p_2)}$$

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,

$$rg_{1.2} = \frac{gCOV_{1.2}}{(\sigma^2 g_1) (\sigma^2 g_2)}$$

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

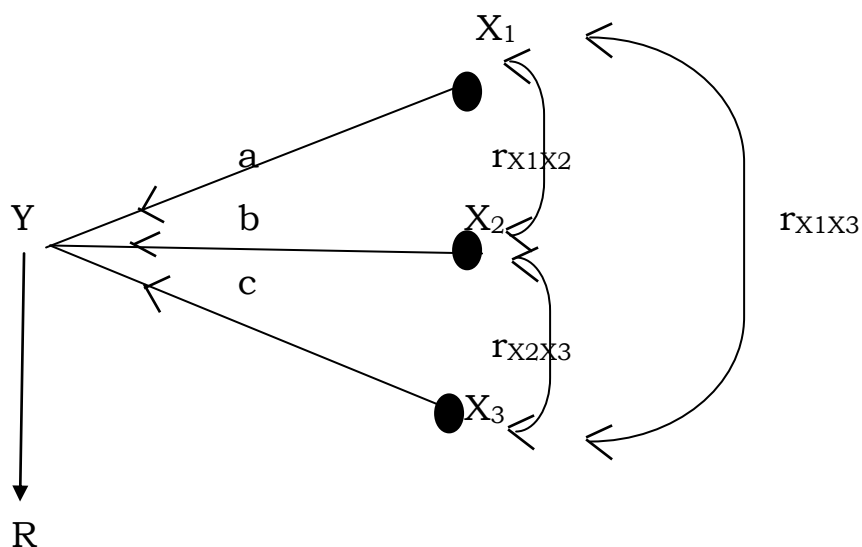
Significance of the various correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedecor and Cochran, 1967).

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 P_{ij} .

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

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

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	$r_{2.3}.....r_{2n}$
r_{ny}	r_{n1}	r_{n2}	$r_{n3}.....1$

Where,

$$r_{1.2} = r_{2.1} \text{ and so on and } r_{ny}$$

= Correlation between one component character and yield

The 'B' matrix was inverted (B^{-1}) and path coefficients (P_{ij}) were obtained as $(P_{ij}) = A \times (B^{-1})$.

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.

$$\text{Indirect effect} = r_{ij} \times P_{ij}$$

Where,

$$i = 1 \text{ to } 12$$

$$j = 1 \text{ to } 12 \text{ and}$$

$$P_{ij} = P_{1Y}, P_{2Y}, \dots, P_{nY}$$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factor (R) were diagrammatically presented. The residual factors i.e. variation in yield unaccounted for by these associations was calculated from the following formula.

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

Where,

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

Where,

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

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

3.3.5 D² analysis

The analysis of divergence was carried out by D² 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 D² 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,

$$X^2_{pq} = V = -m.10 \log e^{\Delta}$$

Where,

$n = N_1 + \dots + N_{K-1}$ = 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 is 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 quantity 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 ($15 + \frac{1}{2}$) terms whose sum is D^2 .

c. Computation of D^2 values

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

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 $\sum D_i^2/n$, where $\sum D_i^2$ 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,

$$\Sigma D_i^2 / (n_i n_j)$$

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 “Variability, path analysis and genetic diversity 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. Out of 55 genotypes twenty five flowered significantly earlier than the population mean. The genotype ICG-8264 (28.50) was the earliest followed by ICG-8286(29.50), ICG-7706 and ICG-7367 (30.50 each). The genotypes TAG-24 (39.00), SB-XI, TPG-41 (38.00 each) and RHRG-6021, ICG-4487 (37.50 each) were comparatively late in days to 50% flowering.

4.1.2 Days to maturity

Twenty seven out of fifty five genotypes showed significantly early maturity when compared with the population mean of 120.59 days. The variation for this character ranged between 114.00 (SB-XI) to 125.00 (ICG-8236) days. The genotype SB-XI recorded the was early in maturity (114.00) followed by

