GENETIC DIVERSITY STUDIES ON PEANUT STEM NECROSIS TOLERANT GROUNDNUT GENOTYPES

BY

P. DHARANI NIVEDITHA

B.Sc (Ag)

THESIS SUBMITTED TO THE
ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

MASTER OF SCIENCE IN AGRICULTURE

(GENETICS AND PLANT BREEDING)

CHAIRPERSON: Dr. M. SUDHARANI

DEPARTMENT OF GENETICS AND PLANT BREEDING
AGRICULTURAL COLLEGE, MAHANANDI
ACHARYA N.G. RANGA AGRICULTURAL UNIVERISTY
GUNTUR – 522 509

2016

DECLARATION

I, **MISS. P. DHARANI NIVEDITHA** hereby declare that the thesis entitled **"GENETIC DIVERSITY STUDIES ON PEANUT STEM NECROSIS TOLERANT GROUNDNUT GENOTYPES"** submitted to the **Acharya N.G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

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Date :

(P. DHARANI NIVEDITHA)
I.D. No.: MAM-2014/06

CERTIFICATE

Ms. P. DHARANI NIVEDITHA has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC DIVERSITY STUDIES ON PEANUT STEM NECROSIS TOLERANT GROUNDNUT GENOTYPES"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any university.

Date :

(**Dr. M. SUDHARANI)**
Chairperson
Associate Professor & Head
Dept. of Genetics And Plant Breeding
Agricultural College, Mahanandi.

CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERSITY STUDIES ON PEANUT STEM NECROSIS TOLERANT GROUNDNUT GENOTYPES"** submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Acharya N.G. Ranga Agricultural University, Guntur, is a record of the bonafide original research work carried out by **Ms. P. DHARANI NIVEDITHA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

Thesis approved by the Student Advisory Committee:

Chairperson	:	**Dr. M. SUDHARANI** Associate Professor & Head Department of Genetics And Plant Breeding Agricultural College Mahanandi, PIN: 518502, A.P	_____
Member	:	**Dr. A. PRASANNA RAJESH** Senior scientist Agricultural Research Station, Kadiri, PIN: 515591 Ananthapur (Dt.), A.P	_____
Member	:	**Dr. P. J. NIRMALA** Associate Professor Department of Biochemistry Agricultural College, Mahanandi, PIN : 518502, A.P	_____

Date of final viva-voce:

ACKNOWLEDGEMENTS

*It is by the blessing of the **Almighty** and the profuse love of my family members I have been able to bring to light this humble piece of work for which I am eternally indebted.*

*With respectful regards and immense pleasure, I express my profound sense of gratitude and indebtedness to the chairman of my Advisory Committee **Dr. M. Sudharani,** Associate Professor & Head, Department of Genetics and Plant Breeding, Agricultural College, Mahanandi for affectionate, sedulous and valuable guidance, constructive criticism and patient counseling instilled in me the spirit of confidence which led to the successful completion of the present study.*

*I am extremely thankful to **Dr. A. Prasanna Rajesh**, **Senior scientist (Groundnut), Agricultural research station, Kadiri, Department of Genetics and Plant Breeding** for his encouragement, sustained interest, prompt and dedicated efforts in providing all the necessary facilities required at the research station without which the successful completion of this task would not have been possible.*

*I sincerely express my gratitude to the revered member of my advisory committee **Dr. P. J. Nirmala,** Associate Professor & Head, Department of Biochemistry, Agricultural College, Mahanandi for her inspiring, meticulous and valuable guidance during the entire period of my investigation.*

I also acknowledge Associate Dean, Agricultural College, Mahanandi for his valuable suggestions and provision of lab and field facilities for the study. I am also grateful to the teaching and non-teaching staff of Agricultural College,Mahanandi and S.V. Agricultural College, Tirupathi for their support during the course of this study, in Particular the Department of Genetics and Plant Breeding, S.V. Agricultural College, Tirupathi.

*I offer my sincere thanks to **Dr. T. Srinivas, Senior scientist (Rice), RARS, Maruteru,** for his valuable suggestions in the preparation of my thesis.*

*I respectfully acknowledge my gratitude to **Dr. A. V. S. Durga Prasad**, **Sri B. V. Ravi Prakash Reddy** Assistant Professors, Department of Genetics and Plant Breeding, Agricultural College, Mahanandi, for their warm and extreme helpfulness in providing necessary information and help required for my work.*

*I also express my gratitude to **Dr. K. S. S. Naik**, Principal Scientist (Groundnut) and Head, ARS, Kadiri for his valuable suggestions and guidance throughout the course of investigation and to Sri **Shankarnarayan**, SRF, ARS, Kadiri and other staff members of ARS, Kadiri for their help during the course of investigation.*

Diction is not enough to express my unboundful gratitude to my beloved parents ***Sri P. Mohanraj*** *and* ***Smt. S. Glory Esther Rani,*** *loving sisters,* ***Usha, Pinky and Sony*** *for their uncountable moral support throughout my educational career. I express my utmost and sincere regards to my beloved grand mother,* ***Smt. Ch. K. G. J. Sundaramma.*** *They have been a fountain of inspiration throughout my life without whose inexhaustible inspiration, everlasting love and moral support I would not have been what I am today.*

I owe a lot to my dear friend and colleagues ***A. Lokeshwar Reddy and K. Bhanu Rekha*** *whose words boosted my self-confidence in the trying circumstances of my life. I thank my colleagues of all the departments* ***Mohammad Raza, Rajeevana, Aparna, Jahnavi, Salma Bhanu, Sreelatha, Ramanjineyulu, Sailaja and Umadevi*** *for their constant encouragement and support. I am also thankful to my seniors* ***Chandra sekhar, Kavitha, Sujatha, Divya and Rajitha*** *and Phd scholars* ***Govardhan, Ravi and Arunodayam*** *and juniors* ***Geethanjali, Madhavi Latha, Vishnu, Surendra and Blessena*** *for their help and co-operation during my study .*

I acknowledge the help of non-teaching staff of Department of Genetics and Plant Breeding, Agricultural College, Mahanandi.

I express my heartiest thanks to A.E.O ***Mr. Subramanyam*** *for timely help and co-operation in various activities of my field work at ARS.*

I humbly thank the authorities of Indian Council of Agricultural Research and ***Acharya N.G. Ranga Agricultural University, Guntur*** *for providing me the opportunity in getting admission into Post graduation and also for all the facilities extended during the period of my post-graduation programme.*

P. Dharani Niveditha ...

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LIST OF ABBREVIATIONS AND SYMBOLS

<	:	Less than
>	:	more than
%	:	Per cent
σ^2	:	Variance
σ	:	Standard deviation
CD	:	Critical Difference
cm	:	Centimetre
df	:	Degrees of Freedom
et al.,	:	And others
Fig.	:	Figure
g	:	Gram
GAM	:	Genetic advance as percent of mean
ha	:	Hectare
K	:	Potassium
kg	:	Kilogram
m	:	Metre
m.ha	:	Million hectare
m.t	:	Million tonnes
N	:	Nitrogen
No.	:	Number
P	:	Phosphorous
per se	:	As such with mean
r_g	:	Genotypic correlation coefficient
r_p	:	Phenotypic correlation coefficient
RBD	:	Randomized Block Design
SCMR	:	SPAD Chlorophyll Meter Reading
SE	:	Standard Error
SPAD	:	Soil and Plant Analyzer Development

ABSTRACT

Author	:	**PRATHAKOTA DHARANI NIVEDITHA**
Title of thesis	:	**"GENETIC DIVERSITY STUDIES ON PEANUT STEM NECROSIS TOLERANT GROUNDNUT GENOTYPES"**
Name of the Author	:	**PRATHAKOTA DHARANI NIVEDITHA**
Major advisor	:	**Dr. M. SUDHARANI**
Submitted for the award of the degree	:	**MASTER OF SCIENCE IN AGRICULTURE**
Faculty	:	**AGRICULTURE**
Department	:	**GENETICS AND PLANT BREEDING**
University	:	**ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**
Year of submission	:	**2016**

The present investigation entitled "Genetic diversity studies on Peanut Stem Necrosis tolerant groundnut genotypes" was carried out with fifty genotypes comprising of released, pre-release cultures and germplasm lines at Agricultural Reasearch Station, Kadiri during *kharif,* 2015 in a randomized block design with two replications. The data were recorded on five randomly selected plants for different yield, yield components and quality traits.

Analysis of variance (ANOVA) revealed highly significant differences among the genotypes for all characters studied indicating the existence of sufficient variation among the genotypes. The characters *viz.,* days to 50 per cent flowering, plant height, number of filled pods per plant, total pods per plant, number of seeds per pod, sound mature kernel per cent, haulm yield per plant, pod yield per plant, kernel yield per plant, shelling per cent, harvest index, 100 kernel weight, SCMR at 60 DAS, oil content and protein content were recorded for fifty genotypes.

The study of *per se* performance indicated that the genotypes *viz.,* 04 x 479-012, K 1501 and K 1643 were found to be superior for most of the yield contributing traits along with yield among the tested entries. These genotypes may be involved in the crossing programme duly estimating the general and specific combining abilities for the future improvement programme.

Study of genetic parameters revealed that kernel yield per plant, pod yield per plant, haulm yield per plant, protein content and number of filled pods per plant recorded high PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean indicating ample scope for improvement of these traits through selection.

The diversity studies grouped fifty genotypes into eight clusters. Among them, cluster II consisted of maximum number of genotypes (22), followed by cluster I (15) and cluster III (8). The clusters IV, V, VI, VII and VIII were monogenotypic and consisted of single genotype. An analysis of the inter and intra-cluster distances revealed maximum inter-cluster distance between clusters IV and VIII followed by VI and VIII, III and V and clusters III and VII, indicating that genotypes from these clusters were highly divergent meriting their consideration in selection as parents for hybridization. Among all the characters studied, SCMR at 60 DAS contributed maximum to the diversity followed by protein content and harvest index.

A perusal of the results of character association revealed positive and significant association of kernel yield with days to maturity, pods per plant, 100 kernel weight, pod yield per plant, shelling per cent, SCMR at 60 DAS and haulm yield per plant, indicating an increase in kernel yield would realize with an improvement in these characters. Therefore, priority should be given to these traits while making selections for kernel yield improvement.

A perusal of the results on path coefficients for yield and yield components revealed high residual effect for both phenotypic and genotypic path coefficients, indicating that other attributes besides the characters studied are contributing for kernel yield and oil content. The results also revealed high positive direct effects of haulm yield per plant, shelling per cent, harvest index and 100 kernel weight on kernel yield per plant and shelling per cent on oil content. Hence, these traits should be considered as important selection criteria in all groundnut improvement programmes and direct selection for these traits is recommended for kernel yield and oil content improvement in groundnut.

Chapter I

INTRODUCTION

Groundnut or Peanut (*Arachis hypogaea* L.) is one of the most important oil and protein producing legume crop of the semi-arid tropics and belongs to the family *Fabaceae,* sub family *Faboideae* (Janila *et al.* 2016). China and India are the leading groundnut producers followed by USA and Nigeria. Groundnut is an annual self pollinating legume native to South America (Brazil) and is a segmental allotetraploid (2n= 4x = 40). Peanut seeds are valued for its oil (45-50%) and protein (25%). It also contains carbohydrates (12-15%) and is a rich source of B-complex vitamins especially thiamine and nicotinic acid. Groundnut kernels contain 40-60 per cent oil, 20-40 per cent protein and 10-20 per cent carbohydrates. They provide 567 kcal of energy from 100g of kernels (USDA nutrient database). Additionally, they also contain several health enhancing nutrients such as minerals, antioxidants and vitamins. They contain antioxidants like *p*-coumaric acid and resveratrol, vitamin- E and many important B- complex groups of thiamine, pantothenic acid, vitamin- B6 foliates and niacin (Janila *et al*. 2016).

India is the largest grower and second producer after China and groundnut crop occupies an area of 44.46 lakh ha. with a production of 71.81 lakh tones and yield of 1615 kg ha^{-1}. Gujarat and Andhra Pradesh are the major groundnut growing states and Andhra Pradesh occupies third place in production in India after Gujarath and Tamilnadu. Groundnut productivity in Andhra Pradesh (1027 kg ha^{-1}) is very low (Annual report 2014-15, Directorate of Groundnut Research) against Indian productivity of 1615 kg ha^{-1} and world productivity of 1675.9 kg ha^{-1}. The low productivity can be attributed to several factors like erratic rainfall pattern, incidence of pests and diseases in addition to cultivation of low yielding varieties. Despite extensive research accomplishments, groundnut till date is considered as an unpredictable legume. Thus, there is a need to improve groundnut productivity through systematic breeding programmes.

Among the biotic stresses peanut stem necrosis (PSND) was initially observed as an epidemic resulting in complete death of young groundnut plants during the *kharif*, 2000 in Anantapur district, Andhra Pradesh. The disease affected nearly 2.25 lakh ha and the crop losses were estimated to exceed Rs 3 billion. Anantapur, Kurnool, Kadapa and Chittoor districts in Andhra Pradesh and Raichur district in Karnataka are being affected by the disease and continuously effecting the productivity (Reddy *et al.* 2002).

Peanut stem necrosis (PSND) is caused by Tobacco Streak Virus (TSV) of genus *Ilavirus* belonging to family *Bromoviridae*. The disease is transmitted by three types of thrips *Frankliniella schultzei, Megalurothrips usitatus, Scirtohrips dorsalis* while *Helianthus, Tagetus, Parthenium, Amaranthus* species are the sources of inoculum. Initially, large necrotic lesions are seen on young quadrifoliates. This symptom will be followed by necrosis of the entire stem located below the necrosed quadrifoliates. If young plants are affected (less than one month old), the entire plant is often necrosed. Necrotic spots are observed on the majority of pods and on branches also in older plants. Further the size of the pods is severely reduced and kernels are not marketable and it was found that the virus is not seed-transmitted.

Kalyani *et al*. (2007) evaluated wild relatives of peanut to identify potential sources of resistance to Tobacco Streak Virus (TSV). 56 germplasm accessions from 20 wild *Arachis* spp in four sections along with susceptible cultivars JL-24 and K 1375 were evaluated under green house conditions. Even though these resistant accessions showed 0-100% TSV infection in inoculated leaves, TSV was not detected in subsequently emerged leaves. This was 1st report on PSND resistance in *Arachis* species. These are cross compatible with *Arachis hypogea* for utilization in breeding for PSND tolerance. ICRISAT suggested the cultivation of tolerant varieties like ICGV 01276, ICGV 92267 and ICGV 99029 (ICRISAT, 2003).

Genetic diversity is a pre-requisite for hybridization programme to obtain desirable genotypes. According to Tomooka (1991), the evaluation of diversity is very important to know the source of genes for particular trait within the available germplasm. This shows that there is need to know the genetic diversity of existing genotypes before undertaking any crop improvement programme. Multivariate statistical methods and numerical taxonomy is being used extensively in summarizing and describing variation and its pattern in a population of crop genotypes. (Makinde *et al.* 2010). The D^2 technique based on multivariate analysis developed by Mahalanobis (1936) is the most effective method for knowing the degree of genetic diversity among the genotypes. It is generally accepted that genetically diverse parents when crossed will show highest heterosis and chances of isolating transgressive segregants will be increased.

The basic key to bring about genetic upgrading in any crop is to utilize the available or created genetic variability. If the variability in the population is largely due to genetic causes with least environmental effect, the probability of isolating superior genotypes will be high. Hence, the knowledge of the variability parameters for different physiological and productivity traits in groundnut such as genotypic coefficient of variation, heritability and genetic advance is essential to formulate effective crop improvement programmes.

Direct selection for yield, however, is not much effective as it is a quantitative character controlled by polygenes and also dependent on several yield component traits. Hence, knowledge about association of characters which directly or indirectly contribute to yield is crucial. Correlation coefficient studies explain the degree of association among the characters. The method of path coefficient analysis developed by Wright (1921) is helpful in partitioning of correlation coefficients into direct and indirect effects and in the assessment of relative contributions of each component to yield.

In this context, the present study was carried out to estimate the nature and magnitude of genetic diversity and variability parameters of productivity traits and quality parameters in a collection of 50 genotypes of groundnut with the following objectives:

1. To study genetic diversity among the PSND tolerant groundnut genotypes for yield, yield components and quality characters.

2. To study variability, heritability and genetic advance for yield, yield components and quality characters, among PSND tolerant groundnut genotypes.

3. To study character associations among yield, yield components and quality characters.

4. To study the direct and indirect effects of different characters on kernel yield and oil content.

Chapter II

REVIEW OF LITERATURE

A brief review of the literature in consonance with the objectives of present investigation in groundnut (*Arachis hypogaea* L.) under the following headings :

2.1 Genetic Parameters
2.2 Genetic Divergence
2.3 Character Associations
2.4 Path coefficient Analysis
2.5 Resistance of genotypes to the disease

2.1 GENETIC PARAMETERS (Variability, Heritability and Genetic advance)

The amount of variability present for different characters in a population and its efficient utilization determines the success of any breeding programme. The effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable. An exploitable and useful measure of the magnitude of genetic variance present in the population is given by genetic coefficient of variability.

Estimation of genetic variability in conjuction with the estimates of heritability and genetic advance indicates the possible improvement achieved through selection. The degree of success depends on the magnitude of heritability [h^2(b)] which measures the relative amount of the heritable portion of total variation and aids in selection.

Genetic advance (GA) under selection gives an idea about how much of the genetic gain was obtained due to selection. Hence, the estimates of genetic variability, heritability and genetic advance will be of immense value in selection and breeding for high yielding strains.

A brief review of literature on variability, heritability and genetic advance of quantitative characters in groundnut is presented here under.

Shinde *et al.* (2010) observed significant differences among the genotypes for all the yield contributing characters except number of primary branches per plant. They registered high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for pod yield per plant, number of immature pods per plant, number of mature pods per plant and biological yield per plant indicating the large extent of genetic variability and less role of environment in the expression of these traits. They found high GCV, high heritability coupled with high genetic advance for pod yield per plant and number of mature pods per plant and concluded that these characters were mainly under the influence of additive gene action indicating the ample scope for further improvement through simple selection.

Zaman *et al.* (2011) evaluated 34 genotypes during *rabi*, 2009-2010 for estimation of genetic variability and genetic parameters for 11 morphological characters and observed highly significant variations among the genotypes for all the characters studied. The highest GCV was observed for kernel yield per hectare followed by kernel yield per plant, branches per plant, immature and mature nuts per plant, 100-kernel weight and plant height. The highest heritability was observed for kernel yield per plant (95.08%) followed by kernel yield per hectare (94.38%), 100 kernel weight (87.01%), immature and mature nuts per plant (82.24% and 80.32%) and branches per plant (79.54%) while, high values of genetic advance were recorded for all the characters except days to maturity and days to 50 per cent flowering.

Rajesh *et al.* (2012) studied variability and genetic association among yield, physiological and confectionary traits in 28 F_2 crosses in groundnut. They observed that PCV was higher than GCV for all the attributes indicating the

influence of environment. They also observed moderate GCV values for kernel yield per plant (21.64) and pod yield per plant (20.33). They registered high heritability coupled with high genetic advance as per cent of mean for pod yield, kernel yield, haulms yield per plant, 100-kernel weight, SLA at 60 and 90 DAS and indicated that these characters are more amenable for selection as they appeared to be predominantly controlled by additive gene action. They also reported moderate heritability coupled with low genetic advance for SCMR at 60 and 90 DAS, shelling percentage and oil content indicating that these characters were highly influenced by the environment and selection may not be rewarding for these characters.

John *et al.* (2013) evaluated 37 genotypes of Spanish bunch groundnut and recorded high GCV estimates for days to 50% flowering and high heritability along with high genetic advance as per cent of mean for plant height, haulm yield per plant, pod yield per plant and kernel yield per plant.

Rao *et al.* (2014) evaluated 50 groundnut genotypes and reported moderate PCV and GCV values for number of pods per plant and plant height, kernel yield, dry pod yield, 100-kernel weight and dry haulm yield. They also observed high heritability coupled with high genetic advance as per cent of mean for 100-kernel weight, dry pod yield, kernel yield, plant height and number of pods per plant indicating the role of additive genes in expression of these traits.

Ramana *et al.* (2015) studied 21 crosses of groundnut derived from a 7 x 7 half diallel and reported high PCV and GCV for number of secondary branches per plant, kernel yield per plant, total phenols content, pod yield per plant, number of kernels per plant and harvest index. They reported high heritability coupled with high genetic advance as per cent of mean for days to 50% flowering, total phenols, number of secondary branches per plant, harvest index, kernel yield per plant and number of kernels per plant indicating that these traits are predominantly influenced by additive genes and suggested the possibility of phenotypic selection for these traits in early generations. They also

reported high heritability coupled with moderate genetic advance as per cent of mean for number of primary branches per plant and moderate heritability coupled with moderate genetic advance as per cent of mean for 100-kernel weight indicating the role of both additive and non additive gene effects with preponderance of additive genetic variance and suggested that selection would be effective to improve these traits.