RHRG-6021, JL-501 (117.00 each). The genotypes ICG-8236, ICG-4492 (125.00 each), and ICG-4049, ICG-4302, ICG-8033 (124.00 each) 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 4.00 and 7.50. Looking to the population mean of 5.66 branches per plant, eight genotypes showed higher branches than population mean. ICG-3806, ICG-4492, ICG-4540, ICG-6381, ICG-9064 JL-501, and TAG-24 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 two 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-7315, ICG-8264, ICG-7367 and ICG-7815 (12.50), ICG-3891, ICG-4508, ICG-7834 and ICG-8827 (12.00) 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-3785, ICG-3829) and 6.00 (ICG-4540), while the population mean was 4.13. Thirty genotypes showed lower number of immature pods per plant than population mean. ICG-3785, ICG-3829, ICG-4490, ICG-6637, ICG-8341, ICG-8827 and

ICG-9064(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 9.50(ICG-3806) and 33.00 (ICG-6637). The population mean for this character was 18.47. Twenty six genotypes showed higher number of mature pods per plant over population mean of which ICG-6637 (33.00), ICG-4303,ICG-5721 (30.50 each), ICG-7620 (26.50), 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 13.65 (ICG-6141) and 30.30 (ICG-5721). Twenty three genotypes recorded significantly more fresh pod yield per plant as compared to the population mean of 19.99 g. The genotype ICG-5721 (30.30) ranked first followed by ICG-6637 (30.24) and ICG-4303 (28.68). However, ICG-6141 (13.65), SB-XI (13.71) and ICG-3814 (14.94) 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 15.91 g. The genotype ICG-6637 (27.52) recorded the highest dry pod yield per plant followed by ICG-5721 (27.17) and ICG-4303 (24.28). The genotype ICG-8286 (9.31) along with ICG-6141(9.50) recorded low yield. Twenty six out of genotypes 55 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-3829) and 41.39 (ICG-3814). Eighteen genotypes out of 55 showed numerically high hundred kernel weight when compared with population mean of 34.42 g. Genotypes ICG-3814(41.39), ICG-3891 (40.43), ICG-4303 (38.47) and ICG-6080 (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-4087 (43.95) recorded the lowest oil content while the genotype ICG-8236 (50.05) recorded highest oil content followed by ICG-3806 (50.00), ICG-4507 (49.22) and ICG-8286 (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-6381) and 26.50 (ICG-4049) with a population mean of 24.19 per cent. The genotypes ICG-4049 (26.50), ICG-6499, ICG-7706 (26.37), and ICG-3891 (26.30) recorded the highest amount of percent protein. In contrast the genotypes ICG-6381 (21.21), ICG-8442 (21.79), ICG-7195 (22.21) recorded lowest values for protein content.

4.1.12 Sugar content (%)

The population mean for sugar content was 12.19 per cent. The genotype ICG-4540 (10.26) recorded the lowest sugar content while the genotype ICG-8083 (13.82) recorded highest sugar content followed by ICG-6080 (13.78) and ICG-

6357(13.67). 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, indicating appreciable amount of variability among the genotypes for studied characters.

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.

For number of mature pods per plant(23.61) recorded the highest estimate for GCV followed by dry pod yield per plant (23.19), number of immature pod per plant (23.08), number of primary branches per plant (20.58), fresh pod yield per plant (18.36) and number of secondary branches per plant (9.15). The highest value of PCV were observed for number of immature pods per plant (27.85), followed by number of primary branches per plant(26.83), dry pod yield per plant (26.57), number of mature pods per plant (26.01), and fresh pod yield per plant (20.93).

**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**	3.08
2	Days to maturity	9.72**	4.18
3	Number of primary branches per plant	1.83	0.94
4	Number of secondary branches per plant	3.36**	1.52
5	Number of immature pods per plant	1.11	0.45
6	Number of mature pods per plant	44.51**	4.27
7	Fresh pod yield per plant (g)	30.40**	3.97
8	Dry pod yield per plant (g)	31.48**	4.25
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 (%)	1.90	0.40

* Significant at 5%

** Significant at 1%

Low estimates of GCV and PCV were observed for the characters days to maturity (1.38 and 2.19), oil content percentage (3.02 and 3.08), protein content percentage (5.91 and 6.05), and hundred kernel weight (g) (4.82 and 7.79).

4.3.2 Heritability (b.s.)

The heritability (b.s.) estimates were high in case of characters *viz.*, percent oil content (96.00), percent protein content (95.00), number of mature pods per plant (83.00), percent sugar content (80.58), fresh pod yield per plant (77.00), dry pod yield per plant (76.00), number of immature pods per plant (68.71) and days to 50% flowering (56.00). It was medium for number of primary branches per plant (58.88), days to maturity (40.00), hundred kernel weight (38.00) and number of secondary branches per plant (38.00).

4.3.3 Genetic advance

The highest magnitude of genetic advance was observed for number of mature pod per plant (8.39) followed by dry pod yield per plant (6.64), fresh pod yield per plant (6.57), days to 50% flowering (3.05), percent sugar content (3.04), protein content (2.87), oil content (2.86), number of primary branches per plant (2.32), days to maturity (2.16), hundred kernel weight (2.11), number of immature pods per plant (2.05). While the lowest genetic advance observed for number of secondary branches per plant (1.21).

Table no. 4.3

Genetic advance as a percent of mean was the highest for number of immature pods per plant (49.75), followed by number of mature pod per plant (44.19), dry pod yield per plant (41.72), number of primary branches per plant (41.07), and fresh pod yield per plant (27.94).

4.4 Correlation

The simple genetic correlation coefficients among the twelve characters were worked out and presented in Table 4.4.

4.4.1 Association of dry pod yield and its components

The characters, fresh pod yield per plant (0.95) and number of mature pods per plant (0.72) showed highly significant and positive association with dry pod yield per plant.

The characters, per cent sugar content (0.16), number of primary branches per plant (0.07) and hundred kernel weight (0.06) showed positive and non-significant correlation with dry pod yield per plant. Whereas, characters days to 50% flowering (-0.17), number of immature pods per plant (-0.25), days to maturity (-0.005), number of secondary branches per plant (-0.50), oil content (-0.15) and protein content (-0.12) 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 significantly negative correlation (-0.2292) with number of mature pods per plant.

Table no.4.4

Days to maturity recorded highly significant and negative correlation (-0.4028) with number of secondary branches per plant.

Number of primary branches per plant showed highly significant and negative correlation (0.7215) with per cent sugar content.

Number of secondary branches per plant exhibited highly significant and positive correlation (0.3367) with percent oil content, while it had significantly negative correlation (-0.5806) with fresh pod yield per plant.

Number of mature pods per plant recorded highly significant and positive correlation (0.7400) with fresh pod yield per plant.

Fresh pod yield per plant showed significant and negative correlation (-0.1927) with per cent oil content.

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 were 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 (1.1371) exerted maximum direct effects toward dry pod yield per plant, followed by number of secondary

Table no.4.5

branches per plant (0.1970), days to 50 percent flowering (0.0115) and number of mature pods per plant (0.0015). However, seven traits *viz.*, number of primary branches per plant (-0.2633), days to maturity (-0.0013), oil content (-0.0615), number of immature pods per plant (-0.1294), hundred kernel weight (-0.14), protein content (-0.1236) and sugar content (-0.170) 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, number of secondary branches per plant, days to 50 percent flowering and number of mature pods per plant exhibited very low indirect effects. Fresh pod yield had positive indirect effects via number of mature pods per plant (0.8414), number of immature pods per plant (0.2104), days to maturity (0.1228), hundred kernel weight (0.1207), number of primary branches per plant (0.1206) and sugar content (0.1051), while it had negative indirect effects via number of secondary branches per plant (-0.6602), days to 50% flowering (-0.2325), oil content (-0.2191) and protein content (-0.0595).

Number of secondary branches per plant had positive indirect effects via oil content (0.0663), number of immature pods per plant (0.0417), number of primary branches per plant (0.0082) and hundred kernel weight (0.0027), whereas it had negative indirect effects via fresh pod yield per plant (-0.1144), number of mature pod per plant (-0.1067), days to maturity (-0.0794), protein content (-0.0215), days to 50% flowering (-0.0126) and sugar content (-0.0004).

Days to 50 percent flowering had positive indirect effects via number of immature pods per plant (0.0045), protein

content (0.0013), days to maturity (0.0011) and hundred kernel weight (0.0002), while it had negative indirect effects via number of primary branches per plant (-0.0026), number of mature pods per plant (-0.0026), oil content (-0.0020), fresh pod yield per plant (-0.0024), number of secondary branches per plant (-0.0007) and sugar content (-0.0007).

Number of mature pods per plant had positive indirect effects via number of secondary branches per plant (0.0008), days to 50 percent flowering (0.0004), hundred kernel weight (0.0002), oil content (0.0002), protein content (0.0001) and sugar content (0.0001), while it had negative indirect effects via number of immature pods per plant (-0.0098), fresh pod yield per plant (-0.0011), days to maturity (-0.0002) and number of primary branches per plant (-0.0002).