2.2 GENETIC DIVERGENCE

Genetic diversity is a pre-requisite for a breeding programme to obtain desirable genotypes. Genetic diversity is very much essential to meet the diverse goals in plant breeding for producing cultivars with increased yield, wider adoption, desirable quality and pest resistance (Nevo *et al.*, 1982). Morphological similarity, eco-geographic diversity, phylogenetic relationships etc. were the few earlier methods used for discriminating divergent populations, which are reinstated by more scientific and advanced biometric techniques, namely, multivariate analysis based on Mahalanobis's D^2 statistic and semigraphic method of metroglyph analysis. Estimation of the degree of divergence between biological populations and computation of relevant contributions of different components to total divergence is done completely by Mahalanobis generalized distance estimated by D^2 statistic (Maurya and Singh, 1977). According to Tomooka (1991), the evaluation of diversity using Mahalanobis D^2 statistic is more reliable method as the requisite knowledge in respect of a mass of characters is available prior to initiation of the crossing programme. The high heterotic nature in the F_1 and broader spectrum of variability in succeeding segregating generations mainly depends upon using of more diverse parents (Arunachalam, 1981).

A brief review of available literature on the genetic divergence in groundnut is presented hereunder.

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Dolma *et al.* (2010 a) evaluated 33 genotypes of groundnut from different geographical regions and grouped them into six clusters. The inter-cluster

distance was maximum between cluster IV and V followed by cluster III and V. Based on inter cluster distance and *per se* performance, the genotypes from these clusters were suggested for inclusion in the hybridization programmes to evolve high yielding and late leaf spot resistant genotypes.

Khote *et al.* (2010) studied the genetic divergence among 30 groundnut genotypes. Inter cluster distance was found to be maximum between cluster II and cluster V followed by cluster I and cluster V, cluster V and VI, cluster III and cluster VI, cluster II and cluster VI, cluster II and cluster V. Cluster I and cluster VI and were identified as genetically diverse clusters that could be utilized for hybridization programmes in crop improvement of groundnut.

Kumar *et al.* (2010) conducted D^2 analysis in 64 groundnut genotypes (39 new germplasm accessions and 25 advanced breeding lines). These genotypes were grouped into seven clusters where, cluster VII was the largest followed by cluster I and cluster VI. Maximum inter-cluster distance was recorded between IV and VI representing wide divergence among these clusters. On the basis of intercluster distance and cluster means the genotypes from these clusters were inferred to be widely diverse and therefore may be considered for future breeding programmes.

Nikam and Thaware (2010) studied genetic divergence among 38 genotypes of groundnut by using Mahalanobis's D^2 statistics. The genotypes were grouped into nine clusters. The maximum inter-cluster distance was observed between cluster VI and VII, followed by cluster II and IX. The genotype in above clusters also revealed substantial differences in the means for important yield contributing characters and were found to be potential parents based on cluster mean and genetic diversity.

Vekariya *et al.* (2010) conducted genetic divergence analysis among 50 groundnut genotypes. The maximum inter-cluster distance was found between clusters III and XIII. The genotypes in above clusters revealed substantial

difference in the means for important yield contributing characters suggesting that the genotypes belonging to these clusters would form ideal parents for improvement in groundnut.

Venkataravana (2010) evaluated 64 genotypes of groundnut and the genotypes were grouped into seven clusters. Specific leaf area (27.67%) was observed to contribute maximum to genetic divergence followed by kernel yield per plant (21.72%), oil content (15.32%) and plant height (7.83%).

Venkateswarlu *et al.* (2011) studied 74 genotypes and grouped them into 12 clusters. Based on inter-cluster distances, the clusters VII vs X, VI vs XII and X vs XII were found to be divergent. The characters, 100-kernel weight, shelling percentage and harvest index were observed to contribute maximum towards genetic divergence. Similarly, Kumar *et al.* (2012) utilized D^2 analysis to classify 50 genotypes of groundnut into five clusters. Harvest index and 100-seed weight were the main contributors to total divergence.

Kandakoor *et al*. (2013) conducted field screening of 56 groundnut genotypes and grouped them into 9 clusters based on per cent damage by thrips. Thirteen genotypes (CTMG-3,4,5, CGV 91114 etc.,) were in 2^{nd} cluster and found to be resistant to thrips. They concluded that the resistance is due to high concentration of phenols and tannins. TMV-2 and JL-24 are highly susceptible for thrips.

Nirmala *et al.* (2013) grouped the 30 genotypes into 14 clusters and reported that maximum inter cluster distance between cluster III and cluster XII. The maximum intra-cluster distance was recorded for cluster X. Among the various traits, the highest contribution towards divergence was found for number of secondary branches per plant followed by crop growth rate (CGR) at 75 days after sowing (DAS) to harvest, CGR at 30-75 DAS, 100 seed weight, plant height, SPAD chlorophyll metre reading and harvest index.

Yadav *et al.* (2014) studied 60 genotypes of groundnut and grouped them into 12 different clusters. The maximum inter-cluster distance was found between cluster III and X while minimum was observed between cluster VII and XI. Cluster III showed high genetic divergence with cluster X followed by cluster V. They advised crossing between the genotypes from cluster I with cluster X, cluster III, cluster V and cluster VIII for the generation of wide spectrum genetic variability and isolation of transgressive segregants for enhancement of pod yield in groundnut.

Rao *et al*. (2014) conducted field experiments with 69 genotypes at 3 dates of sowing and grouped them into four clusters based on the per cent incidence of thrips. The 1st cluster includes genotypes with low incidence of thrips. The resistance in them is due to high leaf & stem trichomes, more leaf thickness and dark green foliage. Some genotypes had characteristic wavy margin and downward folding of leaves which resist the movement of thrips. So these might be used as a source of resistance in breeding programme.

2.3 CORRELATION ANALYSIS

Genetic improvement of yield is the primary concern to plant breeders. However, yield is a complex, quantitatively inherited character and is highly influenced by the environment. A sound knowledge on the extent of association of yield components among themselves and with yield is therefore essential for improving yield. Character association analysis measures the actual relationship between various plant characters and helps the plant breeder in fixing selection criteria for yield in parental lines and segregating populations. Correlation co-efficient reveals the type, nature and magnitude of correlation between any pair of characters. Phenotypic correlation is the association between two characters which can be directly observed and is subjected to changes in the environment. It measures the environmental deviations together with non-additive gene action. Genotypic correlation is the correlation of breeding values *i.e.,* additive + additive x additive gene action.

A brief review of literature available on character association of pod yield and its attributes in groundnut is detailed here under.

Korat *et al.* (2010) evaluated 80 genotypes of Virginia bunch groundnut genotypes under irrigated conditions and observed positive and significant association of pod yield per plant with biological yield per plant and harvest index.

John *et al.* (2011) revealed negative correlation of SCMR with specific leaf area (SLA). Further it was observed the positive correlations of character pairs *viz.*, transpiration rate and photosynthetic rate with pod yield per plant and dry haulm yield per plant with harvest index indicating that selection for these traits might be rewarding in improvement of tolerance to drought besides pod yield in groundnut.

Ravikumar and Reddi Sekhar (2012) reported highly significant positive association of kernel yield per plant, mature pods per plant, pods per plant, harvest index, 100-kernel weight, plant height and shoot weight with pod yield and also observed high estimates of genotypic correlation coefficients than phenotypic correlation coefficients. Hence, they opined that there is a strong inherent association between these characters.

Thakur *et al.* (2013) carried out investigation to determine relationships between pod yield and yield components in 25 groundnut genotypes with three local checks and revealed highly significant positive association of days to maturity, root length, pod width, pod length and kernel length with pod yield per hectare.

Alam (2014) reported that pod yield had significant positive association with secondary branches per plant, harvest index, 100-pod weight, 100-kernel weight, disease incidence and canopy temperature. They also recorded higher genotypic correlation coefficients than phenotypic correlation coefficients indicating strong inherent association between the characters.

2.4 PATH CO-EFFICIENT ANALYSIS

Path co-efficient analysis is a statistical device developed by Wright (1921) which helps in partitioning of the correlation co-efficients into direct and indirect effects of independent variable on dependent variable. The correlation co-efficients do not give a complete picture of the causal basis of association. Path co-efficient analysis of different components of yield provides a true picture of relative importance of their direct and indirect effects and gives a clear understanding of their association with yield. Thus, path co-efficient analysis helps in formulating the selection criterion based on the direct and indirect effects of different yield component characters. Hence, path co-efficient analysis is of much importance in plant breeding programmes.

A brief review of literature on path coefficient analysis is presented here under :

Korat *et al.* (2010) revealed the highest positive direct effects of biological yield per plant and harvest index on pod yield as well as positive indirect effects of 100-kernel weight *via* biological yield per plant and harvest index on pod yield.

Sawargaonkar *et al.* (2010) reported high positive direct effect of kernel yield and indirect effects of oil content, sound mature kernel percentage, days to 50% flowering, test weight, days to maturity and non- reducing sugars through kernel yield on pod yield indicating the importance of these characters to lay emphasis on the selection for rapid improvement in pod yield. Vaithiyalingan *et al.* (2010) revealed maximum direct effect of pods per plant followed by dry matter production and kernel weight on pod yield.

Zaman *et al.* (2011) tested 34 groundnut genotypes and recorded high positive direct effect of number of mature nuts per plant followed by nut size, shelling percentage, days to 50 per cent flowering and days to maturity on kernel

yield per hectare. It was also indicated that branches per plant, plant height, nuts per plant, nut size, kernel size, days to 50 per cent flowering, shelling per cent and days to maturity were identified as the important characters which could be used in selection for yield.

John *et al.* (2011) evaluated 28 groundnut genotypes in F_2 population and revealed that days to 50 per cent flowering had maximum positive direct effect on pod yield per plant followed by dry haulm yield per plant, stomatal conductance, days to maturity and specific leaf area.

Mukhtar *et al.* (2011) revealed the highest positive direct effect of dry matter on pod yield followed by 100-kernel seed weight, seed yield per plant, number of mature pods and number of pods per plant in the decreasing order of the direct effects on pod yield.

Ravikumar and Reddi Sekhar (2012) noticed high direct effect of kernel yield per plant and harvest index on pod yield in a study involving 50 genotypes of groundnut. Further, they suggested that selection based on these characters would result in rapid improvement of pod yield in groundnut.

Thakur *et al.* (2013) carried-out an investigation to determine the path coefficients of pod yield and yield component traits in 25 groundnut genotypes with three local checks and revealed that days to maturity, sound mature kernel per cent, pod length, pod width and kernel length had high positive direct contribution to pod yield per hectare. On contrary, they recorded negative direct negative effects of days to flowering, shoot length, shelling per cent, Sound mature kernel per cent and 100-kernel weight on pod yield per hectare.

Alam (2014) evaluated 45 genotypes of groundnut and revealed that harvest index had highest positive direct effect on pod yield followed by secondary branches per plant and primary branches per plant while SPAD meter reading had maximum negative direct effect on pod yield followed by pod index.

Rao *et al.* (2014) evaluated 50 genotypes of groundnut and reported that kernel yield, days to maturity, number of pods per plant and 100-kernel weight contributed high positive direct effects on pod yield.

2.5 RESISTANCE OF GENOTYPES TO THE DISEASE

Several experiments were conducted to trace out tolerant genotypes for PSND disease. A brief review of literature is presented here under.

ICRISAT 2003 has identified TSV resistance in groundnut is scarce, but extensive screening has identified tolerance in three cultivated varieties (ICGV 01276, ICGV 92267 and ICGV 99029).

Mehta et al. (2013) identified that the absence of resistance genes against biotic stresses like Tobacco streak virus (TSV) within compatible peanut germplasm necessitates the deployment of genetic engineering strategy to develop transgenic resistance. Transgenic resistance in peanut (Arachis hypogaea L.) to peanut stem necrosis disease caused by TSV was obtained by transferring coat protein (CP) gene of TSV through Agrobacterium-mediated transformation of de-embryonated cotyledons and immature leaves of peanut cultivars Kadiri 6 (K6) and Kadiri 134 (K134).

Chapter III

MATERIAL AND METHODS

3.1 LOCATION OF THE EXPERIMENTAL SITE

The present investigation on "Genetic diversity studies on peanut stem necrosis tolerant groundnut genotypes" was carried out during *kharif*, 2015 at Agricultural Reasearch Station (ARS), Kadiri situated at an altitude of 531 m above mean sea level, $14^0$11'N latitude and $78^0$147 E longitude. The experimental soil was of sandy clay loam type. The material used and methods followed pertaining to the present investigation are presented here under.

3.2 MATERIAL

The experimental material consisted of fifty genotypes of groundnut. The material was made available for the study by Agricultural Research Station (ARS), Kadiri, Andhra Pradesh. The list of genotypes is furnished in Table 3.1 and pictures showing the morphological features are presented at Fig. 3.1.

3.3 METHODS

3.3.1 Field layout

The experiment was laid out in a Randomized Block Design with two replications. All the fifty groundnut genotypes were sown on 15th July, 2015. Each genotype was sown in each replication in two rows of 5 m length. A spacing of 30 cm between the rows and 10 cm between plants within a row was adopted.

Table 3.1 list of genotypes and pedigree of fifty groundnut genotypes

S.NO	GENOTYPES	PEDIGREE	BASIS FOR SELECTION
1	03 X 397-031	K 1327 X ICGV 99099	Tolerant to PSND
2	03 X 398-067	K 1569 X ICGV 95386	Tolerant to PSND
3	03 X 427-082	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
4	03 X 427-086	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
5	03 X 427-088	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
6	03 X 427-091	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
7	03 X 427-094	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
8	03 X 427-107	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
9	03 X 427-109	Kadiri Harithandhra X (3 X 155-005)	Tolerant to thrips
10	03 X 461-019	K 1350 X ICGV 99099	Tolerant to thrips
11	03 X 482-036	K 1535 X CTMG-6	Tolerant to PSND
12	03 X 485-001	K 1570 X CIMG-6	Tolerant to PSND
13	03 X 485-024-01	K 1570 X CIMG-6	Tolerant to PSND
14	04 X 477-010	K 1535 X ICGV 95386	Tolerant to PBND
15	04 X 477-018	K 1535 X ICGV 95386	Tolerant to PBND
16	04 X 477-021-1	K 1535 X ICGV 95386	Tolerant to PBND
17	04 X 477-021-2	K 1535 X ICGV 95386	Tolerant to PBND
18	04 X 477-024-1	K 1535 X ICGV 95386	Tolerant to PBND
19	04 X 477-030	K 1535 X ICGV 95386	Tolerant to PBND
20	04 X 477-031	K 1535 X ICGV 95386	Tolerant to PBND
21	04 X 479-002	K 1569 X ICGV 95386	Tolerant to PBND
22	04 X 479-005	K 1569 X ICGV 95386	Tolerant to PBND
23	04 X 479-012	K 1569 X ICGV 95386	Tolerant to PBND
24	04 X 480-007	K 1570 X ICGV 95386	Tolerant to PBND
25	04 X 481-005	K 1574 X ICGV 95386	Tolerant to PBND
26	04 X 481-023	K 1574 X ICGV 95386	Tolerant to PBND

27	K 1643	03X192-074(Kadiri-7 bold X TAG-24)	Tolerant to thrips and PBND
28	K 1563	03X193-003(Kadiri-8 bold X TAG-24)	Tolerant to thrips and PBND
29	K 1715	Kadiri -7 bold – 092 ANP	Tolerant to PBND
30	K 1577	03X193-001(Kadiri-8 bold X TAG-24)	Tolerant to thrips and PBND
31	K 1735	08X174-032(Kadiri-7 bold X JL-24)	Tolerant to PBND
32	K 1576	03X192-001(Kadiri-7 bold X TAG-24)	Tolerant to thrips and PBND
33	K 1725	03X192-110(Kadiri-7 bold X TAG-24)	Tolerant to thrips
34	K 1574	03X019-004(VemanaXJSSP-6VB)	Tolerant to thrips and PBND
35	K 1535	03X154-001(K1240 X NCAC-2242)	Tolerant to thrips and PBND
36	K 1621	11X182-022(ICGV99099 X K4)	Tolerant to thrips and PBND
37	K 1501	02X068-002(K4 X ICGV 930179 P_2)	Tolerant to thrips and PBND
38	K 1799	ICGV96175(Florigiant X NCAC17090) X DH3-20 X PI	Tolerant to thrips and PBND
39	K 1800	ICGV96176(Florigiant X 259747XICGV88312)	Tolerant to thrips and PBND
40	K 1809	Dt.Pop.57(ICGV020054-F2-SSD-SSD-P18-B1)	Tolerant to thrips and PBND
41	K 1717	K 1340 X TAG-24	Tolerant to thrips and PBND
42	K 1641	1567 X (K4 X ICGV 99099)	Tolerant to thrips and PBND
43	K 1650	02X068-002(K4 X ICGV 930179 P_3	Tolerant to thrips and PBND
44	K 1647	K 1340 X JCG-88	Tolerant to thrips and PBND
45	K 1811	Dt.Pop.67(ICGV020055-F2-SSD-SSD-P18-B1)	Tolerant to thrips and PBND
46	Kadiri 6	JL-24 X Ah 316/S	High yielding
47	Kadiri 9	Kadiri-4 X Vemana	High yielding
48	Harithandhra	91/57-2 X 1476177(ICG X 930181 P3)	High yielding
49	Anantha	Vemana X Girnar	High yielding
50	JL-24	Mass selection from Taiwan	Susceptible to PSND

03X397-031 **03X398-067** **03X427-082** **03X427-086** **03X427-088**

03X427-091 **03X427-094** **03X427-107** **03X427-109** **03X461-019**

03X482-036 **03X485-001** **03X485-024-01** **04X477-010** **04X477-018**

04X477-021-1 **04X477-021-2** **04X477-024-1** **04X477-030** **04X477-031**

Plate 3.1 Morphological features of groundnut genotypes utilized in the present study

04X479-002 **04X479-005** **04X479-012** **04X480-007** **04X481-005**

04X481-023 **K 1648** **K 1563** **K 1715** **K 1577**

K 1735 **K 1576** **K 1725** **K 1574** **K 1535**

K 1621 **K 1501** **K 1799** **K 1800** **K 1809**

Plate 3.1 Contd…..

K 1717 **K 1641** **K 1650** **K 1647** **K 1811**

Kadiri 6 **Kadiri 9** **Kadiri Harithandhra** **Anantha** **JL-24**

Plate 3.1. Contd….

3.3.2 Crop husbandry

The field was ploughed and harrowed until a fine tilth of soil was obtained. The crop was provided with fertilizers to supply 20:40:50 N:P:K kg ha^{-1} and 500 kg of gypsum ha^{-1} at peak flowering stage. The crop was raised under completely rainfed conditions. Recommended cultural and agronomic measures were followed during the crop period. Apart from these, need based plant protection measures were adopted during the crop season for controlling diseases and pests.

3.4 METHOD OF RECORDING DATA

Observations were recorded on randomly chosen five competitive plants in each genotype in each replication for all the characters except days to 50 per cent flowering and days to maturity. The latter two characters were recorded on per plot basis. The data of five competitive plants were averaged and expressed as mean of the respective character for that replication. The details of data recorded were as follows.

3.4.1 Days to 50 per cent flowering (DFF) :

Number of days taken from sowing to the date on which 50 per cent of plants in each genotype and in each replication had atleast one blossomed single flower.

3.4.2 Total pods per plant (TP) :

Number of pods in each plant were counted and the mean value of the random sample of five plants was recorded as number of pods at harvest.

3.4.3 No. of filled pods per plant (FP) :

Number of fully filled pods were counted and the mean value of the random sample of five plants was recorded as number of filled pods per plant.

3.4.4 Plant height (cm) (PH) :

Length of main axis from ground level to the tip of the main branch was measured in centimeters and recorded as plant height at harvest.

3.4.5 No. of seeds per pod (S/P) :

Number of seeds in each pod were counted in a random sample of five pods per each plant at harvest and the mean value of the random sample of five plants was recorded as number of seeds per pod.

3.4.6 Sound mature kernels (%) (SMK %) :

The per cent of well filled kernels without cracks shrivels and diseases to the total kernels counted from five random plants in each genotype and replication and expressed as percentage was regarded as sound mature kernels per cent.

3.4.7 Haulm yield per plant (g) (HY) :

The dry weight of stems and leaves after drying for one week in sunlight for each plant was recorded and the average of five random plants was expressed as dry matter per plant in grams.

3.4.8 Pod yield per plant (g) (PY) :

The weight of well sun dried mature pods from each plant was weighed and the mean of randomly chosen five plants was recorded in grams as pod yield per plant.

3.4.9 Kernel yield per plant (g) (KY):

The weight of kernels after shelling of all mature pods of a plant was taken and the mean of a random sample of five plants was recorded as kernel yield per plant in grams.

3.4.10 100-Kernel weight (g) (100 KW) :

For each genotype, in each replication, hundred kernels were counted at random and weighed. The data was recorded in grams.

3.4.11 Shelling percentage (%) (S%) :

Shelling percentage was calculated using the following formula:

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

The mean value of random sample of five plants was recorded as shelling percentage.

3.4.12 SPAD Chlorophyll Meter Reading (SCMR) at 60 days after sowing (DAS) :

The SPAD meter (Soil Plant Analytical Development) is a simple hand held and portable instrument which provides information on the relative amount of leaf chlorophyll content. Fully expanded 3rd leaf from the top on the main axis in each plant was collected from each treatment in each replication for measuring SCMR by SPAD meter of Minolta company, NJ, USA (SPAD 502). Fig. 3.2.

3.4.13 Harvest Index

It is the ratio of the seed yield to the total dry matter was calculated at harvest using the formula

$$\text{Harvest index} = \frac{\text{Pod yield of the sample}}{\text{Total drymatter of the sample}} \times 100$$

3.4.14 Oil content (%)

Oil content in groundnut is estimated by specific gravity method using kerosene. 10 g of split kernels when dipped in kerosene and weighed on the balance the specific gravity of the sample was determined. This is then multiplied with a constant value 176.8 to determine the per cent of oil content in that sample.

Oil content = 176.8 x specific gravity of the sample

SPAD 502 meter

Plate 3.2 General view of the experimental plot and equipment used for estimation of physiological traits

3.4.15 Protein content (%)

To estimate the protein content 2ml of concentrated H_2SO_4 is added to finely powdered seed sample of 0.1 g. To this mixture K_2SO_4 catalytic mixture of one spoon is added and allowed for digestion until the sample become colourless. Then it is titrated with 0.1 N H_2SO_4. The percentage of nitrogen is estimated with the following formula.

$$\text{Nitrogen percentage} = \frac{\text{Titre value x } 0.0014 \text{ x } 100}{0.1}$$

This value is multiplied with a constant value of 6.25 to obtain protein content in the seed sample.

3.5 STATISTICAL ANALYSIS

The treatment means for all the characters were subjected to the following statistical analysis.

1. Analysis of variance
2. Genetic divergence
3. Estimation of genetic parameters (Genotypic coefficient of variation, phenotypic coefficient of variation, heritability in broad sense and genetic advance).
4. Character association
5. Path analysis

3.5.1 Analysis of Variance

The differences between 50 genotypes for different characters were tested for significance by using analysis of variance technique on the basis of model proposed by Panse and Sukhatme (1961).

$$Y_{ij} = \mu + g_i + \gamma_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation on 'i'th genotype in 'j'th replication.

μ = General mean

g_i = Effect of 'i'th genotype

γ_j = Effect of 'j'th replication

e_{ij} = Random error associated with 'i'th genotype in 'j'th replication.

The analysis of variance for each character was carried out as follows:

Source of variation	**Degrees of freedom**	**Sum of squares**	**Expectations of mean sum of squares**	**'F ratio'**
Replications	(r-1)	M_r		M_r/M_e
Genotypes	(t-1)	M_t	$\sigma_e^2 + r\sigma_g^2$	M_t/M_e
Error	(r-1) (t-1)	M_e	σ_e^2	-
Total	(rt-1)			

Where,

r = Number of replications

t = Number of genotypes

M_r = Mean sum of squares due to replications

M_t = Mean sum of squares due to genotypes

M_e= Mean sum of squares due to error.

The significance test was carried out by referring to standard 'F' table values given by Fisher and Yates (1967).

3.5.2 Genetic divergence

3.5.2.1 Collection of data: Data recorded on 50 groundnut genotypes studied in the present investigation for various physiological and productivity traits was used to carry out divergence analysis.

3.5.2.2 Test of significance: Variances were calculated for all the characters under study and significance was tested. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1961). A dispersion table was prepared from the estimates after testing the differences between genotypes for each of the characters. A simultaneous test of significance of differences between the mean values of a number of correlated variables was done (Rao, 1952) by using 'v' statistic which inturn utilizes Wilk's 'λ' criterion (Wilk's, 1932). The sum of squares and sum of products of error and error + variety variance - covariance matrix were used for this purpose. The estimates of 'λ' (Wilk's criterion) was done using the following formula :

$$\lambda = \frac{(E)}{(E+V)}$$

Where,

(E) = Determinant of error matrix

(E+V) = Determinant of error + varieties matrix

$\chi^2_{pq} = V = -m \log_e \lambda$

Where,

χ^2_{pq} = Estimation of χ^2 value at pq degree of freedom

m = n – (p+q+1)/2 with pq degree of freedom

n = Degree of freedom of error + varieties

p = Number of characters

q = Number of genotypes – 1

$Log_e\lambda = 2.3407\ Log_{10}\lambda$

3.5.2.3 Transformation of correlated variables: Transformation was done using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values because D^2 values was reduced to simple enumeration of differences in mean values of various characters of two genotypes *i.e.*,Σdi^2.

3.5.2.4 Computation of D^2 values: Genetic diversity between genotypes was estimated using D^2 analysis as given by Mahalanobis (1936). The D^2 value between 'i^{th}' and 'j^{th}' genotypes for 'P' characters were calculated as

$$D_{ij}^2 = P \Sigma_{t=1} (\overline{Y}_{it} - \overline{Y}_{jt})$$

Where,

$\overline{Y}_{it}$ = Uncorrelated mean value of i^{th} genotype for 't' character

$\overline{Y}_{jt}$ = Uncorrelated mean value of j^{th} genotype for 't' character

D^2_{ij} = D^2 value between i^{th} and j^{th} genotypes

3.5.2.5 Testing the significance of D^2values : The D^2 values obtained for a pair of genotypes were taken as the calculated value of χ^2 and tested against tabulated χ^2 at 'p' degree of freedom where 'p' is the number of characters considered.

3.5.2.6 Grouping of genotypes into different clusters: Grouping of the genotypes into different clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least, on an average show a smaller D^2 value among themselves than those belonging to two different clusters.

The first step in grouping of the genotypes into different clusters was to arrange the genotypes in order to know their relative distance from each other. For this purpose, D^2 values of all the possible combinations of genotypes were estimated as described by Singh and Chaudhary (1977). To start with, the genotypes having the smallest distance from each other were considered first to

which third population having the smallest average D^2 value from the first two genotypes were added. Then comes the nearest fourth genotype and so it goes on. At certain stage, when it was felt that after adding a variety, there was an abrupt increase in the average D^2 value, then that variety was not considered for inclusion in that cluster. Like this the process was continued till all the genotypes were included in one or the other cluster. After the formation of the clusters, the average inter and intra-cluster divergence distances were calculated.

3.5.2.7 Average intra-cluster distance: For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_j/n$

Where, D^2_j = The sum of distances between all possible combinations (n) of the populations included in a cluster.

3.5.2.8 Average inter-cluster distance: Clusters are taken one by one and their distance from other cluster was calculated. The distance between two clusters was the sum of the D^2 values between the members of other clusters divided by the product of number of genotypes in both the clusters under consideration.

3.5.2.9 Cluster diagram: The clusters and their mutual relationships were presented diagrammatically. The square root of average D^2, which was an approximate measure of divergence between groups was used to denote the distance.

3.5.2.10 Contribution of individual characters towards divergence: In all combinations, each character was ranked on the basis of its contribution towards divergence between two entries ($d_i = Y_{it} - Y_{ij}$). Rank 1 was given to the highest mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters. Percentage contribution of each character (X) towards divergence was calculated using the formula.

$$X = \frac{N \times 100}{M}$$

Where,

N = Number of genotype combinations where the character ranked first

M = All possible combinations of number of genotypes

3.5.3 Estimation of genetic parameters

Mean sum of squares and mean sum of products obtained from analysis of variance of various traits studied in the present investigation were utilized for calculation of the following parameters.

i) Variances:

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952)

Genotypic variance $\left(\sigma^2_g\right) = \frac{\text{MSS due to genotypes} - \text{MSS due to error}}{\text{Number of replicaitons}}$

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

σ^2_g = Genotypic variance

σ^2_e = Error variance

ii) Genotypic and phenotypic coefficient of variation:

The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952).

$$\text{GCV (\%)} = \frac{\sigma_g}{\overline{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sigma_p}{\overline{X}} \times 100$$

Where,

σ_g,σ_p and $\overline{X}$ are genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

iii) Heritability (Broad sense) $h^2_{(b)}$:

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [$h^2_{(b)}$] was calculated by the formula given by Lush (1940).

$$\text{Broad sense Heritability} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* (1955), heritability estimates were categorized as

Less than 30% - Low

30 – 60 % - Moderate

More than 60% - High

iv) Genetic advance

Genetic advance refers to the expected gain in the next generation by selecting the superior individuals under certain amount of selection pressure. From

the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.* (1955).

$$GA = k\ \sigma_p\ H$$

where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

H = Heritability (broad sense)

k = Selection differential at 5% selection intensity

v) Genetic advance as percent of mean (GA as per cent mean)

Genetic advance as percent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{GA}{\overline{X}} \times 100$$

Where,

GA = Genetic advance

$\overline{X}$ = Grand mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955).

Less than 10% - Low

10 – 20 % - Moderate

More than 20% - High

3.5.4 Character association

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955).

i) Genotypic correlation coefficient (r_g)

$$r_g(x_i x_j) = \frac{Cov_g(x_i x_j)}{\sqrt{V_g(x_i) \cdot V_g(x_i)}}$$

Where,

$r_g(x_i x_j)$ = Genotypic correlation between 'ith' and 'jth' characters

$V_g(x_i)$ = Genotypic variance of 'ith' character

$V_g(x_j)$ = Genotypic variance of 'jth' character

$Cov_{(g)}(x_i x_j)$ = Genotypic covariance between 'ith' and 'jth' characters.

i) Phenotypic correlation coefficient (r_p)

$$r_p(x_i x_j) = \frac{Cov_p(x_i x_j)}{\sqrt{V_p(x_i) \cdot V_p(x_i)}}$$

Where,

$V_p(x_i)$ = Phenotypic variance of 'ith' character

$V_p(x_j)$ = Phenotypic variance of 'jth' character

$Cov(x_i x_j)$ = Phenotypic covariance between 'ith' and 'jth' characters.

The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degrees of freedom at 5 per cent and 1 per cent levels where, 'n' denotes the number of treatments used in the calculations.

3.5.5 Path coefficient analysis

Path coefficient analysis was carried out by the procedure originally proposed by Wright (1921) which was subsequently elaborated by Dewey and Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

The following set of simultaneous equations were formulated and solved for estimating various direct and indirect effects.

$$r_{1y} = p_{1y} + r_{12}p_{2y} + r_{13}p_{3y} + \ldots\ldots\ldots\ldots + r_{1i}p_{iy}$$

$$r_{2y} = r_{21}p_{1y} + p_{2y} + r_{23}p_{3y} + \ldots\ldots\ldots\ldots + r_{2i}p_{iy}$$

. . . . .

. . . . .

$$r_{iy} = r_{i1}p_{1y} + r_{i2}p_{2y} + r_{i3}p_{3y} + \ldots\ldots\ldots\ldots\ldots + p_{iy}$$

where,

r_{12} to r_{i-1} = Coefficient of correlation among causal factors.

p_{1y} to p_{iy} = Direct effects of characters '1' to i on character 'y'.

The above equations were written in matrix forms as under:

A C B

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ . \\ . \\ . \\ r_{iy} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} \ldots\ldots\ldots\ldots & r_{1i} \\ r_{21} & 1 & r_{23} \ldots\ldots\ldots\ldots & r_{2i} \\ r_{31} & r_{32} & 1 \ldots\ldots\ldots\ldots & r_{3i} \\ . & . & . & . \\ . & . & . & . \\ . & . & . & . \\ r_{i1} & r_{i2} & r_{i3} \ldots\ldots\ldots\ldots & 1 \end{pmatrix} \begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ . \\ . \\ . \\ p_{iy} \end{pmatrix}$$

Then $B = [C]^{-1}A$

where,

$$[C]^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ldots\ldots\ldots\ldots & C_{1i} \\ C_{21} & C_{22} & C_{23} \ldots\ldots\ldots\ldots & C_{2i} \\ . & . & . & . \\ . & . & . & . \\ C_{i1} & C_{i2} & C_{i3} \ldots\ldots\ldots\ldots & C_{ii} \end{pmatrix}$$

Then, direct effects were calculated as follows:

$$P_{1y} = \sum_{i=1}^{I} C_{1i}\, r_{1y}$$

$$P_{2y} = \sum_{i=1}^{I} C_{2i}\, r_{2y}$$

$$P_{iy} = \sum_{i=1}^{I} C_{ii} r_{iy}$$

Besides the direct and indirect effects, the residual effect which measures the contribution of the characters not considered in the causal scheme was obtained as:

$$\text{Residual effect } (P_{RY}) = \sqrt{1-[P_{1y}r_{1y} + p_{2y}r_{2y} + \ldots\ldots\ldots\ldots + p_{iy}r_{iy}]^2}$$

where,

P_{RY} = Residual effect

P_{iy} = Direct effect of 'x_i' on 'y'

r_{iy} = Correlation coefficient of 'x_i' with 'y'.

The scales for path coefficients as proposed by Lenka and Mishra (1973) are as follows:

Value for Direct or Indirect effect	Rate or Scale
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
More than 1.00	Very high

Chapter IV

RESULTS AND DISCUSSION

Groundnut is an important oilseed crop of India. Although India is a world leader in groundnut area, its productivity has remained low, mainly due to many abiotic and biotic stresses. Among many diseases Peanut stem necrosis disease (PSND) is one of the major disease causing severe economic losses. Hybridization and selection of disease tolerant genotypes offers the best long term solution to minimize the risk. For any crop improvement programme, it is essential to know the extent of diversity among the released, pre-release cultures and germplasm lines for yield, yield components and other important quality attributes. Further, kernel yield in groundnut is constituted by different yield components, including several physiological traits, which makes direct selection for kernel yield ineffective, owing to its complex nature of inheritance. The knowledge of genetic parameters like genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability, genetic advance, genetic divergence as well as correlation and path co-efficient analysis are essential for making effective selections from the breeding material either for direct advancement or to formulate efficient crossing programme.

Fifty genotypes were evaluated for variability, genetic parameters, genetic divergence, character associations and path coefficient analysis for fifteen quantitative and qualitative characters in groundnut. The data collected on these characters were used for biometrical studies.

The experimental results obtained from the present investigation were presented and discussed under the following heads.

4.1 Analysis of Variance

4.2 Mean Performance

4.3 Genetic Parameters

4.4 Genetic Divergence

4.5 Character Association

4.6 Path Co-efficient Analysis

4.1 ANALYSIS OF VARIANCE

The analysis of variance (ANOVA) for yield, yield components and quality characters for the 50 groundnut genotypes studied was presented in Table 4.1. The results revealed highly significant differences among the genotypes for all characters studied, indicating the existence of sufficient variation among the genotypes studied. However, the replications were observed to be non- significant for all characters studied. Thus, the analysis of variance revealed ample scope for improvement of these genotypes with regard to the characters studied.

4.2 MEAN PERFORMANCE

The mean performance of these fifty genotypes for fifteen characters was briefly presented in the table 4.2. The general mean, coefficient of variation and critical difference values provides information whether the data collected for the characters included in the study was carried out in a correct procedure and it also permits for further statistical analysis *viz.*, D^2 analysis, correlation and path coefficient analysis for obtaining valid inferences for the objectives with respect to the stated problem. Montogomery and Douglas, 1997.

4.2.1 Days to 50 per cent Flowering (DFF) :

The days to 50 per cent flowering among the genotypes ranged from 28.50 (04 x 477-024- 1) to 37.50 (K 1800) while the general mean was 32.20 days. Six genotypes *viz.*, 03 x 427-094, 03 x 482-036, 04 x 477-021-1, 04 x 477-021-2, 04 x 477-024- 1 and K 1535 were significantly early in flowering than the mean.

Table 4.1. Analysis of variance for fifteen yield, yield components and quanlitative traits in fifty genotypes of groundnut

S. No.	Characters	Mean squares		
		Replications (df:1)	Genotypes (df:49)	Error (df:49)
1.	Days to 50% flowering	4.84	9.61**	1.59
2.	Plant height (cm)	2.43	21.65**	1.58
3.	No of filled (mature) pods per plant	0.32	13.27**	1.75
4.	Total pods per plant	1.21	16.22**	2.14
5.	No of seeds per pod	0.00	0.01	0.00
6.	Sound mature kernels (%)	1.00	28.68**	10.57
7.	Haulm yield per plant (g)	0.00	28.20**	3.59
8.	Pod yield per plant (g)	0.11	21.68**	2.31
9.	Kernel yield per plant (g)	0.06	9.43**	0.95
10.	Shelling percentage (%)	0.45	121.33**	63.65
11.	Harvest index (%)	0.00	0.01	0.00
12.	100 kernel weight (g)	0.13	52.68**	5.42
13.	SPAD Chlorophyll meter reading (SCMR) at 60 DAS	0.02	58.94**	0.77
14.	Oil content (%)	0.17	7.94**	0.86
15.	Protein content (%)	0.16	54.52**	2.30

* Significant at 5% level; ** Significant at 1 % level

Table 4.2. Mean performance of fifty groundnut genotypes for yield, yield components and qualitative traits

S. No.	Genotype	Days to 50% flowering	Plant height (cm)	No. of filled pods per plant	Total pods per plant	No. of seeds per pod	Sound mature kernels (%)	Haulm yield per plant (g)	Pod yield per plant (g)
1.	03 x 397- 031	32.00	22.20	12.80	14.30	1.58	83.00	15.69	11.21
2.	03 x 398- 067	33.50	21.70	11.95	12.80	1.56	86.50	13.40	8.93
3.	03 x 427- 082	33.50	21.40	12.30	13.10	1.58	81.00	13.80	9.54
4.	03 x 427- 086	31.00	25.30	18.50	21.70	1.62	81.50	17.77	13.67
5.	03 x 427- 088	30.50	18.50	11.10	12.10	1.58	78.00	11.22	7.48
6.	03 x 427- 091	31.00	19.30	13.15	15.20	1.52	83.00	12.06	8.04
7.	03 x 427- 094	29.50	19.20	11.90	13.40	1.62	77.00	12.01	8.31
8.	03 x 427- 107	31.00	23.60	11.90	13.40	1.56	81.00	12.69	8.46
9.	03 x 427- 109	33.00	18.30	13.30	16.20	1.64	73.00	13.57	9.38
10.	03 x 461- 019	30.00	19.70	16.30	17.90	1.52	76.00	15.35	10.56
11.	03 x 482- 036	29.50	18.70	13.90	16.10	1.56	84.00	14.82	10.59
12.	03 x 485- 001	31.50	22.10	14.00	17.40	1.64	75.00	15.55	10.76
13.	03 x 485- 024-01	34.00	22.30	15.10	20.30	1.72	77.00	15.08	10.44
14.	04 x 477- 010	33.00	21.65	10.80	11.50	1.58	80.00	14.15	9.80
15.	04 x 477- 018	30.00	19.90	11.00	13.40	1.68	82.00	17.24	13.26
16.	04 x 477- 021-1	29.50	13.90	11.30	13.40	1.54	79.00	15.69	11.58
17.	04 x 477- 021-2	29.50	20.00	12.60	15.40	1.58	82.00	14.93	10.66
18.	04 x 477- 024-1	28.50	27.20	14.70	16.80	1.66	85.00	22.44	17.26
19.	04 x 477- 030	30.00	22.40	10.80	11.50	1.44	78.00	14.01	9.70
20.	04 x 477- 031	30.50	21.40	19.00	20.50	1.64	83.00	18.05	13.89
21.	04 X 479- 002	36.00	16.90	13.90	16.00	1.66	84.00	18.49	14.22
22.	04 X 479- 005	36.00	21.00	14.40	16.30	1.48	83.00	18.88	14.52
23.	04 X 479- 012	33.50	22.30	20.80	22.40	1.56	78.00	27.04	20.80
24.	04 X 480- 007	31.50	18.10	12.85	14.00	1.56	74.00	16.95	12.20
25.	04 X 481- 005	31.50	20.85	10.40	14.80	1.54	81.00	12.57	8.38
26.	04 X 481- 023	31.00	26.00	10.50	12.70	1.60	75.00	14.60	9.74
27.	K 1643	32.00	19.00	13.70	15.70	1.48	76.00	21.99	16.92
28.	K 1563	32.50	22.20	12.80	14.00	1.60	79.00	19.26	14.31
29.	K 1715	36.00	23.40	14.60	16.70	1.54	81.00	21.00	15.08
30.	K 1577	35.00	22.80	9.20	13.10	1.64	79.00	14.65	9.76
31.	K 1735	33.00	19.40	10.80	13.70	1.56	83.00	13.82	10.24
32.	K 1576	30.00	19.10	10.50	13.30	1.56	83.00	16.88	12.06
33.	K 1725	30.00	25.20	15.70	17.10	1.50	80.00	26.39	20.30
34.	K 1574	30.50	22.60	10.70	13.00	1.62	75.00	18.41	13.15
35.	K 1535	29.50	21.00	10.40	12.30	1.58	75.00	14.84	10.28
36.	K 1621	33.00	21.80	15.50	18.80	1.52	71.00	19.04	13.60
37.	K 1501	33.50	22.85	15.60	19.40	1.68	76.00	23.35	17.97
38.	K 1799	33.50	23.30	17.30	19.20	1.56	79.00	16.20	11.57
39.	K 1800	37.50	19.40	16.00	17.00	1.56	82.00	14.60	10.11
40.	K 1809	36.00	20.20	14.40	15.70	1.62	77.00	15.47	11.14
41.	K 1717	35.50	23.20	17.40	20.90	1.60	79.00	22.03	16.94
42.	K 1641	35.00	23.35	12.30	15.40	1.50	74.00	25.34	19.49