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 nine clusters as presented in Table 4.6.

Cluster V with 14 genotypes emerged as the largest cluster followed by cluster II with 13 genotypes, cluster I with 11 genotypes, cluster III with 8 genotypes and cluster IV with 5 genotypes. Cluster VI, VII, VIII and IX included one genotype each (monogenotypic).

Table 4.6 Distribution of fifty five genotypes of summer groundnut into different clusters

Cluster No.	Total number of genotypes included	Genotypes
I	11	ICG4087,4540, 4490,6499, 7406,4492,4109,8341,8033,RHRG6021, TAG-24.
II	13	ICG4057,7315,7358,7681,7834,7367,6096, 4508,4082,8296,7195,4303,8827.
III	8	ICG6141,6387,8328,7620,7815,6381,3814, 8442.
IV	5	ICG-8235,8308,3899,3953,4230.
V	14	ICG-3829,9064,6080,3785,4452, 4507,8236,8264,3806,7706,4049, TPG-41,SB-XI,JL-501.
VI	1	ICG-5721
VII	1	ICG-6637
VIII	1	ICG-3891
IX	1	ICG-4487

4.6.2 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 V exhibited maximum intra cluster distance i.e. (D=7.30), followed by cluster III (D=6.82), cluster II (D=5.67) and cluster I (D=5.53), cluster IV (D=5.46). Being monogenotypic, remaining clusters showed no intra cluster distance.

The maximum inter cluster distance was observed between cluster V and cluster IX (D=17.73), followed by cluster VIII and cluster VI (D=14.74), cluster V and cluster III (D=13.67), cluster VIII and cluster V (D=13.58) and cluster IX and cluster VI (D=13.57). The lowest inter cluster distance was observed between cluster II and cluster VI (D=6.89).

4.6.3 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 highest cluster mean for days to 50 percent flowering was observed in cluster IX (37.50) followed by cluster I (32.91) and lowest cluster mean was observed in cluster VII (32.00) followed by cluster VI (32.50).

In case of days to maturity highest cluster mean was observed in cluster IX (123.50) followed by cluster I (121.55) and lowest cluster mean was observed in cluster VII and VIII (118.00 each) followed by cluster III (119.63).

Table no.4.8

Highest cluster mean for number of primary branches per plant was observed in cluster V (6.07) followed by cluster I (6.00) and lowest cluster mean was observed in cluster VI and VII (4.50 each) followed by cluster III (119.63).

Highest cluster mean for number of secondary branches per plant was observed in cluster VIII (12.00) followed by cluster III (11.31) and lowest cluster mean was observed in cluster IX (8.50) followed by cluster VI and VII (9.50).

Cluster IV (4.60) followed by cluster III (4.56) showed highest cluster mean for number of immature pods per plant and lowest cluster mean was observed in cluster VII (3.00) followed by cluster VI and VII (3.50).

Lowest cluster mean for number of mature pods per plant was observed in cluster IV (33.00) followed by cluster IX (30.50) and highest cluster mean was observed in cluster VI (12.50) followed by cluster VII (16.10).

Highest cluster mean for fresh pod yield per plant was observed in cluster VI (30.30) followed by cluster VII (30.24) and lowest cluster mean was observed in cluster III (18.39) followed by cluster VIII (18.63).

Dry pod yield per plant had observed highest cluster mean in cluster VII (27.52) followed by cluster VI (27.17) and lowest in cluster VIII (12.96) followed by cluster III (14.16).

Hundred kernel weight had observed highest Cluster mean in cluster VIII (40.83) followed by cluster VI (35.79) and lowest cluster mean in cluster VII (32.53) and cluster V (33.96).

In case of percent oil content highest cluster mean had observed in cluster V (48.15) followed by cluster VI (47.93) and lowest cluster mean in cluster VIII (44.41) followed by cluster IX (44.49).

Percent protein content had shown highest cluster mean in cluster VIII (26.30) followed by cluster I (25.55) and lowest in cluster IX (22.26) followed by cluster III (22.37).

Percent sugar content had shown highest cluster mean in cluster VIII (12.45) followed by cluster III (12.44) and lowest in IX (10.56) followed by cluster V (12.06).