S. No.	Genotype	Days to 50% flowering	Plant height (cm)	No. of filled pods per plant	Total pods per plant	No. of seeds per pod	Sound mature kernels (%)	Haulm yield per plant (g)	Pod yield per plant (g)
43.	K 1650	30.00	20.40	11.90	13.60	1.64	82.00	17.83	13.72
44.	K 1647	30.00	17.90	15.20	19.70	1.56	85.00	17.89	13.28
45.	K 1811	33.50	21.40	16.10	18.00	1.58	73.00	15.34	10.61
46..	Kadiri 6	33.00	31.30	10.30	11.80	1.56	85.00	14.24	9.49
47.	Kadiri 9	31.00	30.30	16.50	18.60	1.70	79.00	15.06	10.75
48.	Harithandhra	33.50	30.40	15.60	17.50	1.52	85.00	15.35	10.96
49.	Anantha	32.00	22.30	13.00	13.70	1.56	77.00	11.95	7.97
50.	JL-24	34.00	22.50	14.70	16.70	1.58	76.00	13.73	9.15
	General Mean	**32.20**	**21.78**	**13.59**	**15.75**	**1.58**	**79.42**	**16.65**	**12.04**
	C.V%	3.92	5.78	9.76	9.30	2.93	4.09	11.38	12.63
	Range	28.50 to 37.50	13.90 to 31.30	9.20 to 20.80	11.50 to 22.40	1.44 to 1.72	71.00 to 86.50	11.22 to 27.04	7.48 to 20.80
	CD at 5%	2.54	2.53	2.66	2.94	0.09	6.53	3.81	3.06
	SE(m)	0.89	0.89	0.94	1.04	0.03	2.30	1.34	1.08

Table 4.2. Mean performance of fifty groundnut genotypes for yield, yield components and qualitative traits

S. No.	Genotype	Kernel yield per plant (g)	Shelling Percentage (%)	Harvest index (%)	100 kernel weight (g)	SCMR at 60 DAS	Oil content (%)	Protein content (%)
1.	03 x 397- 031	8.60	76.60	57.33	42.32	30.65	48.15	35.50
2.	03 x 398- 067	7.07	79.13	55.87	39.61	34.45	50.90	21.00
3.	03 x 427- 082	6.49	68.24	48.02	37.46	28.85	51.92	25.50
4.	03 x 427- 086	8.24	60.19	65.51	36.56	30.25	48.09	20.50
5.	03 x 427- 088	5.63	75.12	49.59	36.65	35.45	49.00	28.50
6.	03 x 427- 091	6.04	75.07	53.34	34.31	36.20	52.26	33.50
7.	03 x 427- 094	5.20	63.61	44.51	30.91	30.05	52.20	30.00
8.	03 x 427- 107	5.57	66.47	46.26	35.73	34.15	47.97	29.00
9.	03 x 427- 109	6.39	67.70	58.70	41.82	39.40	48.57	25.50
10.	03 x 461- 019	7.65	73.23	55.76	30.66	41.35	52.04	32.00
11.	03 x 482- 036	7.18	67.82	46.31	42.93	43.20	47.97	29.00
12.	03 x 485- 001	7.61	70.44	41.24	45.46	44.00	47.21	21.00
13.	03 x 485- 024-01	6.65	65.07	41.37	45.83	41.25	50.87	35.50
14.	04 x 477- 010	5.03	51.74	49.08	38.38	46.25	42.52	24.50
15.	04 x 477- 018	5.82	44.06	55.26	47.60	49.80	47.54	24.00
16.	04 x 477- 021-1	6.35	54.36	48.59	36.44	48.65	49.58	30.50
17.	04 x 477- 021-2	6.20	58.78	50.05	47.15	43.15	51.76	25.50
18.	04 x 477- 024- 1	9.61	55.68	51.65	39.57	45.85	51.95	24.00
19.	04 x 477- 030	7.01	72.29	45.86	39.68	47.90	52.99	23.50
20.	04 x 477- 031	10.73	77.33	49.09	37.92	40.95	52.71	26.00
21.	04 X 479- 002	9.72	68.28	65.58	41.49	38.95	51.36	31.00
22.	04 X 479- 005	8.40	57.57	58.49	47.30	37.85	50.15	38.00
23.	04 X 479- 012	14.25	68.74	62.88	40.42	45.95	48.03	30.00
24.	04 X 480- 007	8.77	73.04	54.85	47.74	42.15	51.75	21.50
25.	04 X 481- 005	5.13	60.99	39.65	29.69	43.40	51.49	12.50
26.	04 X 481- 023	5.74	59.03	31.48	33.42	44.15	51.91	35.00
27.	K 1643	10.03	59.59	58.37	40.00	46.10	52.80	27.00
28.	K 1563	9.62	67.77	59.61	41.77	47.05	51.41	24.50
29.	K 1715	10.61	70.88	52.23	43.15	43.90	50.33	32.50
30.	K 1577	6.84	70.14	47.89	39.96	44.60	48.57	26.50
31.	K 1735	7.26	70.93	39.02	42.54	42.35	51.80	31.00
32.	K 1576	6.55	54.00	43.96	35.58	41.75	50.07	26.00
33.	K 1725	13.97	69.21	60.53	44.09	44.40	50.54	33.50
34.	K 1574	8.84	67.28	53.48	43.33	44.20	49.80	24.50
35.	K 1535	5.72	55.89	54.42	36.34	42.75	48.59	31.00
36.	K 1621	9.64	72.24	62.87	41.22	42.20	49.67	23.00
37.	K 1501	9.90	55.85	52.95	41.31	42.05	52.10	24.50
38.	K 1799	7.07	60.89	45.01	33.89	40.65	49.00	32.00
39.	K 1800	6.84	68.29	52.33	29.40	37.55	50.97	39.50
40.	K 1809	6.22	56.86	54.39	36.45	39.00	48.54	33.50
41.	K 1717	11.66	68.72	60.60	43.83	38.85	52.83	21.00
42.	K 1641	11.44	58.74	70.01	44.85	37.05	50.43	26.50
43.	K 1650	8.58	62.49	65.17	44.35	39.95	47.93	31.00

S. No.	Genotype	Kernel yield per plant (g)	Shelling Percentage (%)	Harvest index (%)	100 kernel weight (g)	SCMR at 60 DAS	Oil content (%)	Protein content (%)
44.	K 1647	10.09	75.47	66.84	41.38	42.35	51.05	22.00
45.	K 1811	7.14	67.28	53.06	28.32	38.15	52.29	29.00
46.	Kadiri 6	6.39	67.10	61.28	36.49	29.90	49.29	30.00
47.	Kadiri 9	8.42	79.23	56.20	35.93	38.15	51.54	25.50
48.	Harithandhra	7.40	68.24	57.13	36.58	32.80	48.61	21.50
49.	Anantha	5.32	66.83	66.68	29.11	31.15	51.18	23.50
50.	JL-24	6.80	74.65	60.75	37.31	31.70	50.38	26.50
	General Mean	**7.87**	**65.98**	**54.00**	**39.08**	**40.06**	**50.21**	**27.56**
	C.V%	12.41	12.09	7.43	5.96	2.20	1.85	5.51
	Range	5.03 to 14.25	44.06 to 79.23	31.48 to 70.01	28.32 to 47.74	28.85 to 49.80	42.52 to 52.99	12.50 to 39.50
	CD at 5%	1.96	16.03	0.08	4.68	1.77	1.87	3.05
	SE(m)	0.69	5.64	0.03	1.65	0.62	0.66	1.07

4.2.2 Plant height (PH) :

The plant height among the genotypes varied from 13.90 cm (04 x 477-021-1) to 31.30 cm (Kadiri 6) with a general mean of 21.78 cm. Nine genotypes *viz*., 03 x 427-088, 03 x 427-094, 03 x 482-036, 04 x 477-021-1, 04 x 479-002, 04 x 480-007, K 1643, K 1576 and K 1647 were significantly shorter than the mean plant height of the genotypes.

4.2.3 Number of filled pods per plant (FP) :

The number of filled pods per plant among the genotypes ranged from 9.20 (K 1577) to 20.80 (04 x 479-012) with a general mean of 13.59. Six entries *viz*., 03 x 427-086, 03 x 461-019, 04 x 477-031, 04 x 479-012, K 1799 and K 1717 recorded significantly superior to the general mean.

4.2.4 Total pods per plant (TP) :

The total pods per plant among the genotypes ranged from 11.50 (04 x 477-030, 04 x 477- 010) to 22.40 (04 x 479-012) with a general mean of 15.75. Nine genotypes *viz*., 03 x 427-086, 03 x 485-024-01, 04 x 477-031, 04 x 479-012, K 1621, K 1501, K 1799, K 1717 and K 1647 recorded significantly excelled general mean.

4.2.5 Number of seeds per pod (S/P) :

The number of seeds per pod among the genotypes ranged from 1.44 (04 x 477-030) to 1.72 (03 x 485-024-01) with a general mean of 1.58. Four genotypes *viz*., 03 x 485-024-01, 04 x 477-018, K 1501 and Kadiri 9 exhibited significantly superior number of seeds per pod than the general mean.

4.2.6 Sound mature kernels per cent (SMK%) :

The sound mature kernel per cent among the genotypes varied from 71.00 (K 1621) to 86.50 (03 x 398-067) with a general mean of 79.42. The entry 03 x

398-067 exhibited significantly more sound mature kernel per cent compared to the general mean.

4.2.7 Haulm yield per plant (g) (HY) :

Mean value of haulm yield among the genotypes ranged between 11.22 g (03 x 427-088) and 27.04 g (04 x 479-012) with a general mean of 16.65 g. Among 50 entries eight entries *viz.*, 04 x 477-024-1, 04 x 479-012, K 1643, K 1715, K 1725, K 1501, K 1717 and K 1641 expressed significantly higher haulm yield per plant than the general mean.

4.2.8 Pod yield per plant (g) (PY) :

The mean value of pod yield per plant among the genotypes ranged from 7.48 g (03 x 427-088) to 20.80 g (04 x 479-012) with a general mean of 12.04 g. Eight genotypes *viz.,* 03 x 427-088, 04 x 477-024- 1, 04 x 479-012, K 1643, K 1725, K 1501, K 1717 and K 1641 significantly exceeded the general mean.

4.2.9 Kernel yield per plant (g) (KY) :

The mean value of kernel yield per plant ranged from 5.03 g (04 x 477-010) to 14.25 g (04 x 479-012) with a general mean of 7.87 g. Eight genotypes *viz.,* 04 x 477-031, 04 x 479-012, K 1643, K 1715, K 1725, K 1501, K 1641 and K 1647 showed significantly superior kernel yield per plant than general mean.

4.2.10 Shelling percentage (%) (S %) :

The mean shelling percentage among the genotypes ranged from 44.06% (04 x 477-018) to 79.23% (Kadiri 9) with a general mean of 65.98%. None of the genotypes were found to be significantly superior than the general mean.

4.2.11 Harvest index (%) (HI %) :

The mean values of harvest index among the genotypes ranged between 31.48% (04 x 481-023) and 70.01% (K 1641) with a general mean of 54.00%. Eight genotypes *viz.*, 03 x 427-086, 04 x 479-002, 04 x 479-012, K 1621, K 1641,

K 1650, K 1647 and Anantha showed significantly higher harvest index than general mean.

4.2.12 100 kernel weight (g) (100 KW) :

The 100 kernel weight among the genotypes ranged from 28.32 (K 1811) to 47.74 (04 x 480-007) with a general mean of 39.08. Eight genotypes *viz.*, 03 x 485-001, 03 x 485-024-01, 04 x 477-018, 04 x 477-021-2, 04 x 479-005, 04 x 480-007, K 1641 and K 1650 significantly exceeded the general mean.

4.2.13 SPAD Chlorophyll Meter Reading (SCMR) at 60 days after sowing :

The mean values of SPAD Chlorophyll Meter Reading (SCMR) at 60 days after sowing ranged from 28.85 (03 x 427-082) to 49.80 (04 x 477-018) with a general mean of 40.06. Twenty three genotypes significantly exceeded the general mean.

4.2.14 Oil content (%) (OC) :

The oil content among the genotypes ranged between 42.52 % (04 x 477-010) and 52.99 % (04 x 477-030) with a general mean of 50.21 %. Four genotypes *viz.*, 04 x 477-030, 04 x 477-031, K 1643 and K 1717 recorded significantly higher oil content percentage than the general mean.

4.2.15 Protein content (%) (PC) :

The mean value of protein content among the genotypes ranged from 12.50 % (03 x 481-005) to 39.50 % (K 1800) with a general mean of 27.56 %. Eleven genotypes significantly surpassed the mean value.

The first and the basic tool used by various scientists for selection of parents and hybrids is the per se performance. For rapid success in any hybridization programme, the choice of the parents which can produce superior off springs is very much essential. Parental per se performance has been suggested as an useful index for selection of parents for hybridization. The parents with high mean values

are preferred for hybridization programme as they are expected to produce desirable segregants. (Dwivedi *et al*. 1999).

As over all study of *per se* performance of fifty genotypes indicated that the entry 04 x 479-012 recorded significantly superior mean performance for six characters *viz.*, number of filled pods per plant, total pods per plant, pod yield per plant, kernel yield per plant, harvest index and SCMR at 60 DAS.

The entry K 1501 recorded significantly excelled mean performance for six characters *viz.,* total pods per plant, number of seeds per pod, haulm yield per plant, pod yield per plant , kernel yield per plant and SCMR at 60 DAS. While, the entry K 1643 showed significantly higher mean performance for five characters *viz.*, Plant height, haulm yield per plant, kernel yield per plant , oil content and SCMR at 60 days after sowing.

The entry K 1641 was significantly superior for five characters *viz.*, haulm yield per plant, pod yield per plant, kernel yield per plant, harvest index and 100 kernel weight. Similarly, K 1717 recorded significantly superior performance for five characters *viz.*, number of filled pods per plant, total pods per plant, haulm yield per plant, pod yield per plant and oil content.

Similarly, the entry K 1647 showed significantly superior performance for four characters *viz.,* plant height, total pods per plant, kernel yield per plant and harvest index. Similarly, entry 04 x 477-031 excelled for four characters *viz.*, number of filled pods per plant, total pods per plant, kernel yield per plant and oil content. The entry K 1717 recorded significantly high mean performance for four characters *viz.,* haulm yield per plant, pod yield per plant, kernel yield per plant and SCMR at 60 days after sowing.

The entry, 04 x 477-024-1 was early to flower with lowest plant height compared to other genotypes studied in the present investigation which is very desirable to identify very early segregants with lowest plant plant height by involving this entry in the crossing programme.

Hence the genotypes *viz.*, 04 x 479-012, K 1501, K 1643 and K 1641 were found to be superior among the tested entries in the study with significantly superior performance for many yield attributing characters. These genotypes may be involved in the crossing programme by duly estimating the general and specific combining abilities in the future breeding programme.

4.3 GENETIC PARAMETERS

The estimates of range, variance, phenotypic and genotypic co-efficients of variation (PCV, GCV), heritability in broad sense, genetic advance and genetic advance as per cent of mean for fifteen characters of fifty genotypes of groundnut are furnished in Table 4.3 and Fig. 4.1.

4.3.1 Range

The highest estimate of range was registered for sound mature kernel per cent (86.50) followed by shelling percentage (79.23), harvest index (70%), oil content (52.99 %), SCMR at 60 DAS (49.80), 100 kernel weight (47.74 g), protein content (39.50 %), days to 50 per cent flowering (37.50), plant height (31.30 cm), haulm yield per plant (27.04 g), total pods per plant (22.40), pod yield per plant (20.80 g), number of filled pods per plant (20.80), kernel yield per plant (14.25 g) and number of seeds per pod (1.72) in decreasing order of their magnitude.

4.3.2 Variance

The highest estimate of variance was registered for shelling per cent (V_P = 92.49; V_g = 28.84) followed by SCMR at 60 days after sowing (V_P = 29.86; V_g = 29.08), 100 kernel weight (V_P = 29.06; V_g = 23.62), protein content (V_P = 28.41; V_g = 26.11), sound mature kernel per cent (V_P = 19.63; V_g = 9.06), haulm yield per plant (V_P = 15.90; V_g = 12.31), pod yield per plant (V_P = 12.00; V_g = 9.68) , plant height (V_P = 11.61; V_g = 10.03), total pods per plant (V_P = 9.19; V_g = 7.04), number of filled pods per plant (V_P = 7.52; V_g = 5.76), days to 50 per cent flowering (V_P = 5.60; V_g = 4.01), kernel yield per plant (V_P = 5.19; V_g = 4.24),

oil content (V_P = 4.41; V_g = 3.54), harvest index (V_P = 0.01; V_g = 0.01) and number of seeds per pod (V_P = 0.001; V_g = 0.00) in decreasing order of their magnitude.

Table 4.3. Mean, coefficients of variation, heritability (broad sense) and genetic advance as per cent of mean for fifteen characters in fifty groundnut genotypes

Sl. No.	Character	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic Advance as per cent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50% flowering	32.20	28.50	37.50	4.01	5.60	6.22	7.35	72	4.47	13.88
2.	Plant height (cm)	21.78	13.90	31.30	10.03	11.62	14.54	15.65	86	7.77	35.67
3.	No of filled pods per plant	13.59	9.20	20.80	5.76	7.52	17.66	20.17	77	5.54	40.80
4.	Total pods per plant	15.75	11.50	22.40	7.04	9.19	16.84	19.24	77	6.13	38.92
5.	No of seeds per pod	1.58	1.44	1.72	0.00	0.01	3.08	4.25	53	0.09	5.90
6.	Sound mature kernels (%)	79.42	71.00	86.50	9.06	19.63	3.79	5.58	46	5.40	6.79
7.	Haulm yield per plant (g)	16.65	11.22	27.04	12.31	15.90	21.07	23.94	77	8.15	48.94
8.	Pod yield per plant (g)	12.05	7.48	20.80	9.68	12.00	25.84	28.76	81	7.38	61.27
9.	Kernel yield per plant (g)	7.87	5.04	14.25	4.24	5.19	26.17	28.97	82	4.91	62.43
10.	Shelling percentage (%)	65.98	44.06	79.23	28.84	92.49	8.14	14.58	31	7.91	12.00
11.	Harvest index (%)	0.54	0.31	0.70	0.01	0.01	14.54	16.33	79	0.18	34.19
12.	100 kernel weight (g)	38.08	28.32	47.74	23.62	29.06	12.44	13.79	81	11.57	29.61
13.	SPAD Chlorophyll meter reading (SCMR) at 60 Days after sowing	40.06	28.85	49.80	29.08	29.86	13.46	13.64	97	14.05	35.07
14.	Oil content (%)	50.21	42.52	52.99	3.54	4.41	3.75	4.18	80	4.45	8.87
15.	Protein content (%)	27.56	12.50	39.50	26.11	28.41	18.54	19.34	92	12.93	46.92

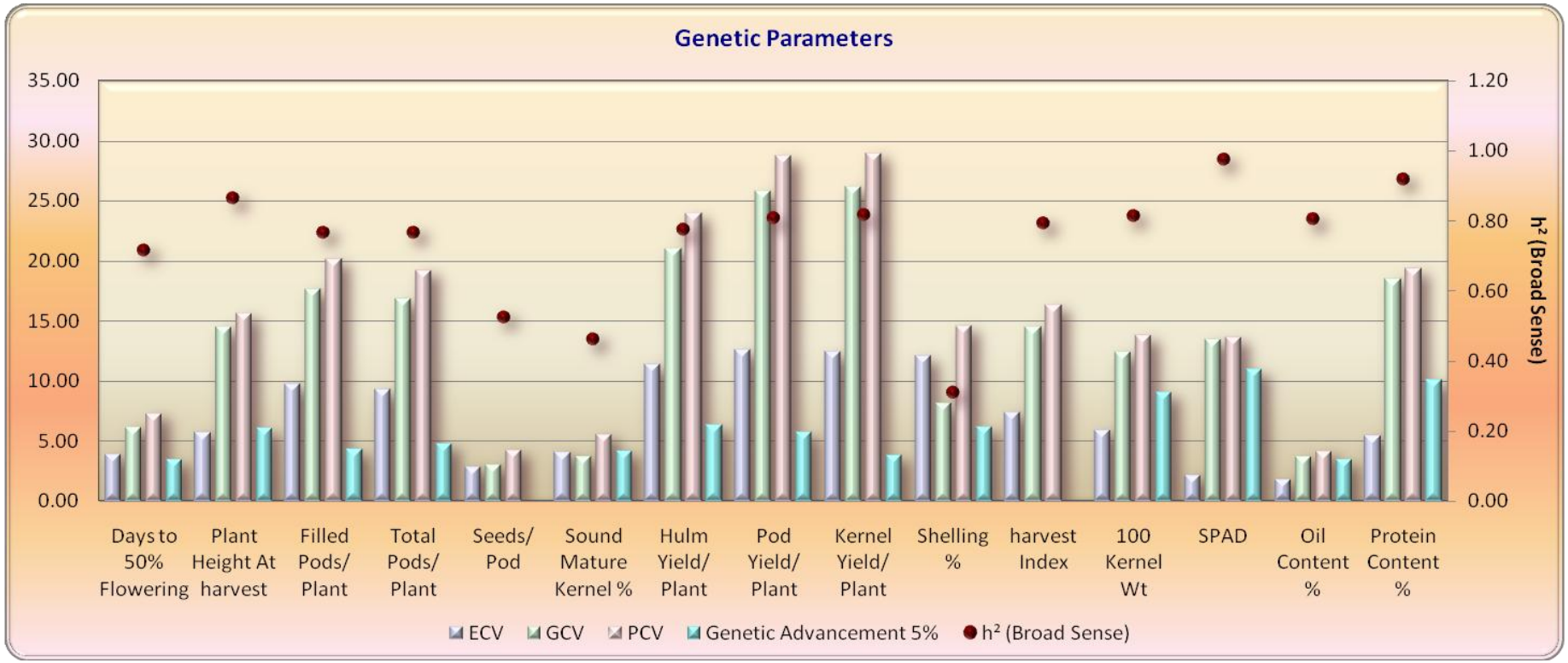

Fig.4.1 Variability, heritability and genetic advance as per cent mean for the traits studied

4.3.3 Variation

In the present study, the estimates of PCV for all the characters were slightly higher than the estimates of GCV, which may be due to the interaction of genotypes with the environment. The results obtained on variability and genetic parameters are presented here under (Table 4.3).

The highest estimate of co-efficient of variation was registered for kernel yield per plant (GCV = 26.17; PCV = 28.97), followed by pod yield per plant (GCV = 25.84; PCV = 28.76), haulm yield per plant (GCV = 21.07; PCV = 23.94), protein content (GCV = 18.54; PCV = 19.34) and number of filled pods per plant (GCV = 17.66; PCV = 20.17) in decreasing order of their magnitude.

On contrary, moderate co-efficient of variation was recorded for total pods per plant (GCV = 16.84; PCV = 19.24), harvest index (GCV = 14.54; PCV = 16.33), plant height (GCV = 14.54; PCV = 15.65), SPAD (GCV = 13.46; PCV = 13.64) and 100 kernel weight (GCV = 12.44; PCV = 13.79). However, low estimates of co-efficient of variation was observed for the remaining characters *viz.,* shelling per cent (GCV = 8.14; PCV = 14.58), days to 50% flowering (GCV = 6.22; PCV = 7.35), sound mature kernel per cent (GCV = 3.79; PCV = 5.58), oil content (GCV = 3.75; PCV = 4.18) and number of seeds per pod (GCV = 3.08; PCV = 4.25).

4.3.4 Heritability

Estimates of high heritability (broad sense) were observed for all the characters under the study *viz.,* SCMR at 60 DAS (97%), protein content (92%), plant height (86%), kernel yield per plant (82%), pod yield per plant (81%) and 100 kernel weight (81%), oil content (80%), harvest index (79%), haulm yield per plant (77%), total pods per plant (77%) and number of filled pods per plant (77%), days to 50% flowering (72%), number of seeds per pod (53%), sound mature kernel per cent (46%) and shelling per cent (31%).

4.3.5 Genetic Advance

The estimate of genetic advance was highest for SCMR at 60 days after sowing (14.05) while it was moderate for protein content (12.93), 100 kernel weight (11.15)

which is an indicative of additive genes in their genetic control. The remaining traits *viz.*, haulm yield per plant (8.15), shelling per cent (7.91), plant height (7.77), pod yield per plant (7.38), total pods per plant (6.13), number of filled pods per plant (5.54), sound mature kernel per cent (5.40), kernel yield per plant (4.91), days to 50 per cent flowering (4.47), oil content (4.45), harvest index (0.18) and number of seeds per pod (0.09) registered low genetic advance in their decreasing order of their magnitude and indicated that most of the traits were controlled by polygenes of non-additive nature.

4.3.6 Genetic advance as per cent of mean

Genetic advance as per cent of mean was recorded as highest for kernel yield per plant (62.43 %) followed by pod yield per plant (61.27 %), haulm yield per plant (48.94 %), protein content (46.92 %), number of filled pods per plant (40.80 %), total pods per plant (38.92 %), plant height (35.67 %), SCMR at 60 DAS (35.07 %), harvest index (34.19 %) and 100 kernel weight (29.61 %), while it was moderate for days to 50 per cent flowering (13.88 %), shelling per cent (12.00 %). The lowest genetic advance as per cent of mean was recorded for oil content (8.87 %), sound mature kernel per cent (6.79 %) and number of seeds per pod (5.90 %).

The amount of variability present for important economic characters and its efficient management in a population determines the success of any breeding programme. The co-efficient of variation is an efficient measure for estimation of range of variability present for different characters in the population. However, the extent of heritable variation cannot be assessed with genetic co-efficient of variation alone. The heritable estimates along with genotypic co-efficient of variation (GCV) would provide a better understanding of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). The genetic gain in conjunction with heritability estimates should form criterion for selection based on phenotypic performance (Johnson *et al.* 1955).

In the present study, the estimates of phenotypic co-efficients of variation for all characters were higher than the estimates of genotypic co-efficients of variation, which may be due to the interaction of genotypes with environment (Table 4.3). The results obtained are discussed here under.

High GCV and PCV estimates were observed for kernel yield per plant, pod yield per plant and haulm yield per plant, protein content, number of filled pods per plant in the decreasing order of their magnitude. Similar kind of high variability for kernel yield per plant was reported by John *et al.* (2008), Nandini *et al.* (2011), Shukla and Rai (2014) and Ramana *et al.* (2015). The high estimates of variability obtained for pod yield per plant were similar to the reports of Mahalakshmi *et al.* (2005), John *et al.* (2008), Nandini *et al.* (2011) and Ramana *et al.* (2015). These findings are in conformity with the findings of Injeti *et al.* (2008) for number of filled pods per plant.

On contrary, moderate estimates of GCV and PCV were recorded for total pods per plant, plant height, harvest index, SCMR at 60 DAS and 100 kernel weight. Similar kind of moderate estimates for total of pods per plant were reported by Prasad *et al.* (2002). These findings are in are in accordance to the earlier reports of Thakur *et al.* (2013) for SCMR at 60 days after sowing.

Low estimates of variability were observed for shelling percentage, days to 50 per cent flowering, sound mature kernel percentage, oil content and number of seeds per pod indicating limited scope for further genetic improvement through selection. The low estimates of variability obtained for days to 50 per cent flowering are in agreement with the findings of Suneetha *et al.* (2004), John *et al.* (2009), Shinde *et al.* (2010) and Nandini *et al.* (2011).

High estimates of heritability were recorded for SCMR, protein content, plant height, kernel yield per plant, pod yield per plant, 100 kernel weight, oil content percentage, harvest index, haulm yield per plant, total pods per plant, number of filled pods per plant and days to 50 per cent flowering. These findings are in agreement with the earlier reports of Hiremath *et al.* (2011) for plant height, 100 kernel weight, pod yield and kernel yield and Patil *et al.* (2014) for haulm yield.

Low estimates of heritability were recorded for number of seeds per pod, sound mature kernel percentage, shelling percentage. Similar results were reported by Thakur *et al.* (2013) for sound mature kernel per cent.

High estimates of genetic advance as per cent of mean were recorded for kernel yield per plant, pod yield per plant, haulm yield per plant, protein content, number of

filled pods per plant, total pods per plant, plant height, SCMR, harvest index and 100 kernel weight. These results are in broad agreement with the reports of Patil *et al.* (2014) for total pods per plant, 100 kernel weight, pod yield per plant, haulm yield per plant and kernel yield per plant.

Moderate estimates of genetic advance as percent of mean were noticed for days to 50 per cent flowering, shelling per cent. While low estimates were recorded for oil content, sound mature kernel per cent and number of seeds per pod. The results are in accordance with reports of Thakur *et al.* (2013).

From the foregoing discussion, it is to conclude that kernel yield per plant, pod yield per plant, haulm yield per plant, protein content, number of filled pods per plant recorded high PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean indicating that these characters are being governed by additive gene action and simple selection could be effective for their further improvement. On the other hand, days to 50 per cent flowering , SCMR at 60 days after sowing and plant height exhibited moderate to low GCV, PCV, high heritability and moderate to low genetic advance. Hence, inter mating of selected genotypes could be suggested to generate variability followed by selection in later generations to identify superior segregants for these characters.

4.4 GENETIC DIVERGENCE

Fifty genotypes of groundnut were assessed for yield, yield components and quality characters adopting Mahalanobis's D^2 statistics.

4.4.1 Test with Wilk's criterion and analysis of variance for dispersion of genotypes

Wilk's 'Λ' (statistic) criterion was used to test the significant differences between the genotypes based on the pooled effects of all the characters. The significance of 'Λ' (statistic) value was tested by χ^2 at 735 degrees of freedom. The 'Λ' statistic value (1653.096) was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously. The analysis of variance for dispersion in fifty genotypes is presented in Table 4.4. The significance of

Table 4.4 Analysis of variance for dispersion in fifty genotypes of groundnut

Source of Variation	Degree of freedom	Mean Sum of Squares
Genotypes	49	1.0543**
Error	48	7.9656**
Total	97	5.3259**

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

Table 4.5. Cluster composition of fifty groundnut genotypes based on Tocher's method

Cluster number	No. of genotypes	Genotypes
I	15	03 x 427-088, 03 x 427-107, 03 x 397-031, 03 x 427-091, JL-24, K 1809, K 1650, 03 x 427-109, 04 x 479-002, K 1811, K 1799, K 1535, 03 x 461-019, 03 x 482-036 and 04 x 479-005
II	22	K 1577, K 1574, 03 x 485-001, 04 x 477-021-2, 04 x 480-007, K 1563, K 1621, K 1647, K 1643, 04 x 477-030, K 1501, K 1576, 04 x 477-031, K 1715, K 1735, 04 x 477-024-1, K 1717, K 1641, K 1725, 04 x 477-021-1, 04 x 479-012 and 04 x 477-018
III	8	03 x 427-082, 03 x 427-094, 03 x 398-067, Anantha, 03 X 427-086, Harithandhra, Kadiri 6 and Kadiri 9
IV	1	K 1800
V	1	04 x 477-010
VI	1	03 X 485-024-01
VII	1	04 x 481-023
VIII	1	04 x 481-005

genotypes clearly indicated the significant pooled effect of all the characters between different genotypes. Hence, further analysis was made to estimate the D^2 values.

4.4.2 Estimation of D^2 values

The mean values of 50 genotypes [(X_1)-(X_2)] were transformed into standardized uncorrelated mean values [(Y_1)-(Y_2)] using pivotal condensation method. The D^2 values were computed for all the possible 1225 pairs of genotypes**.**

4.4.3 Grouping of genotypes into clusters

All the 50 genotypes of groundnut were grouped into eight clusters using Tocher's method (Rao, 1952) and the distribution of genotypes into eight clusters is presented in Table 4.5 and Fig. 4.2. Out of eight clusters, cluster II contained highest number of genotypes (22), followed by cluster I (15), cluster III (8). While clusters IV, V, VI. VII and VIII comprised of only one genotype each. These five genotypes maintained separate identity and they were not included with any other cluster and exhibited high genetic diversity with most of the other clusters. Random genetic drift and selection for specific characters in specified environments cause greater diversity than geographical distance (Murthy and Arunachalam, 1966). Similar results of greater genetic diversity for the genotypes in the mongenotypic clusters were reported by Kumar *et al.* (2012)

4.4.4 Intra and inter-cluster average distance

The average intra and inter-cluster D^2 and D values of eight clusters were furnished in Table 4.6. The maximum intra-cluster D^2 (6101.17) and D (78.11) distances were recorded by cluster III, while the minimum was noticed in the clusters IV, V, VI, VII and VII as they included single genotype each.

The maximum inter-cluster D^2 value was observed between cluster IV and VIII (307.39), while the minimum D^2 value was found between cluster VI and VII (61.07).

Based on inter-cluster distances by Mahalanobis's method of clustering, the clusters IV vs. VIII, VI vs. VIII, III vs. V, III vs. VII and III vs. VI were found to be divergent in the decreasing order of their magnitude. Hence, genotypes of these clusters

Table 4.5. Cluster composition of fifty groundnut genotypes based on Tocher's method

Cluster number	No. of genotypes	Genotypes
I	15	03 x 427-088, 03 x 427-107, 03 x 397-031, 03 x 427-091, JL-24, K 1809, K 1650, 03 x 427-109, 04 x 479-002, K 1811, K 1799, K 1535, 03 x 461-019, 03 x 482-036 and 04 x 479-005
II	22	K 1577, K 1574, 03 x 485-001, 04 x 477-021-2, 04 x 480-007, K 1563, K 1621, K 1647, K 1643, 04 x 477-030, K 1501, K 1576, 04 x 477-031, K 1715, K 1735, 04 x 477-024-1, K 1717, K 1641, K 1725, 04 x 477-021-1, 04 x 479-012 and 04 x 477-018
III	8	03 x 427-082, 03 x 427-094, 03 x 398-067, Anantha, 03 X 427-086, Harithandhra, Kadiri 6 and Kadiri 9
IV	1	K 1800
V	1	04 x 477-010
VI	1	03 X 485-024-01
VII	1	04 x 481-023
VIII	1	04 x 481-005

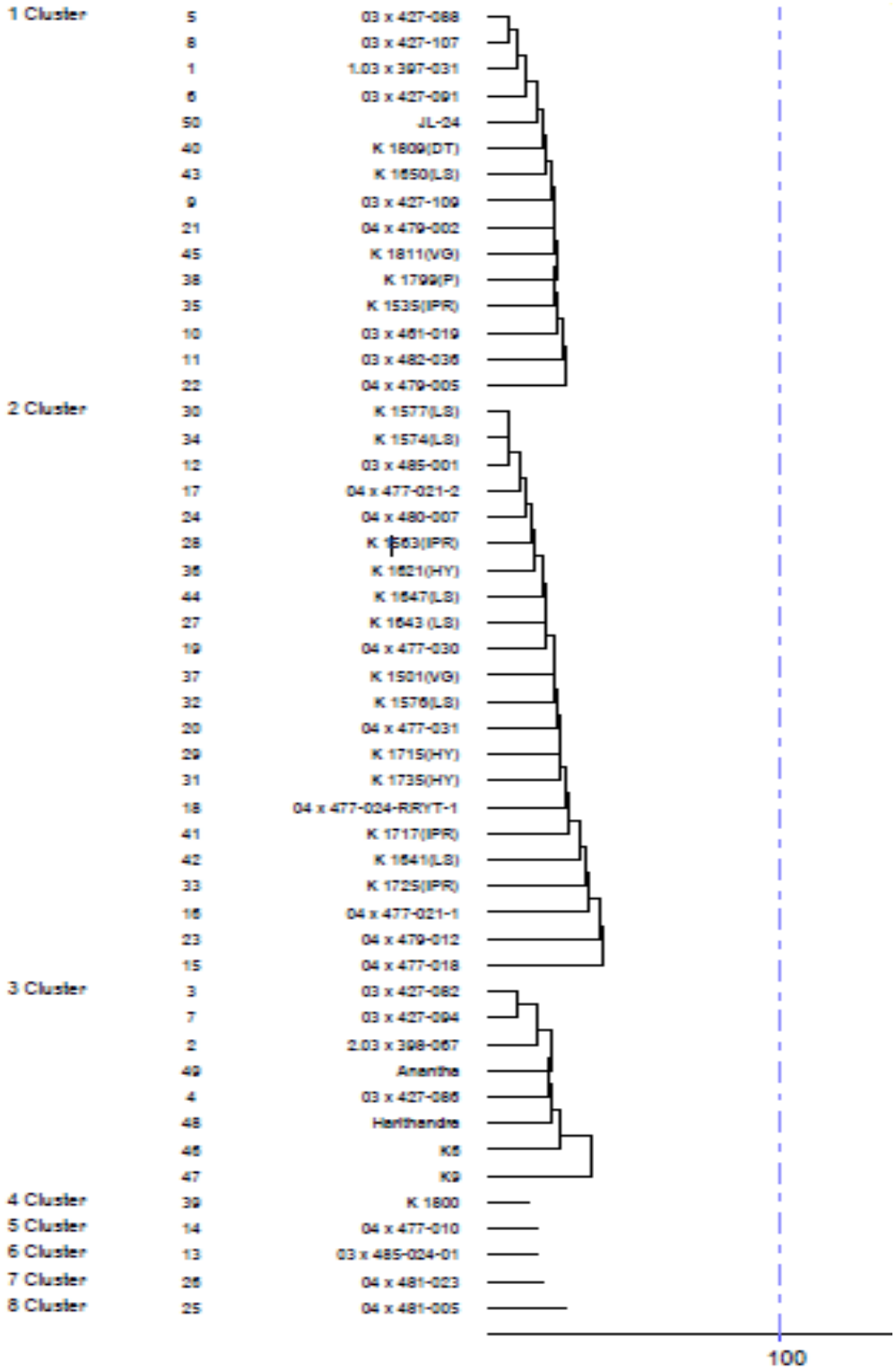

Fig.4.2.Grouping of genotypes into clusters using Tocher's method.

Table 4.6 Average inter and intra cluster distances for the groundnut genotypes studied

Clusters	I	II	III	IV	V	VI	VII	VIII
I	65.28	112.08	122.47	86.33	129.48	86.07	107.70	177.02
II		77.86	206.67	176.81	124.52	115.08	112.83	122.22
III			78.11	184.18	229.41	216.15	225.78	184.53
IV				0.00	214.63	92.12	113.76	307.39
V					0.00	149.35	130.89	151.26
VI						0.00	61.07	247.91
VII							0.00	199.92
VIII								0.00

namely Harithandhra, Kadiri 6, Kadiri 9, Anantha and 03 x 427-082 (Cluster III) and K 1800 (Cluster IV) and 04 x 477-010 (Cluster V) and 03 x 485-024-01 (Cluster VI) and 04 X 481-023 (Cluster VII) and 04 X 481-005 (Cluster VIII) can be utilized as potential parents and crossing among themselves would result in high heterotic expression for yield components and wider segregation among the progenies. The superior recombinants can be obtained by involving such genotypes as parents in hybridization programme.

4.4.5 Cluster means for yield and yield attributes

The cluster means for each of 15 characters are presented in Table 4.7. Considerable differences between clusters means were observed for most of the characters under study. Early flowering was observed in the genotypes of cluster VII (31 days), while delayed flowering was noticed in the genotypes of cluster IV (37.50 days). Maximum plant height was observed in the genotypes of cluster VII (26.00 cm) while minimum was observed in the genotypes of cluster IV (19.40).

The cluster mean for number of filled pods per plant was highest in cluster IV (16.00) and was lowest in cluster VIII (10.40). Total pods per plant ranged from 20.30 in cluster VI to 11.50 in cluster V. The number of seeds per pod was highest in cluster VI (1.72) while it was lowest in cluster VIII (1.54).

More number of sound mature kernels per plant (82.00) was recorded in the genotypes of cluster IV while genotypes of cluster VII (75.00) contained lesser number. The genotype in cluster II recorded the highest haulm yield per plant (19.18 g) while genotype in cluster VIII registered the lowest haulm yield per plant (12.57 g). The genotype in cluster II had high pod yield per plant (14.24 g) while genotype in cluster VIII recorded low pod yield per plant (8.38 g).

The cluster means for kernel yield per plant was highest (9.22 g) in cluster II, while it was lowest (5.03 g) in the cluster V. Similarly, the highest shelling percentage (69.07 %) was recorded by cluster III while genotype in cluster V (51.74 %) registered the lowest.

Table 4.7. Cluster means with respect to yield, yield components and qualitative traits

Character Cluster	Days to 50% flowering	Plant height (cm)	No. of filled pods per plant	Total pods per plant	No. of seeds per pod	Sound mature kernels (%)	Haulm yield per plant (g)	Pod yield per plant (g)	Kernel yield per plant (g)	Shelling percentage (%)	Harvest index (%)	100 kernel weight (g)	SCMR at 60 DAS	Oil content (%)	Protein content (%)
1 Cluster	32.37	20.47	13.70	15.53	1.58	79.13	15.08	10.73	7.11	67.06	0.55	37.99	37.96	49.61	31.00
2 Cluster	31.84	21.37	13.68	16.16	1.58	78.95	19.18	14.24	9.22	65.25	0.54	42.04	43.87	50.68	25.84
3 Cluster	32.13	25.24	13.76	15.32	1.59	81.50	14.20	9.95	6.82	69.07	0.57	35.33	31.95	50.46	24.69
4 Cluster	37.50	19.40	16.00	17.00	1.56	82.00	14.60	10.11	6.84	68.29	0.52	29.40	37.55	50.97	39.50
5 Cluster	33.00	21.65	10.80	11.50	1.58	80.00	14.15	9.80	5.03	51.74	0.49	38.38	46.25	42.52	24.50
6 cluster	34.00	22.30	15.10	20.30	1.72	77.00	15.08	10.44	6.65	65.07	0.41	45.83	41.25	50.87	35.50
7 Cluster	31.00	26.00	10.50	12.70	1.60	75.00	14.60	9.74	5.74	59.03	0.31	33.42	44.15	51.91	35.00
8 Cluster	31.50	20.85	10.40	14.80	1.54	81.00	12.57	8.38	5.13	60.99	0.40	29.69	43.40	51.49	12.50

High harvest index (57 %) was recorded with the genotype in cluster III, while genotype in cluster VII registered the lowest of 31 %. Similarly, the genotype in cluster II recorded highest 100 kernel weight (42.04 g), while genotype in cluster IV recorded lowest 100 kernel weight (29.40 g). The SCMR at 60 days after sowing was maximum in cluster V (46.25) and was minimum in cluster III (31.95). The oil content was highest in cluster VII (51.91%) and was lowest in cluster V (42.52%). The highest protein content was found in cluster IV (39.50 %) and the lowest (12.50%) was recorded in cluster VIII.