4.7Percent 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 percent protein content (40.67) contributed the highest for divergence and was followed by percent oil content (39.33), fresh pod yield per plant (9.09), number of mature pod per plant (6.80), dry pod yield per plant (2.76), days to 50 percent flowering (0.54), days to maturity (0.34), hundred kernel weight (0.34), number of secondary branches per plant (0.7), and sugar content (0.7). However, the contributions of number of primary branches per plant and number of immature pods per plant had no contribution towards divergence. (Table 4.9)

Table 4.9 Contribution of various characters to divergence

Sr. No.	Characters	Times ranked I st	Contribution (%)
1.	Days to 50% flowering	8	0.54
2.	Days to maturity	5	0.34
3.	No. of primary branches per plant	0	0.00
4.	No. of secondary branches per plant	1	0.07
5.	No. of immature pods per plant	0	0.00
6.	No. of mature pods per plant	101	6.80
7.	Fresh pod yield per plant (g)	135	9.09
8.	Dry pod yield per plant (g)	41	2.76
9.	Hundred kernel weight (g)	5	0.34
10.	Oil content (%)	584	39.33
11.	Protein content (%)	604	40.67
12.	Sugar content (%)	1	0.07

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 “Variability, path analysis and genetic diversity 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-headings 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 (114-125 days), no. of secondary branches per plant (7.50-13.00), number of mature pods per plant (9.50-33.00), fresh pod yield per plant (13.65-30.30 g), dry pod yield per plant (9.31-27.51 g), hundred kernel weight (31.12-41.39 g) and oil content (44.05-50.05%).

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, number of primary branches per

plant, dry pod yield per plant, number of mature pods per plant and fresh pod yield per plant. These results confirmed earlier findings of Ganeshan and Sudhakar (1995), Jayalakshmi *et al.* (1998), Rameshkumar *et al.* (1998), Yadav *et al.* (1998), Prakash *et al.* (2000), Aghav (2000) and John *et al.* (2009).

The GCV estimates were higher for number of mature pods per plant, dry pod yield per plant, number of immature pods per plant, number of primary branches per plant, fresh pod yield per plant and number of secondary branches per plants. 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 maturity, hundred kernel weight, percent protein content and percent oil content indicating hardly any scope for improvement of these traits by selection. These results are in conformity with the earlier findings of Korat *et al.* (2009).

5.3 Heritability and genetic advances

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

In general, in self-pollinated crops, characters with high heritability possess high genetic advance which is said to be governed by additive gene action suggesting direct selection for traits. In contrast, high heritability with low genetic

advance or low heritability with high genetic advance are the results of non-additive gene action and selection for such traits may not be rewarding.

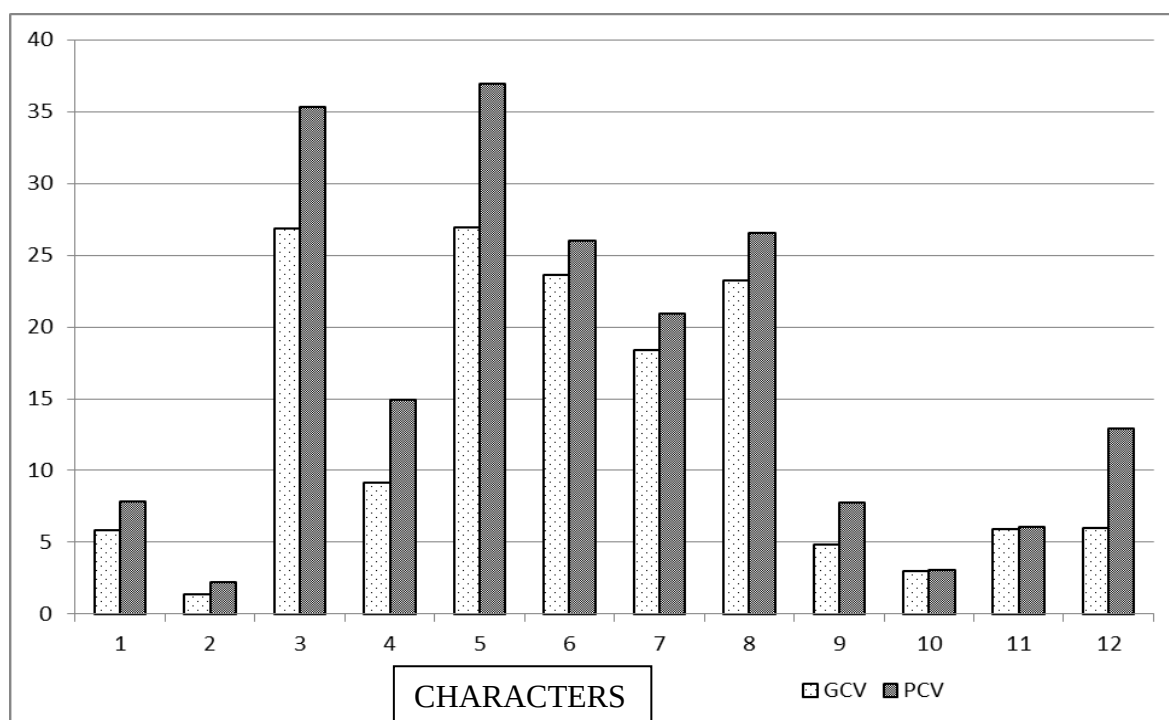


Fig.1. GCV and PCV

In the present investigation, per cent oil content, protein content, number of mature pods per plant, per cent sugar content, fresh pod yield per plant, dry pod yield per plant, number of immature pods per plant and days to 50% flowering had high heritability along with high genetic advance indicating that these traits were governed by additive gene action and simple selection would be effective.

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

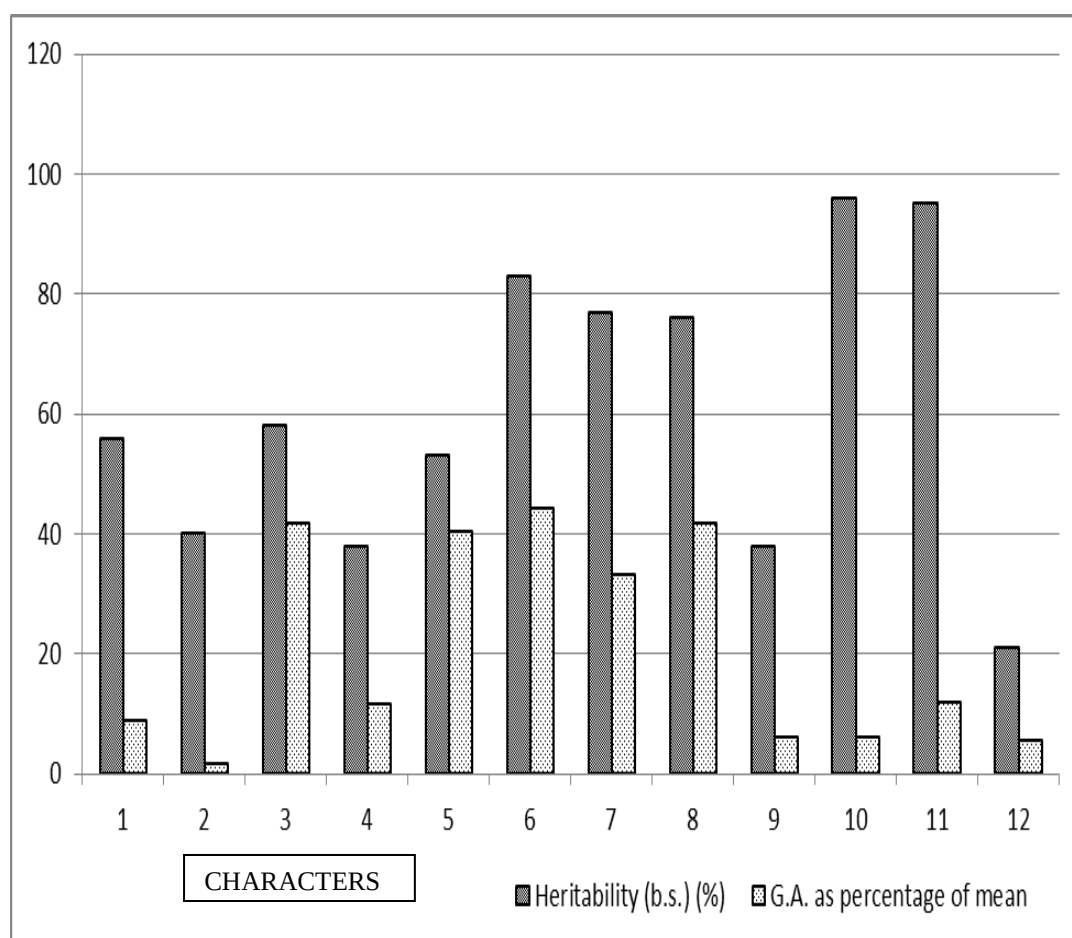


Fig.2. Heritability and GA as a percentage of mean.