A perusal of cluster means for different characters revealed considerable differences among the clusters for all the characters studied (Table 4.7). The genotypes of cluster II registered superior performance for haulm yield per plant, pod yield per plant, kernel yield per plant, 100 kernel weight whereas, the genotypes of cluster III exhibited highest cluster mean for shelling per cent, harvest index and inferior cluster mean for SCMR at 60 DAS. Similarly, genotypes of cluster IV recorded the highest cluster mean for days to 50 per cent flowering, number of filled pods per plant, sound mature kernel per cent and protein content and recorded lowest cluster mean plant height and 100 kernel weight. While genotypes of cluster V were superior for SCMR and inferior for total pods per plant, kernel yield per plant, shelling per cent, oil content. The genotypes of cluster VI exhibited superior cluster mean for total pods per plant, number of seeds per pod. The genotypes of cluster VII were superior for plant height, oil content and low values for days to 50 per cent flowering, sound mature kernel per cent, harvest index. The genotypes in cluster VIII expressed lowest cluster mean performance for number of filled pods per plant, number of seeds per pod, haulm yield per plant, pod yield per plant, protein content. Inter-crossing of the genotypes from these clusters could be suggested to generate a wide spectrum of variability followed by effective selection for these characters.

4.4.6 Relative contribution of each character towards diversity

The number of times that each of the fifteen characters appeared in first position and its respective per cent contribution towards diversity is presented in Table 4.8 and Fig.4.3.

Table 4.8. Contribution of yield, yield components and qualitative traits to total diversity in fifty genotypes of groundnut

S. No.	Character	Times ranked first	Contribution (%)
1.	Days to 50% flowering	15	1.22
2.	Plant height (cm)	61	4.98
3.	No of filled (mature) pods per plant	25	2.04
4.	Total pods per plant	1	0.08
5.	No of seeds per pod	3	0.24
6.	Sound mature kernels (%)	1	0.08
7.	Haulm yield per plant (g)	11	0.90
8.	Pod yield per plant (g)	0	0.00
9.	Kernel yield per plant (g)	17	1.39
10.	Shelling percentage (%)	2	0.16
11.	Harvest index (%)	104	8.49
12.	100 kernel weight (g)	73	5.96
13.	SPAD Chlorophyll meter reading (SCMR) at 60 DAS	498	40.65
14.	Oil content (%)	97	7.92
15.	Protein content (%)	317	25.88

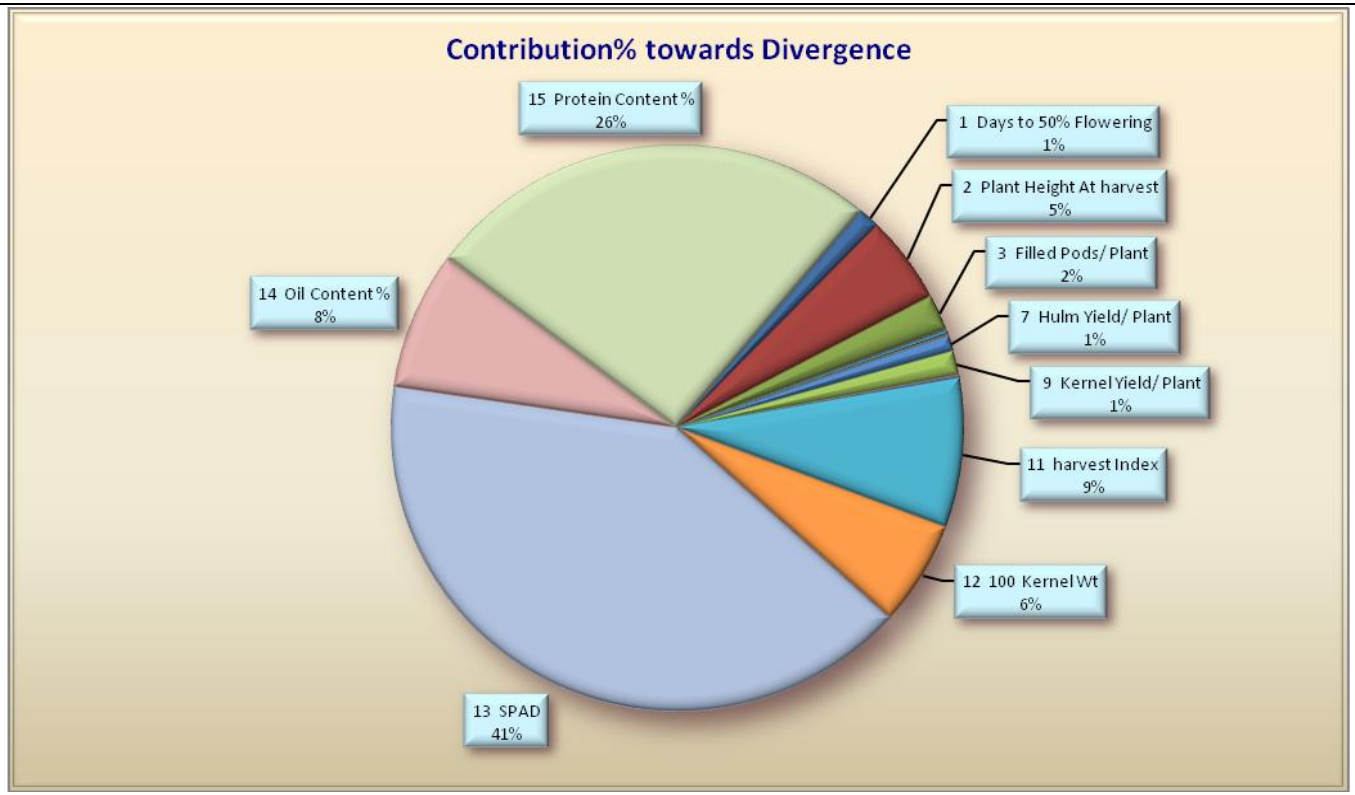

Fig 4.3. Relative contribution of fifteen characters to total genetic diversity in fifty genotypes of groundnut

Among the characters studied, SCMR at 60 days after sowing contributed maximum (40.65 %) to the diversity by taking first rank in 498 times followed by protein content (25.88 %) with 317 times, harvest index (8.49 %) with 104 times, oil content (7.92 %) with 97 times, 100 kernel weight (5.96 %) with 73 times, plant height (4.98 %) with 61 times and number of filled pods per plant per plant (2.04 %) with 25 times.

Similar results of maximum contribution of SCMR at 60 DAS was reported by Nirmala *et al*. (2013). The maximum contribution of protein content towards diversity were similar to the reports of Mukri *et al*. (2014). The highest contribution of harvest index towards diversity were similar to the reports of Reddy & Reddy (1993), Vijayasekhar (2002), Suneetha (2007), Venkateswarlu *et al.* (2011) and Kumar *et al.* (2012). The maximum contribution of oil content towards diversity were similar to the reports of Lakshmidevamma *et al.* (2006), Sonone and Thaware (2009). Similar reports for 100 kernel weight were reported by Nadaf *et al.* (1986), Sigamani (1986), Reddy and Reddy (1993), Vijayasekhar (2002), Dashora and Nagda (2004), Korat *et al.* (2009), Sonone and Thaware (2009), Venkateshwarlu *et al.* (2011) and Nirmala *et al.* (2013). For number of filled pods per plant the results are in conformity with Nadaf *et al.* (1986) and Golakia and Makne (1991).

The characters *viz.*, kernel yield per plant, days to 50 per cent flowering, haulm yield per plant, number of seeds per pod, shelling per cent, sound mature kernel per cent and total pods per plant contributed 1.39, 1.22, 0.90, 0.24, 0.16, 0.08 and 1.00 respectively to the total genetic divergence in decreasing order.

The characters, shelling per cent, sound mature kernel per cent total pods per plant and harvest index showed little contribution to the total genetic divergence which is suggestive of lack of diversity for these traits in the present genetic material which might be due to the operation of directional selection adopted by the breeders in the development of genotypes. Intercrossing of genotypes from these clusters could be suggested to generate a wide range of variability followed by effective selection for these characters.

It was observed that SCMR at 60 DAS, protein content, harvest index, oil content and 100 kernel weight were the major contributors towards divergence (Table 4.8). The

performance of genotypes and the characters with maximum contribution towards divergence should also be considered for improvement of groundnut.

4.4.7 Cluster Diagram

With the help of D^2 values, a cluster diagram was constructed showing the relationship between the different populations (Fig. 4.4). The greatest distance between the two clusters was existed between cluster IV and VIII indicating greatest divergence, whereas the least distance measured between cluster VI and VII indicated the least genetic divergence between them among the eight clusters formed.

4.4.8 Canonical Root Analysis

The canonical root analysis was carried out for fifty genotypes of groundnut as per the method suggested by Rao (1952). The values of six canonical roots and the percentage of variation explained by them were presented in the Table 4.9. The first canonical root accounted for 23.39 per cent of total variability, the second, third and fourth accounted for 18.20 per cent , 12.22 per cent and 10.01 per cent while the fifth and sixth accounted for 7.64 per cent and 6.07 per cent of total variability respectively. The six canonical roots cumulatively accounted for 87.53 per cent of total variability. The mean values of canonical variates for three roots X, Y and Z were furnished in Table 4.10. Two dimensional graphs have been drawn by plotting the mean values of the canonical vectors, Z_1 (X-vector) on 'x' axis and Z_2 (Y-vector) on 'y' axis, Z_1 (X-vector) on 'x' axis and Z_3 (Z-vector) on 'y' axis, Z_2 (Y-vector) on 'x' axis and Z_3 (Z-vector) on 'y' axis and were presented graphically in figure 4.5 respectively.

The amount of contribution of canonical vectors towards total diversity was presented in Table 4.11.

Haulm yield per plant contributed the maximum to the genetic diversity in the vector Z_1 (0.48) followed by shelling percentage (0.41), kernel yield (0.36), number of filled pods per plant (0.33), oil content (0.32), SCMR at 60 DAS (0.23), pod yield per plant (0.23), total pods per plant (0.22), days to 50 per cent flowering (0.14) and protein content (0.07). All the remaining characters *viz.*, plant height, number of seeds per pod,

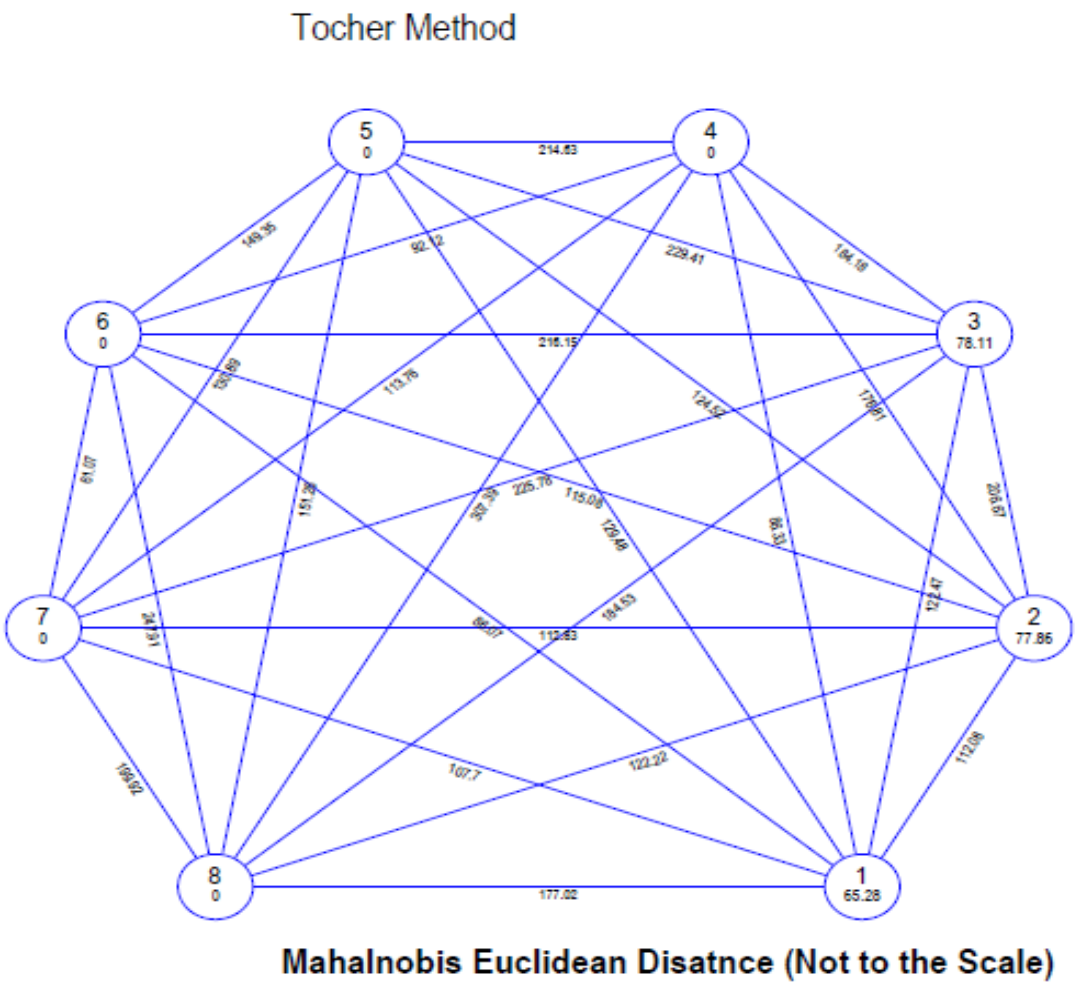

Fig. 4.4. Cluster diagram for the groundnut genotypes studied

Table 4.9. Canonical root values, percent of variation and cumulative variation explained for fifty genotypes in groundnut

Canonical root	Value of canonical root	Percent of variation accounted for	Cumulative total variation accounted for
Z_1	3.51	23.39	23.39
Z_2	2.73	18.20	49.60
Z_3	1.83	12.22	53.81
Z_4	1.50	10.01	63.82
Z_5	1.15	7.64	71.46
Z_6	0.91	6.07	87.53

Table 4.10. Mean values of canonical vectors for fifty genotypes of groundnut

S. No.	Genotype	X Vector	Y Vector	Z Vector
1.	03 x 397- 031	26.74	-3.65	3.47
2.	03 x 398- 067	26.60	-5.09	3.71
3.	03 x 427- 082	25.76	-3.22	3.69
4.	03 x 427- 086	27.06	0.17	3.58
5.	03 x 427- 088	25.75	-6.04	6.11
6.	03 x 427- 091	28.00	-5.79	5.21
7.	03 x 427- 094	25.17	-4.29	5.07
8.	03 x 427- 107	24.89	-4.53	4.47
9.	03 x 427- 109	28.10	-5.43	9.18
10.	03 x 461- 019	31.05	-5.44	6.75
11.	03 x 482- 036	29.38	-10.42	7.26
12.	03 x 485- 001	29.64	-8.65	9.59
13.	03 x 485- 024-01	30.59	-6.89	10.45
14.	04 x 477- 010	26.00	-8.36	7.14
15.	04 x 477- 018	29.05	-13.29	8.79
16.	04 x 477- 021-1	31.14	-13.13	8.62
17.	04 x 477- 021-2	29.08	-11.38	7.81
18.	04 x 477- 024- 1	32.09	-10.07	4.56
19.	04 x 477- 030	30.75	-12.17	6.12
20.	04 x 477- 031	33.26	-7.22	5.65
21.	04 X 479- 002	31.97	-6.39	5.81
22.	04 X 479- 005	31.32	-6.45	4.78
23.	04 X 479- 012	37.52	-5.79	5.96
24.	04 X 480- 007	31.07	-9.71	8.04
25.	04 X 481- 005	28.30	-9.14	6.72
26.	04 X 481- 023	28.97	-9.00	6.99
27.	K 1643	34.92	-10.20	6.30
28.	K 1563	32.45	-9.67	6.32
29.	K 1715	33.75	-7.32	5.95
30.	K 1577	29.05	-8.25	7.87
31.	K 1735	30.71	-11.19	6.60
32.	K 1576	28.85	-10.35	5.95
33.	K 1725	35.73	-9.24	3.50
34.	K 1574	30.15	-9.65	7.21
35.	K 1535	27.29	-8.25	7.11
36.	K 1621	32.29	-5.12	7.82
37.	K 1501	33.82	-6.74	7.41
38.	K 1799	30.25	-4.33	6.48
39.	K 1800	30.41	-2.22	5.54
40.	K 1809	28.78	-3.77	7.09

S. No.	Genotype	X Vector	Y Vector	Z Vector
41.	K 1717	34.26	-4.90	5.61
42.	K 1641	32.83	-4.85	4.10
43.	K 1650	28.58	-8.33	5.32
44.	K 1647	32.33	-8.74	6.36
45.	K 1811	30.21	-2.39	6.72
46.	Kadiri 6	23.18	-0.87	0.59
47.	Kadiri 9	28.51	-2.38	4.81
48.	Harithandhra	26.14	-0.67	1.70
49.	Anantha	24.48	-0.33	3.69
50.	JL-24	26.79	-0.59	5.60

Table 4.11. Canonical vectors for fifteen characters in groundnut

S.No	Character	Z_1	Z_2	Z_3	Z_4	Z_5	Z_6
1.	Days to 50% flowering	0.14	0.35	0.03	0.41	0.08	0.23
2.	Plant height (cm)	-0.06	0.23	-0.31	-0.34	0.09	0.47
3.	No of filled (mature)pods per plant	0.33	0.38	-0.01	-0.21	0.15	-0.06
4.	Total pods per plant	0.22	-0.08	0.41	-0.26	-0.19	-0.06
5.	No of seeds per pod	-0.08	0.01	0.27	-0.58	0.26	0.21
6.	Sound mature kernels (%)	-0.20	-0.28	-0.42	-0.15	0.04	0.00
7.	Haulm yield per plant (g)	0.48	-0.07	-0.03	-0.07	0.02	0.20
8.	Pod yield per plant (g)	0.23	-0.17	-0.51	-0.21	0.10	0.00
9.	Kernel yield per plant (g)	0.36	-0.16	-0.33	0.25	-0.23	0.18
10.	Shelling percentage (%)	0.41	0.32	0.07	-0.01	-0.12	0.10
11.	Harvest index (%)	-0.18	0.37	-0.11	0.00	-0.34	-0.14
12.	100 kernel weight (g)	-0.05	-0.35	0.22	0.20	-0.12	0.50
13.	SPAD Chlorophyll meter reading (SCMR) at 60 DAS	0.23	-0.36	0.20	-0.01	0.08	0.12
14.	Oil content (%)	0.32	-0.21	-0.02	-0.12	-0.07	-0.54
15.	Protein content (%)	0.07	0.01	0.01	0.29	0.80	-0.13

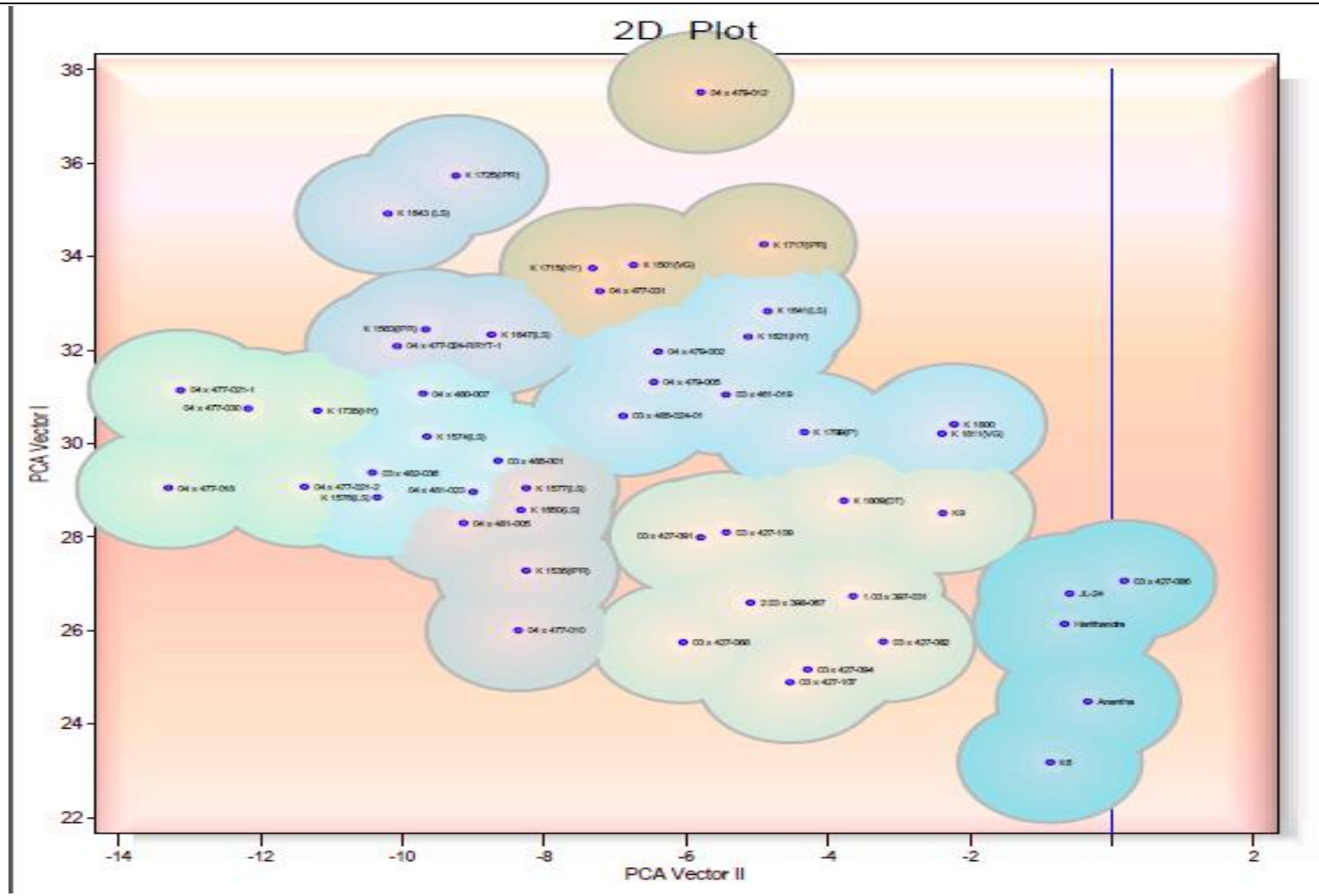

Fig. 4.5. Two dimensional picture of vectors in Principle component analysis (PCA)

sound mature kernel per cent, harvest index and 100 kernel weight contributed negatively to the diversity.

Number of filled pods per plant contributed maximum to the total genetic diversity in Z_2 vector (0.38), harvest index (0.37), days to 50 per cent flowering (0.35), shelling per cent (0.32) and plant height (0.23) in the decreasing order of their contribution. All the remaining characters contributed negatively to the diversity.

Total pods per plant contributed maximum (0.41) to the total genetic diversity in Z_3 vector, followed by number of seeds per pod (0.27), 100 kernel weight (0.22), SCMR at 60 DAS (0.20), shelling percentage (0.007), days to 50 per cent flowering (0.003) and protein content (0.01). The remaining characters contributed negatively to the diversity.

In Z_4 vector, days to 50 per cent flowering (0.41) contributed maximum to the diversity followed by protein content (0.29), kernel yield per plant (0.25) and 100 kernel weight (0.20).

In Z_5 vector protein content (0.80) was contributed positively to the diversity followed by number of seeds per pod (0.26), number of filled pods per plant (0.15), pod yield per plant (0.10), plant height (0.09), days to 50 per cent flowering (0.08) and SCMR at 60 DAS (0.08).

In Z_6 vector the maximum contribution towards diversity was contributed by plant height (0.47) followed by days to 50 per cent flowering (0.23), number of seeds per pod (0.21), haulm yield per plant (0.20), kernel yield per plant (0.18), SCMR at 60 DAS (0.12), 100 kernel weight (0.50) and shelling per cent (0.10).

In the present study, the data collected on the yield, yield components and quality characters in fifty genotypes of groundnut were subjected to D^2 analysis and the genetic diversity was estimated using Tocher's method. This method of grouping is the most widely used procedure of clustering using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters using Tocher's method of clustering.

Among eight clusters formed, Cluster I consisted of a fifteen genotypes whereas, cluster II consisted of twenty two genotypes and cluster III had eight genotypes and

cluster IV,V, VI, VII, VIII had one genotype each, (Table 4.5). Inter-cluster distances were greater in magnitude confirming the presence of diversity among clusters. Minimum inter-cluster distance was observed between the cluster VI and VII revealing the close relationship for most of the characters among the genotypes in these clusters. Maximum inter-cluster distance was noticed between cluster IV and cluster VIII. The genotypes in these clusters can be utilized as potential parents and effecting crosses among these genotypes would result in realizing superior segregants for yield and its components.

Theoretically, the maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to the most divergent clusters. However, for a practical plant breeder, the objective is not only to gain high heterosis but also to achieve high level of production. The performance of genotypes and the characters with maximum contribution towards divergence should also be considered for inclusion of genotypes in the hybridization programme for genetic improvement of groundnut.

To confirm the clustering pattern obtained by D^2 statistics and to plot 50 groundnut genotypes in a two dimensional graph canonical root analysis is used. The six canonical roots accounted for 87.53 per cent of total variation of uncorrelated variables, which indicated that the differentiation of these traits was nearly complete in these genotypes in six phases. The relative distribution of genotypes reflected existence of parallelism between grouping obtained by D^2 analysis and canonical root analysis. The first six canonical roots contribute to 87.53 per cent for getting a clear two dimensional representation.

Haulm yield per plant and shelling percentage contributed maximum to the genetic diversity in first vector whereas, number of filled pods per plant and harvest index contributed maximum followed by days to 50 per cent flowering in second vector. Similarly, total pods per plant followed by number of seeds per pod contributed maximum towards divergence in third vector, while days to 50 per cent flowering followed protein content contributed maximum in fourth vector. Protein content followed by number of seeds per pod contributed maximum towards genetic divergence

in fifth vector. Plant height followed by days to 50 per cent flowering contributed maximum towards divergence in sixth vector. Similarly, days to 50 per cent flowering, plant height, SCMR showed greater contribution towards divergence. This was in agreement with the relative contribution of characters obtained through D^2 analysis. Thus SCMR at 60 days after sowing, protein content, kernel yield per plant and pod yield per plant are the important traits contributing towards divergence and for discerning the genotypes into various clusters.

4.5 CHARACTER ASSOCIATION

Kernel yield in groundnut is a complex trait based on various yield component characters and hence, direct selection for yield would be ineffective. Therefore, selection for various component traits responsible for conditioning of kernel yield in groundnut is advocated. In this context, the nature and magnitude of association among kernel yield and its component traits are important for the breeder to make an effective selection strategy. Further, identification of important kernel yield components and information about their inter-relationship would be useful in developing high yielding varieties. The genotypic and phenotypic correlations for yield and various yield components studied in the present investigation are presented in Table 4.12. A perusal of these results revealed phenotypic and genotypic correlations to be of similar direction and significance. However, genotypic correlations recorded a higher magnitude compared to phenotypic correlations indicating the masking effect of environment. Further, positive and significant association of kernel yield with number of filled pods per plant (r_p=0.5785** and r_g=0.6102**), total pods per plant (r_p=0.5548** and r_g=0.6035**), pod yield per plant (r_p=0.8374** and r_g=0.9825**), harvest index per cent (r_p=0.4804** and r_g=0.5217**), 100 kernel weight (r_p=0.4092** and r_g=0.4418**), shelling per cent (r_p=0.2226* and r_g=0.2496*) and SCMR at 60 DAS (r_p=0.2212* and r_g=0.2512*) ; pod yield per plant with harvest index per cent (r_p=0.4814** and r_g=0.4254**), 100 kernel weight (r_p=0.4789** and r_g=0.4424**) and SCMR at 60 DAS (r_p=0.3438** and r_g=0.3880**) was observed in the present investigation, indicating that an increase in kernel yield and pod yield could be realized with an increased performance of these characters. Therefore, priority should be given to these traits while making selections for

Table 4.12 Genotypic and phenotypic correlations among yield, yield components and qualitative traits in PSND tolerant groundnut genotypes

		DFF	PH	FP	TP	S/P	SMK	HY	PY	S%	HI%	100KW	SCMR	OC	PC	KY
DFF	r_p	1.000	0.0813	0.1693	0.1824	0.0214	-0.0274	-0.1255	0.1116	0.0378	0.1840	0.0447	-0.2105*	0.0031	0.2280*	0.1266
	r_g	1.000	0.0737	0.3067	0.2812	-0.0883	-0.1077	-0.1419	0.1392	0.2365	0.2334	0.0291	-0.2543*	-0.0704	0.2660*	0.2067
PH	r_p		1.000	0.1570	0.1417	0.0914	0.0908	0.0454	0.1251	0.0574	0.0756	-0.0355	-0.2524*	-0.1358	-0.1059	0.1471
	r_g		1.000	0.2064	0.1662	0.1155	0.1619	0.0585	0.1201	0.1757	0.0830	-0.1369	-0.2713*	-0.1759	-0.1232	0.1601
FP	r_p			1.000	0.9120**	0.0449	0.0092	0.0264	0.4261**	0.2121*	0.3019**	-0.0162	-0.0902	0.1479	0.0515	0.5785**
	r_g			1.000	0.9553**	0.1525	-0.0982	-0.0289	0.5454**	0.3596*	0.4081**	-0.0361	-0.0918	0.2568	0.0886	0.6102**
TP	r_p				1.000	0.1604	-0.0360	0.1186	0.4443**	0.1279	0.2440*	0.0956	-0.0088	0.1664	-0.0476	0.5548**
	r_g				1.000	0.2486	-0.1168	0.0742	0.5575**	0.3098	0.3219*	0.0661	0.0061	0.2734	-0.0125	0.6035**
S/P	r_p					1.000	-0.0123	0.1188	-0.0390	-0.0348	-0.0865	0.1226	0.0093	-0.1082	-0.0548	-0.0537
	r_g					1.000	-0.0382	0.1754	-0.0365	-0.3231	-0.1523	0.1317	-0.0014	-0.0888	-0.0806	-0.1601
SMK	r_p						1.000	-0.0393	-0.0444	0.0900	0.0115	0.0386	-0.1310	-0.1223	0.0375	-0.0052
	r_g						1.000	-0.0424	-0.0413	-0.0591	0.0056	0.1026	-0.2185	-0.0833	0.0432	-0.0372
HY	r_p							1.000	0.2317*	-0.2396*	-0.6921**	0.1229	0.5244**	0.1785	0.0900	0.1301
	r_g							1.000	0.3014*	-0.4725*	-0.7386**	0.1748	0.5575**	0.2436	0.1272	0.1504
PY	r_p								1.000	-0.2702	0.4814**	0.4789**	0.3438**	0.0997	0.0216	0.8374**
	r_g								1.000	-0.0913	0.4254**	0.4424**	0.3880**	0.1652	-0.0090	0.9825**
S%	r_p									1.000	0.4804**	0.4092**	0.2212*	0.1593	0.0014	0.2226*
	r_g									1.000	0.5217**	0.4418**	0.2512*	0.3074	0.0007	0.2496*
HI%	r_p										1.000	-0.1377	-0.2672*	0.1833	-0.0457	0.4804**
	r_g										1.000	0.0794	-0.4958*	0.4840	0.0154	0.5217**
100KW	r_p											1.000	-0.2453*	-0.0808	-0.0622	0.4092**
	r_g											1.000	-0.2678*	-0.0814	-0.1255	0.4418**
SCMR	r_p												1.000	-0.1388	-0.0269	0.2212*
	r_g												1.000	-0.1383	-0.0654	0.2512*
OC	r_p													1.000	-0.0791	0.1593
	r_g													1.000	-0.0840	0.3074
PC	r_p														1.000	0.0014
	r_p														1.000	0.0007

r_p= Phenotypic correlation; r_g = genotypic correlation; *, ** Significant at 5% and 1% levels, respectively

DFF=Days to 50% flowering., PH=Plant height., FP=Number of filled pods per plant., TP=Total pods per plant, S/P=Seeds per pod., SMK=Sound mature kernel per cent., HY=Haulm yield per plant., PY=Pod yield per plant, S%=Shelling per cent, HI%=Harvest index per cent., 100 KW=100 Kernel weight., SCMR=SPAD Chlorophyll Meter Reading, OC=Oil content., PC=Protein content

improvement of kernel yield. These findings are in agreement with the reports of Shoba *et al.* (2012) for the traits *viz.*, number of filled pods per plant, total pods per plant, pod yield per plant, harvest index, 100 kernel weight, shelling per cent and SCMR at 60 DAS. Further, Reddy *et al.* (2004) for SCMR at 60 DAS, Reddy *et al.* (1986) and Jayalakshmi *et al.* (2000) for number of filled pods per plant, Ofori (1996) for total pods per plant, Babaria and Dobariya (2012), Toprope *et al.* (2013), Satish (2014) for pod yield per plant, Babaria and Dobariya (2012), Chandrasekhar and Kenchenagoudar (2012) and Alam (2014) for 100 kernel weight, Dolma *et al.* (2010 b) and Shoba *et al.* (2012) for shelling per cent also reported similar findings.

Patil *et al.* (2006) and Makinde *et al.* (2013) reported significant positive association of total pods per plant with pod yield per plant; Dhaliwal *et al.* (2010) and Satish (2014) for haulm yield per plant with pod yield per plant; Narasimhulu *et al.* (2012) and Babaria and Dobariya *(*2012) for pod yield per plant with 100 kernel weight, Rao *et al.* (2013) and Toprope *et al.* (2013) for pod yield per plant with SCMR at 60 DAS.

A perusal of the results on inter-character associations revealed significant and positive association of days to 50 per cent flowering with protein content (r_p=0.2280* and r_g=0.2660*); number of filled pods per plant with total pods per plant (r_p=0.9120** and r_g=0.9553**), pod yield per plant (r_p=0.4261** and r_g=0.5454**), shelling per cent (r_p=0.2121* and r_g=0.3596*) and harvest index per cent (r_p=0.3019** and r_g=0.4081**); total pods per plant with pod yield per plant (r_p=0.4443** and r_g=0.5575**) and harvest index per cent (r_p=0.2440* and r_g=0.3219**); haulm yield per plant with pod yield per plant (r_p=0.2317* and r_g=0.3014*) and SCMR at 60 DAS (r_p=0.5244** and r_g=0.5575**); shelling per cent with harvest index per cent (r_p=0.4804** and r_g=0.5217**), 100 kernel weight (r_p=0.4092** and r_g=0.4418**) and SCMR at 60 DAS (r_p=0.2212** and r_g=0.2512**) in the present investigation, indicating a scope for simultaneous improvement of these traits through selection. These findings are in conformity with the reports of Sharma and Varshney (1990) for number of filled pods per plant with total pods per plant, Sonone *et al.* (2010) for number of filled pods per plant with pod yield per plant and Reddi *et al.* (1986) for number of filled pods per plant with shelling per cent.

In contrast, significant and negative association of days to 50 per cent flowering with SCMR at 60 DAS (r_p=-0.2105* and r_g=-0.2543*); plant height with SCMR at 60 DAS (r_p=-0.2524* and r_g= -0.2713*); haulm yield per plant with shelling per cent (r_p=-0.2396* and r_g=-0.4725**) and harvest index (r_p=-0.6921** and r_g=-0.7386**); harvest index with SCMR at 60 DAS (r_p=-0.2672* and r_g=-0.4958*); and 100 kernel weight with SCMR at 60 DAS (r_p=-0.2453* and r_g= -0.2678*) were observed in the present study, probably due to competition for a common possibility such as nutrient supply, indicating the need for balanced selection while effecting simultaneous improvement of these traits. These findings are in agreement with the reports of Nirmala (2012) for plant height with SCMR at 60 DAS; Parameshwarappa *et al.* 2008 for haulm yield per plant with shelling per cent.

4.6 PATH COEFFICIENT ANALYSIS

Path co-efficient analysis provides an effective means of finding out the direct and indirect causes of association and presents a critical examination of the specific forces acting to produce a given correlation and also measures the relative importance of each causal factor. Hence, the study of direct and indirect effects of yield components on kernel yield per plant was undertaken in the present investigation and the results obtained are presented in Table 4.13 and Table 4.14 and pictures 4.6 and 4.7. A perusal of these results on path coefficients for yield and yield components revealed genotypic and phenotypic path coefficients to be of similar direction and magnitude. Further, the genotypic path coefficients were observed to be of higher magnitude, compared to phenotypic path coefficients indicating the masking effect of environment. The results also revealed high residual effect for both phenotypic (0.3570) and genotypic (0.1631) path coefficients, respectively, indicating that variables studied in the present investigation explained about 64.3 (phenotypic) and 83.7 (genotypic) per cent of the variability in yield and therefore, other attributes besides the characters studied are contributing for kernel yield. The results also revealed high (>0.30) positive direct effects of haulm yield per plant (P_P=0.8434 and P_G=0.6272), shelling per cent (P_P=0.9365 and P_G=1.0877), harvest index per cent (P_P=0.9838 and P_G=0.8560) and 100 kernel weight (P_P=0.1468 and P_G=0.3404), on kernel yield per plant. The results are in conformity with the findings of John *et al* (2011), Mukhtar *et al*. (2011), Vange and

Table 4.13 Genotypic and phenotypic path coefficients of yield components and qualitative characters on kernel yield per plant in PSND tolerant groundnut

Character		DFF	PH	FP	TP	S/P	SMK%	HY	PY	S%	HI%	100KW	SCMR	OC	PC
DFF	Pp	**0.0256**	0.0021	0.0043	0.0047	0.0005	-0.0007	-0.0032	0.0018	0.0010	0.0047	0.0011	-0.0054	0.0001	0.0058
	Pg	**-0.0013**	-0.0001	-0.0004	-0.0004	0.0001	0.0001	0.0002	-0.0032	-0.0003	-0.0003	0.0000	0.0003	0.0001	-0.0003
PH	Pp	0.0018	**0.0226**	0.0035	0.0032	0.0021	0.0021	0.0010	0.0033	0.0013	0.0017	-0.0008	-0.0057	-0.0031	-0.0024
	Pg	0.0118	**0.1601**	0.0331	0.0266	0.0185	0.0259	0.0094	-0.0284	0.0281	0.0133	-0.0219	-0.0434	-0.0282	-0.0197
FP	Pp	0.0422	0.0391	**0.2492**	0.2273	0.0112	0.0023	0.0066	0.0164	0.0528	0.0752	-0.0040	-0.0225	0.0369	0.0128
	Pg	0.0622	0.0419	**0.2029**	0.1938	0.0309	-0.0199	-0.0059	-0.0803	0.0730	0.0828	-0.0073	-0.0186	0.0521	0.0180
TP	Pp	-0.0136	-0.0105	-0.0678	**-0.0744**	-0.0119	0.0027	-0.0088	-0.0253	-0.0095	-0.0181	-0.0071	0.0007	-0.0124	0.0035
	Pg	0.0201	0.0119	0.0681	**0.0713**	0.0177	-0.0083	0.0053	-0.0495	0.0221	0.0230	0.0047	0.0004	0.0195	-0.0009
S/P	Pp	-0.0016	-0.0070	-0.0034	-0.0122	**-0.0761**	0.0009	-0.0090	0.0005	0.0026	0.0066	-0.0093	-0.0007	0.0082	0.0042
	Pg	0.0240	-0.0314	-0.0414	-0.0675	**-0.2716**	0.0104	-0.0476	-0.0095	0.0878	0.0414	-0.0358	0.0004	0.0241	0.0219
SMK	Pp	0.0005	-0.0016	-0.0002	0.0006	0.0002	**-0.0177**	0.0007	-0.0001	-0.0016	-0.0002	-0.0007	0.0023	0.0022	-0.0007
	Pg	0.0053	-0.0079	0.0048	0.0057	0.0019	**-0.0489**	0.0021	-0.0015	0.0029	-0.0003	-0.0050	0.0107	0.0041	-0.0021
HY	Pp	-0.1059	0.0383	0.0223	0.1000	0.1002	-0.0332	**0.8434**	0.0642	-0.2021	-0.5837	0.1037	0.4423	0.1506	0.0759
	Pg	-0.0890	0.0367	-0.0181	0.0465	0.1100	-0.0272	**0.6272**	-0.0231	-0.2963	-0.4632	0.1096	0.3496	0.1528	0.0798
PY	Pp	0.0845	0.0947	0.3225	-0.0253	-0.0295	-0.0336	0.0642	**0.7569**	0.6338	-0.2045	0.3643	0.3625	0.2602	0.0163
	Pg	-0.0662	-0.0571	-0.2593	-0.0495	0.0174	0.0196	-0.0231	**-0.4755**	-0.4671	0.0434	-0.2023	-0.2103	-0.1845	0.0043
S%	Pp	0.0154	0.0235	0.0867	0.0523	-0.0142	0.0368	-0.0979	0.0966	**0.9365**	0.0085	-0.0563	-0.1092	0.0749	-0.0187
	Pg	-0.0338	-0.0251	-0.0514	-0.0442	0.0461	0.0084	0.0675	0.0032	**1.0877**	-0.0515	-0.0113	0.0708	-0.0691	-0.0022
HI%	Pp	0.1810	0.0744	0.2970	0.2401	-0.0851	0.0113	-0.6809	0.1707	0.0204	**0.9838**	0.2005	-0.2413	-0.0795	-0.0612
	Pg	0.1997	0.0710	0.3493	0.2755	-0.1303	0.0048	-0.6322	-0.1526	0.3088	**0.8560**	0.1143	-0.2292	-0.0697	-0.1074
100KW	Pp	0.0066	-0.0052	-0.0024	0.0140	0.0180	0.0057	0.0180	0.0237	-0.0202	0.0299	**0.1468**	0.0445	-0.0204	-0.0039
	Pg	0.0099	-0.0466	-0.0123	0.0225	0.0448	0.0349	0.0595	-0.1534	0.0270	0.0455	0.3404	0.1195	-0.0471	-0.0223
SCMR	Pp	-0.0244	-0.0292	-0.0104	-0.0010	0.0011	-0.0152	0.0607	0.0131	-0.0309	-0.0284	0.0351	**0.1158**	0.0022	-0.0092
	Pg	0.0035	0.0037	0.0013	-0.0001	0.0000	0.0030	-0.0077	-0.0222	0.0068	0.0037	-0.0048	**-0.0138**	-0.0004	0.0012
OC	Pp	0.0000	0.0001	-0.0001	-0.0001	0.0001	0.0001	-0.0001	0.0049	-0.0001	0.0001	0.0001`	0.0000	**-0.0006**	0.0000
	Pg	-0.0192	-0.0479	0.0699	0.0744	-0.0242	-0.0227	0.0663	-0.0587	0.1317	-0.0222	-0.0376	0.0087	**0.2721**	-0.0158
PC	Pp	-0.0011	0.0005	-0.0003	0.0002	0.0003	-0.0002	-0.0004	0.0000	0.0002	0.0003	0.0001	0.0004	0.0002	**-0.0049**
	Pg	0.0135	-0.0062	0.0045	-0.0006	-0.0041	0.0022	0.0064	0.0008	0.0008	-0.0064	-0.0033	-0.0043	-0.0029	**0.0507**
Correlation	Pp	**0.1266**	**0.1471**	**0.5785****	**0.5548****	**-0.0537**	**-0.0052**	**0.1301**	**0.8374****	**0.2226***	**0.4804****	**0.4092****	**0.2212***	**0.1593**	**0.0014**
Kernel yield	Pg	**0.2067**	**0.1601**	**0.6102****	**0.6035****	**-0.1601**	**-0.0372**	**0.1504**	**0.9825****	**0.2496***	**0.5217****	**0.4418****	**0.2512***	**0.3074**	**0.0007**