The traits viz., number of mature pods per plant, dry pod yield per plant, fresh pod yield per plant, days to 50% flowering, 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 and number of mature pods per plant. 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 number of primary branches per plant, hundred kernel weight and per cent 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 percent flowering, oil

content, protein content and days to maturity by Venkataravana *et al.* (2000).

Likewise number of primary branches per plant, oil content, days to maturity, protein content 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. 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 direct casual factors are to be considered simultaneously for selection.

In the present investigation, fresh pod yield per plant, number of secondary branches and days to 50 percent flowering showed positive direct effects. However, eight traits *viz.*, oil content, number of mature pods per plant, days to maturity, number of primary branches per plant, number of immature pods per plant, protein content, and sugar content had negative direct effect on dry 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, number of secondary branches days to 50 percent flowering and number of immature pods per plant 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 protein content, and oil content were high and positive. Similarly, indirect effects of number of secondary branches per plant via protein content, number of mature pod per plant, days to maturity and sugar content were high and positive.

Indirect effects of days to 50 percent flowering via number of primary branches per plant, oil content and sugar content were high and positive.

Thus, it was apparent that fresh pod yield per plant, number of secondary branches and days to 50 percent flowering 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), Ayub 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 nine clusters. The distribution of genotypes into different clusters is presented in Table 4.6. Cluster V with 14 genotypes emerged as the largest cluster followed by cluster II with 13 genotypes, cluster I with 11 genotypes, cluster III with 8 genotypes and cluster IV with 5 genotypes, remaining cluster 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 V ($D=7.30$) which was

followed by cluster III (D=6.82), cluster II (D=5.67) cluster I (D=5.53) and cluster IV (D=5.46). Remaining cluster were monogenotypic, therefore had no intra cluster distance.

The maximum inter cluster distance was observed between cluster V and cluster IX (D=17.73), followed by cluster VIII and cluster VI (D=14.74), cluster V and cluster III (D=13.67), cluster VIII and cluster V (D=13.58) and cluster IX and cluster VI (D=13.57) 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 II and cluster VI (D=7.44). 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 protein content (40.67), oil content (39.33) contributed the highest towards genetic divergence. This was followed by fresh pod yield per plant (9.09), number of mature pods per plant (6.80), dry pod yield per plant (2.76), days to 50 percent flowering (0.54), days to maturity (0.34), hundred kernel weight (0.34), number of secondary branches per plant (0.070 and sugar content (0.07) . The characters number of primary branches per plant (0.00), and number of immature pods per plant (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-6637, ICG-5721, ICG-4303, ICG-3814, ICG-8236, TAG-24 and RHRG-6021 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,VI,VII	3	ICG-6637, ICG-5721, ICG-4303
2.	Number of mature pods per plant	VII	1	ICG-6637
3.	Hundred kernel weight	III	1	ICG-3814
4.	Days to maturity	I	1	TAG-24, RHRG-6021
5.	Oil content percentage	V	1	ICG-8236

6. SUMMARY AND CONCLUSION

The present investigation on “Variability, path analysis and genetic diversity 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 all 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, number of mature pods per plant, fresh pod yield per plant, dry pod yield per plant, days to maturity and days to 50% flowering. Other characters recorded moderate to low heritability. The number of mature pods per plant showed the highest genetic advance followed by dry pod yield per plant, fresh pod yield per plant, and days to 50%

flowering. Other characters showed moderate to low genetic advance.

The genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients. The characters, fresh pod yield per plant and number of mature pods per plant recorded highly significant and positive correlation with dry pod yield per plant. The path coefficient analysis revealed that fresh pod yield per plant, number of secondary branches per plant, days to 50 % flowering and number of mature pods per plant 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, number of secondary branches per plant, days to 50 % flowering 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 nine clusters with substantial genetic divergence between them. Cluster V with 14 genotypes emerged as the largest cluster followed by cluster II with 13 genotypes, cluster I with 11 genotypes and cluster III with 8 genotypes cluster IV with 5 genotypes. Remaining four clusters were monogenotypic. The maximum inter cluster distance was found between cluster V and cluster IX, while the minimum inter cluster distance was found between cluster II and cluster VI. On the basis of cluster means, inter cluster

distances and *per se* performance, following seven genotypes of summer groundnut have been suggested for future hybridization programme.