Residual effect (Phenotypic) = 0.3570; Residual effect (Genotypic) = 0.1631; Diagonal values = Direct effects; Off-Diagonal values = Indirect effects; *, ** Significant at 0.05 and 0.01 levels, respectively

DFF=Days to 50% flowering., PH=Plant height., FP=Number of filled pods per plant., TP=Total pods per plant, S/P=Seeds per pod., SMK=Sound mature kernel per cent., HY=Haulm yield per plant., PY=Pod yield per plant, S%=Shelling per cent, HI%=Harvest index per cent., 100 KW=100 Kernel weight., SCMR=SPAD Chlorophyll Meter Reading, OC=Oil content., PC=Protein content

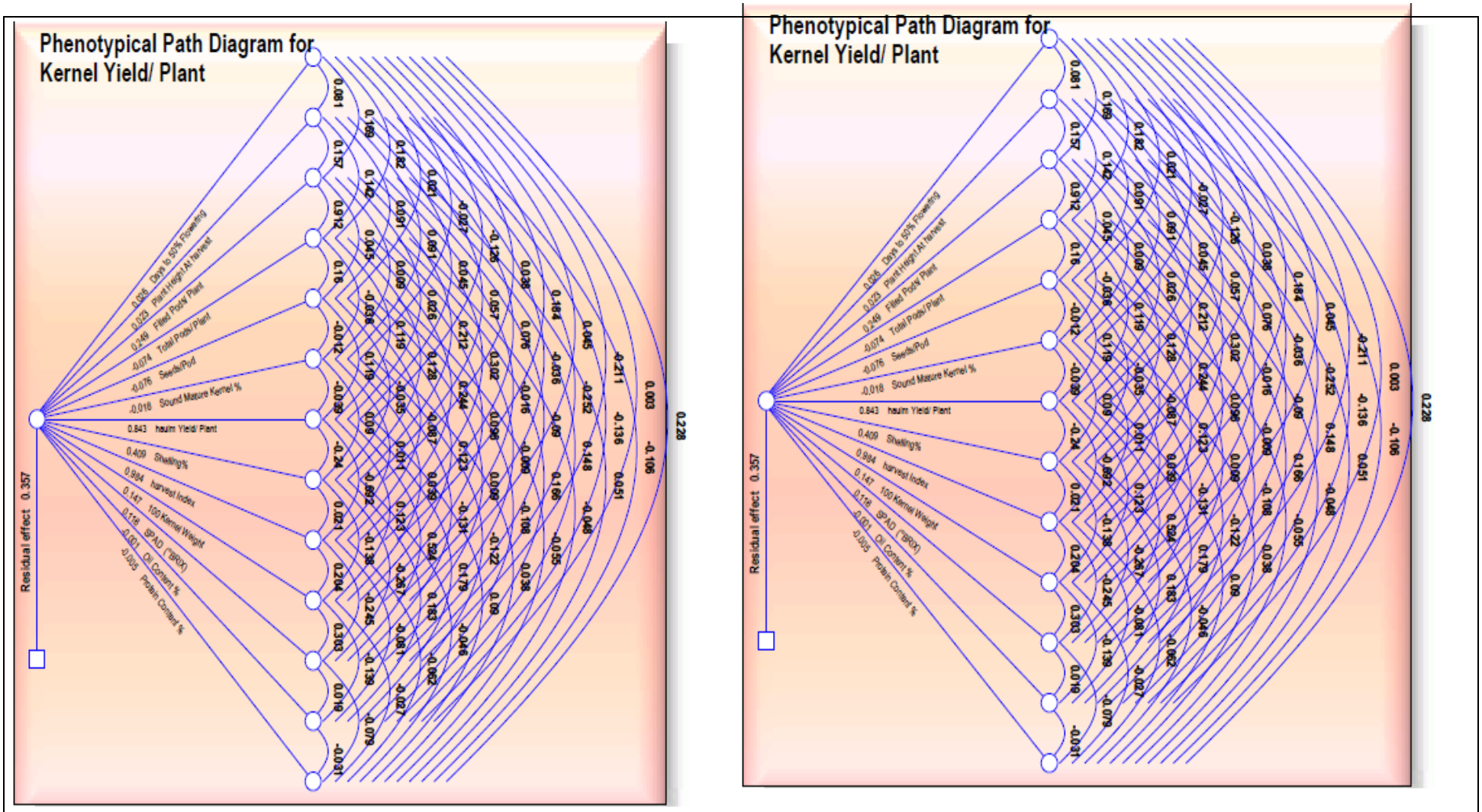

Fig 4.7. Phenotypic and genotypic path diagram for kernel yield per plant

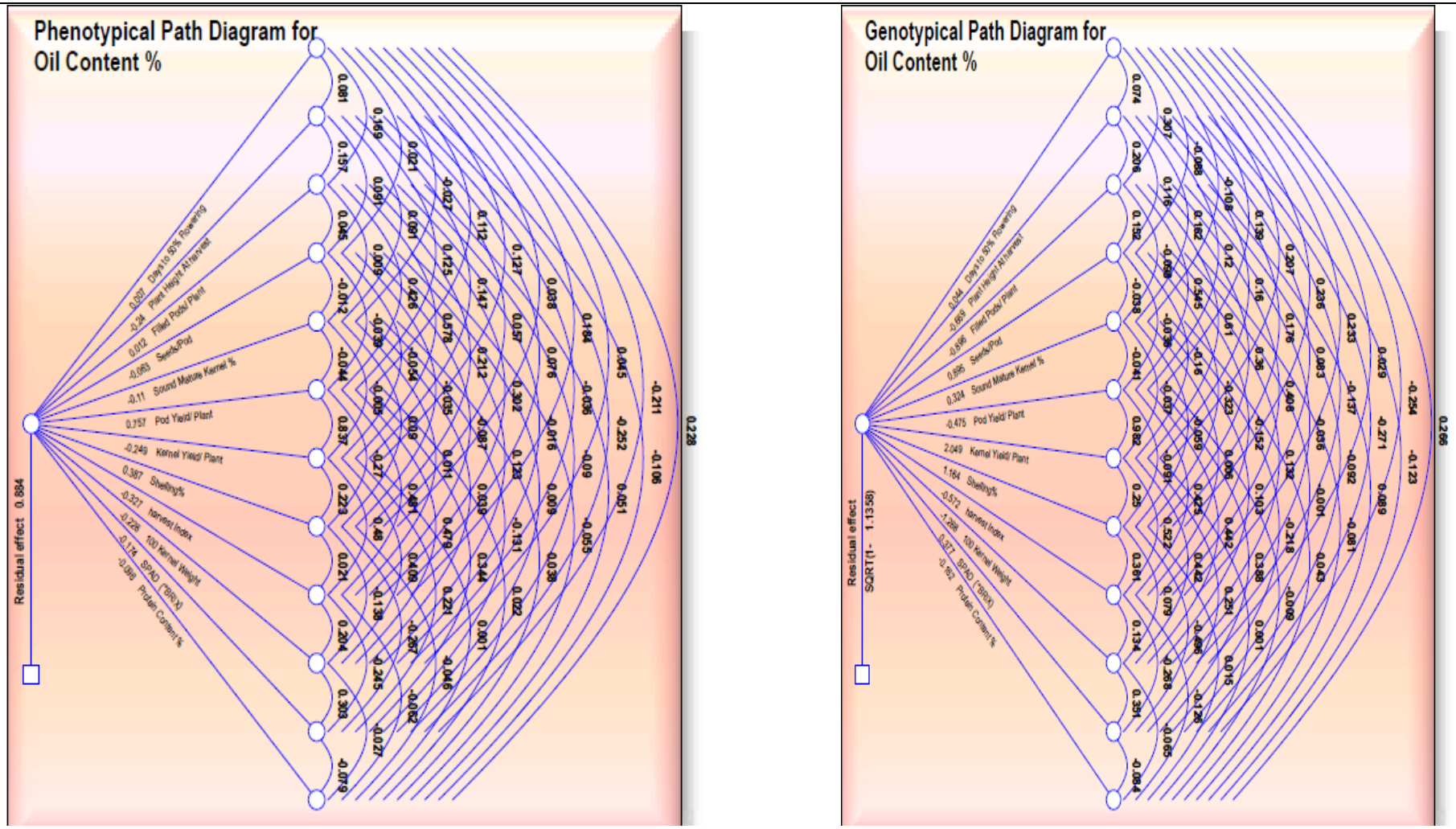

Fig 4.7. Phenotypic and genotypic path diagram for oil content

Maga (2014) for haulm yield per plant, Mane *et al*. (2008) and Dolma *et al.*(2010 b) for shelling per cent and Rao *et al*. (2014), Kwaga (2013) and satish *et al*. (2014) for 100 kernel weight. The character number of filled pods per plant recorded moderate positive direct effect (P_P=0.2492 and P_G=0.2029) on kernel yield per plant. These findings are in conformity with the reports of Zaman *et al. (*2011) and Shanthala and Siddraju (2012). The character plant height recorded negligible direct effect (P_P=0.0226 and P_G=0.1601) on kernel yield per plant. These results are in conformity with the earlier reports of Siddique *et al*. (2006) and Mukhtar *et al*. (2013). The traits *viz.*, Number of filled pods per plant (r_p=0.5785** and r_g=0.6102**), shelling per cent (r_p=0.2226* and r_g=0.2496*), harvest index (r_p=0.4804** and r_g=0.5217**) and 100 kernel weight (r_p=0.4092** and r_g=0.4418**) recorded significant and strong positive association with kernel yield per plant. High direct effects of these traits therefore appear to be the main factor for their strong association with kernel yield. Hence, these traits could be considered as an important selection criteria in all groundnut improvement programmes and direct selection for these traits is recommended for improvement of kernel yield. Further, plant height and haulm yield per plant also recorded direct positive effects in addition to non-significant associations in general with kernel yield per plant, indicating the role of indirect effects and the need for consideration of indirect effects of these traits in PSND tolerant groundnut kernel yield improvement programme.

The results also revealed high residual effect for both phenotypic (0.8839) and genotypic (0.3685) path coefficients, respectively, indicating that variables studied in the present investigation explained about 11.61 (phenotypic) and 63.15 (genotypic) per cent of the variability in yield and therefore, other attributes besides the characters studied are contributing for oil content. The results also revealed high (>0.30) positive direct effects of shelling per cent (P_P=0.3868 and P_G=0.1635) and negligible direct effects of days to 50 per cent flowering (P_P=0.0069 and P_G=0.0443) on oil content. The trait shelling percent also recorded positive association with oil content r_p=0.1833 and r_g=0.4840. In contrast, plant height (P_P=-0.2401 and P_G=-0.6694), harvest index per cent (P_P=-0.3269 and P_G=-0.5724) and 100 kernel weight (P_P=-0.2260 and P_G=-1.2683) recorded high negative direct effect with oil content.

High direct effects of the shelling per cent and negligible direct effect of days to 50 per cent flowering therefore appear to be the main factors due to their strong association with oil content. Hence, these traits could be considered as important for formulating selection strategy in groundnut improvement programmes and direct selection of these traits can be recommended for oil content improvement. However, in view of negative association and high negative direct effect of plant height, harvest index and 100 kernel weight with oil content, balanced selection needs to be adopted while effecting simultaneous improvement for these traits in PSND tolerant groundnut kernel yield improvement programmes.

4.15 Details of promising genotypes identified in the present study

Promising genotypes identified	High mean performance noticed for characters
04 x 479-012	number of filled pods per plant, total pods per plant, haulm yield per plant, pod yield per plant, kernel yield per plant , harvest index and SCMR at 60 days after sowing
K 1501	Total pods per plant, number of seeds per pod, haulm yield per plant, pod yield per plant, kernel yield per plant and SCMR at 60 days after sowing.
K 1643	Plant height, haulm yield per plant, kernel yield per plant, oil content and SCMR at 60 days after sowing.
K 1641	Haulm yield per plant, pod yield per plant, kernel yield per plant, harvest index and 100 kernel weight.
K 1717	Number of filled pods per plant, total pods per plant, haulm yield per plant, pod yield per plant and oil content.
K 1647	Plant height, total pods per plant, kernel yield per plant and harvest index.
04 x 477-031	Number of filled pods per plant, total pods per plant, kernel yield per plant and oil content.
K 1725	Haulm yield per plant, pod yield per plant, kernel yield per plant and SCMR at 60 days after sowing.

K 1717

K 1725

K 1641

K 1501

K 1647

04 x 479-012

Plate.4.1. Promising genotypes identified in the present study

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled "Genetic diversity studies on Peanut Stem Necrosis tolerant groundnut genotypes" was carried out with fifty genotypes comprising of released, pre-release cultures and germplasm lines. The study was focussed to estimate the extent of diversity, in addition to genetic parameters, character associations and path effects for yield, yield components and qualitative traits. The objective of the study was to identify potential and genetically diverse genotypes and to formulate suitable selection strategy for realizing higher kernel yield in PSND tolerant groundnut genotypes. The experiment was conducted during *kharif*, 2015 in a randomized block design with two replications at Agricultural research station, Kadiri, Anantapur district, Andhra Pradesh. The data were recorded on five randomly selected plants for the traits *viz.*, plant height, number of filled pods per plant, total pods per plant, number of seeds per pod, sound mature kernel per cent, haulm yield per plant, pod yield per plant, kernel yield per plant, shelling per cent, harvest index, 100 kernel weight, SCMR at 60 DAS, oil content, protein content and days to 50 per cent flowering on plot basis.

The results revealed highly significant differences among the genotypes for all characters studied, indicating the existence of sufficient variation among the genotypes studied. The entry, 04 x 477-024-1 was early to flower with lowest plant height compared to other genotypes studied in the present investigation which is very desirable to avoid terminal drought.

As over all study of *per se* performance of fifty genotypes indicated that the entry 04 x 479-012 recorded significantly superior mean performance for six characters *viz.*, number of filled pods per plant, total pods per plant, pod yield per plant, kernel yield per plant, harvest index and SCMR at 60 days after sowing.

The entry K 1501 recorded significantly excelled mean performance for six characters *viz.,* total pods per plant, number of seeds per pod, haulm yield per plant, pod yield per plant , kernel yield per plant and SCMR at 60 DAS. While, the entry K 1643 showed significantly higher mean performance for five characters *viz.*, plant height, haulm yield per plant, kernel yield per plant , oil content and SCMR at 60 days after sowing.

Hence, the genotypes *viz.*, 04 x 479-012, K 1501 and K 1643 were found to be superior among the tested entries in the study with significantly superior performance for many yield attributing characters. These genotypes may be involved in the crossing programme by duly estimating the general and specific combining abilities in the future breeding programmes.

An analysis of the results on genetic parameters revealed that kernel yield per plant, pod yield per plant, haulm yield per plant, protein content and number of filled pods per plant recorded high PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean indicating that these characters were governed by additive gene action and simple selection could be used for their improvement. On the other hand, days to 50 per cent flowering , SCMR at 60 DAS and plant height exhibited moderate to low GCV, PCV, high heritability and moderate to low genetic advance. Hence, inter mating of selected genotypes could be suggested to generate variability followed by selection in later generations for realizing the superior segregants for the above characters.

The diversity analysis grouped fifty genotypes of groundnut into eight clusters. Out of these, cluster II contained highest number of genotypes (22), followed by cluster I (15), cluster III (8). While clusters IV, V, VI. VII and VIII comprised of only one genotype each.

Based on inter cluster distances it was observed that IV vs. VIII, VI vs. VIII, III vs. V, III vs. VII and III vs.VI were found to be divergent in the decreasing order of their magnitude. Hence, genotypes of these clusters namely Harithandhra, Kadiri 6, Kadiri 9, Anantha, 03 x 427-082 (Cluster III) and K 1800 (Cluster IV) and 04 x 477-010 (Cluster V) and 03 x 485-024-01 (Cluster VI) and 04 X 481-023 (Cluster VII) and 04 X 481-005

(Cluster VIII) can be utilized as potential parents and effecting crosses in a specific design (Diallel or L X T) would result in identifying highly heterotic segregants.

A perusal of cluster means for different characters revealed considerable differences among the clusters for all the characters studied. The genotypes of cluster II registered superior performance for haulm yield per plant, pod yield per plant, kernel yield per plant, 100 kernel weight whereas, the genotypes of cluster III exhibited highest cluster mean for shelling per cent, harvest index and inferior cluster mean for SCMR at 60 DAS. Similarly, genotypes of cluster IV recorded the highest cluster mean for days to 50 per cent flowering, number of filled pods per plant, sound mature kernel per cent and protein content and recorded the lowest cluster mean for plant height and 100 kernel weight. While genotypes of cluster V were superior for SCMR and inferior for total pods per plant, kernel yield per plant, shelling per cent, oil content. The genotypes of cluster VI exhibited superior cluster mean for total pods per plant, number of seeds per pod. The genotypes of cluster VII were superior for plant height, oil content and low values for days to 50 per cent flowering, sound mature kernel per cent, harvest index. The genotypes in cluster VIII expressed lowest cluster mean performance for number of filled pods per plant, number of seeds per pod, haulm yield per plant, pod yield per plant, protein content. Inter-crossing of the genotypes from these clusters could be suggested to generate a wide spectrum of variability followed by effective selection for these characters.

A perusal of the results on character association revealed positive and significant association of kernel yield with number of filled pods per plant, total pods per plant, pod yield per plant, harvest index per cent, 100 kernel weight, shelling per cent and SCMR at 60 DAS indicating an increase in kernel yield could be realized with the improvement of these characters. Therefore, priority should be given to these traits while making selections for kernel yield improvement. A perusal of the results on inter-character associations revealed significant and positive association of days to 50 per cent flowering with protein content; number of filled pods per plant with total pods per plant, pod yield per plant, shelling per cent and harvest index per cent; total pods per plant with pod yield per plant and harvest index per cent; haulm yield per plant with pod yield per plant and SCMR at 60 DAS; pod yield per plant with harvest index 100 kernel weight, SCMR at 60 DAS and shelling per cent with harvest index, 100 kernel weight and SCMR at 60 DAS in the

present investigation indicating a scope for simultaneous improvement of these traits through selection. In contrast, significant and negative association of days to 50 per cent flowering with SCMR at 60 DAS; plant height with SCMR at 60 DAS; haulm yield per plant with shelling per cent and harvest index per cent; harvest index per cent with SCMR at 60 DAS and 100 kernel weight with SCMR at 60 DAS were observed in the present study indicating the need for balanced selection while effecting simultaneous improvement for these traits.

A perusal of the results of path coefficients for yield and yield components revealed high residual effects for both phenotypic and genotypic path coefficients, indicating that other attributes besides the characters studied are contributing to kernel yield and oil content. The results also revealed high positive direct effects of haulm yield per plant, shelling per cent, harvest index and 100 kernel weight on kernel yield per plant and shelling per cent on oil content. Hence, these traits should be considered as important selection criteria in all groundnut improvement programmes and direct selection for these traits is recommended for kernel yield improvement. However in view of negative association and high negative direct effect of plant height, harvest index and 100 kernel weight with oil content balanced selection needs to be adopted while effecting simultaneous improvement for these traits.

The genotypes *viz.,* 04 x 479-012, K 1501 and K 1643 were found to be superior among the tested entries with significant superiority for many yield attributing characters. These genotypes may be involved in the crossing programme duly estimating the general combining ability (GCA) and specific combining ability (SCA) effects. Study of genetic parameters revealed that kernel yield per plant, pod yield per plant, haulm yield per plant, protein content and number of filled pods per plant recorded high PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean indicating ample scope for improvement of these traits through selection.

The divergence studies revealed maximum inter-cluster distance between clusters IV and VIII followed by VI and VIII, III and V and clusters III and VII indicating that genotypes from these clusters are highly divergent meriting their consideration in selection of parents for hybridization.

A perusal of the results on character association revealed positive and significant association of the traits *viz.*, number of filled pods per plant, total pods per plant, pod yield per plant, harvest index per cent, 100 kernel weight, shelling per cent and SCMR at 60 DAS with kernel yield per plant. Therefore, priority should be given to these traits while making selections for kernel yield improvement. The results also revealed significant positive direct effects of haulm yield per plant, shelling per cent, harvest index and 100 kernel weight on kernel yield per plant and shelling per cent on oil content. Hence, these traits should be considered as important selection criteria in all groundnut improvement programmes. However in view of negative association and high negative direct effect of plant height, harvest index and 100 kernel weight with oil content balanced selection needs to be adopted while effecting simultaneous improvement for these traits.

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