ICG-6637, ICG-5721, ICG-4303, ICG-3814, ICG-8236, TAG-24 and RHRG-6021.

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*** Originals not seen**

8. VITA

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A candidate for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

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(GENETICS AND PLANT BREEDING)

2013

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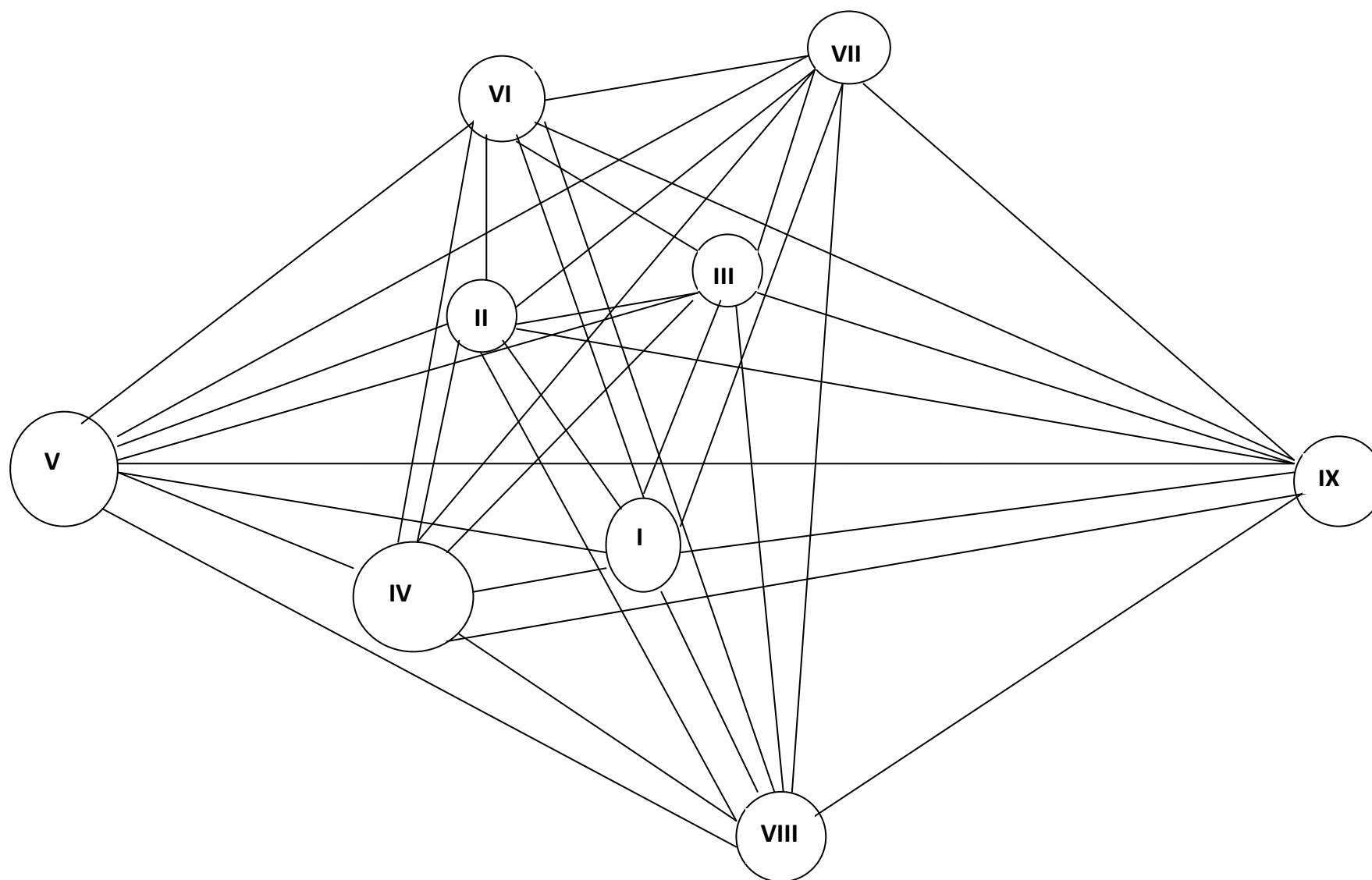


Fig : CLUSTER DIAGRAM (NOT IN SCALE)